

# Botany 2011

## Healing the Planet

The Annual Meeting of 4 Leading Scientific Societies

July 9 -13, 2011

Chase Park Plaza - St. Louis, Missouri



# Abstracts



July 9 – 13, 2011  
The Chase Park Plaza  
St. Louis, Missouri

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President - Mary Eubanks  
Duke University  
Durham, North Carolina

Program Director - Rainer Bussmann  
Missouri Botanical Garden  
St. Louis, MO 63166

Local Representative - Bruce Ponman  
Missouri Botanical Garden  
St. Louis, MO 63166  
Bruce.Ponman@mobot.org

### American Fern Society

President - Michael Windham  
Duke University  
Durham, NC 27708  
(919) 660-7293  
mdw26@duke.edu

Program Director - Kathleen M. Pryer  
Duke University  
Durham, NC 27708  
(919) 660-7380  
pryer@duke.edu

Local Representative and Field Trip Coordinator  
George A. Yatskievych  
Missouri Botanical Garden  
St. Louis, MO 63166  
(314) 577-9522  
george.yatskievych@mobot.org

### American Society of Plant Taxonomists

President - Richard G. Olmstead  
olmstead@u.washington.edu

Program Director - Patrick Herendeen  
Chicago Botanic Garden  
Glencoe, IL 60022  
(847) 835-6956  
pherendeen@chicagobotanic.org

Local Representative - Peter C. Hoch  
Missouri Botanical Garden  
St. Louis, MO 63166  
(314) 577-5175  
peter.hoch@mobot.org

### Botanical Society of America

President - Judy Skog  
George Mason University  
Manassas, VA 20110  
(703) 993-1026  
jskog@gmu.edu

Program Director - David Spooner  
University of Wisconsin  
Madison, WI 53706  
(608) 890-0309  
david.spooner@ars.usda.gov

Local Representative - Allison J. Miller  
St. Louis University  
St. Louis, MO 63103  
(314) 977-7653  
amille75@slu.edu

### Conference Director

Johanne Stogran  
125 Connemara Drive  
Granville, OH 43023  
(740) 927-8501  
johanne@botany.org

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## Plenary Address

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1 RAVEN, PETER

### Saving Plants, Saving Ourselves

The accumulation of information about plants since the time I was a university student in the 1950s has been incredible, but the rate at which we are destroying them, their genetic diversity, and their habitats is astonishing.

At an intensity of which we had no comprehension 50 years ago, we are destroying habitats, drastically and rapidly altering the global climate, and consuming all resources much more rapidly than they can be replenished. In the face of this crisis, we must make serious choices about what we can accomplish and select our goals carefully. Our future food supplies, medicines, climate stability, protection of topsoil, and the provision of clean water, as well as the rich beauty they bring into our lives every day, are worth fighting for.

Ignorance of the scientific method and false assumptions have made the United States the only country in the world where a substantial number of people reject scientific conclusions about evolution, which was well accepted and considered evident well before Charles Darwin proposed his theory about a mechanism to account for it. We are also the only nation on earth with a political constituency that rejects scientific findings about climate change and human beings' role in it for no apparent reason other than assertion and wishful thinking.

In choosing goals for ourselves, our communities, our nation, and the world, we must establish priorities and pursue them actively. There are three people now living for every one who was present when I was born, and we are adding net 200,000 people per day as our population climbs from just under 7 billion to an anticipated 9.5 billion over the course of the next 40 years. We botanists must use our knowledge and our training to educate our fellow citizens, especially children, and maintain a world filled with opportunity, diversity, and beauty.

Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63110, USA

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## Address of the BSA President-Elect

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2 WELLER, STEPHEN

### Broadening Horizons in the Botanical Society of America

The Botanical Society of America is well known for the strong organismal focus of its members, but our interests are expanding and we impact diverse areas of research. An analysis of the papers published in the *American Journal of Botany* indicates that ecology, reproductive biology, systematics, population biology, and anatomy and morphology are well represented. But the influence of BSA members goes well beyond the papers published in the *American Journal of Botany*. We impact a very broad spectrum of research ranging from genomic approaches addressing causes for the dominance of flowering plants, to factors underlying profound ecosystem changes resulting from species invasions. Symposia at our national meetings address questions in genomics, community ecology, and global change. We have diverse research interests, and we influence many disciplines in science. For the BSA to maintain its influential position, we must work hard to reach out to a wider spectrum of our country and ensure the broadest representation possible in the Botanical Society of America. Demographic trends indicate that minority groups will increase dramatically in the United States in the near future. At present, minority representation in the Botanical Society is extremely low. If we wish botanical research to remain a vital part of the scientific community of the future, we must do all we can to encourage greater participation of underrepresented groups. Without this encouragement, the work we value will be relegated to an increasingly smaller part of the workforce and we will miss the potential contributions of some of the brightest minds of the future. BSA programs such as PlantingScience engage middle school students from diverse communities, and our PLANTS program encourages undergraduate minority representation at meetings. These efforts to broaden participation in the society are critical to maintaining the strength of science in our country. We need to take steps at our home institutions as well to engage the broadest possible diversity of students in botanical education and research.

University of California Irvine, Department of Ecology and Evolutionary Biology, 321 Steinhaus Hall, Irvine, CA, 92697, USA

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*Annals of Botany Lecture*

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3 SOLTIS, PAMELA

**Angiosperm Phylogeny: The Role of Polyploidy in Diversification and Genome Evolution**

**A**ngiosperm phylogeny is characterized by a series of rapid radiations that interrupt longer periods of stasis. Attempts to identify the intrinsic phenotypic characteristic(s) or ecological attributes responsible for these shifts in diversification rate have been unsuccessful. More recently, genomic data for *Arabidopsis* and other model organisms have revealed surprising levels of ancient polyploidy within the angiosperms. Furthermore, as genomic and transcriptomic data accumulate for additional species representing previously unsampled branches of the angiosperm tree, new instances of genome duplication are evident, many of which mark significant clades. In addition to ancient polyploidy within angiosperms, genome duplications can be traced to both the most recent common ancestor of all angiosperms and of all seed plants. Is it possible that repeated genome duplications served as catalysts for repeated radiations? Given the ubiquity of ancient polyploidy throughout the history of the angiosperms, it is surprising that most angiosperm genomes behave essentially as diploids, leading to questions of which processes are involved in the diploidization of polyploid genomes. Perhaps clues to the diploidization process may be gleaned from studies of recently formed polyploids, such as *Tragopogon mirus* and *T. miscellus* (Asteraceae), both of which formed in the early part of the 20<sup>th</sup> century. The genomes of these tetraploids, as well as those of wheat, cotton, *Brassica napus*, and others, reveal dynamic interactions between the parental contributions, with shifts in gene expression, changes in karyotype, and loss of chromosomal and genic material from one parental genome or the other. The microevolutionary processes observed in *Tragopogon* and other recent polyploids may provide the mechanisms to explain the essentially diploid genomes of most angiosperms. Furthermore, genome duplication may have triggered radiations by generating novel genomic combinations and thereby novel phenotypes. Given the widespread role of polyploidy as a speciation mechanism in recent angiosperm history, it is perhaps possible that polyploidy has played a long and fundamental role in shaping angiosperm genomes and in angiosperm evolution.

University of Florida, Florida Museum of Natural History, Gainesville, FL, 32611, USA

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**Kaplan Memorial Lecture**

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4 QUATRANO, RALPH

**Mechanisms of cellular polarity: a comparative approach from mosses to seed plant**

**D**r. Ralph S. Quatrano will give the 2011 Kaplan Memorial Lecture in Comparative Development. He received his undergraduate degree from Colgate University (1962) and his Ph.D. in Biology from Yale University (1968). During his career he has held professorships at Oregon State University, where he was the founding director of the Center for Gene Research and at the University of North Carolina at Chapel Hill. Ralph arrived at Washington University in 1998 where he is immediate past Dean of Arts and Sciences and Dean of the School of Engineering and Applied Science. He is also chair of the Executive Council of the Division of Biology and Biomedical Sciences and initiated the joint research program in Plant Sciences with Monsanto. Ralph was the Editor of *The Plant Cell* (1998-2003), and served on the Board of Reviewing Editors for *Science* (1991-98). He served as President of ASPB (1982-93) and is a Fellow of the AAAS, the St. Louis Academy of Science and the ASPB. Dr. Quatrano's research interests are focused on the cellular and molecular mechanisms controlling the development of plant embryos; from the establishment of polarity in the zygote and early embryo, to the hormonal control of gene expression during embryo maturation. He was a leading investigator and corresponding author of an international consortium that sequenced, characterized and published the genome of *Physcomitrella patens* and has been a pioneer in establishing it as an experimental system. He has published over 159 research papers on plants as diverse as *Fucus* and *Arabidopsis*. Ralph will discuss his seminal contributions to our understanding of plant development, specifically, the critical roles of the cytoskeleton, cell wall and hormones in establishing and maintaining cell polarity across different plant groups.

Washington University, St. Louis, MO, 63110, USA

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## Regional Botany Special Lecture

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5 ALBRECHT, MATTHEW

### Conservation of Imperiled Midwest Plants

As a founding member of the Center for Plant Conservation network, the Missouri Botanical Garden (MBG) applies an integrated strategy to support the conservation of the Midwestern flora. To carry-out this strategy, I will discuss how MBG partners with governmental agencies, universities, and non-profit organizations across several states on research and recovery tasks for imperiled plant species. Research efforts that focus on population demography and genetics inform management strategies on how to reverse declining population trends and prioritize conservation efforts. Recovery efforts focus on maintaining genetically appropriate ex situ collections - primarily through seed-banking - and developing ecologically relevant dormancy-breaking and germination protocols. In turn, ex situ collections and protocols form the foundation of population reintroductions, an increasingly utilized conservation tool that can reduce the extinction risk of rare species in the wild. Finally, I will discuss how global climate change poses unique challenges and opportunities for species-level conservation strategies with the Midwestern flora.

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Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166, USA

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## Enhancing Scientist Diversity in Plant Biology Luncheon

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6 CLUTTER, MARY

### 2050 Challenges

The iconic year 2050 is less than 40 years from now. The world then will have changed at least as much as it has from 40 years ago. Over that time a myriad of challenges will confront us. The most important question in an age of increasing dependence on science and technology advances is who will be the practitioners? Who will produce and maintain the advances essential for progress? Among the challenges are feeding 9 billion people, demographic realities, educational reform, merging disciplines, STEM education, funding for research, as well as climate change, biodiversity, biotechnology (GM vs organic issues), globalization, and other political issues. In addressing these challenges, clearly the most important at this juncture in our country is STEM education. That will be the focus of this presentation. Some of the other challenges which impinge on STEM may come up during discussion. The 2050 challenges may be viewed by many as action items for the future. My admonition is: we cannot wait "the future is now."

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American Institute of Biological Sciences, 1900 Campus Commons Drive, Suite 200, Reston, VA, 20191, USA

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## Symposia and Colloquia

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### Charles Heiser Special Contributed Paper Session

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*Sponsored by Society for Economic Botany.*

7      **ANDERSON, GREGORY<sup>\*1</sup>,  
PICKERSGILL, BARBARA<sup>2</sup> and KEPHART,  
SUSAN<sup>3</sup>**

#### **Charles Bixler Heiser, Jr.: A Productive and Inspirational Scientist**

Charles Bixler Heiser, Jr. learned to love Indiana and plant study during early experiences on his grandparent's farm in southern Indiana. That interest became focused on plant evolution, systematics, and "economic botany" under the inspiration of Edgar Anderson and Robert Woodson at Washington University and the Missouri Botanical Garden. The intriguing sunflowers and hybrids present in the vacant lots of St. Louis later became the focus of his doctoral research at UC Berkeley where he was influenced by Lincoln Constance, Herbert Mason, Ledyard Stebbins and a cohort of outstanding student colleagues. After finishing a Ph.D. in just three years, he returned to his home state to begin what became a lifelong professorship at Indiana University. His 120+ papers and six books not only record an impressive career but their influence is reflected in numerous awards, including membership in the NAS. All constitute evidence of the importance of his work. Beyond that written record, however, are the more than 60 formal students (30 PhDs) he mentored, and a very large number of others, each inspired to study and appreciate the diversity of wild and cultivated plants by his scientific publications, interpretive writing, and speaking for wider audiences. Examples of Heiser's impact are the focus of this introduction, that is part overview, and part personal reflections.

<sup>1</sup>University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Road, Unit 43, Storrs, CT, 06269-3043, USA<sup>2</sup>University of Reading, School of Biological Sciences, Whiteknights, Reading, RG6 2AS, United Kingdom<sup>3</sup>WILLAMETTE UNIVERSITY, Department Of Biology, SALEM, OR, 97301, USA

8      **ESHBAUGH, W. HARDY**

#### **A Current View on the Taxonomy of *Capsicum* L. (Solanaceae)**

My research on the genus *Capsicum* began in 1964 soon after I arrived at Indian University and came under the influence of Charles B. Heiser, Jr. It has continued for what is now approaching 50 years. *Capsicum* was an endemic genus to the Americas in pre-Colombian times. However, once discovered it spread

to the Old World and took on an importance that in many ways exceeded its significance in the New World. Chili peppers transformed the diet of the world and continue to do so. People in the Old World, especially in Africa and Asia, do not believe that hot red peppers have a history of no more than 500 years in that part of the world. The mystique of chili peppers, *Capsicum*, and everything about them has evolved into an abundance of books, products, festivals, recipes, and restaurants. *Capsicum* is among the earliest New World domesticates. The archaeological record indicates that chili peppers have a long history in several locations in Latin America. Evidence from a genus-specific starch morphotype indicates that domesticated *C. annuum* dates back to at least 6000 B Pat several locations in the western hemisphere. Linnaeus named several species of *Capsicum* in the 18<sup>th</sup> century. In 19<sup>th</sup> century the size of genus *Capsicum* increased exponentially with the naming of more than 150 taxa. Various experimental studies in the second half of the 20<sup>th</sup> century refined our understanding of species limits with the recognition of no more than 24 species. Now, with new discoveries in the 21<sup>st</sup> century, we recognize at least 36 species with as many as five new species still to be named and described from Peru, Brazil, and Bolivia. Recent studies show that the wild species of *Capsicum* can be divided into two distinct evolutionary lines based on chromosome numbers of  $x = 12$  and 13.

Miami University, Botany, 700 East High Street, Oxford, OH, 45056, USA

9      **FILIPOWICZ, NATALIA<sup>\*1</sup>,  
SCHAEFER, HANNO<sup>2</sup> and RENNEN, SUSANNE<sup>1</sup>**

#### **How many species of *Luffa* (Cucurbitaceae) are there? Relationships in a small genus of worldwide distribution.**

Among the economic plants that interested Charles Heiser was *Luffa*, a pantropical group of annual trailing vines with a suspected 5–6 species (Heiser and Schilling 1988; Heiser et al. 1988). *Luffa aegyptiaca* (incl. *L. cylindrica*) and *L. acutangula* are widely cultivated crops in tropical Asia, and the fruit fibers of the first are used as sponge. As discussed by Heiser, species circumscriptions have been controversial, partly because of naturalized escapes from cultivation. We have studied species circumscriptions and relationships based on combined nuclear and plastid DNA sequences for 50 accessions representing the entire geographic range of loofahs. Study of morphological traits is ongoing. In agreement with Heiser's findings, *L. quinquefida* from Mexico to Nicaragua is distinct from South American *L. operculata* and *L. sepium*. The neotropical species form a clade derived from a paraphyletic Indian/African/Australian group. Sister to all other loofahs is *L. acutangula*, from India and Yemen; followed by *L. aegyptiaca*

from India, Indochina, and tropical Australia; *L. echinata* from India to Egypt; and *L. graveolens* from northern India, Nepal, Bangladesh, and Burma. The Australian material hereto attributed to the latter species represents a new species. *Luffa* thus comprises eight species, and a family-wide phylogeny suggests that *Trichosanthes*, an Asian genus of 100 species, is the sister clade of *Luffa*. The low genetic variability among accessions from vastly distant geographic regions suggests a young age of the species, but the stem age of the genus may be 35 (41-31) million years old (Schaefer et al. 2009).

<sup>1</sup>University of Munich (LMU), Department of Biology, Systematic Botany and Mycology, Menzinger Str. 67, Munich, 80638, Germany  
<sup>2</sup>Harvard University, Department of Organismic and Evolutionary Biology, 22 Divinity Avenue, Cambridge, MA, 02138, USA

## 10 MARTINE, CHRISTOPHER

### Designation of *Solanum* section *Kakadu* (Solanaceae) from Australia

*Solanum* section *Kakadu*, as proposed here, includes two "spiny solanum" (Subgenus *Leptostemonum*) species native to The Northern Territory, Australia: *S. asymmetriphyllum* and the recently-described *S. sejunctum*. Species in this section are dioecious, clonal, woody shrubs to 2 m in height; with stem armature scattered or missing; and with calyx lobes nearly enclosing the berries at maturity. Like all other known dioecious *Solanum* taxa, this breeding system is achieved in section *Kakadu* through the production of inaperturate pollen in morphologically bisexual flowers. Large-scale shifts in climate may have played a role in the geographic and phylogenetic isolation of section *Kakadu*, a clade of two species that has proven difficult to place in taxonomic treatments.

SUNY Plattsburgh, Biological Sciences, 101 Broad Street, Plattsburgh, NY, 12901, USA

## 11 MOODY, MICHAEL\*<sup>1</sup> and RIESEBERG, LOREN<sup>2</sup>

### Sorting through the chaff, nDNA gene trees for phylogenetic inference and hybrid identification of annual sunflowers (*Helianthus* sect. *Helianthus*)

The annual sunflowers (*Helianthus* Sect. *Helianthus*) present a formidable challenge for phylogenetic inference because of ancient hybrid speciation, recent introgression, and suspected issues with deep coalescence. We analyzed sequence data from 11 nDNA genes for multiple genotypes of most species of the section to (1) reconstruct the phylogeny of this group, (2) explore the utility of nDNA gene trees for detecting hybrid speciation and introgression; and (3) test a new empirical method of hybrid identification based on the phylogenetic congruence of nDNA gene trees from

tightly linked genes. We uncovered considerable topological heterogeneity among gene trees with or without three previously identified hybrid species included in the analyses, as well as a general lack of reciprocal monophyly of species. Nonetheless, partitioned Bayesian analyses provided strong support for the reciprocal monophyly of all species except *H. annuus* (0.89 PP), the most widespread and abundant annual sunflower. Previous hypotheses of relationships among taxa were generally strongly supported (1.0 PP), except among taxa typically associated with *H. annuus*, apparently due to the parphyly of the latter. While the nDNA gene tree analyses provided a useful means for detecting recent hybridization, identification of ancient hybridization was problematic for the two most ancient hybrid species, even when linkage was considered.

<sup>1</sup>University of Western Australia, Plant Biology, 35 Stirling Highway, Crawley, WA, 6009, Australia  
<sup>2</sup>University Of British Columbia, Department Of Botany, 6270 University Blvd, Vancouver, BC, V6T 1Z4, Canada

## 12 KEPHART, SUSAN\*<sup>1</sup>, PATZER, JAIME<sup>1</sup>, ARCHIBALD, JENNY<sup>2</sup> and SULTANY, MOLLY<sup>3</sup>

### Demystifying species divergence in *Camassia* (Agavaceae): Integrating phenology, pollination, and floral trait manipulation

Deciphering variability lies at the core of both classic and novel approaches that inform species delimitation, phylogenetic inference, and evolutionary divergence in natural populations. Mosaic genomes and complex morphological patterns pose challenges for classification, particularly in dynamic, yet distinct lineages influenced by hybridization and introgression. Species complexes in the North American genus, *Camassia* (Agavaceae) provide a unique opportunity to study populations in varying stages of divergence and reproductive isolation. *Camassia* is an important spring-flowering perennial in wet prairies and oak savannas. The six species and 10 subspecies include rare and common taxa that exhibit ecological differentiation and span a broad geographic range, with the highest diversity centered in Oregon. We extend prior molecular, phenological, and morphometric analyses by investigating variation in flowering time and floral trait divergence for sister and non-sister species pairs of *C. angusta*, *C. quamash*, *C. howellii*, *C. leichtlinii*, and *C. scilloides*. For two species, we further test the response of pollinators in natural populations to artificial flowers manipulated for key diagnostic traits, including floral symmetry. Previous research suggests that these species comprise distinct phylogenetic lineages, yet specific and subspecific delimitation have been problematic historically due to mosaic patterns of trait differentiation that vary geographically. Thus, we compare sympatric popu-

lations with a long history of divergence, and variable intergradation, with putatively more recent progenitor-derivative pairs. Habitat isolation is evident between several taxa and phenological divergence is strong in all species pairs, with significant differences in sympatry versus allopatry for western *C. quamash* and *C. leichtlinii*. Asymmetric post-mating barriers to hybridization in these species imply that morphological complexity is greatest in sympatric sites where crossability and ecological overlap are high. Our ultimate goal includes a comprehensive classification that will improve taxonomic keys for these ecologically and culturally important monocots. The paired analyses of *in-situ* populations framed in a phylogenetic context will also lend insight into the processes underlying the diverse origins of complex phenotypic patterns and reproductive isolation in plants.

<sup>1</sup>WILLAMETTE UNIVERSITY, Department Of Biology, SALEM, OR, 97301, USA<sup>2</sup>University Of Kansas, RL McGregor Herbarium & Bridwell Botanical Research Lab, 2045 Constant Ave, Lawrence, KS, 66047-3729, USA<sup>3</sup>Lewis & Clark College, Graduate School of Education, 0615 S.W. Palatine Hill Road , Salem, OR, 97219

**13 COATE, JEREMY<sup>1</sup>, LUCIANO, AMELIA<sup>2</sup>, SERALATHAN, VASU<sup>3</sup>, MINCHEW, KEVIN<sup>4</sup>, OWENS, THOMAS<sup>5</sup> and DOYLE, JEFF<sup>6</sup>**

**Anatomical, morphological and physiological changes correlated with recent natural allopolyploidy in *Glycine* subgenus *Glycine***

Polyploidization is a dominant force in plant evolution, and polyploids are often more successful than their diploid progenitors. Photosynthesis plays a fundamental role in plant fitness and previous studies have shown that polyploidy has pronounced effects on photosynthesis-related phenotypes. Most of these studies have focused on synthetic or recently formed autopolyploids, and little is known about the integrated effects of natural allopolyploidy, which involves hybridity and genome doubling, and often incorporating multiple genotypes through recurrent origins and lineage recombination. *Glycine dolichocarpa* is a natural allotetraploid with multiple, biparental origins. We quantified and compared anatomical, biochemical and physiological phenotypes relating to photosynthesis in *G. dolichocarpa* (designated "T2"), and its diploid progenitors, *G. tomentella* ("D3") and *G. syndetika* ("D4"), under controlled, growth chamber conditions. To assess the effects of direction of cross on these phenotypes, we included three T2 accessions having D3-like plastids (T2<sub>D3</sub>) and two T2 accessions having D4-like plastids (T2<sub>D4</sub>). In order to capture the range of variation within the diploid species, we characterized four accessions of each. Allopolyploidy was associated with changes in the anatomy, biochemistry and physiology of photosynthesis in T2.

Guard cell size, chloroplast number per palisade cell, chloroplast number per unit leaf area, palisade cells per unit leaf area, chlorophyll a, chlorophyll a+b, xanthophyll content per unit leaf area, and photosynthetic capacity per cell differed significantly in T2 compared to at least one of its diploid progenitors. Palisade cell volume, chloroplast number, chloroplast volume per unit leaf area, and photosynthetic capacity per unit leaf area differed significantly between T2<sub>D3</sub> and T2<sub>D4</sub>. Additionally, there is considerable variation within T2 that could be due to multiple origins. T2 is characterized by transgressive photosynthesis-related phenotypes (including an approximately two-fold increase in photosynthetic capacity per cell), as well as by significant intra-species variation in several photosynthesis-related phenotypes that correlate with direction of cross.

<sup>1</sup>Cornell University, Plant Biology, 412 Mann Library, Cornell University, Ithaca, NY, 14853, USA<sup>2</sup>Yale University, Department of Pharmacology, 333 Cedar Street, SHM B-208, New Haven , CT, 06520-8066<sup>3</sup>Cornell University, Department of Plant Biology, 412 Mann Library Building, SHM B-208, Ithaca, NY, 14853, United States<sup>4</sup>Bethel University, Department of Biology, 325 Cherry Avenue, McKenzie, TN, 38201, USA<sup>5</sup>Cornell University, Department of Plant Biology, 412 Mann Library Building, SHM B-208, Ithaca, NY, 14853, USA<sup>6</sup>Cornell University, 412 Mann Library Building, ITHACA, NY, 14853-4301, USA

**14 SOLTIS, DOUGLAS<sup>\*1</sup>, BUGGS, RICHARD<sup>2</sup>, CHAMALA, SRIKAR<sup>3</sup>, CHESTER, MICHAEL<sup>3</sup>, SYMONDS, V. VAUGHAN<sup>4</sup>, TATE, JENNIFER<sup>4</sup>, MAVRODIEV, EVGENY<sup>3</sup>, SCHNABLE, PATRICK<sup>5</sup>, BARBAZUK, W. BRAD<sup>3</sup> and SOLTIS, PAMELA<sup>1</sup>**

***Tragopogon* - A model for recent and recurring allopolyploidy**

Elucidating the causes and consequences of polyploidy (genome doubling) is central to understanding the origin and diversification of most eukaryotic lineages. However, much of what we know about these processes is derived from the study of crops and synthetic polyploids. *Tragopogon* provides a unique opportunity to investigate the genetic and genomic changes that occur in natural populations across a range of ages. This single genus contains diploids, natural allopolyploids (*T. mirus*, *T. miscellus*) that have formed repeatedly and are only 60-80 years old, synthetic F<sub>1</sub>s, synthetic allopolyploids, as well as older Eurasian polyploids (0.5 to several mya). To date we have focused on the consequences of polyploidy in recent natural allopolyploids. Using genomic approaches, we have shown that repeated patterns of homeolog loss exceed changes in gene expression. No changes are fixed in populations - we have caught these gene loss and expression changes in the act. We have found extensive chromosomal variation (translocations; reciprocal monosomy/trisomy; reciprocal nullisomy/tetrasomy) in natural populations.

Analyses of synthetic polyploids ( $S_1$ -  $S_3$  generations) indicate that these changes do not appear immediately but accumulate gradually post-polyploidization. We have developed extensive genomic resources including deep transcriptome sequence data, 6X draft genome sequence for a parental diploid (*T. dubius*) shared by *T. mirus* and *T. miscellus*, and are developing linkage and physical maps. We have documented the parentage of an older (0.8-2.8 mya) allotetraploid (*T. castellanus* = *T. crocifolius* X *T. lamottei*) and now propose to develop this system for comparison with the recently formed natural allopolyploids.

<sup>1</sup>University of Florida, Florida Museum of Natural History, Gainesville, FL, 32611, USA<sup>2</sup>Queen Mary University of London, Biology, Mile End Road, London, E1 4NS, UK<sup>3</sup>University of Florida, Biology, Gainesville, FL, 32611, USA<sup>4</sup>Massey University, Institute of Molecular Biosciences, Palmerston North, New Zealand<sup>5</sup>Iowa State University, Center for Plant Genomics, Ames, IA, 50011, USA

## 15 ROSS, NANCI<sup>\*1</sup> and SALICK, JAN<sup>2</sup>

### On the roof of the world: climate change, biogeography & alpine plant diversity, Hengduan Mountains, China

The highest plant diversity and richness in the eastern Himalayas is found in Alpine environments. Furthermore, locally useful plants (e.g., Tibetan medicines) are most abundant in Alpine meadows. Thus, climate change that threatens alpine plants impacts both Himalayan biological and cultural diversity. We assessed species diversity and composition across precipitation and biogeographic gradients within the Hengduan Mountains, NW Yunnan Province, China. Our data indicate that precipitation drives changes in species composition from SW to NE. Two sites, less than 10 km distant that ordinate together with precipitation, are divided by the Mekong(Lansang) river gorge. Interestingly, significant indicator species distinguishing the sites are often from shared genera suggesting a mechanism for the high beta diversity across the region.

<sup>1</sup>Drake University, Biology Department, Olin Hall Room 208, 1344 27th Street, Des Moines, IA, 50311, USA<sup>2</sup>Missouri Botanical Garden, PO Box 299, St. Louis, MO, 63166-0299, USA

## 16 THEISS, KATHRYN<sup>\*1</sup> and HOLSINGER, KENT<sup>2</sup>

### The impacts of harvest on a rare Malagasy orchid

Humans primarily harvest plants for food, shelter and medicine. However, some plants are valued solely for their beauty. We have focused on the harvest of the extremely rare Malagasy orchid, *Erasanthe henrici*, whose only known use is in horticulture. This species is restricted to isolated, highly fragmented forest patches and suffers from low fruit set. In some popula-

tions, fruit set is almost non-existent. In addition, some populations are depleted by collection of plants for resale in the horticultural trade. We built demographic models for six populations based on field observations from 2007-2010 and projected the population sizes using these models 25, 50 and 100 years into the future. We then simulated varying levels of harvest (1, 3, or 5 plants per year) in two ways: (1) choosing the plants to be harvested at random and (2) restricting the harvest to reproductive individuals. Populations declined under both harvest scenarios at any level of harvest, but the declines were most pronounced when harvest was restricted to reproductive plants. Since reproductive plants are more likely to be harvested, annual harvest of even a single plant is more than any of these populations can sustain.

<sup>1</sup>University of Connecticut, Ecology & Evolutionary Biology, 75 N. Eagleville Road, U-3043, Storrs, CT, 06269-3043, USA<sup>2</sup>University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Road, U-3043, STORRS, CT, 06269-3043, USA

## 17 PUSADEE, TONAPHA<sup>\*1</sup>, SCHAAL, BARBARA<sup>1</sup>, RERKASEM, BENJAVAN<sup>2</sup> and JAMJOD, SANSANEE<sup>2</sup>

### Population structure of *Oryza sativa* primary gene pool in Thailand

Thailand lies partly in the center of diversity and domestication of Asian rice (*Oryzasativa*). Rice's gene pool consists of wild rice (*O. rufipogon* Griff.), cultivated rice (*O. sativa* L.) and a weedy form (*O. sativa* f *spon-tanea*). All three components were studied in Thailand to understand evolutionary processes that affect the rice gene pool. Our results indicate that wild rice retains high levels of genetic variation both within and among populations and that variation is structured predominantly by life-history traits e.g., perennial and annual types. In addition, high levels of variation is detected among cultivated varieties with significant differentiation between cultivars, indicating that Thai cultivated rice has a broad genetic base with only 20% reduction of genetic diversity from its wild ancestor. The weedy rice populations reveal varying levels of genetic variation within populations, from nearly as high as wild rice to near zero, to equivalent of modern varieties of cultivated rice. The weedy rice populations are structured by their genetic similarity and differentiation into 2 groups based on their associated cultivated rice varieties, whether the varieties are a modern, high yield or traditional. The spread of invasive weedy rice in Thailand is the result of hybridization and gene flow between native wild rice and local cultivated rice in the areas of co-occurrence in the rice landscape. The predominance of traits associated with outcrossing in the weedy rice, especially an extruded stigma, enables backcrossing to crop rice. This backcrossing in combination with selection pressure due to rice field management has made weedy rice genetically similar to cultivated rice, by the well known

process of crop mimicry. The diversity analysis of the rice gene pool in Thailand has established that this is a dynamic genetic system. Gene flow is ongoing among its three main components, first between cultivated and wild rice which results in weedy rice, which in turn crosses with both cultivated and wild rice.

<sup>1</sup>Washington University, Department Of Biology, CAMPUS BOX 1137, 1 Brookings Drive, St. Louis, MO, 63130-4899, USA<sup>2</sup>Chiang Mai University, Plant Science and Natural Resources, 239 Huay Kaew Rd, Chang Puek, Muang, Chiang Mai, 50200, Thailand

**18 MILLER, ALLISON\*<sup>1</sup>, ROMERO HERNANDEZ, CAROLINA<sup>2</sup> and HUNT, KEN<sup>3</sup>**

### **Relating genetic and phenological variation in pecans (*Carya illinoensis*) growing in a common garden**

Crop genetic resources are critical for sustainable agriculture and food security. Pecan (*Carya illinoensis*), a native North American species, is prized for its oil-rich, nutritious nuts. Breeding collections housing pecan cultivars and native accessions in a common garden present a valuable opportunity to characterize genetic variation in the species, and to examine genetic and environmental influences on phenological traits. In this study, we use neutral molecular genetic data to: 1) characterize genetic variation in a living collection of pecan trees derived from geographically distinct areas; and 2) test the hypothesis that genetic distance is correlated with phenological difference among trees in the common garden. This work was based on trees housed at the University of Missouri Horticulture and Agroforestry Research Center, which maintains a living collection of 160 pecans (two clones each of 80 named accessions). The accessions include 25 cultivars that resulted from human selection (13 resulting from controlled crosses, 12 representing improved seedlings), and 55 accessions derived from native trees. Eight microsatellite loci were used to estimate genetic variation in the HARC pecan collection. A second, independent dataset was produced using amplified fragment length polymorphism (aflp) data generated with five selective primer pairs. Phenological data including the timing of bud break, leaf flush, and nut maturity were collected over seven years. Mantel tests were used to examine correlations between genetic distance and phenological difference in the common garden. Molecular genetic data demonstrate comparable levels of genetic variation in artificially selected trees and native trees, and are consistent with predictions of multiple geographic origins of artificially selected pecan trees. Preliminary analyses indicate that associations between genetic distance and phenological difference are trait-specific. These data are consistent with previous work conducted in pecan, which found that some phenological traits are influenced primarily

by local environmental conditions, while others appear to be under genetic control.

<sup>1</sup>Saint Louis University, Department Of Biology, 3507 Laclede Avenue, St. Louis, MO, 63103, USA<sup>2</sup>PhD Student-Saint Louis University, Biology, 2118A Cleveland Pl, Saint Louis, MO, 63110, USA<sup>3</sup>University of Missouri, Center for Agroforestry, Horticulture and Agroforestry Research Center, 203 Anheuser-Busch Natural Resources Building, Columbia, MO, 65211, USA

**19 EMSHWILLER, EVE\*<sup>1</sup>, EPPERSON, BRYAN<sup>2</sup>, THEIM, TERRA<sup>3</sup>, TAY, DAVID<sup>4</sup> and MEDINA, TULIO<sup>5</sup>**

### **Geographic Distribution of Genetic Diversity of Clonally Propagated Crops: *Oxalis tuberosa* as an example**

In both *ex-situ* and *in-situ* conservation frameworks, vegetatively-propagated (clonal) crops differ from seed-propagated crops in their conservation needs. Understanding of how crop diversity is distributed geographically is critical for conservation of that diversity, and it can be improved by incorporating GIS techniques, spatial statistics and new methods developed in landscape genetics. We studied the Andean tuber crop "oca," *Oxalis tuberosa*, as a model for the evolution of clonally-propagated crops under human influence, specifically how the exchange of planting material among farmers determines the distribution of clonal genotypes in traditional Andean agriculture. We conducted spatial statistical analyses of oca to study how human-mediated dispersal affects the genetic structure of clonal crop populations, and what factors influence the amount of exchange among areas. Cultivated oca was sampled from carefully-distributed localities throughout the Peruvian Andes, and samples were subsequently cultivated in a highland experiment station of INIA (Instituto Nacional de Innovación Agraria) for morphological and molecular analyses. Spatial statistical analyses of AFLP data of 954 oca individuals from 38 localities were done for both individual AFLP alleles and clonal genotypes, the latter determined by both AFLP and morphological data. Importantly, our results found that many oca clonal genotypes have very restricted geographic distributions; most were found in only four or fewer communities. Only a few clonal genotypes were found in widely scattered, discontinuous areas, whereas most were restricted to a particular area in Peru. Our initial spatial autocorrelation analyses (Moran's I and join-count) yielded many very strong but unusual patterns across both spatial scales and genotypes. Wombling analyses of clones and of AFLP alleles also show strong patterns associated with major topographic barriers and linguistic boundaries. These findings have important conservation implications, not only because the clones are so narrowly distributed, but also because they indicate that

other factors besides geographic distance have shaped the distribution of genotypes.

<sup>1</sup>University Of Wisconsin-Madison, Botany Dept, 321 Birge Hall, 430 Lincoln Drive, Madison, WI, 53706-1313, USA<sup>2</sup>Michigan State University, 126 NATURAL RESOURCE BUILDING, East Lansing, MI, 48824-1222, USA<sup>3</sup>University of Wisconsin - Madison, Botany Department, 430 Lincoln Dr, Madison, WI, 53706, USA<sup>4</sup>Centro Internacional de La Papa, Av. La Molina 1895, La Molina., Apartado 1558, Lima 12, Lima, Peru<sup>5</sup>Instituto Nacional de Innovación Agraria, Recursos Genéticos, Av. La Molina # 1981, La Molina., Apartado Postal 2791., Lima, Peru

**20 SPOONER, DAVID\*<sup>1</sup>, GHISLAIN, MARC<sup>2</sup>, DEL ROSARIO HERRERA, MARIA<sup>2</sup>, MONTENEGRO, JUAN DANIEL<sup>2</sup>, CLAUSEN, ANDREA<sup>3</sup> and JANSKY, SHELLEY<sup>1</sup>**

### **A reassessment of *Solanum maglia* in the origin of Chilean landraces of cultivated potato (*Solanum tuberosum* Chilotanum Group)**

**L**andraces potato cultivars of *Solanum tuberosum* occur in two broad geographic regions; the high Andes from western Venezuela south to northern Argentina (*S. tuberosum* Andigenum Group), and lowland south central Chile (*S. tuberosum* Chilotanum Group). Chilotanum is adapted to long days, has a 241 bp plastid DNA deletion (shared with some accessions of the wild potato species *S. berthaultii*, but lacking in the wild potato species *S. maglia*) and differs morphologically by minor characters that are not always Group-specific. The modern "Irish" potato clearly originated from Chilotanum germplasm. Our research investigates the origin of Chilotanum, with one hypothesis proposing an origin from Andigenum, perhaps after hybridization with *S. berthaultii*; and a competing hypothesis suggesting an origin from the wild potato species *S. maglia*, distributed in southern Chile and adjacent western Argentina. Molecular data support both the Andean and Chilean potatoes as members of the same clade, distinct from *S. berthaultii*. The *S. maglia* hypothesis was based on morphological analyses of starch grains of extant and extinct (13,000 years before present) *S. maglia*, and on extant distributional data of *S. maglia* and Chilotanum. Our new starch grain analyses of extinct and extant *S. maglia* using a much wider collection of accessions of both cultivar groups of *S. tuberosum* show extensive overlap. In addition, we could find no evidence of sympatric distributions of extant *S. maglia* and Chilotanum. Therefore, starch grains and distributional data do not support this hypothesis. However, microsatellite data group all accessions of *S. maglia* (Argentinean and Chilean) exclusively with Chilotanum. These results could be interpreted in various ways, but all explanations have problems. One explanation is that *S. maglia* is either a progenitor or product of Chilotanum, but the plastid

deletion of Chilotanum cannot be easily explained. Another explanation is that Chilotanum was formed by hybridization between *S. berthaultii* and *S. maglia* but this conflicts with prior cladistic analyses.

<sup>1</sup>USDA Agricultural Research Service, Horticulture, Univ. Wisconsin, 1575 Linden Drive, Madison, WI, 53706, USA<sup>2</sup>International Potato Center (CIP), P.O. Box 1558, Lima 12, Peru<sup>3</sup>Instituto Nacional de Tecnología Agropecuaria (INTA)

**21 KIETLINSKI, KIEL\* and PRATT, DONALD**

### **Relationships between the weedy *Amaranthus hybridus* and the grain amaranths**

**S**NP and microsatellite markers were utilized to investigate the relationship between the grain amaranths and putative weedy progenitor species (*A. hybridus* and *A. quitensis*). A total of 56 amaranth populations from five species were selected from the USDAs GRIN database based upon geographic distributions, across North and South America, and complete passport data. The 258 tested individuals yielded five complete microsatellite loci (49 alleles) and 73 complete SNP loci (146 alleles). Data analysis indicates that the populations segregate into three distinct groupings, based on geography (U.S., Mexico/Central America, and South America) rather than traditional taxonomic species (*A. caudatus*, *A. cruentus*, *A. hypochondriacus*, *A. hybridus* and *A. quitensis*). We detected multiple possible long distance dispersal events.

Stephen F. Austin State University, Box 13003 SEA Station, Nacogdoches, TX, 75962, USA

**22 CLARKE, ANDREW C.\*<sup>1</sup>, HOLLAND, BARBARA R.<sup>2</sup>, MCLENACHAN, PATRICIA A.<sup>3</sup>, NAKATANI, MAKOTO<sup>4</sup>, MATTHEWS, PETER J.<sup>5</sup>, GREEN, ROGER C.<sup>6</sup> and PENNY, DAVID<sup>3</sup>**

### **Evidence for prehistoric human contact between Polynesia and South America: DNA analysis of the sweet potato (*Ipomoea batatas*)**

**T**he origins of the sweet potato (*Ipomoea batatas*), a crop species fundamental to many agricultural systems in pre-European Polynesia, has been of long-standing scientific interest. The sweet potato, probably along with the bottle gourd, is thought to have arrived in the Pacific from South America. Various lines of botanical, archaeological, linguistic and genetic evidence are consistent with this transfer being effected by Polynesian voyagers who collected the sweet potato from South America between AD 1000 and 1200. The strongest evidence for contact is the Polynesian word

*kumara*, which appears to be derived from the Ecuadorian *cumar*. Despite growing acceptance of this human-mediated transfer, there remain a number of unresolved questions about the sweet potato in Oceania, including: 1) the point on the South American coast where Polynesians made landfall, 2) the number of Polynesian lineages introduced into the Pacific, 3) the dispersal routes of sweet potato within Polynesia, and 4) the influence of Spanish (camote) and Portuguese (batata) introductions of sweet potato in the western Pacific. To address these questions we have used the amplified fragment length polymorphism (AFLP) fingerprinting technique to genotype 270 unique accessions of sweet potato from Asia, Island Melanesia, Polynesia and the Americas. AFLP data have been used to construct phylogenetic trees, and to improve phylogenetic resolution we have developed a new method to optimise AFLP scoring parameters. A putative *kumara* lineage, representing a prehistoric, Polynesian-mediated introduction from South America, has been identified. Sweet potato accessions from Asia to Western Polynesia were found to be genetically diverse, and the relationships between them are complex. The phylogenetic positions of the New Zealand Maori varieties raises questions about their presumed close relationships with other lineages in Eastern Polynesia. Together, these findings suggest a much more complex picture of sweet potato dispersal in Oceania than is currently recognised.

<sup>1</sup>University of Otago, Department of Anatomy and Structural Biology, PO Box 913, Dunedin, 9054, New Zealand<sup>2</sup>University of Tasmania, School of Mathematics and Physics, Private Bag 37, Hobart, TAS, 7001, Australia<sup>3</sup>Massey University, Institute of Molecular BioSciences, Private Bag 11222, Palmerston North, 4442, New Zealand<sup>4</sup>National Institute of Crop Science, Department of Field Crop Science, 2-1-18 Kannondai, Tsukuba, Ibaraki, 305-8518, Japan<sup>5</sup>National Museum of Ethnology, Department of Social Research, Senri Expo Park, Suita City, Osaka, 565-8511, Japan<sup>6</sup>University of Auckland, Department of Anthropology, Private Bag 92019, Victoria Street West, Auckland, 1142, New Zealand

**23 BLACKMAN, BENJAMIN\*<sup>1</sup>,  
KANE, NOLAN<sup>2</sup>, LUTON, HAROLD<sup>3</sup>,  
RASMUSSEN, DAVID<sup>1</sup>, BYE, ROBERT<sup>4</sup>,  
LENTZ, DAVID<sup>5</sup> and RIESEBERG, LOREN<sup>6</sup>**

### Sunflower domestication alleles support single domestication center in eastern North America

Phylogenetic analyses of genes with demonstrated involvement in evolutionary transitions can be an important means of resolving conflicting hypotheses about evolutionary history or process. In sunflower, two genes have previously been shown to be under selection during its early domestication. We have identified a third candidate early domestication gene and conducted haplotype analyses of all three genes to address

a recent, controversial hypothesis about the origin of cultivated sunflower. While the scientific consensus had long been that sunflower was domesticated once in eastern North America, the discovery of pre-Columbian sunflower remains at archaeological sites in Mexico led to the proposal of a second domestication center in southern Mexico. Notably, the identification of these remains as sunflower was initially supported but later contested by Dr. Charles Heiser, and he frequently challenged this and other evidence cited as support for the multiple domestication center hypothesis in his publications over the last decade. Previous molecular studies with neutral markers were consistent with Heiser's favored single origin view. However, only two Mexican indigenous cultivars were included in these studies, and their provenance and genetic purity has been questioned. Therefore, we sequenced regions of the three candidate domestication genes containing SNPs diagnostic for domestication from large, newly collected samples of Mexican sunflower landraces and Mexican wild populations from a broad geographic range. Our evidence from multiple loci supports a single domestication event for extant cultivated sunflower in eastern North America.

<sup>1</sup>Duke University, Biology, Durham, NC, 27708, USA<sup>2</sup>University of British Columbia, Botany, Vancouver, BC, V6R 2A5, Canada<sup>3</sup>Indiana University, Biology, Bloomington, IN, 47405, USA<sup>4</sup>Universidad Nacional Autónoma de México, Jardín Botánico Exterior, Instituto de Biología, DF 04510, Mexico<sup>5</sup>University Of Cincinnati, Biological Sciences, PO Box 210006, Cincinnati, OH, 45221, USA<sup>6</sup>University Of British Columbia, Department Of Botany, 6270 University Blvd, Vancouver, BC, V6T 1Z4, Canada

### 24 EUBANKS, MARY

#### New Light on the Origin of Maize

How the ear of maize with hundreds of naked kernels borne in pairs on a solid rachis covered by husks derived from the shattering teosinte spike of 7-9 grains encased in hard seed coats has perplexed botanists for many years. There are currently two prominent hypotheses to explain the origin of maize. One claims that teosinte (*Zea mays* spp. *parviglumis*) from the Rio Balsas region of Guerrero, Mexico is the progenitor of maize. The other one claims that maize derived from human selection and cultivation of natural recombinants between diploid perennial teosinte (*Zea diploperennis*) and *Tripsacum*. This paper will review the two hypotheses in light of new evidence from the sequencing of the maize genome and from recent archaeological investigations in the Rio Balsas.

University of Texas Brackenridge Field Laboratory, 2709 Lake Austin Blvd., Austin, Texas, 78703, USA

25 WAGNER, GAIL E.

## Sumpweed (*Asteraceae*, *Iva annua*) through Space and Time

Recovery of charred and desiccated sumpweed kernels and cypselae from over 350 archaeological sites allow me to re-examine the use and domestication of this North American plant. Sumpweed (*Iva annua*) was associated with humans for over 7,000 years in eastern North America. It was grown as a domesticated crop, *Iva annua* var. *macrocarpa*, for at least 4,500 years, a period of time perhaps longer than for any other native domesticated plant other than sunflower. Its use by Middle Archaic times (cal. 5970-4945 B.C.) led to an increase in cypselae size and possibly Late Archaic domestication by cal. 3640-2880 B.C.. By the terminal Late Archaic or approximately 1000 B.C. its use was widespread from western North Dakota and central Oklahoma to eastern Kentucky and south-central New York, and from northern Louisiana to southeastern Iowa. Sumpweed reached its peak dietary popularity during the Late Woodland (A.D. 300-1200) and early-middle Mississippian/Middle Ceramic periods (A.D. 700-1400). At times its use extended well beyond its present range of distribution, westward and northward into the Plains, and northeastward into Michigan and southern Ontario. Domesticated sumpweed lingered in several areas -- the Plains, north-central North Carolina, Alabama, and Louisiana -- up into protohistoric and Contact times, but in most areas cropping of sumpweed was discontinued by A.D. 1400.

University of South Carolina, Anthropology, 1512 Pendleton St., Columbia, SC, 29208, USA

26 DUONG, VI and TAYLOR, DAVID\*

## Our Daily Soup: Variability in Vietnamese Plant Utilization in Canh

A fundamental measure of what domesticated/ cultivated plants are important to a people comes via analysis of the elemental foods in the daily diet. The standard daily soup "canh" from Vietnam is such a food, employing many plants. Canh is virtually universally eaten, and varies by region. We have selected canh in order to make comparisons among the plant products used "natively" in Vietnam versus those by expatriates in the US. This first step in the study provides a base line via study of plants in canh from the city of Truc Vunh. Although interviewees all live and work in the same city and have similar educational backgrounds and employment, generational differences and region of family origin appear to be responsible for variation in the plants employed in canh. Understanding the degree of ingredient variability and the factors affecting this variation in southern Vietnam is important when determining how food plant utilization has been maintained (or not) within the substantial South Vietnamese community in

Portland, Oregon. The results of this study will be compared with others evaluating the commitment to fundamental foods among different immigrant populations (e.g., Puerto Rican foods in Puerto Rico versus those in markets in Hartford, CT).

University of Portland, Department of Biology, Swindells Hall 108, MSC 163, 5000 N. Willamette Blvd., Portland, OR, 97203, USA

27 RAGONE, DIANE\*<sup>1</sup>, JONES, ANDREW MAXWELL<sup>2</sup> and MURCH, SUSAN<sup>3</sup>

## Nutritional Diversity in Traditional Cultivars of Breadfruit (*Artocarpus*, Moraceae)

Breadfruit (*Artocarpus*, Moraceae), a high-yielding tropical staple food crop, has been identified under the International Treaty on Plant Genetic Resources for Food and Agriculture for its potential to impact food security. The Breadfruit Institute at the National Tropical Botanical Garden houses the largest breadfruit collection in the world including 300 accessions of breadfruit originating from 34 Pacific islands, the Seychelles, the Philippines and Indonesia. The collection includes *Artocarpus saltilis*, hybrids of *A. altalis* A—*A. mariannensis* TrAcuL, breadfruit's putative ancestral species breadnut (*Artocarpus camansi* Blanco), and dug-dug (*Artocarpus mariannensis* TrAcuL). Cultivars were developed through millennia of traditional breeding for diverse agricultural and nutritional characteristics. The objective of the current research was to compare the nutritional diversity of 94 accessions of breadfruit along with two related species, *Artocarpus camansi* and *Artocarpus mariannensis*, in fresh fruit and flour with the overall goal of selecting highly nutritious cultivars suitable for international distribution for food security. Overall, these data have identified individual cultivars that would provide 20%-25% of the recommended daily adult requirement for protein, approximately 23.5% calcium, 97.4% copper, 19.2% iron, 48.1% potassium, 115.8% magnesium, 33.6% manganese, 0.6% sodium, 53.5% phosphorous, and 21.0% zinc of the recommended daily intake of a female between 19-30 years old, and enough pro-vitamin A carotenoids to fulfill over 60% of the minimum daily vitamin A requirement of adults if eaten as the primary staple food. These data, along with agricultural field data, provide the foundation for introduction of breadfruit as a highly sustainable and nutritious crop for food security throughout the wet tropics.

<sup>1</sup>National Tropical Botanical Garden, 3530 Ppapalina Road, Kalaheo, HI, 96741, USA <sup>2</sup>University of British Columbia, Biology, 3333 University Way, Kelowna, BC, V1V 1V7, Canada <sup>3</sup>University of British Columbia, Chemistry, 3333 University Way, Kelowna, BC, V1V 1V7, Canada

## Onagraceae as a model experimental system

*Sponsored by Systematics Section / ASPT and American Society of Plant Taxonomists.*

28 WAGNER, WARREN<sup>\*1</sup> and HOCH, PETER<sup>2</sup>

### A new classification in Onagraceae

The plant family Onagraceae has emerged as an outstanding model system for evolutionary studies, due in large part to the efforts of Peter Raven and associates. This symposium will celebrate that legacy, summarize at least some of what we have learned, and demonstrate promising new evolutionary approaches for the future. The family has had especially intensive analyses of evolution of breeding and pollination systems, and permanent translocation heterozygosity, which have occupied numerous workers for over a century of genetic and cytogenetic analyses. Recent broad molecular phylogenetic analyses of Onagraceae support the need for changes in the family classification. We propose a revised classification of 22 genera, subdivided into two subfamilies, subfam. Ludwigioideae (only *Ludwigia*) and subfam. Onagroideae (the other genera), and the latter into six tribes, two with only one genus each, three with two genera each, and one (tribe Onagreae) with 13 genera. The most dramatic changes mainly involve the tribe Onagreae, from which we have segregated *Gongylocarpus* as its own tribe, sister to the tribes Epilobieae and Onagreae, and within which we propose changes in the delimitation of *Camissonia* and *Oenothera*. *Camissonia* as currently defined is broadly paraphyletic; our new classification recognizes nine generic lineages (*Camissonia*, *Camissoniopsis*, *Chylismia*, *Chylismiella*, *Eremothera*, *Eulobus*, *Neoholmgrenia*, *Taraxia*, and *Tetrapteron*) that in part form a grade at the base of *Oenothera*. Each of these lineages is well-supported by morphological and molecular data. In contrast, both molecular and morphological data suggest the need to broaden the delimitation of *Oenothera* to include *Calylophus*, *Gaura*, and *Stenosiphon*. This redefined *Oenothera*, strongly supported by molecular data, is marked by at least two morphological synapomorphies: presence of an indusium on the style, and a lobed or peltate stigma. Although the family has its center of diversity in the New World, especially western North America, four of the genera (*Chamerion*, *Circaea*, *Epilobium*, and *Ludwigia*) have colonized and diversified in the Old World, especially in Europe, Asia, Africa, and Australasia.

<sup>1</sup>Smithsonian Institution, Botany, MRC-166 National Museum Of Natural History, PO Box 37012, WASHINGTON, DC, 20013-7012, USA <sup>2</sup>Missouri Botanical Garden, PO. Box 299, St. Louis, MO, 63166-0299, USA

29 SYTSMA, KENNETH<sup>\*1</sup>, HAHN, WILLIAM<sup>2</sup>, WILLIAMS, CODY<sup>3</sup> and KAROL, KENNETH<sup>4</sup>

### *Clarkia*: a Californian chronicle of clades, clocks, chromosomes, and characters

The largely Californian genus *Clarkia* (Onagraceae), although not the focus of Peter Raven's first scientific paper as a teenager, played a pivotal role in his early important scientific discoveries of plant speciation and chromosomal evolution. *Clarkia* has since become a model genus for studying evolutionary phenomena including determinants of species' range sizes, trait plasticity, fitness and adaptation, pollination biology, breeding systems, floral development, population genetics, aneuploidy and polyploidy, rapid speciation, and gene duplication and gene silencing. Despite its scientific importance, a molecular phylogenetic framework for the entire genus is lacking and thus the ability to fully appreciate these important evolutionary events has been hindered. We present here a nuclear and cpDNA based set of relationships for 39 of the 42 species of *Clarkia* representing all recognized sections and subsections in the genus. A small clade of three species (sects. *Eucharidium* and *Clarkia*) represents the sister to all other members of *Clarkia*. Although these trees are largely similar to the latest phylogenetic tree of *Clarkia* based on duplicated genes of nuclear *pgi* (but with more limited taxon sampling), there exists some strong discordance of species relationships between these results compared to those of *pgi*. Under Bayesian frameworks, geographical diversification in space and time, chromosome number and genome size evolution, and floral character state transitions were analyzed. BEAST analysis of a more inclusive clade of Onagraceae, permitting use of fossil calibrations, places the crown radiation of *Clarkia* around 10mya in the late Miocene. Rates of diversification within the genus are considerably greater within the last 2-3my. Diploid  $n=8,9$  sections and their polyploid derivatives form a monophyletic group while the  $n=7$  sections and their derivatives form a paraphyletic grade. The best supported hypothesis of genome evolution is one with two independent increases in size relative to the plesiomorphic condition.

<sup>1</sup>University of Wisconsin-Madison, Department of Botany, 430 Lincoln Dr., Madison, WI, 53706, USA <sup>2</sup>George Washington University, 37TH & O STREETS, WASHINGTON, DC, 20057, USA <sup>3</sup>The New York Botanical Garden, 200 Street & Southern Boulevard, Bronx, NY, 10458, USA

### Evening perfumes: insights from scents and non-scents in the Onagraceae

The scientific and common names of the Evening Primroses (*Oenothera*) call attention to the fragrant, night blooming habit of these remarkable plants. Early studies by Gregory and Stockhouse documented the effectiveness of large hawkmoths as pollinators of the outcrossing species of *Oenothera*, and circumstantial evidence suggested that odors play important roles in guiding such moths to flowers. In this talk, I summarize a decade of collaborative studies aimed at understanding (1) how floral scent guides hawkmoths to *Oenothera* and similar night-blooming flowers, (2) how scent varies among related taxa that differ in breeding system or pollinator spectrum, and (3) how phylogenetic history shapes the chemical composition of such floral scents, within and among lineages of *Oenothera* and other Onagraceae. Scent elicits flower-searching behavior by hawkmoths from a distance and, together with visual cues, guides floral approach and proboscis extension. Most outcrossing *Oenothera* species emit blends of nitrogenous volatile compounds (aldoximes that are precursors to mustard oils) with a sharp, rubbery scent, as well as sweet terpenoid alcohols (geraniol, linalool) and aromatic esters (methyl benzoate) common to hawkmoth-pollinated flowers worldwide, whereas autogamous or day-blooming species in the same lineages (e.g. sect. *Calylophus*) tend to lack these odors. Finally, some scent compounds were found to be restricted to specific clades (e.g. methylnicotinate in sect. *Lavauxia*, 1,8-cineole in sects. *Anogra* + *Kleinia*) irrespective of flower size, pollinator spectrum or breeding system. Similar findings in comparable plant lineages (e.g. *Mirabilis*, *Nicotiana*) suggest that such compounds may serve different roles in floral defense or may simply indicate selectively neutral synapomorphies.

Cornell University, Neurobiology and Behavior, W355 Mudd Hall, 215 Tower Road, Ithaca, NY, 14853, USA

### 31 KRAKOS, KYRA

#### The role of specialization in the reproductive traits of *Oenothera*

Reproductive traits such as pollination and breeding system have been important in angiosperm diversification. Pollination and breeding systems are evolutionarily labile; they easily shift between different states. It is unclear if these shifts are correlated with periods of lineage accumulation. To determine if these shifts result in increased lineage accumulation rates in angiosperms we asked: Do shifts in plant reproductive traits towards specialization drive species diversification in *Oenothera*? Potentially, a shift in a reproductive trait towards specialization is a first step in reproductive isolation and

subsequent speciation of a plant species; however previous studies, which looked only at shifts in pollination system, have conflicting results. These different reproductive traits may shift in a concerted fashion, therefore a more thorough approach that would simultaneously address shifts in pollination and breeding system is needed. In addition, previous phylogenetic studies have not incorporated rigorous ecological data that accurately quantifies pollination system. Therefore, in this study, using 54 species of *Oenothera*, we: 1. Defined pollination systems and floral reward traits to reflect reproductive specialization in *Oenothera*, 2. Developed a phylogenetic context to identify the placement and directionality of the shifts in breeding system, pollination system, and floral reward traits and 3. We determined if *Oenothera* clades with more reproductive trait shifts have higher rates of lineage accumulation than clades with fewer reproductive trait shifts. Our results resolve phylogenetic placement of several *Oenothera* species, reveal the patterns of specialization in the pollination systems, and clarify the role of reproductive trait shifts in the diversification of this important genus.

Washington University, Biology, One Brookings Dr Box 1137, St Louis, MO, 63130, USA

### 32 GREINER, STEPHAN\*<sup>1</sup>, RAUWOLF, UWE<sup>2</sup>, GOLCZYK, HIERONIM<sup>3</sup>, MEURER, JOERG<sup>4</sup> and HERRMANN, REINHOLD G.<sup>2</sup>

#### *Oenothera* - Genomics tools in a model for plant evolution

The genus *Oenothera* has an outstanding scientific history. More than hundred years of genetic research have made *Oenothera* the presumably best studied plant genus of its size. A good deal of information about taxonomy, morphology, cytogenetics, and classical genetics, as well as a rich source of experimental strains is available. *Oenothera* genetics displays a unique combination of non-Mendelian genetic features, like permanent translocation heterozygosity and biparental transmission of plastids. It allows the exchange of plastids between species, which often results in plastome-genome incompatibility (PGI) - a hybridization barrier according to the Dobzhansky-Muller model. In turn, PGI provides molecular access to speciation forces acting on photosynthesis. Furthermore, particular aspects of epigenetics, genome evolution, and population biology can be addressed using *Oenothera* as model system. So far studies in *Oenothera* have been mainly limited to classical genetics and cytology, while molecular approaches have been largely missing. To overcome this limitation, we have established a broad spectrum of biochemical, molecular genetic and cytogenetic methods as well as tissue culture and transformation approaches for the genus. We constructed an EST library, initiated a comparable sequencing of the mitochondria genome, sequenced the five basic plastome types, and provide first candidate loci causing PGI. Moreover, the first

genetic map of bivalent forming *Oenothera* species has been generated assigning more than 1,700 dominant and co-dominant molecular markers to seven coupling groups. Remarkably, homologous recombination was almost completely suppressed in F2 segregants and, if it occurred at all, was restricted to the telomeric regions of the chromosomes. Unusual meiotic behaviour of chromosomes may be responsible for the massive repression of homologous recombination. Our data question the long-standing assumption that HR is primarily repressed due to reciprocal translocation of chromosome arms in ring-forming *Oenothera* species. Our results show that *Oenothera* provides an ideal model for examining hypotheses regarding the evolutionary advantages of sex, as well as of speciation.

<sup>1</sup>Max Planck Institute of Molecular Plant Physiology, Department 3, Am Mühlenberg 1, Potsdam - Gollm, 14476, Germany<sup>2</sup>Botanisches Institut der LMU Muenchen, Department Biologie I, Menzinger Strasse 67, Munich, 80638, Germany<sup>3</sup>John Paul II Catholic University of Lublin - Institute of Biotechnology, Department of Molecular Biology, Al. Krasiwicka 102, Lublin, 20-718, Poland<sup>4</sup>LMU Muenchen, Department I, Chair of Botany, Grosshaderner Str. 2-4, Munich, 82152, Germany

### 33 JOHNSON, MARC

#### From micro- to macroevolution: the contribution of Onagraceae to a modern synthesis of evolutionary ecology

Species in the genus *Oenothera* (Onagraceae), or evening primroses, were among the earliest models for the study of genetics, evolution biology and systematics. Here I describe how the resources provided by a century of research on this system have allowed us to address modern questions in evolutionary ecology. At the microevolutionary scale, we are examining whether there is a dynamic feedback between the ecology and evolution of plant-herbivore interactions. Our field experiments show that the native plant, common evening primrose (*Oenothera biennis*), contains heritable genetic variation for most traits, and that herbivores impose natural selection on many of these traits. Using theory and an experimental evolution approach in the field, we find that natural selection on life-history traits causes rapid genetic and phenotypic evolution within plant populations over just three generations. In turn, this evolution feeds back to influence the abundance and diversity of herbivore populations that specialize on *O. biennis*. We have also scaled up to the macroevolutionary scale to understand how repeated losses of meiotic recombination and segregation (i.e. functional asexuality) across the Onagraceae clade have influenced the evolution and ecology of evening primroses and their interactions with mutualists (pollinators) and parasites (herbivores and pathogens). We find that there have been numerous transitions between sexual and functionally asexual reproduction, and the repeated loss of recombination and segregation is associated within creased speciation

rates, and surprisingly, recombination and segregation can be regained once lost. Transitions to functional asexuality are also associated with numerous ecological and evolutionary consequences, compared to sexual lineages. For example, functionally asexual lineages occur at higher latitudes, invest less resources in flowers to attract pollinators, exhibit decreased resistance to generalist herbivores and exhibit slower rates of adaptive molecular evolution in genes critical in defenses against pathogens. These results illustrate how *Oenothera* can serve as a model to answering biological problems at the nexus of ecology and evolution.

University of Toronto, Mississauga, Biology, Mississauga ON, ON, L5L 1C6, CANADA

### 34 RAVEN, PETER

#### My Life with the Evening Primroses

My studies of Onagraceae began in 1956 under the influence of Harlan Lewis, and they eventually led me all over the world and through all the subdisciplines of botany, joyous excursions that have introduced me to many wonderful colleagues and taught me much about plant evolution. The family, as part of the order Myrtales, probably originated in West Gondwanaland, or in the part of that continental mass that became South America, and it has spread over nearly all habitats suitable for plants subsequently. Outbursts of speciation occurred in Andean South America (*Fuchsia*), New Zealand (*Epilobium*), and especially in the western United States (tribe Onagreae). Anatomy, embryology, vegetative and floral morphology, palynology, cytology, allozymes, nucleic acids, reproductive biology, and many other lines of evidence have helped us clarify relationships within the family over the past 55 years. I have had a remarkable and fulfilling journey that has filled my life with joy, interest, and friends throughout the world.

Missouri Botanical Garden, 2345 TOWER GROVE, St. Louis, MO, 63110, USA

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## History of Botany: The Missouri Connection

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*Sponsored by Historical Section.*

### 35 GRANT, MARISSA\*<sup>1</sup> and KASS, LEE B<sup>2</sup>

#### History of Botany: The Missouri Connection

The Historical Section of the Botanical Society of America wishes to continue its sponsorship of Symposia and/or Special Lectures to highlight the importance of Botany in the Americas. In 2007, the BSA Historical Section sponsored a Symposium on "A Historical Perspective on Chicago Area Botany" and in 2010 the Historical Section along with the Economic Botany and Developmental Sections sponsored "History of Botany in the Rhode Island Area." This year, along with the Developmental and Structural, Economic, Paleobotanical, Southeastern and Systematics Sections, our symposium will highlight botanists who in some way have a Missouri connection and reveal how each has contributed to the development of the field of botany. This symposium will be in conjunction with the annual meeting of Botany 2011, in St. Louis, MO. Our half day Tuesday morning symposium will feature researchers, historians and students of Botanical Science: Nuala Caomhanach, Michael Long, Deborah Q. Lewis, Lynn G. Clark, Kim Kleinman, Dennis and Jan Stevenson, Edward Coe and Lee B. Kass. Speakers will look at the growing appreciation of past generations of botanists including Thomas Nuttall, George Engelmann, Albert Hitchcock, Edgar Anderson, William J. Robbins, Lewis J. Stadler and Barbara McClintock. We anticipate and encourage discussion and socializing during the break and the question/answer period following the presentations. Following the symposium there will be an afternoon field trip to Missouri Botanical Garden where a behind the scenes tour will be given of book and herbarium collections. Participants will view books and specimens belonging to Missouri botanists featured in the morning symposium. Space is limited; interested participants are encouraged to preregister.

<sup>1</sup>Lake Land College, Mattoon, IL, 61938, USA<sup>2</sup>Cornell University, Plant Biology, 412 Mann Library, Ithaca, NY, 14853, USA

### 36 CAOMHANACH, NUALA

#### Thomas Nuttall and 19th Century Botany: The St. Louis Connection

Thomas Nuttall's brilliance as a naturalist and as one of the most adventurous explorer's of the nineteenth century earned him the title of Father of Western Botany. His passion for the natural world serendipitously led this native Englishman to master the known American flora under the tutelage of Benjamin Barton in Philadelphia. In 1809 Barton sent Nuttall westward

to collect botanical specimens, making Nuttall one of the first professionally trained naturalists to explore the western frontier of the United States. Upon arrival in St. Louis, Nuttall would spend six months exploring the environs of the city discovering many species of plants new to science and rousing his eager anticipation of the coming expedition with the Astorians. The result of this expedition on the Missouri River resulted in *The Genera of North American Plants, and a Catalogue of the Species, to the year 1817* (1818), a remarkable two-volume work, written in English, such as had never before been produced in America in the botanical field. Nuttall's reputation as a field naturalist led to an appointment as Curator of the Botanical Garden and Lecturer at Harvard University in 1822. Thomas Nuttall forms an integral connection to St. Louis as a precursor in the establishment of St. Louis as a botanical centre during the nineteenth century.

### 37 LONG, MICHAEL

#### George Engelmann's Fortunate Connections

The 19th-century physician and botanist George Engelmann forged many important bonds with plant collectors, businessmen, and fellow scientists throughout Europe and America. One early connection at university with Louis Agassiz contributed to Engelmann's decision to emigrate from Germany to the American western frontier, where he hoped to become, in good Humboldtian fashion, a traveling naturalist. The decision enhanced the quality of science in the American West. When Engelmann finally settled in St. Louis, he quickly became the leader of its nascent scientific community. His connection with Asa Gray began another lifelong friendship; together they developed a western plant collecting business which helped them gather and describe many new species. Further friendships with prominent St. Louis businessmen Charles P. Chouteau and Henry Shaw led to the formation of two important scientific institutions--the Academy of Science of St. Louis and the Missouri Botanical Garden--both of which Engelmann helped to found and guide.

In later life, as younger scientists in St. Louis rose to prominence, Engelmann played one more important scientific role. During the 1870s he worked with local grape growers and entomologists, as well as French researchers, to counter the invasion of the phylloxera plant louse then crippling European vineyards. His expert knowledge of native species of American grapevines helped save the French wine industry. It is one final example of how Engelmann's connections, formed over a lifetime devoted to science, proved fortunate for the world.

Webster University, School of Communications, 470 E. Lockwood Ave., St. Louis, MO, 63119, USA

38 LEWIS, DEBORAH Q.\*<sup>1</sup> and  
CLARK, LYNN<sup>2</sup>

### Albert Hitchcock Presents - Adventures in Field Work, Types, and Grasses

Albert Spear Hitchcock (1865-1935) left his mark on several institutions as well as on the international botanical community. His higher education and career took him to what are now Iowa State University, University of Iowa, the Missouri Botanical Garden and Washington University, Kansas State University, the US Department of Agriculture, and the Smithsonian Institution. A student of Charles Bessey at Iowa State, Hitchcock received his bachelor's degree in 1884. In 1889-91, during his tenure at the Missouri Botanical Garden, he studied under William Trelease, was an instructor in botany at Washington University, and was curator of the herbarium. His first opportunity for field work abroad, a three-month study of the plants of the West Indies, came in 1890. Hitchcock invented novel ways to accomplish field work in roadless areas and rugged terrain, including a modified wheelbarrow to hold his collecting and camping gear. He pushed this contraption more than 240 miles in 24 days of collecting in Florida. During his career he collected more than 25,000 numbers, mostly grasses, with duplicates distributed widely. As the debate raged between European botanists who favored the Vienna Code of Nomenclature and North Americans who supported the American Code, he served as chairman of the Botanical Society of America's Committee on Botanical Nomenclature. In this role, he was the lead author of and vigorously promoted the "Type-basis Code," which reflected his views on the importance of establishing names in reference to type specimens. Although this proposed Code went considerably beyond a simple compromise position, it was largely adopted in what eventually became the International Code. Hitchcock's body of work, including his long collaboration with Agnes Chase after 1907, stands as the monumental achievement in agrostology of the 20<sup>th</sup> century. He made collecting expeditions to many countries around the world, visited the major herbaria to study types and other specimens, and published more than 200 revisionary and floristic studies of grasses.

<sup>1</sup>Iowa State University, Department of Ecology, Evolution and Organismal Biology, 340 Bessey, Ames, IA, 50011-1020, USA<sup>2</sup>Iowa State University, Department of Ecology, Evolution and Organismal Biology, 253 Bessey, Ames, IA, 50011-1020, USA

39 KLEINMAN, KIM

### Edgar Anderson, The Missouri Botanical Garden and the Rise of Biosystematics

Edgar Anderson--along with W.H. Camp of the New York Botanical Garden and the Bay Area group which included E.B. Babcock, Lincoln Constance, and G. Ledyard Stebbins--helped forge biosystematics in the 1930s and 1940s. Applying genetics to ecological, evolutionary, and taxonomic problems, this generation of workers deepened their practical and theoretical understanding of plants. Anderson came to the Missouri Botanical Garden from Harvard's Bussey Institution in 1922 as "Geneticist to the Garden." With a keen interest in natural history, he gladly accepted the suggestion of his MBG colleagues and students to take a serious interest in taxonomy, working on *Iris* and *Tradescantia* and exploring the Ozarks as well the intersection of genetics and systematics. Anderson's contribution to the rise of biosystematics is rooted in his professional connection to the Missouri Botanical Garden and his field work in Missouri.

Webster University, Academic Advising Center, 470 East Lockwood Ave., St. Louis, MO, 63119, USA

40 STEVENSON, DENNIS\* and  
STEVENSON, JAN

### William J. Robbins: The Missouri Years

William Jacob Robbins (1890-1978) was a distinguished botanist researcher and leader in American science as well as developing a wide range of collaborative and institutional ties with international scientific communities. He received his A.B. (1910) at Lehigh University and Ph.D. (1915) in plant physiology at Cornell University. After serving briefly in World War I as a medical bacteriologist at Yale University, he served as Professor of Botany and Chairman of the Department of Botany of the University of Missouri (1919-1937). During his eighteen years there, he also served as Dean of the Graduate School (1930-1937) and as Acting President (1933-1934). Although trained as a plant physiologist, Robbins was eclectic in his interests. During the Missouri years he wrote two textbooks, *Botany*; a *Textbook for College and University Students* (with H. W. Rickett) and *Principles of Plant Growth*; an *Elementary Botany*. He, also, encouraged the study of genetics in part through his support of the appointment of Barbara McClintock, thus, setting the stage for excellence in this area that still exists today at the University of Missouri. His administrative experience and success in that endeavor at the University of Missouri paved the way for his continuing leadership in science at large and his research abilities led to his membership in the National Academy of Sciences.

The NY Botanical Garden, 2900 Southern Blvd, Bronx, NY, 10458-5126, USA

### Lewis J. Stadler: The Nature of the Gene, and a Clue to DNA

Lewis John Stadler was born and raised in St. Louis, Missouri. A giant of theoretical genetics, he was a brilliant experimenter into the nature of genes. His remarkable prescience about the chemical nature of the genetic material was fulfilled as his career closed, when Watson and Crick accurately described DNA. Surprisingly, no special future was evident early: by his own report he was 57th in his high school class of 69. Even in graduate school days he failed to impress faculty during a brief stay at Cornell in 1919. He completed the PhD at the University of Missouri in 1922 and spent his career on the University faculty, appointed jointly from 1930 on with USDA, until 1954. His early research was on hybridization and selection of pure lines in crops, and on natural variability and diversity. By 1924 he was studying (1) variability of crossing-over and (2) spontaneous and induced mutation, which presaged his career contributions. Soon he demonstrated x-ray induced mutation (1928), coincident with studies by Muller on *Drosophila*. A classic 1929 study showed that mutation rate decreases with increased ploidy. McClintock used materials and advice received from him during her postdoctoral visit (1931). His intellectual leadership by 1936 drew together vigorous, interacting, creative scientists who treasured lunchtime exchanges. With typical elegant design he applied different ultra-violet wave-lengths as a possible clue to the chemical nature of the substance which absorbs the radiation producing genetic effects" (1939) and correctly predicted that DNA was the genetic material. Intensive research on spontaneous changes in one selected locus further drew upon his analytical skills, superbly displayed in his valedictory paper, "The Gene" (1955). He was elected to the National Academy of Sciences and held numerous other honors and responsibilities. His correspondence shows significant humanitarian actions. Rhoades notes in a Memoir for NAS that Stadler had a rich, warm personality, full of understanding and sympathy for points of view different from his own."

UNIV OF MISSOURI, 202 CURTIS HALL, Columbia, MO, 65211-7020, USA

### 42 KASS, LEE B

#### Barbara McClintock at the University of Missouri (1936-1942): The Road to Transposition

Barbara McClintock was appointed Assistant Professor of Botany at the University of Missouri in 1936. A year earlier, Lewis J. Stadler had identified McClintock as the best cytologist in the world for the appointment in his genetics research institute. Stadler's Rockefeller Foundation grant initially paid Mc-

Clintock's salary, but the renewal was contingent upon the university assuming financial responsibility for her appointment, which they did. McClintock taught many courses at Missouri; developing their first course in Cytogenetics. She was major advisor or directed research for seven graduate students and offered guidance to many visiting researchers. She presented seminars at neighboring universities and regularly attended annual meetings of the Genetics Society of America. There in 1936 and 1937, she reported on ring chromosomes, a study she had initiated as a National Research Council Fellow (1931-1933) with Stadler. She soon published a complete account of that work and the research that grew from the initial study. Continuing these investigations during the next three years at Missouri (1939-1941), she wrote three papers elucidating the mechanisms for the breakage-fusion-bridge cycles in maize, which led to her Nobel-award-winning discovery of transposable elements. Upon learning that Stadler's genetics research group might be terminated if Stadler left the University and that there might be an opening for her at the Department of Genetics, Carnegie Institution of Washington, Cold Spring Harbor (CSH), New York, McClintock requested a leave of absence and spent the summer of 1941 at CSH. There she was offered a visiting investigator appointment for the duration of her leave. When Missouri learned that she was subsequently offered a permanent staff position at CSH, they immediately counter offered with a large raise to supplement her previously recommended promotion with tenure. CSH offered a full-time research investigator appointment, with no interference and complete freedom to pursue research without teaching responsibilities, committee work, graduate student advising or publication deadlines. McClintock resigned from Missouri in August 1942.

Cornell University, Plant Biology, 412 Mann Library, Ithaca, NY, 14853, USA

**Incorporating microbes into plant community ecology**

*Sponsored by Mycological Section.*

**43 BEVER, JAMES DAVID**

**Conceptual frameworks for understanding soil microbial impacts on plant communities**

Resource partitioning has played a prominent role in the thinking about plant community structure. Yet this and other commonly held frameworks in plant ecology have an aboveground bias that neglects soil organisms. However, recent work has illustrated that the presence and composition of soil microbial communities can have large impacts on plant community diversity and composition. Therefore, a complete understanding of plant community structure and dynamics requires integration of a microbial perspective with frameworks for plant-plant interactions. I outline three ways in which microbes can impact plant community dynamics and coexistence. The first two mechanisms act through microbial modification of plant resource competition, either through microbial mediation of plant resource partitioning (expansion or contraction), or through resource sharing via common mycorrhizal networks. The third mechanism, plant-soil community feedbacks, does not depend upon competition for resources for plant species coexistence. Rather, the dynamics of soil microbes (changes in density and composition) can reinforce or work against the fitness of the most abundant plant species. I describe and illustrate these mechanisms of microbial mediation of plant-plant interactions, and discuss their implications for the dynamics and management of plant communities.

Indiana University, Department of Biology, Bloomington, Indiana, 47401, USA

**44 STEIDINGER, BRIAN\*, DALLING, JIM<sup>2</sup> and TURNER, BEN<sup>1</sup>**

**Resource partitioning of soil organic phosphorus: Investigations from a tropical montane forest**

The partitioning of soil nutrients into chemically unique resources has been demonstrated with nitrogen, but not phosphorus (P). Soil P exists in several different organic forms, including monoesters (glucose-phosphate), inositols (phytic acid), and diesters (DNA, RNA). As soils age, the proportion of the total soil P pool in inorganic/organic monoester forms decreases, while the proportion in inositol/diester forms increases. Concomitantly, arbuscular mycorrhizal (AM) plants are associated with young soils, while ectomycorrhizal (EM) and nonmycorrhizal (NM) plants are associated

with older soils. Therefore, I hypothesized AM, EM, and NM trees exploit different forms of soil P and that plant species turnover across soil age gradients is mediated by preference for these different forms. I collected seedlings of AM (*Mollinedia darensis*, *Podocarpus oleoifolius*), EM (*Oreomunna mexicana*), and NM (*Roupala montana*) from P-limiting soils at the Fortuna Forest Reserve, in Western Panama. Seedlings were grown in a hydroponic growth medium containing exclusively inorganic, monoester, diester, or inositol-P. The plants were harvested at 4 months and used to calculate relative growth rate (RGR) and foliar and whole-plant P content. Treatment differences in mean RGR within species were analyzed using ANOVA and least significant difference ( $p < 0.05$ ) in SAS. Inter-species comparisons of growth between the organic P groups to the inorganic groups were conducted to evaluate the significance of the species\*treatment interaction. Growth in the mycorrhizal species was high in inorganic-P and organic monoester-P and low in organic inositol and diester-P treatments. The NM species (Proteaceae) exhibit significantly greater growth on inositol phosphate ( $p = 0.0004$ ) and nearly-significantly greater growth on diester phosphate ( $p = 0.058$ ) than the mycorrhizal species. I found no significant differences between AM and EM species' growth response on different treatments. This indicates that partitioning of soil P may occur between mycorrhizal and NM plants, but not between AM and EM plants. Measurements of the foliar and whole-plant P-content are currently in progress.

<sup>1</sup>Smithsonian Tropical Research Institute, Mrc 0580-12, Unit 9100 Box 0948/Dpo Aa 34002-9998, Panama City, Panama, Panama  
<sup>2</sup>University of Illinois Urbana-Champaign, Plant Biology, 265 Morrill Hall, 505 South Goodwin Avenue, Urbana, IL, 61801, USA

**45 HORTON, TOM**

**Structure and function of mycorrhizal networks: A complex foundation for plant communities**

In 1988 Newman outlined the ecological significance of mycorrhizal linkages in plant communities. Our understanding of the structure and function of mycorrhizal networks has developed further with the application of isotopic tracers and methods for identifying individuals and species of fungi. Fungal communities are species rich, and we are beginning to learn about the functional roles of those species. I define a common mycorrhizal network as a continuous thallus (mycelium of an individual) linking two or more plant individuals of the same or different species. The sum of multiple common mycorrhizal networks can be thought of as a complex mycorrhizal network, and with this complexity comes all the variations in structure and function that each species of fungus brings. The size of a fungal individual varies by species, but typically ranges from meters to tens of meters. Larger genetic individuals are likely made up of multiple ramets, but even if an indi-

vidual is continuous, the scale of directin fluence on plants in a common network is likely centimeters to a few meters. Non-self fusions between thalli are rejected in Basidiomycota and Ascomycota (variously forming ecto-, ericoid, arbutoid, monotropoid and orchid mycorrhizae) through the vegetative incompatibility system. Species in Glomeromycota (forming arbuscular mycorrhizae) develop genetically mixed thalli. The fungi in a complex mycorrhizal network are a guild of organisms competing for resources. The fungi have enzymatic capacities for accessing forms of nutrients unavailable to plants such as organic nitrogen and recalcitrant forms of phosphorus. Competition for soil nutrients is likely a function of root-to-root competition for plant available forms and mycelial competition for plant unavailable forms. We have good evidence that C, N, and P move through networks, but we are in need of studies elucidating which species are moving them in these complex systems, how they interact with host species, and what molecules are transferred to the hosts.

SUNY-Environmental Science and Forestry, Environmental Biology, 241 Illick Hall, Syracuse, NY, 13210, USA

46 MANGAN, SCOTT A.\* and SCHNITZER, STEFAN A.

### Plant-soil feedbacks and relative tree species abundance in a tropical forest in Panama

Negative interactions between plants and their soil biota have been hypothesized to be important in maintaining plant diversity and determining plant relative abundance in both grassland and forest ecosystems. Negative plant-soil feedbacks (NPSF) occur when species-specific soil enemies accumulate under established plants, and in turn, reduce the recruitment of conspecific offspring relative to heterospecific offspring, thereby preventing any one species from dominating the plant community. In a previous study, we showed that variation in strengths of negative feedback caused by some aspect of the soil biota is important in determining relative abundance of tropical trees in Panama. Here, we present results from a fully reciprocal biocide experiment designed to test whether an important group of soil-borne enemies (oomycetes) are the primary soil-borne enemies driving NPSF at the seedling stage. We hypothesized that if oomycetes are sufficiently species-specific with their hosts and drive NPSF, then the strength of NPSF should lessen with the application of an oomycete-specific biocide. Contrary to our hypothesis, the addition of the biocide significantly increased the strength of community-wide NPSF relative to unmanipulated soil communities ( $P = 0.010$ ). Specifically, the strength of NPSF per species increased in all five species examined, and significantly so in three of those species. The unequal effect of biocide on NPSFs among species led to the breakdown in the relationship between the strength of feedback and relative abundance. In un-

manipulated soils, tree species exhibiting stronger negative feedbacks were less common as adults than those species exhibiting weaker negative feedbacks or positive feedbacks ( $R^2 = 0.82$ ,  $P = 0.034$ ). However, no relationship between the strength of feedback and abundance was detected in biocide-treated soils ( $R^2 = 0.19$ ,  $P = 0.458$ ). Our multiple plant-species approach contradicts single-species studies and suggests that oomycetes are not direct drivers of NPSFs. Instead, oomycetes appear to be generalists and may compete with other species-specific organisms important to this process.

University of Wisconsin - Milwaukee, Department of Biological Sciences, P. O. Box 413, Milwaukee, WI, 53201, USA

47 WALKER, JOHN F.\*<sup>1</sup> and JUMPPONEN, ARI<sup>2</sup>

### Seasonal Dynamics of Mycorrhizal Fungus Communities

Communities of rhizosphere-associated fungi are diverse and variable temporally and spatially. Fungi that form ectomycorrhizal symbioses are particularly diverse across small spatial scales, with communities typically comprised of few abundant core taxa and numerous rare species. Elucidating the degree to which intra-annual temporal variation in these communities affects diversity and functionality would allow important inferences about partitioning of fungal symbionts across the season, transitions between functional guilds of fungi, and host plant plasticity at the soil interface. We present results from three recent studies focusing on temporal dynamics of root-associated fungi. *First*, a comparison among ectomycorrhizal associates of red oak seedlings in a temperate eastern forest retrieved from mid-summer and early fall suggested that richness of certain ectomycorrhizal fungus groups changes over the season. *Second*, an investigation of fungal diversity on roots of *Quercus* spp. in non-forested rural and urban sites in the Flint Hills region (KS, USA) indicated a transition from putative root-associated antagonists and saprobes that were abundant early in the growing season to common ectomycorrhizal fungi later. Changes in the richness of ectomycorrhizal groups were again observed, although the specific pattern was not consistent with the previous study. *Third*, an investigation of changes in fungal communities associated with a dominant C4 prairie grass (*Andropogon gerardii*) forming arbuscular mycorrhizal symbioses indicated a similar transition from pathogenic/saprobic fungi in the spring to dominance by mycorrhizal associates later in the growing season. Drivers for these shifts in fungal communities and their functional consequences remain unclear. However, root turnover in the spring may be a primary factor combined secondarily with differences in environmental tolerances and niche preferences of the fungi. Determining whether the observed seasonal shifts in broad functional groups are universal and whether patterns of seasonal partitioning in mycorrhizal

zal groups are biome- or ecosystem-specific are valuable future research directions.

<sup>1</sup>Appalachian State University, Biology, 572 Rivers St, Boone, NC, 28608, USA<sup>2</sup>Kansas State University, Division of Biology, 116 Ackert Hall, Manhattan, KS, 66506, USA

**48 MCCORMICK, MELISSA<sup>1</sup>, SZLAVECZ, KATALIN<sup>2</sup> and WHIGHAM, DENNIS<sup>1</sup>**

**Alteration of microbial communities by non-native earthworms**

Non-native species can dramatically alter the availability of nutrients and the microbial community, including alteration of mycorrhizal networks that are essential for efficient resource acquisition by most plant species. We used field manipulations to determine the effects of non-native earthworms on mycorrhizal fungi and tree seedling growth. We manipulated earthworm density and leaf litter in plots into which seedlings of two arbuscular (AM; *Liriodendron tulipifera* and *Acer rubrum*) and two ectomycorrhizal (ECM; *Quercus rubra* and *Fagus grandifolia*) trees were planted. We measured enzyme activity, microbial abundance and composition in the plots as well as seedling growth and mycorrhizal colonization. In a second experiment we separately manipulated hyphal disruption, soil mixing, and soil fertility, in addition to adding non-native earthworms, to determine how different earthworm activities affected mycorrhizal fungi. In both experiments we used taxon-specific quantitative PCR to measure the abundance of bacteria, fungi, AM and ECM in the soil. We combined these analyses with assessment of enzyme activity to separate direct and indirect effects of non-native earthworms on seedling growth and survival. ECM and AM fungi were less abundant in plots with more earthworms and results of the second experiment suggested that earthworms primarily affected mycorrhizae through soil mixing. Both mycorrhizal groups were also more abundant in mature compared to successional forests. ECM seedlings were smaller in high density earthworm plots, while the reverse was true for AM seedlings but effects depended on forest land-use history. Earthworm biomass was consistently higher in plots with tulip poplar litter than those with beech litter, suggesting earthworm invasion may have changed feedbacks between the plant and microbial communities. In these experiments we found that earthworm-driven alterations in the microbial community, especially effects on the mycorrhizal community, directly affected the plant community, while plant effects on the microbial community were also mediated by earthworms.

<sup>1</sup>Smithsonian Institution, Smithsonian Environmental Research Center, 647 Contees Wharf Rd., Edgewater, MD, 21037, USA<sup>2</sup>The Johns Hopkins University, Dept. of Earth and Planetary Sciences, 3400 N. Charles St., Baltimore, MD, 21216, USA

**49 WILSON, GAIL W. T.<sup>\*</sup>, HICKMAN, KAREN R. and WILLIAMSON, MELINDA M,**

**Invasive species alter arbuscular mycorrhizal densities: implications for restoration**

Soil organisms play important roles in regulating ecosystem-level processes and the association of arbuscular mycorrhizal (AM) fungi with a plant species can be a central force shaping plant species' ecology. These plant-fungal associations have been reported to both constrain and facilitate the ability of an invasive species to successfully expand its range. Understanding how mycorrhizal associations are affected by plant invasions may be a critical aspect of the conservation and restoration of native ecosystems. We assessed AM intra- and extra-radical hyphal densities of two expanding plant species of the Central Great Plains, *Bothriochloa* spp. (Old World Bluestems) and *Juniperus virginiana* (Eastern redcedar). Restoration following eradication of these species was also examined. Old World Bluestems are a group of warm-season perennial grasses of Eurasian origin that are a great threat to native prairies of the southern and central Great Plains. These species are functionally similar to native warm-season grasses of these grasslands, and both *Bothriochloa* and native warm-season grasses are obligate mycotrophs. Eastern redcedar are native to the tallgrass prairie, but are rapidly encroaching into native grasslands in response to global land use change. Examination of soil microbial communities beneath both Old World Bluestem and Eastern redcedar indicated AM inter- and intra-radical colonization increased substantially, compared to adjacent native prairie. We examined plant-soil feedbacks of Old World Bluestem by assessing biomass production and AM colonization of native warm-season grasses planted into soil collected beneath Old World Bluestem. Our results indicated the major driver in plant growth suppression following invasion by Old World Bluestem was the alteration in soil microbial communities. Plant growth was tightly correlated with AM root colonization demonstrating mycorrhizae play an important role in the invasion of these systems by Old World Bluestem and indicating the native AM fungal community may be a fundamental consideration for the successful restoration of native plant communities into invaded sites.

Oklahoma State University, Natural Resource Ecology & Mngt, Stillwater, Ok, 74078, USA

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## Healing the planet: Conservation of the world's tropical forests

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*Sponsored by William L. Brown Center.*

50 ASNER, GREG P.

### Monitoring Tropical Forests for Conservation: Science to Policy Breakthrough

For decades, monitoring of tropical forests by satellites has revealed the grim picture of deforestation that threatens the most biodiverse regions of our planet. In recent years, remote sensing science and technology have evolved beyond deforestation monitoring, providing new opportunities to further understand human impacts in tropical regions, and to remotely explore some of the most unique remaining forests in the tropics. At the same time, new social and economic opportunities have emerged to help slow the rate of tropical forest losses. To work, these new programs rely on a vastly improved monitoring capability. We have just entered a new era in tropical forest monitoring, created by remote sensing scientists to meet the demand for expanding scientific knowledge and for improving forest conservation and management. The technology must be made available to non-experts if transparency and trust are to be created among stakeholders. With emerging partnerships between science institutions, international organizations and national governments, the hope of curbing forest losses and protecting remaining biodiversity has never been stronger.

Greg Asner, Department of Global Ecology, Carnegie Institution for Science, 260 Panama St., Stanford, CA, 94305, USA

51 HUBBELL, STEPHEN P.

### Understanding tree species' rarity in tropical forests and its implications for conservation

Tropical lowland wet forests contain an extraordinary diversity of tree species, but most of these species are rare to exceedingly rare, occurring at adult densities of only a few adult trees per square kilometer. The global network of large, permanent tropical forest plots contains over 4.5 million trees of approximately 8,500 tree species, representing about 10% of the known tree species in the tropics. However, half of these tree species collectively make up less than 1% of the individuals. What is poorly known is the extent to which locally rare species are also globally rare. This paper considers the implications of rarity for the conservation of tropical forest tree diversity.

University of California, Los Angeles, Ecology and Evolutionary Biology, 621 Charles E. Young Dr., South, Los Angeles, CA, 90095-1606, USA

52 PIMM, STUART L.

### Conserving Tropical Forest: Where Things Stand

Conventional wisdom holds that tropical forests hold the great majority of plant species, that human activities are shrinking these forests rapidly, and that deforestation is the single most important driver of terrestrial extinctions. These three assertions require careful documentation. I will provide statistical estimates of the numbers of flowering plants missing from the taxonomic record. Overall, about 15% more species remain to be discovered. They will be found in biodiversity hotspots — areas where exceptionally high levels of habitat destruction collide with high levels of endemism. These facts predict that about 30% of all plant species are in danger of extinction. To be effective, conservation efforts must greatly reduce the present rate of deforestation and do so in key areas. Some recent efforts through REDD have started to reduce deforestation. However, given the already extensive losses of forests in key areas, conservation will need to restore presently degraded areas. I will provide examples of how this may be done effectively.

Duke University, Nicholas School of the Environment, Box 90328, Duke University, Durham, NC, 27708, USA

53 LAURANCE, WILLIAM

### Paradise in Peril: Emerging Threats to Tropical Forests

I will highlight new and emerging threats to tropical forests, the world's most biologically diverse ecosystems. The drivers of tropical forest destruction and key perils to biodiversity have changed over the past two decades. Industrial drivers of forest conversion—such as logging, large-scale soy and cattle farming, oil-palm plantations, and oil and gas development—have escalated in importance in recent decades, buoyed by rapid globalization, economic growth, and rising standards of living in developing nations. Biofuels are likely to grow rapidly as a driver of future forest destruction. Climate change is increasingly emerging as a potentially serious driver of change in the tropics, and some fauna, such as amphibians, are being decimated by emerging pathogens. In general, old-growth forests are vanishing rapidly and being replaced by fragmented, secondary, and logged forests. These various environmental insults often operate in concert, magnifying their impacts and posing an even greater threat to tropical forests and their biodiversity.

James Cook University, School of Marine and Tropical Biology, PO Box 6811, Cairns, Queensland, 4870, Australia

### A Wild Solution to Climate Change

Half of the excess CO<sub>2</sub> in the atmosphere comes from destruction and degradation of ecosystems over the past three centuries. An important amount can be removed by ecosystem restoration providing benefits for ecosystems as well as reducing the concomitant amount of climate change. The ideal would be to maximize the amount of biodiversity conservation benefit -- e.g., restoration in biodiversity hotspots like the Atlantic forest region of Brazil.

The Heinz Center, 900 17th Street, NW, Suite 700, Washington, DC, 20006, USA

### 55 BAWA, KAMAL

#### Saving Tropical Forests: Usable Knowledge, Institutions and Participatory Governance

Despite tremendous advances in sustainability science, and improved policies and concerted conservation action to save biodiversity, rates of deforestation in the tropics remain high. Curtailing the rate of biodiversity loss would require progress on many different fronts. I focus on the role of usable knowledge, means to generate such knowledge, and the ways to widen participation of civil society in using this knowledge to reduce environmental degradation. I cite examples from South Asia to elaborate my arguments. No other region of the world is perhaps more challenging than South Asia in our efforts to simultaneously conserve biodiversity and improve human condition. Thus lessons drawn from the region have wide applicability to other parts of the tropics.

University of Massachusetts, Boston, Biology, 100 Morrissey Blvd., Boston, MA, 02125, USA

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### The fruitful outcome of graduate student-designed curricula: research modules, publishing opportunities, and outreach inspired by the NSF's Graduate STEM Fellows in K-12 Education (GK-12) Program

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*Sponsored by Teaching Section and BSA Education Committee.*

### 56 MEYER, RACHEL<sup>\*1</sup> and LOIZIDES, LAUREN<sup>2</sup>

#### One hundred researchable questions sprouting in NYC parks

Many graduate students in the biological sciences will have several teaching opportunities over the course of their programs. Involving graduate students in designing teaching modules is beneficial (though sometimes unrealized) to their research, publications, and professional experiences. The City University of New York NSF GK-12 Program is designed to maximize benefits to graduate students as well as partnering institutions. Through the program, graduate students work under the guidance of teachers to develop and teach elementary and secondary-level curricula inspired by one's own scientific research experiences. Working collaboratively, the graduate student and teacher share their expertise and apply novel approaches to science education. This is a unique opportunity for graduate students to hone skills in teaching and communication, and to develop publications, unique local educational programs, and future research projects. Here, we present a curriculum that was developed and pilot tested in high school science classes as part of the GK-12 program. The curriculum theme is on generating researchable questions, collecting data, and communicating results by means of nature journaling and documentary-making. Originally part of an Environmental Science class, this inquiry-based module can be applied to any class within the natural sciences. The curriculum is now being packaged to become a College Now course, which will be implemented by other teachers across New York City in after-school programs. Further, the curriculum is being used for science education research: we have collected data on how it has transformed student inquiry skills and attitudes toward science and nature. In this presentation, we will share strategies to maximize the applications (i.e. new educational programs and publications) as well as the benefits pertinent to professional development that can stem from new curricula.

<sup>1</sup>The City University of New York Graduate Center, Biology, 365 Fifth Avenue, New York, NY, 10016, United States<sup>2</sup>Baruch College Campus High School, 55 East 25th Street, New York, NY, 10010, United States

### From the rainforest to the classroom: connecting students with field research

Introducing middle school-aged children to current scientific investigations can help them make connections between real-world issues and concepts they are learning in the classroom. Through the NSF GK-12 program at the Environmental Science Institute at The University of Texas at Austin, sixth and seventh-grade students at Fulmore Middle School in Austin and Park Crest Middle School in Pflugerville, TX learned about water quality issues, the importance of biodiversity, phytoremediation, and invasive species. Using scientific studies from biology, environmental science, aquatic science, geology, and botany, the primary focus of the program was to enlighten students about the impacts of environmental change on Texas habitats and residents. Expanding science lessons beyond Texas ecosystems, through a website called the Jungle Journal designed specifically for this program, students interacted with a botanical researcher while she traveled to Bolivia and Peru on a plant-collecting trip. On this website, the botanist posted daily journal entries and trip photos. Students viewed the postings and asked questions. In this presentation, specifics of those lessons along with fun student stories will be shared. These student-researcher interactions increased the graduate student's ability to communicate difficult science concepts to grade school students, stimulated student interest in scientific studies, and inspired new lesson ideas for middle school teachers.

University of Missouri-Columbia, Biological Sciences, 1201 Rollins St.-Bond LSC 311, Columbia, MO, 65211, USA

### 58 GONZALEZ, FAVIO<sup>1</sup> and PABON-MORA, NATALIA\*<sup>2</sup>

#### Evo evo on a budget: An effort to update the plant developmental biology curriculum for public universities in Colombia

Plant development in an evolutionary biology perspective (evo-devo) requires the integration of phylogenetics, comparative morphology and anatomy, and a substantial molecular biology background. Built upon such background, evo-devo then formulates questions about the relationship between gene expression and function with specific phenotypes. As many other scientific disciplines, evo-devo has undergone a "romantic" phase followed by an "empiric" phase before reaching an academically mature status. Leading international institutions in the field have successfully integrated all disciplines, and for the most part have achieved such status. However, research has been focused on model organisms such as *Arabidopsis*, rice and corn. On the other

hand, universities in many developing countries strive to train and recruit local scientists in several of the basic fields, able to undertake integrative approaches aimed at research on non-model organisms. These organisms, usually tropical, grow under complex ecological requirements, being thus difficult or impossible to grow in greenhouses. In this talk we will present ongoing case studies carried out in the National University of Colombia, one of the leading public institutions in the country. We have selected some neotropical plant taxa for these projects, on the basis of several criteria: 1) the occurrence of atypical floral or fruit characters in members of Aristolochiaceae, Chlorantaceae, Papaveraceae, Proteaceae, and Solanaceae; 2) the extremely diverse morphological traits on leaves, flowers and fruits, as e.g. in genera of Orchidaceae, Berberidaceae and Piperaceae; and 3) the morphological stasis of flowers in neotropical Coriariaceae, Gunneraceae and Winteraceae. These projects attempt to provide a stronger background regarding phylogenetic relationships, and character evolution as the basis for more academically mature phases of evo-devo. We will highlight the major challenges standardizing a state-of-the-art evo-devo program in Colombia. Lastly, we will discuss which molecular biology tools should be implemented to assess gene expression and function in non-model species and how are we beginning to incorporate them in our ongoing projects.

<sup>1</sup>Universidad Nacional De Colombia, Instituto De Ciencias Naturales, Ciudad Universitaria Universidad Nacional, Bogota, 1, Colombia <sup>2</sup>Graduate Center, City University of New York, 365 Fifth Avenue, New York, NY, 10016, USA

### 59 STROZAK, VICTOR S.

#### Authentic Research Modules: a strategy to integrate GK-12 Fellows' research into science classes in New York City high schools and the CUNY College Now Program

Authentic Research Modules in Science (ARMs) are the primary strategy that CUNY's GK-12 Program uses to integrate fellows' research into science courses in New York City high schools. Each ARM incorporates some aspect of the fellow's research and has specific components that focus on basic literacy and computational skills. ARMs curriculum development, including pilot testing, offers fellows a common core training experience that embodies best practices in learning theory, instructional design, and evaluation. It is the major training mechanism by which fellows become skilled at effectively communicating complex scientific ideas to a lay audience. Collaborating with high school teachers to design and implement research activities increases the fellows' competencies in communication, teamwork, curriculum design and instruction. The goal of the ARM is to give high school students an opportunity to think like scientists and have a genuine research experience. Urban environments in general

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## The fruitful outcome of graduate student-designed curricula:

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and New York City in particular offer a rich, untapped resource for student research projects. By investigating their own backyard and developing research projects on some aspect of the urban environment, students become engaged in doing science for the first time. They learn specific research skills as well as general science process skills. They also gain content knowledge and improve overall science literacy. This presentation will describe specific research courses that have been developed and how they have become courses in the CUNY College Now Program.

The Graduate Center, CUNY, Center for Advanced Study in Education, room 3300.12, 365 Fifth Avenue, New York, NY, 10016, USA

### 60 AHMED, SELENA

#### Bringing Classroom Research to Publication and Beyond

This paper explores strategies to disseminate research results for both educators and students as a key component of inquiry-based curricula in K-12 and undergraduate classrooms. Written, oral, community outreach, and multi-media dissemination strategies will be presented. These strategies include publication in education journals, professional development workshops, community-based activities, storyboard videos, and interactive websites. Drawing on experiences of teaching ethnobotany inquiry-based curricula in field, classroom, and laboratory settings, this paper discusses the challenges and opportunities of guiding students through the process of disseminating research results. It further examines how educators can reflect on their inquiry-based curricula and package their lessons as self-sustaining modules, courses, and school-wide programs. This dissemination model seeks to develop scientific communication skills, advance knowledge, and promote activism in science education while addressing the broader impact criteria of many grant-giving organizations.

Tufts University, Boston, MA, 02111, USA

### 61 DOUGLAS, JASON

#### Engaging students through environmental justice research

Young people are more often than not very well aware of social, political, and environmental issues in their neighborhood and the world, but what can awareness achieve if there is only a limited understanding of the issues? When environmental issues seem too enormous and all encompassing to have a workable solution, it can lead to people feeling further removed from nature -- particularly in the urban context. Environmental issues at the scale of global warming have been associated with a sense of removal when considering cause and effect, and often a sense of incapac-

ity regarding the ability to take action on such matters (Devine-Wright et al., 2004). A decontextualized style of learning can result in a sense of removal from the issues that are being considered (Berman, 1997). How can educators, researchers and practitioners help to instill a sense of responsibility in youth and society when they are up against society's increasing removal from nature? Drawing on my work with young adults in an after-school environmental research program, this paper explores young people's material and conceptual remaking of nature and society as they participate in a research program concerning environmental issues in New York City, e.g. air pollution and access to green space. Further, it examines theory and practice concerning experience, community engagement, mentorship, and democracy as pathways to the development of efficacy and environmental stewardship.

The Graduate School and University Center -- City University of New York Environmental Psychology, 365 5th Avenue, New York, NY, 10016, USA

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## Healing the planet: medicinal plants and the legacy of Richard E. Schultes

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*Sponsored by Society for Economic Botany and Economic Botany Section.*

### 62 BUSSMANN, RAINER

#### "I know every tree, every single tree one can see" - The life and legacy of Richard E. Schultes

If any body could be named as the father of Ethnobotany, it would be Richard E. Schultes (1915-2001). No researcher has ever done more field research, more to promote the discipline, and has encouraged more students to become ethnobotanists, with almost every senior scientist in the field acknowledging some connection to Schultes. Well known scholars like Mike Balick, Robert Bye, Wade Davis, Doel Soejarto and Andrew Weil were all Schultesians, but Schultes also inspired generations of non-academics and always freely shared his time and advice. Schultes published almost two dozen books and almost 500 papers, collected over 30000 herbarium numbers, often with dozens of copies, conducted continuous fieldwork in the Amazon for over 14 years, and created what can only be called the golden age of Economic Botany. How did Schultes, growing up in a poor second generation immigrant family, come to such fame? Who was this man, fluent in ten languages, who spent his entire career linked to or at Harvard, and became the focal point of generations of useful plant researchers and plant users, and created this by any account magical work setting that gave unrivaled opportunities to students, staff and visitors? And how could it happen, that the legacy of a widely decorated scholar got quickly forgotten at his home institution, and his incredible plant material and artifact collection is left to accumulate dust in a Harvard attic?

Missouri Botanical Garden, William L Brown Center For Plant Genetic Resources, PO Box 299, St. Louis, MO, 63166-0299, USA

### 63 BYE, ROBERT

#### Passage through Mexico - the influence of RES on Mexican economic botany

Richard Evans Schultes dedicated his life to studying the interrelationships between plants and people as well as sharing his enthusiasm with members of academic and public circles. His botanical formation was grounded in the Harvard University's tradition of taxonomy and "useful" plants. After completing original field work on peyote in Oklahoma (USA), his interdisciplinary vision shifted to Mexico. At these southern latitudes, he discovered more members of this mind-altering ethnobotanical complex and pioneered

interdisciplinary studies on mushrooms and ololiuqui. After completing his doctoral thesis on the useful plants of northeastern Oaxaca in 1941, he moved onto northwestern South American where his focus resided for the remainder of his life and where he built his international eminence. Northeastern Oaxaca was the area with which RES became best acquainted. His introduction to the area by the German B. P. Reko allowed him to survey the economic plants of the mountains of the Sierra Madre of Oaxaca; later, he presented the area, the people and the sacred mushrooms to ethnomycologists such as Roger Heim and Gordon Wasson. His broad interest as "the last Victorian explorer" followed the paths by European botanists of the previous century. Other plants caught his attention and he began to publish a series (*Plantae Mexicanae*) dedicated to expanding the taxonomic, floristic and economic botany of this region. In the late 1950s, he finished writing about Mexican plants, in particular with articles on orchids and the Oaxacan spice, *Quararibea funebris*. Although northwestern South America dominated his field work, he maintained contact with the second center of New World sacred narcotics through collaboration with researchers conducting field and laboratory investigation in Mexico. Even though the public does not associate RES with Mexican ethnobotany, the intellectual foundation and the implementation of Mexico's contemporary programs in sacred plants, medicinal plants, interpretation of plants found historical sources, and maize conservation are strongly influenced by RES's Mexican passage.

Universidad Nacional Autónoma de México, Jardín Botánico del Instituto de Biología, , Mexico, DF, 04510, MEXICO

### 64 SOEJARTO, DR. DJAJA D.

#### Medicinal Plants and the Legacy of Richard Evans Schultes

The late Professor Richard Evans Schultes is a renowned and accomplished ethnobotanist. He is also an accomplished plant taxonomist and bioprospector, who focused on narcotic and hallucinogenic plants. I was initiated into a bioprospecting career by Professor Schultes early in my graduate years at Harvard. The highlight of my career as a bioprospector was when I received in 1986 a contract with the US National Cancer Institute, on behalf of the University of Illinois at Chicago, to explore Southeast Asian plant diversity to collect plants for anticancer and anti-HIV screening, as part of the revival of the NCI's new plant screening program. This contract was renewed every 5 years through 2004. A major contribution that resulted from this exploration program was the discovery by the NCI of the anti-HIV compounds, the calanolides, isolated from species of *Calophyllum* collected in Sarawak, Malaysia. Calanolides were licensed to an Illinois-based pharmaceutical company for development as a drug to treat AIDS. The discovery of the calanolides also led to an im-

portant turning point in the biodiversity conservation and bioprospecting laws of the government of Sarawak, with the establishment of the Sarawak Biodiversity Centre (SBC) in 1998. While this NCI contract was still ongoing, a multidisciplinary team of botanists, ethnobotanists, natural product chemists, biochemist, economists, biotechnologists, and attorneys, under my leadership, was awarded an ICBG Grant to study the biodiversity of Vietnam and Laos. The goals of this program are to discover new bioactive compounds as potential candidates for development into pharmaceuticals for therapy against cancer, AIDS, malaria, and tuberculosis and, at the same time, to promote the conservation of the biodiversity of Vietnam and Laos, as well as to advance community economic standings in the study areas. Our ICBG project is still on-going to this date. It has been a great privilege and honor to be a student of Professor Schultes and to inherit and to push on his legacy in the study of medicinal plants.

College of Pharmacy, University of Illinois at Chicago, Chicago, Department of Medicinal Chemistry and Pharmacognosy, 833 S. Wood St., Chicago, IL, 60612, USA

## 65 ZARUCCHI, JAMES

### Richard Evans Schultes in the Northwest Amazon

Richard Evans Schultes, a native Bostonian and leading ethnobotanist of the 20<sup>th</sup> century, conducted the vast majority of his field studies among the native people in the Northwest Amazon of eastern Colombia. In the Comisaría del Vaupés, Schultes first surveyed the Rão Apaporis, a major tributary of the Amazon basin and southern boundary of the Vaupés, for native rubber trees as part of the allied war effort; he later collected many thousands of samples over several decades that record the high level of plant diversity found in that region as well as documented the use of numerous species by the indigenous population. Many hundreds of species new to science were obtained and described by either Schultes or his botanical colleagues. *Vaupesia* R. E. Schultes (Euphorbiaceae) was described as a new genus of rubber producing tree. *Resia* H. E. Moore (Gesneriaceae), *Schultesianthus* Hunziker (Solanaceae), and *Schultesiophytum* Harling (Cyclanthaceae) are genera named in honor of this legendary plant collector, conservationist, and professor of ethnobotany.

Missouri Botanical Garden, Research, PO Box 299, St. Louis, MO, 63166-0299, USA

## 66 BALICK, MICHAEL

### Reflections on Richard Evans Schultes, the Society for Economic Botany and the trajectory of ethnobotanical research

The life and work of Richard Evans Schultes—teacher, mentor and friend—resulted in a most extraordinary legacy that impacted an entire academic discipline as well as the tropical rainforest where he spent so much of his time. His life and times have been brilliantly chronicled by Wade Davis in the biography "One River: Exploration and Discoveries in the Amazon Rain Forest" (Simon & Schuster, 1997). At this, the tenth anniversary of his passing in 2001, we celebrate, with this symposium, his life and academic contributions. Professor Schultes, as his students always called him with such great reverence, was a founder of The Society for Economic Botany in 1959 and edited our journal for 18 years, from 1962-1979. His multidisciplinary scientific research program began in 1936 with that well-known trip to Oklahoma and lasted far beyond his retirement from Harvard in 1985. Professor Schultes' mentorship of dozens of Ph.D. students during his career at Harvard, combined with his teaching, lecturing and inspiration of tens of thousands of students throughout his long and distinguished career, did much to influence the trajectory of ethnobotany and economic botany. His values are deeply infused in the lives and professional activities of his numerous students, and I will elaborate on this, using examples from my own work.

New York Botanical Garden, 200th St and Southern Blvd., Bronx, NY, 10458, USA

## 67 SCHULTES, NEIL P.

### The Leaf falls near the Tree: my Father and my Career in Plant Biology

Find myself in the unique position of being not only one of Richard Evans Schultes many students (as an undergraduate in his *Plants and Human Affairs* course) but also a recipient of half his genome. Is it the *nature* of a Schultes or the *nurture* in the Schultes household that led to my career choice as a plant biologist? One might think that as my father and I share similar fates - attending undergraduate and graduate school at Harvard and choosing plant science as a career - that there might have been a hefty dose of generational grooming. Surprisingly, this was not the case. What my father offered me, as well as to many others, were opportunities and experiences. These undoubtedly helped me decide upon my career. Today I work at The Connecticut Agricultural Experiment Station in New Haven CT as a plant molecular biologist. There, colleagues and I work as part of a large effort in the plant community to identify and understand how maize genes give rise to C4 photosynthesis. Despite the gap between field botany and lab research it never ceases to amaze me how often I reach

back and retrieve informational gems from his course to use in my own seminars and teaching. Truly his legacy extends beyond the *nature* of Economic Botany and into the *nurturing* of the next generation of plant biology students.

The Connecticut Agricultural Experiment Station, Biochemistry & Genetics, 123 Huntington St., New Haven, CT, 06511, USA

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## Innovations in organismal botany - a tribute to the pioneering studies of Donald A. Eggert

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*Sponsored by Paleobotanical Section.*

68 TAYLOR, THOMAS\*<sup>1</sup> and ROTHWELL, GAR<sup>2</sup>

### Innovations in organismal botany - a tribute to the pioneering studies of Donald A. Eggert

Donald A. Eggert's groundbreaking studies of Paleozoic vascular plants represent not only a major shift in how fossil plants can be studied and analyzed, but also in how such original approaches can be used to integrate concepts about the biology of living and fossil species. Of the many research areas initiated by Eggert, several have fundamentally changed our ideas about the structure, development, and phylogenetic position of certain fossil plants, and how these processes and patterns are reflected in closely related extant taxa. Eggert's research has left an indelible mark on multiple areas of biology and his detailed studies serve as both a source of inspiration and measure of extraordinary scientific quality. This symposium will highlight five of the major research areas explored by Eggert to demonstrate not only the breadth of his interests, but also his level of scientific accomplishment. Each of the speakers will demonstrate the state of the discipline before Eggert's involvement, the accomplishments that Eggert made, and the questions and challenges that remain.

<sup>1</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-7600, USA<sup>2</sup>Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, 97331, USA

69 TOMESCU, ALEXANDRU

### Recognition, reconstruction, and characterization of ancestral filicalean ferns

In the late 50's and early 60's, when Don Eggert turned his attention to the fossil record of ferns, filicalean fern diversity included only extant families and rare hints of putative leptosporangia in Carboniferous fossils. The Coenopteridales, an extinct pteridophytic group comprising small, monostelic plants, were regarded as potential intermediates between the basal trimerophytes and living ferns. The four families of coenopterid ferns (Stauropteridaceae, Zygotpteridaceae, Botryopteridaceae, Anachoropteridaceae) were based on detached vegetative segments, with little knowledge of fertile parts, and many suspected that this classification, as well as the order as a whole, were artificial constructs. While there was growing agreement that coenopterids

may, in fact, represent several distinct lineages, Eggert was the first to produce plant reconstructions that highlighted the need for reconsideration of coenopterid classification and initiated the disintegration of the order. More important, his reconstructions which reconciled coenopterid vegetative parts with newly discovered fertile structures, showed that some coenopterids were in fact filicalean ferns belonging to two new families: the Tedeleaceae, based on the zygopterid *Ankyropteris*, and the Sermayaceae, based on anachoropterid plants. Continued work on the coenopterid plexus in the vein pioneered by Eggert led to reconstruction of several other taxa and ultimately generated a novel understanding of Devonian-Carboniferous fern diversity and relationships. Disintegration of the Coenopteriales resulted in the establishment of two new orders, the Stauropteriales and Zygopteriales, as well as the recognition of six extinct filicalean families which form what came to be called the 'first filicalean radiation': the old Botryopteridaceae and Anachoropteridaceae, Eggert's Tedeleaceae and Sermayaceae, and the Psalixochlaenaceae and Kaplanopteridaceae. These add considerably to filicalean taxonomic diversity and contribute a wealth of morphologies featuring combinations of characters absent in living filicales. Perhaps most important, disintegration of the Coenopteriales and the novel combinations of characters of extinct filicaleans have allowed for reevaluation of euphyllophyte phylogenies, leading to exciting new perspectives that challenge the dogma on relationships within the group.

Humboldt State University, Department of Biological Sciences, 1 Harpst Street, Arcata, CA, 95521, USA

## 70 TOMLINSON, P. BARRY.

### Carboniferous arborescents in relation to the architecture of modern trees

Don Eggert's interpretation of Carboniferous lepidodendroids was innovative because, faced with the reconstruction of such tall trees from scattered fragments, he produced a result that emphasized developmental dynamics, encapsulated in the concepts of epidogenesis and apoxogenesis, with an ultimate suggestion of determinate growth. This anticipated in an essentially pioneering fashion the later concept of "tree architecture" based on the study of modern trees, in which "deterministic" and "opportunistic" processes combine to produce a tree's canopy within a forest environment. Given this, we can ask the question - did early tree forms demonstrate the process of "reiteration"?; i.e., the partial or total repetition of a tree's architecture, as when subject to some disturbance within a biological environment. Simply put, how did a lepidodendroid tree respond to branch breakage, bearing in mind that its branches developed by stem apical dichotomy. The paleobotanical literature says little about this, so maybe early trees did not reiterate. If so, how did later trees gain this ability? A possible explanation is because they de-

veloped axillary branching, which seems correlated with the development of the megaphyll (providing the leaf axil) and the presence of secondary growth from a bifacial vascular cambium (which permits the development of the attachment of a branch to the parent axis). We will explore this idea with reference to unusual examples in modern trees which in turn raises the question of why the leaf axil is almost always the site of branching in modern trees, but in highly diverse, but little studied ways.

National Tropical Botanical Garden, The Kampong, 4013 Douglas Rd, Miami, FL, 33133, USA

## 71 TAYLOR, EDITH\* and RYBERG, PATRICIA

### Donald A. Eggert's contributions to the study of fossil phloem structure and evolution

Phloem tissue is rarely preserved in the fossil record, even in deposits of permineralized or petrified plants. Although several authors had noted the presence of phloem and described the cellular preservation earlier, Donald Eggert was the first to do detailed and modern studies on this tissue and to describe primary versus secondary phloem. Eggert, along with his students, published only three papers on the subject, one each on lycopsid, sphenophyte, and calamite phloem, but he inspired other researchers to take a closer look at phloem in fossil plants, especially in seed plants, and showed that it is possible to infer physiology based on the anatomy of the cells and tissue. His work on the root phloem of the calamite, *Astromyelon* (with Marion L. Wilson), remains one of the few known examples of secondary phloem produced by a vascular cambium in a pteridophyte and as such, raises interesting questions about the growth and development of these extinct plants. Following Eggert's work in the mid to late 1970s, other researchers have detailed phloem in fossil plants, beginning with Middle Devonian progymnosperms and extending to Cretaceous conifers and benettitaleans. In the secondary phloem, it appears that the basic cell types and cellular arrangements found in extant seed plants were established early. The bifacial cambium and secondary phloem constructed of sieve cells, phloem parenchyma, and fibers first appear in the aneurophytalean progymnosperms. In the Paleozoic pteridosperms, the same cell types occur, and some examples exhibit repeating tangential rows of alternating cell types, as seen in some modern conifers. Overall, secondary phloem in seed plants appears to be a remarkably conservative tissue through time, perhaps related to the exacting physiological requirements of phloem loading, unloading, and transport.

University Of Kansas, Department Of Ecology & Evolutionary Biology, 1200 Sunnyside Ave., Lawrence, KS, 66045, USA

### The contributions of the fossil record to understanding the evolution of morphological and functional innovations in the seed plant microgametophyte

The latter half of the 20<sup>th</sup> century witnessed the rise of scientists that began shifting the intellectual center of paleobotany from primarily a taxonomic inventory of the fossil record that provided data on the polarity and evolution of various plant characteristics and taxa, to a discipline that increasingly became concerned with the paleobiology of fossil taxa. Don Eggert was one of the early scientists that began to transition to the new paradigm. His contributions not only explored new methods, but new questions that inspired contemporaries to not only draw on comparative morphological data, but explore and extract data from disciplines that were traditionally thought to be restricted to the study of extant plants, e.g., development. In this presentation the innovations of Don Eggert's contributions to paleobiological questions is reviewed. A survey of the important evolutionary changes in the seed plant microgametophyte are discussed, i.e., the spore / pollen transition and its bearing on our understanding of subsequent changes in polarity and aperture formation and function, functional significance of the spore / pollen wall, morphological changes of the microgametophyte related to reproductive biology, pollination biology and ultimately to the evolution of higher seed plants.

East Tennessee State University, Biological Sciences, Box 70703, Johnson City, TN, 37614-1710, USA

### Rooting the Paleozoic's largest trees; morphology, development, and homologies of *Stigmaria*

The morphogenus *Stigmaria* Brongniart is probably the most ubiquitous and extensively studied of all late Paleozoic wetland plant fossils. *Stigmaria* has long been regarded as the well-understood rooting system of arborescent lycopsids; yet, in the 1960s Don Eggert embarked on a detailed reexamination and reevaluation of the structure, development, homologies, and biological affinities of this magnificent fossil. Eggert's studies and the subsequent studies they spawned have fundamentally altered perceptions of the first giant forest trees, of the homologies for organs of the quillwort *Isoetes*, and of the evolution of polar auxin regulation for the development of plant rooting systems. This presentation emphasizes the unique insights Eggert brought to this research agenda, the numerous advancements in understanding of Carboniferous wetland vegetation that they simulated, and recent studies that have brought together plant molecular biology and plant paleontology to develop a much deeper understanding of land plant evolution and phylogeny.

Ohio University, Department of Environmental and Plant Biology, Athens, OH, 45701, USA

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## Plant reproductive strategies under environmental stress

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Sponsored by Ecological Section and Genetics Section.

74    **SESHADRI, ARATHI<sup>\*1</sup> and  
MOLANO-FLORES, BRENDA<sup>2</sup>**

### Plant reproductive strategies under environmental stress

With increasing evidence for wide ranging changes in climatic conditions, evolutionary responses of plant sexual reproduction can have wide spread implications on population changes and food production. We aim to bring together researchers addressing different aspects of plant reproductive strategies and thus provide a synthesis of current research. It has become increasingly evident that global climate change is bound to have large impacts on many biological processes. Changes in phenotypic traits of different plant species strongly suggest that natural populations are responding to these altered environmental conditions. The sexual phase of plant reproduction, a particularly vulnerable developmental process, under active selection offers the unique potential to understand the role of environmental stress in the adaptive processes that modulate plant reproduction. While sexual strategies in flowering plants are diverse and a majority of plants are hermaphrodites, the extent and manifestation of reproductive functions differs based on sexuality, breeding systems and life histories. Understanding the impacts of climate change on the evolutionary potential of plant populations is the need of the hour especially given the fact that a successful food production from agricultural crops depends on successful functioning of plant reproduction. In this symposium, we aim to bring together diverse researchers to present their current research and share ideas on consequences of environmental stress on plant reproductive strategies.

<sup>1</sup>Colorado State University, Biology, 1878 Biology, Fort Collins, Colorado, 80523, USA <sup>2</sup>ILLINOIS NATURAL HISTORY SURVEY, CENTER FOR WILDLIFE AND PLANT ECOLOGY, 1816 South Oak Street, CHAMPAIGN, IL, 61820-6970, USA

75    **SESHADRI, ARATHI<sup>\*</sup> and MUDD,  
SAMUEL J**

### A comparison of reproductive responses in plants growing under varying levels of temperature and water availability

Unprecedented climatic changes over the last decade have resulted in plant species experiencing large variations in atmospheric CO<sub>2</sub> levels, average temperatures and precipitation patterns. These variables are described as environmental stresses and plants experi-

encing such stressful conditions exhibit altered vegetative and reproductive traits either as plastic responses or genetic changes or both. Knowledge of stress-mediated responses, role of selection in the prevailing conditions and possible epigenetic changes can provide important insights into plant evolutionary potential. Increase in selfing is seen in plants adapting to changing environments with the predominant mechanism being a variation in floral traits facilitating autonomous selfing. Inbreeding depression, an associated cost of increased selfing can vary with stress and the nature of interaction between stress and inbreeding depression is not entirely resolved. Focusing on plasticity in the expression of floral traits facilitating selfing, we aim to understand the modulation of reproductive strategies and patterns of inheritance under varying levels of temperature and water-availability. Using greenhouse populations of *Collinsia heterophylla*, a hermaphroditic annual, we compared flower size, herkogamy and autonomous selfing success in experimental plants. While the onset of flowering and peak flowering duration are different under temperature and water stress, nature of variation in flower size is similar for both variables. Only temperature stress resulted in a significant reduction in herkogamy but autonomous selfing was higher in both temperature and drought stressed plants indicating that the floral trait known to be correlated with autonomous selfing success varies with the kind of stress. In conclusion, our results indicate that acclimation to temperature and water stress elicits differential responses in plants. Further analyses will explore the interaction between stress types and levels. Implications of our findings in relation to adaptation by increased selfing and inbreeding depression under stress will be discussed.

Colorado State University, Biology, 1878 Biology, Fort Collins, Colorado, 80523, USA

76    **MAZER, SUSAN<sup>\*1</sup>, DUDLEY,  
LEAH<sup>1</sup>, HOVE, ALISA<sup>1</sup>, EMMS, SIMON<sup>2</sup> and  
VERHOEVEN, AMY<sup>2</sup>**

### The evolution of mating system, life history, and physiology in *Clarkia*: does selection for drought-avoidance drive the evolution of selfing?

Plant mating systems are highly evolutionarily labile; in the wildflower genus *Clarkia*, for example, the shift between outcrossing and self-fertilization has occurred > 12 times among <40 taxa. In addition to exhibiting lower pollen:ovule ratios and smaller flowers, regularly selfing *Clarkia* taxa flower earlier and have faster floral development rates than their outcrossing counterparts. The most common explanations for the evolution of selfing focus on its *direct* advantages. For example, selection may favor selfing where pollinators are scarce or unreliable; where plants with large, attractive flowers are at risk of desiccation or herbivory; or

where short growing seasons require rapid reproduction (which is promoted by selfing). But selfing could also evolve as a "by-product" of selection on correlated traits, even if there is no direct advantage to selfing. Currently, we're investigating genetic correlations between flowering date and traits that influence mating system (e.g., the degree of herkogamy and dichogamy). If these correlations are sufficiently strong (e.g., if early flowering is associated with rapidly developing flowers with low herkogamy and dichogamy), then selfing may evolve in *Clarkia* not (only) because of its direct advantages, but as a correlated response to selection favoring earlier flowering (e.g., where the growing season is short). If this is generally the case, then adaptation of annual spring wildflowers to earlier or unpredictable summer drought could involve a rapid increase in selfing rates (and inbreeding depression), potentially reducing their adaptive potential. We're also examining whether the shorter life span of selfing *Clarkia* is reflected in their physiological performance. Selfing taxa appear to achieve their earlier flowering through faster photosynthetic rates, but this comes with higher rates of evapotranspiration. Consequently, the evolution of selfing may assume both *physiological as well as genetic risks*, and therefore be restricted to certain habitats or environmental conditions.

<sup>1</sup>University of California, Santa Barbara, Ecology, Evolution & Marine Biology, University of California, Santa Barbara, Life Sciences Building, Santa Barbara, CA, 93106, USA<sup>2</sup>University of St. Thomas, Biology Department, Saint Paul, Minnesota, 55105, USA

77 CARUSO, CHRISTINA<sup>\*1</sup>, CASE, ANDREA<sup>2</sup> and BAILEY, MAIA<sup>3</sup>

### Why do *Lobelia* females like it hot? Potential effects of environmental stress on the expression of male sterility

In many gynodioecious species, high temperature and/or low precipitation are correlated with higher ratios of female to hermaphrodite plants within populations. If sex is determined by both nuclear and cytoplasmic genes, then these environmental stressors can affect the relative fitness of the sexes via two mechanisms. First, stress may increase seed production of females relative to hermaphrodites (reproductive compensation). Second, stress may reduce the relative pollen or seed fitness of hermaphrodites that carry more male fertility restorer alleles (cost of restoration). Although models suggest that the cost of male fertility restoration is the key determinant of variation in population sex ratios, much more is known about the effect of environmental stressors on compensation than on cost. *Lobelia siphilitica* is an excellent system for studying the effects of environmental stressors on population sex ratios for two reasons. First, females are more common in sites with higher annual mean temperatures. This correlation suggests that temperature affects the relative fitness of female and hermaphrodite *L. siphilitica*. Second, *L. siphilitica* is one

of the few gynodioecious species where there is evidence for a cost of restoring male fertility. Hermaphrodite *L. siphilitica* that carry more nuclear male fertility restorer alleles have lower pollen viability. This reduction in pollen fitness should limit the spread of restorer alleles and thus increase the frequency of *L. siphilitica* females.

We develop the hypothesis that annual mean temperature and female frequency are correlated in *L. siphilitica* because of genotype-by-environment effects on the cost of restoration. We predict that restorer alleles will have a larger negative effect on pollen viability when *L. siphilitica* is growing at higher temperatures. Such genotype by environment interactions could result in *L. siphilitica* populations becoming more female-biased in response to increasing global temperatures. More generally, we suggest that understanding the ecology and genetics of the cost of male fertility restoration is key for predicting the effects of environmental stress on reproductive strategies of gynodioecious species.

<sup>1</sup>University Of Guelph, Department Of Integrative Biology, New Science Complex, 50 Stone Road East, GUELPH, ON, N1G 2W1, Canada<sup>2</sup>Kent State University, Box 5190, 256 Cunningham Hall, Kent, OH, 44242-0001, USA<sup>3</sup>Providence College, Department of Biology, 1 Cunningham Square, Providence, RI, 02918, USA

78 SIMONS, ANDREW

### Life-history evolution under changing environments

Environmental change can lead to extinction of previously well-adapted organisms. Adaptive tracking and phenotypic plasticity are well studied modes of response to changing environments. The evolution of risk averse, "bet-hedging" strategies is often overlooked, but may also be an important mode of response. In a review of empirical evidence for bet hedging, I find that the taxonomic distribution in over 100 studies of bet hedging suggests their ubiquity, yet the empirical evidence tends to be weak. I report on two empirical tests of bet hedging from my lab. First, in a five-year study of *Lobelia inflata* (Campanulaceae), we find the magnitude of fluctuating selection acting on the timing of seed germination to be sufficient to explain the degree of bet-hedging diversification behavior characteristic of individuals of this species. Second, we borrow a fungal model organism (*Neurospora crassa*) to test Cohen's classic 1966 model of seed dormancy as bet hedging. We allow ascospore dormancy fraction to evolve under five selection regimes that differ in the frequency of 'bad' years. Dormancy fraction evolved in proportion to the frequency of bad years, a result consistent with Cohen's predictions. Differential survival through environmental change may thus be mitigated by the evolution of bet hedging, and further knowledge of the prevalence of bet hedging in nature is needed.

Carleton University, Department of Biology, Nesbitt 209, 1125 Colonel By Drive, Ottawa, ON, K1S 5B6, Canada

79 SHERRY, REBECCA

### Response of flowering phenology and duration of reproduction to warming and soil moisture in a tallgrass prairie

Warming typically advances spring flowering and been reported to delay later summer flowering. Here phenological responses of 12 species in a 1 year step warming and double precipitation experiment were examined the year following the treatment year. Changes in phenology due to the previous year's warming were in the opposite direction to those observed during the treatment year. Six species responded to warming in 2004, delaying flowering 6.2 days and fruiting 7.9 days. Unlike 2003, no species advanced flowering phenology in 2004. Delays resulted from a soil moisture deficit in formerly warmed plots that lasted 3 months or more after warming ended. Increased precipitation altered phenology in one species but did not affect duration of reproductive phases. While 10 of 11 responsive species entered bud phase earlier under warming than in controls in 2003, in only 2 species showed a phenological delay at the beginning of the bud phase in 2004. Warming tended to shorten flowering and fruiting stages and total duration in spring annuals. Together, these results suggest that climate anomalies can influence plant reproductive phenology in the following year; here due to a lag in soil moisture recharge.

University of Oklahoma, Botany & Microbiology, 770 Van Vleet Oval, Rm. 136, Norman, OK, 73019, United States of America

80 CULLEY, THERESA

### Differential expression of chasmogamy and cleistogamy in light-limited environments

As sedentary organisms, plants must respond quickly and adapt to changing environments in order to survive. One of the best known examples of such adaptation is the chasmogamous/cleistogamous breeding system in which both open, showy chasmogamous (CH) flowers and closed, self-pollinated cleistogamous (CL) flowers are produced on the same individual. This occurs largely in response to changing resource levels that vary either temporally or spatially. For example, many species of *Viola* begin to flower in the early spring in response to warming soil temperature and/or increasing day length. CH flowers are produced first before tree leaf-out when light levels are high and insect pollinators are most frequent; CL flowers subsequently appear only after the forest canopy forms when light levels and pollinator activity dramatically decline. Because of this dependence of flowering on environmental variation, changes in availability of a resource such as light can shift relative windows of CH and CL flower production, thereby indirectly impacting the mating system (i.e. relative rates of outcrossing and outcross-

ing). This may lead to changes in the genetic composition and structure of populations over time, potentially impacting the evolutionary ability of populations to continue to adapt to environmental changes. Given the ability of global climate change to promote shifts in early flowering of temperate forest herbs as well impacts on insect activity, it is likely that differential expression and reproductive output of CH and CL will be changed as well. This presentation will emphasize the importance of considering not only shifts in flowering in response to global climate change and environmental stress, but also the finer-scale effects such actions may have on the mating system and population genetic structure of plant species around the world.

University Of Cincinnati, Department Of Biological Sciences, 614 Rieveschl Hall, Cincinnati, OH, 45221-0006, USA

81 MOLANO-FLORES, BRENDA

### Abiotic factors contributing to the breakdown of self-incompatibility

Self-incompatibility encourages outcrossing by preventing self-fertilization. In a self-incompatible plant, if pollen from the same plant or a similar genotype reaches the stigma, pollen tube germination (sporophytic) or growth (gametophytic) will be stopped along the pistil and fertilization of the ovule will not occur. Nearly half of all flowering plants utilize self-incompatibility as a strategy to force outcrossing. However, many natural populations show variation in the strength of the expression of self-incompatibility as the result of environmental conditions or physiological changes. In addition, self-incompatibility can be overcome by abiotic factors. The main goal of this presentation is to provide a review of the abiotic factors that can breakdown self-incompatibility and the techniques that can be employed to artificially induce self-compatibility. Particular emphasis will be placed on the use of carbon dioxide and temperature. Several case studies will be presented from agricultural and native systems to demonstrate the physical location, chemical reactions and genetic variation associated with the breakdown of self-incompatibility. In addition, a case will be made for why some of these abiotic factors (temperature and carbon dioxide) can no longer be ignored in natural populations of species with self-incompatibility. As carbon dioxide levels and temperatures increase due to global warming, could we see an increase in the switch from self-incompatibility to self-compatibility among natural populations? How will this change affect outcrossing rate, inbreeding depression and reproductive assurance? Could this lead to changes in plant species composition of communities? Although in the laboratory an abiotic factor can be used to breakdown self-incompatibility, in their natural habitat plants are exposed simultaneously to multiple abiotic factors making the interactive effect of these factors even more complex.

University of Illinois, Illinois Natural History Survey, 1816 S. Oak St., Champaign, IL, 61820, USA

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## Advances in Plant Systematics and Population Genomics: Applications of Next Generation Techniques

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Sponsored by Ecological Section and Genetics Section.

**82 UDALL, JOSHUA\*<sup>1</sup>, BAJGAIN, PRABIN<sup>1</sup> and RICHARDSON, BRYCE<sup>2</sup>**

### Natural sequence diversity of *Artemisia tridentata* in the western United States

**A**rtemisia tridentata (big sagebrush) is one of the most widely distributed and ecologically important shrub species in western Northern America. This species serves as a critical habitat and food resource for many animals and invertebrates. Habitat loss due to disturbances, usually wildfire, followed by establishment of invasive plant species is a serious threat to big sagebrush ecosystem sustainability. Taxonomic relationships within this species remain in question. Based on morphological, ploidy and chemical tests, big sagebrush is divided into three widespread subspecies. However, previous studies have shown that hybridization could be common and distinguishing subspecies based on the characters mentioned above can be problematic. Using 454 sequencing, we recently generated the first set ESTs for this species. Partial gene sequences (~360 bp) from 48 genes were targeted for re-sequencing from individuals across the range of big sagebrush (~350 individuals, 11 western states). Amplicons were generated using Fluidigm AccessArray and they were sequenced using 454. Based on these sequences, we present insight into the underlying phylogeographic and population genetic structure of big sagebrush.

<sup>1</sup>Brigham Young University, Plant and Animal Science Dept, 292 Widstoe Building, Provo, UT, 84602, USA<sup>2</sup>USDA Forest Service, Rocky Mountain Research Station, 735 North 500 East, Provo, Utah, 84606, USA

**83 SCHLUETER, JESSICA\*<sup>1</sup>, SAFARI, SAJEDEH<sup>1</sup>, BEINE, JAIME<sup>1</sup>, WHALEY, ADAM<sup>1</sup>, BURKEY, KENT<sup>2</sup> and CARTER, THOMAS<sup>2</sup>**

### Determining molecular responses to environmental change in soybeans

**A**s the global climate changes, plants will be challenged by environmental stresses that are more extreme and more frequent. The average yield loss due to environmental stresses is currently estimated to be more than 50% for major crop species and is the major limitation to world food production. The discovery of resistance to environmental stresses has been hampered by the complexity of these traits as well as the difficulty in measurement of the plant responses. Recent stud-

ies have identified a small family of soybean genotypes from a breeding program in Fiskeby, Sweden, that are resistant or partially resistant to atmospheric ozone pollution as well as other environmental stress conditions. Ozone pollution is often perceived as an urban issue, but the problem is actually regional and includes many agricultural areas. Ozone has been shown to reduce growth and yield in many crops and soybean is known to be an ozone sensitive species Utilizing Illumina RNA-seq we have surveyed both resistant, Fiskeby III, and susceptible, Mandarin (Ottawa), varieties under both control (low) and high ozone conditions.

<sup>1</sup>University of North Carolina at Charlotte, Bioinformatics and Genomics, Bioinformatics 261, 9201 University City Blvd, Charlotte, NC, 28223, USA<sup>2</sup>United States Department of Agriculture, Agricultural Research Service, 3127 Ligon St, Raleigh, NC, 27607, USA

**84 BARKER, MICHAEL S.**

### Old problems, new solutions, and some obstacles for next-generation plant evolutionary biology

**N**ext-generation sequencing has created unprecedented opportunities for the study of plant evolution. Relatively rapid and inexpensive access to genome-scale data has created new opportunities for studying the evolutionary history of plants. Although next-generation technologies have presented new solutions to old problems, there are a number of new obstacles, especially limitations of current next-generation sequencing and bioinformatic analyses of existing data. I will present recent bioinformatic advances in the analysis of gene duplications, polyploidy, and hybridization and compare how well competing technologies perform under these algorithms. In particular, I will provide an overview of the pros and cons of two predominant next-generation sequencing technologies, 454 and Illumina, as well as a first look at the "post-light" sequencing technology from Ion Torrent. Finally, I will outline the significant challenges associated with next-generation plant evolutionary biology and identify potential directions for overcoming these remaining obstacles.

University of Arizona, Ecology & Evolutionary Biology, P.O. Box 210088, Tucson, AZ, 85721, USA

**85 KANE, NOLAN C\*, GRASSA, CHRIS, ANDREW, ROSE, RENAUT, SEBASTIEN and RIESEBERG, LOREN**

### Genetic underpinnings of divergence and adaptation in *Helianthus*

**N**umerous taxa remain morphologically distinct in the face of hybridization with other species. It is often assumed that gene flow from other species only affects a small proportion of the genome, but recent work suggests that reproductive barriers may be quite porous,

allowing some gene flow over much of the genome. We have used high resolution genomic scans to estimate locus-specific and genome-wide effective migration rates and levels of differentiation for multiple pairs of sunflower taxa that vary in divergence time, strength of reproductive isolation and degree of geographically separation. We show that genomic regions of differentiation are small, only exceeding a handful of genes in a few areas of low recombination. While these scans can identify possible "speciation genes" under strong divergent selection, these loci appear to affect gene flow at only very localized regions of the genome.

University Of British Columbia, Department Of Botany, 6270 University Blvd, Vancouver, BC, V6T 1Z4, Canada

**86 EGAN, ASHLEY N<sup>\*1</sup>, SCHLUETER, JESSICA<sup>2</sup> and DOYLE, JEFF<sup>3</sup>**

### Comparative genomics of phaseoloid legumes: what 454 transcriptomics can tell us about phylogeny

The legume family (Leguminosae; Fabaceae) is one of the most diverse plant families on earth, having ~18,000 species. The phaseoloid group contains many economically important species such as the cultivated soybean (*Glycine max*; a polyploid) and Kudzu (*Pueraria montana*; a highly invasive species in the U.S.). Polyploidy (whole genome duplication) has played an important role in the diversification of legumes, both anciently and in the more recent evolutionary past. Polyploidy events are easily inferred from doubled (or multiplicative) base chromosome numbers of species relative to related evolutionary lineages. However, ancient polyploidy may go unnoticed due to reduction in chromosome number (diploidization), making ancient polyploidy cryptic. To assess the prevalence of polyploidy in phaseoloid legume evolution, we sequenced the transcriptomes of several species using Roche 454 pyrosequencing. We examined signatures of polyploidy by creating a distribution of synonymous substitutions across duplicated gene pairs within each genome. Using the soybean genome and cDNA database as a reference, we compare ancient signatures of polyploidy across species to obtain a robust estimate of the time of ancient polyploidization within legumes. We discuss the pros and cons of using next-gen sequencing for Ks estimation and compare outcomes with other estimates of polyploidy in the soybean genome using Expressed Sequence Tags (ESTs). In addition, we present a phylogenomic hypothesis of phaseoloid relationships using orthologous genes culled from transcriptome data.

<sup>1</sup>East Carolina University, Biology, Howell Science Complex N303a, Mailstop 551, Greenville, NC, 27858, USA<sup>2</sup>University of North Carolina - Charlotte, Bioinformatics and Genomics, 9201 University City Blvd , Bioinformatics Building 261 , Charlotte, NC, 28223, USA<sup>3</sup>Cornell University, 412 Mann Library Building, ITHACA, NY, 14853-4301, USA

**87 CRONN, RICHARD<sup>\*1</sup>, KNAUS, BRIAN<sup>1</sup>, LISTON, AARON<sup>2</sup>, MAUGHAN, JEFF<sup>3</sup>, PARKS, MATTHEW<sup>4</sup>, SYRING, JOHN<sup>5</sup> and UDALL, JOSHUA<sup>6</sup>**

### Simplifying the complex: Targeted sequencing strategies for population, phylogenetic, and genomic studies in plants

The recent and dramatic advances offered by modern DNA sequencers annually re-define the amount of sequence data that can be gathered for comparative genetic analysis. Even with the achievements in sequencing to date, plant genomes present formidable obstacles that can make it difficult to execute large-scale population and evolutionary genetic studies. Many factors - wide genome size variation (from ~100 Mbp to well over 100Gbp), extensive variation in the contribution of organellar DNA to total DNA, polyploidy, and gene number/redundancy - contribute to these challenges, and they demand powerful and customizable genome reduction strategies to achieve the desired goals.

In this talk, we summarize the many available genome reduction strategies that can be used to target partial-to-complete organelle genomes, and known and anonymous nuclear targets. These methods fall under four general categories; PCR-based enrichment, hybridization-based enrichment, restriction enzyme-based enrichment, and physical enrichment of sub-genomic partitions. Central to all methods is multiplex DNA sequencing, a process that enables simultaneous sequencing of multiple target pools. We provide examples of how these strategies have been successfully used in three specific applications: (1) enriching and sequencing partial-to-complete chloroplast genomes for phylogenetic analysis; (2) enriching and sequencing nuclear loci to identify population- and taxon-specific polymorphism; and (3) enriching transcriptomes for gene discovery, polymorphism identification, and gene expression analysis. While the benefits of targeted sequencing are greatest in plants with large genomes, most comparative projects can benefit from the improved throughput offered by targeted multiplex DNA sequencing, particularly as the amount of data produced from a single instrument far exceeds 100 billion bases per run.

<sup>1</sup>USDA Forest Service, 3200 SW Jefferson Way, Corvallis, OR, 97330, USA<sup>2</sup>Oregon State University, Department Of Botany & Plant Pathology, 2082 Cordley Hall, Corvallis, OR, 97331-2902, USA<sup>3</sup>Brigham Young University, Plant and Wildlife Science Dept, 285 Widstoe Building, Provo, UT, 84602<sup>4</sup>Oregon State University, Department of Botany & Plant Pathology, Cordley Hall, Corvallis, OR, 97331-2092, USA<sup>5</sup>Linfield College, 900 SE Baker St, McMinnville, OR, 97128, USA<sup>6</sup>Brigham Young University, Plant and Wildlife Science Dept, 292 Widstoe Building, Provo, UT, 84602, USA

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Strategies for healing our coast lines: Deepwater Horizon oil spill in the Gulf of Mexico, erosion and urban degradation: progress for the North American future marine macro-plants

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*Sponsored by Physiological Section.*

88 THORHAUG, ANITRA\*<sup>1</sup> and COONS, JANICE<sup>2</sup>

**Healing the Biodiversity of Dominant Plants of the Atlantic, Gulf of Mexico, and the Greater Caribbean Coastlines after Industrial pollutants and Development Degradation.**

During many centuries, man's activities have claimed large quantities of biodiversity of Atlantic and Gulf of Mexico estuaries: dredge and fill, salinity diversion, sewerage effluents, and industrial outflows. About 13% of the sea's surface area contains sites of the highest global biodiversity: he estuaries and nearshore. This is one of the least understood botanically in the array of global ecosystem resources, and is full of complexity while difficult to access. The eco-physiology of marine macro-plants and their restoration principles are just beginning to be elucidated. A great deal of the intense oceanic productivity is immediately next to shore where the terrestrial nutrients from riverine systems plus shallow waters allows light penetration to relatively the shallow bottoms creating enormous productivity. At the intersection between these two massive ecosystems, the Mississippi Delta and the upper reaches of the Western Hemisphere's largest inland sea, the Gulf of Mexico . Here the estuary of one of the world's largest rivers, draining toxins from 38 states reaches the low energy end of the Gulf of Mexico. We will discuss: 1.) Examples of successful restoration of the dominant coastal plant species under difficult situations with contamination still present is occurring; 2.) Knowledge of physiological responses of coastal macro-plants to oil, and to dispersed oil and other ongoing pollutants must be gathered and analyzed; and 3.) Past examples of coastal vegetative ecosystems coming in contact with large-scale oil spills especially in the Gulf of Mexico and Caribbean (Ixtoc, Yum, Panama).

<sup>1</sup>Yale University, School of Forestry and Environmental Sciences, 359 Prospect St., New Haven , Ct. , 06901, USA<sup>2</sup>Eastern Illinois University, Biological Sciences, 600 Lincoln Ave, Charleston, IL, 61920, USA

89 ZEDLER, JOY\*<sup>1</sup> and DOHERTY, JAMES<sup>2</sup>

**Major restoration efforts are healing biodiversity in Californian coastal marshes**

Despite the historical loss of 90% of California's coastal marsh area, and despite recent challenges (including extreme flooding, sea storms, and a "homeland security fence" at the US-Mexico border), stakeholders are sustaining Tijuana Estuary and much of its plant and animal diversity. Despite budgetary constraints, The State Coastal Conservancy and others have funded restoration planning and implementation; a non-governmental organization (Southwest Wetlands Interpretive Association) has engaged local citizens; and education and research coordinators at the National Estuarine Research Reserve helped K-12 and university students study and learn about biodiversity conservation. During 30 years of vegetation monitoring, Tijuana Estuary's 400-ha salt marsh lost its historical diversity in 1984, when the mouth closed and an 8-month drought eliminated stream flow. Soils became dry and extremely hypersaline, and two short-lived species (*Salicornia bigelovii*, *Suaeda esteroa*) were greatly reduced in distribution--but not extirpated. Once tidal influence was restored, all but the short-lived species regained their historical distributions. In 1997 a field experiment began to link changes in diversity to ecosystem services. Replicate plots on an excavated marsh plain were planted with 0, 1, 3, and 6 native species. After 2 growing seasons, indicators of the salt marsh's ability to support biodiversity (biomass, height, canopy layering, resistance to invasion) were positively correlated with the number of species planted. By 2009, however, those services were mostly provided by *Salicornia virginica*, *Jaumea carnosa* and *Frankenia salina*. Nevertheless, additional research demonstrated that each of the eight marsh-plain halophytes makes a unique contribution to salt marsh functioning. All are likely necessary for resilience in the face of major disturbances (e.g., rapidly rising sea level or catastrophic flooding). Episodes of sedimentation tend to promote dominance at the expense of diversity, but armed with such knowledge, managers can restore and maintain biodiversity in Californian salt marshes.

<sup>1</sup>University Of Wisconsin, Botany, 430 Lincoln Drive, Madison, WI, 53706, USA<sup>2</sup>University of Wisconsin, Department of Botany, 312 Birge Hall, 430 Lincoln Drive, Madsion , WI, 53706 - 1381, USA

90 TEAS, HOWARD<sup>1</sup>, THORHAUG,  
ANITRA<sup>2</sup> and COONS, JANICE\*<sup>3</sup>

### Healing Mangrove Biodiversity: oil spills, dispersants and mangrove restoration

One of the highest marine shoreline biodiversities and productivities, and also a source of very high sequestered carbon in the world's marine and estuarine tropics and subtropics is from mangroves, a group of higher plants from a variety of evolutionary pathways adapted to high salt tolerance, some of which grow directly in the intertidal marine zone, others of which grow upland in areas of salt intrusion and spray. The problem of mangrove tolerance to a variety of anthropogenic substances has been studied intensively. Oil and dispersed oil particularly has been tested on seedlings and adults resulting in the fact that a series of dispersants can alleviate massive mortality of mangroves if placed onto fresh oil sheen prior to petroleum entering a mangrove forest. If the oil sheen reaches the mangroves on low tidal cycle, then permeates to the roots, the mortality is far higher. The Panama spill and Ixtoc in the Greater Caribbean Sea are examples of this in the field as are other spill results also indicating mortality when sediments are permeated by oil. Restoration of mangroves has been carried out extensively in the Gulf of México and Caribbean including South Florida by Teas and others. The restoration on a variety of impacted sites including oiled sediments has also been carried out. The dispersed oil and dispersant alone data from our testing of mangroves vs. dispersed oil, as well as Greater Caribbean Basin spills and their restoration in a variety of anthropogenic situations will be discussed.

<sup>1</sup>University of Miami, Department of Biology, Coral Gables, Fl, 33133, USA<sup>2</sup>Yale University, School of Forestry and Environmental Sciences, 359 Prospect St., New Haven, Ct., 06901, USA<sup>3</sup>Eastern Illinois University, Biological Sciences, 600 Lincoln Ave, Charleston, IL, 61920, USA

91 THORHAUG, ANITRA

### The Subtropical/Tropical USA Seagrasses in Gulf of Mexico and South Atlantic USA Coastal Areas: Healing the biodiversity by Restoration Under a Variety of Pollution sources including Oil, and Dispersed Oil

There are 95,142 ha of seagrass in Texas, plus 1,092,651 ha in Florida, 4,511 ha in Louisiana, 298 ha in Mississippi, and less than 200 ha in Alabama with additional large populations on the USA Atlantic Seacoast from north Carolina to Maine on soft bottoms. This is estimated to be far less than 50% of the pre-World War II seagrass extent so that a large loss of biodiversity has occurred. Additionally, the Caribbean and Gulf of Mexico is one of the most intense petroleum extraction and transport sites in the world, with a large

percentage of the US, Mexican and Venezuelan oil drilling transiting the area along with additional oil transport from the Middle East and oil through the Panama Canal. When seagrasses are restored biodiversity of its ecosystem has been seen by a variety of investigators to reassemble epiphytes, invertebrates, and vertebrates in general. The Gulf of Mexico basin's and Florida projects to heal the biodiversity of damaged seagrass communities, number in the thousands of restored seagrass hectares and are among in the earliest global efforts of seagrass restoration. A discussion of healing biodiversity post-seagrass-restoration in the face of ongoing various pollutants will be presented focusing on *Thalassia testudinum*, *Halodule wrightii*, and *Ruppia maritima* in a particular review of investigations of restoration efforts on the 2010 oil spill species. A second discussion of the investigations of responses of dominant seagrass species *Thalassia testudinum* and *Halodule wrightii* to various oils and dispersed oils in laboratory and field will occur, as well as a discussion of seagrass ecosystem responses to a series of large-scale spills in the Greater Caribbean Basin. The healing of biodiversity of seagrasses in the face of industrial, infrastructure building and diversion of water ( Mississippi and Florida), the urban and agricultural runoff, and point source pollutants from mining, power plants and sewerage is remarkable and will be examined.

Yale University, School of Forestry and Environmental Sciences, 359 Prospect St., New Haven, Ct., 06901, USA

92 SHAFER, DEBORAH

### Using seeds to increase and heal biodiversity in Large-scale submerged aquatic vegetation restoration in the Chesapeake Bay

In 2003, the Chesapeake Bay Program developed a strategy to accelerate the large-scale restoration of seagrasses and other submerged aquatic vegetation (SAV) within Chesapeake Bay, one of the world's largest estuaries. One of their goals involved planting more than 1,000 acres of SAV in order to restoration populations to historic levels. Seeding was determined to be one of the most cost-effective means of planting and restoring large, self-maintaining, genetically diverse SAV beds. However, protocols for the harvest, processing, storage, and subsequent dispersal of seeds of most SAV species were largely non-existent. An interagency research program was launched in 2003 in Maryland and Virginia to develop tools, techniques, and protocols for using seeds in large-scale SAV restoration. We now have protocols available for multiple SAV species, spanning the salinity gradient from polyhaline to oligohaline waters. Costs of planting are on a downward trend as our knowledge and experience increase. The process of developing these protocols for using seeds in SAV restoration should be widely applicable in other regions.

US. Army Corps of Engineers., Engineer Research and Development, 3909 Halls' Ferry Road, Vicksburg, MS, 39108, USA

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## Grab that Research Baton and Teach: Bessey Award Winners

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*Sponsored by Teaching Section.*

93 HAZELWOOD, DONNA\*<sup>1</sup> and BAKER, STOKES<sup>2</sup>

### Scholarship and education pioneers Charles Edwin Bessey, the Bessey Teaching Award and the first awardee, Samuel N Postelthwait

Born in Minton, Ohio, 1 May 1845, Charles Edwin Bessey entered Michigan Agricultural College (MAC) in July 1886. He originally planned to return to Ohio as a civil engineer or surveyor, and had to be persuaded to specialize in botany. After college, his first position was as assistantship at MAC that placed him in charge of the greenhouses, he taught at Iowa State College of Agriculture at Ames, IA, worked with Asa Gray at Harvard, later obtained a Master's Degree from MAC, and was awarded a Ph.D. from the University of Iowa. He taught at and served as Dean of the University of Nebraska Agricultural College and as chancellor of the University of Nebraska Lincoln. Along the way he was invited to share his views on problems in agricultural education and to provide solutions. After lecturing for a year he was well on his way as a power figure in botany and education. Among his many honors, he was a charter member of the BSA and served as the President in 1895. He was elected to the American Association for the Advancement of Science (AAAS) and became its President in 1911. He revolutionized the teaching of botany, and wrote influential text books. The Charles Edwin Bessey Teaching Award, given by the BSA, honors teachers who exhibit outstanding scholarship and commitment to teaching. The first award, in 1989, was to Samuel Noel Postelthwait, who opened the door to multimedia presentations with the "Audio Tutorial Method." The Teaching Section of the BSA is reactivating the Postelthwait award honoring both remarkable scientists and educators.

<sup>1</sup>DAKOTA STATE UNIV, COLL OF ARTS AND SCIENCES, Science Center, 820 N. Washington Ave, MADISON, SD, 57042, USA<sup>2</sup>University of Detroit Mercy, Biology Department, 4001 W. McNichols Rd., Detroit, MI, 48221

94 BROWN, BEVERLY

### Innovation in Education: What would Bessey do?

Charles E. Bessey was an exceptional botanist and teacher. During his life he conducted research on wide-ranging botanical topics. He did so while advocating for direct student engagement with botanical specimens in classes and practical application of botanical knowledge. He took steps to bridge gaps between students and botany by writing the first botanical text book in the United States and implementing the use of teaching laboratories at universities. This is a proud heritage that the Botanical Society of America (BSA) continues to build on. The PlantingScience project has introduced thousands of students to scientist mentors who help teachers immerse students in research experiences in their classrooms and on-line. Just as Bessey provided texts for students, the BSA is also providing resources to teachers and students to support their exploration of botanical questions. The establishment and growth of our on-line teaching resource database makes accurate and engaging botanical information freely available to teachers at every level. Finally, the BSA, primarily through the Education Committee and Teaching Section, works to incorporate research on best practices for teaching into every member's consciousness. These innovations in science education guarantee that Bessey's work lives on and proudly prospers within the BSA and beyond.

Nazareth College Of Rochester, Biology, 4245 East Avenue, ROCHESTER, NY, 14618, USA

95 WANDERSEE, JAMES

### How can botanic gardens help us prevent plant blindness?

Getting a person's attention is not easy these days. Our research studies have previously shown that the general public, especially in first-world nations and in large cities, often exhibits what we have termed *plant blindness*--the failure of people consciously to notice, understand, and value the plants around them. By 2007, the world's urban population exceeded the number of people living in rural areas for the first time in history. Plant blindness is indeed on the increase, in spite of the fact that, as the RBG-Kew reminds us, *all life depends on plants*. Enigmatically, if we cannot turn the urban public's attention to plants, how can our carefully crafted botany education efforts possibly be successful? In contrast to the rather reserved approaches that botanic gardens employ to draw visitors, Hollywood studios use theater marquees worldwide to attract attention to their latest movies. *Marquee* is the name given to the large sign overhanging a theater entrance announcing the current attraction, with bold and colorful text sur-

rounded by bright, flashing lights. At *Botany 2001*, a report by our research group introduced and defined the term *marquee plant* as: 1. A plant species that strongly attracts the public's attention and invites its direct observation; 2. A plant species that, during some or all of its life cycle, is capable of drawing a crowd at a botanic garden; 3. A plant species that may serve as a portal to increasing public understanding of plants. Since then, we have expanded our research-based characterization and knowledge of marquee plants, and have documented the linkages between attracting people's attention to plants and expanding the urban public's understanding of plants.

Louisiana State University, Educational Theory, Policy, and Practice, Graduate Studies in Biology Education, 223 Peabody Hall, Baton Rouge, LA, 70803, USA

### 96 SUNDBERG, MARSHALL

#### Research Methods in Pedagogy

Both qualitative and quantitative assessment strategies have their place in designing and testing pedagogical tools and techniques for improving student learning. Qualitative strategies include focus groups, journals, interviews, concept mapping, textbook annotation, and a variety of short in-class activities such as minute papers and muddiest point writings. Quantitative strategies include pre- and post-tests, surveys, and use of clickers. Examples of successful implementation of many of these strategies will be provided for student active lecture courses, inquiry-based laboratory courses and integrated lecture/laboratory courses.

Emporia State University, Department Of Biological Sciences, 1200 COMMERCIAL, EMPORIA, KS, 66801, USA

### 97 ARMSTRONG, JOSEPH

#### Evaluating learning in the laboratory classroom: portfolios instead of lab reports and quizzes

Quizzes and reports have long been the bane of laboratory teaching. And yet how else do we evaluate learning? In labs with diverse activities and many observations a portfolio can better reflect the material covered and by showing interrelations of materials and observations students can better reflect learning as well. Lab quizzes often produce miserable results, deflating and discouraging to both student and instructor. The portfolio came to the rescue. The digital format of portfolios allows text, data, illustrations, images, still and video, to be meaningfully interrelated and juxtaposed. A simple grocery list of fruits and vegetables shows little learning. Grouping fruits and vegetables into taxonomic and/or type categories shows understanding of basic lessons. Rather than short term memorization, students learn by working with images and diverse materials to assemble

a meaningful portfolio, a practice that generates better long-term learning. Students require guidance and instruction so they understand what shows learning and the evaluation rubric that will be applied is based on this. The portfolio process has several advantages. First, it uses digital technologies and students end up recording more of what they do than via standard reports. Second, the portfolios provide tangible evidence of what they covered and learned, i.e., they have a better educational product at the end, one that they keep for future use. The realization that they are doing this for themselves, for their future use, produces some quite impressive efforts. Third, over all students spend more time working with laboratory materials, and demonstrate good retention of materials covered, good recognition of specimens, and a decent ability to apply the knowledge when needed.

Illinois State University, School of Biological Sciences, Campus Box 4120, Normal, IL, 61790-4120, USA

### 98 MARTINE, CHRISTOPHER

#### Three ways to conduct research at an undergraduate institution, including one way to never publish again

A generation ago, the singular goal of science faculty at many undergraduate institutions was to excel in the classroom while balancing the demands of teaching three to five courses per semester. Recent hires at many undergraduate institutions are encountering a new paradigm, however. That is, one in which teaching loads are the same but the expectations for scholarly productivity are quite different. The new model requires excellence in the classroom and a high level of scholarly productivity - often with a premium placed upon including undergraduates in one's research program. For junior faculty especially, meeting these teacher-scholar expectations is a daunting task. Three examples of research programs at undergraduate institutions are presented as disparate models. Each illustrates a different set of outcomes for both the faculty member and the students involved.

SUNY Plattsburgh, Biological Sciences, 101 Broad Street, Plattsburgh, NY, 12901, USA

### 99 HANGARTER, ROGER

#### The Un-still Life of Plants

As a group, plants are among the slowest forms of life. With their barely perceptible movements, plants merit little notice for most humans. With industrialized agriculture, increasing urbanization, the availability of realistic-looking artificial plants that do not require human interaction, and a world that is moving at an ever-increasing pace, we are becoming further removed from the rhythms of plants. As a consequence, the appreciation of the importance of plants is receding in our collective consciousness to the point that, for many people plants are regarded as little more than ornamental objects. In this presentation, time-lapse technology will be used to demonstrate the remarkable

dynamics of plant life. We will see how keenly aware plants are of their environment throughout their life as they navigate the space around them and respond to the various stimuli they encounter. The sense of intrigue and mystery revealed by time-lapse imaging enhances our own awareness of plant life and, hopefully, provides a deeper appreciation of our relationship to plants and our environment.

Indiana University, Biology, 915 E 3rd St., Bloomington, IN, 47405

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## Education Sharing our Ethnobotany Curriculum: the Open Science Approach

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*Sponsored by Society for Economic Botany.*

**100 BARFIELD, KERI\* and HARRISON, PATRICIA**

### **Sharing Our Ethnobotany Curriculum: The Open Science Approach**

The Open Science Network (OSN) is a National Science Foundation funded project, coordinated by the Botanical Research Institute of Texas. OSN has been leading a worldwide collaboration of ethnobiology educators through the continual exchange and enrichment of educational techniques, materials, and experiences. This Network champions open educational resources and uses the latest web technologies to encourage sharing, generation, and management of educational tools and curriculum for the traditional and non-traditional classroom. Ethnobiological teaching resources have been made openly available by researchers and educators based at the University of Hawaii at Manoa, Frostburg State University, University of South Carolina, University of Arkansas for Medical Sciences, and University of Kent among others.

Botanical Research Institute of Texas, 1700 University Drive, Fort Worth, TX, 76107, USA

**101 DEPASS, ANTHONY**

### **Technology in Biology Education: Shifting Paradigms for Content Access and Dissemination**

The quest for finding more effective ways to teach and learn has meant for most, the incorporation of the newest technologies into the classroom. The increasingly rapid pace of technological advancement has transformed the volume and quality of information that is accessible to faculty and students in and outside of the classroom, and that has redefined the learning environment. Besides impacting teaching, technology has had a major impact on the growth of teachable information, in part due to the faster pace of scientific discovery, and has raised issues as to what should be taught. The vastly inclusive encyclopedic approach has been the basis for a teaching model that has dominated science education for more than a century has grown more impractical. The recent NSF supported report on *Vision and Change in Undergraduate Biology Education: A call to Action*, argues for a focus on core concepts and competencies as a model that will serve to better educate future scientists and an informed citizenry. Its implementation will impact content in the determination of the core concepts that are to be taught to the desired level of critical

understanding. The role of technology, not for its own sake, but to bring inquiry-based pedagogy to the learner will be of significant consideration. However, this brings us back to the question of access. Recent publications have indicated that access may be defined by the way technology is used, and that such use vary significantly between segments of our population. The paradigm for the incorporation of technology in learning, especially at the university level, may potentially serve to deepen disparities and widen gaps in achievement as measured by outcomes that are intimately tied to these newer approaches.

Long Island University, Biology, 1 University Plaza, Brooklyn, NY, 11201, USA

### 102 LEWIS, WALTER

#### **How an Ethnobotanical/Medicinal Course Evolved Forty Years ago at Washington University**

What will be described in this symposium is how a new course so broadly defined could be included as a serious contribution to the Department of Biology curriculum. It took some doing, starting with a short between semester mini-course, and eventually ending up as an upper level undergraduate/graduate course with the largest student enrollment in the department. I will also describe how the course was enhanced each semester by professors from the Schools of Medicine and Dentistry, by five tutorials held weekly for those requiring extra tutoring particularly in botany, chemistry, and medical terminology, and an extra unit for those who wished to attend an informal weekly seminar. All this was enhanced by our first text book, *Medical Botany, Plant Affecting Man's Health* in 1977 and a larger edition in 2003. Field work included one or several day-long trips to surrounding parks and semi-wilderness areas and for a lucky 15 over Easter recess a trip deep into the Amazon basin of Peru for ten days where, for example, each student completed an individually selected project. As time permits other aspects will also be discussed during the symposium.

Washington University In St. Louis, DEPT OF BIOLOGY-BOX 1137, One Brookings Drive, St. Louis, MO, 63130, USA

### 103 MCCLATCHEY, WILL C

#### **Bitter Pills: Lessons Learned While Developing Medical Ethnobotany**

An advanced undergraduate course in medical botany was taught for 12 years using a combination of pharmacognosy and plant diversity content. Students were expected to have strong backgrounds in biology and chemistry with specific training in plant systematics and organic chemistry. As part of an NSF curriculum development project in 2007, the course was redesigned

to focus on ethnobotany and to incorporate modern instructional methods and assessments. In 2008 and 2009 the course was taught using a problem-based learning (PBL) methodology that included nested iterative formative assessments. This method was selected because this course is primarily taken by pre-medical students who go on to attend the University of Hawai'i Medical School which uses PBL as the focus of its training system. Students worked as individuals and in groups with different combinations explored in order to develop practical scientific workskills beyond knowledge of medical ethnobotany. Students reported mixed perspectives about the modified course format. For some the change was very stressful with too much work being expected early in the cycle. Others flourished within the modified environment and appreciated the opportunity to learn how to work within the PBL environment before getting into medical school. Student grades (outcomes) for the course were similar to those earned in prior years, but because the assessments were so different it was not possible to provide a direct comparison. New teaching methods are valuable for engaging students and encouraging them to work with information in ways that they will encounter it within the real world. This process needs to happen as early as possible within the educational system. It appears that students who encounter this later may have a difficult time adjusting to a new reality, but it is likely that the same phenomenon would have happened when they moved from academia into the real world.

Botanical Research Institute of Texas, Research, 1700 N. University Avenue, Fort Worth, TX, 76107, USA

### 104 VOUGIOUKALOU, SOFIA ANTHI

#### **Online resources for open innovation in ethnobotany: towards a more engaged science**

Open innovation is a concept that assumes that organisations can and should collaborate with external ideas and expertise as well as internal ideas to advance research and development and create new opportunities. Importing this idea into higher education, it becomes clear that the use of online resources as collaborative platforms can lead to enriched teaching and learning environments, innovative intra- and inter-university joint working and increase potential access to more diverse sources of funding. Not all knowledge resides within universities, and online resources enable two-way engagement which can improve both the relevance and the impact of university knowledge and expertise. Exploding the notion of the "ivory tower", more permeable boundaries between a higher education institution and its environment enable new innovations to be co-developed and knowledge to be constructively re-contextualised, thus creating mutually beneficial relationships between the university and external parties. In an era where academic research has to demonstrate

its public value and socioeconomic impact, universities do not need to rely entirely on their own resources and produce outputs for an internal audience. Instead, making use of the wide distribution of knowledge online and offline, students and staff can use information from - and produce outputs for - other educational institutions and businesses as well as public, voluntary and community sector organisations. In this way, ethnobotany can transcend the margins of social and natural sciences and demonstrate its relevance and value in providing solutions to contemporary issues of social and environmental importance. The challenges and complexities involved in working across institutional and disciplinary boundaries will be addressed using examples of open innovation in teaching, research and knowledge exchange partnerships with external organisations in two higher education institutions in the UK.

## 105 BROSÌ, SUNSHINE

### **Curriculum Peer-Review and Inter-Institutional Collaboration Assisted by the Open Science Network in Ethnobiology**

Undergraduate degree programs in Ethnobotany are limited in the United States to the University of Hawaii, Manoa, and Frostburg State University in Maryland. However, courses in Ethnobiology can be found within multiple departments at various international institutions. With a few exceptions, ethnobotanists are often geographically isolated from colleagues and potentially stunted in collaboration opportunities when compared to other sub-disciplines within plant biology. The Open Science Network in Ethnobiology (OSN) connects ethnobotany educators in order to increase inter-institutional collaboration and provide opportunities for curriculum development, evaluation, and advancement. Resources which are organized at OSN's website allows instructors to connect concepts in ethnobiology across various geographic boundaries and areas of expertise. For example, courses at Frostburg State University have been enhanced by incorporation of online learning modules from the University of Hawaii. Lectures with specific learning objectives can incorporate examples from throughout the world and incorporate knowledge from diverse colleagues with various backgrounds. Additionally collaboration of faculty within the network includes sharing of syllabi, specific assignments, grading rubrics, and other curricular activities. For example, students in courses at Frostburg State University and Hollins University in Roanoke, Virginia completed annotated bibliographies on various different species to create a more comprehensive database for plants in Appalachian region. Students at Frostburg State University have also developed online learning modules specific to plants and people of the Appalachian region including American ginseng, native

plant dyes, making paper and ink from exotic weeds, and Appalachian dulcimer production. Regional distinctions and global connections will emerge as students and faculty from across the globe develop similar learning modules. In addition, the OSN fosters collaboration which results in peer-review of materials for courses and instructional approaches. This collaboration assists in determining core skills which ethnobiologists need to understand and peer-review of various methods of teaching these skills to students. These resources have been instrumental in developing an open-philosophy in which educators readily share materials in order to advance the discipline.

Frostburg State University, Biology, 101 Braddock Road, Frostburg, MD, 21532, USA

## 106 HUIISH, RYAN DAVID

### **Developing curriculum for improving ethnobiology education and field research through collaborative resource pooling**

Ethnobiology today is a synergetic combination of sciences that is drawing the interest of an increasing number of students. Field research in ethnobiology is an invaluable way to teach and experience this multifaceted science first hand. However, the intensive, interdisciplinary, and intercultural nature of field research presents various unique challenges and generally requires significant training and preparation that begins months before in classroom and laboratory settings. Development of rigorous curriculum addressing such specifics as the acquisition of international research and specimen collection permits, institutional review board proposals unique to ethnobiological concepts, intellectual property rights, reciprocity and so forth, all within complex cultural contexts is vital for successful research, but difficult to develop and maintain. The Open Science Network is a powerful platform facilitating educational resource pooling. In conjunction, the use of online professional networking software, such as Zotero, has proven useful in overcoming the difficulties of creating resource libraries specific to topics and projects across disciplines and between universities. Such an online forum for resources is easy to search and export into lesson plans, is more frequently updated than a textbook, and is a direct, interactive resource for students. The open forum and inclusion of colleague and student feedback further promotes the continued accuracy and utility of resources. Examples from course work and field experience will further address challenges faced by educators and highlight how collaborations in curriculum development will better prepare students to make future contributions to this evolving discipline.

Hollins University, Biology, 7916 Williamson Rd., Roanoke, VA, 24020, USA

## 107 PRETTYPAINT-SMALL, VALERIE

**Research Agendas on Native American Reservations: Who Should be in the Drivers Seat and Why Its Important**

Tribal colleges continue to lead their respective communities into the 21<sup>st</sup> century by developing a science and technology curriculum that incorporates cultural values and their respective native languages. Despite efforts to assimilate Native Americans into non-Indian society, most tribes within the US have, and continue to assert their rights of sovereignty over cultural resources and indigenous knowledge. However, the unfortunate history of research scientists conducting studies without benefit to the community have spurred tribal colleges to lead the way in securing intellectual rights to said knowledge. Given the financial benefits to universities by way of federal funding to conduct research on indigenous issues, university-led research has often led to self-serving or individualistic topics that provide no real-world benefit to the community within which they study. Furthermore, many federally funded research fellowships and internships require tribal college students to leave their respective reservations, rather than working with tribal colleges and their respective communities to help solve real-world contemporary native issues. Universities can help to provide resources that are often lacking at tribal colleges due to budget shortfalls and a history of underfunding native students. These studies, however must be driven by the needs of the communities within which they serve and tribal colleges should be at the forefront to control the research process, rather than universities and non-Indian students forcing their own research agendas.

Colorado State University, Weed Sciences , Plant Sciences Building, Fort Collins, CO, 80523, USA

## 108 CAIN, SHAWNA\* and CAIN, ROGER

**The Cherokee Native & Art Plant Society**

The Cherokee Native & Art Plant Society (CNAPS) is a self-organized, tribal community not-for-profit organization. Incorporated in 2008, CNAPS was set into motion by Cherokee National Treasures for the purpose of teaching and learning traditional arts and ecological practices that depend upon one another. The mission of CNAPS is "To Support and Promote Cherokee Elders, Traditions, Artistic Expressions and Natural Environments." CNAPS focuses upon the Cherokee lens where Cherokee National Treasure Elders are viewed as experts in the field of Traditional Ecological Knowledge, often aware of the subtle nuances required to successfully carry on Cherokee ecological traditions to future generations. Cherokee National Treasures play an integral role as "tradition keepers" and individuals distinguished by

Cherokee Nation as artists who demonstrate traditional skills and knowledge intertwined with the natural environment, especially those who continue to keep these traditions alive. As a grass-roots organization, CNAPS works with tribal entities, public/private schools, universities, colleges and tribal community organizations to ensure that traditional ecological knowledge and South-eastern artistic expressions are continued in meaningful contexts that promote conservation of natural resources.

Some current CNAPS projects include teaching about traditional hunting and gathering of culturally significant plants, natural dyes, basketry, pottery, stomp dance, traditional food preparation, oral traditions and herbal remedies. Through an intergenerational approach that encourages mentoring and small group-building projects, CNAPS strives to create lasting connections between Cherokee people, their natural landscapes, and their cultural traditions.

The Cherokee Native & Art Plant Society, 308 N. Muskogee Avenue, Tahlequah, OK, 74464, USA

## 109 HALL, KAREN C.

**Digital Storytelling for Students: Critical connections to traditional knowledge**

Storytelling is a powerful medium used by human cultures throughout time and across the globe, providing meaning, interpretation, and education. With the advent of less expensive and more widely available equipment, software and websites, students now have a means of capturing or creating stories of their own through digital media. This presentation will discuss the importance of digital storytelling as a means of connecting students to traditional knowledge, including how and why these stories are useful exercises for all.

Clemson University, School of Agriculture, Forestry and the Environment, 261 Lehotsky Hall, Clemson, SC, 29634, USA

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## 70 Years After Schultes: Economic Botany from the Andes to the Amazon

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*Sponsored by Society for Economic Botany.*

**110 CAMARA LERET, RODRIGO<sup>\*1</sup>,  
PANIAGUA Z, NAREL Y.<sup>2</sup> and MACÍA,  
MANUEL J.<sup>1</sup>**

### **Quantitative ethnobotany of palms with indigenous, afroamerican and mestizo inhabitants of the Amazon, Andean & Choco forests of northwestern South America**

A protocol for gathering information on ethnobotanical and socio-economic variables of palms and human communities in different tropical rain forest is discussed. Using this protocol we present our study in quantitative ethnobotany of palms with different human groups: indigenous, afroamerican, and mestizo communities that inhabit the Amazon, Andean and Choco forests of Colombia, Ecuador, Peru and Bolivia. By gathering a data set unrivaled in previous studies, with over 2700 informants in 32 localities from the four countries, several ecoregions and human groups, this analysis will enable a better understanding of how traditional knowledge and management systems of palms have evolved, how they have been adapted to changes, and what possible factors determine the use and conservation of a species and in turn of the forests in which they grow. Although the protocol was designed for northwestern South America, the purpose is to standardize a protocol to be used at the global scale, allowing for comparing patterns of palm use between different countries, ecoregions, habitats, human groups and use categories.

<sup>1</sup>Universidad Autónoma de Madrid, Departamento de Biología, Campus de Cantoblanco, Calle Darwin, 2, Madrid, Madrid, 28049, Spain <sup>2</sup>Herbario Nacional de Bolivia, La Paz, Bolivia

**111 PANIAGUA Z, NAREL Y.<sup>\*1</sup>,  
CAMARA LERET, RODRIGO<sup>2</sup>, BUSSMANN,  
RAINER<sup>3</sup> and MACIA, MANUEL<sup>2</sup>**

### **Differences in traditional use of palms reflect the life history of users - the case of indigenous and campesino communities in Beni, Bolivia**

The life history of the local population is often reflected in the usage patterns of resources in their surrounding environment. We studied two human groups living in the same ecosystem, with the same species of palms present. The indigenous Chacobo reached their

present settlement area about 60 years ago, when American missionaries established a homeland for the tribe. The campesino communities settled around 40 years ago at the end of the local rubber (*Hevea brasiliensis*) boom. Our study showed that the campesinos mostly rubber tappers or their children know and use a larger number of palm species for a more diverse range of applications. This knowledge is a result of their extensive voyages during rubber collection, which gave them the opportunity to learn about and experiment with a large number of species. This knowledge has been transferred into their present day lives, and is used to find new income sources from products derived from palms. The Chacobo in contrast use palms mostly for subsistence, for a low number of uses.

<sup>1</sup>Herbario Nacional de Bolivia, La Paz, Bolivia <sup>2</sup>Universidad Autónoma de Madrid, Campus de Cantoblanco, Departamento de Biología, Área de Botánica, Calle Darwin, 2, Madrid, 28049, Spain <sup>3</sup>Missouri Botanical Garden, William L. Brown Center, PO Box 299, St. Louis, MO, 63166-0299, USA

**112 BALSLEV, HENRIK**

### **Palm harvest impact in the western Amazon, Andes and Pacific lowlands**

Palms are the most useful group of plants in tropical American forests and in this project we study the effect of extraction and trade of palms on forest in the western Amazon, Andes and Pacific lowlands. We determine the size of the resource by making palm community studies in the different forest formations and determine the number of species and individuals of all palm species. The genetic structure of useful palm species is studied to determine how much harvesting of the species contributes to genetic erosion of its populations, and whether extraction can be made without harm. We determine how much palms are used for subsistence purposes by carrying out quantitative, ethnobotanical research in different forest types and we also study trade patterns for palm products from local markets to markets that involve export to other countries and continents. We study different ways in which palms are managed and we propose sustainable methods to local farmers, governments, NGOs and other interested parties. Finally we study national level mechanism that governs extraction, trade and commercialization of palm products, to identify positive and negative policies in relation to resilience of ecosystems and use this to propose sustainable policies to the governments. The results are disseminated in a variety of ways, depending on need and stake holders, from popular leaflets and videos for farmers, reports for policy makers to scientific publication for the research community. The team behind the proposal represents 10 universities and research institutions in Europe and northwestern South America.

Aarhus University, Bioscience, Ny Munkegade 114, Aarhus, 8000, Denmark

113 MACÍA, MANUEL J.\*<sup>1</sup>, CAMARA LERET, RODRIGO<sup>2</sup>, PANIAGUA Z, NAREL Y.<sup>3</sup>, BALSLEV, HENRIK<sup>4</sup> and PARDO-DE-SANTAYANA, MANUEL<sup>5</sup>

### Palm Uses in Tropical Rainforests of North-western South America

A thorough review concerning palm uses in tropical rainforests of north-western South America was carried out to understand patterns of palm use throughout ecoregions (Amazonia, Andes, Choco), countries (Colombia, Ecuador, Peru, Bolivia), and among the different human groups (indigenous, mestizos, afroamericans, *colonos*) that occur there. A total of 194 useful palm species, 2395 different uses and 6141 use-reports were recorded from 255 references. The average (SD) number of different uses per species was 12.3 (18.7) although great variability was observed between different species. Ethnobotanical information was recorded for 54 indigenous groups, which represent 49% of the total indigenous groups living in the study area. The Amazon was the ecoregion with the highest palm use: 134 useful species (90% of those potentially present), 82% of total different uses, 84% of total use-reports, an average (SD) of 14.7 (20.0) uses per species, and 81% of total bibliographic references found. Fewer, but similar uses were recorded for the Andes and Choco. Ecuador was the most intensively studied country. The main uses of palms in north-western South America were in the categories *Human Food* (70%), *Utensils and Tools* (66%), *Construction* (63%) and *Cultural Uses* (56%). Indigenous people knew more palm uses than mestizos, afroamericans and *colonos*. The use of palms was not random and the main uses were the same throughout the studied ecoregions and countries. Palms satisfy basic subsistence needs and have great importance in traditional cultures of rural indigenous and peasant populations in our study area. Areaceae is probably the most important plant family in the Neotropics, in relation to use diversity and abundance.

<sup>1</sup>Universidad Autónoma de Madrid, Biology, Botany Unit, Calle Darwin 2, Madrid, 28049, Spain <sup>2</sup>Universidad Autónoma de Madrid, Departamento de Biología, Campus de Cantoblanco, Calle Darwin, 2, Madrid, Madrid, 28049, Spain <sup>3</sup>Herbario Nacional de Bolivia, La Paz, Bolivia <sup>4</sup>Aarhus University, Department of Biological Science, Ecoinformatics & Biodiversity Research Group, Denmark <sup>5</sup>Universidad Autónoma de Madrid, Biology, Botany Unit, Calle Darwin 2, Madrid, 28049

114 BUSSMANN, RAINER\*<sup>1</sup> and PANIAGUA Z, NAREL Y.<sup>2</sup>

### Traditional knowledge in a changing world - new insights from the Chacobo in Bolivia

The Chacobo are a Panoan speaking tribe of about 500 members in Beni, Bolivia. Originally nomadic, the Chacobo were relocated in their current main settlement in the 1960s, after American missionaries convinced the Bolivian government to set up a homeland for the tribe, and migration ceased. The first large ethnobotanical study on the tribe was conducted by Brian Boom in the 1980s.

During the last decade, the status of indigenous groups in Bolivia has markedly improved, and the Chacobo now have legal title to a territory of about 450,000ha. Our present work represents the start of a follow up ethnobotanical inventory of the tribe. The departure of permanent missionaries, access to markets, with an all weather road constructed in the last few years, as well as a larger territory, seem to already have markedly changed plant use, knowledge patterns and lifestyle of the population. All children now learn Chacobo as their first language in school, the use of important plant species centers more on income generation, and the more sedentary lifestyle of the tribe is again replaced by migration patterns, based on seasonal availability of resources.

<sup>1</sup>Missouri Botanical Garden, William L. Brown Center For Plant Genetic Resources, PO Box 299, St. Louis, MO, 63166-0299, USA-

<sup>2</sup>Herbario Nacional de Bolivia, La Paz, Bolivia

115 FADIMAN, MARIA

### *Pambil*: Use, conservation and socioeconomics of the palm *Iriartea deltoidea*, (Arecaceae) in the Mache-Chindul Ecological Reserve, Ecuador

The palm, *pambil*, *Iriartea deltoidea*, (Arecaceae) provides material for shelter, construction, and food. This study examines how locals use the palm, and how that relates to their conservation incentive for the palm, and the forest in which it grows. The study area is in the Mache-Chindul Ecological Reserve, a protected area of the humid tropical rainforest in Ecuador. This is an area of interest for conservationists and development groups as it is one of the hotspots of biodiversity with only 5% remaining of this kind of forest in Ecuador. Three different ethnic groups live in and around this area: *Mestizo* and Afro-Ecuadorian colonists and the indigenous group of Chachi. This paper looks at how these different groups utilize the palm for thatch, building and food and how the importance of plant use relates to rainforest conservation. Particular attention

is focused on deforestation, economic incentives, ease of collection, socioeconomic associations, and cultural differences in collection and management. Uncut forest provides the best habitat for the palm, thus there is a growing awareness of how deforestation affects this resource. Although many leave the palm standing in their fields, it is common knowledge that these palms are weaker, and this less useful than those growing in primary forest. This case study explores the concept that using forest species can act as an internal incentive for ecosystem conservation.

Florida Atlantic University, Geosciences, 777 Glades Rd, Boca Raton, FL, 33431, USA

## 116 WILLIAMS, SOPHIE

### Cultivation of harvested species as a conservation strategy

The harvesting of plants from the wild is a major component of the livelihoods and subsistence for many people throughout the world. However, over-exploitation threatens many harvested plant populations. One option to combat over-exploitation is the cultivation of a species, effective only if the cultivation substitutes for wild harvesting. Xate (*Chamaedorea ernesti-augustii*) is harvested illegally in Belize by Guatemalans and exported to the US and Europe for use in the floricultural industry. The industry is estimated to be worth approximately US \$4 million in 2000 and the levels of harvest are thought to be unsustainable. In Guatemala, community initiatives have begun to establish xate plantations. In 2004 a training programme coordinated by Belize Botanic Garden taught Belizean farmers xate cultivation techniques. The aim of this research was to assess the impact of the training programme upon the relationship between Belizean farmers and the xate palm. Using questionnaire surveys and semi-structured interviews we evaluated the knowledge farmers in relation to xate, investigate whether the training made people more likely to cultivate xate (accounting for socio-economic predictors), and qualitatively assessed the barriers to xate cultivation. Trained farmers had a higher knowledge of xate cultivation than farmers not trained ( $t = 9.85, p < 0.01, df = 79$ ). Training was an important predictor of xate cultivation. Older people who are trained and own forest are the most likely to be cultivating xate. The primary barrier to cultivation was access to seeds to establish plantations. The lack of market to sell xate when harvested also deterred people from growing xate. Training can influence knowledge and behaviour of participants. However, there are barriers other than knowledge that restrict xate cultivation. To develop cultivation as a conservation strategy these barriers need to be addressed. The next stage in the research is to identify the conditions under which cultivation of xate would reduce pressure on the wild harvested

populations using a bio-economic modelling approach.

Royal Botanic Gardens, Kew and Bangor University, School of Environment, Natural Resources and Geography, Thoday Building, Deinol Road, Bangor, Gwynedd, LL57 2UW, UK

## 117 FILIPOWICZ, NATALIA\*<sup>1</sup> and RENNER, SUSANNE<sup>2</sup>

### *Brunfelsia* (Solanaceae): A single entry from South America into the Antilles followed by repeated radiations, and pollinator shifts involving butterflies, moths, and hummingbirds.

Among the hallucinogenic plants that most fascinated Richard Schultes, and later his student Timothy Plowman, was *Brunfelsia grandiflora*. *Brunfelsia* comprises c. 50 species of shrubs and treelets in the Antilles and South America, and the group's medicinal importance was already known in 1534 (herbal of Otto Brunfels). Plowman's revision of *Brunfelsia* distinguishes three sections that differ in flower and fruit morphology: section *Brunfelsia* (23 species) from the Antilles, *Franciscea* (ca. 18 spp.) in northwest South America, and *Guaianenses* in the Amazon basin (6 spp.). *Brunfelsia* species have gamopetalous white or purple flowers of various sizes, sometimes with abundant nectar, nocturnal scent, or colour-changing petals, and the centre of endemism are the Greater Antilles with 23 species. We inferred pollination mode changes and geographic relationships using combined plastid and nuclear DNA sequences for 65 accessions representing 38 species. Trees were rooted on 8 representatives of the Petunieae. *Brunfelsia* is monophyletic, and the deepest split is between an Antillean clade and a South American clade (each with 100% bootstrap support). Section *Guaianenses* is polyphyletic. The Caribbean clade is ancestrally moth-pollinated, with one shift to hummingbird pollination, while the South American clade is mostly butterfly-pollinated with one possible shift to moths. *Brunfelsia* entered the Antilles from South America once, and the single Panamanian species is related to the South American, not the Antillean clade. Cuba harbours a clade of 11 species that is sister to a Jamaican clade of 6 species, and each island was colonized only once, while Puerto Rico (5 species) was colonized twice. The type species of *Brunfelsia*, *B. americana* from Hispaniola and the Lesser Antilles, is polyphyletic, and since the name is based on a Plumier plate we have yet to resolve its application. Another problem species is the polyphyletic, horticulturally important South American *B. uniflora*. Using average nucleotide substitution rates to calibrate genetic distances yields a crown age of *Brunfelsia* of 13–21 Myr.

<sup>1</sup>University of Munich (LMU), Department of Biology, Systematic Botany and Mycology, Menzinger Str. 67, Munich, 80638, Germany-  
<sup>2</sup>Systematic Botany and Mycology, Department of Biology, University of Munich (LMU), Munich, 80638, Germany

118 ISLAM, MELISSA\*<sup>1</sup> and RANKER, TOM<sup>2</sup>

### The Evolutionary History of the Cultivated Coca (*Erythroxylum*)

The tropical, flowering shrubs in the genus *Erythroxylum* P. Brown (230 species) are commonly known as coca and occur throughout the tropics. Two species each with two varieties are exploited for their production of the secondary metabolite, cocaine. Most studies of coca are devoted to understanding the economic and medical impact of the legal and illegal uses of cocaine. Until now, the evolutionary relationships among the cultivated species and their closest wild relatives remained untested in a modern phylogenetic framework. Based on their morphological similarity, the cultivated species were hypothesized to be more closely related to each other than to any other *Erythroxylum* species. Both species belong to section *Archerythroxylum*, which should include their closest relatives. This section includes approximately 60 species from the Neotropics. Two nuclear loci (nrITS and *idhb*) and one chloroplast locus (*rpL32F*), along with morphological characters, was sampled from approximately 70 species to infer the evolutionary relationships among the cultivated species and to determine their closest wild relatives. The *idhb* locus was sampled from only 35 species. Based on the phylogenetic analyses, the two cultivated species, *E. coca* Lam. and *E. novogranatense* (Morris) Hieron, and their varieties form separate well-supported clades and are supported as distinct species. Although the two cultivated species are closely related, their monophyly is not supported. Their closest wild relatives are *Archerythroxylum* species with deciduous leaves.

<sup>1</sup>Denver Botanic Gardens, Research & Conservation, Denver, CO, 80206, USA<sup>2</sup>University of Hawaii at Manoa, Department of Botany, 3190 Maile Way, Room 101, Honolulu, HI, 96822, USA

119 BENNETT, BRADLEY C.

### Hunting, Hallucinogens and Health: The use of canine ethnoveterinary medicines by the Shuar and Quichua of Amazonian Ecuador

Archaeological records for the presence of domesticated dogs (*Canis lupus familiaris*) in the Americas date only to 9,000 years before present. Their relatively recent arrival from Europe and Asia belie their importance to native cultures in the Americas. The Shuar believe that dogs are gifts from Nunkui, the earth mother. Dogs may be nursed by a Shuar woman along with her own children. In many American indigenous cultures, dogs serve more than the role of a household pet - they are crucial for hunting and warfare success. For this reason native peoples in the Americas devel-

oped an ethnoveterinary pharmacopeia to treat illnesses in their canine companions and to improve their animal's ability to track game animals. These practices are not restricted to New World cultures. For example, Macronesian peoples employ *Zingiber officinale* and *Dendrobium* spp., among others, to improve the hunting ability of dogs. Here, I describe canine ethnoveterinary plants used by two cultures from Amazonian Ecuador, Shuar and lowland Quichua. Both peoples practice horticulture and supplement their diets through hunting and fishing. These native Ecuadorian cultures use seven species specifically to treat dogs including *Anthurium eminens* and *Anthurium gracile* to kill botfly larvae, *Caladium bicolor* and *Ficus insipida* as anthelmintics, and *Casearia commersoniana* to cure mange. Fifteen species are used to improve the hunting ability of dogs. These species include *Fittonia albivenis*, *Alternanthera bettzichiana*, *Tabernaemontana sananho*, and *Caladium schomburkii*. Of even more interest, both cultures give sacred psychoactive plants to their hunting dogs: *Brugmansia* spp., *Osteophloeum platyspermum*, *Virola duckei*, and *Ilex guayusa*. The latter is a potent stimulant, due to the methyl xanthine alkaloid caffeine. The former species are employed as shamanic hallucinogens due to their dimethyltryptamine or tropane alkaloids. The effects of hallucinogens on hunting dogs has not been studied. Shamans, under the influence of hallucinogens, experience enhanced auditory and olfactory perception. The same mechanisms may act in canines but a definitive answer will require controlled studies.

Florida International University, Biological Sciences, Miami, FL, 33199, USA

120 LAW, WAYNE\*<sup>9</sup>, MACKENZIE, RICHARD<sup>2</sup>, JENKINSON, THOMAS<sup>3</sup>, PERRY, BRIAN<sup>4</sup>, DESJARDIN, DENNIS<sup>5</sup>, LORENCE, DAVID<sup>6</sup>, EPERIAM, EMOS<sup>8</sup>, LENGSI, REILO<sup>8</sup>, SANNEY, JACOB<sup>9</sup>, CIANCHINI, CARLOS<sup>9</sup> and BALICK, MICHAEL<sup>10</sup>

### Increased local demand for *sakau* (*Piper methysticum*) in Micronesia, and the impact on biodiversity

As the demand for *sakau* (*Piper methysticum*) increases on the island of Pohnpei, Federated States of Micronesia, the supply of roots of this cultivated plant now comes from plants grown on Pohnpei as well as the nearby island of Kosrae (where it is locally known as *sukah*). A species essential to the local culture, it is consumed on a regular basis by many Pohnpeians, and no longer reserved only for high ranking individuals and ceremonies. Pohnpeian farmers clear cut areas of the pristine upland forest along streams to access nutrient rich soils to grow *sakau*. On the neighboring island of Kosrae where *sakau* is grown for export, clearings are done on a smaller scale and only in lowland secondary

forests along streams. Our study has analyzed the impact of these two cultivation methods on the ecosystem by recording the changes in vegetation, and how deforestation further alters the fleshy fungi community and stream biodiversity and its function. Relevé plots to measure plant and fungi species diversity were set up within, above, and below *sakau* plantations and in forested areas at similar elevations. Stream reaches in these plots were established to create a paired design. *Sakau* plantations are significantly shifting plant species composition and allow invasive species into the study areas. This had led to differences in diversity of fleshy fungi, and alters stream biodiversity, which we attribute to an increase in algal biomass that affects other organisms resident in the streams. As some of the species identified during this project are taxa new to science, we have developed specific conservation recommendations to protect the unique biodiversity of these islands, and these are being implemented as part of a region-wide program to preserve terrestrial and marine habitats. Further work on this multidisciplinary and highly collaborative program will include discussion with *sakau* farmers to encourage cultivation in a manner less impactful to these fragile island ecosystems.

<sup>1</sup>Kosrae Conservation and Safety Organization, P.O. Box 1007, Kosrae, FM, 96944, Federated States of Micro<sup>2</sup>USDA Forest Service, Pacific Southwest Research Station, Institute of Pacific Islands Forestry, 60 Nowelo Street, Hilo, HI, 96720, USA<sup>3</sup>San Francisco State University, Department of Biology, 1600 Holloway Avenue, San Francisco, CA, 94132, USA<sup>4</sup>University of Hawaii, Hilo, Department of Biology, 200 W. Kawili St, Hilo, HI, 96720, USA<sup>5</sup>San Francisco State University, Department of Biology, 1600 Holloway Avenue, San Francisco, CA, 94132, USA<sup>6</sup>National Tropical Botanical Garden, 3530 Papalina Road, Kauai, Hawaii, 96741, USA<sup>7</sup>Conservation Society of Pohnpei, P.O. Box 2461, Pohnpei, FM, 96941, Federated States of Micro<sup>8</sup>Conservation Society of Pohnpei, P.O. Box 2461, Pohnpei, FM, 96941, Federated States of Micro<sup>9</sup>Kosrae Conservation and Safety Organization, P.O. Box 1007, Kosrae, FM, 96944, Federated States of Micro<sup>10</sup>New York Botanical Garden, 200th St And Southern Blvd., Bronx, NY, 10458, USA

121 VANDEBROEK, INA\*<sup>1</sup> and BALICK, MICHAEL<sup>2</sup>

### Ethnobotany and Medical Education

**B**ackground: Ethnobotany is a useful tool for medical education, particularly of value in informing and training health care providers in becoming more culturally sensitive to the knowledge, beliefs and practices of patients from diverse cultures. The use of ethnobotanical information in the clinical encounter is pivotal in establishing a relationship of trust between physicians and their minority and often underserved patients, and to promote an environment where the use of herbal remedies by patients is more readily disclosed. Non-disclosure may be potentially harmful, as unforeseen drug-herb interactions are possible if herbal remedies are taken concomitantly with prescribed medications. Methodology: A series of information ses-

sions, practical exercises and guided visits were designed to train healthcare providers and students from medical institutions in New York City (Albert Einstein College of Medicine, Montefiori Medical Center, Bronx-Lebanon Hospital Center, Columbia University Medical Center), including PowerPoint presentations, role play exercises, medical Spanish training, ethnomedical interview exercises, and guided visits to local herbal shops, called *Botanicas*. Results: The training sessions were very well received. A self-administered evaluation instrument in cultural competence showed significant improvement in the knowledge, attitudes and skills of the learner groups after the training. Next steps: Currently, cultural competency training mostly exists as elective classes in the medical curriculum. Additional research and advocacy is needed to gather more comparative ethnobotanical information from different cultural groups that can be converted into curricular materials and promote the role of ethnobotany in medical cultural competency training.

<sup>1</sup>New York Botanical Garden, 2900 Southern Boulevard, Bronx, NY, 10548, USA<sup>2</sup>New York Botanical Garden, 200th St And Southern Blvd., Bronx, NY, 10458, USA

122 GERIQUE, ANDRES

### Biodiversity as a resource: plant use, land use, and nature conservation in Shuar, Saraguro, and Mestizo communities in southern Ecuador

**T**he tropical premontane and montane rainforests of the eastern Andean slopes of southern Ecuador constitute one of the most important hotspots of plant diversity. However, this region contains some of the world's most rapidly changing landscapes due to deforestation. Most land conversion can be attributed to settlers or colonists, but indigenous peoples as well are turning to more intensive land use and are assimilating themselves into local and regional market economies. The experience in international nature conservation during the past decades has shown that, to be effective, biodiversity conservation in inhabited areas should serve the goals of both nature safeguarding and the use claims of the local population. The strategy could be to provide welfare through the use of forest biodiversity for local peoples who coexist with it under the philosophy "use it or lose it" coined by Janzen in Costa Rica. Based on the foregoing, this study pursued the following targets: (1) to document the ethnobotany of the different ethnic groups who live in the area of study - namely the Shuar, the Saraguros, and the Mestizos - in order to avoid the loss of plant knowledge through possible acculturation and other modernization processes, and to identify species of economic value; (2) to analyse actual land use strategies; a better understanding of local land use allows for the development of income generating alternatives to current non-sustainable land uses. The last goal (3) was to evaluate the suitability of the implemen-

tation of agroforestry systems, ecotourism, payments for environmental services, and bioprospecting as instruments in line with the "protection by use" concept.

University of Erlangen-Nuremberg, Institute of Geography, Kochstr. 4/4, Erlangen, 91054, Germany

## 123 VOEKS, ROBERT

### ***Economic Botany* (1947-2010): Then and Now**

The journal *Economic Botany* has changed considerably since its inaugural issue in 1947. This paper explores these changes, and how they reflect on the field of economic botany/ethnobotany, by means of a review of the 2,187 published research articles that have appeared. Contributions have changed over the decades from largely descriptive reviews of lesser known useful taxa to explorations of people-plant relations grounded in hypothesis testing and (largely) quantitative methods. Original research in the field was rarely employed in the early years, but by 2010, 78% of projects included field work. Early research focused on the US and neighboring countries, but by 2005, a minority of original research was being conducted in industrial and post-industrial developed nations. The use of laboratory methods peaked in the 1970s, and has held fairly steady at about 25% of articles. A clear research methodology was rare until the 1970s, but today appears in nearly 100% of published articles. One of the clearest trends is the internationalization of the journal. In the five-year span from 1950 to 1954, 82% of contributors were American, the remainder hailed from only nine other countries. But between 2005 and 2009, only 37% of contributors were American, while 73% came from a total of thirty-two other countries, foremost among these Mexico, Brazil, China, Spain, and the UK. Finally, the content and objectives of submissions has changed significantly, as researchers increasingly concern themselves with botanical conservation and sustainability, ethnobotanical theory, domestication and diffusion, traditional ecological knowledge, the value of non-timber forest products, botanical history and archaeology, gender, and ethnobotanical change.

California State University--Fullerton, 800 N. State College Blvd, Fullerton, CA, 92631, USA

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## Developmental and Structural Section

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See also *Biomechanics and Evolutionary Developmental Biology (Evo-Devo)*.

### ORAL PAPERS

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124 PABON-MORA, NATALIA\* and LITT, AMY

#### Functional redundancy of non-core eudicot *FUL*-like paralogs in regulating flowering time and petal development

The *APETALA1/FRUITFULL* gene lineage is mostly known for the critical roles of the *Arabidopsis* duplicates *API* and *FUL* in floral meristem identity, in sepal and petal identity (*API*), and in fruit development (*FUL*). *API* and *FUL* are members of the *euFUL* and the *euAPI* clades respectively, that resulted from a major gene lineage duplication concurrent with the diversification of the core eudicots. The functions reported for *API* and *FUL* are for the most part conserved in other *euAPI* and *euFUL* genes. In order to evaluate the role of the duplication in the functional divergence of these genes, we have carried out functional studies of the pre-duplication *FUL*-like genes found in non-core eudicots. Particularly, we are studying the function of *FUL*-like genes in Papaveraceae. Species of Papaveraceae possess at least two *FUL*-like paralogs which differ in sequence mostly at the C-terminus. Functional studies assessing the role of each *Papaver* *FUL*-like paralog showed that the two copies appear to have similar functions; downregulation of each independently showed they regulate axillary meristem growth, floral meristem and sepal identity, as well as fruit development. The close similarity of phenotypes from downregulation of each gene suggests the two may function cooperatively in these processes. However, when both copies are downregulated simultaneously, additional roles emerge in regulating flowering time and specifying proper petal identity, indicating both are required for these processes. Downregulation of both copies results in similar but not identical phenotypes in another member of the family, *Eschscholzia californica*. These data suggest that functional divergence of Papaveraceae *FUL*-like genes has occurred independently in different taxa. Our data gathered from Papaveraceae will be discussed with preliminary data gathered from downregulation of *FUL*-like genes in *Aquilegia coerulea* (Ranunculaceae). Changes in protein motifs among the duplicates and protein networks will be discussed in the light of these data.

The New York Botanical Garden, 200th St and Southern Blvd, Bronx, New York, 10458, USA

125 YOCKTENG, ROXANA\*<sup>1</sup>, ALMEIDA, ANA MARIA<sup>2</sup> and SPECHT, CHELSEA<sup>1</sup>

#### The role of *SEPALLATA* genes in floral evolution in the Zingiberales

*SEPALLATA* genes are class E MADS-Box transcription factors that are required for the specification of all whorls of floral organs in model plants studies so far. Although there are still no functional studies in non-model plants, expression studies suggest a role of *SEP* genes in flower organ determination and both neo- and sub-functionalization of *SEP* genes have been implicated in the evolution and development of monocot floral diversity. Zingiberales is an order of tropical monocots that contains around 2500 species and show a striking diversity of floral forms. Evolution of floral morphology in the Zingiberales is mainly related to changes in the stamen and petal whorls. Here, we hypothesize that duplication of the *SEP* gene family, together with B and C gene family duplications, might underlie the evolution of floral form in the order through diversification of protein-protein interaction networks. Our preliminary results in the Zingiberales show that *SEP* genes have undergone explicit patterns of duplication events, especially in the *SEP*-3 clade. Expression studies thus far are in agreement with a framework in which gene duplications play a role in morphological diversification. Explicit protein-protein interaction studies are proposed to fully test our hypothesis.

<sup>1</sup>University California, Berkeley, Plant and Microbial Biology, 111 Koshland Hall, Berkeley, CA, 94720, USA <sup>2</sup>University of California at Berkeley, Plant and Microbial Biology, 111 Koshland Hall, Berkeley, CA, 94720-3120, US

126 ALMEIDA, ANA MARIA\*<sup>1</sup>, OTONI, WAGNER<sup>2</sup>, YOCKTENG, ROXANA<sup>1</sup> and SPECHT, CHELSEA<sup>1</sup>

#### Gingers BCs: The role of MADS-box genes in floral evolution in the Zingiberales

Despite the vast diversity of angiosperm floral forms, studies on the evolution of floral development have focused in few model species and a limited number of floral shapes. In order to fully understand the evolution of floral form in the angiosperms, the study of new systems with different morphological traits is fundamental. In the classical model of flower development - the ABC model - combinatorial expression of A, B, and C class MADS box genes determine the identity of the floral organs. B (*DEF/AP3* and *GLO/PI*) and C (*AG*) class genes, in particular, are involved in the determination of petal, stamen and gynoecium identity. The Zingiberales - an order of tropical commelinid monocots - contains approximately 2,500 species roughly divided into two groups: the banana (Musaceae, Lowiaceae, Streliziaceae, Heliconiaceae), and the ginger

(Costaceae, Zingiberaceae, Cannaceae, Marantaceae) groups. In the Zingiberales changes in floral form are mainly due to changes in the petal and stamen whorls: the acquisition of a complete differentiation between the first (sepals) and second (petals) whorls after the divergence of the banana lineage; the impressive reduction in the number of fertile stamens in the ginger group; and the acquisition of a novel floral structure, the labellum, as a result of the fusion of infertile stamens in Zingiberaceae and Costaceae. By taking a candidate gene approach, we asked: Are B and C class genes correlated with changes in floral morphology in the Zingiberales? It is evident from our results that B and C class genes expanded within the Zingiberales. Evolution of both *GLO/AP3* and *AG* gene families suggest a Zingiberales-specific duplication event, right after its divergence from the other commelinid monocots. Our results support the idea that B and C class gene family expansion and functional diversification are correlated to the main morphological changes in Zingiberales flowers. However, functional studies are still needed to address whether B and C class genes are causally related to such changes.

<sup>1</sup>University of California at Berkeley, Plant and Microbial Biology, 111 Koshland Hall, Berkeley, CA, 94720-3120, US<sup>2</sup>Universidade Federal de Viçosa, Departamento de Biologia Vegetal, Departamento de Biologia Vegetal - UFV, Viçosa, Minas Gerais, 36570-000, BR

## 127 RANDLE, APRIL MICHELLE\* and DIGGLE, PAMELA

### The role of flower position and sex in explaining intra-plant variation in flower size

Identifying the factors that contribute to intra-plant variation in floral size is critical for addressing several key questions in plant evolutionary and developmental biology. In plant species with unisexual flowers, differences in floral size are often attributed to adaptive differences in allocation to male or female function. However, the sexual identity of a flower is often confounded with location within an inflorescence. In some species, flower position alone can explain the differences between sexes in floral size. Most studies of positional effects on flower size have been conducted in simple, raceme-like inflorescences. Here, we examine flower size variation within compound umbels of eight species of Apiaceae that vary in their sexual expression (hermaphrodite, weakly-andromonoecious, strongly-andromonoecious). We find that in andromonoecious species of Apiaceae, both sex and flower position influence the size of secondary sexual characters. Hermaphroditic species also show flower size differences related to position. The differences in size that are related to flower position within an inflorescence do not appear to be due to gradients of resource availability, but rather appear to be due the inherent variation found in repetitive units within a plant (e.g., plant architecture).

University of Colorado, Ecology and Evolutionary Biology, Ramaley N122, Boulder, CO, 80309-0334, USA

## 128 MATSUNAGA, KELLY K.S.\*<sup>1</sup>, MESLER, MICHAEL R.<sup>2</sup> and TOMESCU, ALEXANDRU<sup>1</sup>

### Nectary Structure of *Scoliopus bigelovii* (Liliaceae)

*Scoliopus bigelovii* (slinkpod, fetid-adder's tongue) is a member of the Liliaceae native to California's redwood forests, whose ill-scented flowers are self-incompatible and pollinated by fungus gnats. Although a handful of papers document various anatomical features, no detailed description of nectary structure exists. The perigonal nectaries of *S. bigelovii* are located in a median groove on the proximal portion of the sepals and do not visibly produce nectar, although foraging behavior of pollinators suggests that nectar is provided. In this study the presence of nectar was confirmed, and the anatomy of the nectary region was described using light and scanning electron microscopy. The nectaries consist of a band of parallel ridges of nectariferous tissue that extends from near the base of the sepal to just beyond where the sepals recurve. The nectariferous tissue is composed of a uniseriate, secretory epidermis overlying one to four layers of nectary parenchyma. Nectariferous cells were identified by their relatively small size and conspicuously dense cytoplasm containing small vacuoles. Although this tissue lacks its own vasculature, the nectary appears to be supplied by the main sepal bundles through a band of large, tightly packed subglandular parenchyma cells, in which the bundles are embedded. SEM reveals abundant protoplasmic material in cells of the subglandular and nectariferous tissues, with greatest density in the epidermis during anthesis. Considerably less material was observed in the mesophyll abaxial and lateral to the nectary region. A very thin cuticle lines the nectary, and we infer that the small volume of nectar produced permeates this cuticle without rupturing it. Moreover, the lack of both specialized vasculature and visible nectar, hallmarks of nectar-secreting tissues when present, can be explained by the small quantity of nectar produced and ultimately required for rewarding pollinators. Nevertheless, the position of the nectary remains consistent with other Liliaceae, and these findings contribute to our knowledge of the anatomical diversity of nectaries within the family.

<sup>1</sup>Humboldt State University, Department of Biological Sciences, 1 Harpst Street, Arcata, CA, 95521, USA<sup>2</sup>Humboldt State University, Department of Biological Sciences, 1 Harpst St., Arcata, CA, 95521, USA

129 HAMPLIOS, KATHERINE E.\*<sup>1</sup>, THADEO, MARCELA<sup>2</sup>, MOORE, MICHAEL<sup>3</sup> and STEVENSON, DENNIS<sup>4</sup>

### Anatomy and development of fleshy fruits in the monocots

Though fruits in the monocot clade are predominantly capsular, baccate fruits are present in several distantly related monocot orders and families. Capsules are generally accepted as the ancestral fruit type for the monocots, and the presence of baccate fruits in various unrelated monocot groups is considered the result of convergent evolution. The independent evolution of fleshy fruits multiple times in the monocot clade implies that separate lineages of baccate fruits may have varying developmental pathways. However, information on the ontogeny and anatomy of monocot fruits is scarce. In a recent study by Rasmussen et al. (2006), capsular and baccate fruits from the Asparagales were examined to determine the evolution of fruit type in the order. This study aims to expand upon that of Rasmussen et al. by examining the anatomy and development of baccate fruits in select genera from the Commelinales, Dioscoreales, Liliales, and Poales in addition to the Asparagales in order to better understand the evolution of fruit types in the monocot clade on a larger scale.

<sup>1</sup>Oberlin College, Biology, Science Center K123, Oberlin College, Oberlin, OH, 44074, USA<sup>2</sup>The New York Botanical Garden, Science, 200th Street And Southern Blvd, Floor 2, Bronx, New York City, NY, 10458, USA<sup>3</sup>Oberlin College, 119 Woodland St., Science Center K111, Oberlin, OH, 44074, USA<sup>4</sup>THE NY BOTANICAL GARDEN, 2900 SOUTHERN BLVD, BRONX, NY, 10458-5126,

130 HASENSTAB, KRISTEN

### Leaf Anatomy and Trichome Morphology in the genus *Varronia* (Cordioideae: Boraginaceae: Boraginales)

The genus *Varronia* (Cordioideae: Boraginales), with ca. 100 species, has largely been thought to have homogenous vegetative features. Anatomical sections of leaves instead reveal that a surprising amount of variation exists, including isobilateral leaves which were have not previously been described in the genus. Additionally, scanning electron microscopy (SEM) revealed a wide range of variation in leaf trichome morphology across species of *Varronia*. Trichomorphotypes include stellate, muricate, strigulose, glandular and apically hooked. These anatomical and micromorphological characters will provide insights in an evolutionary context toward understanding the diversification of *Varronia*. Species of *Varronia* often occur in dry habitats and the genus appears to have radiated across topographically diverse regions of the Neotropics. The structural traits documented here may provide insight into the relationship between habitat and diversification rates

Rancho Santa Ana Botanic Garden, Research, 1500 N College Ave, Claremont, CA, 91711, USA

131 BUDKE, JESSICA\*, GOFFINET, BERNARD and JONES, CYNTHIA

### Experimental Manipulation of the Moss Calyptra: The effect of cuticle removal and desiccation on sporophyte development in *Funaria hygrometrica*.

In mosses and other bryophytes, the sporophyte is small, unbranched, and physically attached to the maternal gametophyte. A cap of gametophyte tissue, called the calyptra, covers the sporophyte apex during early development and throughout seta elongation in mosses. The calyptra is necessary for sporangium formation and ultimately sporogenesis. Calyptra-less sporophytes wilt unless grown in high humidity chambers suggesting that the maternal calyptra may prevent desiccation of the developing sporophyte. We have confirmed that the calyptra is covered by a multi-layered cuticle. Furthermore this cuticle is thicker than the cuticle on all other parts of the moss plant.

A manipulation experiment was carried out to test the role of the calyptra by determining the effect of cuticle removal and desiccation on sporophyte development. A complete block design with three treatments and a control (removal of calyptra, removal then replacement with calyptra intact, removal then replacement with calyptra cuticle removed, un-manipulated control with calyptra intact) was carried out for sporophytes of *Funaria hygrometrica* at a pre-meiotic developmental stage. Following these manipulations, plants were grown under four humidity levels, ranging from 30 to 99% RH, for 6 hours and then returned to 99% RH for the remainder of their development.

Preliminary results indicate that calyptrae without their cuticle are less effective in preventing desiccation of the sporophyte apex at lower humidity levels; resulting in decreased sporangium development, stunted growth, and sporophyte death. Additionally, measurements of spores per capsule and spore viability are currently underway to quantify the experimental effects on maternal gametophyte fitness and sporophyte reproductive success. We propose that the calyptra and its cuticle provide a unique mode of maternal care, which may have favored a taller moss sporophyte stalk via the seta meristem and increased architectural complexity of the moss capsule.

University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Rd. U-3043, Storrs, CT, 06269, USA

132 MALAHY, MICHAEL\* and DOUST, ANDREW

### Pattern of vegetative architectural development in green millet (*Setaria viridis*) under varied planting densities

**V** egetative architecture refers to the three-dimensional arrangement of branches in space. In grasses, vegetative architecture influences the ability of the plant to compete for light and other resources and ultimately affects economically important traits such as grain yield and biomass. Green millet (*Setaria viridis* (L.) P. Beauv.) is a small, weedy, panicoid grass and the wild progenitor of foxtail millet (*Setaria italica* (L.) P. Beauv.), which is being developed as a model genetic system for biofuels grasses such as switchgrass. Patterns of vegetative development in green millet were analyzed in non-limiting conditions and under different planting densities to determine the effect of shading on vegetative architecture. In non-limiting conditions, axillary branches were produced acropetally from the base beginning 12 days after planting and continued until anthesis of the main culm. Four orders of branches were observed with the pattern of development on secondary and tertiary branches recapitulating the pattern of the culm. This pattern was observed again under reduced planting density, however, at high planting density, size and number of axillary branches was highly variable. At high planting density, phenotypic characters that relate to the overall size of the plant, such as height and branch number, were highly variable as compared to the relative phenotypic uniformity of individuals in the reduced density block.

Oklahoma State University, Botany, 104 Life Sciences East, Stillwater, OK, 74078, USA

133 SCHWARTZ, ALLISON<sup>1</sup>, ORTIZ, IRMA<sup>1</sup>, SANDERS, ERIN R.<sup>2</sup>, DEMASON, DARLEEN<sup>3</sup> and HIRSCH, ANN M.<sup>4</sup>

### A newly isolated *Bacillus* strain affects legume plant architecture and pea nodule morphology by secreting auxin

**A** Gram-positive, elongated bacterium, designated 30N-5, was isolated from the Mildred E. Mathias Botanical Garden by UCLA undergraduate students after plating the soil suspension on a nitrogen-free medium. A phylogenetic analysis of a partial 16S rDNA sequence of strain 30N-5 revealed it to be 100% similar to *Bacillus simplex* strain NH259. Even though the initial isolation was made on a nitrogen-free medium, no evidence for *nifH*, one of three structural genes encoding the enzyme nitrogenase, was observed. Nevertheless, a profoundly positive effect on plant growth was observed. Upon inoculation onto the roots of both wild-type and the cytokinin-receptor mutant *hit1-1* of

*Lotus japonicus*, a model legume, *B. simplex* 30N-5 was found to alter the architecture of the inoculated plant by increasing root and shoot length as well as lateral root number and plant biomass. The auxin responses of the plants were visualized using a DR5::GUS reporter construct in pea (1). The DR5-auxin responsive element drives the beta-glucuronidase (GUS) reporter gene. Differences in nodule morphology were observed through a comparison of pea roots from uninoculated, *Bacillus*- and *Rhizobium*-inoculated roots, as well as from roots co-inoculated with both bacteria. The data strongly suggest that this new *Bacillus* strain influences nodule morphology in an auxin-dependent manner.

(1) DeMason DA, Polowick PL (2009) Patterns of DR5::GUS expression in organs of pea (*Pisum sativum*). Inter J Plant Sci 170: 1-11. We acknowledge the financial support of the Shanbrom Family Foundation and the UCLA Office of Instructional Development for courses MIMG 121A and MCDB150L. Irma Ortiz was supported by NIH grant GM55052 to Dr. Richard L. Weiss (UCLA). Other undergraduates who participated in this research are Rudy Benitez, Nigar Yusufova, Christine Kim, Ethan Mathews, Mary Motamedinia, Archie McCoy, Han Soul Kim, Kayoko Hanamoto, Walter Kim, Judy Wong, Brittany Yee, and Faith Oh.

<sup>1</sup>University of California-Los Angeles, Molecular, Cell & Developmental Biology, 621 Charles Young Dr, South, Los Angeles, CA, 90095-1606, USA<sup>2</sup>University of California-Los Angeles, Dept. of Microbiol, Immunol, and Mol Genetics, Los Angeles, CA, 90095, USA<sup>3</sup>University Of California, Botany And Plant Sciences, 900 University Ave., Riverside, CA, 92521, USA<sup>4</sup>University of California-Los Angeles, MCD Biol and Mol Biol Inst, 621 Charles Young Dr, South, Los Angeles, CA, 90095-1606, USA

134 WU, CHI-CHIH<sup>\*1</sup>, DIGGLE, PAMELA<sup>2</sup> and FRIEDMAN, WILLIAM<sup>3</sup>

### The impact of the lower genetic relatedness of endosperm to its compatriot embryo on maize seed development

**I**n most flowering plants, a developing seed commonly contains an embryo and an endosperm. As a result of double fertilization the embryo and endosperm within a seed are identical in terms of allele identities but commonly differ in ploidy. In contrast with an embryo, endosperm does not transmit its genetic contents to the next generation. Rather, an endosperm nourishes its compatriot embryo during seed development and germination, and ultimately dies. Evolutionary models based on kin selection suggest that the "sacrifice" of an endosperm for the benefit of its embryo may be advantageous because of the greater coefficient of relatedness of the endosperm to its associated embryo than to other embryos. To empirically test such theoretical interpretations, we took advantage of the phenomenon of heterofertilization in maize, in which double

fertilization is accomplished by sperm from two genetically distinct pollen grains, and the embryo and endosperm have different fathers. Because the coefficient of relatedness between an embryo and its compatriot endosperm is lower in heterofertilized kernels (seeds) than in homofertilized kernels, inclusive fitness theory predicts that in heterofertilized kernels the endosperm might behave less cooperatively with its embryo with the result that the embryo would be relatively smaller than in homofertilized kernels. We used five genetically distinct maize lines and a crossing design that allowed us to control for genetic background effects. Dry masses of dissected embryo and endosperm of heterofertilized and adjacent homofertilized kernels were compared. Preliminary results show that the dry weight of endosperm is not significantly different between heterofertilized and homofertilized kernels, but the weight of the embryo of heterofertilized kernels is slightly decreased. The lower weight of embryos in heterofertilized kernels is consistent with our prediction: endosperm behaves less cooperatively and provides less nourishment to its compatriot embryo in heterofertilized kernels than in homofertilized kernels.

<sup>1</sup>University Of Colorado Boulder, Campus Box 334, Boulder, CO, 80309, USA<sup>2</sup>University of Colorado , Ecology and Evolutionary Biology, Ramaley N122 , Boulder , CO, 80309-0334, USA<sup>3</sup>Harvard University and Arnold Arboretum, Organismic and Evolutionary Biology, Cambridge, MA, USA

**135 KITIN, PETER\*<sup>1</sup>, BEECKMAN, HANS<sup>1</sup> and KIRCHOFF, BRUCE<sup>2</sup>**

### **A visual based microscopic identification key for 37 Central African wood species**

The traditional work on wood identification is time-consuming and requires extensive expertise in specimen preparation, microscopy, and with wood anatomical terminology. Identification of wood specimens is typically made using dichotomous keys with text-based wood anatomical characters. Use of these types of keys often results in high error rates. To help overcome these problems we substituted micrographs for text-based characters and used direct comparison of images of unknown wood with reference images from microscope slides. A database of more than 2,000 microstructure images of the wood of 37 commercially important Central African species was created. We attempted to visually capture the important diagnostic features for the 37 species with light microscopy and SEM. Between two to five specimens of each species were investigated, with the goal of documenting as much intra-specific variation as possible. We discuss the development of image-based identification key and interactive teaching for Central African wood species.

<sup>1</sup>Royal Museum for Central Africa, Brusselssesteenweg 13, Tervuren, 3080, Belgium<sup>2</sup>University Of North Carolina At Greensboro, Department Of Biology, PO BOX 26170, GREENSBORO, NC, 27402-6170, USA

**136 WILLIAMS, TIM R.\*<sup>2</sup>, ROTHWELL, GAR<sup>1</sup>, WYATT, SARAH<sup>2</sup> and SANDERS, HEATHER<sup>3</sup>**

### **The role of auxin in isoetalean body plans**

There are only two major lineages of plants that evolved giant trees: lignophytes (including seed plants) and isoetalean lycophytes. The formation of giant trees requires at least two traits. These are increase in girth by secondary growth (i.e., wood) and bipolar growth which allows for a large rooting system. In living plants both traits are regulated by polar auxin transport. Because the closest common ancestor of lignophytes and isoetaleans had neither of these traits, both evolved independently in the two clades. Lignophytes form the canopy-dominant trees of modern vegetation, but the tiny quillwort *Isoetes* is the only surviving genus of isoetalean lycophytes. So unusual is the growth morphology of *Isoetes*, that without the fossil record it would be virtually impossible to interpret. Comparison of the growth and structure of *Isoetes* to the entire fossil history of lycophytes reveals several changes in basic morphology, all of which are associated either with polar auxin transport or the failure of auxin regulation in living plants. These differences include gravitropism in shoot systems, patterning of secondary vascular tissue, and cellular elongation associated with apical growth. Auxin treatments have been used to test hypotheses of auxin regulatory failures during the evolution of *Isoetes*, and as an attempt to rescue extinct phenotypes of isoetalean trees. Preliminary results of these experiments have yielded a transformation in morphology of the rooting apex from a linear meristem to a circular meristem characteristic of extinct forms; increased apical branching of rootlets (i.e., leaves modified for rooting); and shedding of secondary cortical tissues.

<sup>1</sup>Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, 97331, USA<sup>2</sup>Ohio University, Department of Environmental and Plant Biology, Athens, OH, 45701, USA<sup>3</sup>Oxford University, Department of Plant Sciences, South Parks Road, Oxford, OX1 3RB, UK

**137 SCHNEIDER, EDWARD\*<sup>1</sup> and CARLQUIST, SHERWIN<sup>2</sup>**

### **Equisetum Xylem: SEM Studies and their Implications**

Scanning electron microscope (SEM) studies of xylem of three species of *Equisetum* reveal numerous details not previously visible with light microscopy. SEM images of thick (ca. 1 mm) sections reveal pit shapes, cell contexts, and microstructure of pit membranes. Pit shapes are remarkably diverse in comparison to those of ferns or conifers. Nodal tracheary elements are isodiametric to fusiform in shape, and have crowded circular (mostly) to elongate prominently bordered pits and uniformly thick secondary walls. Internodal trache-

ary elements, by contrast, have relatively large circular pits with inconspicuous borders. Secondary walls of internodal tracheids are thin, with thickenings that are annular, looplike, or of some intermediate form. Metaxylem internodal tracheary elements face carinal canals (= proxylem lacunae), and many of the large circular (often crateriform) pits facing the canals may lack pit membranes, especially in *E. giganteum* and *E. myriochaetum*. Because dye experiments show that carinal canals can conduct water in stems of *Equisetum*, internodal tracheary elements facing the canals may have perforations (many of the pits in *E. myriochaetum* lack pit membranes despite careful handling techniques). This opens the possibility that internodal tracheary elements may, in some species, be vessel elements that permit conduction from the carinal canals of one internode node to those of the next internode (carinal canals are not intercontinuous between internodes), aided by metaxylem tracheids of the nodal plates. Such vessel elements would not be the same as those reported by Bierhorst, who found vessels only a few vessel elements long in rhizomes.

<sup>1</sup>Department of Horticultural Sciences, University of Minnesota, St. Paul, MN<sup>2</sup>Santa Barbara Botanic Garden, 1212 Mission Canyon Rd, Santa Barbara, CA, 93105

### 138 LITTLE, STEFAN<sup>\*1</sup>, COOPER, RANESSA<sup>2</sup> and JERNSTEDT, JUDY<sup>1</sup>

#### Developmental anatomy of branch architecture in *Ginkgo biloba*

*Ginkgo biloba* is notable in having highly dimorphic shoots. Long shoots produce elongate axes with leaves separated by internodes several centimeters long. Spur shoots/short shoots are produced in the axils of leaves of long shoots, and can occur as the ultimate shoot tip of a branch. Short shoots often persist for several years, producing leaves with crowded internodes, and either axillary pollen strobili in male trees or axillary ovulate structures in female trees. In investigations of experimentally induced vegetative branching of short shoots, we (and others) have noted the relatively narrow diameter of axes bearing several year-old short shoots. Analysis of tree architecture and branch anatomy reveals that short shoots have highly divergent development and structure compared to that of long shoots. Typical pycnoxylic wood with several growth increments is found in long shoots, but only a single increment of xylary tissue is found in short shoots. Short shoot axes do not widen appreciably with age, and the xylem is constructed more like that of a monoxylic cycad axis. Relating the age of short shoots to the growth increments in their subtending long shoots reveals cryptic growth rings that can be very narrow. In especially long-lived branches that bear only short shoots (both laterally and terminally), the hypothesized 1:1 ratio of short shoot age to subtending long shoot growth rings appears to be decoupled; branches that are 20+ years old may only bear 3-10 annual rings in long shootwood, and only 1-2 apparent rings in short shoot steles. Short

shoot development bears anatomical signatures of both primary thickening and radially aligned metaxylem, another similarity to axes of cycadophytes. Xylem of short shoots is mainly primary unless shoots convert to long shoot growth. Results suggest, therefore, another line of evidence that *Ginkgo* short shoots are analogous to the pachycaul axes of cycads. Supported in part by a Katherine Esau Postdoctoral Fellowship (SAL).

<sup>1</sup>University Of California Davis, Department Of Plant Sciences, Davis, CA, 95616-8515, USA<sup>2</sup>HILLSDALE COLLEGE, 33 E COLLEGE ST, HILLSDALE, MI, 49242, USA

### 139 SPICER, RACHEL<sup>\*1</sup> and TISDALE-ORR, TRACY<sup>2</sup>

#### Auxin response and transport during the initiation of secondary growth in *Populus*

The plant hormone auxin (indole-3-acetic acid) is a master regulator of plant morphology, but despite its prominent role in vascularization and apical dominance, little is known about the role of auxin in woody plant development. We sought to visualize auxin response in a woody stem during the transition from primary to secondary growth by developing several transgenic lines of *Populus tremula* x *alba* expressing GUS under the control of the synthetic auxin-responsive promoter DR5. Exogenous application of both auxin and the auxin transport inhibitor NPA induced significant GUS expression, with the latter occurring above the point of NPA application. GUS expression patterns in untreated pDR5-GUS *Populus* suggest that two separate routes of basipetal auxin transport exist in young woody stems, one formed by the primary xylem parenchyma of leaf traces, and one formed by the vascular cambium. Further up the stem, just beneath the shoot apex and before the appearance of a unified vascular cambium, GUS expression occurred in arcs of developing primary xylem. Current work is focused on improving methods of tissue preservation and sectioning of the vascular cambium to determine if the GUS expression is in fact restricted to cambial initials, or if it is instead concentrated in expanding xylem. The latter observation would be consistent with the GUS expression in the expanding primary xylem above, as well as a well-documented role of auxin in developing vasculature. However, current published measurements of auxin quantified by mass spectrometry suggest high concentrations in the vascular cambium itself. Transport assays with radiolabeled auxin confirmed the existence of two routes of basipetal auxin transport, an outer route near the vascular cambium and an inner route via the primary xylem parenchyma. Future work will focus on combining visualization of the auxin response in pDR5-GUS *Populus* with radiolabeled auxin transport assays to determine the route of auxin transport from the developing leaves into the nascent vascular cambium and/or the expanding vessel elements.

<sup>1</sup>Connecticut College, Department of Botany, 270 Mohegan Avenue, New London, CT, 06320, USA<sup>2</sup>Harvard University, Rowland Institute, 100 Edwin H. Land Boulevard, Cambridge, MA, 02142, USA

140 KITIN, PETER\*<sup>1</sup>, ROBERT, ELISABETH M.R.<sup>2</sup>, NTAMWIRA, NIRANDA<sup>3</sup>, VAN DEN BULCKE, JAN<sup>4</sup>, TAKATA, KATSUHIKO<sup>1</sup>, BEECKMAN, HANS<sup>5</sup> and LACHENBRUCH, BARBARA<sup>6</sup>

### Three-Dimensional Structure of Stems formed by Successive Cambia

Plant stems formed by successive cambia contain alternating layers of xylem and phloem, embedded in conjunctive tissue. The three-dimensional structure and the functional significance of the stem architecture with alternating vascular bands are little known. In *Salacia reticulata*, and *Sericostachys scandens*, successive cambia and new vascular increments were initiated from parenchyma cells at the outer side of the recently-formed phloem. Radial transport within a vascular increment may occur through the frequent tangential-wall pitting at the xylem/cambium interface. Radial transport between vascular increments may occur through rays and also along stem axis as successive vascular increments were inter-connected at different vertical positions along the stem. Moreover, *S. scandens* contained large vascular rays with vascular bundles, each initiating from an inner xylem increment and ending in the outer bark. Such 3-D network of subsequent vascular increments would confer an improved safety for the long-distance vascular transport in the case of injury or dysfunction of portions of the vasculature. In *Avicennia*, one of the main mangrove genera, the amount of internal phloem as well as the complexity of its reticulate structure inside the stem is found to change with changing environmental conditions. In more stressful conditions such as higher salinity levels, an increased proportion of internal phloem as well as a more complex internal structure can be observed suggesting an ecological advantage from the internal phloem in harsh environmental conditions by water storage and embolism repair. A database analysis showed 84.9% of the woody shrub and tree species with concentric internal phloem occur in either dry or saline environments. Other functional attributes that may result from this stem structure include allowing stems to flex and twist with less damage to the vasculature, and providing abundant and close phloem and conjunctive tissues for the xylem that could serve for carbohydrate storage, wound repairs and defenses against pathogens, as well as for meeting local demands for growth and maintenance.

<sup>1</sup>Akita Prefectural University, Institute of Wood Technology, Noshiro-shi, Japan<sup>2</sup>Vrije Universiteit Brussel (VUB), Laboratory for Plant Biology and Nature Management (APNA), Brussels, Belgium<sup>3</sup>Official University of Bukavu, DP Congo<sup>4</sup>Ghent University, Faculty of Bioscience Engineering, Laboratory of Wood Technology, Gent, 9000, Belgium<sup>5</sup>Royal Museum for Central Africa, Laboratory for Wood Biology, Tervuren, 3080, Belgium<sup>6</sup>DEPT WOOD SCI & ENGIN, 119 Richardson Hall, Oregon State University, Corvallis, OR, 97331, USA

141 MORAWETZ, JEFFERY

### Haustorial structural diversity across parasitic Orobanchaceae

Orobanchaceae present an ideal system for studying evolution of the parasitic habit in flowering plants: with a single origin of parasitism, the full range of trophic modes is represented, from non-parasites to facultative and obligate hemiparasites and holoparasites. This parasitic ability is conferred through an organ unique to parasitic plants: the haustorium. The Orobanchaceae are parasitic on the roots of their host plants through terminal and/or lateral haustoria that develop along the parasite's root system. Haustoria have a generalized internal structure, being composed of a vascular core, hyaline body, and endophyte, often with a bridge of xylem cells connecting the vasculature of host and parasite. Reports of phloem connections between host and parasite in Orobanchaceae are rare, and detailed comparative studies of haustorial structure within and across the main parasitic lineages of the family are lacking. Haustoria, representing four of five parasitic lineages within the family, were collected from plants excavated in the field, and were subsequently embedded in paraffin and plastic for structural examination. Xylem bridges were observed in all taxa examined. The proximity of parasite and host phloem, and the presence of parenchyma including transfer cells at the host-parasite interface were variable, and characteristics of these elements will be further discussed. What are the structural modifications involved in phloem-to-phloem transfer between the host and parasite in Orobanchaceae and does this include direct sieve element connections?

Rancho Santa Ana Botanic Garden, 1500 North College Ave., Claremont, CA, 91711, USA

142 HORNER, HARRY\*<sup>1</sup>, RUCHTI, TIRANEE<sup>2</sup>, YOON, HANA<sup>2</sup> and SAMAIN, MARIE-STEPHANIE<sup>3</sup>

### Differences in Leaf Anatomies and Crystal Macropatterns Between the Species-rich Sister Genera *Peperomia* and *Piper* (Piperaceae)

The majority of angiosperms produce calcium oxalate crystals in some or all of their plant organs, and most notably in their leaves. The crystals have different individual or aggregate shapes, and are spatially distributed within an organ. These two characters are species specific. Leaves are most amenable for study as they are plentiful and easy to process. Cleared fresh or herbarium leaves, using household bleach, ethanol and xylenes, display semi-transparent views of retained cell walls and inorganic crystals when viewed be-

tween crossed polarizers with a light microscope. Leaf crystals of *Peperomia* and *Piper* species were revealed as having distinctly different: 1) leaf anatomies; 2) crystal shapes; and 3) crystal locations or macropatterns. The 178 *Peperomia* species exclusively display druses throughout or concentrated over the veins in the small palisade parenchyma below a typically multilayered adaxial hypodermis, and sometimes either raphide bundles or prisms occur in the spongy parenchyma; all creating at least seven leaf crystal macropatterns. Fifty-nine species of *Piper* studied so far have a more complex array of crystals shapes and macropatterns that consist of: crystal sand and raphide bundles being most common, followed by prisms/styloids, sphaerites and very small 'druses', and various combinations of them. Most of these crystals occur in the palisade and spongy parenchymas sandwiched between the upper epidermis and its hypodermis and the lower epidermis and its hypodermis. *Piper* leaves are typically thinner than *Peperomia* leaves but the abundance of crystals in almost all of the species of both genera suggests a potential functional attribute associated with photosynthetic efficiency based on habitat. Finally, the observed macropatterns will be compared to published phylogenetic trees for the two genera to determine if species with the same or similar crystal macropatterns in each genus are closely associated with each other or not. These results will be further used to ascertain whether crystal shape and crystal macropatterns serve as useful taxonomic and phylogenetic characters within each genus.

<sup>1</sup>Iowa State University, Genetics, Development And Cell Biology Dept, 3A Bessey Hall, AMES, IA, 50011-1020, USA<sup>2</sup>Iowa State University, Undergraduate Biology Major, Ames, IA, 50011, USA<sup>3</sup>Ghent University, Department of Biology, Research Group Spermatophytes, K.L Ledeganckstraat 35, Gent, 9000, Belgium

### 143 DEMASON, DARLEEN\*<sup>1</sup> and JAGANATHA CHETTY, VENKATESWARI<sup>2</sup>

#### Interactions between GA, auxin and *UNI* expression controlling shoot ontogeny and leaf morphogenesis in garden pea (*Pisum sativum*)

*Unifoliata* (*UNI*) is a major gene controlling the number of pinna pairs produced during leaf morphogenesis in pea. There are two mutant alleles known: *uni* and *uni-tac*. Leaves on wild type plants have 2-3 pairs of proximal leaflets, 3 pairs of distal tendrils and a terminal tendril. Leaves on *uni* mutants are simple, bifoliate or trifoliate. Leaves on *uni-tac* mutants are intermediate with 2-3 pairs of proximal leaflets, 0-1 pair of distal tendrils and a terminal leaflet. A number of gibberellic acid (GA) biosynthesis mutants are known in pea including *le* and *nana* (*na*). Leaves on *na* mutants are miniaturized and possess 2 pairs of proximal leaflets, 1-2 pairs of distal tendrils and a terminal tendril. We used genetic, hormone application, and qRT-PCR experiments to explore the interactions between GA and auxin, and *UNI* gene expression that control shoot ontogeny and leaf morphogenesis. The rate of leaf complexity increase

during shoot ontogeny (i.e. heteroblasty) and adult leaf complexity are controlled by GA through *UNI*. Leaves on greenhouse grown *le uni-tac* and *na uni-tac* plants are rescued by weekly GA or auxin treatments. Shoot tips of *LE uni-tac* have higher *UNI* and class I *Knox* mRNA levels than shoot tips of *le uni-tac* and *na uni-tac* plants demonstrating a regulatory relationship for GA. Auxin increases *UNI* mRNA levels in *uni-tac* shoot tips as well as that of other genes including class I *Knox*. Therefore GA and auxin positively promote leaf dissection during morphogenesis by increasing *UNI* expression, which subsequently prolongs the time period during which acropetally initiated pinna pairs are formed. GA and auxin play common and supportive roles in pea leaf morphogenesis as they do in many other aspects of plant development.

<sup>1</sup>University Of California, Botany And Plant Sciences, 900 University Ave., Riverside, CA, 92521, USA<sup>2</sup>University of California, Botany and Plant Sciences, 1125 Batchelor Hall, Riverside, CA, 92521, USA

### 144 GRAHAM, LINDA<sup>1</sup>, ARANCIBIA, PATRICIA<sup>2</sup>, TAYLOR, WILSON<sup>3</sup>, STROTHER, PAUL<sup>4</sup> and COOK, MARTHA\*<sup>5</sup>

#### Aeroterrestrial *Coleochaete* (Streptophyta, Coleochaetales) Models Early Plant Adaptation to Land

The streptophyte water-to-land transition was a pivotal event in Earth history but it is poorly understood. While some early-diverging modern streptophyte algae are aeroterrestrial (capable of living in sub-aerial habitats), *Coleochaete*, identified by some as sister to the embryophytes, is generally regarded as obligately aquatic. We tested the ability of two *Coleochaete* species to grow and reproduce asexually in non-aquatic sub-aerial conditions. We assessed the ability of aeroterrestrial *Coleochaete* to resist chemical degradation - a trait indicative of fossilization potential. When grown on agarized mineral media or on quartz sand, *Coleochaete* occurred as distinctive hairless multistratose hemispherical bodies having unistratose lobes or irregular clusters of cells with thick, layered chemically resistant walls. When exposed to liquid water, aeroterrestrial *Coleochaete* produced typical asexual propagules (biflagellate zoospores). Cells that had been air-dried for periods up to several months maintained their integrity and retained their green pigmentation. Structural and reproductive features of modern aeroterrestrial *Coleochaete* suggest that ancient complex streptophyte algae could have grown and reproduced in moist terrestrial habitats, persisted through periods of desiccation, and left distinctive fossilizable remains.

<sup>1</sup>University Of Wisconsin, Botany Dept, 211 Birge Hall, 430 Lincoln Drive, Madison, WI, 53706, USA<sup>2</sup>UNIVERSIDAD DEL BIO-BIO, DEPTO DE CIENCIAS BASICAS, CHILLAN, Chile<sup>3</sup>UNIVERSITY OF WISCONSIN - EAU CLAIRE, DEPT OF BIOLOGY-PHILLIPS HALL, 105 Garfield Avenue, P.O. Box 4004, EAU CLAIRE, WI, 54702-4004, USA<sup>4</sup>Boston College, Paleobotany Laboratory, Weston Observatory, 381 Concord Road, Weston, MA, 02493, USA<sup>5</sup>Illinois State University, School of Biological Sciences, Campus Box 4120, Normal, IL, 61790-4120, USA

145 BACHELIER, JULIEN\*<sup>1</sup> and  
FRIEDMAN, WILLIAM<sup>2</sup>

### Female gametophyte competition in early-diverging lineages of flowering plants.

Just over the last twenty years, molecular studies have greatly contributed to the resolution of the phylogenetic relationships amongst flowering plants at all systematic levels. In addition, the resolution of a basal grade of three early-diverging lineages, referred to as the ANITA grade, provided a new and robust framework for ancestral character reconstruction, which revealed that the first flowering plants were surprisingly far more diverse than it was long assumed. Recently, we reported in *Trimenia*, an extant member of the ANITA grade, a remarkable mechanism of female gametophyte development. In each ovule, multiple female gametophytes are differentiated remotely from the site of fertilization and they initiate a pattern of intercellular tip growth in the nucellus central tissue. They grow concurrently like tubes, intertwined with each other from the base to the apex of the nucellus, and only one of them will yield the unique embryo of each seed. Such a development strikingly resembles that of pollen tubes growing in the transmitting tissue of the carpel, and suggests that *Trimenia* has evolved a unique mechanism of female gametophyte competition. However, our phylogenetic analysis reveals that such a mechanism is not unique in angiosperms and that it may be variously expressed. For instance, the initiation of multiple female gametophytes exhibiting a pattern of tip growth is rare in angiosperms and only occurs in a few unrelated taxa, whereas the occasional production of more than one female gametophyte is frequent in some extant members of the ANITA-grade and other basal clades. Therefore, a mechanism of female gametophyte (egg) competition may have played a central role in the reproductive biology of the first flowering plants and, in addition to male gametophyte (sperm) competition and maternal mate choice, may have contributed to their rapid diversification and tremendous diversity.

<sup>1</sup>Harvard University, Arnold Arboretum - Organismic And Evolutionary Biology, 1300TH CENTRE STREET, BOSTON, MA, 02131, USA<sup>2</sup>University Of Colorado, DEPT OF EPO BIOLOGY, Boulder, CO, 80309-0334, USA

146 LESLIE, ANDREW

### Branching architecture and reproductive allocation in conifers

Several lineages of living and extinct conifers (Cupressaceae, Podocarpaceae, fossil Araucariaceae, and fossil Cheirolepidiaceae) contain species that exhibit a growth form characterized by small, highly ramified branches bearing scale leaves. In contrast, other conifer lineages produce fewer, larger branches (Pina-

ceae, living Araucariaceae). These different branching habits can potentially constrain how reproductive tissue is deployed, since small branches cannot bear large reproductive cones. Quantifying pollen production in species with different branching habits is one way to explore this effect, and conifers are particularly suited to this approach because their pollen is produced in conspicuous unisexual cones. Direct counts of the number of pollen grains produced per pollen cone combined with surveys of the number of pollen cones produced per tree in several species of Cupressaceae, Taxaceae, and Pinaceae growing in southern Connecticut show that taxa with small branches produce much smaller pollen cones, but they typically produce several orders of magnitude more cone-bearing branches. This often results in roughly similar amounts of total pollen production (typically on the order of tens of billions of pollen grains) in individual trees of both small and large-branched species. These results suggest that vegetative morphology and growth form can play an important role in constraining reproductive morphology as well as determining how reproductive resources are allocated over the plant body.

Yale University, School of Forestry and Environmental Studies, 195 Prospect St., New Haven, CT, 06511, USA

147 RUSSELL, SCOTT\*<sup>1</sup>, GOU, XIAOPING<sup>2</sup>, ZHANG, YANAN<sup>1</sup>, MIAO, SEN<sup>3</sup> and TIAN, HUI-QIAO<sup>1</sup>

### Genome-wide transcriptional profiles of the pre-and post-fertilization rice gametes reflect unique contributions from the egg and sperm cell

Microarray technology permits relatively small quantities of total RNA to be collected and amplified to allow examination of transcripts present in the male and female gametes of flowering plants. Rice (*Oryza sativa* spp. *japonica*) were used because of its availability, well known timetable, cell cycle readiness and development of protocols for collection of enriched intact gametic cells. Linearly amplified labeled transcript template material was hybridized to the 57K genomic microarray of Affymetrix according to manufacturer's instructions and analyzed using Affymetrix microarray processing equipment and software. Normalization was conducted using dChip software by MBEL. Presence and absence calls were determined using the MAS 5 algorithm with  $p < 0.05$  for present,  $0.05 < p < 0.07$  for marginal and  $p > 0.07$  for absent. When probe sets were normalized using unique mapping, a majority of genes were expressed in both the egg and sperm cells with enriched expression in the egg cell. Most of these represent genes which are present in essentially all rice cell types examined to date and thus maybe regarded as a conserved set of presumed "housekeeping genes". Since cytoplasm of the sperm cells is believed to be transmitted

in many plants during plasmogamy, some sperm genes may be expressed in the zygote and embryo, as with *Arabidopsis*; however, the relative abundance of these genes is subject to significant change after fertilization. With maturation of the zygote, another distinct suite of genes establish the transcriptome of the embryo.

<sup>1</sup>Xiamen University, School of Life Sciences, Xiamen, 361005, China<sup>2</sup>Lanzhou University, School of Life Sciences, Lanzhou, 730000, China<sup>3</sup>University of Oklahoma, Department of Botany and Microbiology, Norman, OK, 73019

## POSTERS

### 148 BRAUER, LAURA\*<sup>1</sup> and CARLSWARD, BARBARA<sup>2</sup>

#### Rehydration Techniques for Dried Leaf Tissue of *Badiera* (Polygalaceae)

Leaf samples were treated in boiling water with Aerosol OT surfactant, 3% potassium hydroxide, and 14.8 N ammonium hydroxide. All specimens were then washed and stored in 70% ethyl alcohol. For paraffin processing, specimens were dehydrated in a graduated tertiary butyl alcohol/ethyl alcohol series, embedded in paraffin, and sectioned at 10  $\mu\text{m}$  on a rotary microtome. Sections were stained with Heidenhain's iron-alum hematoxylin and safranin and mounted on slides with Permount. Potassium hydroxide treatments removed all protoplasmic contents but generally returned cells to full turgor. Water with Aerosol OT did not remove cell contents but resulted the most distorted mesophyll. Ammonium hydroxide treatment not only preserved cell contents but also returned cells to full turgor. While water with Aerosol OT is the most cost effective and least time consuming, ammonium hydroxide gives the best overall results and is the least cost effective and most time consuming.

<sup>1</sup>Eastern Illinois University, 600 Lincoln Avenue, Charleston, IL, 61920, USA<sup>2</sup>Eastern Illinois University, Biological Sciences, 600 Lincoln Avenue, Charleston, IL, 61920, USA

### 149 AMPONSEM, OHENE<sup>1</sup>, WESTON, ERICA<sup>2</sup>, INGRAM, BRIAN<sup>2</sup> and COTE, GARY\*<sup>2</sup>

#### Regulation, Histochemistry, and Structure of Crystal-Producing Idioblast Cells in *Dieffenbachia seguine* (Araceae)

Many plants, especially in the Araceae, have idioblast cells which produce crystals of calcium oxalate. Some aroid species, including *Dieffenbachia seguine*, have an unusual type of crystal idioblast, termed the biforine, which is able to forcibly expel the crystals. It has often been proposed that these crystals, particularly those in biforines, might play a role in defending

against herbivory. If this is true we would hypothesize that plants regulate the number of crystal idioblasts in foliage, producing more if the plant is under threat from herbivores. To test this we have examined the abundance of crystals in leaves of plants treated with simulated herbivory or with plant hormones that signal various kinds of stress. We found that crystal abundance drops with age; this is consistent with the hypothesis, since younger leaves are often more tempting to herbivores. However, none of the experimental treatments had any effect on the abundance of crystals, contradicting the hypothesis. We are extending this work by maintaining leaf pieces in peel culture so that leaf cells are directly in contact with the test substances. We are also studying the cell walls of biforines, which are noticeably thicker and more robust than those of other leaf cells, to the point that they survive blending or grinding with a mortar and pestle, which destroy all other leaf cells. Histochemical studies indicate the cell walls are remarkably free of lignin and other phenolics. We have also begun scanning electron microscopy studies of the structures of the crystals themselves.

<sup>1</sup>Radford University, Biology, 501 Stockton Street, Radford, VA, 24142, USA<sup>2</sup>Radford University, Biology, 501 Stockton Street, Radford, VA, 24142, USA

### 150 GHOSH, DR. NABARUN\*<sup>1</sup> and SMITH, DON<sup>2</sup>

#### Fluorescent Microscopy on BSBMV infected sugar beet (*Beta vulgaris*) and clonal propagation via *in vitro* culture

Sugar beets (*Beta vulgaris* L.) support the sweetener industry in the United States. Beet soil borne mosaic virus (BSBMV) is a soil borne virus and member of the genus Benyvirus that infects sugar beets. Rhizomania, caused by BNYVV (Beta Necrotic Yellow Vein Virus) is a type member of the genus Benyvirus, vectored by a fungus *Polymyxa betae*, and BSBMV (Beet Soil Borne Mosaic Virus), is a devastating disease of sugar beet in US responsible for the vast decline of production in the last decade. The Southwest region and Texas included in the Great Plains region are the only ones that have experienced a decline in production in the 10 years. Our approaches were: 1. Localization of viruses in the plant tissue using fluorescence microscopy and 2. Cloning and propagation for new sugar beet varieties. To study the leaves and petioles with epifluorescence, thin sections were cut from the beet leaves and petioles and stored in 75-80% glycerin. Sections were observed and images were captured using a BX-51 Olympus Scope, a Digital Camera and UV source. Sections were treated with berberine hemi-sulfate and counterstained with aniline blue. Another set was stained in Fluorol yellow for possible localization of the suerbin components in the cork tissue. UV source helped in fluorescing by the lignified tissue very well under FITC. We observed the sections from the leaves and petioles at different magnifications

for possible localization of viral elements. Autofluorescence was recorded in the epidermis and hypodermis region of the petiole. Sugar beet leaves emit Blue-green fluorescence that results in autofluorescence. Variation of fluorescence was recorded between the infected and non-infected regions while using the FITC filters. IAA (0.5 mg/l) and BAP (2mg/l) were used to modify the MS medium to induce dedifferentiation of somatic cells. Rooting was obtained by using IAA and IBA (0.5 mg/l) Root and shoot formation occurred directly from the explants or from regenerable callus were observed. Modification and refinement of *in vitro* techniques allowed us to obtain regenerable callus that had the capability of entire plant regeneration.

<sup>1</sup>WEST TEXAS A&M UNIVERSITY, Life, Earth and Environmental Sciences, 2403 Russell Long Blvd., Canyon, Texas, 79015, USA<sup>2</sup> University Of North Texas, 1155 Union Circle #305220, Denton, TX, 76203-5017, USA

**151 MICKLE, JAMES<sup>\*1</sup>, LUMAGA, MARIA ROSARIA BARONE<sup>3</sup>, MORETTI, ALDO<sup>2</sup> and DELUCA, PAOLO<sup>3</sup>**

### **Micromorphological Insights on the Systematic Position of *Bowenia* and *Stangeria* (Cycadales)**

Cycad cuticular micromorphology was examined in *Stangeria* and *Bowenia*. *Stangeria eriopus* (Kuntze) Baillard is from Africa and has a subterranean stem with pinnate leaves whose leaflets possess a midrib. *Bowenia serrulata* Chamberlain and *B.spectabilis* Hooker are from Queensland, Australia and have subterranean stems and bipinnate leaves. Some workers place these genera in the same family, Stangeriaceae, while others suggest that they are not as closely related. Foliar samples were taken from the middle of mature leaves from greenhouse-grown plants (Duke University; Università di Napoli). Leaf material was fixed in FAA; cuticles were isolated in 20% Cr<sub>2</sub>O<sub>3</sub> for up to 72 hours. Specimens were coated with gold-palladium and observed under SEM. *Stangeria* abaxial external cell surface is smooth, with scattered granulate particles and cell outlines partially visible. Stomata are on the same level as epidermal cells with a slightly elevated flange. Stomatal pores show raised lips extending  $\frac{3}{4}$  of guard cell length. Distinct striations extend to 0.1 mm from stomatal poles. Similar striations surround hair bases. Internally, surfaces of abaxial epidermal cells are felty, well demarcated, and intervenal cells are randomly arranged. Guard cell cuticles are in shallow pits and finely granulate. Thick flanges flank stomatal apertures. Short polar extensions are present. Stomatal complex is surrounded by a flange with serrate margin, felty inner surface and 5-6 divisions. *Bowenia* abaxial internal epidermal cell cuticle surface is lightly granular. Epidermal cells are well-marked, elongate and irregularly spindle-shaped. Cuticular flange between guard cells is thickened at the middle, giving it a diamond-shaped

platform appearance. Stomatal opening extends 1/2 the length of stomatal apparatus. Adjacent to the cuticular flange, on either side, is an enlarged buttress with two diagonally-extended pegs. Laterally there is a low ridge on each side. Inner cuticular walls of guard cells is rugose. Polar extensions are flattened. Subsidiary cells are 5-6 and irregular, with two polar subsidiary cells. Stomatal long axes are aligned with epidermal cell long axes. Cuticular micromorphology does not show close similarity between these genera, supporting a more distant relationship of these genera.

<sup>1</sup>North Carolina State University, Department of Plant Biology, Campus Box 7612, 2115 Gardner Hall, Raleigh, NC, 27695-7612, USA<sup>2</sup>DIPT DI BIOLOGIA VEGETALE, VIA FORIA 223, NAPOLI, I-80139, Italy<sup>3</sup>Orto Botanico, Via Foria 223, Napoli, 80139, Italy

**152 DUARTE, DAVID<sup>\*1</sup>, BOBICH, EDWARD<sup>2</sup>, PAK, SARAH<sup>3</sup>, PHAM, SHAWN<sup>3</sup>, UTSUMI, YASUHIRO<sup>4</sup> and EWERS, FRANK<sup>5</sup>**

### **Seasonal changes in the vessel anatomy of adults and resprouts of California black walnut trees following wildfire.**

Following a wildfire at Bonelli Park in San Dimas, CA, unburned adult trees and new growth resprouts of *Juglans californica* S. Watson were examined to determine the anatomical basis for seasonal variation in hydraulic conductivity and mechanical flexibility and strength. Differences between growth forms were also considered. Stems from nine individuals per adult and resprout growth forms were sampled monthly from February through June of 2008. Stem samples were sectioned to analyze for variances in vessel diameter, hydraulic vessel diameter, vessel frequency, percent conductive, and percent vessel lumen area. The results showed a significantly greater vessel frequency in adults than in resprouts with a decrease of frequency through the season. In addition, the vessel lumen areas tended to be greater in adults, whereas the mean and hydraulic vessel diameters tended to be greater in resprouts. Both growth forms demonstrated positive increases in percent conductive, percent vessel lumen area, and hydraulic vessel diameter going from February through June. All the seasonal changes can be attributed to the production of a new xylem growth ring. The resprouts especially showed much larger mean and much larger hydraulic mean vessel diameters in the outer growth ring. In adults, vessel frequency and percent vessel lumen area were especially high in the outer growth ring. A separate study on these plants showed that hydraulic conductivity increased greatly between the months of April and May for adults and resprouts, likely related to the production of the outer growth ring. Overall differences between growth forms in vessel diameter and fre-

quency were correlated to higher mechanical strength (lower vessel frequency and percent vessel lumen area) and higher hydraulic conductivity (greater hydraulic diameter) in sprouts than in adult trees.

<sup>1</sup>California State Polytechnic University, Biological Sciences, 3801 West Temple Avenue, Pomona, CA, 91768, USA <sup>2</sup>California State Polytechnic University, Pomona, 3801 W. Temple AVE, Pomona, CA, 91768, USA <sup>3</sup>California State Polytechnic University, Pomona, Biological Sciences, 3801 West Temple Avenue, Pomona, CA, 91768, USA <sup>4</sup>Kyushu University, Tsubakuro 394, Sasaguri, Fukuoka, N/A, 811-2415, Japan <sup>5</sup>California State Polytechnic University, Pomona, Department of Plant Biology, 3801 West Temple Avenue, Pomona, CA, 91768, USA

## 153 DOTZEK, JANA

### Putative mitochondria-mediated speciation barriers in *Oenothera* - An example for recombination between mitochondrial genomes in sexual crosses?

The genus *Oenothera* (evening primrose) has an outstanding scientific tradition and was developed as model for cytoplasmic inheritance and speciation over the past century. Due to biparental transmission of plastid genomes within intra-specific crosses of *Oenothera* species, frequently so called plastome-genome incompatibility or plastid-mediated incompatibility, is observed. These incompatibilities are speciation barriers under the Dobzhansky-Muller model of speciation. However, besides the plastid-mediated there are also other incompatibilities described in the genus, which are independent from plastid, as well as from nuclear inheritance. They point to a biparental inheritance of a further cytoplasmic component. One of these incompatibilities is the so-called *falcifolia*-syndrome, which arises in reciprocal crosses between strains of *Oe. glazioviana* and *Oe. biennis* with different frequency, depending on the mixing ratio of the involved cytoplasms. Since plants which inherit their plastid genomes biparental often also display biparental inheritance or paternal leakage of mitochondrial genomes, it is reasonable to assume the mitochondrial genome as genetic base for the *falcifolia*-syndrome. This would be the first case of a hybridization barrier, which is mediated alone by the mitochondria genome, probably due to recombination between the two mitochondria genomes involved. To address this question we established a protocol for mitochondria isolation in the biochemically challenging genus *Oenothera* and obtained pure mtDNA for next generation sequencing approaches. So far we did a comparative sequencing of seven mitochondrial genomes from different *Oenothera* species, including lines which display the *falcifolia*-syndrome in sexual crosses. First studies on the inheritance of the mitochondrial genome in *Oenothera* will be presented.

Max-Planck-Institute of Molecular Plant Physiology, Potsdam-Golm, Germany

154 DIE, AGATHE<sup>1</sup>, KITIN, PETER\*<sup>2</sup>, VAN ACKER, JORIS<sup>3</sup>, KOUAMÉ, FRANÇOIS N'GUESSAN<sup>4</sup> and BEECKMAN, HANS<sup>1</sup>

### Cambial activity and formation of growth rings of xylem and phloem in teak (*Tectona grandis*) in Ivory Coast

We investigated plantation teak that grows in conditions of one dry season from mid November to mid February and a long rainy season with two peaks, during June - July and October. Cambium was dormant or least active from November until January (monthly precipitations 30 - 50 mm). The largest cambial zone and widest layers of differentiating xylem and phloem occurred in June (400% thicker cambium relative to the dormant stage during the driest months December and January). The cambium had reduced thickness and ceased activity at the end of the rainy season in October when the monthly precipitation was still relatively high (100 mm). Reactivation started in February together with vegetative bud break at monthly precipitations below 50 mm. Cambial divisions occurred firstly at the phloem side while expanding cells were present at the xylem side. The first fully expanded vessel elements with developing secondary walls were observed in the beginning of March. A false annual ring of xylem was formed in the period February - May. In June, the current-year xylem included a fully formed layer of earlywood, wide zone of differentiating earlywood, and several cell layers of developing latewood. New phloem differentiation was initially slow and became active with the increase of the precipitation rate and development of new foliage. At least two growth rings of phloem, marked by alternating layers of sieve tubes and sclerenchyma bands, were formed in the current year. The high correlations between annual rhythm of cambial activity, phenology, and monthly precipitations show good adaptation of this imported commercial species to the local environment.

<sup>1</sup>Royal Museum for Central Africa, Laboratory for Wood Biology, Leuvensesteenweg 13, Tervuren, 3080, Belgium <sup>2</sup>Oregon State University, Richardson Hall 119, Corvallis, OR, 97331, USA <sup>3</sup>Gent University, Faculty of Bioscience Engineering, Laboratory of Wood Technology, Ghent, 9000, Belgium <sup>4</sup>Université Cocody-Abidjan, Laboratoire de Botanique, Abidjan, Ivory Coast

**Anatomical and morphological characteristics among *Fusispermum* spp. and *Rinorea apiculata* group (Violaceae) can be useful for understanding the phylogenetic relationships**

Within the Violaceae, *Fusispermum* spp. and *Rinorea apiculata* clade are strongly supported as being successively sister to the rest of the family; while the monogeneric Goupiaceae are sister to Violaceae. Few comprehensive empirical studies have ever been published on Violaceae, especially on *Fusispermum* spp. and *Rinorea apiculata* group. Furthermore, those studies have focused on the most widely available genus *Viola*, not a typical one in the family, being largely herbaceous and temperate, while most of its members are woody and tropical in distribution. Leaf, seeds, androecium and gynoeceum of *Fusispermum laxiflorum*, *F. minutiflorum*, *F. rubrolognosum*, *Rinorea apiculata* group (*R. apiculata*, *R. crenata*), *Rinorea* s. str. (*R. lindentiana*, *R. squamata*, *R. paniculata*, *R. dasyadena*, *R. viridifolia*), and *Goupia glabra* (Goupiaceae) were examined. Structures in most of these species were illustrated for the first time, namely *Fusispermum* spp. and the *Rinorea apiculata* group. This new information may provide characters that can be understood in the context of hypothesis of relationships within Violaceae, and between Violaceae and Goupiaceae. The results of this research show that: *G. glabra* has a nodal anatomy (3:1) similar to the Violaceae. The petioles of *R. apiculata* clade have double vascular bundle. *Fusispermum* spp. has a special adaxial glandular tissue on the leaf. Cuticle of *Fusispermum* spp. has straight anticlinal walls, and *Rinorea* spp. has undulate to sinuous anticlinal walls. The androecia of Goupiaceae, *Fusispermum* spp. and *R. apiculata* clade has an apical appendage on the anthers. A glandular disc surrounds the ovary in Goupiaceae, *Fusispermum* spp., *R. apiculata* clade; in *Rinorea* s. str. there is a gland adnate to each filament. The ovary of Goupiaceae, *Fusispermum* spp., and *R. apiculata* clade are glabrous; in *Rinorea* s. str. different types of hairs cover the ovary. The seed of *Rinorea apiculata* clade has different morphology from *Rinorea* s. str. The flowers on early stages of *Fusispermum* spp. and *Rinorea* spp. development are not actinomorphic.

University Of Missouri Saint Louis, Missouri Botanical Garden, 2012 Maury Avenue 1N, Saint Louis, MO, 63110, USA

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**Ecological Section**

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*See also Conservation Biology, Advances in Plant Systematics and Population Genomics: Applications of Next Generation Techniques and Plant reproductive strategies under environmental stress.*

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**ORAL PAPERS**

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156 WOODS, TERESA\*<sup>1</sup>, JONAS, JAYNE<sup>2</sup> and FERGUSON, CAROLYN<sup>3</sup>

**The invasive *Lespedeza cuneata* attracts more insect pollinators than native congeners, with variable impacts**

Invasive plant species can exert competitive effects as well as facilitative effects on insect pollination services of native species. Through high relative abundance and/or prolific floral display, invasive plants that rely on insect pollination can successfully compete with some native plant species for shared pollinators. Alternatively, invasive plants can facilitate pollination of native plants by supporting and attracting shared insect populations. Factors that influence the effects of alien plant species on pollination services to native plants include the degree of shared pollinator species, synchronous flowering phenology, similar flower morphology and color, relatedness of invasive and natives, and showiness and densities of flowers. To investigate such plant-pollinator dynamics, this study compared the invasive *Lespedeza cuneata* and three native congeners, all sympatric with synchronous flowering, using *in situ* populations over two years during peak floral displays. The invasive demonstrated significantly higher insect visitation rates per plant in both years. Positive correlations were found between floral density and visitation rate per plant in all the native species. Although there was no such correlation found in the invasive *L. cuneata*, floral density was at least twenty times higher than the native species and likely saturated the pollinator community. When insect visitation rates of native plant species were compared with or without the presence of the invasive, *L. cuneata* showed a competitive effect on two native species, but a facilitative effect on one. The native plant species that experienced a facilitative effect had the highest degree of shared insect visitors with the invasive, and is morphologically most similar to the invasive, compared to the other native *Lespedeza* species. Insect visitor taxonomic analyses indicated each of the *Lespedeza* species had common insect visitors, with one major exception: the common honeybee, *Apis mellifera*, a primary visitor to the invasive plant species, was never observed on the native *Lespedeza* species.

<sup>1</sup>Kansas State University, Olathe Campus, 22201 W. Innovation Dr., Olathe, KS, 66061, USA<sup>2</sup>Colorado State University, Forestry, Rangeland and Watership Stewardship, 1472 Campus Delivery, Fort Collins, CO, 80523, USA<sup>3</sup>Kansas State University, Division of Biology, Ackert Hall, Manhattan, KS, 66506, USA

157 MATLAGA, DAVID\*<sup>1</sup>, DAVIS, ADAM<sup>1</sup> and QUINN, LAUREN<sup>2</sup>

### Evaluating the invasive potential of *Miscanthus* biofeedstocks: Estimating population parameters for current and hypothetical candidate species

Bioenergy crops have been promoted as environmentally friendly alternatives to petroleum, with widespread efforts underway to identify candidate species. However, many species under consideration share key traits (e.g. rapid growth, vegetative spread) with invasive species, creating concern that feedstock crops may escape cultivation and establish aggressive feral populations. In the North Central region of the USA, the C4 grass *Miscanthus x giganteus* (*Mxg*), a sterile Asian hybrid, is one of the top candidates for biomass production. In its current form *Mxg* is sterile but efforts underway to restore fertility to this species. Our goal was threefold: 1) characterize the relationship between demographic performance and *Mxg* age; 2) use matrix projection models to understand the population trajectory for *Mxg* in its current form; 3) conduct simulations to understand how changes to recruitment parameters (seed fertility and rhizome fragmentation and establishment) will influence population trajectories. We collected demographic data from 13 experimental plantings of *Mxg* throughout Illinois which spanned a range of ages (1-7 years). Survival of *Mxg* is strongly age-dependent, with low survival in the first year after planting (~29%) and high survival occurring after four years post-planting (<92%). A matrix projection model parameterized with fitted estimates of survival and seed production from our field data estimated a population growth rate ( $\lambda$ ) for *Mxg* of less than 1 ( $\hat{\lambda} = 0.929$ ), indicating gradual population decline over the long-term. Simulations indicate that a growing population ( $\hat{\lambda} > 1$ ) will occur if greater than one in 100,000 seeds can successfully establish or if adult plants produce greater than one rhizome fragment per every two individuals. Future efforts will incorporate the dispersal abilities of seeds and vegetative expansion of adult plants to parameterize models *Mxg* population spread.

<sup>1</sup>USDA-ARS Global Change and Photosynthesis Research Unit, Turner Hall, Goodwin Ave, Urbana, IL, 61801, USA<sup>2</sup>Energy Biosciences Institute, Long Pocket Laboratories, 1206 W. Gregory Drive, Urbana, IL, 61801, USA

158 VITT, PATT\*<sup>1</sup> and KNIGHT, TIFFANY<sup>2</sup>

### Optimal management frequency for population viability and genetic diversity

Many plant species need disturbance to establish and/or maintain viable populations, and several studies have used demographic models and data to calculate how frequent the disturbances must be to allow for viable populations. In addition, many plant species will outcross at a higher frequency in years following a disturbance event, if, for example, plants produce more chasmogamous flowers in these years. Here, we ask whether the optimal disturbance frequency for maintaining population size differs from that which maximizes population genetic diversity. *Viola conspersa* is an Illinois state-listed short-lived perennial that performs best in the years following disturbances, such as tree-falls, animal activity such as digging, local flooding, or human disturbance such as logging or plowing. In the Midwest, invasion by buckthorn forms a densely closed canopy that might reduce reproduction, survivorship and patterns of reproduction, potentially causing local extinction. We studied the size-specific demography of 6 populations for 10 years, and sampled a wide variety of environmental variation experienced by this species, including highly invaded habitats and those with active habitat restoration. We created an individual-based model that considers how different frequencies of disturbance (via habitat restoration) correspond to population viability and patterns of within-population genetic diversity. We parameterized this model with our demographic field data and a hypothetical quantitative trait composed of 10 loci each with two alleles. We find that plants produce slightly more chasmogamous flowers following a disturbance, and that disturbance frequencies required to maintain population size and to maximize genetic diversity of populations are similar.

<sup>1</sup>Chicago Botanic Garden, 1000 Lake Cook Road, Glencoe, IL, 60022, USA<sup>2</sup>

159 ZYLKA, JASON\*<sup>1</sup>, MOLANO-FLORES, BRENDA<sup>2</sup> and WHELAN, CHRISTOPHER<sup>2</sup>

### Floristic Quality of Seed Banks and Standing Vegetation Across a Management Spectrum

Based on management practices and land history, there are a number of different vegetation cover types that occur in the Midwest. While the outcome of different management decisions are easily visible in the standing vegetation, their impact on seed bank composition are not. This study aims to analyze the floristic quality of different landscapes to determine what effect

land management is having on the seed bank as well as the standing vegetation. Of particular interest is determining if higher quality standing vegetation results in a higher quality seed bank. Six different management histories were surveyed for this study: remnant prairie, restored prairie, row crop, old field, historic pasture, and pasture recently converted from row crop at the Midewin National Tallgrass Prairie (Will Co., IL). In 2008, vegetation surveys and soil cores were collected in July and October, respectively, for a total of 30 sites (five sites per management history) and 300 soil cores (10 cores per site). Soil cores were grown in a greenhouse and seedlings were identified to species. Results indicate that the seed banks vary per management history and there is little correlation between above ground vegetation and the seed bank. While some general similarities in floristic quality exist, these results suggest that significant gains in floristic quality should not be expected from the seed bank.

<sup>1</sup>University of Illinois Urbana-Champaign, Natural Resources and Environmental Sciences, 1816 S. Oak Street, Champaign, IL, 61820<sup>2</sup>University of Illinois, Illinois Natural History Survey, 1816 S. Oak St., Champaign, IL, 61820, USA

**160 MYERS, JONATHAN A.\*<sup>1</sup>, CHASE, JONATHAN M.<sup>1</sup>, JIMÉNEZ, IVÁN<sup>2</sup>, JØRGENSEN, PETER M.<sup>2</sup>, ARAUJO, ALEJANDRO<sup>3</sup>, PANIAGUA Z, NAREL Y.<sup>4</sup> and SEIDEL, RENATE<sup>5</sup>**

### **Disentangling regional, environmental, and spatial influences on beta-diversity in temperate and tropical forests**

**T**urnover in species composition (beta-diversity) often increases towards the tropics. Although this pattern may reflect differences in local ecological processes between biogeographic regions, it may also reflect sampling effects owing to differences in regional species pools (gamma-diversity). Using a null-model approach that controls for gamma-diversity of woody plant communities in North (Missouri, gamma-diversity ~45 species) and South America (Bolivia, gamma-diversity ~600 species), we show that sampling effects mask the signature of environmental and spatial processes in temperate and tropical forests. Before controlling for gamma-diversity, environment and space combined explained more beta-diversity in temperate forests. After controlling for gamma-diversity, however, environment and space explained similar, and more, beta-diversity in both regions, suggesting that local ecological processes may have similar influences on community assembly in temperate and tropical forests.

<sup>1</sup>Washington University in St. Louis, Department of Biology and Tyson Research Center, Campus Box 1137, One Brookings Drive, St. Louis, MO, 63130, USA<sup>2</sup>Missouri Botanical Garden, St. Louis, MO, 63166, USA<sup>3</sup>Museo de Historia Natural Noel Kempff Mercado, Bolivia<sup>4</sup>Herbario Nacional de Bolivia, La Paz, Bolivia<sup>5</sup>Universidad Mayor de San Andrés, Instituto de Ecología, La Paz, Bolivia

**161 MCGIVERN, JAMES\*, BOCIAN, LINDSEY, BROWN, NATHALIE-ANN, PERENIC, JOSEPH and GANGER, MICHAEL**

### **Life on the fringe: characterization of a forest-field ecotone in the Erie Bluffs State Park using hierarchical clustering and indicator species analysis**

**T**he Erie Bluffs State Park is a 450-acre park located in northwestern Pennsylvania. The park includes many communities including broadleaf terrestrial forest, broadleaf terrestrial woodland, broadleaf palustrine forest, terrestrial herbaceous openings, as well as agricultural fields. Approximately 441 vascular plant species occur within these communities, including species rare to Pennsylvania. One ubiquitous plant community found within the park is an ecotone formed where the forest and field habitat converge, hereafter referred to as the fringing habitat. This fringing habitat is composed of species typical to forests and fields, along with a few species unique to this ecotone. Within the fringing habitat are 158 species of the total 441 found within the park itself (approximately 36%). The long-term development of the park includes converting currently farmed areas into old field habitats. The fringing habitat may serve as a source of colonists for these old fields and therefore an accurate understanding of the composition of the species within the fringing habitat is crucial in predicting the long term development of these fields. To characterize the vegetation, 146 quadrats were established within the fringing habitat. Quadrats were 1 m wide and were located 50 m apart. The presence of vascular plant species within quadrats was determined, and two methods of vegetation analysis were applied to characterize the fringing habitat. Hierarchical clustering and indicator species analyses were used jointly to classify the fringing habitat. Hierarchical analysis organized the quadrats by species similarity into a dendrogram. Indicator species analysis was then applied to divide the dendrogram into 5 branches, representing the most ecologically meaningful groupings. The distribution of these groups was organized spatially along environmental gradients. The environmental factors associated with the groups include soil type, sun exposure, and arboreal influences. The vegetation patterns in the fringing habitat can be used to predict future field development after they are allowed to go fallow.

Gannon University, Biology, 109 University Square, Erie, PA, 16541, USA

162 GORCHOV, DAVID\*<sup>1</sup>,  
CASTELLANO, STEVE<sup>2</sup>, FRANK, PETER A.<sup>1</sup>  
and KHANAL, SUJAN<sup>1</sup>

**Using age structure to infer dispersal processes in the invasion of an exotic shrub, *Lonicera maackii* (Rupr.) Herder (Caprifoliaceae), Amur honeysuckle, in forest fragments**

A fundamental question in invasion biology is the importance of expanding fronts (diffusion) vs. long-distance dispersal events. As part of a broader study to understand the patterns and processes of the invasion of *Lonicera maackii*, we are using age structure to infer whether populations were founded by diffusion or long-distance dispersal. This upright shrub, native to northeast Asia, does not reproduce clonally, but is self-compatible. Because individuals do not reproduce before age 4, the age structure of a population founded by one or a few long-distance colonists would be expected to have 1-few old individuals followed by a gap of several years. Alternatively, we expect a continuous age distribution if populations were founded by diffusion from nearby sources, where propagule pressure could deliver seeds each year. We quantified the age structure of *L. maackii* in 17 woodlots in an agricultural matrix in a 20 km<sup>2</sup> recently invaded region in Darke County, Ohio. Woodlots ranged in size from 1-10 hectares and generally 50 - 1000 m from potential propagule sources. For small populations (N < 30) we sampled all individuals; for larger populations we sampled the largest 30 shrubs. Individuals are readily located in spring and fall because of this species' extended leaf phenology. For each individual we collected the basal portion of the largest 2-4 stems, made clean cuts with a miter saw, scanned cross sections, processed the images with Image J and counted annual rings. Individuals ranged in age from 2 to 21, with populations (oldest individual) ranging from 4 to 21. Most populations analyzed to date show continuous age distributions, consistent with diffusion rather than long-distance dispersal. We interpret these findings in light of evidence from microsatellite markers for diffusion vs. long-distance dispersal, and discuss implications for management and control.

<sup>1</sup>Miami University, Botany<sup>2</sup>Miami University, Botany, 316 Pearson Hall, 700 East High Street, Oxford, OH, 45056, USA

163 HINCHLIFF, CODY\*<sup>1</sup> and  
ROALSON, ERIC<sup>2</sup>

**The latitudinal diversity gradient: evidence from the sedges**

The latitudinal gradient in species richness is one of the oldest and most enigmatic topics in modern biology. Species richness decreases rapidly with distance from the equator, and despite numerous hypotheses about why this might occur, a satisfactory explanation remains elusive. To address this question, we use the globally important sedge family (Cyperaceae) to test an important prediction: that rates of diversification may vary meaningfully with distance from the equator. This prediction follows from the theoretical work proposed by Wiens and Donoghue in 2004, known as the tropical conservatism hypothesis. We used GenBank data as well as novel genetic sequences to reconstruct the phylogeny of over 1,000 species of Cyperaceae, and estimated character-dependent diversification rates on the resulting phylogenetic trees to test the correlation between diversification rate and distance from the equator. Preliminary evidence suggests that these rates vary widely among lineages within the family, indicating the importance of several major species radiations (incl. the genus *Carex*) in the creation of global patterns of sedge diversity.

<sup>1</sup>Washington State University, School of Biological Sciences, 239C Abelson Hall, Pullman, WA, 99164-4236<sup>2</sup>Washington State University, School of Biological Sciences, 332 Abelson Hall, Pullman, WA, 99164-4236

164 STANTON-GEDES, JOHN\*<sup>1</sup>,  
TIFFIN, PETER<sup>2</sup> and SHAW, RUTH<sup>1</sup>

**Ecological and genetic contributions to range limits in *Chamaecrista fasciculata***

The stability of species range limits is a conundrum to evolutionary biologists: what limits species from expanding their ranges via adaptation to conditions beyond the range edge? Theoretical and empirical work suggest that both ecological and evolutionary forces can be involved in the stability of range edges. We examined these processes on limiting range expansion of the native annual legume *Chamaecrista fasciculata* at its northern and western range edges in the Upper Midwest of the United States. First, to determine the relative importance of abiotic (e.g. climate) and biotic (e.g. competitors) factors, we established experimental populations simulating a colonization event with seeds transplanted into sites within the range, at the northern and western range edges, and beyond both these edges. At each site, we reduced neighboring vegetation in half the experimental populations. The results demonstrate that absolute fitness is below population replacement

beyond both range edges, but that the effect of neighbors varies from facilitative to competitive at different life-history stages. Second, we evaluated population structure and gene flow between populations within the range and at the range edge using sequence data from nine nuclear loci. The results suggest that these populations are not at equilibrium, with evidence for a stepping-stone model of poleward range expansion in response to Pleistocene glacial retraction. Overall, these results suggest that the distribution of *C. fasciculata* is limited by a combination of ecological factors reducing absolute fitness at the range edge, and genetic factors reducing adaptive potential to these environments.

<sup>1</sup>University of Minnesota - Twin Cities, Ecology, Evolution and Behavior, St. Paul, MN, 55108, USA<sup>2</sup>University of Minnesota - Twin Cities, Plant Biology, St. Paul, MN, 55108, USA

### 165 CLARK, JOHN\*, HEIN, FRANK and DE LA ROSA, CARLOS

#### Santa Catalina Island - past, present, and future study of a near-continent island system

Santa Catalina Island is one of the eight California Channel Islands, located approximately 35 km southwest of Los Angeles. At 194 km<sup>2</sup>, 88% of which is managed by the non-profit land trust Catalina Island Conservancy, Santa Catalina is the third largest Channel Island and is the second tallest with an elevation of 639 meters. Mediterranean in climate, at least 8 defined plant communities have been identified on the island, from coastal scrub, to oak woodlands, to open grasslands. Over 400 species of plants are native to the island and nearly 200 non-native introductions. Only a few mammals are native and include the Catalina Island fox, a ground squirrel, and a few other rodents. Birds are numerous and include an endemic subspecies of California quail and year-round resident bald eagles. Various ungulates have been introduced to the island over the last 150 years and have been managed and/or removed from the island in recent times. These characteristics, combined with a diverse and long history of land use and recovery, make Santa Catalina Island a unique living laboratory for island-based scientific research. The island is the most accessible of all the Channel Islands adding to the appeal of Santa Catalina as a long term research station. Past, present and future studies are described here and opportunities for novel projects and immediate research needs are presented. Collaborations with the Catalina Island Conservancy are encouraged and contact and research goals are provided.

Catalina Island Conservancy, PO Box 2739, Avalon, CA, 90704, USA

### 166 BIRNBAUM, AMANDA\* and HUSTON, MICHAEL

#### Plant Growth and Chemical Response to Variation in Soil Properties by a Texas Sand Ridge Endemic *Monarda viridissima* (Lamiaceae)

The purpose of this study is to compare two closely related, co-occurring congeners, *Monarda punctata* and *M. viridissima*, both in *Monarda* subgenus *Cheilyctis*, section *Cheilyctis*. *Monarda punctata* is geographically widespread and has a variety of phenotypes found in varying habitats. *Monarda viridissima* is a narrow endemic restricted to the Carrizo sand formation in south Texas. By comparing edaphic and environmental conditions of sites where *M. viridissima* and *M. punctata* grow with sites where only *M. punctata* grows, I hope to determine whether there are growth or chemical responses to environmental conditions that could be responsible for range restriction in *M. viridissima* and some of the ecological differences between the two species.

Texas State University - San Marcos, Department of Biology, 601 university Drive, San Marcos, TX, 78666, USA

### 167 KITTELSON, PAMELA\*<sup>1</sup> and LESICA, PETER<sup>2</sup>

#### Precipitation and temperature are associated with advanced flowering phenology in a semi-arid grassland.

Advances in spring blooming of wildflowers have been associated with climate change; however, the majority of long-term community-level studies have been conducted in humid-temperate regions. Less is known about phenological changes in herbaceous, semi-arid plant communities. We recorded first-bloom date of common spring wildflowers in a semi-arid grassland in the Rocky Mountains from 1995 through 2009 and analyzed these data along with mean monthly temperature and precipitation. Advanced flowering predominated; 75% of the 32 species displayed a negative linear regression slope, and this trend was strong for nine species (slope > 1.0,  $p < 0.10$ ). Only one species showed a strong trend for later flowering. Mean advance for all 32 species was 0.61 days/year and mean advance for the nine species displaying a strong tendency to flower earlier was 1.6 days/year. Species flowering early in the spring showed stronger trends toward advanced flowering than later species. Average March temperature and January plus December precipitation, falling mainly as snow, were explanatory variables in the best multiple linear regression model for mean first flowering date of strongly advanced species. Our results suggest that flowering phenology may be changing fast-

er and precipitation may play a more important role in semi-arid grasslands than in humid-temperate systems.

<sup>1</sup>Gustavus Adolphus College, Department Of Biology, 800 W. College Ave., St. Peter, MN, 56082, USA<sup>2</sup>University Of Montana, Biological Sciences, Missoula, MT, 59812, USA

168 MORAN, EMILYV\*<sup>1</sup> and KUBISKE, MARK E<sup>2</sup>

### Selective impacts of CO<sub>2</sub> and ozone on aspen (*Populus tremuloides*)

Genetic variation in plants influences many community and ecosystem properties. If global change factors cause shifts in the genetic composition of plant populations, this could have cascading effects on processes such as herbivore community assembly, nutrient cycling, and carbon storage. While a number of studies have examined adaptive responses to CO<sub>2</sub> and O<sub>3</sub> in herbaceous plants, few have examined the potential for adaptive responses in trees. Making use of data from the AspenFACE experiment, we ask: Can these atmospheric pollutants exert a measurable selective effect on a woody plant over short timescales? To address this question, we developed a hierarchical Bayesian model to test whether genotype x environment interactions are necessary to explain patterns of tree mortality. We hypothesized that fast-growing clones would tend to have an advantage, particularly in the more competitive high [CO<sub>2</sub>] environment, but that factors other than growth (such as stress tolerance) would also be important for survival. We find that G x E interactions in mortality lead to altered dominance hierarchies and decreased evenness under elevated CO<sub>2</sub> and O<sub>3</sub>. These responses are largely due to differences in growth responses between clones. While one might have expected a tradeoff between growth and stress tolerance, this was not observed. These results support the hypothesis that elevated [CO<sub>2</sub>] favors fast-growing genotypes and those with a higher-than average growth response to CO<sub>2</sub>, while high [O<sub>3</sub>] selects for genotypes that can maintain their growth despite exposure to this leaf-damaging pollutant. This suggests that managers might be able to increase carbon sequestration in temperate forests by selectively planting genotypes with these traits, which are identifiable in young saplings; however, because of possible tradeoffs between growth and tolerance of drought and/or frost, further study is needed.

<sup>1</sup>NIMBioS, 1534 White Avenue, University of Tennessee, Knoxville, TN, 37996, USA<sup>2</sup>USDA Forest Service, Northern Research Station, Rhinelander, WI, 54501, USA

169 FELTRIN, RAQUEL<sup>1</sup>, SCHEFFER, FERNANDA<sup>1</sup>, GULLO, MANOELLE<sup>1</sup>, VILELA, DANIELA<sup>2</sup>, ANTONELLI, PRISCILLA<sup>3</sup>, FERREIRA, LUCAS<sup>4</sup>, RODRIGUES, GUILHERME<sup>5</sup>, SMITH, CARL<sup>6</sup>, HUGHES, STEVEN<sup>6</sup>, WALKER, CHARLES<sup>6</sup>, BURKE, BRYCE<sup>6</sup>, MCGEE, JERVIS<sup>6</sup>, HAMEL, PAUL<sup>6</sup> and DEVALL, MARGARET\*<sup>6</sup>

### Changes in the Overcup Oak Research Natural Area

The Overcup Oak Research Natural Area (RNA) is a bottomland hardwood stand in the Delta National Forest, Mississippi, that was set aside for nonmanipulative research and education in 1943. The oldest trees in the RNA are 200-250 years old. A tornado occurred in part of the Overcup Oak RNA in 2008, providing an opportunity to observe succession in this old growth RNA after a natural disaster, to compare the damaged and undamaged areas and to compare the present conditions to the baseline data that were collected previously. Plots were established in the damaged and undamaged areas and a survey of the trees, shrubs, herbaceous plants and down woody debris was carried out. Importance values were calculated for the dominant trees, shrubs and herbaceous vegetation. Overcup oak (*Quercus lyrata*), American elm (*Ulmus americana*), and Nuttall oak (*Quercus nuttallii*) are important canopy species in the RNA. Other species occurring on the site are red maple (*Acer rubrum*), green ash (*Fraxinus pennsylvanica*), and sugarberry (*Celtis laevigata*). There are scattered individuals of sweetgum (*Liquidambar styraciflua*), water hickory (*Carya aquatica*), possumhaw (*Ilex decidua*), persimmon (*Diospyros virginiana*), dogwood (*Cornus* spp.), hawthorn (*Crataegus viridis*), willow oak (*Quercus phellos*), winged elm (*Ulmus crassifolia*), swamp privet (*Forestiera acuminata*), and baldcypress (*Taxodium distichum*). Predominant species in the understory are greenbriars (*Smilax* spp.) and scattered palmetto (*Sabal minor*).

<sup>1</sup>Universidade Estadual Paulista, Botucatu, SP, Brazil<sup>2</sup>University of Sao Paulo, Piracicaba, SP, Brazil<sup>3</sup>Escola Superior de Agricultura 'Luis de Queiroz', Piracicaba, SP, Brazil<sup>4</sup>Universidade Federal Rural de Rio de Janeiro, Seropedica, Brazil<sup>5</sup>Universidade Federal Rural, Seropedica, Brazil<sup>6</sup>Center for Bottomland Hardwoods Research, Stoneville, MS, 38776, USA

## Prey Preference in Aquatic Bladderworts (*Utricularia* spp.; Lentibulariaceae) Across the Eastern North America

Carnivorous bladderworts form integral parts of aquatic ecosystems and are particularly sensitive to environmental conditions such as eutrophication. My lab continues to conduct a study on prey preference over a wide geographic area, probably the widest area ever studied for these plants. The study area to date includes the Eastern US from Maryland to Florida and west to Indiana. We hope to make this a long-term ecological study and to extend it to eastern Canada and to some Western states in the US as we work to find out whether aquatic bladderworts (*Utricularia* spp.; Lentibulariaceae) of three basic morphologies show differences in prey preference. That is, do bladderworts with the same basic architecture select the same kind of prey (size, behavior, etc.) from the different prey available at a particular site. These three morphologies include architectures which can be described as thin and string-like (e.g. *U. gibba*), ropy (e.g. *U. macrorrhiza*, *U. foliosa*), and dimorphic with subterranean trapping shoots (e.g. *U. intermedia*). This project is an extension of our past lab work simulating natural habitats and prey populations. That part of our project showed a clear connection between the prey preference of particular aquatic carnivorous plants and the behavior of the favored prey. Most of those organisms which were trapped spent significant time resting in and on the non-carnivorous parts of the plant, as opposed to merely swimming throughout the trapping regions. Our work in the lab made it clear that prey preference depended on the architecture of the particular aquatic carnivorous plant studied. Our data so far indicate a clear distinction in prey preference among the three architectures which we are studying.

Indiana University Southeast, Department of Biology, 4201 Grant Line Road, New Albany, IN, 47150-6405, USA

## 171 RUFFATTO, DANIELLE M.\*<sup>1</sup> and MOLANO-FLORES, BRENDA<sup>2</sup>

### Variation in gender ratios of the gynodioecious prairie species *Lobelia spicata* L. across a latitudinal gradient

The high variability in gender ratio observed for gynodioecious species has been linked to genetic, biotic and abiotic factors among populations and across a latitudinal gradient. This study focuses on assessing whether two abiotic factors, temperature and precipitation, are driving the relationship between gender ratio/reproductive output measurements across a latitudinal gradient for the gynodioecious prairie species *Lobelia spicata* L. Data on latitude, gender ratio, reproductive

output [i.e. fruit set, seed number per fruit, seed biomass, percent seed germination] and mean temperature and precipitation from May to July [growing season] were collected for 11 populations across Illinois during the summer of 2008 and 2009. As with studies conducted on other gynodioecious species, the percent of females within *L. spicata* populations showed a strong negative relationship with latitude, such that there were higher percentages of females in southern than in northern populations. Temperature is likely the driving force behind the latitude/gender ratio relationship because it showed a strong negative relationship with latitude and a significant positive relationship with gender ratio in both 2008 and 2009. However, less precipitation in southern populations during intermittent years may also account for some of the latitudinal variation in gender ratio. The reproductive output measurements did not show any trends with the exception of female and hermaphrodite seed biomass, which showed a consistent negative relationship with latitude and strong positive relationship with temperature. Thus, it appears that stressful conditions, such as high temperatures and low precipitation, may favor the success of female plants within populations of *L. spicata* while high temperatures result in the production of larger seeds by both female and hermaphrodite plants.

<sup>1</sup>University of Illinois, Department of Plant Biology, 1816 S. Oak St., Champaign, IL, 61820, USA<sup>2</sup>University of Illinois, Illinois Natural History Survey, 1816 S. Oak St., Champaign, IL, 61820, USA

## 172 KARIYAT, RUPESH\* and ANDREW, STEPHENSON

### Volatile mediated indirect defense signaling is disrupted by inbreeding and genetic variation in Horsenettle (*Solanum carolinense* L.)

Inbreeding is commonly observed in natural plant population with negative effects on fitness traits and susceptibility to herbivory. Herbivorous insects remove photosynthetic leaf area from plants thereby affecting fitness and also inducing defense responses such as the emission of herbivore induced volatile organic compounds (VOC) and subsequent attraction of predators and natural enemies. Although host plant genetic diversity and inbreeding are likely to influence induced plant chemistry, few studies have examined induced response phenotypes across different genetic backgrounds. This study was designed to examine whether genetic background (maternal family) and inbreeding affect qualitative and quantitative aspects of herbivore-induced VOCs; and whether these differences affect herbivores and their natural enemies under field conditions, using common horsenettle (*Solanum carolinense* L.) as the study system. Our results suggest that breeding influences volatile emissions both quantitatively and qualitatively, and that genetic background (starting popu-

lation) also influences emissions, with inbred plants emitting more volatiles when undamaged but less when damaged compared to the outbred plants.

The analysis of insect attraction in the field indicates that breeding, damage, and breeding x damage are all highly significant with damaged outbred plants with higher volatile emissions able to attract higher number of parasitoid hymenopterans and undamaged inbred plants with higher volatile emission attracting higher number of herbivorous coleopteran and dipteran insects. Our study takes a novel approach in tritrophic interactions because few studies have combined lab and field experiments as a means of investigating indirect plant defense signaling, focusing on the effects of inbreeding and genetic background (maternal family) influence the quantity and quality of VOC blends produced constitutively and in response to specialist herbivore feeding, and that inbreeding in particular plays a strong role in determining the attraction of herbivorous and predatory insects in the field, suggesting that inbreeding disrupts the indirect defense phenotype.

173 BROKAW, JOSHUA\*<sup>1</sup> and  
HUFFORD, LARRY<sup>2</sup>

### Allopolyploid Speciation in Edaphic Specialists: *Mentzelia mollis* and *Mentzelia packardiae*

*Mentzelia mollis* and *M. packardiae* are narrow endemics found on unusual substrates in the northern Great Basin. These substrates have been found to support a large number of rare endemics while excluding common components of surrounding vegetation. Assays of substrate chemical and physical properties reveal extremely high concentrations of sodium and potassium salts. Comparisons of habitat data for *M. mollis* and *M. packardiae* indicate significant ecological divergence from each other and from other extant members of *Mentzelia* section *Trachyphytum*. In agreement with their geographic proximity, phylogeny reconstructions based on plastic intergenic spacers and the low-copy nuclear gene isocitrate dehydrogenase suggest that *M. mollis* is one of two progenitors of *M. packardiae* through allopolyploidization. Further, this suggests that despite its specialization and rarity, the genome of *M. mollis* has contributed to the evolution of *M. packardiae* as a new species with unique adaptations.

<sup>1</sup>Abilene Christian University, Biology Dept, Abilene Christian University, ACU Box 27868, Abilene, TX, 79699-7868, USA<sup>2</sup>Washington State University, SCHOOL OF BIOLOGICAL SCIENCES, 312 Abelson Hall, PULLMAN, WA, 99164-4236, USA

174 WILDENBERG, AMANDA\*,  
COONS, JANICE and COUTANT, NANCY

### Royal Catchfly (*Silene regia*) Floral Development in Response to Photoperiod

Royal Catchfly, *Silene regia*, is a prairie forb that is endangered in multiple states. Successful propagation of the species, which may include floral development, is essential to recovery programs. Within Caryophyllaceae, floral initiation often is linked to photoperiod. As *S. regia* prepares to flower, stems elongate. Our objective was to determine if flowering for *S. regia* was affected by photoperiod or developmental age. Seeds were planted in high porosity soilless mix with an Osmocote 14-14-14 four-month slow release solid fertilizer at 14.6 g/L. Plants were divided into two groups which were placed in different but identical growth chambers. One group was grown with a long day photoperiod of 16 hours light/8 hours dark with light intensity of 185  $\mu\text{mol}/\text{m}^2/\text{sec}$ . The second group was grown with a short day photoperiod of 8 hours light/16 hours dark with light intensity of 368  $\mu\text{mol}/\text{m}^2/\text{sec}$ . Each group contained 36 plants with three replications of twelve plants each. After 9 weeks, crown diameter was measured. Basal rosette leaves were counted weekly. As elongated stems developed, weekly counts for number of nodes, number of axillary stems, number of flower buds, and number of open flowers were made. Long day plants developed a significantly greater number of elongated stems than the short day plants, with elongated stems developing for 30.6% of plants in long days and for 0% of plants in short days. Short day plants had significantly fewer basal rosette leaves than the long day plants at 9 weeks, but had the same number of basal leaves by 16 weeks. Overall, stem elongation with subsequent floral initiation in *S. regia* was triggered by a long day photoperiod rather than a short day photoperiod or developmental age. This information is useful for the production of flowering plants when developing genetically diverse populations in natural areas.

Eastern Illinois University, Biological Sciences, 600 Lincoln Ave, Charleston, IL, 61920, USA

175 MILLER-STRUTTMANN, NICOLE

### Reproductive biology and stress-adaption in Ozark glade endemic plants reveals a counter-intuitive relationship between rarity and reproductive specialization

The traditional stress-competition tradeoff in niche theory states that traits adaptive for high stress environments are maladaptive when competition for shared resources is high. Historically, this tradeoff has been conceptualized as competition for abiotic resources, but biotic interactions, such as competition for pollinator

services, are also limiting in many habitats and could lead to the extinction of local populations via reduced reproductive success. In this study, I test the hypothesis that stress-adaptive traits (*sensu* Chapin's stress-resistance syndrome) reduce the competitive ability of locally-abundant, regionally rare (LARR) Ozark glade plant in comparison to closely-related, common species (CC). Greenhouse and growth chamber experiments estimated the stress resistance of LARR taxa and their CC congeners to drought and high heat conditions. Individuals of each congeneric pair were exposed to a series of manipulated, abiotic conditions, in accordance with *in situ* field observations and optimized in the greenhouse, and their fitness responses were compared. A field observational study documented the degree of pollination specialization for LARR taxa and their CC congeners, and a field competition experiment explicitly tested the relative competitive abilities of the LARR and CC taxa for shared pollinators. Contrary to our predictions, LARR plants were not more resistant to high-stress condition, and they had higher pollination specialization scores and were better competitors for pollinators in comparison to their CC congeners. These results indicate that LARR plants are not locally adapted to heat or drought stress, and that reproductive specialization and competition for pollinators, not stress-adaptive traits, may be more important for the maintenance of populations in stressful environments.

## 176 GEHRING, JANET

### Variation in seed mass among maternal plants of experimental *Gentiana puberulenta*

Studies of many plant species have shown seed size is an ecologically important trait influenced by numerous environmental factors but theory predicts selection will result in a single, optimal seed size within populations. The goal of my research was to identify sources of seed mass variation in *Gentiana puberulenta*, a tallgrass prairie forb. Because *G. puberulenta* is a sub-canopy, short-statured species that flowers late in the growing season, I hypothesized maternal resource levels would be a major factor contributing to seed size variation. I collected seeds from 8-14 open-pollinated individuals in nine central-Illinois populations of *G. puberulenta* and transplanted the resulting seedlings into two experimental plots in October 2008. In July 2010, total stem length of surviving plants was determined and plants were assigned to one of three experimental groups (control, supplemental water, and supplemental water + fertilizer) based on their size and population of origin. Experimental treatments were initiated after the first plant began flowering. Flowers were open to pollinators and also received supplemental non-self pollen. Seed mass was determined in batches of 100 and analyzed based on either average seed mass in fruits or

average seed mass of plants. The fruit-level analysis ( $N = 506$ ) indicated seed mass varied significantly among populations, maternal parents (nested within populations), and node. Sources of variation that contributed significantly to average seed mass of plants ( $N = 138$ ) were population, maternal parent (nested within population) and length of longest leaf of maternal plant. My results indicate genetic differences among maternal plants are an important source of seed mass variation in *G. puberulenta*.

BRADLEY UNIVERSITY, Department Of Biology, 1501 W. Bradley Avenue, PEORIA, IL, 61625, USA

## 177 WEEKLEY, CARL\*<sup>1</sup> and MENGES, ERIC<sup>2</sup>

### The population dynamics of the endangered herb *Liatris ohlingerae* (Asteraceae) in Florida scrub and roadside habitats

Variations in disturbance regimes may alter the population dynamics of plant species. We investigated the demography of *Liatris ohlingerae* (scrub blazing-star), a perennial herb endemic to the Lake Wales Ridge, in roadsides and in Florida scrub sites differing in time-since-fire. We compared mean annual survival, plant size at flowering, reproductive activity, and the impact of herbivory in six roadside and 13 scrub populations. To further explore fire effects, we conducted a "clip and burn" experiment. Mean annual survival did not differ between roadside and scrub populations nor with time-since-fire. Scrub plants had significantly greater total stem length than roadside plants in all eleven years analyzed. In eight years, scrub plants had significantly fewer stems and fewer herbivorized stems than roadside plants, and in seven years, scrub plants had significantly more flowering heads. Time-since-fire generally had little impact on vital rates or herbivory. In the "clip and burn" experiment, survival of clipped and burned plants did not differ significantly from the control. Our results show that *L. ohlingerae* plants in scrub sites are larger and more fecund than roadside plants and that scrub populations are tolerant of individual fires and a range of fire return intervals.

<sup>1</sup>Archbold Biological Station, Plant Ecology Program, PO Box 2057, Lake Placid, FL, 33862, USA <sup>2</sup>ARCHBOLD BIOLOGICAL STATION, PO BOX 2057, LAKE PLACID, FL, 33862, USA

178 DESAI, MANISHAN

### Biological Spectrum with some other ecological attributes of the flora and vegetation of Shamlaji Forest, Gujarat, India

Based on the current available information on the flora and vegetation of the Shamlaji Forest, spectra on life form and some other ecological attributes were analyzed and reviewed in different sub-ecosystem of the investigated area. The floristic list consists of 346 species belonging to 85 families of 74 dicotyledons and 11 monocotyledons. Fabaceae and Asteraceae were dominating family in the study area. According to the Raunkiaerian life form therophytes (49.42%) followed by phanerophytes (42.77%) were dominant in the area. Contribution of Cryptophytes (3.47%), Hemicryptophytes (0.87%) and Chaemophytes (3.47%) is very less in the establishment of vegetation structure in the area. Deciduous vegetation is characterized by the largest percentage of therophytes and it falls under the category of therophytic type of phytoclimate. In this region, the vegetation expression was predominantly deciduous, although the tree flora has few elements of evergreen species. Physical climate of the area is arid and dry with three main seasons, monsoon, winter and summer. On average there are 40 rainy days in a year. Average rainfall is 760mm (10years) with a wide range of variation year to year. Temperature varies as per the season and the seasonal variation is very wide. Humidity is generally high during monsoon, otherwise dryness prevails. Soil in General observed sandy with varying proportion of loam and redish brown to grayish brown in colour. The dominance of phanerophytes appears to be due to sufficient rainfall, high temperature and low biotic pressure. However, the population of therophytic species is increasing in highly grazed and eroded areas.

Bhavan's Sheth R. A. College of Science, Ahmedabad,, Botany; Vidyagauri Nilkanth Marg, Khanpur, Ahmedabad, Gujarat, 380015, India

179 WEBER, STEFAN\*<sup>1</sup>, CARUSO, CHRISTINA<sup>1</sup> and MAHERALI, HAFIZ<sup>2</sup>

### The role of floral traits in the assembly of spring ephemeral communities

Although plants compete for pollination services through their flowers, floral traits are rarely considered in community-assembly theory. Plants with similar traits are likely to share ecological niches and therefore compete for space and resources. Superior competitors may exclude species with similar traits from coexisting in the same community. Because closely related species share similar traits, competitive outcomes may be predicted by phylogenetic relation-

ships between taxa as well. We tested the hypothesis that plant communities are structured by competition for pollination by studying 52 species of early-blooming forbs. We inventoried community composition at forest sites across south-western Ontario and Michigan. We measured seven aspects of flower colour, morphology and phenology and compared similarity in these traits among co-existing species. We tested observed patterns against those generated in theoretical null communities to judge if neighbouring species were more or less similar in floral traits than expected by chance. We also measured the phylogenetic relatedness of community members to account for trait-conservatism in coexistence patterns. We found evidence that both competition for and facilitation of pollination structures spring ephemeral assemblages. Communities were composed of species with more dissimilar flower sizes than expected under the null model. This over-dispersion of flower size suggests that competition excludes species that attract similar-sized pollinators from coexisting. However, communities were composed of species that flowered more synchronously and had more similar floral hues than expected under the null model. This clustering of species with similar flowering phenology and flower color suggests that facilitation of pollination also influences community-assembly. Phylogenetic relatedness did not explain community composition, because few floral traits were conserved. Our results demonstrate that visually attractive traits promote facilitation of shared pollinators while morphological traits act to partition resources in response to competition. We suggest that pollinator attraction represents an ecological niche through which species can be sorted in a community, and that floral similarity can explain co-existence patterns among plants.

<sup>1</sup>University Of Guelph, Department Of Integrative Biology, New Science Complex, 50 Stone Road East, GUELPH, ON, N1G 2W1, Canada<sup>2</sup>University Of Guelph, Department Of Integrative Biology, GUELPH, ON, N1G2W1, Canada

180 MCEWAN, RYAN\*<sup>1</sup>, CHIANG, JYH-MIN<sup>2</sup> and YI-CHING, LIN<sup>3</sup>

### Topographic and biotic regulation of aboveground carbon storage in subtropical broadleaved forests of central Taiwan

There is a growing need to understand, and ultimately manage, carbon storage by forest ecosystems. Broadleaved evergreen forests of Taiwan provide an outstanding opportunity to examine factors that regulate ecosystem carbon storage. We utilized data from three Taiwan Forest Dynamics Plots (FS, LHC, and PTY) in which every tree is tagged and mapped, to examine factors regulating carbon storage as estimated from aboveground biomass. Allometric equations were used to estimate the aboveground biomass

of each tree, and a maximum-likelihood model building procedure was used to examine relationships between plot-level aboveground biomass (AGB; Mg/ha) and a suite of topographic and biotic factors. We found that our study sites have AGB values comparable to some of the most carbon dense forests in the world. Across all three sites, maximum biomass was contained in the taxonomic families Fagaceae, Lauraceae and Theaceae. In the FS site, we identified slope convexity ( $P = 0.03$ ) and elevation ( $P < 0.001$ ) as topographic predictors of AGB. Within plots, maximum AGB was found in topographically flat areas. In FS, stem density ( $P < 0.001$ ) was a significant biotic predictor of AGB and the maxima occurred at intermediate densities. In LHC, we found that convexity ( $P < 0.001$ ) and slope ( $P < 0.001$ ) were significantly related to AGB which was maximized along a topographic ridge in the plot. Species richness ( $P < 0.001$ ) was a significant biotic predictor of AGB in LHC, and the relationship indicated slightly higher AGB at higher levels of species richness. The only significant factor related to AGB in PTY was species richness ( $P = 0.02$ ). Additional work is needed to further understanding of topographic factors as regulators of AGB and to carefully scrutinize the role of species richness in forest carbon storage. In particular, future work will test the hypothesis that AGB is positively correlated with species richness because of complementarity among species where adding species increases functional diversity, increasing the sites carbon storage.

<sup>1</sup>University Of Dayton, Biology, 300 College Park, Dayton, OH, 45469-2320, USA<sup>2</sup>Tunghai University, Department of Life Science, No. 181, Sec. 3, Taichung Port Rd., Taichung, 40704, Taiwan<sup>3</sup>Tunghai University, Department of Life Science, No. 181, Sec. 3, Taichung Port Rd, Taichung, 40704, Taiwan

**181 SINCLAIR, JORDAN\*<sup>1</sup> and FREEMAN, CARL**

### **Incest, Specialization and the Environment: A New Model for the Evolution of Dioecy**

**D**ioecy has evolved independently in many plant families. This suggests that dioecy is a viable sexual system in circumstances that independently reoccur. Historically, the two selective pressures attributed to this evolution are selfing coupled with inbreeding depression and specialization among the unisexual plants. The proposed model incorporates these factors and expands the concept of inbreeding to include consanguineous matings as well as environmental conditions to predict the circumstances under which dioecy is likely to evolve. When neither inbreeding nor specialization is considered, male and female sterile mutants are quickly eliminated from the population. When selective advantages are given to these mutants they can persist and, if their relative fitness is high enough, they can invade. Both of these results are in accordance with previous predictions. What is novel is our ability to combine the

inbreeding and specialization advantages, allowing us to see how the two forces interact and the influence this can have on the evolutionary process. The addition of a heterogeneous environment allows us to examine why dioecious species are often found in stressful environments, and to what extent the environment can influence the evolution from a population of hermaphroditic to unisexual individuals.

<sup>1</sup>Wayne State University, Department of Biological Sciences, Detroit, MI, USA

**182 AYODELE, MUYIWA SEGUN\*<sup>1</sup>, AWORINDE, D. O.<sup>1</sup> and ILORI, O. J.<sup>2</sup>**

### **Variations in Frond-sheath Fibers and Moisture Collection Strategies among three West African Palms**

**T**hree palms namely: *Cocos nucifera* L. (Coconut palm), *Elaeis guineensis* Jacq. (Oil palm) and *Phoenix dactylifera* L. (Date palm) were investigated for characteristic features of leaf fibers and development orientation along tree trunk. Fibers were anatomically examined by macerating primordial leaf sheath (net-like structure) for the nature of fibers, the pits; taking dimensions (length and width) of the fibers in  $\mu\text{m}$ . Fiber sheaths pictures and photomicrographs of fiber characteristics are presented for detail comparison. Fiber characteristic simplifications are correlated with the moisture availability regimes for the different plants in their ecological habitats. Leaf fibers in *Cocosnucifera* are woven into a sheet, wrapped around the base of each frond; neatly tucked into the inner developing frond. The sheath enlarges as the tree trunk increases in height. *Elaeis guineensis* has less conspicuous woven sheath, only noticeable in younger fronds. Older fronds have fiber sheaths gradually transformed into a pile stuffing each frond axils. In *Phoenix dactylifera*, conspicuous strands of crunchy fibers are alternately woven around each frond base along the tree trunk forming a continuous cushion of fibers on the trunk. Anatomical study results show that in the three species, fibers are pointed at both ends and all the walls have bothered pits except in oil palm which is half bordered. Fibers are longest in Date palm ( $974 \pm 4 \mu\text{m}$ ) and shortest in Coconut palm ( $100 \pm 10 \mu\text{m}$ ). Ecological implications of observations: high frequency of long fiber is indicative of high conductive safety to avoid embolism. Increase in fiber width suggests an increased conductive efficiency. Date palm usually found in the dry ecological habitat (except those used for aesthetics) combines the attribute of good conductive efficiency fibers with crunchy fiber strands pad on frond axils. Some adventitious roots were noted situated underneath each frond base pad. Thus, there is ample provision for the absorption of any available moisture for conservation by the fiber pads which in turn would make such available for the hidden roots underneath the frond pads. This scenario is absent in coconut whose habitat is usually along the moisture lad-

en beach terrain. The Oil palm is intermediate in these features suggestive of its ability to colonize habitats between the sea and the dry savanna areas

<sup>1</sup>Biological Sciences Department, University of Agriculture, Abeokuta.<sup>2</sup>Biology Department, Adeyemi College of Education, Ondo

**183 KOPTUR, SUZANNE\*<sup>1</sup>,  
RICO-GRAY, VICTOR<sup>2</sup>, DIAZ-CASTELAZO,  
CECILIA<sup>3</sup> and PALACIOS-RIOS, MONICA<sup>1</sup>**

**Nectar secretion on fern fronds is associated with lower levels of herbivore damage: field experiments with *Pleopeltis crassinervata*, a widespread epiphyte of Mexican cloud forest remnants**

Though it is not from the section of the genus *Polypodium* known to have some species bearing nectaries, *Pleopeltis crassinervata* frequently has sooty mold at the base of its fronds. This mold indicates nectar secretion, and suggested that this species may, like other epiphytic *Polypodium* species, benefit from ant protection supported by nectar secretion on its developing fronds. Previous experiments used sticky resin to exclude ants, but the fronds of this species are often lying flat against the tree trunks upon which they grow; we used nylon polish to cover the nectaries instead. We chose twenty-two pairs of fronds (each pair on separate plants), matched for size and developmental stage; on one of each pair we covered the nectaries with polish (experimental treatment), on the other we put polish on another part of the frond (control). Developing fronds on experimental plants (with nectaries covered) suffered greater damage than did fronds on control plants with nectaries functioning normally, suggesting nectaries attract visitors that protect the fronds against herbivores. We conducted the same experiment on a fern that does not have nectaries (*Polypodium furfuraceum*), and found no difference between experimental and control fronds. We found seven species of ants visiting the nectaries of *Pleopeltis crassinervata*, and assessed their protective abilities with caterpillar placement experiments; there was a wide range of response. Variation in ant behavior towards herbivores may explain why some individual plants showed no evident benefit from protection in this facultative association. Nectaries attracting protective agents may help *Pleopeltis crassinervata*, the most widespread epiphytic species, persist despite habitat disturbance, surviving on shade trees in coffee plantations in former cloud forest areas of Veracruz.

<sup>1</sup>Instituto de Ecología, A.C., Herbarium, Apto. 63, Xalapa, Veracruz, 91000, Mexico<sup>2</sup>Universidad Veracruzana - Xalapa, Instituto de Neuroetología, Calle Dr. Luis Castelazo s/n, Col. Industrias Animas, Xalapa, Veracruz, 91190, Mexico<sup>3</sup>Instituto De Ecología, A.C., Apto. 63, Xalapa, Veracruz, 91000, Mexico

**POSTERS**

**184 CHEN, YING\*<sup>1</sup> and HOLLAND, MARJORIE<sup>2</sup>**

**Seasonal Changes in Coastal Vegetation Biomass**

Surges and waves generated by hurricanes and other severe storms can cause devastating damage to property and loss of life in coastal areas. Vegetation in wetlands and coastal fringes can reduce storm surges and waves while complementing traditional coastal defense approaches such as permanent levees, seawalls and gates. Moreover, the roots and rhizomes of marsh plants help coastal sediments cohere and consolidate. Soil and plant samples were collected from December 2009 to November 2010 in both low and high marsh zones directly along a coastal edge as well as further inland in eight transects at Graveline Bayou and at the Grand Bay National Estuarine Research Reserve (GND-NERR) on the Mississippi Gulf Coast. In these eight transects, four transects are located in coastal areas and four are in the inland marsh sites. The inland marshes are dominated by *Juncus roemerianus* (needlegrass rush), while *Spartina alterniflora* (smooth cordgrass) dominates the coastal marshes. Hydrologic and chemical data including salinity, pH, and water depth have been obtained from the monitoring stations at GND-NERR. Field measurements include collection of soil cores and plant samples within a 0.25 m<sup>2</sup> quadrat, plant heights, percent cover, and elevation. Laboratory analyses of the soil samples include moisture, bulk density, organic matter, mean grain size, and percentage of sand, silt, and clay. Laboratory analyses of the plant samples include measurements of above- and belowground biomass and rhizome thickness. Initial results suggest that above- and belowground biomass differs significantly over Spring, Summer, and Fall in coastal and inland marsh sites. Both above- and belowground biomass is highest in Summer and lowest in Spring in the coastal marsh sites. Although there is no significant difference in elevation gradients between the coastal and inland marshes, native vegetation at lower elevations with lower density in close proximity to storm surges within the coastal marsh sites tends to have lower above- and belowground primary production.

<sup>1</sup>University of Mississippi, Biology, Oxford, MS, 38677<sup>2</sup>University Of Mississippi, Biology, P.O. Box 1848, Shoemaker Hall, University, MS, 38677, USA

185 WARD, MEGAN<sup>\*1</sup> and MARTINE, CHRISTOPHER<sup>2</sup>

### The Current Status of a New Potential Invasive Plant Species within Clinton County, New York: *Mycelis muralis* (Asteraceae)

Invasive plant species have proven to be a common issue within communities where they can disrupt natural habitats and cause a loss of biodiversity. *Mycelis muralis* (Asteraceae) is a well-documented and well-studied invasive species in New Zealand, but has been recently recorded two years ago in SUNY Plattsburgh's Rugar Woods and nearby localities. *Mycelis muralis* has not been studied beyond being apart of general plant surveys within North America. To develop a better understanding of this apparent newcomer to northeastern New York, a two-step surveying technique shall be used. The first step in the process is to determine how dense the population of *M. muralis* is, and second, a more thorough, diverse survey shall be taken to use to analyze how *M. muralis* affects co-occurring plants and pollinator communities. This second survey will also be used to develop baseline data for diversity within Rugar Woods, something that has not been previously done. Preliminary testing shows that *M. muralis* in Clinton County shows similar site preference, including soil pH, as the invasive populations in New Zealand. These comparisons may prove to be critical to predicting future impacts of *M. muralis* within the region.

<sup>1</sup>State University of New York At Plattsburgh, Biological Sciences, 101 Broad Street, Plattsburgh, NY, 12901, USA<sup>2</sup> State University Of New York At Plattsburgh, 101 Broad Street, Plattsburgh, NY, 12901-2681, USA

186 DEWSBURY, BRYAN<sup>\*1</sup>, KOPTUR, SUZANNE<sup>2</sup> and FOURQUREAN, JAMES<sup>3</sup>

### Biodiversity and biogeochemical patterns along a chronosequence in a pine rockland habitat

Pine rocklands are critically endangered habitat whose community structure is primarily determined by periodic fire. In south Florida, slash and burn agriculture by native indians and modern day development have reduced this habitat to approximately 3% of its original acreage. Experiments in pine rocklands typically focus on the nature, periodicity and spatial scale of the fires that are responsible for keeping this ecosystem in a state of early succession. These studies suggest that periodic natural fires are necessary to allow clearance of the understory, and facilitate the growth of specific species. In the absence of fire, a buildup of organic matter can cause a shift in species composition and ultimately community structure. While the delivery and timing of

fires in this system have been well-studied, the biogeochemical changes that occur in the absence of fire are not as well understood. We sampled various sites in a pine rockland system to quantify the bottom-up effects on plant community structure in this system, and to characterize how this relationship might change in the absence of fire over large temporal scales. In this study we used the different burn schedules of spatially variant pine rocklands in Long Pine Key, Everglades National Park, Florida, to construct a chronosequence representing possibly different successional stages of this ecosystem. For logistical ease, as well as to draw comparisons to a parallel study in seagrass beds, we surveyed each site for mid level shrub species only, ignoring grasses, sedges and large (>6 feet) trees. We report that recently burned sites heavily favored the presence of *Ardisia escallonioides*, *Morinda royoc* and low coverage of *Myrica cerifera*. Sites burnt ten years ago had high coverage of both *Sereinoa repens* and *Sabal palmetto*. Other mid level shrubs varied highly between and within sites.

<sup>1</sup>Florida International University, Biology Department / Fourqurean Lab, 11200 SW 8th St, Miami, FL, 33199, USA<sup>2</sup>Florida International University, Department Of Biological Sciences, 11200 SW 8th St, Miami, FL, 33199, USA<sup>3</sup>Florida International University, Biological Sciences, 11200 SW 8th Street, OE 167, Miami, FL Florida, 33199, USA

187 SVOBODA, HARLAN<sup>\*</sup> and VAN KLEY, JAMES

### Effects of Exotic Species Removal at the SFA Pinewoods Native Plant Center on Native Forest Understory Vegetation

Chinese privet (*Ligustrum sinense*) is a non-native invasive shrub that is capable of replacing native forest understory with a near-monoculture. The Pinewoods Native Plant Center (PNPC) on the campus of Stephen F. Austin State University, Nacogdoches, Texas includes a wet-mesic bottomland forest which was heavily infested with privet. During the summer of 2009, much of the privet on the property was mechanically removed with subsequent follow-up spot herbicide treatments. During 2010, thirty 10m<sup>2</sup> plots were established in order to monitor vegetation changes associated with the privet removal effort. Plots were located in three treatment areas: 1) uncleared privet-infested, 2) recently (summer 2009) privet-cleared, and 3) a portion of the property that had been maintained privet-free for at least 20 years by hand-removal. Data were subject to canonical correspondence analysis (CCA) and multivariate classification and the Shannon-Wiener diversity index was calculated for each plot to observe any differences in the flora between the three sample areas. Even after removing effects of environmental co-variables of soil texture and micro-elevation, floristic differences were evident between the three treatments and plots from the three were located largely in distinct regions of a partial-CCA ordination space. Species richness was not significantly different between the three groups of

samples but the Shannon-Wiener diversity index was lower for the uncleared privet plots. Total vegetative coverage was higher in the uncleared privet plots than in the others but coverage in the recently-cleared plots was not significantly different from that of the privet-free plots. The results suggest that diversity and species richness were not adversely effected by the mechanical removal of *L. sinense* and the first-season post-removal community had already substantially recovered.

Stephen F. Austin State University, Biology, 1936 North St., Nacogdoches, TX, 75962, USA

## 188 TIPTON, ALICE G.\*<sup>1</sup> and GALEN, CANDACE<sup>2</sup>

### The ghost of glades past: ectomycorrhizal community abundance in degraded and restored dolomite glades

With the onset of fire suppression in the early twentieth century, many dolomite glade habitats throughout Missouri were invaded by cedars and other woodland species, causing the loss of these unique open habitats that once persisted on the southwestern slopes of Missouri hills. However, extensive restoration has begun at many of these historical glade sites. Differences in plant communities, soil mycorrhizal communities, and abiotic factors between glades and the surrounding woodland make glades an interesting system for studying edge effects on plant/mycorrhizal interactions. For example, oak (*Quercus*) species of Missouri woodlands host ectomycorrhizal fungi (ECM), while most of the herbaceous glade plants host arbuscular mycorrhizae (AMF). Because glades are harsh dry environments with shallow rocky soil, it is likely that mycorrhizal relationships between plants and their partnering fungi are important to the health and diversity of the plant community and restoration success. We sampled the ectomycorrhizal soil community in five glades of varying sizes and restoration ages (5-20 ybp) throughout central and southern Missouri. We also sampled 13 historic and overgrown glade sites in the same region, located at Tyson Research Center. The Tyson historic glade sites were cleared of tree species in the summer of 2010 but restoration has not yet begun. In both the historic Tyson glades and the 5-20 year old restored glades, ectomycorrhizal colonization decreased from the edge to the center of the glade site. Moreover, ectomycorrhizal colonization rates overall did not differ between historical glade sites at Tyson and restored glade sites. These results suggest that glades restrict ECM colonization and that such restriction persists long after glades have been converted into woodland. We are currently surveying the morphotypes of ECM species found in the glade samples, to determine if ECM vary in sensitivity to glade environments and accordingly in invasion potential.

<sup>1</sup>University of Missouri-Columbia, Biological Sciences, 105 Tucker Hall, Columbia, MO, 65211, USA<sup>2</sup>University Of Missouri, Biological Sciences, 105 TUCKER HALL, Columbia, MO, 65211, USA

## 189 FOARD, MEGHAN\*<sup>1</sup> and MARSICO, TRAVIS<sup>2</sup>

### Chinese privet invasion decreases botanical species richness in a riparian forest

Some recent research suggests that species invasions are the second greatest cause of extinctions, while other scientists consider invasions a side effect of habitat loss. MacDougall and Turkington (2005) propose possible ways to identify the role invasive species play in the reduction of biodiversity. They suggest models to determine if invasive species are drivers of ecosystem degradation or if they are passengers on the ride of habitat alteration. One way to assess the drive of invasive species is to compare the diversity of species that remain in a fully invaded ecosystem to species diversity in similar habitats with less invasion. Invasive species that are considered drivers compete directly with native species for limiting resources, resulting in reduced species richness and biodiversity. Based on preliminary species richness survey data, we demonstrate that the invasive shrub, *Ligustrum sinense* (Chinese privet), is likely a driver of its own invasion. In the riparian zone along the Wolf River in Shelby Farms Park Conservancy, Memphis, Tennessee, we evaluate botanical species richness within sites that are fully invaded by *L. sinense* and sites with less *L. sinense*. Our inventory suggests that in areas with the highest *L. sinense* cover there is reduced botanical richness when compared with the lower privet areas. Based on currently identified collections, 38 species were found in areas with 90-100% *L. sinense* cover and 52 were found in areas with 60-89% cover. The species richness (S) is 37% higher in the less-invaded regions relative to the most invaded sites. The implications of these observations are that *L. sinense* is a driver and has reduced the richness of native species. Based on these field observations and a thorough literature review, we discuss best practices for implementing a recovery plan in *L. sinense* invaded ecosystems.

<sup>1</sup>Arkansas State University, Department Of Biological Sciences / Marsico Lab, PO Box 599, Arkansas State University, State University, AR, 72467, USA<sup>2</sup> Arkansas State University, Department Of Biological Sciences, PO Box 599, State University, AR, 72467, USA

190 SHEARMAN, TIMOTHY\*<sup>1</sup> and  
MARTINE, CHRISTOPHER<sup>2</sup>

### Long term comparison of wetland plant communities in Ausable Marsh, Clinton County, NY 1978-2011: Preliminary Results

Plant community structure and composition can be altered for a number of reasons such as succession, invasion, or changes in climate or hydrology. This study seeks to identify community changes that have occurred over the past thirty years in Ausable Marsh, a large, complex wetland on Lake Champlain. Field maps of plant communities from a study in 1978 were digitized in GIS, where random nested plots were generated in each stratum identified. Preliminary results from the first of two field seasons (2010 and 2011) show that Sorensen's similarity index between 7 sampled strata and their 1978 counterparts varied. Overstory similarity was relatively high, with most strata over 60%. Due to lack of reference data, midstory and understory layers could not be compared in all strata. However, in those that could be compared, similarity was low (mostly under 40%) indicating that community changes may have occurred in these layers. Among the major changes were the spread of non-native species such as European frog-bit (*Hydrocharis morsus-ranae* L.), which was not present in the baseline data, and purple loosestrife (*Lythrum salicaria* L.), which greatly increased its range in the marsh. Native species such as wood nettle (*Laportea canadensis* [L.] Weddell) and ostrich fern (*Matteuccia struthiopteris* [L.] Todaro) also increased in abundance. The 2011 field season will provide more conclusive data regarding community change in the marsh. This project will set up a long-term research study that will enhance our ability to record and understand large-scale shifts in diversity and ecosystem function in wetland habitats of the Sixth Great Lake. It can also provide critical information in developing a management plan for non-native species in the marsh.

<sup>1</sup>SUNY Plattsburgh, Natural Science Graduate Program, 101 Broad St., Plattsburgh, NY, 12901, USA<sup>2</sup>State University Of New York At Plattsburgh, 101 BROAD STREET, PLATTSBURGH, NY, 12901-2681, USA

191 CHAPMAN, JULIA\* and MCEWAN,  
RYAN

### Tree regeneration ecology of an old-growth central Appalachian forest: Diversity, temporal dynamics, and disturbance response

Diversity and compositional dynamics in deciduous forests of eastern North America are increasingly subject to an array of drivers including natural small- and large-scale disturbances, invasion by exotic species, pathogens, insect pests, and anthropogenic influences. In order to understand reactions to these drivers, there is a pressing need to understand baseline dynamics in these forests. In particular, these forests are thought to be undergoing a long-term dominance shift in which maples (*Acer* spp.) are replacing oaks (*Quercus* spp.). We examined dynamics of woody understory species in an old-growth central Appalachian forest to 1) document baseline dynamics over a decade and 2) investigate the reaction of the seedling and shrub-layer vegetation to a recent fire in one portion of the study site. We were also interested in understanding in how species diversity in the woody understory reacted to gradients of productivity and to the recent fire. Over a ten-year interval (2000 - 2010), *Acer* spp. sapling densities decreased significantly ( $P < 0.01$ ) and *Quercus* spp. sapling densities did not change significantly. Seedling densities of *Acer* spp. increased significantly ( $P < 0.01$ ) while mean cover decreased significantly ( $P < 0.01$ ). For a few *Quercus* species, seedling densities increased significantly ( $P < 0.01$ ), and mean cover of *Quercus alba* seedlings increased significantly ( $P < 0.05$ ). Significant unimodal relationships ( $P < 0.01$ ) were exhibited between diversity and productivity in both understory strata. Plots burned by fire had significantly lower sapling layer density and species richness ( $P < 0.001$ ) in 2010 compared to pre-disturbance data in 2000. In the same area, the seedling layer did not show a clear response to this fire disturbance. Further work is needed to understand how various ecosystem drivers are influencing the composition of forest regeneration layers and how those trends relate to overstory succession. The factors that constrain or promote diversity to create a unimodal relationship with productivity also need to be examined.

University Of Dayton, Biology, 300 College Park, Dayton, OH, 45469-2320, USA

192 CARUSO, CHRISTINA\*<sup>1</sup>,  
LAMBERT, ALLISON M.<sup>2</sup>, GALE, NIGEL V.<sup>3</sup>,  
SEIFERT, ELIZABETH K.<sup>3</sup>, MILLS, EMILY  
R.<sup>3</sup>, MADSON, HANNAH J.<sup>1</sup>, BAILEY,  
MAIA<sup>4</sup> and CASE, ANDREA<sup>5</sup>

### Predictors of outbreeding depression in *Lobelia siphilitica* (Lobeliaceae)

Outbreeding depression is defined as a decline in fitness caused by mating between distantly related individuals, and can have significant consequences for the success of habitat restoration projects. To avoid outbreeding depression, some restoration projects use local seed sources. However, the geographic distance between parental populations may not adequately predict genetic and ecological distance, and consequently the potential for outbreeding depression. We tested for outbreeding depression in *Lobelia siphilitica* (Lobeliaceae), a wildflower commonly used in prairie, woodland, and wetland restorations in the midwestern United States. We then determined whether the magnitude of outbreeding depression was correlated with the geographic, ecological, and/or genetic distance between parental populations. We crossed *L. siphilitica* plants from six focal populations with individuals from their home population and from each of 20 away populations. Four fitness components were measured for each cross: seeds per fruit, percent germination, early offspring size, and final aboveground biomass. These fitness components will be used to estimate the magnitude of outbreeding depression for each combination of home and away populations. We will use climate data to estimate the ecological distance, and chloroplast genome sequence data to estimate the genetic distance between home and away populations. Mantel tests will then be used to determine if geographic, ecological, and genetic distances are correlated with each other. Finally, we will test which of these distance metrics best predicts variation in the magnitude of outbreeding depression. Our results will indicate whether the geographic distance between parental populations is a good predictor of the magnitude of outbreeding depression, or if additional ecological and genetic information is necessary to select seed sources for the restoration of *L. siphilitica* populations.

<sup>1</sup>Kent State University, Department of Biological Sciences, Kent, OH, 44242, USA<sup>2</sup>University of Florida, Fort Lauderdale Research and Education Center, 3205 College Avenue, Fort Lauderdale, FL, 33314, USA<sup>3</sup>University of Guelph, Department of Integrative Biology, New Science Complex, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada<sup>4</sup>Providence College, Department of Biology, 1 Cunningham Square, Providence, RI, 02918, USA<sup>5</sup>Kent State University, Box 5190, 256 Cunningham Hall, Kent, OH, 44242-0001, USA

193 BOCIAN, LINDSEY\*<sup>1</sup>, MCGIVERN,  
JAMES<sup>1</sup>, BROWN, NATHALIE-ANN<sup>2</sup>,  
PERENIC, JOSEPH<sup>3</sup> and GANGER,  
MICHAEL<sup>1</sup>

### The Vascular Plant Species of the Fringing Habitat Ecotone in the Erie Bluffs State Park

The Erie Bluffs State Park is a 450-acre property located in northwestern Pennsylvania along Lake Erie. The park contains various habitats including broadleaf terrestrial forest, broadleaf terrestrial woodland, broadleaf palustrine forest, terrestrial herbaceous openings, agricultural fields, and a fringing ecotone habitat, hereafter referred to as the fringing habitat. The management plan for the park includes converting the agricultural fields to native habitat. Given that the fringing habitat surrounds these fields, this habitat is likely to serve as a source of colonists. Therefore, the characterization of the fringing habitat is crucial to successfully predicting the post-conversion community. In the summer of 2010, 146 quadrats, one meter wide and 50 meters apart, were established within the fringing habitat. The vascular plant species present in each quadrat were recorded. A comparative analysis was conducted to compare the native/non-native status of species to those present throughout the park, as well as the number of species unique to the fringing habitat. Life history data, species richness data, frequency of species, and frequency across families were also obtained for all of the species in the fringing habitat. A comparison was made between the species found in the one agricultural field that was allowed to go fallow in 2009 and the species found in the fringing habitat. The fringing habitat was found to contain 158 of the 441 species present in the park overall, despite containing roughly 2% of the park's area. These species include forest and field species along with 64 species (41%) unique to the habitat. Most species, 65%, were perennials indicating a persistent community. Approximately 40% of the species were non-native. Of species in the one abandoned field, 98% also occurred in the fringing habitat. Together, these data highlight the importance of the fringing habitat in old field succession. Managing the fringing habitat prior to agricultural field abandonment is therefore crucial to managing the transition from agricultural fields to native habitat.

<sup>1</sup>Gannon University, Biology, 109 University Square, Erie, PA, 16541, USA<sup>2</sup>Gannon University, Biology Department, 109 University Square, Erie, PA, 16541, USA<sup>3</sup>Gannon University, Biology Department, 109 University Square, Erie, PA, 16541, USA

194 COLLINS, HILARY<sup>\*1</sup> and  
DRENOVSKY, REBECCA<sup>2</sup>

### Shade Tolerance and Early Life History Stages Of a Problematic Invasive, *Rosa multiflora* Thunb. (Roseaceae)

Invasive biology is a relevant and pressing current topic; however, little research has been focused on the ability of plants to invade forested ecosystems. Previously, forests have been considered resistant to invasive plants, but recent work suggests that forests are susceptible and could be severely impacted by invasives. *Rosa multiflora* is a common invasive species of edge habitats, and isolated individuals or small populations of *R. multiflora* also grow in the forest interior. We hypothesized that *R. multiflora* is shade tolerant, potentially enabling it to become invasive in the forest interior. We compared light levels and shrub density at the forest edge and interior in Cuyahoga Valley National Park, OH. To learn more about the reproductive characteristics of *R. multiflora*, we recorded the fecundity of select shrubs and took soil samples to determine the number of seeds in the edge and interior seed bank. Although there was no significant difference between shrub density in edge versus interior plots, there was a trend for higher density in edge plots ( $F=4.822$ ,  $P=0.093$ ). *R. multiflora* shrubs at the edge did produce significantly more flowers ( $t=5.7$ ,  $P<0.0001$ ) and hips ( $t=5.7$ ,  $P<0.0001$ ), than in the interior. However, few *R. multiflora* seeds were found in the seed bank in either edge or interior plots. Evidence of high levels of frugivory of *R. multiflora* hips by white-tailed deer was observed during the study, which could be facilitating the spread of *R. multiflora* throughout the forest. Our data suggest that *R. multiflora* is partially shade tolerant, as it is able to survive and grow vegetatively in the forest interior, although its ability to reproduce is likely limited by shade. In forests where frequent disturbance events occur (which can create canopy gaps), *R. multiflora* could become problematic.

<sup>1</sup>John Carroll University, Biology Department, 20700 North Park Blvd, University Heights, OH, 44118, USA<sup>2</sup>John Carroll University, Biology, 20700 North Park Blvd, University Heights, OH, 44118, USA

195 BINGGELI, CASEY<sup>\*1</sup>,  
MIHUC, TIMOTHY<sup>2</sup> and MARTINE,  
CHRISTOPHER<sup>3</sup>

### Impact of invasive aquatic plants on macroinvertebrate and zooplankton communities in Lake Champlain

There are 48 invasive species in Lake Champlain. Thirteen of the 48 invasive species are plants and yet, very little research has been done on the effects of invasive aquatic macrophytes on associated macroinvertebrate communities in Lake Champlain. The purpose of this study was to determine the impact invasive macrophytes have on macroinvertebrate and zooplankton communities. Invasive macrophytes examined during this study include *Trapa natans* (water chestnut), *Hydrocharis morsus-ranae* (European frog-bit), *Nymphoides peltata* (yellow floating heart) and *Myriophyllum spicatum* (Eurasian watermilfoil). Native species included *Nymphaea odorata* (American white water-lily), *Nuphar lutea* (yellow pond lily) and *Ceratophyllum demersum* (coontail). Plant and macroinvertebrate communities were collected using a 250  $\mu$ m veliger net. Zooplankton samples were collected using a 63  $\mu$ m Wisconsin net. Comparisons were made between the macroinvertebrate communities utilizing invasive plants and those utilizing native plants of similar growth habit. Each plant species sampled had a unique macroinvertebrate community composition. Differences between macroinvertebrate communities found on native versus invasive macrophytes included an increase in Amphipoda, Coleoptera, Ephemeroptera and Hemiptera in native plants.

<sup>1</sup>SUNY Plattsburgh, Dept. Biological Sciences, 101 Broad Street, Plattsburgh, NY, 12901, USA<sup>2</sup>Lake Champlain Research Institute, Center for Earth and Environmental Science, 101 Broad St, Plattsburgh, NY, 12901, USA<sup>3</sup>SUNY Plattsburgh, Biological Sciences, 101 Broad Street, Plattsburgh, NY, 12901, USA

196 MCDONALD, BRIENNA and  
GEHRING, JANET<sup>\*</sup>

### A comparative study of the response of two *Helianthus* species to water availability

Differences in the local distribution of congeners can result from adaptation to biotic and abiotic factors in their respective habitats. We studied two species of sunflowers, *Helianthus grosseserratus* and *H. occidentalis* that grow in different environments. *Helianthus occidentalis* is found in dry, open environments such as sand and hill prairies whereas *H. grosseserratus* is typically found in areas with higher moisture availability. We hypothesized functional traits related to drought tolerance would differ between the two *Helian-*

*thus* species and coincide with their typical habitats. We also hypothesized phenotypic plasticity would differ between the two species in response to water availability. To test our hypotheses, we exposed individuals of both species to three levels of water availability. Relative water content (RWC) at harvest indicated our experimental treatments were effective; relative water content was highest in high-water plants and decreased with water availability. Our results show that *H. grosseserratus* grew faster and larger than *H. occidentalis*, even under low water conditions. *Helianthus grosseserratus* was largest in high-water conditions whereas *H. occidentalis* gained the most biomass in the medium water treatment. Specific leaf area (SLA) of *H. occidentalis* was lower than in *H. grosseserratus*, suggesting *H. occidentalis* leaves are thicker and may have higher water-use-efficiency. Furthermore, *H. occidentalis* adjusted its SLA in response to water availability to a much greater extent than did *H. grosseserratus*, which may have contributed to the ability of *H. occidentalis* to maintain RWC. We conclude that *H. occidentalis* is restricted to dry open environments both because it is adapted to dry conditions but also because it may be excluded from high-water habitats.

#### 197 MAKINGS, ELIZABETH

##### "Found Then Drowned" Noteworthy Collections from Tempe Towne Lake riverbed, Tempe, Arizona

Tempe Town Lake is a water body created by inflatable bladder dams that were constructed along the highly regulated and formerly-perennial Salt River in Phoenix, Arizona. The dam ruptured on 20 July 2010, exposing organic and clay-dominated lake bed sediments that had been submersed for approximately 10 years. A unique plant community sprung up in the immediate aftermath - dominated by graminoid wetland vegetation and reminiscent of cienega marshlands that historically blanketed many rivers in the Southwest. During a site visit on 27 Sept 2010 twenty taxa were collected. Three species turned out to be of interest: *Cyperus michelianus* ssp. (Rottb.) Asch. & Graebn. (Cyperaceae) - a North American record; *Ludwigia erecta* (L.) Hara (Onagraceae) - an Arizona record with a disjunct of some 1,200 miles; and *Ammannia coccinea* Rottb. (Lythraceae) - historically rare in Arizona, but suddenly abundant in this particular reach of the temporary wetland of the Salt River. The habitat is now gone as the bladder dams were replaced, and the Lake refilled, but the exercise underscores the importance of collecting in sometimes overlooked urban watersheds that may harbor novelties.

Arizona State University, School of Life Sciences, PO Box 874501, Tempe, AZ, 85287-4501, USA

#### 198 HUEBNER, CYNTHIA D.

##### Changes in invasive plant species abundance over five years in disturbed and undisturbed forests

Invasive plants establish and spread because they are opportunists, superior competitors, or both. As opportunists, invasive plants take advantage of disturbance-related resource changes. The goal of this study was to determine if existing exotic plant species cover in both disturbed and undisturbed forests increased over time, and if the increases were most likely to occur in disturbed forests and mesic land types. Forty-eight stands in a deciduous temperate forest with half in each of two disturbance types (80+ year-old second growth forests and 15-year old clear cuts) were selected with 7-9 stands in each of three land types. The 80+ stands were sampled in May-July in 2001 and again in 2006; the clear cuts were sampled in May-July in 2002 and again in 2007. Differences in percent cover of all plant species, with a focus on the exotics and common native species, were determined and compared using a Kruskal-Wallis test. There were 5 exotic (2 invasive) plants in the 80+ stands in 2001 and 6 exotic (1 invasive) plants in 2006. There were 18 exotic (5 invasive) plants in the clear cuts in 2002 and 16 exotic (5 invasive) plants in 2007. Only *Rosa multiflora* significantly increased in cover, and only in the clear cuts. There was no significant relationship between *R. multiflora* change in cover and land type. Changes in cover of three common native species that are not preferred by deer all increased significantly in the clear cuts but not in the 80+ stands. There were no significant changes in cover related to land type or disturbance for two native species preferred by deer. These findings confirm that the invasive species found in these stands were opportunists who responded positively to disturbance, but were not superior competitors. Similar increases in cover in the clear cuts were also found for some of the native species.

Northern Research Station, USDA Forest Service, 180 Canfield St., Morgantown, WV, 26505, USA

#### 199 STODDARD, MATTHEW<sup>\*1</sup> and MELOCHE, CHRISTOPHER<sup>2</sup>

##### Morphological variation, developmental stability, and genetic diversity in an Alpine Avens.

Alpine Avens (*Geum rossii*) is the most widespread and abundant plant in the alpine tundra of Colorado. Due to the short growing season of this high altitude environment, shoots of *G. rossii* undergo extreme developmental preformation. On the tundra, *G. rossii* is distributed across a steep gradient of soil moisture and growing season length. Across this gradient the mature

size of leaves varies by as much as 90% but is inversely correlated with growing season length. In spite of large changes in mature morphology across the gradient, the duration of preformation and the proportion of development completed during preformation do not vary significantly. Plants must develop to achieve a much greater size in less time in wet, short growing season environments. Because *G. rossii* is extensively clonal, spreading rhizomatously belowground, the relative contribution of asexual and sexual reproduction remains unclear. To determine if the contrasting development is purely phenotypic plasticity or if it has a genetic component, DNA was extracted and three microsatellite loci specific to *Geum* were amplified using PCR. Preliminary genetic analysis suggests that genetic variation does exist across strong the strong environmental gradients in the Colorado Alpine.

<sup>1</sup>Metropolitan State College of Denver, Department of Biology, P.O. Box 173362, Campus Box 53, Denver, CO, 80217-3362, USA<sup>2</sup>Metropolitan State College Of Denver, P.O. Box 173362, Campus Box 53, DENVER, CO, 80217-3362, USA

200 DENTON, RENEE

### Biodiversity and hydrology of swales in blueoak woodlands of the west central Sierra Nevada

Western foothills of the Sierra Nevada represent some of the most biologically diverse ecosystems in California. Wetlands associated with these ecosystems are of particular interest as they represent a spatially and temporally unique yet floristically rich subset of this diversity. Swales are a class of foothill wetlands apart from springs, seeps, and intermittent streams. During the rainy season, the flush of water infiltrating the shallow, sandy upland soils flows into lowland swales before seeping into cracks in the granitic substrate as ground water recharge. Swales form a network across the landscape linked directly to the uplands yet represent a small proportion of the total land area. In order to conserve foothill wetland biodiversity in the future, it will be crucial to identify the components of importance for conservation and sustainable use, and to determine how anthropogenic practices influence these components across the landscape. How will grazing as a tool, or even the absence of grazing, be used to modify the landscape? To this end, research is ongoing at the San Joaquin Experimental Range to better understand how climate variability and grazing affect plant biodiversity and related hydrologic function. Five swale complexes were selected wherein to replicate two seasonal mowing treatments and allow control plots representing release from grazing. Plant species (alpha) and patch (beta) diversity was collected for all 15 swales at the peak of flowering using the multi-scale Modified Whitaker plot method (Stolgren et al. 1999). Common native plant species include *Eleocharis palustris*, *Calandrinia ciliata*, *Mimulus guttatus*, *Ranunculus californicus*, and

*Sidalcea hartwegii*. Ground water height was sampled in each swale with 2 stratified rows of 9 stand pipe piezometers. Moisture in the soil profile from ground surface to bedrock was measured using the Deviner 2000 system. Variation in total plant biomass was evaluated each season along with all other parameters for five years. Best methods for managing and restoring the structure, composition, and function of wetland ecosystems will be developed.

USDA Pacific Southwest Research Station, 2081 E. Sierra Ave., Fresno, CA, 93710, USA

201 CALLEN, STEVEN\*<sup>1</sup>, KNOUFT, JASON<sup>1</sup> and MILLER, ALLISON<sup>2</sup>

### Assessing the environmental niches of native and introduced *Pueraria montana* (kudzu)

Similarities in niche characteristics of native and introduced ranges have been implicated as important factors contributing to invasion success. Comparative analysis of the environmental niches of introduced populations and the native populations from which they originated facilitates the identification of environmental factors associated with successful invasion. Kudzu, *Pueraria montana* var. *lobata*, native to Asia, was introduced into the United States in 1876 and has since established populations in nearly 30 states, often dominating the landscape and displacing native taxa. In order to identify potential differences in the native and introduced environmental niches that may be contributing to the success of kudzu in the United States, GIS-based techniques in ArcGIS v9.3 and Maxent were used to describe the environmental niches of native (Asia) and introduced (United States) kudzu populations. While annual precipitation was the most important variable characterizing both ranges, temperature seasonality was important for predicting the extent of the native range, while precipitation of the driest month and annual mean temperature were of primary importance for predicting the introduced range. Environmental niche models created with environmental variables from the introduced range and projected onto the native range predicted 99% of the localities, where as models generated using environmental variables from the native range and projected onto the introduced range predicted only 74% of the localities. While biotic factors such as release from specialist enemies and community structure likely play a role in the kudzu invasion, these preliminary results suggest apparent differences in abiotic factors characterizing the native and introduced ranges of kudzu.

<sup>1</sup>Saint Louis University, Biology, 3507 Laclede Avenue, St. Louis, MO, 63103, USA<sup>2</sup>Saint Louis University, Department Of Biology, 3507 Laclede Avenue, St. Louis, MO, 63103, USA

202 COLLINS, JENNIFER\*<sup>1</sup> and  
MARTINE, CHRISTOPHER<sup>2</sup>

***Hydrocharismorsus-ranae* (European frogbit, Hydrocharitaceae): Growth response of an aquatic invasive plant to additions of nitrogen and phosphorous**

*Hydrocharis morsus-ranae* (Hydrocharitaceae), commonly known as European frog-bit, is a free-floating invasive aquatic plant residing in mostly shallow, marsh-like waters in parts of southern Canada and the northern U.S. The species creates a dense mat of interlocking plants on the surface of the water. European frog-bit is believed to have negative effects on the communities it invades, including impeding water flow and blocking out light that is essential for submerged native flora. These two problems may, in turn, affect native fauna by creating a less oxygen-rich environment and by reducing attachment sites for aquatic invertebrates. The focus of this undergraduate research study, in collaboration with the Lewis Creek Association (Vermont), is to identify the effects of nitrogen and phosphorous inputs on established populations of *H. morsus-ranae*. Using individuals collected in Lake Champlain, measurements of leaves and rosettes, plus total plant biomass, will be taken as a means to track the influence of nitrogen and phosphorous additions to lake water. Results of the study may influence policy in the Lewis Creek watershed, where agricultural run-off is thought to contribute to the vigor of established *H. morsus-ranae* populations, thus presenting an additional challenge to ongoing eradication efforts.

<sup>1</sup>SUNY Plattsburgh, Biology, 101 Broad St, Plattsburgh, NY, 12901, USA<sup>2</sup>State University at Plattsburgh, Biological Sciences, 101 Broad St, Plattsburgh, NY, 12901, USA

203 DUCHICELA, JESSICA\*<sup>1</sup>,  
VOGELSANG, KEITH M<sup>1</sup>, SCHULTZ,  
PEGGY A.<sup>1</sup>, KAONONGBUA, WITTAYA<sup>2</sup>,  
MIDDLETON, ELIZABETH<sup>3</sup> and BEVER,  
JAMES<sup>4</sup>

**Non-native plants and soil microbes contribute to reduced soil aggregate stability in disturbed N. American grasslands.**

Soil aggregate stability is an important ecosystem property that reflects the soil vulnerability to erosion and its potential to sequester carbon. Soil aggregate stability has been shown to decline with anthropogenic disturbances, but the consistency, duration, and causes of these declines in aggregate stability are untested. We assessed aggregate stability in paired remnant and post-disturbance old fields across California grasslands,

shortgrass prairie and tallgrass prairie. We found that the proportion of water-stable aggregates was lowest in shortgrass prairie and that sites recovering from anthropogenic disturbance consistently had lower aggregate stability than remnant sites, with the negative effect of a prior history of tillage being greater than that of grazing. Across all grasslands, non-native plant diversity was a significantly negative predictor of soil aggregate stability and mediates part of the effect of prior disturbance. The negative effect of non-native plants on aggregate stability was confirmed in a mesocosm experiment focusing on the California grasslands. Moreover, an inoculation study focusing on the tallgrass prairie soils demonstrated that the degradation of the microbial community also contributed to the decline in soil aggregate stability. Overall the results suggest that alteration of both plant and microbial composition underlie the continued prevents the recovery of aggregate stability following anthropogenic disturbance. Therefore, restoration practitioners need to address these biological components in the ecosystem in order to recover the important ecosystem service of soil stabilization.

<sup>1</sup>Indiana University, Biology, Jordan Hall; 1001 East Third Street, Bloomington, IN, 47405, USA<sup>2</sup>Indiana University, Biology, 1001 E. 3rd St, Jordan Hall 142, Bloomington, IN, 47405, USA<sup>3</sup>Indiana University, 1001 E Third Street, Bloomington, IN, 47405, USA<sup>4</sup>Indiana University, Biology, 1001 East Third Street, Bloomington, IN, 47405, USA

204 VERRICO, BRITTANY\*<sup>1</sup> and  
KILGORE, JASON<sup>2</sup>

**Life stage fluctuations in garlic mustard (*Alliaria petiolata*) abundance: incorporating long-term ecological monitoring into an undergraduate curriculum**

Garlic mustard (*Alliaria petiolata*) is an invasive biennial forb of eastern North American deciduous forests that exhibits oscillating life stage abundance within a given population. As part of a Long-term Ecological Monitoring (LEM) program, garlic mustard abundance will have been monitored by undergraduate interns (Summers 09, 10) and students from introductory biology (Fall 09, 10), botany (Spring 10, 11), and experimental biology (Summer 11) courses. Abundance of rosettes and adults were recorded from 80 plots over 10 transects in a 57-acre biological field station. From Summer 2009 to 2010, abundance of garlic mustard rosettes significantly decreased in 3 of 8 transects (95% CI of difference in means), while abundance of adults significantly decreased in 2 transects; the other transects had no significant ( $\alpha = 0.05$ ) difference in abundance of either life stage across years. Within plots, change in rosette abundance was negatively correlated ( $r = -0.39, p < 0.001$ ) with change in adult abundance. This relatively weak relationship may be due to

late Summer germinants contributing to the following year's adult cohort; we plan to track germinants through the Summer to test this hypothesis. These results support the notion that populations of this invasive biennial undergo fluctuations in life stage abundance, likely as a result of high seed production and strong density dependence, including an interaction between rosette and adult life stages. Furthermore, monitoring of garlic mustard populations as part of the LEM program has successfully been integrated into the biology curriculum thus exposing a wider range of students to long-term botanical studies.

<sup>1</sup>Washington & Jefferson College, 50 South Lincoln Street, Box 1328, Washington, PA, 15301, USA<sup>2</sup>Washington & Jefferson College, 60 South Lincoln Street, Washington, PA, 15301, USA

## 205 CARABALLO-ORTIZ, MARCOS\* and CARLO, TOMAS

### Coevolution of American mistletoes with tree families

Mistletoes are obligate parasitic plants that depend on host trees for their establishment, growth, and mineral nutrition. Although mistletoes play an important ecological role in plant communities, little is known about the coevolution between mistletoes and their hosts. To determine if mistletoes are host specific (a measure of coevolution), we selected the two largest mistletoe families in America (Loranthaceae and Viscaceae) and assembled a database using thousands of parasitism records from herbarium specimens and the literature. Next, we compared the frequency of host parasitism among the most common tree families and genera present in the Americas. We found that mistletoe parasitism is not random across plant families, and although parasitism has been recorded in more than 100 tree families, mistletoes were significantly more frequent in families such as Leguminosae, Fagaceae, Malvaceae, Rutaceae, and Pinaceae. To gain insight in the level of host specificity, we performed a reciprocal transplant experiment in the field using mistletoes in the genus *Dendropemon* (Loranthaceae). We carried out the experiment in Northeastern Puerto Rico where two very similar *Dendropemon* species coexist in different host trees: *D. bicolor* in *Tabebuia* (Bignoniaceae) and *D. caribaeus* in *Citharexylum* (Verbenaceae). The results of the reciprocal transplant suggest that *Dendropemon* mistletoes are host specific. These data also suggest that the global pattern of coevolution between mistletoes and their hosts is influenced by the taxonomic identity and the local interactions of both the parasite and its host.

Penn State University, 208 Mueller Lab, University Park, PA, 16802, USA

## 206 SALAZAR, GERARDO\* and BALLESTEROS-BARRERA, CLAUDIA

### Using niche modeling to assess potential further spread of the African invasive orchid *Oeceoclades maculata* in Mexico

*Oeceoclades maculata* is a terrestrial orchid first discovered in Brazil early in the XIX century but now believed to be native to tropical Africa. In the few last decades it spread out from South America throughout Central America and the Caribbean islands, and into Florida, USA. In the early 1990's a first population of *O. maculata* was recorded in the Yucatan Peninsula, Mexico and since then the species has dispersed widely in south-eastern Mexico, thriving in moderately disturbed as well as in well-conserved, wet- to seasonally dry tropical forest habitats. However, so far *O. maculata* is restricted in Mexico to the Gulf slope and its northern limit of distribution is coincident with the north-western edge of the Isthmus of Tehuantepec (foothills of the Sierra de los Tuxtlas in southern Veracruz and the area of Tuxtepec in northern Oaxaca). In this study we performed ecological niche modelling based on georeferenced occurrence data and environmental data layers analysed with the Maxent software package to generate potential distribution maps for *O. maculata*. Our aim was identifying additional areas with potentially suitable environmental conditions for this species in parts of Mexico where it has not been recorded. Two models were generated, one using only data from Mexican localities and the other based on all available records from the global distribution of the species. The potential distribution modelled only from Mexican records closely matches the known distribution of *O. maculata* in this country but fails to predict its presence in other areas where it has been confirmed (e.g. Florida). On the other hand, the projection based on all global records identifies large expanses of suitable environmental conditions both on the Gulf slope (most lowland areas of Veracruz and adjacent states, north to central Tamaulipas) and on the Pacific watershed, where the species has never been found, suggesting that, at least as to environmental abiotic conditions, *O. maculata* is likely to continue expanding its range in Mexico

Departamento de Biología, Universidad Autónoma Metropolitana Iztapalapa, Mexico City, Distrito Federal, Mexico

207 FALCON, WILFREDO\*<sup>1</sup>,  
TREMBLAY, RAYMOND<sup>2</sup> and ACKERMAN,  
JAMES<sup>1</sup>

**Population biology of an invasive orchid:  
The emerging dominance of *Spathoglottis  
plicata* in Puerto Rico**

**A**bstract Unavailable.

<sup>1</sup>University of Puerto Rico, Biology, Faculty of Natural Sciences, PO Box 70377, San Juan, PR, 00936-8377, USA<sup>2</sup>COLEGIO UNIVER DE HUMACAO, DEPT BIOLOGIA/EST POST C.U.H., HUMACAO, PR, 00791-4300, USA

208 CRAWFORD, KERRI MARGARET\*  
and RUDGERS, JENNIFER

**Effects of plant species diversity and  
genetic diversity on aboveground and  
belowground processes**

**B**iodiversity is a critical element of community properties and ecosystem processes. Both plant species richness and genetic diversity positively affect processes ranging from primary production, ecosystem stability, and the maintenance of diversity. In nature, it is likely that species diversity and genetic diversity interactively affect how communities are structured and ecosystems function. However, their relative contributions and potential interactive effects have been rarely documented. A potentially important (but relatively unexplored) consequence of declining plant diversity is the alteration of soil microbial community structure and function. Soil microbes are important drivers of ecosystem functions and can be important determinants of plant community structure. Here, we report results from a common garden experiment conducted in a coastal freshwater dune habitat at Sleeping Bear Dunes National Lakeshore in Empire, MI. We manipulated plant species diversity (0, 1, 3, or 6 species) and genetic diversity (0, 1, 3, or 6 populations) within a dominant, dune-building species (*Ammophila breviligulata*) to address how both levels of diversity simultaneously influence aboveground and belowground properties and processes. Preliminary results suggest that plant diversity influences a wide range of responses. Plant species diversity and genetic diversity synergistically influence aboveground biomass production but no effects of plant diversity on belowground biomass were detected. Soil nematode abundance doubled with both increasing species diversity and genetic diversity, although there were no interactions between the two levels of diversity. Furthermore, there is a strong trend for diversity to interactively influence arbuscular mycorrhizal fungal spore abundance. Soil physical properties were also affected. Potassium was generally

lost from experimental communities during 2009 to 2010. However, there was a significant species diversity by genetic diversity interaction such that in plots with high levels of genetic diversity, potassium was not lost, but instead increased with increasing species diversity. These results suggest that interactions between levels of diversity are an important aspect of how diversity structures communities and mediates ecosystem processes.

Rice University, Ecology & Evolutionary Biology, 6100 Main Street, MS - 170, Houston, TX, 77005, USA

ORAL PAPERS

209 GYLLENHAAL, CHARLOTTE\*<sup>1</sup>,  
KADUSHIN, MARIAN<sup>1</sup>, WALLER,  
DONALD<sup>2</sup> and SOEJARTO, DR. DJAJA D.<sup>3</sup>

**Ethnobotanical versus random plant  
collections in natural product drug  
discovery**

Natural product drug discovery encompasses the search for new medications from plants and other natural sources. Discussion is ongoing as to proper sourcing of plant materials to optimize the yield of new medications or of new phytochemical compounds that may serve as leads for pharmaceutical drug development. Two primary approaches in use to acquire plant samples for discovery are the ethnobotanical and the random approaches. In a project to discover new bioactive compounds from plants of Vietnam and Laos (1998-2008) we used both approaches. Under a cooperative agreement, plants were acquired, on one side, through traditional medicine use from healers throughout Laos, and from villages surrounding a national park in Vietnam (the ethnobotanical collection pool). On the other side, plants were acquired using the random collection method from the forests of Cuc Phuong National Park, Ninh Binh Province, Vietnam (the random collection pool). All plants were extracted in Laos and Vietnam, respectively, and the extracts sent to the University of Illinois at Chicago and other cooperating laboratories for testing in a variety of cancer cell lines, HIV, malaria, tuberculosis and cancer chemoprevention. Botanical identification, ethnobotanical information and laboratory results were managed in a comprehensive database, the Natural Products Information System (NAPIS, White Point Systems). Chi-square analysis was used to test the hypothesis that plants used in traditional medicine were more likely to test positively in the various bioassays, and that plants with uses related to specific bioassays were more likely to test positively in the related bioassay. Results will be presented for the individual bioassays and all bioassays analyzed together.

<sup>1</sup>University of Illinois at Chicago, Department of Medicinal Chemistry and Pharmacognosy, 539 Pharmacy, mc 781, 833 South Wood Street, Chicago, IL, 60612, USA<sup>2</sup>University of Illinois at Chicago, Department of Biopharmaceutical Sciences, 335 Pharmacy, MC 865, 833 South Wood Street, Chicago, IL, 60612, USA<sup>3</sup>College of Pharmacy, University of Illinois at Chicago, Chicago, Department of Medicinal Chemistry and Pharmacognosy, 833 S. Wood St., Chicago, IL, 60612, USA

210 DE GEZELLE, JILLIAN M.\*<sup>1</sup> and  
MAHADY, GAIL<sup>2</sup>

**Phytoestrogen Use in Q'eqchi Maya  
Fertility Regulation and Reproductive  
Ethnomedicine in Southern Belize**

**I**ntroduction: The Q'eqchi Maya of Belize have an extensive traditional pharmacopoeia of plants used for reproductive health and fertility regulation. Such plants provide compelling leads for compounds with novel hormone-mimicking bioactivity. These plant-based medicines have wide-reaching therapeutic potential including protection from reproductive cancers and neurodegenerative disorders, as well as the treatment of menopausal symptoms and infertility. Objectives: This study was conducted in conjunction with the Belize Indigenous Training Institute (BITI) in the hopes of comprehensively documenting traditional treatments for reproductive health, and revitalizing traditional Maya medicine in Belize. BITI shares an interest in further validating Q'eqchi traditional wisdom through verification of medicinal qualities of their plant medicines. Methodology: Semi-structured interviews, forest and home garden interviews, photo elicitation, and plant collections were used to collect data with 32 Q'eqchi adults over 18 months of fieldwork in Belize between 2007 and 2010. Ten plant species were collected to assay for estrogenic activity. A total of thirteen methanol extracts were tested using a reporter gene assay at the UIC/NIH Center for Botanical Dietary Supplements Research. Results: The Belizean Q'eqchi utilize at least 70 plant species in 35 families for 47 conditions related to reproductive health. The highest numbers of species were used to treat heavy menstruation, for use as contraception, to treat infertility, for use during pregnancy, and for treating menopause. In addition to medicinal plants, healers use massage, prayer, and ritual in their ethnomedical treatments. Of the 13 extracts assayed, 11 displayed estrogenic activity and 2 were cytotoxic. Discussion: Traditional Q'eqchi medicine maintains the use of hormone-mimicking plants for the treatment of reproductive ailments and for fertility regulation. However, there has been an accelerated loss of women's traditional knowledge in particular, due to several cultural, socioeconomic, and geographic factors. Validation of the efficacy of these plants will aid in returning prestige to this rich system of traditional medicine and revitalizing endangered healing traditions in Belize.

<sup>1</sup>The New York Botanical Garden, Institute of Economic Botany, Bronx, NY, 10458, USA<sup>2</sup>University of Illinois at Chicago, Department of Pharmacy Practice, 833 S Wood Street, Chicago, IL, 60612, USA

211 STRUWE, LENA\*<sup>1</sup>, GRAZIOSE, ROCKY<sup>2</sup>, BRODY, STACY<sup>2</sup>, SUGUMARAN, M<sup>3</sup>, SMITH, PETER<sup>4</sup>, RASKIN, ILYA<sup>2</sup> and POHLIT, ADRIAN<sup>1</sup>

### Tropical *Fagraea* and *Tachia* (Gentianaceae) as potential sources of antimalarial treatments

Malaria is a major global health problem, with hundreds of millions of cases each year. Drug resistant strains of *Plasmodium* are evolving, so commonly-used antimalarial treatments are no longer effective in many areas. Plants contain vast resources of known and unknown bioactive compounds and are potential sources of new antimalarial drugs. Species in *Fagraea* and *Tachia* (Gentianaceae; tribes Potalieae and Helieae, respectively) have traditionally been used to treat malaria and fever in the tropics. We investigated the chemical and bioactivity basis for their ethnobotanical uses as medicinal herbs in malaria treatment. Extracts were prepared and tested to determine the antiplasmodial activity and cytotoxicity of four species of *Fagraea*: *F. fragrans*, *F. crenulata*, *F. racemosa*, and *F. auriculata*. *Fagraea fragrans* and *F. crenulata* all relatively large trees and *F. racemosa* is a small shrub, whereas *F. auriculata* is usually hemiepiphytic. They are closely related to species of *Anthocleista* from Africa, another antimalarial herbal. We expected to see antiplasmodial activity at least from *F. fragrans*, as two antimalarial substances, the monoterpene fagraldehyde and the monoterpene alkaloid gentianine, have been isolated from this species. The *in vivo* antiplasmodial activity of aqueous root extracts of Brazilian *Tachia* has been known for two decades. Two antimalarial compounds have now been found in Brazilian *Tachia*, amplexine (previously only found in *Anthocleista*) and decussatin, also confirming its value as a traditional antimalarial medicine. The presence of antimalarial compounds in widely divergent and poorly investigated tropical gentians suggests that further studies in this taxonomic group should be prioritized.

<sup>1</sup>Instituto Nacional de Pesquisas da Amazônia - INPA, Coordenação de Pesquisas em Produtos Naturais - CPPN, Laboratório de Princípios Ativos da Amazônia - LAPAAM, Avenida André Araújo 2936, Petrópolis - Manaus, Amazonas, CEP 69060-001, Brazil<sup>2</sup>Rutgers University, Plant Biology And Pathology, 59 Dudley Road, New Brunswick, NJ, 08901, USA<sup>3</sup>Rimba Ilmu Botanic Garden, Institute of Biological Sciences, Faculty of Science, University of Malaya, Kuala Lumpur, 50603, MALAYSIA<sup>4</sup>University of Cape Town Medical School, k45OMB Groote Schuur Hospital, Observatory, 7925, South Africa

212 HERRERA, KATHERINE\*<sup>1</sup>, MEASOR, KEVIN<sup>2</sup>, BAMSHAD, MARYAM<sup>3</sup> and BALICK, MICHAEL<sup>4</sup>

### Effect of Kava (*Piper methysticum* G. Forst.) on Social and Affect Behaviors of Prairie Voles (*Microtus ochrogaster*)

The lateral roots of the Kava plant (*Piper methysticum* G. Forst.) have been used for centuries by Western Pacific Islanders to make a beverage. The properties of this beverage and its chemical constituents have been shown to have anxiolytic effects in humans, mice, and chicks. Based on ethnobotanical studies of the traditional use of Kava, it is also hypothesized that Kava reduces aggression and fosters social bonding among those drinking it. To test this hypothesis, we used prairie voles (*Microtus ochrogaster*) because they display social and affect behaviors that are similar to humans, and it will aid to elucidate the neuronal mechanisms of Kava's effect on behavior. Two methods of Kava administration were utilized. The first method consisted of using commercially available powdered Kava to make a solution similar to what would be traditionally imbibed by humans. This was given to a group of sexually naïve females for a period of approximately 48 hrs in place of their regular water source. The second method of administration used commercially available Kava extract that was serially diluted and injected intraperitoneally to a separate group of females. After administration of Kava, the voles' anxiety levels were tested using two different tests, the elevated plus maze and the habit trail. To observe any aggression and affiliation behavioral changes, a third test was used. Results indicate that Kava lowered anxiety in the experimental voles; however, experimental voles did not demonstrate more affiliative behavior as predicted. These subjects spent significantly less time in direct contact with the stimulus voles as compared to their control counterparts. This suggests an alternative effect that Kava may be having on social behaviors.

<sup>1</sup>The New York Botanical Garden, Institute of Economic Botany, 200 St. & Kazimiroff Blvd., Bronx, NY, 10458, USA<sup>2</sup>Lehman College, Biological Sciences, Bronx, NY, 10468<sup>3</sup>Lehman College, Biological Sciences, Bronx, NY, 10469, United States<sup>4</sup>New York Botanical Garden, 200th St And Southern Blvd., Bronx, NY, 10458, USA

## 213 ROSE, JANNA

### Bacterial Inhibition and Cytotoxic Properties of Plants used to Treat Diarrhea in Central Anatolian Villages

In this study, 15 Central Anatolian plant extracts were evaluated for their safety and their efficacy in inhibiting the growth of 21 bacterial strains that commonly infect the human intestinal tract and cause diarrhea. Ethnobotanical research was carried out in Central Anatolia for one year, beginning in September 2008. Following interviews and a thorough literature review, plants used to treat diarrhea were collected for research. Voucher specimens were deposited in Gazi University's Herbarium. Plant materials were collected and processed in bulk, with methanolic and aqueous extracts prepared from culturally relevant parts of the plants for a total of 34 extracts. An antibacterial assay was carried out using microtiter broth dilutions to CLSI standards, and an Alamar Blue Cytotoxicity Assay was used to evaluate the safety of the plants for human ingestion. The percent inhibition was used to calculate the effectiveness of the 34 extracts in inhibiting one or more of the 21 bacterial strains. *Rosa canina*, *Hypericum perforatum*, *Vitex agnus-castus*, and *Rhus coriaria* showed significant inhibition at low concentrations (32, 16, 8, and 4 µg/ml) against 8 bacteria (*Enterococcus faecalis*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Shigella flexneri*, *Vibrio parahaemolyticus*, and *Yersinia pseudotuberculosis*). Further evaluation of these Turkish plants could lead to an easily accessible, readily available plant-based remedy for diarrhea in the region.

Florida International University, Biological Sciences, 11200 SW 8th Street, Owa Ehan 167, Miami, FL, 33199, USA

## 214 QUAVE, DR. CASSANDRA L.

### Medicinal plants as modulators of microbial pathogenesis

Historically, most studies on the anti-infective potential of botanical CAM therapies have focused on microbicidal or -static activity. However, recent work has led to the discovery of anti-virulence agents that target microbial pathogenesis rather than growth or survival. This approach offers the advantage of specificity to distinct molecular targets while reducing selective pressures for the development of drug resistance. Some prominent examples include the proanthocyanidins from *Vaccinium macrocarpon* that disrupt adhesion of P-fimbriated *E. coli* to uroepithelial cells, accounting for efficacy in preventing recurrent urinary tract infections. Likewise, *Allium sativum* has been found to attenuate virulence by inhibiting hyphae formation in *Candida albicans* and also by blocking quorum sensing in *Pseudomonas aeruginosa*. Several Italian medicinal plants used in the traditional treatment of skin and soft tissue infec-

tion have also been found to inhibit *S. aureus* quorum-sensing and biofilm formation. My research objectives are to assess the anti-pathogenic properties of medicinal plant products in the treatment of infectious disease. Natural products offer a distinct advantage over their synthetic counterparts due to their rich structural diversity, chirality, and extensive functional group chemistry. Data on the anti-pathogenic properties of select medicinal plants will be presented and a general overview of this approach to drug discovery will be provided.

University of Arkansas for Medical Science, Microbiology and Immunology, 4301 W. Markham St., #511, Little Rock, AR, 72205-7199, USA

## 215 BRENDLER, THOMAS

### Regulatory Legislation for Herbal Products in the European Union. A model worth adopting?

Herbal products can enter the market place in various ways and categories, ranging from herbal medicines, supplements, foods and food ingredients, all the way to cosmetics and cosmetic ingredients. These access routes are governed by national legislation which varies widely from blissful ignorance to, in the case of herbal medicines, full drug compliance. The European Union is in the process of harmonizing the regulatory framework for each of those categories in order to ensure product quality, safety and efficacy. Individual routes of access are described and discussed with regard to their relevant regulatory requirements. Focus is put on market authorizations of herbal medicines for full drug status, as bibliographic registrations for well-established use, under the framework provided in the Traditional Herbal Medicinal Products Directive (THMPD), and on food supplements in their various regulatory manifestations, specifically regarding related functional and health claims.

Plantaphile, Belforter Strasse 20, Berlin, 10405, Germany

## 216 BROWN, PAULA\* and MURCH, SUSAN

### The Traditional and Modern Uses of Cranberry (*Vaccinium macrocarpon* Ait.) and Related species

Moerman (1998) reports the use of wild cranberries (*Vaccinium macrocarpon*) by the Algonquin, Chippewa, Ojibwa and Iroquois in baked, dried and raw foods, mixed with cornbreads and sold as cash crops. Berries were gathered from August through the fall, even when still unripe, allowed to ripen and then eaten either fresh or cooked (Kuhnlein HV and Turner NJ, 1996). In traditional preparation of pemmican, cranberries were sometimes mixed with meat and melted fat of large game animals such as buffalo, elk or deer.

Likewise, Turner (2004) reported that the indigenous people of Haida Gwaii used 2 species of cranberry native to their region, viz. *Vacciniumoxycoccus* L and *Vaccinium vitis-idaea* L as dried or preserved fruits, usually cooked for a long time before eating. In the modern marketplace, cranberry (*V. Macrocarpon*) is one of the significant success stories of the functional foods industry. Cranberries are perhaps most well known for the treatment and prevention of Urinary Tract Infections (UTIs). Research suggests that phytochemical constituents of cranberry inhibit *Escherichia coli* from adhering to uroepithelial cells in the urinary tract or may reduce symptoms of UTI through broader anti-inflammatory effects. However, the specific individual cranberry compounds responsible for the medicinal effects remain to be identified. The overall objectives of our research were to document the growth and harvest of cranberry from field plots in the lower mainland of British Columbia and wild populations of native BC cranberries from the Haida Gwaii, to compare the concentrations of known cranberry anthocyanins in samples from across BC and to determine whether the Haida Gwaii collections had similar compositions of medicinal metabolites. There was an average anthocyanin content of 7.8% in the commercially grown cranberries with a highest concentration of 14.2%. Overall anthocyanins containing galactose as the sugar moiety were present in significantly higher amounts than the corresponding arabinoside counterparts and glycosylated peonidin was present in higher levels than glycosylated cyanidin in most berries. Together, these data provide foundational knowledge about the chemotaxonomy of the *Vaccinium* genus and provide new insights into the maintenance of health in the traditional diets of North Americans.

University of British Columbia, Chemistry, 3333 University Way, Kelowna, BC, V1V 1V7, Canada

## 217 BULLARD-ROBERTS, ANGELLE\* and BENNETT, BRADLEY

### Treating Sugar: Antidiabetic herbal remedies in Trinidad and Tobago

In Trinidad and Tobago (T&T), the colloquial expression *having sugar* refers to having symptoms of the condition Type II diabetes mellitus (DM). In this southern Caribbean republic, DM is the third leading source of mortality excluding infectious diseases. Literature published between 1976 and 2006 have indicated that forty-two local plants are used by the multi-ethnic *Trinbagonians* (as they are locally called) in the treatment of DM. Considering the increasing prevalence of DM and the lack of pharmacological data on the efficacy and safety of the local antidiabetic remedies, we sought to determine what plants Trinbagonians currently use and how they prepare and administer these plants to treat symptoms of DM. This information will be used to guide laboratory analysis of the antidiabetic properties of these plants. We interviewed fifty persons from

fifteen communities who were recruited on the basis of their knowledge of local medicinal plants. Interviewees were asked to provide information about all of the medicinal plants which they knew, the ailments which those plants were used for, the method of preparation and the source of the plants. From the general body of information they provided, any plants which were specifically mentioned for treating *sugar* were noted. We noted twenty-two antidiabetic plant species. For twelve of these plants, our data is the first record of their use against DM in T&T, though most are employed by Trinbagonians for other ailments. Two species represent new additions to T&Ts recorded pharmacopoeia: the shrub *Hamelia patens* Jacq., and the grass *Paspalum vaginatum* Sw. Like the majority of medicinal remedies in T&T, the leaves of these plants are prepared as *bush-tea* by steeping them in hot water. The most frequently cited antidiabetic was *Momordica charantia* L. Fabaceae and Rubiaceae were represented most frequently with citations of three species from each family. Sixty percent of these antidiabetics are cultivated food or ornamental species.

Florida International University, Biological Sciences, 11200 SW 8th Street, Miami, FL, 33199, USA

## 218 OFFRINGA, LISA

### Medicinal Plants of Northern Thailand Used by Traditional Doctors to Improve Cognitive Impairment in the Elderly

Dementia is a progressively debilitating disease affecting cognition, memory and behavior primarily in the elderly population. The prevalence of dementia is expected to increase dramatically in south and east Asian countries in the next 30 years. Thailand lies at the center of three biological diverse areas, the Indo-Burmese, Indo-Chinese and Malaysian regions, and shares its flora with these three regions providing Thai healers with a rich basis for their materia medica. This study identified medicinal plants used by traditional doctors in Northern Thailand with potential to prevent and treat cognitive impairment. Interviewed doctors report plant formulas used to increase memory, tonics for the brain and long life, and specific formulas for the symptoms of dementia. The multi-plant formulas and selected individual plants will be tested for their activity in vitro and in vivo bioassays. These formulas could possess synergistic properties that enhance the activity of the individual plants as well as reduce unfavorable side effects that can occur with single plant remedies. This project, in collaboration with Thai academic and botanical institutions, aims to identify and collect medicinal plants reported as efficacious by traditional doctors, and test them against the causes of dementia as a means to substantiate traditional knowledge with scientific methodology. Locating effective plant therapies could alleviate the suffering of those afflicted with cognitive impairment and support the ability of traditional medicine to

provide solutions to modern problems.

The Graduate Center at The City University of New York, Biology Department, 365 Fifth Avenue, New York, NY, 10016, USA

**219 MORTENSEN, DANIELLE\* and BRENDLER, THOMAS**

**Inventory and rapid throughput screening of indigenous utilized plant species of Namibia for the purpose of developing new natural products**

We present the outline and methodology of a project conducted in collaboration with Rutgers University, GIBEX, and AAMPS, which is funded by the Namibian Millennium Challenge account. This is a work in progress, having started in March 2011 and to be completed within approximately one year. We have surveyed and inventoried the utilized indigenous Namibian flora for the purpose of identifying potentially new ingredients for indigenous Namibian natural products in foods, flavors, health, nutrition, and cosmetic products in a context of local sustainable economic development. The survey and inventory has drawn from all available sources including early explorer's and other historical accounts in order to include traditional plant use which may have been lost over time. From this inventory some 100 species are being selected for investigation based on a variety of criteria, with focus on local stakeholder's interests. Samples and herbarium specimen are being collected and uses will be verified in the field. Plant material is subjected to Screens-to-Nature technology, where we introduce 11 portable, field-deployable pharmacological screens, and facilitate into Namibia the training associated with their use. This approach does not remove any natural resources from its country of origin for the purpose of analysis. Based on the results of the screening process, select species will be subjected to further investigation including chemical profiling, development of quality assurance standards, regional and international market assessments, sustainability (wild-crafting vs. cultivation) and feasibility of creating a product development value chain benefitting Namibian PPOs. This work will lead to a shortlist of around 10 candidate species for product development employing science-based marketing strategies and establishing public-private sector partnerships.

Plantaphile, Belforter Strasse 20, Berlin, 10405, Germany

**220 SCHOOLEY, ERIKA\* and HUIISH, RYAN DAVID**

**Antimicrobial properties of the Tongan medicinal plant *Syzygiumcorynocarpum*: Bioassays in support of ethnobotanically-guided research**

Much of the traditional medicine of Tonga specifically treats infections. In a previous study, *Syzygium corynocarpum* not only showed significant inhibition rates of *Staphylococcus aureus* in laboratory bioassays, but was also the plant most frequently referenced by Tongan healers for use in treating infections. This correlation alludes to the benefits of ethnobotanically-guided drug research. Furthermore, in medicinal preparations, Tongan healers specifically use the young leaves of *S. corynocarpum*, which are a characteristic red-purple color changing to dark green at maturity. Extracts of mature leaves and bark, as well as the young leaves, are being tested for inhibition rates of *S. aureus* to compare efficacy and strengthen the case for ethnobotanically-guided research in the search for novel drugs.

Hollins University, Biology, 7916 Williamson Rd., Roanoke, VA, 24020, USA

**221 KITONDE, CATHERINE\*, LUKHOBA, CATHERINE and DOSSAJI, SAIFUDDIN**

**Antimicrobial and Phytochemical Study of *Vernonia glabra* (Steetz) Oliv. & Hiern. in Kenya.**

Infectious diseases are prevalent and life threatening. In Kenya, a majority of the sick are seeking herbal remedies in such for effective, safe, and affordable cure. This project aims to investigate the antimicrobial activity and phytochemical compounds present in different parts of *Vernonia glabra*, a plant used by herbalists in various regions of Kenya claimed to treat different microbial infections. The plant was collected in January, 2010 in Machakos, and the different plant parts ground into powder and extracted in Dichloromethane:Methanol (1:1) and water. These were tested against bacterial and fungal organisms using disc diffusion technique. It was observed that the organic crude extracts of the flower, leaf, stem, root and/or entire plant, showed activity against at least one of the four test micro-organisms and at concentrations lower than the water crude extracts. The organic crude extract of the leaf showed the highest activity against *Staphylococcus aureus* (Mean inhibition, 1.83) and *Aspergillus niger* (mean inhibition, 1.43), and also recorded higher activity those of the standard ds. Organic crude extract of flower showed significant activity against one only

organism- *Staphylococcus aureus*. Thin Layer Chromatography-Bioautography Agar Overlay, showed that saponins were eliciting over 60% of all the antimicrobial activity. These results suggest that *Vernonia glabra* may contain phytochemicals of medicinal properties and also justifies the use of *Vernonia glabra* in herbal medicine for the treatment of microbial diseases. In particular, the *V. glabra* leaf may contain broad spectrum antibacterial and antifungal agents that could be useful in the development of competent antimicrobial drugs. Further investigation to isolate, determine the pure and safe antimicrobial compounds is recommended for scientific verification and validation of the drugs from *Vernonia glabra*.

University of Nairobi, School of Biological Sciences, P.O. Box 30197,00100, Nairobi, Kenya

**222 BRADBURY, ELIZABETH JANE<sup>\*1</sup>,  
TAY, DAVID<sup>2</sup> and EMSHWILLER, EVE<sup>3</sup>**

### Understanding Domestication Resulting in Opposing Crop Phenotypes: (2) Organic Acid Accumulation in Oca (*Oxalis tuberosa* Molina) Tubers

Crops displaying directly opposing domesticated biochemical phenotypes could provide valuable insight to the effects on the domestication process of conflicting selective pressures in the agricultural ecosystem. One relatively well-known example is cassava (*Manihot esculenta* Crantz), which has high-cyanide and low-cyanide varieties that are grouped into two distinct use-categories, those cassava that are processed prior to consumption and cassava that are consumed after cooking without processing. Small-scale studies conducted by Bradbury and Emshwiller (2011) revealed that *Oxalis tuberosa* Molina, "oca", may represent another example of such a crop system, with opposing high oxalic acid and low oxalic acid cultivars. Each cultivar set ("use-category") also has different cultural food preparation practices. In order to establish a more thorough understanding of the biochemical basis for the different use-categories of oca, we conducted a common garden experiment in the Mantaro River Valley in the Junán Department of Peru. In September 2009, we planted 45 unique cultivars replicated five times throughout the field using a randomized block design. Tubers were harvested June 2010 and organic acid extractions were conducted following the hot 2M HCl protocol outlined by Ross and colleagues (1999). Six organic acids were quantified using HPLC analysis: oxalic, malic, tartaric, succinic, ascorbic, and glutaric acids. Our results indicate that there is a statistically significant difference in organic acid accumulation between the oca use-categories, demonstrating that oca displays what we are referring to as "opposing crop phenotypes" with high-acid cultivars processed prior to consumption and low-acid cultivars consumed after cooking without prior pro-

cessing.

<sup>1</sup>University of Wisconsin-Madison, Botany, 430 Lincoln Drive, Birge Hall, Madison, WI, 53706, USA <sup>2</sup>El Centro Internacional de la Papa, Division 2, Av. La Molina 1895, La Molina, Lima, Peru <sup>3</sup>University Of Wisconsin-Madison, Botany Dept, 321 Birge Hall, 430 Lincoln Drive, Madison, WI, 53706-1313, USA

**223 WITHERUP, COLBY<sup>\*1</sup>, ZEREGA,  
NYREE<sup>2</sup> and ZUBERI, M. IQBAL<sup>3</sup>**

### Measuring and preserving diversity in a Bangladeshi food crop: Jackfruit (*Artocarpus heterophyllus*, Moraceae)

*Artocarpus heterophyllus* (Jackfruit) is one of two economically important crops in the genus *Artocarpus* (with *A. altilis*, or breadfruit) in the mulberry family (Moraceae). Jackfruit is a monoecious tree that produces the largest tree-borne fruit structure in the world. It is found in cultivation at low elevations throughout Southeast Asia and has been introduced in the Philippines, Australia, and throughout Africa and the Neotropics. Jackfruit is the national fruit of Bangladesh, a country whose natural areas are severely threatened by overpopulation and climate change, but very few studies have focused on jackfruit there. In Bangladeshi villages, jackfruit trees are grown in almost every yard, but it is feared that genetic variation is being lost due to deforestation, a decline in seed propagation, and the introduction of high-yielding, uniform cultivars. Loss of crop diversity is an issue of international concern. The demand for genetic material for breeding new adapted cultivars relies on diverse germplasm from both wild and modified sources. In Southeast Asia, international organizations (Global Facilitation Unit for Underutilized Species, International Centre for Underutilized Crops, International Plant Genetic Resources Institute) are looking to under-utilized crops like jackfruit to provide a new level of food security and income. Leaf samples and ethnobotanical data were collected from several sites throughout Bangladesh in July 2010. Using microsatellite analysis, my research will give a broad view of jackfruit diversity in Bangladesh. By analyzing my lab results in connection to my ethnobotanical data, I will investigate claims of genetic erosion and attempt to identify possible causes.

<sup>1</sup>Chicago Botanic Garden/Northwestern University, Plant Science, 1000 Lake Cook Road, Glencoe, IL, 60022, USA <sup>2</sup>Northwestern University, Program In Biological Sciences, 2205 Tech Drive, 2-144 Hogan Hall, Evanston, IL, 60208, USA <sup>3</sup>University of Rajshahi, Rajshahi, 6205, Bangladesh

### Paleoethnobotanical Remains from Guijarral, a Late Classic Maya Site in Northwestern Belize

Most studies of ancient Maya subsistence are based on ethnographic and historical accounts that model a reliance on maize (*Zea mays*), beans (*Phaseolus vulgaris*), and squash (*Cucurbita* sp.). Our investigations of botanical remains recovered from an array of shovel tests and sealed contexts at Guijarral, a Late Classic (AD 600-900) Maya farmstead, have shown an expanded botanical repertoire beyond the maize, bean, and squash trinity. Some plant genera distributions suggest the importance of wild plants and their uses, as well as allow us to construct hypotheses regarding the locations of activities within the site and begin to reconstruct the agroecology associated with Late Classic provisioning. Data presented here demonstrate the importance of considering the potential for local control of perennial foodstuffs in local ritual, subsistence, and power dynamics.

University of South Carolina, Anthropology

### 225 BLAIR, CHARLES

#### Invasive Aquatic and Riparian Weeds and Mosquitoes; Challenges, Successes, and Opportunities

The adverse effects of invasive aquatic and riparian weeds on water quality; hydrology, native plant communities, and wildlife habitat and their consequences for mosquito control efforts, public health and nuisance problems, have been often implied, but could be better articulated. This presentation will present some of these relationships and highlight collaborative activities among vector and weed control agencies. Invasive aquatic and riparian weeds result in several adverse changes in these settings. Displacement of native flora degrades habitat for fauna that feed on mosquito larvae and pupae. The use of biorational larvicides, some derived from bacterial sources that do not harm this fauna supplements the effectiveness of this predation, which can reduce or eliminate the necessity of aerial adulticide application. There are situations where the density of invasive flora has been shown to interfere with application of these agents. Mosquito breed in standing water, which can include still-water natural areas, such as ponds, and small lakes and also moving water areas streams and tidal areas with changing levels which leave isolated standing water areas. Manmade sources include landscaping, irrigation canals, ponds, storm drain holding areas, and wastewater recharge basins. Examples of specific problems in particular settings will be described: for still-water, *Ludwigia spp.*; for estuarine;

*Spartina spp.*; and riparian, *Arundo donax*. Successful projects that can be applied elsewhere; lessons that can be learned from unsuccessful activities; and the need for continuing investigations will be discussed.

176 ALCOR AVE, LOMPOC, CA, 93436, USA

### 226 KITAGAWA, JUNKO\*<sup>1</sup>, YAMADA, KAZUYOSHI<sup>2</sup>, OHYAMA, MOTONARI<sup>3</sup>, HOSHINO, YASUHARU<sup>3</sup>, SHINOZUKA, YOSHITSUGU<sup>4</sup>, YONENOBU, HITOSHI<sup>2</sup> and YASUDA, YOSHINORI<sup>1</sup>

#### Analysis of recent vegetation change for the successful regeneration of Kiso-hinoki cypress

*Kiso-hinoki* cypress is one of the most beautiful trees in Japan. The forest was severely deforested in the early 17th century, but it was regenerated by the conservation during Edo period. The result from the Taritsu lake on Shirasu mountain pass showed the recovery of forest, however, the productivity has been less than before 17th century. It is said the regeneration of forest is not successful because of the recent less activity of cutting undergrowth. The main undergrowth is *Sasa* in *Kiso-hinoki* cypress forest. To make a forest policy, it is essential to understand the management of the forest during Edo period when the regeneration was successful. Phytolith analysis of the core sediment from Taritsu Lake was conducted at the depth of around AD1610, late 19th century when Meiji restoration occurred and close to the present. In addition, pollen from Fukami-ike Lake in Nagano prefecture was analyzed annually from the early 20th century to understand the recent change of the forest. The result shows that there is no remarkable difference in the number of phytolith of *Sasa* type among the samples. Not cutting undergrowth seems not to be the factor which prevents the regeneration of cypress trees. In both samples from around AD 1610 and the late 19th century, the phytolith of *Pleioblastus* type was observed. It indicates that *Pleioblastus* invaded to the open space where cypress trees were cut down. However, the phytolith of *Pleioblastus* type was not observed in the sample from present. The area has become the place which received little sunshine. Pollen analysis indicated that the rate of evergreen tree increased after the World War II. It might be caused by the plantation of *Cryptomeria japonica* and the decrease of deciduous oak. Together with phytolith analysis, it may be concluded that the increase of the rate of evergreen trees in the forest hinders of the regeneration of cypress forest.

<sup>1</sup>International Research Center for Japanese Studies, 3-2 Oeyama-cho, Goryo, Nshikyo-ku, Kyoto, 610-1192, Japan <sup>2</sup>Naruto University of Education, 748 Nakashima, Takashima, Naruto-cho, Naruto, 772-8502, Japan <sup>3</sup>Tohoku University, 12-2, Kawauchi Aoba-ku, Sendai, 980-0862, Japan <sup>4</sup>Hokkaido University, North 10, west 4, Sapporo, Japan

227 RAKOTOARIVELO, NIVO  
HARINIAINA

**Vohibe Forest: an invaluable source of useful plants**

The low to mid elevation evergreen rainforest of Vohibe is classified as New Protected Area, and covers 3117 ha. It is located in the Ambalabe rural Commune, at 72 km northwest of Vatomandry in the Eastern Region of Madagascar. This Commune is very isolated in geographic terms and was threatened before by the practice of slash and burn cultivation. But this forest is still very rich in biodiversity and has a high specific endemic up to 80%. This richness prompted us to do an ethnobotanical study about useful plants and the local people knowledge to ensure their sustainable use and their future conservation.

In Madagascar's rural areas, forests are the only source for people's daily needs, such as water, food, medicinal plants, and materials for construction, handcraft, tools and firewood. Vohibe forest is no exception. Our initial ethnobotanical survey found that of ca. 180 species of plants used by local people, about 50% are collected in the forest. The leaves, bark and root are commonly used as medicine and for handcrafts, while the trunk is mainly used in construction and for manufacturing tools. Fruits are often used as food. The choice of species depends also on the needs: hard wood and resistant species are used for building, healing plants for traditional medicine and fiber plants for handcrafts.

Missouri Botanical Garden, Research and Conservation Program, PO Box 3391, Antananarivo, Analamanga, 101, Madagascar

228 ODHAMBO, JUDITH\*,  
LUKHOPA, CATHERINE and DOSSAJI,  
SAIFUDDIN

**Ethnomedicinal knowledge in the traditional management of human ailments in Lake Victoria Basin, Kenya**

Though the majority of inhabitants in the Kenya rely on ethnomedicinal plant species to manage a wide range of human ailments, much the indigenous knowledge largely remains undocumented. An ethnomedicinal study was conducted to document the plant species used medicinally in the Lake Victoria Basin. Data was collected by interviewing the herbalists from the region. A total of thirty four plant species distributed in twenty one botanical families were identified. The plant family with highest number of plants used for medicine was Compositae, followed by Leguminosae then Labiatae. The herbals were prepared mainly as concoctions and decoctions and were majorly administered orally and dermally to treat ailments such as typhoid, malaria, and

chest and skin related complications. A rich knowledge of medicinal plants was recognized and phytochemical and bioactivity analyses of these herbal plants are recommended to determine their safety and efficacy.

University of Nairobi, School of Biological Sciences, P.O. Box 30197,00100, Nairobi, Kenya

229 REEDY, DAVID\* and  
MCCLATCHEY, WILL

**Adopting Invasives; Lessons from a Moorean Mat Fiber**

In 1769 Captain James Cook stopped in his voyage at the Society Islands. On June 1<sup>st</sup>, the naturalist on this voyage, Joseph Banks set sail for nearby Mo'orea. There he collected many items of material culture including a highly decorative and unique mat. This mat returned to England and eventually became interred at the Pitt Rivers Museum in Oxford. We have used microscopic analysis to compare fibers of this mat to fibers of other known Polynesian mat fiber plants. This comparative analysis later extended to other fibers known to be used in Polynesian material culture. The fiber from Cook's collection did not match fibers from any known pre-European contact Polynesian plant. Continued examination of the fibers revealed this mat to be identical to the stem fibers of *Typha domingensis*. However, this species is thought to not have reached the Society Islands until the mid-Nineteenth century. Our recent ethnographic data from the Society Islands suggest that *T.domingensis* is only used by a small number of residents on the island of Mo'orea.

Botanical Research Institute of Texas, 1700 University Drive, Fort Worth, TX, 76107, USA

230 HAZLETT, DONALD\*<sup>1</sup> and  
TORRES HERRERA, JENNIFER C.<sup>2</sup>

**Socioeconomic Value and Growth of Naturalized *Musa balbisiana* L. A. Colla Leaves in Honduras**

*Musa balbisiana* (Musaceae) is a diploid, seed-producing banana indigenous to Southeast Asia. After it was introduced into the Lancetilla Experimental Garden in Honduras (ca. 1960s), it became naturalized in nearby second-growth areas of the north coast. Local residents were quick to recognize the socioeconomic value of leaves from this weedy banana as a wrap for traditional Honduran *nacatamales*. To estimate the monetary value and to provide preliminary data on leaf harvest sustainability a 3 month study (July to September) was undertaken in 2009. For 3 months each of 38 harvesters averaged a weekly sale of 4,400 cut, de-veined and blanched *Musa* leaves. These sold for Lps. 550.00 (ca. \$30.00 US) to truckers, who transported them to major markets to resell at a profit. The number of use-

ful leaves produced by a single *Musa* plant in 3 months was documented by 2 methods: 1) the traditional way of cutting the entire banana stem to remove leaves and 2) a more careful method of cutting off only the useful leaves. Both methods yielded a total of 6 or 7 useful leaves after 3 months (including the original leaf cut at the onset), but the more careful method did yield significantly more immature and larger leaves. A longer study may show an increase in leaf production per plant associated with the more careful leaf harvest method. This is the first estimate of useful leaf production (for *nacatamales*) from this exotic *Musa*. No management plans exist for sustainable leaf production from this species since all leaves are currently harvested from wild populations. However, a few land-owners in the Langetilla area are protecting and charging a fee to harvest *Musa* leaves. The sale and cultural use of *M. balbisiana* leaves in Honduras is an example of an exotic species that has positive socioeconomic benefits. This naturalized *Musa* appears to have few, if any, of the negative impacts typically attributed to exotic plants.

<sup>1</sup>Denver Botanic Gardens, Research, 909 York Street, Denver, CO, 80206, USA<sup>2</sup>Instituto Nacional de Conservación y Desarrollo Forestal, Áreas Protegidas y Vida Silvestre, Región Forestal Pacífico, Tegucigalpa, Francisco Morazan, Honduras

## 231 FULLER, DR. REBEKAH

### Using mobile phones and ODK to collect and preserve indigenous ethnobotanical knowledge

Open Data Kit (ODK) is a free suite of tools created to help organizations and researchers collect, aggregate and visualize their data. Run as an open-source project it allows the collection of data on mobile phones and data submission to a central web based server. The system can be modified to suit particular research and to date has yet to be applied to the conservation of indigenous ethnobotanical knowledge. Protecting and preserving ethnobotanical knowledge is of up most importance to Maori, the indigenous people of New Zealand. The aim of this pilot study was to test ODK as a community friendly suite of tools capable of collecting, collating and storing Maori ethnobotanical knowledge. The study site is described as the rohe (traditional boundaries) of the Maori tribe of Ngāpuhi, North Island, New Zealand. Questions were developed to test a number of options available to ODK, including open, multiple-choice and location questions. Data recorded included social variables and ethnobotanical information on the cultivated and non-cultivated crops grown in home gardens. Interviews were completed with the assistance of Te Runanga-A-Iwi-O-Ngāpuhi a representative body of the tribe. Three main benefits for communities were identified. Firstly, in an interview situation ODK was easy to use and interviewees were comfortable with mobile phones being used. Secondly, there is benefit in formatting and managing a secure online database

protecting intellectual property rights and guardianship of the information. Thirdly, the suite of tools has an in-built flexibility to be able to collect different data types including interview responses, GPS locations, images and video recordings. Although a powerful research tool, ODK may be difficult to be set up and run by community groups. There may also be issues with the use of GPS functions that rely on cellular network coverage. Modifying or creating a similar system able to be directed towards communities would be of great value for protecting and conserving indigenous ethnobotanical knowledge in the future.

University of Auckland, School of Biological Sciences, 23a Symonds Street, Auckland Central, Auckland, New Zealand

## 232 TURI, CHRISTINA\* and MURCH, SUSAN

### Medicinal and Spiritual Use of North American *Ligusticum* species, Commonly Known as "osha"

North American *Ligusticum* species (Apiaceae) are a wild harvested medicinal crop and sold commercially as "osha" as treatment for muscles aches, anxiety, colds and flues. The use of "osha" is supported in ethnobotanical literature. Opler (1923) reported that the Tonkwa require that one must possess *L. porteri* in order to partake in the peyote ceremony, while Camzine and Bye (1980) observed among the Zuni that both patient and medicine man would chew upon the roots of *L. porteri* during healing rituals. Jordan (2008) recorded instances of the Plains Apache throwing roots of *L. porteri* over a fire to help console individuals during rituals associated with mourning. Turner (1980) reported that the Okanagan-Colville peoples used smoke produced from *L. canbyi* to treat individuals believed to be in a trance, possessed by spirits, or who are ceremonially unconscious. Currently, commercial demand for "osha" has led to a market-driven wild harvest of *Ligusticum* species, which may be threatening wild populations. Despite growing demand, there is relatively little information available describing the traditional, medicinal and/or spiritual uses, phytochemistry, conservation status, production systems or sustainable use. *In vitro* grown plants have the potential to provide tissues for commercial products without impacting wild populations. Thus, our research is focused on determining the conservation status of wild populations of *Ligusticum* in British Columbia, while also developing methods for conservation of *Ligusticum* germplasm through tissue culture. Furthermore, we are interested in examining the neurotransmitter biochemistry of "osha". Melatonin and serotonin, human neurotransmitters associated with depression, migraines and seasonality disorders, have been detected at relatively high levels in roots and shoots of mature plants and seedlings of *Ligusticum porteri* and *Ligusticum canbyi*. Together, the studies are leading to new understandings of *Ligusticum* phy-

tochemistry in hopes of conserving this genus in North America.

University of British Columbia, Chemistry, 3333 University Way, Kelowna, BC, V1V 1V7, Canada

**233 MCCLURE, KATRINA\*,  
KINDSCHER, KELLY, CORBETT, STEVE  
and LONG, QUINN**

**Creating an Ethnobotanical Database:  
Native Edible and Medicinal Plants of  
Kansas as a Case Study**

This project illustrates how an ethnobotanical database can provide information on plants relevant to tribal groups. Our case study, using regression analysis, is one example of how an ethnobotanical database can be used to extract information over many contexts, be it geographical or cultural (i.e., tribal or cultural group or organization). The Prairie Ethnobotanical Database at the University of Kansas provides important insights into the proportion of plants that have medicinal value, as well as a wide range of additional use criteria, including: plant part utilized, treatment types, tribal affiliation, regional expanse, and physical categorizations such as duration and growth habit. This case study uses data limited to medicinal plants in Kansas across plant families. There are 2,232 species in Kansas, of which 711 are recorded as having medicinal uses. Thirty-two percent of Kansas plants are used for medicine, and 68 percent are categorized as non-medicinal. Regression analysis of plant families are ranked and compared with results for all of North America and areas of interest are identified. Within the state of Kansas, not unexpectedly, Asteraceae (sunflower family) is ranked highest, but surprisingly Fabaceae (bean family) ranks exceedingly high with regard to medicinal use. We highlight here just one method where an ethnobotanical database can be used as a model to retrieve valuable information regarding the historical uses of native plants. The regression analysis used reveals distinctions between plant families in Kansas. This method of analysis, along with others, can be expanded into various contexts. Tribes interested in developing or utilizing existing ethnobotanical databases could use this resource as a way to develop culturally relevant projects related to the study and identification of traditional foods, medicinal plants, and plants used for basketry, art, and other materials.

University of Kansas, Kansas Biological Survey, 2101 Constant Ave, Lawrence, KS, 66047, USA

**234 WALKER, KAREN**

**Honoring Those Who Came Before:  
Native American Ethnobotany at the  
Missouri Botanical Garden**

For centuries, the Lakota and Dakota (Sioux) People have accumulated knowledge about their environment. Within this realm of knowledge they have developed skills in using plants that grow around them for food, medicine, building materials and clothing. For generations this knowledge was passed from one family to the next through oral traditions of story telling, songs, and teachings. Much of their traditional knowledge is still being passed on today but there is an overwhelming potential for this knowledge to be lost in our modern society. Many elders and tribal members are working to preserve TEK, as well as incorporating this knowledge into community, health, and education programs. The Missouri Botanical Garden is collaborating with the Crow Creek and Standing Rock Indian Reservations in South and North Dakota to promote the preservation and use of traditional ecological knowledge.

Missouri Botanical Garden, William L. Brown Center, P.O. Box 299, St. Louis, MO, 63166, USA

**235 MERLIN, MARK D.**

**Cultural ecology, mythology and the  
use of the opium poppy in the Ancient  
Hellenic World**

The major psychoactive drug plant in ancient Greece was *Papaver somniferum* L., the opium poppy. Use of this true narcotic was certainly of great medical importance more than two millennia ago in the Hellenic world. It also had ritual and ecstatic use in the region that predated the ancient Greek use in the eastern Mediterranean. The ecological relationships of the key cereals and the poppy in ancient Greek agriculture were symbolized in the pantheistic mythology of ancient Greece, specifically of Demeter and her daughter Persephone. This well-known story was a symbolic rendering of the seasonal cycle of grain farming in the ancient Mediterranean world which connected the mind-altering and therapeutic use of the opium poppy with nutritional basis of the society. The linkage of this alkaloid-rich poppy with the great cereal crops of the region was a hallmark of Demeter's appearance, informing the Greek people about the conscious cultivation of wheat and barley and fortuitous commensal association of the opium poppy and its tiny seeds in the grain fields of Hellenistic farmlands. A combination of up-to-date ethnobotany, ecology, archaeobotany, archaeology, mythology and history remind us of what key species fed and helped heal people in the ancient eastern Mediterranean world and underscore their basic ecological relationships.

University of Hawaii at Manoa, Botany, Department of Botany, St. John 101, Honolulu, HI, 96822, USA

236 KHAN, SARAH K.\*<sup>1</sup>, CALLOWAY, STEPHANIE A.<sup>2</sup>, MAIDA, I. TATIANA<sup>3</sup> and RAKEL, DAVE P.<sup>1</sup>

**Block Spanish food frequency screeners, eating out, shopping and Nutrition Environment Measures Survey in a predominantly Latino community, Milwaukee WI**

More than 60% of Wisconsin's Latino population is overweight or obese compared to 23% of the US population. UW-Madison Department of Family Medicine, CORE/El Centro, and Aurora Walker's Point Community Clinics partnered to document the eating habits and research the nutrition environment of a predominantly urban Latino community. Two community-based clinics offer primary care, integrative modalities, exercise, and wellness services to all, regardless of ability to pay in Milwaukee, WI. Spanish Block Food Frequency Screeners for fruit, vegetable, and fat consumption, and a survey assessing where clients shopped for food and ate out were administered. Based on the most frequented shopping outlets, Nutrition Environment Measurement Surveys (NEMS-Stores) were administered in stores. Clinic participants surveyed (n=225) reported good fruit and vegetable intake (approximately four servings/day). Participants also reported good fat intake (19-24% calories from fat/day). When fat intake was broken down by gender, men's fat intake was reported as fair (25-33% calories from fat/day), whereas women's fat intake remained good. The grocery and convenience stores (n = 13) assessed generally offered a good selection of healthier food options; stores generally offered high quality fruits and vegetables; though overall higher prices for healthier food options predominated relative to a regular food choices. We would like to present our results and get feedback about our planned next steps in terms of Latino Health improvement through urban gardens, culturally appropriate health and culinary education and intervention programs.

<sup>1</sup>UW-Madison, Dept Family Medicine-Integrative Medicine, Madison, WI<sup>2</sup>CORE/El Centro, CORE/El Centro, Food & Environmental Health Coordinator, Milwaukee, WI<sup>3</sup>Nutrition Health Educator, CORE/El Centro, Milwaukee, WI

237 LINARES, EDELMIRA\* and BYE, ROBERT

**Gastronomy and biodiversity conservation in Mexico**

Given the status of being one of the five megadiversity biota of the world and the privilege of being one of the three major centers of origin of agriculture, Mexico faces the challenge of conserving its natural capital for future inhabitants as well as protecting the germplasm of many of the world's economically important plants. With over 10% of the species being edible, the consumption of roots, stems, leaves, flowers, fruits and seeds can be detrimental as well as beneficial to the sustainable use of Mexican flora. The shift from being a rural to an urban nation has forced Mexico to rely on the importation of staple foods while the general public has lost its appreciation of local edible plants. Ethnobotany contributes to biodiversity conservation by rescuing knowledge, practices, plants, and plant products and, consequently, promoting respect and utilization of these processes and foodstuffs. Given that many of the edible plants have evolved with Mexican ethnic groups in agricultural fields, anthropogenic sites and nearby wild habitats, the key to their conservation is the maintenance of plant-human interactions - in particular, eating. Mexican gastronomy, though founded upon the basic Mesoamerican triad of maize, bean and squash, is varied due to geographically local additives that vary taxonomically and to the cultural diversity of food preparation and gastronomic palette. In collaboration with various governmental and non-governmental organizations, our Botanical Garden has applied various approaches to conserving this gastronomic biodiversity at various levels through local schools, regional fairs, and national programs. Recently, Mexico pioneered the international paradigm of culinary recognition through UNESCO's Representative List of the Intangible Cultural Heritage of Humanity. An evaluation of our different programs indicates that enlightening person experiences and readily availability are key to increasing the public's pro-active participation in biodiversity conservation.

Universidad Nacional Autónoma de México, Jardín Botánico del Instituto de Biología, , Mexico, DF, 04510, MEXICO

238 ELKINGTON, BETHANY G.<sup>\*1</sup>,  
SYDARA, KONGMANY<sup>2</sup>, HARTMANN,  
JOHN F.<sup>3</sup>, SOUTHAVONG, BOUNHONG<sup>2</sup>  
and SOEJARTO, DR. DJAJA D.<sup>4</sup>

### Epidemiology from Palm Leaf Manuscripts of Laos

In an effort to preserve traditional medicine knowledge and to uncover information about disease patterns and treatment in the Lao People's Democratic Republic, linguistic experts have searched centuries-old medical records incised on palm leaf manuscripts. A list of more than 7000 records has resulted, mostly from Buddhist monasteries, covering folk categories of diseases, symptoms and remedies. The records shed light on the medical history and traditional medicine heritage and folk beliefs of the people of Laos.

<sup>1</sup>University of Illinois at Chicago, Department of Medicinal Chemistry and Pharmacognosy, 833 South Wood Street (M/C 781), Chicago, IL, 60615, USA<sup>2</sup>Institute of Traditional Medicine, Ministry of Health, Ban Phonpao, Vientiane, Laos<sup>3</sup>Northern Illinois University, Department of Foreign Languages and Literatures, Watson Hall 314, DeKalb, IL, 60115, USA<sup>4</sup>

239 SHRESTHA, SUSHMA

### Integrating ecological and ethnobotanical knowledge for biodiversity conservation at Manaslu Conservation Area, Nepal

Most conservation approaches are extra-locally derived yet they influence local livelihoods and rely on local actions for effective outcomes. If the goal is to gain local participation in biodiversity conservation, then local knowledge becomes critical information. This preliminary study compiles and integrates local knowledge about landscapes and forest community types for the study of woody plant diversity at the Manaslu Conservation Area (MCA) of Nepal. Eighteen participatory maps were acquired from nine Gurung and Tibetan ethnic villages to examine how local people view their landscape spatially. These participatory "ethnecological" maps were then georegistered with remote sensed images to produce land cover/land use maps for the study villages. Participants mapped and named natural and human-created features across a heterogeneous landscape and included their recognition of dominant plant species. Participatory maps show a high number of land cover types that include culturally and ecologically important landscape features invisible on the classified images. Between the lowest mixed temperate forests at 1500m to the evergreen forests around 3800m, 115 ecological plots were established. Concurrent ethnobotanical interviews were conducted to document the number of uses and categories of uses. More than 80% of the recorded plants have local names and

all have recorded uses (medicine, construction, food, fuel, fodder, ceremonies, etc.), indicating the importance of these plants to the local people. Plants that provided fuel, fodder, and construction materials dominated the list of the most important species. This data show patchy distribution of key forest resources in a heterogeneous landscape and the relationships between resource diversity and local ethnobotanical knowledge about woody plants. Integration of ecological and ethnobotanical knowledge can contribute towards learning about local places and potentially guide biodiversity conservation agendas that are sensitive to human livelihoods.

Miami University, Botany, 316 Pearson Hall, Oxford, OH, 45056, USA

240 RASHFORD, JOHN

### The Meaning of the name "god tree" in the Caribbean

The name "god tree", which appears in dictionaries and other reference works, is generally defined as a Caribbean name for the massive buttressed tropical giant called the silk cotton tree or kapok (*Ceiba pentandra*). While this is true, the aim of this paper is to show that in the Caribbean, "god tree" was originally applied to species of the genus *Ficus*, and that this tradition, which is widely represented in the folklore of the region, is similar to ideas associated with figs trees in the African Brazilian religious tradition called Candomble. The reason for the later association of "god tree" with the silk cotton tree will also be explored.

241 KRINGS, NATHAN

### Sources of a Scent - the Enduring Legacy of Sandalwood

The diffusion of the products of the family *Santalaceae* and the appreciation for their unique qualities has gone hand in hand with the spread of Buddhism and other common Asian values. The process continues to this day - even as the original religious impetus behind traditional Japanese and Chinese material and spiritual culture seems to be slowing. The purpose of this work is to trace the historical diffusion of sandalwood and examine its current situation. The cultural significance of sandalwood, specifically *Santalum album*, is examined in detail. Cultivation, harvesting, and processing of *S. album* are also detailed in the light of laws and regulations enacted by the Indian government. The conflicting interests of business and conservation are weighed, along with the ongoing threat of smuggling. These findings are useful toward an understanding of the commodity in the global and local economies, as well as its recent price fluctuations, which have seen values in excess of 1000USD per kg.

242 MEYER, RACHEL<sup>1</sup>, DUVAL,  
ASHLEY<sup>2</sup> and JENSEN, HELEN<sup>\*3</sup>

### Patterns and dynamic processes in crop domestication: a historical review of global food crops

Crop domestication has been a structuring element of human societies for the past 10,000 years. The changes (genetic, morphological, chemical, etc.) that accompany domestication provide insight into the selection pathways of crop evolution and reflect the needs and values of societies that cultivate them. For a subset of major crops, the domestication syndromes, and selection pathways, are well characterized. However, much less is known about these processes for most crops, particularly those of minor economic importance. Even many crops of substantial economic and cultural importance are under-studied with limited information available in reviews on their domestication syndrome, selection pathways and original uses. With limited reference information, it is difficult to compare lesser-known crops to well-studied model crops in guiding new research or educational efforts. In this study, we review and compare data on a broad cross-section of crops to highlight patterns of domestication and identify potential novel research directions in the field of crop evolution. We selected over 125 food crops with origins throughout the world and compiled taxonomic, archaeological, ethnobotanical, genetic, physiological, phylogeographic and conservation information. These data were summarized in tables, timelines, and narratives. Cluster analyses were performed to identify similar patterns among subsets of crops and also to identify gaps in the literature indicating domestication syndromes and selection pathways that have not been thoroughly investigated. We identified an important subset of crops whose original uses differ significantly from their contemporary primary uses as food. Additionally, data suggests that genetic bottlenecking, resulting from intensive selection, often occurred relatively recently despite exploitation of a species for thousands of years. This review highlights the dynamic and ongoing nature of domestication processes and the threats posed by genetic erosion, varietal extinction and loss of crop wild relatives. We identify both common trends and divergent patterns in crop evolution. The review also provides a reference for studies on crop plants, particularly those for which limited data and reviews are available.

<sup>1</sup>The City University of New York Graduate Center, Biology, 365 Fifth Avenue, New York, NY, 10016, United States <sup>2</sup>Yale University, School of Forestry and Environmental Studies, 195 Prospect Street, New Haven, CT, 06511, USA <sup>3</sup>McGill University, Department of Biology, 1205 Dr. Penfield Avenue, Montreal, QC, H3A 1B1, Canada

## POSTERS

243 MBUGUA, PAUL KAMAU

### Traditional Uses Of Four *Sansevieria* Species In Kenya

*Sansevieria* is a tropical plant of great use to the locals. In this paper research was done to find out how useful this plant is growing in the wet and semi-arid lands of Kenya. Four species were investigated and a comparison done between two districts: Nakuru and Maragwa. The results showed a heavy dependency on this wild plant for various community needs such as hedges, medicinal, fibres and even making bricks.

Kenyatta University, Plant and Microbial Sciences, P.O. Box 43844, 00100 GPO, Nairobi, Nairobi, 00100, Kenya

244 GHORBANI, ABDOLBASET<sup>\*2</sup>,  
LANGENBERGER, GERHARD<sup>2</sup> and  
SAUERBORN, JOACHIM<sup>2</sup>

### Comparison of medicinal and food plant use among Lahu and Hani ethnic minorities in SW China

Naban River Watershed National Nature Reserve (NRWNNR) located in Xishuangbanna Prefecture, SW China, is rich in biocultural diversity. The Nature Reserve comprises approximately 30 villages and a total population of more than 5000 people and is managed based on "the Man and Biosphere" concept of IUCN. Lahu are living in 12 villages and Hani in 7 villages in highlands of the area. Ethnobotanical survey was conducted to document and analyze the knowledge of plant use among Lahu and Hani. Data collection was done through conducting freelist interviews, semi-structured interviews, field walks and botanical sample collections. Botanical samples were identified scientifically and cultural importance of useful plants has been calculated. A total of 93 species of wild food and 289 medicinal species are used by Lahu and 143 species of food plants and 199 species of medicinal plants by Hani. Most culturally important food plants for Lahu are *Diplazium esculentum* (Retz.) Sw. (Salient Index: 0.58), *Musa acuminata* Colla (0.56), *Houttuynia cordata* Thunb. (0.34) and *Piper longum* L. (0.26) and for Hani are *Diplazium esculentum* (Retz.) Sw. (0.51), *Oenanthe javanica* (Bl.) L. (0.43), *Solanum americanum* Mill. (0.38) and *Musa acuminata* Colla. (0.36). Most salient medicinal plants for Lahu include *Aristolochiasp.* (0.19), *Fibraurea recisa* Pierre (0.12), *Helicteres angustifolia* L. (0.09) and among Hani are *Dendrobium crepidatum* Lindl. ex Paxt. (0.41), *Aristolochia* sp. (0.31), *Microstegium ciliatum* (Trin.) A. Camus (0.13) and *Eupatorium coelestinum* L. (0.12). Used plants were categorized based on habitats and collection sites. The results show

that although Lahu and Hani are living in the same area with similar vegetation, patterns of plant use are not very similar. Both minorities use anthropogenic vegetations as main source of food plants whereas most of the medicinal plants are collected from collective or secondary forest. The presented data could be used in land use planning and management as well as sustainable harvest planning in the area.

<sup>1</sup>Institute for Plant production and Agroecology in the Tropics and Subt, Uni. Hohenheim, Garbenstr. 13, Stuttgart, Baden-Wurtemberg, 70599, Germany<sup>2</sup>Institute for Plant production and Agroecology in the Tropics and Subt, Uni. Hohenheim, Garbenstr. 13, Stuttgart, Baden-Wurtemberg, 70599, Germany

## 245 IMURA, HIROE

### Utilization of Useful Plants, Focusing on Foods in the Liangshan Yi Autonomous Prefecture, China

The result of this research concerns the utilization of the food plants among a few of the villages of the Yi ethnicity in Ganluo County, Liangshan Yi Autonomous Prefecture, Sichuan, China. In Gan luo xian, at the center of the town where the train station is located, people of the Yi ethnicity utilize potatoes (*Solanum tuberosum* L.), soybeans (*Glycine max*(L.)Merrill), Maize (*Zea mays* L.), buckwheat (*Fagopyrum esculentum* Moench.), oat (*Avena sativa* L.) and sorghum (*Sorghum bicolor* (L.) Moench) as their main food plants which they carefully cultivate, prepare and process by traditional methods. These plants are very important to the Yi ethnic group, as they are the main source of sustenance. The Yi ethnic group prepares their traditional primary foods through a very basic method called "Fu". The ingredients used in this process are millets and maize. By the "Fu" method, ingredients are first dried, pulverized, kneaded with water, rounded evenly, and finally boiled. After time passes and foods become cold, they will be warmed up in the ash of a stone hearth on the floor called "Geke" before served. Also, sorghum is kept as an ingredient of the traditional liquor for the Yi. The Yi call this liquor "Gangan-jiu" and serve it during social gatherings such as festivals or having guests visit. In addition, sorghum is also used as a material to make brooms called "Nohe". Despite the ongoing changes in society, the cultivation and utilization of the traditional plants has been carefully followed by the Yi. Therefore I conclude that each of these traditional names in the Yi's indigenous language have passed on their ancestor's traditional knowledge to subsequent generations and have shown their own environmental consideration. Keywords: Ethnobotany, Useful plants, Millets, Yi ethnicity(China)

Turukawa women's junior college, Miwa-cho,1135, Machida-shi, Tokyo, 1950054, JAPAN

## 246 DAWODU, ABIMBOLA\* and FASOLA, TAIYE. R

### Diurnal variation in the phytochemical composition of some Nigerian plants used in ethnomedicine.

It is believed by traditional herbal practitioners that herbs must only be collected before sunset as those collected after will not be potent. This has prompted the investigation of 15 plant species used in the treatment of diabetes in Nigeria. The leaves and stem barks of the plants were both harvested at 9am and 9pm. The harvested samples were dried at room temperature and powdered for phytochemical screening following standard methods.

The studies on Day and Night variations in phytochemicals showed differences in their quantities for the morning and evening samples. The evening samples of *Momordica charantia*, *Morinda lucida*, *Alstonia boonei*, and *Mangifera indica* leaves had the values of (140, 139, 100, 100) mg/100g respectively in the tannin content which was higher than the morning samples at (94, 94, 88, 69) mg/100g respectively. The Alkaloid content of *Ageratum conyzoides*, *Mimosa pudica*, *Lantana camara*, *Terminalia cattapa*, *Rauwolfia vomitoria* leaves had the values (2130, 7290, 3480, 2110, 3820) mg/100g respectively which was also higher than their morning counterparts at (380, 1420, 2200, 1170, 2590) mg/100g respectively. The evening samples of *Vernonia amygdalina*, *Carica papaya*, *Ocimum gratissimum*, and *Moringa oleifera* Leaves showed a significant difference in Flavonoid quantity (3130, 14400, 2560, 3140) mg/100g when compared with those collected in the morning (20, 3430, 1510, 2450) mg/100g. The Saponin content of *Mangifera indica* stem bark had a difference, while differences were also observed in the quantity of Terpenoid, Saponin, Flavonoid, Alkaloid, Tannins, Phenolic and Antioxidant content in the stem bark of *Azadirachta indica*, *Plumeria rubra* and *Xylopiya aethiopicum*.

The variations in the secondary metabolites of these medicinal plants may give a clue to the best time of their collection when needed for therapeutic efficacy.

University of Ibadan , Department of Botany , Ibadan, IB, NIGERIA"

247 TSHISIKHAWE, MILINGONI  
PETER\*, BALOYI, OLIVIA and MASEVHE,  
NDIVHALENI ANOX

### **Ethnobotanical survey of medicinal plants used by traditional healers with *Securidaca longepedunculata* Fresen. in the treatment of HIV/AIDS and related sicknesses**

In South Africa, about 5.7 million people are infected with HIV/AIDS. The use of herbal medicine has been recognized as a critical part in primary health care and as a system to reaching the goal of dealing with target on health. In this study we aim to document all the medicinal plants used by traditional healers to treat HIV/AIDS and related opportunistic infections such as cough and fever, and to document the existing knowledge and practices related to HIV/AIDS conditions and treatment in the Vhembe district of Limpopo province in South Africa

The information was gathered by a means of structured questionnaires. Thirty one plants were found to be used with *Securidaca longepedunculata* in the treatment of HIV/AIDS and related sicknesses. Trees made up the largest percentage of those medicinal plants while the roots were the most sought after parts in medicinal preparation.

University of Venda, Botany, Private Bag X5050, Thohoyandou, Thohoyandou, Limpopo Province, Za, RSA

248 KARIYAT, RUPESH\*<sup>1</sup>,  
STEPHENSON, ANDREW<sup>2</sup> and SCANLON,  
SARAH<sup>3</sup>

### **Effects of inbreeding and herbivory over generations in Horsenettle (*Solanum carolinense* L)**

The effects of inbreeding depression are reported to be stronger in species that typically outcross than in species that typically self (Johnston and Schoen, 1996); moreover, the effects of inbreeding can vary among families within populations (Dudash et al., 1997). However, there is little information regarding the long-term effects of inbreeding depression in wild plant populations across multiple generations under natural conditions. This study investigated differences between inbred and outbred progeny from 8 maternal families of Horsenettle (*Solanum carolinense* L) in fitness, susceptibility to herbivory, and production of new sprouts. Sixteen plants - one inbred and one outbred progeny from each family - all carrying a different combination of self incompatibility alleles (Variants of the Polymorphic S locus) were planted in each of 2 fields in 2008, and data on fruit number, seeds per fruit, and overall fitness was

collected. After the first growing season, plants overwintered and new sprouts emerged in early summer 2009. Data on time of sprouting, number of sprouts, leaf damage, and number of fruits, seeds/fruit and overall fitness was collected for the second generation. To examine how herbivory differentially affected the fitness of inbred and outbred progenies, one of the fields was sprayed with the contact insecticide Carbaryl 0.05% four times during the growing season. Genomic DNA was extracted and amplified from leaf samples of the new sprouts and self incompatibility alleles were identified to determine parentage. We found that (1) outbreds (both parents and second generation sprouts) produced significantly higher number of fruits and seeds, and had better fitness than inbreds, (2) outbred parents produced significantly higher numbers of new sprouts in the second generation and their sprouts germinated at least 2-3 days earlier, (3) both inbreds and outbreds from the sprayed field produced higher number of fruits and seeds, but (4) herbivory had a greater impact on the fruit production and fitness of inbred progeny.

<sup>1</sup>The Pennsylvania State University, Plant Biology, 208 Mueller Lab, Dept Of Biology, State College, PA, 16801, USA<sup>2</sup>Pennsylvania State University, Department Of Biology, 208 MUELLER LAB, UNIVERSITY PARK, PA, 16802, USA<sup>3</sup>

249 MOLINAR, RICHARD<sup>1</sup>, YANG,  
MICHAEL<sup>1</sup> and DEAN, ELLEN\*<sup>2</sup>

### **Hmong culinary and medicinal plants grown in Fresno County California**

Fresno County, California has over 4,000 small family farmers. More than 1,300 of these farmers are refugees from Laos, Cambodia, and Vietnam, including about 850 Hmong, 350 Lowland Lao, and the remaining are Mien, Khmu, Lahu, and Chinese. Since 2003, Fresno County UC Cooperative Extension researchers have been collecting Asian vegetables and herbs from Hmong farmers, both at farms and at farmers markets, for identification and outreach purposes. This grew into a small farms outreach project and hoophouse collection of live plants that specifically targeted plants grown by Hmong farmers. A researcher fluent in Hmong was integral in the success of the project. Plants are available for viewing at the University of California Kearney Field Station in Parlier, CA and were sent to the UC Davis Center for Plant Diversity herbarium for identification and mounting. To date, researchers have documented and identified 48 culinary and/or medicinal plants that are grown by Hmong farmers. The well known chicken soup herbs for pregnant females are part of the collection.

<sup>1</sup>UC Cooperative Extension, Fresno County, 1720 South Maple Avenue, Fresno, CA, 93702, USA<sup>2</sup>UC Davis Center for Plant Diversity, Plant Sciences, m.s. 7, One Shields Ave., Davis, CA, 95616, USA

250 MOLLIK, MD. ARIFUL HAQUE\*<sup>1</sup>, RAHMAN, MD. MAHAFUZUR<sup>1</sup>, FERDAUSI, DILARA<sup>1</sup>, AZAM, MD. NUR KABIDUL<sup>1</sup>, RAHMAN, MD. SAHIDUR<sup>1</sup>, AHMED, AHASAN<sup>2</sup>, CHOWDHURY, MAJEEDUL H.<sup>3</sup>, JAHAN, ROWNAK<sup>2</sup> and RAHMATULLAH, MOHAMMED<sup>1</sup>

### A medicinal plant study of Koira region in Khulna district: First hand information from field investigation in Bangladesh

Traditional medicinal practitioners known commonly as Kavirajes fulfill the medical needs of most rural as well as a significant section of the urban population of Bangladesh. It is the objective of this ongoing study program to find out more information on medicinal plant usage amongst various Kavirajes, since such usage varies between Kavirajes of different regions. The present survey was conducted amongst the Kavirajes of Koira region in the southern district of Khulna, Bangladesh. Interviews were conducted of the Kavirajes with the help of a semi-structured questionnaire. Medicinal plant specimens as pointed out by the Kavirajes were photographed, collected and identified at the Bangladesh National Herbarium. Information on the use of thirty-nine medicinal plants or plant parts was obtained. The medicinal plants (with ailments treated given in parenthesis) included *Clerodendrum infortunatum* (malaria, dermatitis), *Nymphaea nouchali* (atherosclerosis), *Phyllanthus nodiflora* (rheumatoid arthritis, eczema), *Barringtonia acutangula* (cancer), *Wrightia antidysenterica* (tuberculosis, tumor, spleen enlargement), *Shorea robusta* (syphilis), *Vanda tessellata* (rheumatoid arthritis), *Callicarpa americana* (dermatitis, tumor), *Phragmites karka* (jaundice, malaria), *Pongamia pinnata* (wound, dermatitis), *Curculigo orchioides* (infertility, fever), *Xanthium italicum* (tumor, headache, dermatitis), *Ludwigia hyssopifolia* (eczema), *Abutilon indicum* (tuberculosis), *Sonneratia apetala* (gonorrhoea, malaria), *Melia azedarach* (cancer, rheumatoid arthritis), *Heritiera fomes* (diabetes, diarrhea, pain), *Persicaria minor* (sedative), *Terminalia arjuna* (hypertension, bone fracture), *Asparagus racemosus* (snake-bite), *Cynodon dactylon* (tonsillitis, atherosclerosis), *Terminalia chebula* (leucorrhoea, tumor, tuberculosis), *Swertia chirata* (bronchitis, diuretic), *Terminalia bellirica* (diuretic, leprosy), *Ageratum conyzoides* (indigestion, impotency), *Alternanthera sessilis* (colic), *Dendrocnide sinuata* (dermatitis, stomachache), *Zingiber officinale* (cancer, liver diseases, paralysis), *Leucas aspera* (edema, snake-bite), *Cymbopogon citratus* (myopathic spasm), *Bombax ceiba* (leucorrhoea, pneumonia, snake-bite), *Aloe vera* (asthma, cancer, gonorrhoea), *Hibiscus rosa-sinensis* (cold), *Blumea lacera* (diarrhea, edema), *Solanum virginianum* (asthma, snake-bite), *Phyllanthus niruri* (typhoid, diabetes), *Wedelia chinensis* (alopecia, cancer),

*Tamarindus indica* (jaundice, anti-inflammatory), and *Piper longum* (cholera, tetanus, hypertension). It is to be noted that the above medicinal plants included mangrove species like *Heritiera fomes* and *Sonneratia apetala*, the medicinal uses of which are very little available or known.

<sup>1</sup>University of Development Alternative, Biotechnology and Genetic Engineering, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh <sup>2</sup>University of Development Alternative, Pharmacy, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh <sup>3</sup>New York City College of Technology, Biological Sciences, 300 Jay Street, Brooklyn, NY, 11201, USA <sup>4</sup>University of Development Alternative, Molecular Medicine and Bioinformatics, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh

251 LUKHOB, CATHERINE

### Use of Ethnobotanical Data in the Search for and Identification of Potential Drug Plants: A case study of *Ocimum* and *Plectranthus* species (Labiatae) in Kenya.

Traditional medicine has utilized plants to palliate, cure and/or prevent diseases in both humans and animals. The acquisition of knowledge has been through trial and error, and observation. Today, the enhanced search for botanical drugs throughout the world has increased the need for accurate means of identifying plants with possible pharmacological and biological activity. This paper discusses the value of ethno-botanical data in the preliminary search for potential drug plants using the case of *Ocimum* and *Plectranthus* species in Kenya.

University of Nairobi, School of Biological Sciences, P.O. Box 30197, 00100, Nairobi, Kenya

252 VICKERS, AMANDA\*<sup>1</sup>, BROSI, SUNSHINE<sup>2</sup>, HOWELL, JAMES<sup>3</sup> and PUTHOFF, DAVID<sup>2</sup>

### Chromatographic Quantification of Medicinal Compounds in Flowering and Non-flowering Wild-Harvested *Actaea racemosa* L.

Black cohosh (*Actaea racemosa* L.) is a perennial herb native to deciduous woodlands in eastern North America producing a flowering raceme persistent from midsummer into the fall. Traditionally, black cohosh has been used as a specific remedy for musculoskeletal pain and to support uterine function. Today, extracts of black cohosh are marketed primarily for use in relieving hotflashes associated with menopause. A majority of the raw material which supplies the global market for black cohosh products is harvested from naturally occurring wild populations in Appalachian woodlands. Although floral characteristics greatly as-

sist correct differentiation between *A. racemosa* and the concurrent species *A. pachypoda* Ell. and *A. podocarpa* DC., there is currently no incentive for wild harvesters to select only flowering individuals. This research addresses the question of whether harvest based on the presence or absence of a flowering raceme could allow a wild harvester to increase the yield of medicinal constituents in the rhizomes, while insuring correct identification based on floral characteristics. Rhizomes of flowering and non-flowering black cohosh plants were quantified using HPLC with PDA and UPLC with MS. The levels of several active ingredients including actein, 23-epi-26 deoxyactein, caffeic acid, ferulic acid, and kaempferol were quantified. Plants which had produced a flowering raceme failed to differ in rhizome mass from those which had not ( $p = 0.429$ ) indicating no negative impact of selection criteria on weight of harvested rhizome. In addition to yielding comparisons that are directly applicable to wild harvesting, intensive quantitative analysis will allow comparison with both cultivated and cell-cultured plant material. Improvements in the ability to produce these compounds in vitro will also enable conservation efforts by reducing demand on wild populations.

<sup>1</sup>Frostburg State University, Biology, 100 Braddock Road, Frostburg, MD, 21532, USA <sup>2</sup>Frostburg State University, Biology, 101 Braddock Road, Frostburg, MD, 21532, USA <sup>3</sup>Alligany College of Maryland, Biology, 12401 Willow Brook Road, Cumberland, MD, 21502, USA

**253 RAHMAN, MD.SAHIDUR\*<sup>1</sup>, SERAJ, SYEDA<sup>2</sup>, CHOWDHURY, ANITA RANI<sup>3</sup>, JAHAN, FARHANA ISRAT<sup>3</sup>, KHUDHA, MD. MONJUR-E-<sup>3</sup>, KHAN, MD. SHAMIUL HASAN<sup>3</sup>, APORNA, SADIA AFRIN<sup>3</sup>, JAHAN, ROWNAK<sup>3</sup> and RAHMATULLAH, MOHAMMED<sup>3</sup>**

### **A survey of medicinal plants used by the traditional healers of the Bede community of Bangladesh for treatment of rheumatism**

Rheumatism is widely prevalent particularly among the elderly people through out the world. It is a debilitating disease, causing not only intense pain but also may result in loss of movement and stiffness of joints. The Bedes are an indigenous community of Bangladesh, who unlike other indigenous people is nomadic in nature. They live on boats and make their living by traveling often on the river-ways and selling various merchandise to the village people. Their other occupations include snake catching and traditional medicinal practices. The Bede healers rely mostly on medicinal plants for treatment of various ailments. The objective of the present study was to conduct an ethnomedicinal survey among the Bede healers to gather information on medicinal plants used by them for treatment of rheumatism. It was observed that the plants used by the

Bede healers for treatment of rheumatism included *Justicia adhatoda*, *Crinum asiaticum*, *Datura stramonium*, *Calotropis gigantea*, *Terminalia arjuna*, *Bombax ceiba*, *Sansevieria roxburghiana*, *Mangifera indica*, *Ananas squamosa*, *Carissa carandas*, *Thevetia peruviana*, *Leucas aspera*, *Ricinus communis*, *Xanthium indicum*, *Leonurus sibiricus*, *Brassica napus*, *Chrozophora rotteileri*, *Cassia fistula*, *Sida acuta*, and *Careya arborea*. Since there are no modern allopathic drugs that can cure rheumatism, the afore-mentioned plants offer potential for discovery of novel compounds to treat this debilitating disease.

<sup>1</sup>University of Development Alternative, Biotechnology and Genetic Engineering, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh <sup>2</sup>University of Development Alternative, Faculty of Life Sciences, House No. 78, Road No. 11A, Dhanmondi, 1205, Bangladesh <sup>3</sup>University of Development Alternative, Faculty of Life Sciences, House No. 78, Road No. 11A, Dhanmondi, Dhaka, 1205, Bangladesh

**254 RAHMAN, MD.SAHIDUR\*<sup>1</sup>, KHUDHA, MD. MONJUR-E-<sup>2</sup>, CHOWDHURY, ANITA RANI<sup>2</sup>, JAHAN, FARHANA ISRAT<sup>2</sup>, KHAN, MD. SHAMIUL HASAN<sup>2</sup>, APORNA, SADIA AFRIN<sup>2</sup>, JAHAN, ROWNAK<sup>2</sup> and RAHMATULLAH, MOHAMMED<sup>2</sup>**

### **A survey of medicinal plants used by the traditional healers of the Bede community of Bangladesh for treatment of physical weakness**

Physical weakness in humans can arise from a number of factors including old age, malnutrition, physical and mental stress, and diseases. The Bedes are a nomadic community of Bangladesh, who reside on boats and live a river-based life of traveling and plying their trade of selling various merchandise, snake catching, and disease treatment. For the latter occupation, they have their own traditional medicinal practitioners, who mostly administer medicinal plants for treatment of various ailments. Physical weakness is among one of the ailments treated by the Bede healers and for which they are highly regarded by the village people, who form the majority of their patients. The objective of the present survey was to document the medicinal plants used by the Bede traditional healers of a Bede community at Savar, Bangladesh for treatment of physical weakness. Informed consent was obtained from the healers and information gathered with the help of a semi-structured questionnaire and the guided field-walk method. It was observed that the plants used by the Bede healers for treatment of physical weakness included *Mangifera indica*, *Carum copticum*, *Phoenix sylvestris*, *Phyllanthus emblica*, *Terminalia chebula*, *Terminalia bellerica*, *Nigella sativa*, *Bombax ceiba*, *Terminalia arjuna*, *Tagetes erecta*, *Glycyrrhiza glabra*, *Codiaeum variegatum*,

*Tamarindus indicus*, *Litsea glutinosa*, *Aloe barbadensis*, *Abroma augusta*, *Psidium guajava*, and *Aegle marmelos*. The selection of plants by the Bede traditional healers depended on the cause of physical weakness.

<sup>1</sup>University of Development Alternative, Biotechnology and Genetic Engineering, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh<sup>2</sup>University of Development Alternative, Faculty of Life Sciences, House No. 78, Road No. 11A, Dhanmondi, Dhaka, 1205, Bangladesh

255 HUGHES, MARK and BLAIR, CHARLES\*

### Invasive Aquatic Weeds; Implications for Mosquito and Vector Management Activities

Healthy natural wetlands ARE FAR LESS LIKELY to be breeding areas for disease-carrying mosquitoes than degraded ones. Degradation of these bodies of water by invasive aquatic weeds and other influences can result in their being potential habitat for mosquitoes that can carry the West Nile Virus, encephalitis, and other diseases. Control of these invasive plants can be an important part of the Integrated Weed/Pest Management efforts of both Weed Management Areas and Mosquito and Vector Control Agencies. Adverse effects of Water Hyacinth, *Eichhornia crassipes*, hydrilla, *Hydrilla verticillata*, Water Evening-primrose, *Ludwigia spp.*, Smooth Cordgrass, *Spartina spp.*, *S. densiflora x foliosa*, and other species on water quality and facilitating mosquito breeding will be shown. Presentations on the importance of *S. spp.* in San Francisco Bay were made at recent statewide Cal-IPC and Mosquito and Vector Control Conferences. Demonstration of these relationships can enhance both agency and public awareness of their importance.

176 ALCOR AVE, LOMPOC, CA, 93436, USA

256 HOSSAN, MD SHAHADAT\*<sup>1</sup>, SERAJ, SYEDA<sup>2</sup>, SWARNA, AUDITY<sup>2</sup>, RAHMAN, MEHREEN<sup>2</sup>, ISHIKA, TASNEEMA<sup>2</sup>, BISWAS, KAKOLI RANF<sup>2</sup>, MONALISA, MIRZA NIPA<sup>2</sup>, KHAN, TANIA<sup>2</sup>, KHUDHA, MD. MONJUR-E-<sup>2</sup>, JAHAN, ROWNAK<sup>3</sup> and RAHMATULLAH, MOHAMMED<sup>4</sup>

### Medicinal plants consumed by the Bede community by the Turag River at Kamarpara, Tongi, Bangladesh for prevention of diseases

The Bedes, otherwise known as the River Gypsies, are not widely known outside Bangladesh. They live in small groups throughout the country, and earn their living through selling miscellaneous items, snake catching, and performing various medicinal practices. They reside in boats and travel on the river-ways visiting various villages in turn to ply their trade. Since they lack access to modern medical facilities, they rely on their own healers, who in turn, prescribe medicinal plants for both therapeutic as well as preventive purposes. The objective of the present study was to conduct an ethnomedicinal survey among the Bede healers of the Bede community residing by the Turag River in Tongi area of Bangladesh to gather information on medicinal plants that they consumed at various times of the year for prevention of a number of diseases. These medicinal plants (with diseases that the Bede healers claimed to be prevented) included *Colocasia esculenta* (blood poisoning), *Amaranthus spinosus* (pain), *Amaranthus tricolor* (anemia, debility), *Chenopodium album* (gastric troubles), *Spinacea oleracea* (loss of appetite), *Enhydra fluctuans* (leucorrhoea), *Xanthium indicum* (rheumatic pain), *Ipomoea aquatica* (wastage of body, prevention of whitish discharge in urine), *Brassicapus* (fever, cold, coughs), *Cucurbitapepo* (debility), *Momordica charantia* (blood poisoning, skin disorders, jaundice), *Cajanus cajan* (jaundice), *Lagenariaciceria* (cardiovascular disorders), *Lathyrussativus* and *Vigna mungo* (flatulence, constipation), *Leucas aspera* (pain), *Molugo spergula* (fever, debility, gastrointestinal disorders), *Aegialitisrotundifolia* (loss of appetite), *Nigellasativa* (blood poisoning, skin disorders), *Citrus grandis* (throat pain, fever, debility), and *Corchorus capsularis* (debility, loss of appetite).

<sup>1</sup>University of Bedfordshire, Bedfordshire & Hertfordshire Postgraduate Medical School, 3B Oxgate Gardens, London, NW2 6EA, United Kingdom<sup>2</sup>University of Development Alternative, Pharmacy, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh<sup>3</sup>University of Development Alternative, Molecular Medicine and Bioinformatics, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh<sup>4</sup>University of Development Alternative, Biotechnology and Genetic Engineering, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh

257 HOSSAN, MD SHAHADAT\*<sup>1</sup>, SERAJ, SYEDA<sup>2</sup>, JAHAN, FARHANA ISRAT<sup>2</sup>, CHOWDHURY, ANITA RANI<sup>2</sup>, KHUDHA, MD. MONJUR-E-<sup>2</sup>, KHAN, MD. SHAMIUL HASAN<sup>2</sup>, APORNA, SADIA AFRIN<sup>2</sup>, JAHAN, ROWNAK<sup>3</sup> and RAHMATULLAH, MOHAMMED<sup>4</sup>

### A survey of medicinal plants used by the traditional healers of the Bede community of Bangladesh for analgesic purposes

The Bedes are an indigenous community of Bangladesh, who live on boats and do not remain stationary at any given place for a long time. Very little is known about this community because of their nomadic nature. Because they travel by boats on the river-ways of the country, they are referred to as the River Gypsies. The Bedes usually shun modern allopathic medical practices and rely on their own healers for treatment of various ailments. Because of their continuous travel throughout the country, the healers possess quite extensive knowledge of the medicinal plants of the country and their manifold uses. Since pain due to various causes is widely prevalent amongst all human beings, it was the objective of the present study to gather information on medicinal plants that they use for analgesic purposes. Interviews were conducted of the Bede healers with the help of a semi-structured questionnaire and the guided field-walk method. The medicinal plants used by the Bede healers for treatment of pain included *Justicia gendarussa*, *Coccinia grandis*, *Cassia sophora*, *Ruellia tuberosa*, *Anonasquamosa*, *Carissa carandas*, *Scindapsus aureus*, *Cocos nucifera*, *Cotulahemispherica*, *Bixa orellana*, *Heliotropium indicum*, *Crataeva magna*, *Datura metel*, *Chenopodium ambrosioides*, *Euphorbia hirta*, *Cassia occidentalis*, *Ageratum conyzoides*, *Kalanchoe pinnata*, and *Tragia involucrata*. Taken together, the plants present considerable potential for discovery of novel analgesics, which can be efficacious and at the same time, avoid the gastrointestinal discomforts associated with a number of allopathic pain-killing drugs.

<sup>1</sup>University of Bedfordshire, Bedfordshire & Hertfordshire Post-graduate Medical School, 3B Oxgate Gardens, London, NW2 6EA, United Kingdom<sup>2</sup>University of Development Alternative, Pharmacy, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh<sup>3</sup>University of Development Alternative, Molecular Medicine and Bioinformatics, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh<sup>4</sup>University of Development Alternative, Biotechnology and Genetic Engineering, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh

258 HOSSAN, MD SHAHADAT\*<sup>1</sup>, SERAJ, SYEDA<sup>2</sup>, KHUDHA, MD. MONJUR-E-<sup>2</sup>, APORNA, SADIA AFRIN<sup>2</sup>, KHAN, MD. SHAMIUL HASAN<sup>2</sup>, JAHAN, ROWNAK<sup>3</sup> and RAHMATULLAH, MOHAMMED<sup>4</sup>

### Medicinal plants used in amulets by the Bede community of Savar, Bangladesh for prevention of diseases

The Bedes are otherwise known as the River Gypsies of Bangladesh. They live in boats and travel throughout the year within the country, residing for a few days to a few weeks at different river-side villages. They have their own healers, who prescribe medicinal plants for therapeutic purposes, as well as prescribe medicinal plants to be worn in amulets for prevention of various diseases or other types of disorders. The objective of the present study was to conduct an ethnomedicinal survey among a large Bede community, who resides in Savar, which falls within Dhaka district, Bangladesh to gather information on medicinal plants prescribed to be worn in amulets by the Bede healers. After obtaining informed consent from the healers, the actual survey was conducted with the help of a semi-structured questionnaire and the guided field walk method. In this method, the healers showed various medicinal plants that they used within the amulets, and mentioned their local names and uses. All plant specimens were identified at the Bangladesh National Herbarium. The various plant species used in the amulets (with diseases given in parentheses) included *Helicteres isora* (unconsciousness in children), *Ruellia ciliosa* (mental tension due to disagreements between husband and wife), *Adenanthera pavonina* (excessive bleeding during menstruation), *Sapindus mukorossi* (prevent evil eye from children), *Elaeocarpus ganitrus* (bed wetting in children), *Musa sapientum* and *Bryonopsis laciniata* (infertility in women), *Martynia arnua* (waist pain), *Bixa orellana* (injury), and *Alstoniascholaris* (wet dream).

<sup>1</sup>University of Bedfordshire, Bedfordshire & Hertfordshire Post-graduate Medical School, 3B Oxgate Gardens, London, NW2 6EA, United Kingdom<sup>2</sup>University of Development Alternative, Pharmacy, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh<sup>3</sup>University of Development Alternative, Molecular Medicine and Bioinformatics, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh<sup>4</sup>University of Development Alternative, Biotechnology and Genetic Engineering, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh

259 WALSH, BRIAN M.\*<sup>1</sup> and  
EMSHWILLER, EVE<sup>2</sup>

### Phylogeny of American *Chenopodium* species with focus on origins of the domesticated taxa

The edible seeds of Quinoa (*Chenopodium quinoa*, Amaranthaceae) have gained popularity worldwide, based on nutritional qualities and ease of growing. Most people do not know quinoa is one of four cultigens of *Chenopodium* domesticated in the Americas: *C. quinoa* and *C. pallidicaule* from South America, *C. berlandieri* ssp. *nuttalliae* from Mesoamerica, and the extinct *C. berlandieri* ssp. *jonesianum* recovered from archaeological sites throughout eastern North America. Despite nearly 100 years of debate researchers still do not agree on the relationship among these domesticates. Conflicting hypotheses have been proposed asserting whether cultigens were domesticated independently or represent introductions into neighboring regions. Alternative hypotheses suggest two, three, or four independent domestications of *Chenopodium* in the Americas, and proposed several putative wild progenitors of the cultigens. To investigate the relationships among cultigens of *Chenopodium* and assess potential wild progenitors, a phylogenetic framework of the genus emphasizing New World species is required. Phylogenetic analyses of DNA sequences of non-coding loci, both nuclear (*SOS1* intron 17, *COS at103*, *ITS*) and plastid (*trnQ-rps16*, *trnL-trnT*, *ndhJ-trnF-trnL*, *psbD-trnT*, and *psbM-ycf6*), were conducted using parsimony, maximum likelihood, and Bayesian analyses. Taxon sampling includes 19 *Chenopodium* species from North and South America, with focus on the extant cultigens and subspecific taxa within *C. berlandieri*.

Findings include the following: *Chenopodium pallidicaule* is genetically distinct from other extant cultigens.

Sampled cultivars of the Mesoamerican cultigen, *C. berlandieri* ssp. *nuttalliae*, unite in a single subclade, nested within, but distinct from wild *C. berlandieri*.

*Chenopodium quinoa* is nested within the *C. berlandieri* complex, but not within the *C. berlandieri* ssp. *nuttalliae* clade. Interestingly, the southern-most range of wild *C. berlandieri* is southern Mexico, where as Quinoa is cultivated in Ecuador, Peru, and Bolivia. These findings are consistent with independent domestications of the extant cultigens. Using nucleotide markers unique to *C. berlandieri* ssp. *nuttalliae*, ancient-DNA analyses will be conducted to determine the relationship of the extinct cultigen, *C. berlandieri* ssp. *jonesianum*.

<sup>1</sup>University of Wisconsin - Madison, Botany, 430 Lincoln Dr., Madison, WI, 53706, USA<sup>2</sup>University Of Wisconsin-Madison, Botany Dept, 321 Birge Hall, 430 Lincoln Drive, Madison, WI, 53706-1313, USA

260 PANTUSO, TRACI\*, DRUM, RYAN  
and LUND, KALEB

### Immunomodulating Effects of *Oplopanax horridus*

Devil's Club, *Oplopanax horridus* (Sm.) Miq. (Araliaceae) (syn. *Fatsia horrida* (Sm) Benth. & Hook.; *Echinopanaxhorridus* (Sm.) Decne. & Planch; *Panaxhorridum* (Sm.)), is a deciduous shrub of the Araliaceae or Ginseng family native to the Northwestern United States. Native Americans of British Columbia and the Northwestern United States regard Devil's Club as an important medicinal plant. Traditional medicinal uses of *Oplopanax horridus* (OH) include its use as an antibacterial, antifungal, antimycobacterial, antiviral and as an immunomodulator for rheumatism and diabetes. Previously it has been shown that extracts of OH have antibacterial, antifungal, antiviral and anti-mycobacterial properties. The mechanisms of action of OH's effects have not been established and there are few studies that have presented chromatographic profiles of OH extracts. OH extracts have demonstrated a dose dependent decrease in nitric oxide (NO) production in LPS stimulated RAW264.7 macrophage cell line, which may partially explain the traditional use of OH as an immunomodulator for both rheumatism and diabetes. Macrophage populations are a heterogeneous group of myeloid derived cells that are found in many different tissues and demonstrate population dependent protein expression. LPS induced bactericidal macrophages release increased levels of pro-inflammatory biomarkers, such as reactive oxygen species (ROS), nitric oxide (NO), tumor necrosis factor alpha (TNF- $\alpha$ ), Interleukin-6 (IL-6) and IL-12, which are all required to fight intracellular pathogens such as *Mycobacterium tuberculosis* and are implicated in the pathogenesis of diabetes and rheumatoid arthritis. To further understand the effects of OH extract on LPS stimulated macrophage activation, the bark of recumbent stems of *Oplopanax horridus* were collected in Skagit County, Washington and ethanol and water extracts were prepared and assessed for their anti-nitric oxide and anti-TNF- $\alpha$  activities in an *in vitro* RAW264.7 macrophage cell line model. The ethanol extract showed increased nitric oxide and TNF- $\alpha$  inhibition compared to the water extract.

Bastyr University, Research, 14500 Juanita Drive NE, Kenmore, Wa, 98028, USA

261 GUEL, ANEL\*<sup>1</sup>, PENN, JIM<sup>2</sup> and ATÍAS VASQUEZ, GLADIS<sup>3</sup>

### Use of the chambira palm (*Astrocaryum chambira*) in rainforest communities of the Peruvian Amazon: Household involvement in a commercial artwork for export and tourists

Near a large new community reserve in the Peruvian Amazon, women in local communities have been involved in weaving chambira fiber artwork to raise household incomes and alleviate rural poverty. Despite the promotion of this expanding business as an ecofriendly activity that offers needed economic opportunities for ribereño women, no studies have been conducted on how women and their households become involved in this business, nor the economic impact on their households and communities. Moreover, there is no research demonstrating how they obtain the palm fibers, and if it is harvested in a sustainable manner.

To determine the reasons why women became involved in chambira weaving, their income from artwork sales, where they obtain fiber, and if the fiber is harvested in a sustainable manner. The results of the study will give the women, their communities and development planners key insights about how the chambira artwork business can both help and hinder community development as they consider conservation priorities.

Structured socioeconomic surveys were conducted in 122 households from 5 different communities. Using GPS and ArcGIS 10, chambira harvest areas and gardens were surveyed and mapped out. With each survey, the density of chambira palms was determined and the harvest of new shoots was recorded.

Household income from the sale of chambira artwork showed high variance between communities, along with levels of participation in the export program. Densities of chambira palms varied greatly across different landscapes. Harvest levels for the palms ranged from medium to very high, with most palms harvested from relatively small areas.

Current demand for chambira fiber far exceeds the available supply in community lands. Each of the five communities must plant more chambira to supply the expanding artwork market and lower harvest pressure on wild chambira. Participation must increase so that more women and their families can take advantage of the increased demand for chambira artwork and raise their household income.

<sup>1</sup>Grand Valley State University, Department of Geography and Planning, 12 National Ave NW, Grand Rapids, Michigan, 49504, USA<sup>2</sup>Grand Valley State University, Department of Geography and Planning, B - 4 - 205 Mackinac Hall, Allendale, MI, 49401, USA<sup>3</sup>The Rainforest Conservation Fund, Peru

262 BOTTS, ELIZABETH<sup>1</sup>, KEINSLEY, MATTHEW<sup>2</sup>, BRIMMER, COURTNEY<sup>2</sup>, MILLER, TANNER<sup>2</sup>, SUMMERS, KELLEY<sup>2</sup>, DUDLE, DANA<sup>1</sup> and HANSON, BRYAN\*<sup>2</sup>

### The Effect of Climate Change on the Medicinal Plant Purslane (*Portulaca oleracea*)

Climate change is a form of stress to plants. Increased temperatures, drought and salinity are expected to have significant effects on the growth and chemical composition of medicinal plants. We have been investigating the effect of drought and salinity on the medicinal plant purslane, known for its high levels of important fatty acids and betalain pigments, using methods from both ecology and chemistry. Several genotypes of purslane were grown under various stress levels in a genotype by environment experiment. Plant growth and fitness were monitored via morphological parameters. The chemical response to stress was measured by a combination of single point measurements (e.g. antioxidant levels) and metabolomic approaches (spectroscopic methods such as visible spectra and IR spectra). We will report on the results to date.

<sup>1</sup>DEPAUW UNIVERSITY, Department Of Biology, 114 Olin Hall Of Biological Sciences, 1 E. Hanna Street, GREENCASTLE, IN, 46135, USA<sup>2</sup>DePauw University, Chemistry & Biochemistry, 602 S. College Ave, Greencastle, IN, 46135, USA

263 FUENTES-CROSS, PATRICIA\*<sup>1</sup> and CROSS, HUGH<sup>2</sup>

### Genetic Diversity of a native Australian fruit, *Santalum acuminatum*, in South Australia

The native Australian fruit quandong, *Santalum acuminatum*, is widely dispersed across the southern arid regions of Australia. Along with two other endemic species of *Santalum* (*S. spicatum* and *S. murrayanum*) it has been listed as threatened. Wild populations are impacted by harvesting, browsing by feral animals, and habitat fragmentation. We use a phylogeographic approach to study remnant populations in South Australia, to reconstruct the historical processes underlying their geographic distributions, reveal their current genetic structure, and determine which of the external stresses have had the greatest impact. We collected leaf samples from wild populations and these have been genotyped using chloroplast and nuclear microsatellite markers, and DNA sequences were obtained from the nrDNA marker ITS. Thus far, our results indicate a high degree of genetic variation both between and within populations of South Australia. More detailed genetic and morphological study of the species and its relatives will help to uncover the historical processes underlying

the current distributions, and to determine what biotic and abiotic factors have had the largest impacts on their genetic diversity.

<sup>1</sup>The University of Adelaide, School of Earth and Environmental Sciences, North Terrace Campus, Darling Bldg. Room 205A, Adelaide, South Australia, SA, 5000, Australia<sup>2</sup>Department of Environment and Natural Resources, State Herbarium of South Australia, P.O Box 3732, Kent Town, South Australia, 5000, Australia

**264 SOEJARTO, DJAJA DJENDOEL\*<sup>1</sup>, SOUTHAVONG, BOUNHONG<sup>2</sup>, SYDARA, KONGMANY<sup>3</sup>, BOUAMANIVONG, SOMSANITH<sup>4</sup>, XAIVEU, MOUACHANH<sup>5</sup>, ELKINGTON, BETHANY G.<sup>6</sup>, GYLLENHAAL, CHARLOTTE<sup>7</sup>, KADUSHIN, MARIAN R.<sup>1</sup>, RILEY, MARY C.<sup>1</sup> and ZHANG, HONGJI<sup>7</sup>**

**A survey of medicinal plants of Lao People's Democratic Republic toward the discovery of bioactive compounds as potential candidates for pharmaceutical development**

**E**thnobotanical interviews on medicinal plants of Lao People's Democratic Republic were conducted for the period of 1999 through 2008, as part of an effort of a Vietnam-Laos ICBG project, Studies on Biodiversity of Vietnam and Laos, to discover new bioactive compounds from plants of Laos as potential candidates for development into drugs for therapies against cancer, AIDS, malaria and tuberculosis. Interviews were performed throughout the country in the Lao language by the scientific staff of the Institute of Traditional Medicine [ITM] of the Ministry of Health of Laos in Vientiane, in cooperation with scientists from the University of Illinois at Chicago [UIC]. A disease-based semi-structured interview method [UIC IRB Research Protocol # 2003-0636] was used. A total of 81 healers [mostly male; age 65-82:27; age 50-64:37; age 40-49:17] in 15 of the 17 provinces of Laos were interviewed. Following the completion of an interview session, the interviewee guided the interviewer(s) to the site of the plants in a garden or in the field (forest). For each interview, a set of voucher herbarium specimens was prepared [taxonomically identified at a later date] and plant samples [plant parts] mentioned to be used for disease treatment were collected. A total of 991 plant samples were collected for biological assay. The identity of 750 of these has been determined with confidence, as belonging to 578 species of angiosperms, in 107 families. Samples were extracted at the laboratories of ITM, using a standardized extraction protocol. Extracts were dispatched to UIC for bioassay at UIC laboratories. In the event of active leads, the active species were recollected for bioassay-guided chemical isolation of the active compounds. Results of ethnobotanical survey will be presented, and results from the laboratory [biology and

chemistry] analyses will be discussed. This project has been supported by NIH Grants 1-UO1-TW-001015-01 and 2-UO1-TW-001015-06.

<sup>1</sup>University of Illinois at Chicago, College of Pharmacy, Medicinal Chemistry and Pharmacognosy, m/c 781, 833 S. Wood St., Chicago, IL, 60612, USA<sup>2</sup>Institute of Traditional Medicine, Xoy 1 Ban Thongkang, Vientiane, Vientiane, Lao People's Democratic R<sup>3</sup>Institute of Traditional Medicines, Xoy 1 Ban Thongkang, Vientiane, Vientiane, Lao People's Democratic R<sup>4</sup>Office of the Prime Minister, National Herbarium, Vientiane, Vientiane, Lao People's Democratic R<sup>5</sup>Institute of Traditional Medicines, Pharmacognosy, Xoy 1 Ban Thongkang, Vientiane, Vientiane, Lao People's Democratic R<sup>6</sup>University of Illinois at Chicago, Department of Medicinal Chemistry and Pharmacognosy, 833 South Wood Street (M/C 781), Chicago, IL, 60615, USA<sup>7</sup>University of Illinois at Chicago, Department of Medicinal Chemistry and Pharmacognosy, 539 Pharmacy, mc 781, 833 South Wood Street, Chicago, IL, 60612, USA

**265 REESE, R.\*<sup>1</sup>, WYZGOSKI, FAITH<sup>2</sup>, PAUDEL, LILADHAR<sup>3</sup>, RINALDI, PETER<sup>4</sup>, GIUSTI, MONICA<sup>5</sup>, JOHNSON, JODEE<sup>6</sup>, SCHEERENS, JOSEPH<sup>10</sup>, BOMSER, JOSHUA<sup>8</sup>, HARDY, JAMES<sup>4</sup>, GE, XIJIN<sup>9</sup>, CHANON, ANN M.<sup>10</sup> and MILLER, A. RAYMOND<sup>10</sup>**

**Modeling of High Field NMR Spectra of Black Raspberry (*Rubus occidentalis* L.) Fruit Polyphenol Composition and the Chemopreventive Properties of the Fruit Extracts in Human Cancer Cells (HT-29)**

**P**olyphenolic-rich black raspberry (BR) fruit extracts have shown chemoprotective activity against oral, esophageal, colonic and rectal forms of aerodigestive cancers. Several studies have identified potentially important biologically active compounds from BR, but understanding the complex interactions of constituents in the BR extracts in modulating cancer cell-growth requires a metabolomic approach. Comparing <sup>1</sup>H nuclear magnetic resonance (NMR) based analyses of BR extracts with their inhibition of proliferation of HT-29 colon cancer cells, we constructed statistically based models that permitted quantitation of structure-activity relationships. Anthocyanins (cyanidin 3-rutinoside, cyanidin 3-xylosylrutinoside, cyanidin 3-glucoside, cyanidin 3-sambubioside, and pelargonidin 3-rutinoside) were shown to be important antiproliferative constituents of the extracts. Additionally, non-anthocyanin phenolic compounds including hydroxybenzoic acids, quercetin, myricetin, ellagic acid, and their glycosylated and methoxylated derivatives were found to be impor-

tant to the overall antiproliferative activity of the fruit.

<sup>1</sup> South Dakota State University, Bio/Micro, SNP 249B, Box 2140D, Brookings, SD, 57007, USA<sup>2</sup>The Ohio State University-Mansfield, Department of Chemistry, 1760 University Drive, Mansfield, OH, 44906<sup>3</sup> University of Akron, Department of Chemistry, Akron, OH, 44325-3601<sup>4</sup>University of Akron, Department of Chemistry, Akron, OH, 44325-3601<sup>5</sup> The Ohio State University, Department of Human Nutrition,, Columbus, OH, 43210<sup>6</sup>The Ohio State University , Department of Human Nutrition, Columbus, OH,, 43210<sup>7</sup>The Ohio State University, Ohio Agricultural Research and Development , Department of Horticulture and Crop Science, 1680 Madison Avenue, Wooster, OH, 44691<sup>8</sup> The Ohio State University, ,, Department of Human Nutrition,, Columbus, OH, 43210<sup>9</sup>South Dakota State University, Department of Mathematics and Statistics, Brookings, SD, 57007<sup>10</sup>The Ohio State University, Ohio Agricultural Research and Development , Department of Horticulture and Crop Science, 1680 Madison Avenue, Wooster, OH, 44691

## 266 JAHAN, NUSRAT

### Effect of different media and growth regulators for callus formation and organogenesis of *Juniperus species*

The effect of various concentrations and types of plant growth regulators were checked to optimize the efficient media for propagation. The young shoots of *Juniper excelsa* and *Juniper horizontalis* brought from Ziarat were cultured on MS,WPM, N<sub>6</sub> media supplemented with different concentrations of 2, 4-Din combination with BAP. The explants were cultured in the woody plant media (WPM) containing 0.50 mg/L 2, 4-D and BAP 50mg/L. Rich solid mass of brown-green callus was produced. Large number of shoots were produced in medium containing 0.50mg/L BAP. Rooting started on the same media when plant attained height of 3cm. After the production of roots the plants were transplanted individually in small pots and kept in the close tunnel where the humidity was approximately 70%. After acclimatization plants were shifted to green house.

Balochistan University of IT, engineering and management sciences, Plant sciences and Informatics, Faculty of Life Sciences and Informatics, Quetta, Baluchistan, 83700, Pakistan

## 267 PAUDEL, BABU RAM

### Ethno-Phytotherapy in the Lekhnath Municipality, Kaski, the Mid-Hills of Nepal

Lekhnath Municipality, extends, in the Oriental Realm<sup>1</sup>, between the north parallels of 25° 7' and 28° 10' and east meridians of 83° 50' and 84° 50'. Situated in the mountainous region of the southern Himalayas and trapped between the higher Himalayas in the north and Mahabharat range in the south, it occupies central position in the country. Lekhnath Municipality is rich in both biodiversity and cultural diversity. It includes the biodiversity rich forest and wetlands, both of which

are declared as biodiversity hot spot in Nepal. The study analyzed the indigenous knowledge of medicinal plants and their uses among the different ethnic groups living within the municipality. Data were collected in one year period through interviews, interaction and workshop with local people , traditional healers (Baidhya, Dhami and Amchis) and traditional followers. A total of 217 plants were found being used by the local healers for the treatment of more than 50 different prevailing diseases within the communities. Spiritual belief, minimum or no side effect, cheap and easy availability are the causes of dependency on traditional healing practice. Enforcement of local bodies in management of plant resources and legitimating traditional knowledge and practice could help to preserve indigenous knowledge.

Tribhuvan University, Shubhashree College, Kathmandu, Nepal

## 268 ZAIDI, MUDASSIR

### Seasonal forage mineral concentrations, nutritional and medicinal value of *Berberis baluchistanica* as fodder from arid environments of Balochistan.

This study was conducted to find out seasonal variations in mineral composition of a palatable shrub *Berberis baluchistanica* (Family Berberidaceae) in high elevations at Walitangi, Quetta, Balochistan. This province is well known for its wealth of a large number of medicinal plants and unique plants being used by men and animals. In this area a large population depends on animals for their livelihood. *Berberis baluchistanica* is a wild plant used as fodder for grazing animals this plant is also used as medicine by local people. They used the roots decoction for the cure of internal injuries and ophthalmic problems, beside this it is also used for the removal of kidney stones, as it contains berberine which is known to be useful for a number of diseases. Its mineral concentrations as fodder were assessed seasonally for two years. It was found to be good source of macroelements but deficient in Fe and Na so must be supplemented with some other forage. The fresh leaves and ash was analyzed for its mineral composition through X-ray fluorescent spectrophotometer and Atomic absorption spectrophotometer. High Phosphorus, Potassium, Calcium, Mg content (0.49%, 0.42%, 0.39%, 0.30% DM respectively) were observed during spring and summer seasons. These minerals gradually decreased in autumn and winter seasons. Iron and Sodium concentration were lower than the amounts required for small ruminants (0.05%, 0.04% DM respectively) and their concentrations were not effected by the seasons.

University Of Balochistan, C-9, University Colony, Sariab Road, Quetta, 83700, Pakistan

269 AZIZ, IDRIS JAMEEL\* and  
BASHIR, ANBREEN

### Plants And Vision

Life on this planet would not be complete without the role played by plants. The multidisciplinary approach of ethnobotany gives us an insight into the role played by plants in many cultures including their medicinal use. The Himalayan mountain range, well known for its richness in floral diversity, extends along the northern frontiers of countries like Nepal and India. Traditional health care systems have long been used in these places for healing. Information about medicinal plants was written on palm leaves (Saushrut Nighantu) as early as 879 AD. Our aim was to study the medicinal plants that could treat various eye diseases. Plants like *Evetamia coronaria* and *Achyranthes aspera* have widely been used for eye diseases like conjunctivitis by various tribes in Nepal and India. Medicinal plants are still being used by eastern homeopathic treatment institutes in these countries. Many factors like habitat loss and deforestation combined with over harvesting have resulted in dwindling of some of this herb treasure. Secondly, we wanted to identify the main causes of decline in the number of medicinal plants and the status of their conservation.

Harris-Stowe State University, Arts & Science, Laclede Ave., St. Louis, MO, 63103, USA

270 NOVY, ARI\*<sup>1</sup>, SMOUSE, PETER E.<sup>2</sup>, HARTMAN, JEAN MARIE<sup>3</sup>, STRUWE, LENA<sup>4</sup>, HONIG, JOSHUA<sup>5</sup>, MILLER, CHRIS<sup>6</sup> and BONOS, STACY<sup>6</sup>

### Genetic Variation of *Spartina alterniflora* Loisel. in the New York Metropolitan Area and Its Relevance for Marsh Restoration

We determined the genetic population structure of *Spartina alterniflora* in Jamaica Bay, Queens, NY and the surrounding area by microsatellite genotyping in order to assist the ongoing restoration of Jamaica Bay by the U.S. Army Corps of Engineers. AMOVA analysis indicated that population differences accounted for only 15% of molecular variance ( $\Phi_{PT} = 0.15$ ,  $p = 0.001$ ). Observed heterozygosity ( $H_o$ ) ranged from 0.62 to 0.73. A Mantel test indicated a weak and non-significant correlation between Nei genetic distance and geographic distance matrices ( $r = 0.34$ ,  $p = 0.12$ ). A PCA revealed no obvious grouping pattern for the sampled populations. Based on these data, we determined that the studied populations contained similar genetic variability to other populations in the New York vicinity and to those of the entire region. It seems likely that collection of germplasm from within the general region

will provide sufficient variation to maintain overall genetic variation in restoration plantings. Given the small amount of genetic structure among populations within Jamaica Bay, however, it would be prudent to collect widely within the target marsh. We also recommend the practice of propagating plugs of *S. alterniflora* from wild seed, as opposed to vegetative propagation, when creating planting stock, in order to maximize genetic diversity in restored marshes.

<sup>1</sup>Rutgers University, Departments of Plant Biology and Landscape Architecture, 59 Dudley Rd., New Brunswick, NJ, 08901, USA<sup>2</sup>Rutgers University, Ecology and Evolution, 14 College Farm Road, New Brunswick, NJ, 08901, USA<sup>3</sup>Rutgers University, Landscape Architecture, 93 Lipman Drive, New Brunswick, NJ, 08901, USA<sup>4</sup>Rutgers University, Room 237 Foran Hall, Room 237 Foran Hall, 59 Dudley Rd, New Brunswick, NJ, 08901, USA<sup>5</sup>Rutgers University, Plant Biology, 59 Dudley Road, NJ, 08901, USA<sup>6</sup>US Department of Agriculture, Plant Materials Center, Cape May, NJ, USA

271 BASHIR, ANBREEN

### Dwindling Himalayan Mayapple

The importance of plants to life on earth is immeasurable. The impact of human activity on the existence of some of the most beneficial plants has been of increasing concern. One of the hot spots of economically important plants is the majestic Himalayan mountain range surrounding Kashmir valley of India. It is the home of a large number of medicinal plants including *Podophyllum hexandrum*, which is progressing towards extinction. The plant has a rhizome which is a source of a very essential resinous substance known as podophyllotoxin, an active ingredient for several drugs like podophyllin. This has made the species vulnerable for over exploitation. This indiscriminate extraction of podophyllotoxin along with several other factors has led to the near extinction of the Himalayan Mayapple.

Harris-Stowe State University, Math And Natural Science, Laclede Avenue, St Louis, MO, 63103, USA

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## Genetics Section

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See also *Genomics / Proteomics, Molecular Biology, Molecular Ecology and Evolution, Population Genetics, Advances in Plant Systematics and Population Genomics: Applications of Next Generation Techniques and Plant reproductive strategies under environmental stress.*

### ORAL PAPERS

272 NOVY, ARI<sup>\*1</sup>, FLORY, LUKE<sup>2</sup> and HARTMAN, JEAN MARIE<sup>3</sup>

#### Rapid evolution of phenology during invasion of the grass *Microstegium vimineum* in North America

*Microstegium vimineum* (Poaceae, tribe Andropogoneae) is a C<sub>4</sub>, shade tolerant, short-day flowering, annual grass considered to be among the most invasive plants in the eastern United States. It forms dense monocultures in forests, fields and disturbed areas where it can suppress native species and disrupt ecosystem function. *M. vimineum* was first recorded in North America in Knoxville, TN in 1919, though it may have been introduced elsewhere. By 1972 its range extended from Florida to New Jersey, and west to Ohio and Mississippi. It is currently found as far north as Massachusetts, as far west as Texas and Missouri, and as far south as Puerto Rico. To examine evolution of invasive *M. vimineum* phenology, and to evaluate the potential impact of this evolution on range expansion, we collected 10 populations of *M. vimineum* from throughout its invasive range. Populations were grown in controlled environment growth chambers under two distinct light regimes: one simulating daylength conditions near the northern limit of the invasive range and one simulating conditions near the southern limit. We found that the average critical flowering day length for each population was significantly predicted by latitudinal origin under both treatments ( $R^2=0.89$ ,  $p<0.001$  and  $R^2=0.85$ ,  $p<0.001$  for northern and southern treatments respectively). Since herbarium records indicate that *M. vimineum* was introduced in the southeastern United States and then radiated outward, we conclude that the variation in phenologic phenotypes recorded from populations outside the original introduction area must have arisen by evolution during the last 100 years. Our results indicate that rapid evolution in *M. vimineum* phenology may have contributed to range expansion in this invasive grass.

<sup>1</sup>Rutgers University, Departments of Plant Biology and Landscape Architecture, 59 Dudley Rd., New Brunswick, NJ, 08901, USA-

<sup>2</sup>Indiana University, Department of Biology, 1001 East 3rd Street, Bloomington, IN, 47405, USA<sup>3</sup>Rutgers University, Department of Landscape Architecture, 93 Lipman Drive, New Brunswick, NJ, 08901, USA

273 RILEY, LYNN<sup>\*1</sup>, MCGLAUGHLIN, MITCHELL E<sup>2</sup> and HELENURM, KAIUS<sup>3</sup>

### Phylogeography of two California Channel Island endemic *Eriogonum* (Polygonaceae)

The California Channel Islands harbor many endemic animals and plants, including several endemic species and subspecies within the genus *Eriogonum* (Polygonaceae). Although a few Channel Island phylogeographic studies have been published, patterns of colonization and divergence have not been inferred for any Channel Island plant taxon. The current study uses DNA sequence divergence to infer colonization and gene flow patterns within and between two Channel Island endemic *Eriogonum* species. Data are presented from the monotypic endemic species *Eriogonum arborescens* and the three subspecies of the endemic species *E. giganteum*. Six populations of *Eriogonum arborescens* and fourteen populations of *E. giganteum* were sampled from throughout the archipelago. One to three individuals from each population were sequenced for three chloroplast regions (ca. 2K total aligned base-pairs), the ribosomal internal transcribed spacer (ITS) and one low copy nuclear gene region (*LFY*). Distinct patterns of DNA diversity and divergence were detected between different taxa, and within taxa on different islands. Additionally, discordant phylogenetic signals were recovered with the chloroplast and nuclear sequence data. Implications for colonization patterns and inter-island gene flow are discussed.

<sup>1</sup>University Of South Dakota, Biology, 414 E. Clark Street, Vermillion, SD, 57069, USA <sup>2</sup>University of Northern Colorado, Biology, 501 20th St, Greeley, CO, 80639, USA <sup>3</sup>University Of South Dakota, Department Of Biology, Vermillion, SD, 57069, USA

274 SHI, TAO<sup>\*</sup> and BARKER, MICHAEL S.

### Paleopolyploidy and diversification of Actinidiaceae and related Ericales

Analyses of plant genomes suggest that ancient polyploidy may have led to a dramatic increase in diversity in several angiosperm lineages. However, additional genomic analyses are needed to precisely locate ancient polyploidy in the plant phylogeny and assess the contribution of genome multiplication to correlated radiations. Previously, we demonstrated three ancient genome duplications in *Actinidia* (kiwifruit). Using newly generated Illumina transcriptome data (~1GB/species), we sampled each genus of the Actinidiaceae (*Actinidia*, *Clematoclethra*, and *Saurauia*) and their closest families in Ericales including two carnivorous families- Roridulaceae and Sarraceniaceae, and ornamental plants among the Ericaceae. Analyses of gene families among

these species support our previous results with one paleopolyploidy in the ancestry of extant Actinidiaceae species (Ad- $\alpha$ ), another ancient polyploidy shared by all the species we sequenced as well as *Camellia sinensis* (Ad- $\beta$ ), and the well-established At- $\gamma$  WGD that occurred prior to the divergence of all taxa examined. Preliminary analyses indicate significantly faster rates of species diversification were found in Actinidiaceae correlated with the most recent WGD (Ad- $\alpha$ ) than those without, i.e. Roridulaceae and Sarraceniaceae. Ongoing research is directed towards identifying the novel contribution of paleopolyploid-derived genes to the Actinidiaceae genome and identifying candidates associated with diversification. These results represent one of the first case studies of paleopolyploidy and diversification where members of all involved clades are represented by genomic data, and kiwifruit may serve as a model system for studying polyploidy and diversification among angiosperms.

University of Arizona, Ecology & Evolutionary Biology, P.O. Box 210088, Tucson, AZ, 85721, USA

275 CHESTER, MICHAEL<sup>\*1</sup>, GALLAGHER, JOSEPH<sup>2</sup>, SYMONDS, V. VAUGHAN<sup>3</sup>, VERUSKA C. SILVA, ANA<sup>4</sup>, MAVRODIEV, EVGENY<sup>5</sup>, LEITCH, ANDREW R.<sup>6</sup>, SOLTIS, PAMELA<sup>7</sup> and SOLTIS, DOUGLAS<sup>1</sup>

### Population cytogenetics of a neoallopolyploid species, *Tragopogon miscellus* Ownbey (Asteraceae)

*Tragopogon miscellus* is one of only a few allotetraploid species known to have arisen within just the past few hundred years. This allotetraploid was first reported in 1950 and has formed multiple times from the diploids *T. dubius* and *T. pratensis*, which were introduced to the USA in the early 1900s. Thus, this model system provides natural populations in which to observe the early stages of polyploid evolution. Molecular analyses conducted to date suggest that *T. miscellus* is genetically unstable, with frequent losses of DNA detected. Preliminary cytological studies have also identified individuals with karyotypes that are not simply additive of the diploid progenitors. The cytology of *T. miscellus* was examined at the population level by sampling seeds collected from seven localities in the Palouse region of Washington and Idaho. Karyotypes were constructed from somatic metaphase chromosomes subjected to genomic *in situ* hybridization (GISH). Nuclear microsatellites were used to identify and delimit independently derived polyploid lineages of *T. miscellus*. Results show that many polyploid individuals have a non-additive karyotype, yet most of these aneuploids still have the euploid number of 24 chromosomes. Most dosage alterations appear compensated by putative homeologous chromosomes, resulting in monosomy-trisomy or

nullisomy-tetrasomy. Significantly, monosomy-trisomy and nullisomy-tetrasomy have not been previously reported from nature. Both nullisomy and non-reciprocal translocations are likely to contribute to progenitor-specific DNA losses.

<sup>1</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA<sup>2</sup>University of Florida, Department of Biology, Gainesville, Florida, 32611, USA<sup>3</sup>Massey University, Private Bag 11222, Palmerston North, N/A, 4410, New Zealand<sup>4</sup>Embrapa Coastal Tablelands, Aracaju, 49025, Brazil<sup>5</sup>University Of Florida, Florida Natural History Museum, Florida Museum Of Natural History, PO Box 117800, Gainesville, FL, 32611-7800, United States<sup>6</sup>Queen Mary, University of London, School of Biological and Chemical Sciences, Mile End Road, E1 4NS, UK<sup>7</sup>University of Florida, Department of Biology, FLMNH, Dickinson Hall, P.O. Box 117800, Gainesville, FL, 32611-7800, USA

**276 JORDON-THADEN, INGRID\*<sup>1</sup>, FACIO VICCINI, LYDERSON<sup>2</sup>, BUGGS, RICHARD<sup>3</sup>, CHESTER, MICHAEL<sup>1</sup>, VERUSKA C. SILVA, ANA<sup>4</sup>, CHAMALA, SRIKAR<sup>1</sup>, DAVENPORT, RUTH<sup>1</sup>, WU, WEI<sup>5</sup>, SCHNABLE, PATRICK<sup>5</sup>, BARBAZUK, W. BRAD<sup>1</sup>, SOLTIS, DOUGLAS<sup>1</sup> and SOLTIS, PAMELA<sup>6</sup>**

### **Exploring genome evolution and gene expression in natural and synthetic polyploids (*Tragopogon*, Asteraceae) based on growth chamber experiments**

We present an integrated study of genome evolution, gene expression, and phenotype in two recently formed allotetraploid species (*Tragopogon miscellus* and *T. mirus*), their diploid parents (*T. pratensis*, *T. dubius*, and *T. porrifolius*), and synthetic allotetraploids. Using SNPs identified from 454 and Illumina sequencing of the diploids, we designed primers for Sequenom Mass-ARRAY analysis. We established a growth chamber randomized block experiment for comparison of diploids and natural and synthetic allotetraploids. SNP variation between the diploid parents is used to assess homeolog loss and changes in gene expression in the allotetraploids relative to their parents and to compare broadly sampled wild individuals with synthetics. We recorded phenotypic variation in many quantitative traits and linked these data to the gene loss/gene expression data. Phenotypes scored include growth rate, physiological robustness (measured in photosynthetic efficiency), foliar anatomical variation, and reproductive timing and fitness. Karyotypes of selected polyploids were examined using FISH and GISH to investigate the role of aneuploidy and chromosomal

rearrangements as drivers of homeolog loss.

<sup>1</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA<sup>2</sup>Universidade Federal de Juiz de Fora, Departamento de Biologia, Instituto de Ciências Biológicas, Minas Gerais, Juiz de Fora, 36036-900, Brazil<sup>3</sup>Queen Mary-University of London, The School of Biological and Chemical Sciences, Mile End Road, London, E1 4NS, UK<sup>4</sup>Embrapa Coastal Tablelands, Aracaju, 49025, Brazil<sup>5</sup>Iowa State University, Center for Plant Genomics, Ames, IA, 50011, USA<sup>6</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA

**277 AHMAD, HABIB\* and AFREDI, SAHIB**

### **Tea Cultivars of Pakistan: Phylogenetic Affinities and Genetic Diversity Estimated through Numerical and Molecular Markers**

Numerical trait analysis and DNA finger printing were employed for elaborating genetic diversity and establishing affinities among the tea cultivars grown in Pakistan. Thirteen cultivars were identified with the help of numerical analyses which were tested with DNA finger printing of 130 plants i.e. 10 plants per cultivar. Numerical elaboration was done with 18 quantitative and 7 qualitative traits. The analyses of leaf, shoot and seed parameters differentiated all the genotypes into two groups viz., broad and narrow leaved, corresponded to the Chinese and Assam type of tea, respectively. Most of the narrow leaved cultivars introduces from different origins segregated into similar types both for the qualitative and quantitative traits. DNA analyses through RAPD and SSR primers detected 115 and 103 alleles, in 87 and 75 plants, respectively. Genetic distance estimates analyzed through RAPD and SSR markers was 0-100%, showing high level of genetic diversity. The cluster analysis of RAPD data showed mixed grouping profile of the samples, however, samples from different plants of a particular cultivar segregated into independent sub-clusters. The findings of molecular data was generally in coincidence with the results obtained from numerical trait analysis, concluding close genetic affinity among the tea cultivars separated on the leaf morphology. The variations between, and within plants of the same cultivar confirmed the differences in origin of the cultivars. Information obtained from numerical trait analysis was generally in conformity with the information obtained from DNA finger printing. Failure of placing some broad-leaved cultivar into clearly will-defined clusters may be attributed due to genetic introgressions because of cross pollination.

Hazara University, Department of Genetics, Dhodial, Mansehra, Khyber Pakhtunkhwa, 21300, Pakistan

**278 MILES, NICHOLAS<sup>\*1</sup>,  
YAMAGUCHI, TAKAHIRO<sup>2</sup>, SOLTIS,  
DOUGLAS<sup>3</sup>, TSUKAYA, HIROKAZU<sup>4</sup> and  
SOLTIS, PAMELA<sup>5</sup>**

### **Leaf Evolutionary Developmental Genetics in Pitcher Plants**

**T**he evolution of carnivorous plants involves spectacular changes in form and function of the leaf. Significantly, the carnivorous pitcher form evolved independently three times in angiosperms. The three distantly related pitcher families, Cephalotaceae, Nepenthaceae, and Sarracenaceae, all have pitchers with the inside of the ascidium corresponding to the former adaxial side of a normal bifacial leaf and the outside of the pitcher corresponding to the former abaxial side. The genetic model of bifacial leaf development provides hypotheses of possible genetic changes associated with pitcher development and evolution. We address these hypotheses using genes isolated from the Western Australian pitcher plant, *Cephalotus folicularis*. Members of the *YABBY* and *HD-ZIP Class III* gene families were isolated using degenerate primers designed from *Arabidopsis thaliana* and data from the transcriptome sequencing project 1KP. The pattern of expression of these leaves was then examined using *in situ* hybridization.

<sup>1</sup>University Of Florida, Florida Museum Of Natural History, Dickinson Hall, Gainesville, FL, 32611-7800, USA<sup>2</sup>National Institute for Basic Biology, Nishigonaka 38, Myodajji, Okazaki, 444-8585, Japan<sup>3</sup>, University Of Florida, Department Of Botany, 220 BARTRAM HALL, Gainesville, FL, 32611, USA<sup>4</sup>The University Of Tokyo, 7-3-1, Graduate School of Science, Science Building #2, Univ. Tokyo, Hongo, Bunkyo-Ku, Tokyo, N/A, 113-0033, Japan<sup>5</sup>University of Florida, Department of Biology, FLMNH, Dickinson Hall, P.O. Box 117800, Gainesville, FL, 32611-7800, USA

**279 WICKETT, NORMAN J<sup>\*1</sup>, HONASS,  
LOREN<sup>1</sup>, WAFULA, ERIC<sup>2</sup>, TIMKO,  
MICHAEL<sup>3</sup>, WESTWOOD, JAMES<sup>4</sup>,  
YODER, JOHN<sup>5</sup> and DE PAMPHILIS,  
CLAUDE W<sup>6</sup>**

### **Using stage specific cDNA sequencing to uncover the origin and evolution of parasitism in Orobanchaceae**

**T**he Parasitic Plant Genome Project is a collaborative effort to use stage specific cDNA sequences to understand the genomic changes that led to, and resulted from, the acquisition of a parasitic life history in Orobanchaceae. Transcriptomes of three Orobanchaceae species that vary in their nutritional strategies were sequenced using both 454 and Illumina technologies: the facultative hemiparasite *Triphysaria versicolor*, the obligate hemiparasite *Striga hermonthica*, and the holoparasite *Orobanche (Phelipanche) aegyptiaca*. Within each

species, transcriptomes were sequenced from multiple developmental stages from germinating seeds, to early attachment to host, to above-ground reproductive and vegetative tissues. Using this comparative framework, we are developing a set of genes that may play an important role in haustorium formation (a parasitic plant specific organ that is used to invade the host plant), host invasion, and nutrient acquisition. Additionally, these data are being used to test hypotheses of molecular evolution and to explore the history of polyploidy in this lineage.

<sup>1</sup>Penn State University, Biology, 403 Life Sciences Building, University Park, PA, 16802, USA<sup>2</sup>Penn State University, Biology, 403 Life Science Building, University Park, PA, 16802, USA<sup>3</sup>University of Virginia, Biology, Gilmer Hall 044, PO Box 400328, Charlottesville, VA, 22904-4328, USA<sup>4</sup>Virginia Tech, Plant Pathology, Physiology, and Weed Science, 401 Latham Hall (0390), Blacksburg, 24061, VA, USA<sup>5</sup>University of California, Davis, Plant Sciences, Mail Drop 3, 137 Asmundson Hall, Davis, CA, 95616, USA<sup>6</sup>Pennsylvania State University, Department Of Biology, 101 LIFE SCIENCES BUILDING, UNIVERSITY PARK, PA, 16802, USA

**280 ZHANG, JIAN<sup>\*1</sup>, KANG, MING<sup>2</sup>,  
LIU, XIANG<sup>3</sup>, FRANKS, ROBERT<sup>4</sup> and  
XIANG, QIUYUN (JENNY)<sup>5</sup>**

### **Comparative 454 sequencing of leaf and inflorescence transcriptomes in *Cornus canadensis* and *C. florida* - data for developing molecular markers and identifying candidate**

**C**omparative transcriptome sequencing is a useful tool to search for candidate genes contributing to phenotypic differences and to develop molecular markers to be applied to evolutionary studies. Using GS-FLX 454 Titanium system, we present the *de novo* transcriptome sequencing of two species of *Cornus*, *C. canadensis* and *C. florida*, that produce different inflorescence architectures. The sequencing was run for one normalized cDNA library from leaves of *C. canadensis* and two unnormalize cDNA libraries from inflorescence buds of these two species on half a Titanium plate. A total of 96245, 251799 and 114648 raw reads, with a medium length of 443 bp, were obtained for the leaf transcriptome of *C. canadensis* (Ccl), inflorescence transcriptomes of *C. canadensis* (Cci) and *C. florida* (Cfi), respectively. These reads were trimmed and assembled into 1265 contigs and 30704 singletons for Ccl, 2859 contigs and 58594 singletons for Cci, and 1193 contigs and 33039 singletons for Cfi, respectively. All contigs and singletons were annotated by similarity search of four protein databases: TAIR10 *Arabidopsis* protein database, UniProtKB/Swiss-Prot annotated protein database, GenBank all green plants protein database, NCBI non-redundant(nr) protein database using the BLASTx algorithm with an E-value threshold of  $10^{-5}$ . The best five protein hits for each query sequence were parsed out

to create annotated tables, and further annotated with Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) orthology(KO) identifiers. The three transcriptome datasets were further used to generate expression profiles and identify SNPs. The data provide an important information platform for functional genomics and evolutionary developmental genetics in *Cornus*, in addition to developing phylogenetic markers, microsatellite markers, and mining for SNPs.

<sup>1</sup>North Carolina State University, Plant Biology, Gardner Hall 2115, Campus Box 7612, Raleigh, NC, 27695, USA<sup>2</sup>South China Botanical Garden, Plant Conservation Genetics And Evolutionary Genetics, Xingke Road 723, Tianhe District, Guangzhou, Guangdong Province, 510650, P.R. China<sup>3</sup>North Carolina State University, Plant Biology, Raleigh, NC, 27695, USA<sup>4</sup>North Carolina State University, Genetics, Raleigh, NC, 27695, USA<sup>5</sup>North Carolina State University, Plant Biology, Gardner Hall 2115, Raleigh, NC, 27695, USA

## 281 PARKS, MATTHEW\*<sup>1</sup>, CRONN, RICHARD<sup>2</sup> and LISTON, AARON<sup>3</sup>

### Separating the Wheat from the Chaff: Mitigating the Effect of Noisy Data in Plastome Phylogenomic Analyses

Through next-generation sequencing, the amount of sequence data potentially available for phylogenetic analyses has increased exponentially in recent years. Simultaneously, the risk of incorporating "noisy" data with misleading phylogenetic signal has also increased, and such data may disproportionately influence the topology of weakly supported nodes and lineages with rapid radiations and/or elevated rates of evolution. We investigated the influence of phylogenetic noise on large data sets using plastome sequences from 102 species of *Pinus* and six Pinaceae outgroups. Nucleotide sites in our 142 kbp alignment were ranked by variability and serially removed in 100 bp partitions. Maximum likelihood topologies were determined for each alignment partition (minus removed variable sites) and the corresponding cumulative partition of removed variable sites. Topologies were compared using the Robinson-Foulds test to determine the point of topological consistency, predicted to be the point where "noisy" data has largely been removed from the alignment. In our alignment, this coincided with the removal of the most variable 3.8% of sites (5.5 kbp). Nonetheless, tree-wide bootstrap support remained high (median value >99%) until removal of the most variable 6% (8.7 kbp) of sites, suggesting that phylogenetic noise did not impact overall nodal support. However, closer investigation of two taxa with historically unresolved phylogenetic positions (the four species of subsection *Contortae* and the morphologically distinctive, flat-needled *Pinus krempfii*), revealed dramatically different responses to data removal. Whereas topological resolution and bootstrap support for *Pinus krempfii* peaked as noisy sites were removed, subsection *Contortae* resolved most strongly when all sites were included. When compared to previous phylogenetic analyses of nuclear loci and morphological data, the

most highly supported topologies seen in our plastome analysis are consistent for *Pinus krempfii* but inconsistent for subsection *Contortae*, indicating that removal of noisy sites can result not only in increased resolution for poorly supported nodes, but serve as a tool for identifying highly supported, but likely incorrect topologies.

<sup>1</sup>Oregon State University, Department of Botany & Plant Pathology, Cordley Hall, Corvallis, OR, 97331-2092, USA<sup>2</sup>USDA Forest Service, 3200 SW Jefferson Way, Corvallis, OR, 97330, USA<sup>3</sup>Oregon State University, Department Of Botany & Plant Pathology, 2082 Cordley Hall, Corvallis, OR, 97331-2902, USA

## 282 CHALLAGUNDLA, LAVANYA\*<sup>1</sup> and WALLACE, LISA<sup>2</sup>

### Evolution of B chromosomes in the genome of *Xanthisma gracile* (Asteraceae)

B chromosomes are unusual genetic elements that occur in addition to the normal chromosome complement of the A genome. B chromosomes have been found in 15% of eukaryotic species, most widely in flowering plants. The prevalence of B chromosomes in eukaryotic genomes in addition to variability in the mechanisms of action and perpetuation of B chromosomes across genomes creates many interesting questions about their origin and function within cells. In this project we have studied the origin of B chromosomes in the spiny daisy, *Xanthisma gracile* (Asteraceae) by comparing molecular genetic similarities between A and B chromosomes. Previous studies of *X. gracile* based on morphological, cytological and molecular genetic data suggest the possibility of interspecific hybridization with related species, which may have contributed to the origin of B chromosomes. Thus, we test the alternative hypotheses that the B chromosomes are derived from the A-genome vs. an external source through hybridization with a closely related species. Natural samples were collected from multiple populations in Arizona and seeds were germinated for experimental study. The DNA content of plants with and without B chromosomes was characterized using Flow Cytometry. Flow sorted chromosomes as well as regular metaphase chromosomes were used for FISH to assess the nature of B chromosomes using markers both from the A genome as well as related sister species. Patterns of heterochromatin relative to A chromosomes have been examined through G- banding which serves as an indicator of the presence of repeat regions. Flow cytometry indicated the cDNA content of *X. gracile* is ~ 2 pg, which is consistent with recent reports but differs from the value in the Kew Database of Angiosperm C-values. The results of this study will be discussed in light of the evolutionary origin and diversification of *X. gracile* in relation to other closely related species and will lead to a better understanding of the molecular nature of its B chromosomes.

<sup>1</sup>Mississippi State University, Biological Sciences, 34 N Wallace Circle, Mississippi State, MS, 39762, USA<sup>2</sup>Mississippi State University, PO Box GY, Mississippi State, MS, 39762, USA

**283 ESTEP, MATT C<sup>\*1</sup>, GOWDA, BHAVAN<sup>2</sup>, HUANG, KAN<sup>2</sup>, TIMKO, MICHAEL<sup>2</sup> and BENNETZEN, JEFFREY<sup>3</sup>**

### Genomic characterization for parasitic weeds of the genus *Striga* by sample sequence analysis

Generation of ~2200 Sanger sequence reads or ~10,000 454 sequence reads for seven *Striga* DNA samples allowed identification of the highly repetitive DNA content in these genomes. The fourteen most abundant repeats in these *Striga* species were identified and partially assembled. Annotation indicated that they represent eight long terminal repeat (LTR) retrotransposon families, three tandem satellite repeats, one LINE retroelement, and one DNA transposon. All of these repeats are most closely related to repetitive DNAs in other closely-related plants, and are not products of horizontal transfer from their host species. These repeats were differentially abundant in each species, with the LTR retrotransposons and satellite DNAs most responsible for variation in genome size. Each species had some repetitive elements that were more abundant and some less abundant than the other *Striga* species examined, indicating that no single element or any unilateral growth or decrease trend in genome behavior was responsible for variation in genome size and composition. Genome sizes were determined by flowsorting, and the values of 615 Mb (*S.asiatica*), 1330 Mb (*S. gesnerioides*), 1425 Mb (*S. hermonthica*) and 2460 Mb (*S. forbesii*) suggest a ploidy series, a prediction supported by repetitive DNA sequence analysis. Phylogenetic analysis employing six chloroplast loci indicated the ancestral relationships of the five most agriculturally-important *Striga* species, with the unexpected result that the one parasite of dicotyledonous plants (*S. gesnerioides*) was found to be more closely related to some of the grass parasites than many of the grass parasites are to each other.

<sup>1</sup>University of Missouri-St. Louis, Department of Biology, R223 Research building, St. Louis, MO, 63121, USA<sup>2</sup>University of Virginia, Department of Biology, Charlottesville, VA, 22903, USA<sup>3</sup>University of Georgia, Department of Genetics, Athens, GA, 30602, USA

**284 TAYLOR, SUNNI<sup>\*1</sup> and MARTIN, NOLAND<sup>2</sup>**

### Homoploid hybrid speciation in Louisiana Iris

Natural hybridization is common in plants and has played an important role in the evolution of plant biodiversity. Although hybridization commonly results in the production of hybrids that are less fit than the parental species, some hybrid lineages may be fit in a novel habitat such that the hybrid lineage can diverge from the progenitor species. Homoploid hybrid specia-

tion involves the evolution of reproductive isolation between such a hybrid lineage and the originally hybridizing taxa. When originally described, *Iris nelsonii* was hypothesized to be a homoploid hybrid species derived from hybridization between three widespread species of Louisiana Iris (Iridaceae): *Iris brevicaulis*, *I. fulva*, and *I. hexagona*. In order to investigate the hypothesized hybrid origin of *I. nelsonii*, we conducted a survey of genetic variation in populations of the three widespread species and *I. nelsonii*. Results from this molecular work revealed that *I. nelsonii* shares genetic variation with all three purported progenitor species, supporting the hypothesis that *I. nelsonii* is indeed a homoploid hybrid species. Such homoploid hybrid speciation is thought to be a relatively rare event and the Louisiana Irises provide a unique system for studying this interesting evolutionary process.

<sup>1</sup>Texas State University-San Marcos, Biology, 601 University Dr., San Marcos, TX, 78666, United States<sup>2</sup>Texas State University, Biology, 601 University Drive, San Marcos, TX, 78666, USA

**285 BRAUKMANN, THOMAS<sup>\*</sup> and STEFANOVIC, SASA**

### Comparative plastid genome evolution in mycoheterotrophic Ericaceae

Heterotrophic plants exhibit a wide range of evolutionary degradation of photosynthetic ability and rely entirely or partially on their hosts to supply water and nutrients. These plants are divided into two distinct, but evolutionary artificial groups, parasitic and mycoheterotrophic plants. Haustorial parasitism has evolved at least 11 times independently and there are at least 10 independent origins of mycoheterotrophy in angiosperms. Each lineage represents an independent origin of heterotrophy and heterotrophs are not well characterized outside a few well-studied examples. Ericaceae, the heather family, is a large and diverse group of plants with elaborate symbiotic relationships with mycorrhizal fungi, including several mycoheterotrophic lineages. Grounded within a phylogenetic framework and broad taxonomic sampling, a comparative investigation of plastid genomes was conducted in the family using a slot-blot Southern hybridization approach. This survey contained lineages within Ericaceae with different life histories and trophic levels, including multiple representatives from the hemi-mycoheterotrophic pyroloids and holo-mycoheterotrophic monotropoids. A number of fully photosynthetic (autotrophic) members were included to best represent the other major clades within Ericaceae. This survey used 55 probes derived from all categories of protein-coding genes typically found in the plastomes of photosynthetic plants. Our results indicate that monotropoids exhibit extensive loss of genes relating to photosynthetic function and retain genes with possible function outside photosynthesis. Furthermore, hemi-mycoheterotrophic plants retain most genes relating to photosynthesis but are polymorphic for the plas-

tid *ndh* genes. Our survey extends previous inferences that plastid gene losses occur prior to becoming holoheterotrophic and that mycoheterotrophic Ericaceae exhibit gene losses similar in pattern to parasitic plants.

University Of Toronto At Mississauga, Department Of Biology, 3359 Mississauga Rd N, Mississauga, ON, L5L 1C6, Canada

## POSTERS

286 GALLAGHER, JOSEPH<sup>1</sup>, CHESTER, MICHAEL<sup>1</sup>, SYMONDS, V. VAUGHAN<sup>2</sup>, VERUSKA C. SILVA, ANA<sup>3</sup>, MAVRODIEV, EVGENY<sup>4</sup>, LEITCH, ANDREW R.<sup>5</sup>, SOLTIS, PAMELA<sup>4</sup> and SOLTIS, DOUGLAS<sup>1</sup>

### Are independently derived populations of *Tragopogon miscellus* Ownbey (Asteraceae) reproductively isolated?

*Tragopogon miscellus* is an allopolyploid that has formed recently (fewer than 80 years ago) in the Palouse region of Washington and Idaho. Previous studies have shown that the species has formed multiple times. So far, evidence for genetic exchange between independently derived populations has been equivocal. That is, based on microsatellite data, some co-occurring individuals with distinct genotypes have resulted from separate origins (with one genotype a recent migrant to the location) with no clear evidence of subsequent hybridization and recombination between these genotypes. In contrast, hand-pollination between *T. miscellus* individuals of distinct origins results in viable F<sub>1</sub> hybrids. Here we survey populations across an urbanized area in the north of the Palouse where *T. miscellus* has become one of the most prevalent weeds. In this area there may be more opportunities for inter-population gene flow due to the closer proximity among populations. To determine if gene flow is occurring between independently derived *T. miscellus* populations we used genomic *in situ* hybridization (GISH) to generate karyotypes for a large number of individuals from seven localities. Translocations appear to be fixed in some populations. We used nuclear microsatellites to examine genetic structure among these same individuals. By combining these data, we are able to determine which individuals within these populations are migrants from another population, which individuals are the results of crossing, and what effects karyotypic variation may have on gene flow among independent origins. This study will help estimate the prevalence of crossing between recent allopolyploid populations with different origins.

<sup>1</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA<sup>2</sup>Massey University, Institute of Molecular Biosciences, Palmerston North, New Zealand<sup>3</sup>Embrapa Coastal Tablelands, Aracaju, 49025, Brazil<sup>4</sup>University of Florida, Florida Museum of Natural History, Gainesville, FL, 32611, USA<sup>5</sup>Queen Mary University of London, School of Biological and Chemical Sciences, Mile End Road, London, E1 4NS, UK

287 S, DEEPA<sup>1</sup>, DUNCAN, KAYLIA<sup>2</sup>, ANNAMALAI, PANNEERSELVAM<sup>3</sup>, PRABHAKARAN, MUTHUCHAMY<sup>3</sup>, NOORUDDIN, THAJUDDIN<sup>1</sup> and MUTHUKUMARAN, GUNASEKARAN<sup>2\*</sup>

### Biodiversity, Antimicrobial Activity and Molecular Characterization of Actinomycetes from Salt Pan Environment

The marine environment is an untapped source for many useful drugs and an assessment of this potential is imperative. It is well known that the antibiotics are medicinally valuable and that the actinomycetes are the potential sources of antibiotics, which could be profitably used in the pharmaceutical industries; new antibiotics to control many bacterial, fungal and neoplastic diseases of plants, animal and human beings. A perusal of the literature clearly indicates that reports on the antimicrobial activity actinomycetes from the marine environment are very scanty. The marine soil of Tamil Nadu has rich potential of microbial diversity. Nevertheless, they have not been extensively explored for the registration of novel actinomycetes. In the present study soil sample were collected from salt pan region of Vedharanyam, Nagapattinam District, Tamil Nadu. The Physico - chemical parameters of soil sample were analysed. Totally 16 actinomycetes strains were isolated viz., *Actinbispora sp.*, *Actinobispora yunnanensis*, *Dactylosporangium sp.*, *Jonesia sp.*, *Micromonospora sp.*, *Nocardia sp.*, *Nocardioides sp.*, *Saccharomonospora sp.*, *Saccharopolyspora sp.*, *Streptomyces albus*, *S. cyaneus*, *S. exfoliatus*, *S. griseoflavus*, *Streptoverticillium sp.*, *S. baldaccii*, *Tettrabacter sp.* The isolated strains were identified based on the morphological, biochemical, and physiological characteristics. All the 16 actinomycetes were selected for antimicrobial activity. The Antibacterial activity was determined against two pathogenic bacteria such as *Staphylococcus aureus*, *Klebsiella pneumoniae*: *Streptomyces griseoflavus* was showed maximum activity against *Staphylococcus aureus* and *Klebsiella pneumoniae*. Antifungal activity was determined against two fungal pathogenic such as *Aspergillus niger*, *Fusarium moniliforme*. *Streptomyces griseoflavus* was showed maximum level of inhibition against *Aspergillus niger* followed by *Fusarium moniliforme*. Molecular characterization of *Streptomyces griseoflavus* were evaluated by PCR amplification of 16s rDNA gene. The genomic DNA and amplified products were separated in agarose gel and the 16s rDNA gene of *Streptomyces griseoflavus* species isolated from soil was partially sequenced using specific 16s rDNA sequence primer. 8F:[51AGA GTT TGA TCC TGG CTC AG-31]. 1492 R: [51- ACG GCT ACC TTG TTA CGA CTT-31].

<sup>1</sup>Bharathidasan University, Microbiology, School of Life sciences, Tiruchirappalli, Tamil Nadu, 620 024, India<sup>2</sup>Fisk University, Biology, 1000 17th Ave North, Nashville, TN, 37208, USA<sup>3</sup>A.V.V.M. Sri Pushpam College, Botany and Microbiology, Poondi, Tamil Nadu, 613 503, India

**The Genetic Basis for a Red Flower  
Mutant in Sweet Pea (*Lathyrus odoratus*)**

Floral color is a trait that not only attracts pollinators, but has also attracted centuries of researchers because of its association with genetic, ecological and evolutionary questions. The Sweet pea (*Lathyrus odoratus*) has served as a model system for genetic studies of floral color during the early 20th century, and therefore, many of the hereditary factors responsible for a color switch from wild type to color mutants, have been identified. A single factor *A* is responsible for a color change from the wild type purple and blue bicolor (cultivar 'Cupani') to a red and white bicolor form (cultivar 'Painted Lady'). The genetic control of such a color switch was investigated in this study. HPLC analysis of pigment extracts indicated a major switch of enzyme flux from producing delphinidin and its derivatives to the production of cyanidin and its derivatives. However, RT-PCR showed no difference in the expression levels of *f3'5'h*, responsible for the switch of flux in the Anthocyanin Biosynthetic Pathway (ABP). Cloning and sequencing of *f3'5'h* from cDNA revealed a non-synonymous coding SNP changing the amino acid from G (Glycine) in 'Cupani' to D (Aspartic acid) in 'Painted Lady'. A co-segregation analysis is being carried out between this SNP marker with the 'Painted Lady' phenotype in the F2 generation, to determine whether there is an association between the *f3'5'h* allele and the red mutant phenotype. Preliminary results are presented in this poster and their significance is discussed.

University of British Columbia, Department of Botany, Biodiversity Research Centre, 2212 Main Mall, Vancouver, BC, V6T 1Z4, Canada

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**Historical Section**

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See also *History of Botany: The Missouri Connection*.

**ORAL PAPERS**

289 TOUWAIDE, ALAIN

**When History Meets Genetics.  
Horseradish in Antiquity**

Genetics is able to reconstruct the phylogenesis of plant species. Without a validation from history, such reconstruction is theoretical, however exact and useful it may be. Horseradish offers a paradigmatic case to check the validity of this hypothesis. The paper will present the textual evidence about the diffusion of horseradish from its area of origin to the Mediterranean, and check whether such data correlate with the result of genetical analysis. In so doing it will show how ancient textual data (which should preferably be confirmed with archaeological data) complete the results of genetic history and transform them from a flat image into a three-dimensional one, which adheres closely to reality. In the field of economic botany, this is particularly relevant as this type of inquiry makes it possible to identify the actors whose uses economic botany studies, together with their places and time. The paper will capitalize on the recent work by botanists and geneticists and expand on it by bringing to light the data of historical research.

Institute for the Preservation of Medical Traditions, Research, PO Box 7606, Washington, DC, 20044, USA

290 TOUWAIDE, ALAIN

**History and Economic Botany: Some  
Methodological Reflections**

In recent years, history has been increasingly present in economic botany inquiries. Economic-botanists collect data from historical documents (from pre-printed books [manuscripts] to early printed books) as a basis for their investigations. In this way, the range of primary sources for the economic botany inquiries is considerably expanded, also making it possible to compare current practice (often known by oral transmission) and the written record of ancient uses (often resulting from a century-long tradition). Though perfectly founded and legitimate, such use of ancient documents as sources is not always sound from the historical method viewpoint. The paper aims to present some methodological reflections based on case studies taken from the historical documentation. The purpose is to generate a border-crossing dialogue between the many disciplines that contribute to economic botany research.

Institute for the Preservation of Medical Traditions, Research, PO Box 7606, Washington, DC, 20044, USA

## 291 SUNDBERG, MARSHALL

### Botanical Education in the United States II. Asa Gray through Charles Bessey and the New Botany

Amos Eatons success at Rensselaer was the stimulus for two divergent trends of botanical instruction in the 19<sup>th</sup> century. On the one hand his disciple Almira Lincoln Phelps, and later Alphonso Wood, were producing botanical textbooks emphasizing the process of botany and student-active approaches, particularly for high schools and younger students. Content was de-emphasized with a focus on basic conceptual ideas. On the other hand, Asa Gray, Eatons botanical rival, and protege of Eatons own protege, John Torrey, was critical of Eatons botany and of his approach to botanical teaching. The prolific Gray brought professionalism to American botany and his textbooks were the standard for college instruction until Besseys publication of *Botany for High Schools and Colleges* in 1880. This book, based on Sachs great German botanical textbook, emphasized the new botany by focusing on plant anatomy and physiology as well as taxonomy. Bessey and his contemporaries in the Midwest, including Barnes and Coulter among others, led the progressive change in botanical instruction even as they collaborated to form the Botanical Society of America.

Emporia State University, Department Of Biological Sciences, 1200 COMMERCIAL, EMPORIA, KS, 66801, USA

## 292 FLANNERY, MAURA

### Blanche and OakesAmes: A Relationship of Art and Science

Oakes Ames (1874-1950) was a wealthy New Englander who developed a fascination with orchids as a boy. He had his own greenhouse, and eventually his own library, herbarium, and laboratory - at home. He was educated at Harvard University where he joined the faculty after receiving his A.M. degree. He later donated his herbarium of over 100,000 specimens, as well as his library, to the University. He made many contributions to the orchid literature describing over 1,100 new species and 9 new genera. In 1900, Oakes married Blanche Ames (1878-1969) who had graduated with top honors in art from Smith College. Throughout their long marriage, Blanche did many illustrations for Oakes's publications. In 1947, the couple published *Drawings of Florida Orchids*, with Blanche as first author and Oakes listed as a contributor a reversal of their usual publication arrangement. The volume included drawings made from early in their marriage up to the time of the publication. Not all the images were scientific illustrations, some were floral landscapes. Blanche Ames did not limit herself to botanical illustra-

tion. She also painted sophisticated portraits, political cartoons, and murals. But it is her botanical work that I am most interested in, and in particular the pen-and-ink illustrations that not only ended up in publications but on herbarium sheets as well. Many of the sheets in the Oakes Ames Herbarium are rich in a diversity of ways of illustrating plants. Yes, they have dried specimens attached to the page, and packets with seeds and other plant structures. But many also have photographs and pencil drawings by Oakes as well as more finished images by Blanche. The sheets are thus the products of this collaboration and documents of a marriage as well as of species. In this paper, I will discuss what these sheets reveal about orchids, art, and feminism, of which Blanche was a staunch proponent.

28 Atlas Ave., Malverne, NY, 11565, USA

## 293 MARANZ, STEVEN

### Evidence for an alternative evolutionary and ethnopharmacological role for anti- malarial plants in Sub-Saharan Africa

Africa's human populations have numerous genetic adaptations linked to resistance to malaria. In addition to Duffy negative blood groups that confer almost complete resistance to *Plasmodium vivax* and hemoglobinopathies that reduce *P. falciparum* pathogenicity, there is a relatively higher threshold for bitter taste detection that corresponds geographically to endemic malaria areas. Traditional African anti-malarial therapies feature some extremely bitter treatments, such as *touloucouina* ('bitter oil') from *Carapa procera* DC (Meliaceae). However, tolerance to bitter taste may exist in non-human primates as well and probably pre-dates the development of conscious ethnomedicine. This raises the intriguing possibility that dietary compounds may influence malaria. Experiments using a mouse model of malaria demonstrate that a high oral intake of dietary flavonoids significantly reduces parasite loads and enhances the acquisition of immune memory. However, *in vitro* assays show that flavonoids marginally inhibit *P. falciparum* at physiological concentrations. Most *in vitro* investigations of African anti-malarial plants have likewise found only weak anti-plasmodial activity. This discrepancy may be resolved by the higher active compound concentration required to directly kill the parasite compared to the levels needed to modify the host endothelial environment. If flavonoids and other treatment compounds act primarily on the host rather than the parasite, the key effects will not be detectable *in vitro*. Thus, the current system of relying on *in vitro* screening of African plant extracts for direct anti-plasmodial activity is misplaced. Indeed, the epidemiological record of the past century shows that compounds with anti-plasmodial potency at nanomolar doses invariably select for drug resistant parasites. If indigenous equivalents to chloroquine or artemisinin had emerged in Africa's past, they would in all likelihood have failed as

well. Given Africa's long exposure to malaria and extensive ethnobotanical experimentation with both diet and therapies, it is more likely that host-acting compounds that are not easily overcome by *Plasmodium* parasites would have been preferentially retained in the indigenous food ways and pharmacopeia.

Cornell University, Weill Medical College, Microbiology & Immunology, 1300 York Av, New York, NY, 10021, USA

**294 RUSSELL, RUSTY\*<sup>1</sup>, VAN CAMP, ANNE<sup>2</sup> and SHEFFIELD, CAROLYN<sup>1</sup>**

### The Field Book Project

The Field Book Project is a collaborative project for improving access to primary source materials related to biodiversity research. Led by the US National Herbarium and Smithsonian Institution Archives, this project is developing a Field Book Registry based on existing standards and community input. In this presentation, we will introduce the project in terms of envisioned benefits for the botanical community, current implementation status, and future goals. Field books are the original documents that describe the events and circumstances leading up to and including the collection and description of biological specimens. The Smithsonian houses thousands of these unpublished journals, notes, and images related to field research, most falling into the category of *hidden* collections, or collections for which little or no documentation exists. Funding for this project comes from the Council on Library and Information Resources (CLIR) and is restricted to describing, cataloging and providing access to the item records. We will present on the status of achieving these immediate goals as well as our longer term goals of extending functionality and expanding the scope of the Registry. Longer term goals focus on making field books accessible via a public-facing, online Field Book Registry that will serve as an international toolkit for management of biodiversity field books. In this second phase of the project other organizations will be able to contribute their field book content. This collaborative effort is being defined with partner institutions including Harvard University Herbaria and Archives, Peabody Museum (Harvard), New York Botanical Garden, Academy of Natural Sciences, Missouri Botanical Garden, and California Academy of Sciences. Page level digitization and delivery is another long term objective. Working with the Biodiversity Heritage Library (BHL) we are assessing possible strategies for accomplishing this monumental task.

<sup>1</sup>Smithsonian Institution, United States National Herbarium, MRC-166, Botany, P.O. Box 37012, Washington, DC, 20013-7012, USA-

<sup>2</sup>Smithsonian Institution, SI Archives, Capitol Gallery #3000, 600 Maryland Ave., SW, Washington, DC, 20024-2520, USA

## POSTERS

**295 NEILL, AMANDA K., REHMAN, TIANA FRANKLIN\*, KIESCHNICK, SAM, SWADEK, REBECCA, MARKSTIENER, PATTY and NORTON, KIM**

### A moving story: Workflows for relocation and expansion of the BRIT-SMU-VDB Herbarium at the Botanical Research Institute of Texas

The combined BRIT-SMU-VDB Herbarium at the Botanical Research Institute of Texas (BRIT) houses over one million plant specimens representing much of the Earth's plant diversity. These specimens are widely used by students and professionals as well as the general public. After many years of planning a permanent building, construction was completed in early 2011 on the new home for this independent non-profit research institution. The new, two-story herbarium space occupies over 20,000 square feet. The herbarium proper is fully compactorized, and the previously-owned 585 metal cabinets are supplemented by an additional 325 new metal cabinets. Of the new cabinets, nearly all are doublewidths, so the expansion space more than doubles the herbarium's capacity. Compactorization of the collections with modern storage equipment allows the incorporation of a large backlog of boxed specimens of great scientific value and provides a safe environment for their preservation. Grants from the US National Science Foundation and the Institute of Museum and Library Services supported the purchase and installation of the mobile storage units and herbarium cabinets. Reaching the herbarium for the move took more than six months of labor by herbarium staff and a huge crew of volunteers. Since this was the second move in four years, this process has been twice-tested. Workflows of preparations for moving, including boxed backlog organization, cabinet labeling and mapping, and reorganization are described.

Botanical Research Institute of Texas, 1700 University Drive, Fort Worth, TX, 76107-3400, USA

See also *Incorporating microbes into plant community ecology.*

POSTERS

296 ZOLJ, SANDA, PAWLEY, MELISSA D., ALI, T'SHURA S.A., GOINES, JILLIAN C., ROBINSON, DAVE and LAU, JOANN\*

**Effect of extracts from reishi mushroom (*Ganoderma lucidum*) on lung cancer cell proliferation.**

For centuries, Chinese herbalists have used the reishi mushroom (*Ganoderma lucidum* [Curtis] P. Karst) as a remedy for human diseases like hepatitis, bronchitis, and cancer. This study examined the effects of *G. lucidum* extract on proliferation of lung cancer. Female and male lung cancer cell lines were treated with various concentrations of *G. lucidum* and monitored 1, 2 and 5 days post-treatment. Overall, there was a dose-dependant, as well as time-dependent, decrease in cell proliferation. Immunoblot analysis was used to examine the levels of apoptotic and cell cycle proteins (Bcl-xL, Bcl-2, Bax, Cdc2, Cdk4, and Cyclin D) in the cell cultures following treatment. Results suggest that the decrease in cancer cell proliferation was due to signaled cell death (apoptosis). Previous studies with other cancer cell-lines have been contradictory in regards to the active component in reishi mushroom. Some reports suggest that the active component is a polysaccharide, while others point to triterpenoids. To better understand the active components responsible for cell death, triterpenoids and polysaccharides were separated from *G. lucidum* and further assayed in this system. Our results suggest that the triterpenoid component of *G. lucidum* is the bioactive component. Biochemical characterization of this ancient herbal remedy could hold promise for the treatment of lung cancer.

Bellarmine University, Biology, 2001 Newburg Road, Louisville, KY, 40205, USA

297 DAVOODBASHA, MUBARAKALI<sup>1</sup>, RAMASAMY, PRAVEENKUMAR<sup>1</sup>, STOKES, IMARGOBE<sup>2</sup>, THIYAGARAJAN, SHENBAGAVALLI<sup>1</sup>, THAYALAN, MARI NIVETHA<sup>1</sup>, ASOKRAJA, ILAVARASI<sup>1</sup>, ABDULAZEES, PARVEEZ AHAMED<sup>1</sup>, NOORUDDIN, THAJUDDIN<sup>1</sup> and MUTHUKUMARAN, GUNASEKARAN<sup>\*2</sup>

**Morphological, biochemical, molecular and antimicrobial characterization of *Trichoderma viride* NTDMF01**

*Trichoderma viride* is one of the important biocontrol fungi showing their vital role in the field of agriculture and medicine. In the present study *Trichoderma viride* NTDMF01 was isolated from terrestrial soil sample and characterized by morphological and biochemical methods. In order to characterize these isolate at molecular level, genomic DNA was isolated and subsequently ITS and 28S rDNA genes were amplified using specific primers and sequenced. The 28S rDNA and ITS sequences of *T. viride* NTDMF01 were submitted in GenBank with accession no GU585845 and HM217756 respectively. DNA barcode was developed based on the Internal Transcribed Spacer gene sequences from Barcoding Of Life Data system (BOLD) with Barcode id NTDMF001-10. Phylogenetic tree was constructed to know the taxonomic position of isolated strain. The crude extracts of *T. viride* NTDMF01 showed antifungal activity against various human and plant pathogens such as *Trichophyton* sp., *Epidermophyton* sp., *Nigrospora* sp., *Aspergillus* sp. etc. The active antifungal fractions were further purified and analyzed using FTIR, GC-MS, NMR for structure characterization.

<sup>1</sup>Bharathidasan University, Microbiology, School of Life sciences, Tiruchirappali, Tamil Nadu, 620 024, India<sup>2</sup>Fisk University, Biology, 1000 17th Ave North, Nashville, TN, 37208, USA

## Paleobotanical Section

See also *Innovations in organismal botany - a tribute to the pioneering studies of Donald A. Eggert.*

## ORAL PAPERS

298 BENCA, JEFFREY\*<sup>1</sup>, STROMBERG, CAROLINE<sup>1</sup> and CARLISLE, MAUREEN<sup>2</sup>

**Morphological variation in the panglobal Devonian lycopsid genus *Leclercqia*: A new species from Washington state**

The basal lycopsid genus *Leclercqia* had a vast geographic range, inhabiting both Gondwana and Euramerica during the Early-Middle Devonian (~400-385 Ma). Despite its broad distribution, only two species have been described to date (*L. complexa* and *L. andrewsii*). A new Middle Devonian flora in northern Washington State has yielded a new morphotype for the genus. To determine whether this morphotype represents a new species, we developed a series of measurements capturing vegetative and reproductive morphology to assess the morphological and taxonomic diversity within the genus. Analysis of Variance (ANOVA) of measurements shows that the new morphotype from the Chilliwack Group is statistically significantly different from both *L. complexa* and *L. andrewsii* in four out of twelve characters, *L. complexa* in ten out of twelve characters, and *L. andrewsii* in nine out of twelve characters. In addition, *L. complexa* shows statistically significant differences from *L. andrewsii* in nine of the twelve characters measured. Multivariate techniques using vegetative characters similarly separate the new morphotype from *L. complexa* and *L. andrewsii*. To test whether intraspecific and interspecific variation are distinguishable in modern lycopsids, these same analyses were used to compare extant variants and species of *Lycopodium*. The analyses showed that biological species are distinguishable from one another while intraspecific variants are not. Based on these results, we suggest the addition of a new species to the genus: *Leclercqia scolopendra*. Additionally, intraspecific comparison of *L. complexa* from localities spanning six continents showed that some regional morphological variation exists within this species, providing another possible line of evidence for continental proximities during the Early-Middle Devonian. This study represents the first global morphometric analysis of a Devonian lycopsid genus and demonstrates that this method can be used to quantify degrees of taxonomic and morphological diversity between and within long-extinct plant groups using relatively few diagnostic features.

<sup>1</sup>University of Washington, Biology, 24 Kincaid Hall, Box 351800, Seattle, WA, 98195-1800, USA<sup>2</sup>Burke Museum, University of Washington, Box 353010, Seattle, WA, 98195-301, USA

299 HOFFMAN, LAUREL\*<sup>1</sup> and TOMESCU, ALEXANDRU<sup>2</sup>

**An early origin of secondary growth in the Early Devonian of Gaspé**

Secondary growth may have evolved independently in as many as five plant lineages. The earliest occurrences are seen in Middle Devonian euphyllophytes-progymnosperms and cladoxyllaleans. By the Late Devonian, sphenopsids, some ferns, and lycopsids had also evolved secondary growth. Secondary tissues arising from a vascular cambium are recognizable based on a suite of characters, including presence of axial and radial components, radially aligned cells as seen in cross sections, and addition of radial cell files by multiplicative divisions. Investigation of anatomically preserved plants in the Early Devonian (Emsian, ca. 405 Ma) Battery Point Formation (Gaspé, Quebec) has yielded a specimen exhibiting features of the secondary growth syndrome. The specimen consists of a cylinder of xylem 1.7 mm in diameter, devoid of extraxylary tissues, and is associated with *Psilophyton dawsonii* material. Although its anatomy is reminiscent of *P. dawsonii*, the specimen cannot be indisputably assigned to that species due to its lack of extraxylary tissues and because it falls outside the range of defining parameters of *P. dawsonii*. The specimen is protostelic with a small amount of crushed metaxylem around the central protoxylem. Primary tissues make up only a small fraction of the xylem, and are surrounded by a significant amount of tissue with secondary growth characteristics: conspicuous radial arrangement of tracheids and numerous instances of multiplicative division. The specimen is compressed laterally and features radial ruptures representing rays (probably uniseriate) which, due to their parenchymatous nature, provided the weakest structural planes that cleaved during diagenetic compression. Together, these features are indicative of secondary growth. Irrespective of its exact taxonomic affinities, anatomy and age place this plant at the base of the euphyllohyte clade, demonstrating that secondary growth had evolved prior to the divergence of cladoxyllaleans and progymnosperms. The Gaspé plant demonstrates another independent origin of secondary growth, pushing the earliest emergence of this developmental feature down into the Early Devonian.

<sup>1</sup>Humboldt State University, Department of Biological Sciences, 1 Harpst St., Arcata, CA, 95521, USA<sup>2</sup>Humboldt State University, Department of Biological Sciences, 1 Harpst Street, Arcata, CA, 95521, USA

300 CARUSO, JOSEPH A.\*, BARRETT-WATSON, HANNA and TOMESCU, ALEXANDRU

### New gametophytes from the Early Devonian Beartooth Butte Formation (Wyoming)

The Beartooth Butte Formation hosts the only extensive Early Devonian plant assemblages in western North America and has recently yielded fossils reminiscent of thalloid bryophyte gametophytes. The fossils are <10 mm and fall within three morphological types. Type 1 includes radially symmetrical thalli with 4-6 branches diverging from a central point. Branches are 0.8-1.5 mm wide at the base, up to 3 mm long, sometimes with two orders of branching, and rounded or bilobed tips. Type 2 consists of bilaterally symmetrical thalli. Branches fan out from a central area in two directions, forming a "butterfly shape". Each of the two fans, consisting of 5-6 branches, widens to almost 180°, with the outermost branches recurved and overlapping corresponding branches of the opposite fan. Branches are 0.6-1.3 mm wide at the base, up to 3.3 mm long, sometimes with two orders of branching and rounded tips. Type 3 thalli are smaller (up to 6 mm) and exhibit bilateral symmetry. Two branches, 1.5-2.2 mm wide at the base and up to 2.2 mm long with lobed tips, diverge in each of the two directions of growth. The absence of fertile structures makes it difficult to resolve the taxonomic affinities of these gametophytes. Type 1 thalli resemble *Ricciellopsis* and *Riccopsis* from the Middle Devonian of Podolia and the Triassic-Jurassic of Iran and Sweden, but are different from these in some characteristics. Type 3 thalli resemble *Marchantites* fossils from the Cretaceous of Spain, but type 2 thalli are not comparable to any known fossil gametophyte. Some extant Ricciaceae are reminiscent of type 1 gametophytes in their radial symmetry and diminutive sizes, but the pronounced bilateral symmetry seen in type 2 and type 3 gametophytes has no counterpart among extant bryophytes. Palynostratigraphy indicates a late Lochkovian - early Praghian (ca. 410 Ma) age for the Wyoming gametophytes, therefore they are slightly older than the early vascular plant gametophytes of the Rhynie chert and German Schiefergebirge.

Humboldt State University, Department of Biological Sciences, 1 Harpst Street, Arcata, CA, 95521, USA

301 HILLIER, KAITLIN\*<sup>1</sup> and ROTHWELL, GAR<sup>2</sup>

### Evidence for the filicalean fern genus *Senftenbergia* in Pennsylvanian sediments of western North America

Specimens considered to be compression fossils from putative Pennsylvanian sediments of central Oregon and originally described as *Pecopteris oregonensis* Arnold have been reexamined revealing that they have anatomically preserved vascular tissues and are assignable to the filicalean family Tedeliaceae. Fern fragments include segments of rhizome with diverging rachides as well as interconnected frond segments that document four orders of pinnately dissected pinnae with lobed pinnules. Individual pinnules display open dichotomous venation with one vein terminating each rounded lobe. Fertile pinnules have large, stalked, solitary sporangia attached at the margin adjacent to a vein ending, and the sporangia are uniformly arranged with their apices oriented toward the center of the pinnule along the abaxial surface. This arrangement of sporangia is more reminiscent of the genus *Senftenbergia* Corda than *Ankyropteris* Stenzel or *Tedelia* Eggert and Taylor, both of which display clusters of abaxial sporangia. The rachis trace is roughly anchor shaped in cross section, with two lateral protoxylem strands and oval primary pinnae traces that diverge in an alternate pattern to form a planar frond. The rhizome displays long internodes, and distinctive dense coarse trichomes are preserved on the rachis and primary pinnae. The overall morphology of this fern conforms closely to that of *Ankyropteris brongniartii* (Renault) Bertrand (sensu Mickle 1980), and appears to be a liana. This extends the geographic and stratigraphic ranges of *Senftenbergia* from Europe and Eastern North America to Oregon in western North America, and from the Mississippian to the Pennsylvanian. This species supports the earlier interpretation that *Ankyropteris* and *Senftenbergia* are closely related filicalean ferns. Examination of the associated plants in the flora reveals that the only common tree was a species of *Calamites* Brongniart with *Asterophyllites* Brongniart foliage and *Phyllothea* Brongniart cones. If this association reflects plant interactions then this is the first instance of a fern vine that grew on a calamite tree.

<sup>1</sup>Ohio University, Department of Environmental and Plant Biology, Athens, OH, 45701, USA <sup>2</sup>Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, 97331, USA

302 SCHWENDEMANN, ANDREW\*,  
TAYLOR, THOMAS and TAYLOR, EDITH

### Investigating Leaf Hydraulics in Fossil Plants from the Permian and Triassic of Antarctica

Water transport in plants is an important physiological topic that has received a lot of attention, including studies that focus on water transport in fossil plants. To date, this work has primarily concentrated on water transport through fossil stems. Fossilized leaves are more common and represent an excellent opportunity to study plant paleophysiology due to the many interactions between leaves and their environment. Leaf venation architecture varies greatly across plant species and is often used to differentiate leaf fossils into separate morphotaxa. Venation architecture plays an important role in leaf biomechanical support, the delivery of nutrients and photosynthates, and in hydraulic supply. In turn, leaf hydraulic supply influences the maximum photosynthetic rate of the plant as well as the amount of water lost to the atmosphere. Although hydraulic studies in plants mostly focus on stem hydraulics, leaves contribute at least one-fourth of the total resistance to water movement in the whole plant. In general, water conductance in a leaf increases with increased midrib conductivity and minor vein density. Although the Hagen-Poiseuille equation can calculate individual vein conductivity, it does not incorporate the venation architecture of the whole leaf. Here, a spatially explicit model for studying the leaf hydraulics of extant angiosperms is applied to fossil leaves from the Permian and Triassic of Antarctica. Leaf morphotypes included in this study include *Glossopteris*, *Dicroidium*, and *Heidiphyllum*. Such an analysis allows for the comparison of relative hydraulic construction costs and maximum photosynthetic rates. Due to the inherent assumptions of the conductance model and the inherent incompleteness associated with fossils, absolute values are impossible to obtain. The model does, however, allow for comparisons to be made to leaf types across latitudinal gradients and through time. This model will be used to study potential physiological changes in leaf types at different paleolatitudes as well as examine possible physiological reasons for the dominance of some plant groups.

University of Kansas, Ecology and Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-7534, USA

303 BERGENE, JULIE\*, TAYLOR, EDITH and TAYLOR, THOMAS

### Anatomically preserved *Dordrechtites* from the Middle Triassic of Antarctica

*Dordrechtites* is an enigmatic seed-bearing structure previously known only from South Africa and Australia. The discovery of compressed and permineralized specimens of this taxon at the base of Mt. Falla (upper Fremouw Formation) in the central Transantarctic Mountains extends the geographical distribution of the genus and increases the known floral diversity of the Triassic of Antarctica. It is also the first permineralized material of the taxon and thus provides additional characters that can help elucidate affinities of the structure by linking anatomical detail to surface compressions. The fossils appear to be preserved as compressions on the surface, but sections through the matrix reveal that they are permineralized within and can be studied by means of the peel technique. *Dordrechtites* specimens represent dispersed megasporophylls. Each is conspicuously T-shaped with a central, flattened area bearing the ovule, and two long slender extensions previously described as sterile arms or horns. The megasporophyll surface shows longitudinal striations. The central region is pyramidal in shape with an average length of 10 mm. The T-shaped sporophyll extensions are about 12 mm long by 1 mm wide and bend towards the central ovule-bearing region. Each structure bears one ovule with an adjacent presumed air pocket. Sporophyll tissue consists of large thick-walled sclerenchyma cells that are 40-70  $\mu$ m wide. The integument consists of a bi-layered sclerotesta. The inner sclerotesta is densely packed with indistinct cells while the outer part is 5-20 cells deep; individual cells are  $\sim$  10  $\mu$ m wide with oval to oblong rectangular cells that have thickened walls. A discontinuous layer consisting of radial files of cells occurs on the chalazal end of the ovule adjacent to the outer sclerotesta and may represent some type of abscission zone. The four previously described species, which are thought to be associated with *Heidiphyllum*, are very similar in size and shape to the Antarctic material, therefore the permineralized fossils can be directly compared to the compression forms.

University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-7600, USA

304 HARPER, CARLA\*<sup>1</sup>, TAYLOR,  
THOMAS<sup>1</sup> and KRINGS, MICHAEL<sup>2</sup>

### Fungi from the Permian and Triassic of Antarctica

Fungi are an integral part of modern ecosystems, and it is believed that they were equally important as constituents of ancient communities. The recent re-discovery of the advantages of petrographic thin sections over acetate peels has resulted in a wider recognition of fossil fungi. Exceptionally well-preserved fungi have recently been discovered from Skaar Ridge (Permian) and Fremouw Peak (Triassic) in Antarctica. These include several different types of hyphae and mycelia in Permian plant tissue, one of which is characterized by irregular septations and numerous papilla-like hypha projections. It is interesting to note that this type of hypha forms coils in some host cells. Large thick-walled fungal spores (Glomeromycota?) from Skaar Ridge are unusual because some forms contain a number of small spherical structures, each about 13  $\mu\text{m}$  in diameter. Fungi from the Fremouw Peak locality include an intracellular meshwork of tenuous hyphae or filaments less than 1  $\mu\text{m}$  in diameter. Some appear septate and possibly possess clamp connections. Fungal spores similar to those from Skaar Ridge have been found in the chert matrix from Fremouw Peak. These spores are up to 170  $\mu\text{m}$  in diameter and many contain small spores or propagules of other fungi. The internal structures are predominately spherical-pyriiform and born terminally on narrow hyphae. These reports emphasize the abundance of well-preserved fungal remains in peat deposits from the late Paleozoic-early Mesozoic of Antarctica and offer new sources of information on fungal diversity and interactions.

<sup>1</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-2106, USA<sup>2</sup>Bayerische Staatssammlung Für Paläontologie Und Ge, Richard-Wagner Strasse 10, Munich, Germany, D-80333, Germany

305 KLYMIUK, ASHLEY\*<sup>1</sup>, STOCKEY,  
RUTH<sup>2</sup> and ROTHWELL, GAR<sup>2</sup>

### A taxodioid (Cupressaceae) seed cone from the Upper Cretaceous of British Columbia, Canada

A single anatomically preserved seed cone was recovered from the Eden Main locality (Vancouver Island), a Coniacian succession of marine sandstones with phytodetrital remains preserved in  $\text{CaCO}_3$  concretions. The elliptical cone measures 25 mm long and 7 mm wide, and has helically arranged bract/scale complexes which are almost entirely fused. The axis contains a narrow parenchymatous pith, surrounded by a slightly

dissected vascular cylinder. The parenchymatous cortex contains 11-13 large resin canals. In transverse section, there appears to be an abscission layer where bract/scale complexes attach to the axis. The cylindrical vascular trace to the bract/scale complex is 100  $\mu\text{m}$  in diameter, and is accompanied by one resin canal, 170-200  $\mu\text{m}$  wide, which runs the entire length of the bract. The bract extends at a right angle from the cone axis for 2 mm, before narrowing and angling apically for a further 3.8 mm. Within the inflated portion of the bract, the resin canal ramifies laterally, producing 4-8 additional canals. These canals are smaller in diameter, and do not continue into the distal portion of the bract, which is sclerotic and triangular in cross section. The adaxial surface of the bract/scale complex bears three inverted winged ovules, 600  $\mu\text{m}$  long and 375-550  $\mu\text{m}$  wide, some of which contain megagametophyte tissue. Seeds are vascularized at their chalazal ends, and borne upon a parenchymatous pad. This parenchymatous tissue is arranged in periclinal files and is laterally continuous with a similar abaxial zone, which abruptly transitions to a sclerotic hypodermis near the outer margin of the cone. The small ovuliferous scale seen distal to the seed is 0.6 mm long, free from the bract at its tip, and densely sclerotic. Of the basal taxodioid members of the Cupressaceae, this new cone is most similar to the Jurassic *Hughmillerites juddii* (Seward et Bancroft) Rothwell, Stockey, Mapes et Hilton, but shows a suite of characters that place it in a new taxon.

<sup>1</sup>University Of Alberta, Biological Sciences, CW 312 Biological Sciences Building, 116th And Sask. Drive, Edmonton, AB, T6G 2E9, Canada<sup>2</sup>Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, 97331, USA

306 RICHEY, JON\*<sup>1</sup> and UPCHURCH,  
GARLAND<sup>2</sup>

### Inference of $\text{pCO}_2$ Levels and Climate in the Late Cretaceous from Fossil Lauraceae

Botanical estimates of  $\text{pCO}_2$  for the Late Cretaceous have most commonly used Stomatal Index (SI) in fossil *Ginkgo*. Recently, SI in fossil Lauraceae has been used to infer changes in  $\text{pCO}_2$  at the Cenomanian-Turonian boundary, based on the relation between SI and  $\text{pCO}_2$  in extant *Laurus* and *Hypodaphnis*. To provide a broad-scale picture of  $\text{pCO}_2$  based on fossil Lauraceae, we examined dispersed cuticle of the leaf macrofossil genus *Pandemophyllum* from: 1) the early to middle Cenomanian of the Potomac Group of Maryland (Maulden Mountain locality, lower Zone III) and 2) the Maastrichtian of southern Colorado (Raton Basin, Starkville South locality). These samples fall within the Late Cretaceous decline in  $\text{pCO}_2$  inferred from geochemical modeling and other proxies. SI was calculated from fossil cuticle fragments using ImageJ and counts of up to 56,000 cells per sample;  $\text{pCO}_2$  levels were estimated using the relation between SI and  $\text{CO}_2$  published for *Laurus nobilis* and *Hypodaphnis zenkeri*. Early to

middle Cenomanian atmospheric pCO<sub>2</sub> is estimated at 473 parts per million (ppm) from the *L. Nobilis* equation and 418ppm from the *H. zenkeri* equation (95% confidence interval (CI) = 401-550ppm), while late Maastrichtian pCO<sub>2</sub> is estimated at 461ppm from the *L. Nobilis* equation and 405ppm from the *H. zenkeri* equation (95% CI = 357-522ppm). The Maastrichtian estimates falls within the range of published estimates from other proxies. The Cenomanian estimate, in contrast, is low relative to other estimates. The 95% confidence intervals of our pCO<sub>2</sub> estimates overlap each other and those of other pCO<sub>2</sub> estimates for the Late Cretaceous based on Lauraceae, suggesting no significant difference. This could indicate that pCO<sub>2</sub> was relatively constant through the Late Cretaceous. Alternatively, it could indicate that Lauraceae show low sensitivity to high CO<sub>2</sub>, or other modern taxa should be used for inferring pCO<sub>2</sub> with Late Cretaceous Lauraceae.

<sup>1</sup>Texas State University-San Marcos, Biology, 601 University Drive, San Marcos, TX, 78666, USA<sup>2</sup>Texas State University, Department of Biology, 601 University Drive, San Marcos, TX, 78666, U.S.A.

### 307 BENEDICT, JOHN

#### The fossil history of Zingiberales and new insights based on fossil and extant members

The fossil record of Zingiberales extends from the late Cretaceous to the Pliocene in Europe and to the Eocene in North America. Fossils recognized in this order include leaves (e.g. *Zingiberopsis* and *Musops*), rhizomes and 7 fruit and seed species. The most widely distributed and most completely studied fruit genus is *Spirematospermum*, which is known from many localities in Europe and at least one site in eastern North America. Originally described as *Gardenia wetzleri* Heer (Rubiaceae), the genus was renamed *Spirematospermum wetzleri* by Chandler who suggested its affinities were with Zingiberaceae. The most informative fossils of *Spirematospermum* are anatomically preserved fruits from the middle Miocene flora of FASTERHOLT, Denmark studied by Friedrich and Koch. *Spirematospermum* has been assigned to either Musaceae or Zingiberaceae based on a combination of fruit and seed characters. One of the main characters that was used to ally *Spirematospermum* with Musaceae is the transverse septum at the chalazal end of the seed that delimits the chalazal chamber. This character was thought to be unique to Musaceae, however it is now also known in some species of *Alpina* (Zingiberaceae). Because this character is not limited to Musaceae today, it cannot be used to conclusively place *Spirematospermum* in this family. Anatomically preserved fossil seeds from the late Paleocene of North Dakota that are very similar to *Spirematospermum* are being studied serially

by the cellulose acetate peel method. The presence of a *Spirematospermum*-like plant in the Paleocene of North Dakota is intriguing since it further documents the floristic elements shared with the Almont-Beicegel Creek floras and those from Europe.

Arizona State University, School Of Life Sciences, PO Box 4601, Tempe, AZ, 85287-4601, USA

### 308 BOONCHAI, NAREERAT<sup>\*1</sup>, MANCHESTER, STEVEN<sup>2</sup> and LOTT, TERRY<sup>1</sup>

#### Southwestern Wyoming Fossil Plants Expedition 2010: retracing petrified wood sites of the 1970s-80s

In 2009, about a hundred Eocene silicified wood specimens with an excellent anatomical preservation were donated to the Paleobotany collection, Florida Museum of Natural History. These specimens were collected during 1972-1984 by James B. Stichka from seven well known lapidary-quality petrified wood localities in southwestern Wyoming. Unfortunately, very little research on wood anatomy in this area has been done to identify the kinds of trees represented. To obtain precise GPS data, relevant geological information, and collect additional specimens, Mr. Stichka, now 94 years old, guided us back to his original collecting sites, successfully retracing his routes in the Eden Valley area of Wyoming from 30-40 years earlier. The localities we collected were Big Sandy Reservoir, Blue Forest, Parnell Draw, and Blue Rim. From the anatomical study of fifty petrified wood samples from the site east of Big Sandy Reservoir (early Eocene Bridger Formation), these stems belonged to Anacardiaceae (*Edenoxylon* sp.), Lauraceae (*Laurinoxylon* sp.), another undetermined dicotyledonous wood, and Palmae (*Palmoxylo* sp). The diversity of trees from this site is low, dominated by anacardiaceous wood and palm. We are still investigating the taxonomic affinities of wood from other sites. In addition, other plant organs and animal fossils have been found at these sites, e.g., leaves of *Lygodium*, *Populus*, *Pseudosalix*, and fruits of *Landeenia*. These fossil wood specimens provide another opportunity to augment the floristic composition and paleoclimate of the Eocene floras from southwestern Wyoming, which is generally in agreement with other fossil evidence from the Early Eocene in this region. The dicotyledonous woods recovered so far are diffuse porous and semi-ring porous, suggesting moderate seasonality. These wood taxa imply that the paleoclimate was subtropical rather than the semi-arid conditions that are present today.

<sup>1</sup>Florida Museum of Natural History, Natural History, Museum Rd & Newell Dr, University of Florida, Gainesville, FL, 32611, USA<sup>2</sup> University of Florida, Florida Museum of Natural History, PO Box 117800, Gainesville, FL, 32611, USA

### Environmental vs. Anthropogenic Landscape Effects: the demise of the Maya

Ideas regarding the positive or negative impact on Classic Maya landscape modifications have sparked controversy that needs a resolution. Some have argued that the landscape modification spawned the end of the Maya civilization while others conclude that other factors created the downfall, and the Maya method of land management sustained their culture throughout both the rise and the fall. My research analyzes the Maya landscape via two directions of analysis: living plant specimens collected from around a Classic Maya center and sediment cores from pools near the center. These lines of analysis form the basis for my preliminary research into the Maya landscape and the resulting demise of the Maya civilization. I argue that, while the people remained on the landscape, the environmental consequences of their later land management combined with climatic impacts resulted in the collapse of this mighty civilization. However, their landscape conservation techniques provide the framework for further analysis into how the Maya were able to construct terrains that survived centuries and still positively influence the forest today.

University of Illinois Urbana-Champaign, Plant Biology, 505 South Goodwin Avenue, Urbana, IL, 61801, USA

### 310 LE, THIEN-Y\*<sup>1</sup>, DUNN, REGAN<sup>1</sup> and STROMBERG, CAROLINE<sup>2</sup>

#### The Effects of Light Quantity on Grass Epidermal Cell Shape

Phytoliths, microscopic plant silica bodies, inform us about the types of plants that remain in the fossil record, allowing for reconstruction of past ecosystems. Phytoliths are produced abundantly in grasses, and their variation in epidermal cell wall undulation (waviness) might allow us to infer the structure of ancient vegetation (open habit vs. closed canopy). We looked at the effects of sunlight variation on epidermal cell shapes of modern grasses as a first step in creating a proxy for determining habitat type from the fossil record. Long and short cells of five species of grasses (*Chusquea culeou* 'Gigantea' (CC), *Poa secunda* (PS), *Schizachyrium scoparium* (SS), *Sporobolus asper* (SA), and *Stipa viridula* (SV)) were grown in 20%, 60%, 100% (control), and 120% light. Morphometric measurements of individual long and short cells were made from epidermal peels using Adobe Photoshop. For each cell, the degree of waviness was calculated using the undulation index (UI), a dimensionless value representing the ratio of the circumference of the measured cell to the circumference of a circle with the same area. Silicified cells were extracted from the leaves so that heights of the short and

long cells can also be examined. Data for SS, SA, and SV long and short cells, and PS short cells showed that light quantity does have an effect on UI of epidermal cells, but that the pattern between treatments can be non-linear, especially for short cells. Although there are overall statistical differences in UI between light treatments in both species and types of cells, data from SS, SA, and SV long cells show the greatest promise for use in the fossil record because of the bimodal distribution of UI between the deep shade (20% light) and enhanced light (120% light) treatments.

<sup>1</sup>University of Washington, Biology, 24 Kincaid Hall, Box: 351800, Seattle, WA, 98195-1800, USA <sup>2</sup>University of Washington, Biology, 24 Kincaid Hall, Box 351800, Seattle, WA, 98195-1800, USA

### 311 TAYLOR, WILSON\* and GONTAREK, BRYAN

#### The search for extant analogues for early land plant algal progenitors

The aquatic algal ancestors that gave rise to the earliest terrestrial plants are not normally expected to have left much in the way of fossil remains, lacking as they likely were in recalcitrant (hence preservable) tissues. The one possible exception to this is the dispersal bodies (spores). Palynologists have long recognized the widespread and continuous record of microscopic, acid-insoluble, acetolysis-resistant bodies from various depositional environments, but have had mixed success at efforts to establish the biological affinities. One potential source of extant analogues that has been relatively unexplored is moribund algal monocultures. We collected and sampled taxa from the UW Madison culture collection, examined and photographed them, then subjected those with evidence of possible resistant cells to acetolysis to see if recognizable remains survived. This approach of using acetolysis as "simulated fossilization" is not new, but its application to a broad array of taxa under conditions that may be expected to have forced the organisms into whatever "survival mode" they are capable of, may be. At the same time, a more targeted assortment of algal cultures with known desiccation tolerance was provided by Dr. Louise Lewis and subjected to the same treatment. Despite previous reports in the literature of resistant wall components in several of the tested taxa, only two survived acetolysis with anything beyond fragmentary or amorphous remains: *Botryococcus* and *Protosiphon*. TEM examination of these remains is ongoing. This is one approach in a multipronged study that includes field collections in the desert southwest of the US and the dry valleys of Australia in the coming year.

University of Wisconsin-Eau Claire, Biology, Eau Claire, WI, 54701

312 DUNN, MICHAEL\*<sup>1</sup>, GENSEL, PATRICIA<sup>2</sup> and BLAKE, MITCH<sup>3</sup>

**The Alta Flora of the Price Formation (Mississippian, Tournaisian/Visean) of southern West Virginia**

The Alta locality of the Price Formation in southern West Virginia is a relatively recently discovered outcrop that continues to produce a diverse assemblage of Mississippian age plants. The strata are only broadly dated as Tournaisian to Visean due to nearby complex faulting, and may represent a series of overbank flood deposits that preserved the plant remains as compressions in fine-grained sandstones to mudstones. This report summarizes previously described taxa from the site and adds new data to produce a comprehensive floristic survey of the assemblage. The flora consists of at least 10 morphotaxa representing seed plants, lycopsids, and possibly progymnosperms. Foliage taxa include *Charbeckia macrophylla*, *Genselia compacta*, *Chlidanophyton* sp., *Rhodea* sp., and *Protobarinophyton* sp., and stem taxa include specimens previously assigned to *Lepidodendropsis*. Ovules and ovulate cupules include *Lagenospermum*, *Gnetopsis*, and several undescribed specimens. New data from the site include fertile axes assignable to *Chlidanophyton* that produce ovate sporangia borne on the terminal ends of equal to unequal dichotomizing branches of naked axes in sparse clusters. Sporangia split open apically but no evidence of a dehiscence slit or other dispersal mechanism has been observed. These data add to our rapidly increasing understanding of the distribution and diversity of Mississippian age plants from North America.

<sup>1</sup>CAMERON UNIVERSITY, 2800 Gore Blvd, LAWTON, OK, 73505, USA<sup>2</sup>University Of North Carolina, Department Of Biology, 403 Coker Hall, University Of North Carolina, CHAPEL HILL, NC, 27599-3280, USA<sup>3</sup>West Virginia Geological Survey, 1 Mont Chateau Rd, Morgantown, WV, 26508-8079, USA

313 SERBET, RUDOLPH\*<sup>1</sup>, HAGEMAN, SCOTT<sup>2</sup>, HOFFMAN, BRIAN<sup>2</sup>, KRINGS, MICHAEL<sup>3</sup>, TAYLOR, EDITH<sup>4</sup> and TAYLOR, THOMAS<sup>4</sup>

**Lycopterid seed fern diversity from the Pennsylvanian of Missouri.**

An Upper Pennsylvanian locality (Bonner Springs Shale, Kansas City Group, Middle Missourian) in western Missouri is currently providing diverse and well preserved fossils of both plants and arthropods. The plant material that consists of both impressions and compressions and is composed of fertile and vegetative remains of various fern, seed fern, sphenophyte, lycopsid, cordaite and conifer taxa. The discovery of a branched putative lycopterid pollen organ from this

site demonstrates that this group of Paleozoic seed ferns was more diverse than previously known. The pollen organ is characterized by a primary axis with alternately arranged secondary and tertiary axes; with the latter producing flattened, shield-shaped units characterized by a thick equatorial margin and bearing pollen sacs on the abaxial surface. Each unit is approximately 5 mm in diameter and contains approximately 16 sporangia. Gland-like structures occur on the surface of the pollen organ. Pollen grains are radial and approximately 45 µm in diameter; surface ornamentation includes the presence of both grana and coni. Fronds of the *Spheopteris*-type are commonly assigned to the lyginopterids and this morphotype is associated with the new pollen organs. The new pollen organ morphology is similar in basic organizational morphology to that of several lyginopterid pollen microsporangiate organ types, including *Feraxotheca* and *Crossotheca*, however, there are distinct differences suggesting that this organ represents a new morphogenus.

<sup>1</sup>University Of Kansas, Division Of Paleobotany, NAT HIST MUS & BIODIV RES INST, 1200 Sunnyside Avenue, Lawrence, KS, 66045, USA<sup>2</sup>Park University, Department of Natural and Physical Sciences, Parkville, MO, 64152, USA<sup>3</sup>Bayerische Staatssammlung Für Paläontologie Und Ge, Richard-Wagner Strasse 10, Munich, Germany, D-80333, Germany<sup>4</sup>University of Kansas, Ecology and Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-7534, USA

314 RYBERG, PATRICIA\*<sup>1</sup>, TAYLOR, EDITH<sup>2</sup> and TAYLOR, THOMAS<sup>3</sup>

**Mt. Acherar: A window into Antarctic glossopterid diversity**

Impressions of glossopterid reproductive organs are known in Antarctica from the Horlick Mountains to southern Victoria Land. To date, two impression ovulate genera have been described and they do not have overlapping ranges of distribution. This study provides the first evidence of a locally diverse flora at Mt. Acherar in the Central Transantarctic Mountains. Three genera of glossopterid ovulate structures, including the multiovulate *Plumsteadia* and *Scutum* as well as a new morphotaxon, were found approximately 18 meters below the level from which a permineralized forest was previously described within the upper part of the Upper Permian Buckley Formation. The new morphotaxon consists of cupules helically attached to a stem. A single vein enters the base of a cupule and then diverges five to six times with secondary veins extending to the margin of the lobed cupule. Cupules measure 4.0–6.6 mm in length and 4.8–8.0 mm wide. Up to five biwinged ovules, each measuring 3.0–3.7 mm by 2.9–3.7 mm, are attached in each cupule. Two morphogenera of ovulate structures in the glossopterid clade are currently identified as bearing cupules, which either extend from the midrib of a leaf or are attached at the end of an isolated stalk. Unlike these previously described morphogenera,

however, the new taxon from Mt. Achernar bears cupules attached to an axis in a helix. In addition to this new taxon, the presence of *Scutum* represents the first record of the genus in Antarctica. *Plumsteadia* has been documented at Mt. Achernar but collections from the 2010–2011 Antarctic field season reveal specimens at a higher density than previously recorded, perhaps indicating that numerous ovulate structures were produced in some organized structure not yet observed. Previous studies on Antarctic glossopterids have provided only a hint to the glossopterid diversity of Antarctica, and the Mt. Achernar locality provides a localized snapshot of the heterogeneity of the glossopterids in Antarctica.

<sup>1</sup>University Of Kansas, Department Of Ecology & Evolutionary Biology, 1200 Sunnyside Ave., Lawrence, KS, 66045, USA<sup>2</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-7600, USA<sup>3</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-2106, USA

### 315 TAYLOR, THOMAS<sup>\*1</sup>, KRINGS, MICHAEL<sup>2</sup> and DOTZLER, NORA<sup>3</sup>

#### Where are the fossil zygomycetes?

Molecular evidence suggests that the Zygomycota is an ancient lineage of Fungi that may have extended back into the Precambrian. Modern zygomycetes are characterized by a special mode of sexual reproduction that involves gametangial fusion and the formation of a zygospore within a zygosporangium. Historically the fossil record of this group was believed to be extensive, but after the establishment of the Glomeromycota fossil evidence of true Zygomycota is rare. One interesting type of fossil that has been variously associated with the Zygomycota are structures commonly referred to as sporocarps. These structures, which range from the Carboniferous into the Triassic, are composed of interlaced hyphae that surround a central cavity. Although the precise systematic position remains controversial, new evidence from the Carboniferous of France indicates that at least some sporocarps represent mantled zygospores like those of some modern Zygomycota. Other evidence from the Middle Triassic of Antarctica indicates that at least some of the structures termed sporocarps were produced together within a sac-like structure very similar to that found in modern sporocarp-forming Zygomycota. In this presentation we review the biodiversity of what have been termed fossil sporocarps, and highlight those forms that that may be assigned to the Zygomycota with some degree of confidence.

<sup>1</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-2106, USA<sup>2</sup>Bayerische Staatssammlung fuer Palaeontologie, Richard-Wagner Strasse 10, Munich, 80333, Germany

### 316 BOMFLEUR, BENJAMIN<sup>\*1</sup>, SERBET, RUDOLPH<sup>2</sup>, KRINGS, MICHAEL<sup>3</sup>, TAYLOR, EDITH<sup>4</sup> and TAYLOR, THOMAS<sup>5</sup>

#### What is *Dejerseya*?

The Triassic foliage morphotype *Dejerseya lobata* comprises entire-margined to partly pinnate leaves with secondary veins forming fan-shaped to pinnate clusters within the lobes. The leaves are unevenly amphistomatic, and stomata are composed of moderately sunken guard cells surrounded by papillate subsidiary cells. Associated reproductive organs are assigned to new species of *Matattella* (ovulate organs) and *Townrovia* (pollen organs). The ovulate organ is characterized by pinnately arranged, primarily shield-shaped megasporophylls divided into three to four narrow lobes, each with a single recurved naked ovule on the lower surface. The pollen organ arises from a reproductive bud, and consists of a slender axis bearing pinnately arranged, stalked, elongate receptacles, each with about 20 unilocular, club-shaped pollen sacs. Pollen is non-taeniolate bisaccate and monosulcate, and corresponds most closely with *Falcisporites australis*. Co-occurrence data indicate that the isolated organs derive from a single natural plant species. Based on structural similarities with well-established peltasperm taxa, we suggest that this new seed fern, in addition to several other enigmatic pteridosperm fossils from Gondwana, represents a member of a previously unrecognized group of Mesozoic peltasperms. Paleocological analyses indicate that these plants were opportunistic, early-successional inhabitants of stressed wetland environments in polar latitudes during the Triassic.

<sup>1</sup>University of Kansas, Department of Ecology and Evolutionary Biology, Haworth Hall, 1200 Sunnyside Ave., Lawrence, KS, 66045, USA<sup>2</sup>University Of Kansas, Division Of Paleobotany, NAT HIST MUS & BIODIV RES INST, 1200 Sunnyside Avenue, Lawrence, KS, 66045, USA<sup>3</sup>Bayerische Staatssammlung Für Paläontologie Und Ge, Richard-Wagner Strasse 10, Munich, Germany, D-80333, Germany<sup>4</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-7600, USA<sup>5</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-2106, USA

317 DECOMBEIX, ANNE-LAURE<sup>\*1</sup>,  
TAYLOR, EDITH<sup>2</sup> and TAYLOR, THOMAS<sup>3</sup>

**Anatomy and affinities of permineralized  
corystosperm trunks from the Middle  
Triassic of Antarctica: new data and  
synthesis.**

Anatomically preserved stems of Middle Triassic corystosperm seed ferns from the Central Transantarctic Mountains include (1) trunks of *Jefersonioxylon* from Gordon Valley found in association with *Dicroidium* leaf compressions and (2) young stems of *Kyklloxylon* from Fremouw Peak bearing *Dicroidium* leaf bases. Neither taxon is comparable to the corystosperm trunk morphogenus *Rhexoxylon*, and it has been suggested that the habit of the Antarctic corystosperms differed from the tree-fern like reconstruction based on the association of *Rhexoxylon* and *Dicroidium* in the Triassic of South America. We have previously hypothesized, based on portions of trunks with preserved bark from Fremouw Peak, that stems with a *Rhexoxylon*-like dissected xylem cylinder actually correspond to the outer part of fluted trunk bases. New specimens from Fremouw Peak, including material collected during the 2010-2011 austral field season, support this concept. Permineralized trunks 50 cm or more in diameter are preserved in fluvial sandstone channels at the locality. The base of the trees is often surrounded by silicified peat and is the only region where the bark is preserved. The secondary xylem is locally highly lobed, with included bark tissues, and isolated fragments somewhat resemble the outer part of a *Rhexoxylon* axis. The decorticated, more distal part of the trees shows a fluted secondary xylem cylinder. The central part of the trunks, as well as branches also found in the enclosing sandstone, however, lack evidence of the complex vascular system typical of *Rhexoxylon*. The simple stelar anatomy is indeed more comparable to that of young stems of *Kyklloxylon* known from the permineralized peat at the same site. The similarities of the Antarctic specimens with South American corystosperm trunks with a so-called normal cylinder axis, such as *Cuneumxylon* and *Tranquiloxylo*, will be discussed.

<sup>1</sup>University Of Kansas, 1200 Sunnyside Ave., Haworth Hall, Lawrence, KS, 66045-7534, USA<sup>2</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-7600, USA<sup>3</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-2106, USA

318 GARCIA MASSINI, JUAN L.<sup>\*1</sup>,  
FALASCHI, PAULA<sup>2</sup> and ZAMUNER, ALBA<sup>3</sup>

**Fungal-arthropod-plant interactions from  
the Jurassic petrified forest *Monumento  
Natural Bosques Petrificados*, Patagonia,  
Argentina**

Fungal-arthropod-plant interactions are described from the Middle Jurassic *Monumento Natural Bosques Petrificados*, Deseado Massif, Patagonia, Argentina. Fossils consist of silicified araucarian logs that appear differentially decayed and display systems of galleries bored in patterns resembling those produced by extant wood-boring beetles. Galleries are filled with frass that is reworked into smaller galleries containing circular to elliptical coprolites that are of possible mite origin and composed of fungal and plant remains. Fungi are also found growing from the walls of the galleries and from the coprolites. Identifiable fungal propagules include asexual structures typical of extant imperfect fungi. Comparison with modern wood with similar patterns suggests axilophagous role for the wood borer, whereas the narrower galleries and coprolites likely are products of a smaller xylophagous/fungivorous woodborer. Decay patterns in the silicified woods are like those produced by extant saprotrophic and pathogenic wood-rotting fungi in modern ecosystems. The fungus on the walls of the galleries and on the coprolites most likely played a saprotrophic role. However, additional indirect and direct interactions (i.e., phorisms) similar to those between conifers, mites, beetles, and fungi in modern ecosystems can be hypothesized. This report provides fossil evidence of multi-trophic fungal-arthropod-plant interactions and suggests the possibility that complex interactions like those in modern conifers might have been in place by at least the Jurassic. These results underscore the importance of fungi as key elements of past ecosystems, acting as drivers of biological cycles and symbionts with a variety of organisms.

<sup>1</sup>Centro Regional de Investigaciones Científicas y Transferencia Tecnológica, Biología, Entre Ríos y Mendoza s/n, Anillaco, La Rioja, 5301, Argentina<sup>2</sup>Universidad de Buenos Aires, Laboratorio de Paleobotánica, Intendente Güiraldes 2620, Buenos Aires, Buenos Aires, 1428, Argentina<sup>3</sup>Universidad Nacional de La Plata, División Paleobotánica, Paseo del Bosque s/n, La Plata, Buenos Aires, 1900, Argentina

319 STOCKEY, RUTH\*<sup>1</sup>, ROTHWELL,  
GAR<sup>1</sup> and JOHNSON, KIRK<sup>2</sup>

**A new species of *Cobbania* (Araceae) from the Cretaceous (Upper Maastrichtian) of South Dakota**

A large number of new specimens of the floating aquatic aroid genus *Cobbania* Stockey, Rothwell et Johnson have been recovered from pond sediments in the Hell Creek Formation of Harding County, South Dakota. Specimens are preserved as compression/impressions in a greyish brown, sandy siltstone. At least 12 rosettes of whole plants with branched aquatic roots, some of which are interconnected by stolons, show the characteristic trumpet-shaped, pubescent *Cobbania*-type leaves with a central aerenchymatous zone. Stems of the new plant are smaller and more delicate; leaves have shorter petioles, a larger number of primary veins, and considerably wider rims than those of *C. corrugata*. Leaves of both species show an apical notch and collective veins in the margin with 2-3 marginal veins and a fimbrial vein in the rim. In the new specimens the leaf rim is quite narrow near the base, but expands dramatically (6-7 times the size) toward the apex. Both plants show a similar over-all venation pattern with a large number of (up to 19 in the new species) abaxial primary veins that extend from the petiole. Stolons in the Hell Creek plants are up to 1cm wide and show evidence of probable internal vascular tissues, not seen in *C. corrugata*. These new *Cobbania* fossils come from the Upper Maastrichtian, near the end of the 10 million year geologic range for the genus, and reveal that these aquatic Araceae were more diverse just prior to the K/T boundary.

<sup>1</sup>Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, 97331, USA<sup>2</sup>DENVER MUSEUM OF NATURE & SCIENCE, 2001 COLORADO BLVD, Denver, CO, 80205-5798,

320 HU, SHUSHENG\*<sup>1</sup>, TAYLOR,  
DAVID<sup>2</sup> and HICKEY, LEO<sup>3</sup>

**A new Turonian flower of Ericalean affinity from the South Amboy Fire Clay Member of the Raritan Formation, Linden Clay Pit, Middlesex County, New Jersey**

Charcoalified plant mesofossils, including flowers, inflorescences, fruits, and seeds, have been recovered from carbonaceous clay of inferred estuarine origin belonging to the South Amboy Fire Clay Member of the Raritan Formation from the Linden Clay Pit, Middlesex County, New Jersey. Based upon dispersed angiosperm pollen, including *Complexiopolis* sp. and *Pseudoplicapollis* sp., these samples fall in Zone V of Doyle and Robbins (1977) and are of late Turonian Age. Among the three dimensionally preserved mesofossils is a minute, pentamerous flower with in situ ovules and adherent

pollen. The flower is 2.0 mm long and 1.2 mm wide. The preserved basal remnants of the perianth form a single ring resulting from the fusion of an inner and an outer whorl of sympetalous and synsepalous corolla elements. An annular disc is located inside of the stamens, into which is inserted a large nectary gland opposite to the filament bases. The ovary is superior, syncarpous, and 5-carpellate, 1.1mm long, and 0.9 mm wide. The style is at least 0.5 mm long and hollow. The stumps of five filament bases are present and opposite the petals. Pollen grains, which are found adhering to the filament bases and also lying between the petals and the ovary wall, are oblate, 14 x 21 Åµm, tricolporoidate, with short colpi, scabrate to regulate sculpturing, and a solid tectum and foot layer. The ovules are rectangular, 105 x 66 Åµm in length and width, arranged horizontally, and axile, with more than 50 ovules per locule. Based upon the floral and pollen characteristics, such as a connate corolla, an annular disc, a syncarpous and 5-locular ovary, a hollow style, horizontal ovules, axile placentation, and tricolporoidate pollen with a solid tectum and foot layer; the fossil flower appears to have its closest affinity with the Order Ericales.

<sup>1</sup>Yale University, Peabody Museum of Natural History, 170 Whitney Avenue, New Haven, CT, 06511, USA<sup>2</sup>INDIANA UNIVERSITY SOUTHEAST, Department Of Biology, 4200 GRANT LINE ROAD, NEW ALBANY, IN, 47150, USA<sup>3</sup>Yale University, Peabody Museum Of Natural History, P.O. Box 208109, 170 Whitney Avenue, New Haven, CT, 06520-8109, USA

321 ESTRADA-RUIZ, EMILIO\*<sup>1</sup>,  
UPCHURCH, GARLAND<sup>1</sup>, WHEELER,  
ELISABETH<sup>2</sup> and GREG, MACK H.<sup>3</sup>

**Late Cretaceous dicotyledonous woods from the Crevasse Canyon and McRae Formations, south-central New Mexico, USA: Part I**

Late Cretaceous angiosperm woods from the Western Interior, U.S.A., are poorly known relative to palynomorphs and leaf macrofossils. Recently, abundant and diverse angiosperm woods have been reported from the Campanian to Maastrichtian of Coahuila, Mexico, and Big Bend National Park, Texas, but less is known about angiosperm wood diversity in coeval deposits to the north. The Campanian Crevasse Canyon Formation and Maastrichtian McRae Formation of south-central New Mexico, U.S.A., provide an abundant record of silicified woods that expands our knowledge of dicot wood diversity during the Late Cretaceous. The Crevasse Canyon Formation yields woods belonging to *Metcalfeoxylon* (Malvales) and *Paraphyllanthoxylon* (probably Lauraceae), two genera previously described from the Western Interior Cretaceous. The Jose Creek Member of the McRae Formation yields the genus *Platanintium* (Platanaceae) and woods that appear to represent new genera. These latter woods include one species of Celastraceae, two types of probable Myrtales,

and a eudicot of uncertain affinity. A range of plant sizes and life forms is indicated by the woods. *Metcalfeoxylon* known from *in situ* stumps with maximum basal diameters up to 0.75m respectively, and woods of *Paraphyllanthoxylon* known from other areas come from trunks up to 1 m in diameter. The woods of Celastraceae and possible Myrtales have axis sizes consistent with their derivation from small trees, large shrubs, and/or vines, while the eudicot of uncertain affinity has a small diameter axis and wood anatomy consistent with its derivation from a small plant (low density of small vessels and large quantities of parenchyma). Our work indicates that certain taxa, such as *Paraphyllanthoxylon* and *Metcalfeoxylon*, were important angiosperm trees from paratropical regions of North America, and that others may have been more endemic in their distribution and/or plants of smaller stature.

<sup>1</sup>Texas State University, Department of Biology, 601 University Drive, San Marcos, TX, 78666, U.S.A. <sup>2</sup>North Carolina State University, Department of Wood and Paper Science, Raleigh, NC, 27695, U.S.A. <sup>3</sup>New Mexico State University, Department of Geological Sciences, Las Cruces, NM, 88003, U.S.A.

### 322 UPCHURCH, GARLAND\*<sup>1</sup>, KIEHL, JEFF<sup>2</sup>, SHIELDS, CHRISTINE<sup>2</sup> and SCOTESE, CHRISTOPHER<sup>1</sup>

#### Plants, clouds, and climate models: Understanding warm climates of the latest Cretaceous

The nature of past warm climates has been a major area of disagreement between paleobotanists and climate modelers. Paleobotanical proxies for temperature such as foliar physiognomy indicate equable conditions and reduced latitudinal temperature gradients for warm intervals such as the Late Cretaceous, while climate models typically produce cold conditions and steep latitudinal temperature gradients. Paleobotanical proxies for atmospheric pCO<sub>2</sub>, such as Stomatal Index, indicate only moderate increases in atmospheric pCO<sub>2</sub> for times such as the Late Cretaceous, while climate models generally require significant increases in pCO<sub>2</sub> to simulate the warmth indicated by paleobotany and geochemistry. Fully coupled simulations using the low-resolution version of the Community Climate System Model, version 3 (CCSM3) demonstrate high congruence between paleobotanical and geochemical temperature indicators and climate model output for the latest Cretaceous (Maastrichtian). In these simulations we explore the combined roles of greenhouse gases, vegetation cover, and the properties of liquid clouds in creating warm and equable conditions. Our model successfully reproduces warm polar temperatures and the latitudinal gradient of Mean Annual Temperature without overheating the tropics, using paleobotanically realistic levels of atmospheric pCO<sub>2</sub>. The best fit for Mean Annual Temperature is a simulation that prescribes 560 ppm pCO<sub>2</sub> (2x preindustrial), 2000 ppb CH<sub>4</sub>, realistic

vegetation, and liquid cloud properties that most likely reflect pre-anthropogenic levels of cloud condensation nuclei. If Late Cretaceous pCO<sub>2</sub> levels were lower than 560 ppm, as suggested by stomatal index studies of fossil Lauraceae, additional warming mechanisms are probably needed. One good candidate is reduced rates of transpiration in Late Cretaceous vegetation, which would have resulted from the evolution of vein density in Cretaceous angiosperms and reduced fractional cover of angiosperms during the Cretaceous relative to the Cenozoic.

<sup>1</sup>University of Texas, Department of Earth and Environmental Sciences, Box 19049, Arlington, TX, 76019, USA <sup>2</sup>National Center for Atmospheric Research, 1850 Table Mesa Drive, Boulder, CO, 80307, USA

### 323 AXSMITH, BRIAN\*<sup>1</sup>, STULTS, DEBRA<sup>2</sup>, KNIGHT, TERRELL<sup>3</sup> and BINGHAM, PATRICK<sup>4</sup>

#### The conifer *Araucaria bladenensis* and associated large pollen and ovulate cones from the Upper Cretaceous Ingersoll shale (Eutaw Formation) of Alabama

**A**raucarian conifer remains from the Upper Cretaceous Ingersoll shale Konservat-Lagerstätte (Eutaw Formation) of Alabama include leafy shoots of *Araucaria bladenensis*, an associated pollen cone, an ovulate cone, and an isolated bract-scale complex that were probably produced by the same plant species. Well-articulated *A. bladenensis* specimens with preserved cuticles reaffirm the original generic determination, and show similarity to branches of the extant species *A. bidwillii*. The large pollen cone is remarkable as the earliest example comparable in size and pollen sac number to those of the largest extant *Araucaria* species. The co-occurrence of this cone with *Upatoia barnardii* in the Eutaw Formation also demonstrates that typical fossil araucarians with small pollen cones coexisted during the Late Cretaceous with modern appearing, large-coned species. The intact ovulate cone is large and ovoid but poorly preserved. An associated bract-scale complex displays lateral wings and a ligule. Comparisons with other fossil and extant araucarian conifers indicate affinity with section *Bunya*. These fossils reaffirm that araucarian conifers were a significant component of the southeastern U.S. Cretaceous flora, and provide a temporal and biogeographic context for the currently unexplained transition from small to large pollen cones in the family.

<sup>1</sup>University Of South Alabama, Department Of Biological Sciences, LSCB 124, MOBILE, AL, 36688-0002, USA <sup>2</sup>University of South Alabama, Marine Sciences, Life Sciences Building 124, Mobile, AL, 36688, United States <sup>3</sup>Auburn University, Department of Geology and Geography, Auburn, AL, 36849-5305, United States <sup>4</sup>Auburn University, Geology and Geography, Auburn, AL, 36849-5305, United States

324 CREPET, WILLIAM\*<sup>1</sup>, NIXON,  
KEVIN<sup>2</sup> and GANDOLFO, MARIA<sup>3</sup>

### The Mismeasure of a mystery: Angiosperm origins and Phylogenetics

Angiosperms have been a focus of evolutionists for over a century and the "Abominable Mystery" of Darwin has been a diadem in the treasury of the great questions that science has failed to resolve. Consequently, the "mystery" has been the focus of powerful new analytical tools grouped under "phylogenetics". Yet, instead of clarifying angiosperm origins, contradictory results of applications of phylogenetic methodologies have further confused our understanding of angiosperm relationships. This systemic incongruence has been exacerbated by conflicting treatments of potentially illuminating fossil taxa such as Bennettitales, seed ferns, and *Archaeofructus*. Complicating matters is the subtle influence of historical thought which seems to have: 1. Affected the way these taxa are coded, 2. Affected the construction of the matrices themselves, and 3. Resulted in selective presentation of results of various analyses. Therefore, cladograms based on structural features or on analyses that include them may reflect outcomes based on more than objective readings of available evidence. Moreover, there has been an inconsistently applied tendency to demand rigor in defining angiosperms and in identifying their characters. Resulting restricted definitions sometimes exclude possibly relevant fossils from analyses thereby obscuring their true affinities. Further confusing the issue is a contrasting tendency to group certain fossils with angiosperms and to then code certain of their characters as homologous, often based on complex scenarios of change. Elimination of encoded hypotheses, recognition of the limits of fossil data, and more objective analysis may improve our ability to identify likely angiosperm ancestors by bringing into play information now hiding in plain sight.

<sup>1</sup>Cornell University, Department Of Plant Biology, 413 Mann Library, Ithaca, NY, 14853, USA<sup>2</sup>Cornell University, L. H. BAILEY HORTORIUM, 408 MANN LIBRARY, ITHACA, NY, 14853-4301, USA<sup>3</sup>Cornell University, L. H. BAILEY HORTORIUM, 410 Mann Library Building, ITHACA, NY, 14853-4301, USA

325 HORIUCHI, JUNJI\*<sup>1</sup> and  
MANCHESTER, STEVEN<sup>2</sup>

### The Paleocene Yachinaka flora of the Minato Formation from Kuji, northeastern Honshu, Japan

Well preserved Paleocene fossil plants have been recovered from several locations in the vicinity of Kuji, northeastern Honshu, Japan. Here we provide an overview of the Yachinaka flora--one of the most diverse and well-collected assemblages. The flora is useful in reconstructing the local vegetation and climate, and is interesting biogeographically in comparison with Paleocene floras known from other parts of the Northern Hemisphere. The Yachinaka flora contains three kinds of ferns, *Ginkgo*, Cupressaceae (*Metasequoia*, and two other genera), Platanaceae (two genera), *Fagopsisiphylum*, *Alnus*, *Corylites*, *Ulmites*, *Trochodendroides*, *Zyziphoides*, *Nyssidium*,

*Nordenskioldia*, a legume, *Acer*, *Deviaeacar*, a pentamerous flower, *Celtis aspera*, bignoniaceous seeds, and several unidentified angiosperms. Most of the genera, and some of the species in this flora are also known also from North America, Greenland, Scotland, Xinjiang, and Kamchatka. These fossils support the concept of a relatively homogeneous widespread, mostly deciduous vegetation surrounding the Northern Hemisphere in the Paleocene.

<sup>1</sup>Tokyo Gakuji University, Attached School, Tokyo, Japan<sup>2</sup>University of Florida, Florida Museum of Natural History, PO Box 117800, Gainesville, FL, 32611, USA

326 DILLHOFF, RICHARD\*<sup>1</sup>,  
DILLHOFF, THOMAS<sup>2</sup>, DEVORE,  
MELANIE<sup>3</sup>, GREENWOOD, DAVID<sup>4</sup> and  
PIGG, KATHLEEN<sup>5</sup>

### The Eocene Thomas Ranch flora, Allenby Formation, Princeton, British Columbia, Canada

The first descriptions of Eocene fossil plants from the Allenby Formation, south-central British Columbia, Canada were published over a century ago. Both compression and permineralized floras are known from this formation. Since 1973, the Princeton Chert flora alone has generated over 45 publications. Compression floras at Thomas Ranch and One Mile Creek have yielded several new species including *Pseudolarix arnoldi* (Pinaceae); *Tetracentron hopkinsii* (Trochodraceae); *Betula leopoldae*, and *Palaeocarpinus stonebergae* (Betulaceae); *Stonebergia columbiana* and *Neviusia dunthornei* (Rosaceae) and several species of *Acer* (Sapindaceae). However, these individual localities have not been assessed for their floral diversity and paleoenvironmental reconstruction. We have surveyed the Thomas

Ranch locality using plant mega- and microfossils. The fossils record a diverse mixed floral assemblage of gymnosperms and angiosperms. Collections to date have yielded a total of 71 megafossil morphotypes representing at least 61 nominal species when multiple organs and leaf morphologies of the same species are eliminated. Thirty-three morphotypes are identified to at least generic level, including: *Ginkgo*, *Abies*, *Pinus*, *Pseudolarix*, *Acer*, *Alnus*, *Betula*, *Fagus*, *Sassafras*, Platanaceae, *Prunus*, and *Ulmus*. Over 70 pollen and spore types are recognized, 37 of which are assignable to family or genus. The pollen samples are heavily dominated by conifers (85-97%), with Betulaceae accounting for most of the angiosperm pollen. *Azolla*-dominated beds and gypsum deposits suggest periodic fluctuations in water level. Leaf physiognomic (CLAMP, LMA and other approaches) and taxon-based analog methods have been used to provide climate estimates for the Thomas Ranch site. Differences between the mean annual temperature (MAT) estimates provided by these two approaches reflect inherent uncertainties in the methods, but both estimates are at the low end of the MAT range that has been published for other Okanagan Highland localities, indicating a temperate climate consistent with the floristic character of a mixed conifer-deciduous forest.

<sup>1</sup>1307 212TH AVE NE, SAMMAMISH, WA, 98074, USA<sup>2</sup>10521 37th St SE, Lake Stevens, WA, 98258, USA<sup>3</sup>Dept Of Biology & Env. Science, GC & SU Campus Box 81, MILLEDGEVILLE, GA, 31061-0001, USA<sup>4</sup>Brandon University, Brodie Science Building - Room 3-15, 270 18TH Street, BRANDON, MB, R7A 6A9, Canada<sup>5</sup>Arizona State University, SCHOOL OF LIFE SCIENCES FACULTY & ADMIN, BOX 874501, Tempe, AZ, 85287-4501, USA

### 327 ERDEI, BOGLARKA\*<sup>1</sup> and MANCHESTER, STEVEN<sup>2</sup>

#### Dioonopsis leaves from the Eocene of Western North America--a cycad shared with the Paleogene of Japan

Reexamination of western North American Cenozoic cycad leaves, with attention to epidermal anatomy as well as morphology and venation, indicates that species formerly assigned to extant genera *Ceratozamia*, *Dioon* and *Zamia* from the Eocene of California and Alaska do not actually represent these modern cycad genera. Reinvestigation of cycad leaf and leaflet remains from the Eocene floras of Hamilton Bay, Alaska and La Porte, California leads to the recognition that they belong to *Dioonopsis*, an extinct genus first recognized in the Paleogene of Japan. The leaves are simply pinnate. The pinnae that vary from entire margined to minutely spinose are inserted suboppositely on the rachis with broad bases, similar to species of *Dioon*. Venation is parallel, with common dichotomies and occasional anatomoses. Leaves are hypostomatic with haplocheilic stomata scattered, and randomly arranged in intercostal areas. Guard cells are sunken and overarched by subsidiaries (4-7) forming a strongly cutinized coronal rim.

Ordinary epidermal cells are isodiametric and slightly elongated over veins. The epidermal features distinguish these fossils from extant genera but coincide well with the extinct genus *Dioonopsis*. Confirmation of *Dioonopsis* in the Eocene of western North America as well as Japan, combined with its apparent absence in the European Tertiary, indicates that it probably spread via the Beringial phytogeographic pathway. This contrasts with our current knowledge of another extinct cycad, *Eostangeria*, shared between the Paleogene of North America and Europe which suggests linkage across the North Atlantic connection. The presence of *Dioonopsis* in southern Alaska during the Eocene, along with current understanding that these fossiliferous strata were nearly in their modern latitudinal position by the Eocene, leads to the conclusion that these cycads were able to occupy high latitude environments. This, however, implies that Alaskan *Dioonopsis* was exposed to light stress contrary to the present-day environment of modern cycads where light is not a limiting factor. This investigation was supported by a Fulbright award to the first author.

<sup>1</sup>Hungarian Natural History Museum, Botanical Department, Budapest, H-1476, POB222, Hungary<sup>2</sup>University of Florida, Florida Museum of Natural History, PO Box 117800, Gainesville, FL, 32611, USA

### 328 DEVORE, MELANIE\*<sup>1</sup> and PIGG, KATHLEEN<sup>2</sup>

#### Fossil evidence for temperate family evolution: Rosaceae from Republic, Washington and other Okanagan Highlands Eocene sites

Combining morphological and molecular data from extant plants with information from the fossil record is increasingly becoming essential for estimating times of divergence of lineages from higher taxonomic levels (e. g., family or above) to genera. Protocols for working with data from extant plants are well established, and the degree of resolution that can be expected from given types of molecules is becoming well known. Understanding what information can be obtained from fossils remains a less uniform process, as it is more difficult to find the essential localities and floras that are ideal for providing such data. The early middle Eocene Republic flora from northeastern Washington State is an excellent example of a diverse flora with a strong record of significant temperate angiosperm families. One family that is particularly well represented is Rosaceae, a group that shows its first documented major radiation in the fossil floras from Republic and related Okanagan Highlands sites of central British Columbia. Among the over a dozen rosaceous genera are forms that fall within three basic categories: (1) some are extant genera that are well established by the Eocene (*Photinia*, *Neuuisia*, *Prunus*, *Oemleria*); (2) others are Eocene forms are close to, but perhaps not exactly like, extant genera (cf. *Spi-*

*raea*, *Rubus*, *Cratageus*, *Amelanchier*, *Malus*/*Pyrus*, cf. *Pyracantha*, *Hespermeles*); and (3) still others are extinct genera with affinities at higher taxonomic levels (*Stenbergia* and other forms). Recent and ongoing studies of floral and vegetative remains from these sites show that major lineages within the family are well established in western North America by the early middle Eocene.

<sup>1</sup>Dept Of Biology & Env. Science, GC & SU Campus Box 81, MILLEDGEVILLE, GA, 31061-0001, USA<sup>2</sup>Arizona State University, SCHOOL OF LIFE SCIENCES FACULTY & ADMIN, BOX 874501, Tempe, AZ, 85287-4501, USA

**329 STROMBERG, CAROLINE<sup>\*1</sup>,  
DUNN, REGAN<sup>2</sup>, KOHN, MATTHEW<sup>3</sup>,  
MADDEN, RICHARD<sup>4</sup> and CARLINI, ALFREDO<sup>1</sup>**

### **Did South America herald Earth's earliest grasslands? New plant silica records from Gran Barranca, Argentina**

**B**ased on the study of faunas from Patagonia, South America, it has long been assumed that savanna grasslands spread in the Middle Eocene (40-45 Ma) in southern South America, ~20 million years earlier than on other continents. Paleobotanical lines of evidence are contradictory, with plant silica (phytolith) assemblages supporting the idea of open, grassy habitats by the Late Eocene, whereas macrofossils and palynofloras from Patagonia indicate closed forests during the Eocene and Oligocene. To test the South American early grassland hypothesis we conducted a high-resolution study of phytolith assemblages in the Sarmiento Formation at Gran Barranca, Chubut Province, Argentina. This section, which is known to produce well-preserved phytoliths, spans 42-18.5 Ma and is the most complete and important record of South American faunas. Phytolith analysis shows that a variety of forest indicators, including palms and woody dicotyledons, dominated phytolith assemblages throughout the section, with palms being particularly abundant during the Eocene and Oligocene. Grasses are present throughout the section, but initially consisted primarily of grasses likely related to bamboos. Phytoliths typical of open-habitat grasses (poids, PACMADs) do occur by at least 38 Ma, marking the earliest appearance of these two clades, but are quite rare (typically <5%). By the Late Oligocene/Early Miocene, pooid open-habitat forms dominate grass phytolith assemblages, and increase in frequency to 30% of assemblages overall. This expansion of grasses coincided with markedly lower palm phytolith abundances, possibly suggesting drier or colder climates. This record is consistent with previous interpretations of macrofossil and palynological data and rejects the notion that open, grass-dominated habitats spread in southern South America before at least the late Early

Miocene (18.5 Ma).

<sup>1</sup>Museo de La Plata, Paleontología de Vertebrados, Paseo del Bosque s/n, La Plata, B1900 FWA, Argentina<sup>2</sup>University of Washington, Biology, 24 Kincaid Hall, Box 351800, Seattle, WA, 98195-1800, USA<sup>3</sup>Boise State University, Geosciences, 1910 University Drive, Boise, ID, 83725-1535, USA<sup>4</sup>Duke University, Evolutionary Anthropology, 07 Bio. Sci. Bldg, Biological Sciences Building, Campus Box 3170 Med Ctr, Durham, NC, 27708-0680, USA

**330 STULTS, DEBRA<sup>\*1</sup>, AXSMITH,  
BRIAN<sup>2</sup> and WAGNER-CREMER,  
FRIEDERIKE<sup>3</sup>**

### **Atmospheric paleo-CO<sub>2</sub> estimates based on *Taxodium distichum* (Cupressaceae) fossils from the Miocene and Pliocene of Eastern North America**

**T**he extant cupressaceous conifer species, *Taxodium distichum*, has a record from the Late Miocene Brandywine Formation of Maryland and the Late Pliocene Citronelle Formation of southern Alabama based on the gross morphology of fossil leafy shoots, isolated leaves, pollen cones, isolated seed cone scales, and seeds. This determination is now corroborated by the presence of a species-specific arrangement of stomatal bands (narrow adaxial and wide abaxial bands) on preserved leaf cuticles from both formations. A calibration curve constructed from stomatal densities of modern leaves of *T. distichum* that were collected over the last century of anthropogenic CO<sub>2</sub> increase has been produced. The stomatal density of fossil leaf cuticles from the Brandywine Formation and Citronelle Formation have been directly compared to this curve and produced paleo-CO<sub>2</sub> mean estimates of 360 and 351 ppmv, respectively. Although the temporal resolution of the fossil sites is somewhat low, these results are in general agreement with multiple independent proxies, and demonstrate the utility of *T. distichum* leaves as instruments for stomatal frequency analysis. It also shows the reliability of stomatal frequency as an important terrestrial proxy for Neogene paleo-CO<sub>2</sub> estimates.

<sup>1</sup>University of South Alabama, Marine Sciences, Life Sciences Building 124, Mobile, AL, 36688, United States<sup>2</sup>University Of South Alabama, Department Of Biological Sciences, LSCB 124, MOBILE, AL, 36688-0002, USA<sup>3</sup>Utrecht University, Department of Palaeoecology, Utrecht, the Netherlands

331 BOYCE, CHARLES\*<sup>1</sup> and  
ZWENIECKI, MACIEJ<sup>2</sup>

**A record of plant microenvironment from  
the anatomy of permineralized leaf fossils**

Because leaves are the primary interface between plant and environment, fossil leaf morphology has been widely proven to be a valuable source of information regarding past climates and atmospheric compositions. From the leaf's perspective, however, the plant to which the leaf is attached is as much a part of its environment as regional climate. Thus, fossil leaves may also preserve an untapped wealth of information concerning the habit and ecology of the parent plant as well as the vegetation structure of the landscape. Previous modeling and laboratory experiments indicated that--regardless of leaf venation pattern--hydraulic capacity is maximized when the distance between veins ( $d$ ) equals that from vein to leaf surface ( $\hat{l}'$ ). This relationship was born out by measurements made in diverse extant plants:  $d = \hat{l}'$  for plants of exposed environments. Having  $d < \hat{l}'$ , i.e. high vein density in a thick leaf, would provide no benefit for the costs associated with the extra vein production and has not been seen in nature. Having  $d > \hat{l}'$ , i.e. low vein density in a thin leaf, would lead to rapid overheating or desiccation in an exposed environment because hydraulic supply would be unable to accommodate demand, but can be tolerated in a plant as long as it is in a sheltered environment with a low vapor pressure deficit. Thus the  $d/\hat{l}'$  ratio provides an indicator of microhabitat readily accessible from anatomically preserved fossils. Fossil leaves that have been sampled occupy a similar range of  $d-\hat{l}'$  combinations as living plants. Where whole-plant habit is known, the fossil plants that fall well off the  $d = \hat{l}'$  line are reasonable candidates for sheltered understory environments, suggesting this proxy can provide useful information regarding the many other fossil plants for which whole plant reconstructions are not available and only the leaf is known.

<sup>1</sup> University Of Chicago, Department Of Geophysical Sciences, 5734 S. Ellis Ave., Chicago, IL, 60637, USA<sup>2</sup> Arnold Arboretum of Harvard University, Jamaica Plain, MA, 02130, USA

332 PAN, AARON\*<sup>1</sup>, CURRANO,  
ELLEN<sup>2</sup>, JACOBS, BONNIE<sup>3</sup> and  
HERENDEEN, PATRICK<sup>4</sup>

**Late Oligocene - Early Miocene moist  
forest legumes (Fabaceae) from  
northeastern Africa**

Since the late Eocene, the Fabaceae has been an important group in terms of diversity, prominence, richness, and ecological significance in tropical moist African forests. Recent discoveries from the late Oligocene and early Miocene of Ethiopia show a diverse legume record including members of the Detarieae *sensu lato*, Mimosoideae, and Faboideae. These fossils include the oldest confirmable records of *Azelia* and *Newtonia*, and along with other proxies indicate that northeastern Afro-Arabia harbored luxuriant tropical moist forest vegetation during this time interval. Comparisons of the legume and palm (Arecaceae) fossil records indicate two very different evolutionary histories in Africa. The palms are diverse and abundant during the early Paleogene, but become depauperate through successive extinctions and extirpations and only play minor roles in forested communities during the Neogene. The Fabaceae appear in the Paleocene, become prevalent in the middle Eocene and are major components of forests throughout the remaining Eocene to the present.

<sup>1</sup>Fort Worth Museum Of Science & History, 1600 Gendy Street, Ft. Worth, TX, 76107, USA<sup>2</sup>Miami University, Department of Geology, 501 East High Street, Oxford, OH, 45056, USA<sup>3</sup>Southern Methodist University, Environmental Science Program, P.O. Box 750395, Dallas, TX, 75275-0395, USA<sup>4</sup>Chicago Botanic Garden, Senior Scientist, 1000 Lake Cook Road, Glencoe, IL, 60022, USA

333 STULTS, DEBRA\*<sup>1</sup> and AXSMITH,  
BRIAN<sup>2</sup>

**Quantitative paleoclimate estimates from  
two Late Neogene floras of eastern North  
America**

Floras of two Late Neogene formations in eastern North America, the Late Miocene Brandywine Formation located within the Mid-Atlantic Coastal Plain, and the mid-Pliocene Citronelle Formation which spans the northern Gulf of Mexico Coastal Plain, have been used to generate quantitative climate information for this time period. A Co-existence Analysis of plant taxa of the Brandywine Formation has produced figures indicating that temperatures during the Late Miocene, although in the same overall climate category as today, i.e., warm temperate, were a little warmer than currently exists in the area. Late Miocene warm month mean annual temperatures (WMMT) are estimated at 25.6 C, cold month mean temperatures (CMMT) have a range of 0.1 to 7.8°C, and mean annual temperatures are with-

in 13.3 -16.1°C. Mean annual precipitation (MAP) was 897-1206 mm and the annual pattern of precipitation apparently was similar to the current pattern. Coexistence Analysis results from the Citronelle Formation indicate the region during the mid-Pliocene had a humid/subtropical climate. The WMMT range estimate is 25.6 to 27.9 C, the CMMT estimate is 4.3 to 12.6 C, and the MAT estimate is 14.4 to 20.8 C. This correlates closely to temperatures in the area today. Interestingly, the MAP estimate of 1122-1250 mm indicates that precipitation during the Citronelle Formation depositional period was less than current precipitation totals. It is also possible that the annual pattern of precipitation (i.e., wet months, dry months) was different than the current pattern. Future study will compare the results of this analysis to a planned, physiognomic climate analysis using these same fossils. Comparisons will also be made to results obtained from other climate proxies.

<sup>1</sup>University of South Alabama, Marine Sciences, Life Sciences Building 124, Mobile, AL, 36688, United States<sup>2</sup>University Of South Alabama, Department Of Biological Sciences, LSCB 124, MOBILE, AL, 36688-0002, USA

**334 ERWIN, DIANE\*<sup>1</sup>, MYERS, JEFFREY A.<sup>2</sup> and SCHORN, HOWARD E.<sup>3</sup>**

### **Are there Neogene "lowland" floras preserved near the modern-day crest of the central Sierra Nevada, CA?**

In light of ongoing debate about the uplift history of the Sierra Nevada, a question remains concerning whether or not several Neogene floras preserved near today's crest represent "lowland" forests that grew at <915 m (3000 ft.) elevation. The Mt. Reba and Elephants Back (EB) assemblages sit above treeline at >2637 m (8650 ft.) leaving one to indeed wonder about the landscape and climate in which they grew. As currently described, the Mt. Reba includes cypress (*Cupressus*), Douglas fir (*Pseudotsuga*), two evergreen oaks (*Quercus*, *Lithocarpus*), two pines (*Pinus*), fir (*Abies*), giant sequoia (*Sequoiadendron*), and juniper (*Juniperus*). Using the "similar living species" method paleoelevation estimates were between ~762 to 915 m (~2500 - 3000 ft.) suggesting a post-7 Ma uplift of ~1829 m (6000 ft.). Similarly, the Lower (~16 Ma?) and Upper EB (~7 Ma) floras described as mixed broad-leaved evergreen and deciduous hardwood forest with no conifers implied growth at ~762 to 915 m (~2500 - 3000 ft.) elevation. From our floristic analysis of the Mt. Reba plants we estimate a MAT of 8-9°C (not 13.3°C) and elevation of at least 1524m (5000 ft.), if not higher, given the relatively warmer and wetter late Miocene climate. With respect to the EB floras, the age and stratigraphic position of the Lower assemblage, in particular, is problematic. The Upper EB has three taxa: *Lyonothamnus*, *Nerium*, and several cf. *Quercus alba*-type leaves. Only the oak is identifiable to genus. The Lower EB includes deciduous hardwoods (e.g., *Populus*, *Salix*, *Juglans*, *Ulmus*,

*Quercus*, *Platanus*) and evergreen shrubs that are not exclusively low elevation taxa, but conifers are absent. If the Lower EB flora is ~16 Ma based on new geologic mapping and radioisotopic dates, floral analysis must take into account growth during the Mid-Miocene Climatic Optimum, a time of elevated global temperatures, increased precipitation and humidity that would allow forest growth at elevations >915 m (3000 ft.).

<sup>1</sup>University of California, Museum of Paleontology, 1101 Valley Life Sciences Building, Berkeley, CA, 94720, USA<sup>2</sup>Western Oregon University, Department of Geology, Monmouth, OR, 97361, USA<sup>3</sup>337 Mari Court, Ridgecrest, CA, 93555, USA

## **POSTERS**

**335 QUAN, CHENG\*<sup>1</sup>, LIU, YUSHENG<sup>1</sup> and UTESCHER, TORSTEN<sup>2</sup>**

### **Paleogene evolution of precipitation in northeast China supporting the mid Eocene intensification of the East Asian monsoon**

The early development of the East Asian monsoon in the geological past is highly critical in paleoclimatological study, but few quantitative results are known. Based on fossil plants from Fushun of NE China, we here present a quantitative estimation on the evolution of the precipitation in this area during the mid Paleocene - late Eocene. The results demonstrate that the seasonal precipitation prevailed during the interval, suggesting that the early monsoonal system had already developed in this period. Comparing Paleogene climatic results from different latitudes spanning eastern China, we conclude that the East Asian monsoon must have had been significantly enhanced after the late mid Eocene (~41-40 Ma), due to the evidently increased precipitation differentiation between wet and dry months as shown in the present study. Both the uplift of the Da Hinggan Mountains in NE Asia on the regional topographical background and the India-Asia collision in the global context might have conjointly contributed to the early monsoon intensification by the influence on the air mass movement and associated precipitation pattern in the monsoonal realm.

<sup>1</sup>East Tennessee State University, Department Of Biology, PO Box 70703, Johnson City, TN, 37614-1710, USA<sup>2</sup> Bonn University<sup>4</sup>, Steinmann Institute, Bonn, 53115, Germany

336 QUAN, CHENG\*<sup>1</sup>, LIU, YUSHENG<sup>1</sup>  
and UTESCHER, TORSTEN<sup>2</sup>

### Paleogene seasonal variation and climate evolution of northeast China

The continental Paleogene climates have been well studied in Europe and North America, but very little is known from Asia because only a few climatic results were reported on particular geological intervals. Based on 29 floral assemblages from 8 well age-controlled fossiliferous sites, we here quantitatively reconstruct the climates throughout the Paleogene of northeast China and discuss related seasonal variations. Our results demonstrate that the gradient of the mean annual temperature (MAT) was fairly shallow (0.27 °C/1° latitude) during the Paleocene throughout this region. In the Eocene, the climates were equably distributed, but the seasonality was predominant in the region, indicated by obvious thermal and hydrological differentiations between winters and summers of the sites. The paleo-East Asian monsoon must have had intensified at least in the mid late Eocene, substantially shown by apparent differences in annual climate distribution of all the sites. Regarding the climatic evolution of northeast Chinese Paleogene, our quantitative results suggest that the MAT overall declined from a warm condition in the Paleocene and Eocene to a moderate condition in the Oligocene, sharing a comparable trend with those of marine records. Two significant cooling events are recognized in the early and mid Eocene with temperatures dropped 3.4 °C and 3.8 °C for the MAT, and 5.8 °C and 4.7 °C for the winter temperature, respectively, in similar magnitudes to corresponding variations of Europe and North America. Furthermore, the present results show that the MAT rebounded in the late mid Eocene and then decreased till the Oligocene, in consistent with the pattern of Europe in the mid Eocene to Oligocene interval.

<sup>1</sup>East Tennessee State University, Department Of Biology, PO Box 70703, Johnson City, TN, 37614-1710, USA<sup>2</sup>Bonn University, Steinmann Institute, Bonn, Germany

337 ZHOU, ZHIYAN<sup>1</sup>, QUAN, CHENG\*<sup>2</sup> and LIU, YUSHENG<sup>2</sup>

### Tertiary *Ginkgo* ovulate organs with associated leaves from North Dakota, USA and its evolutionary significance

The evolutionary history of *Ginkgo*, a living fossil once flourished in the geological time, has been better understood for the Mesozoic Era, but was still elusive in the Tertiary because of the rarity of reproductive organs. We here describe a new species, *Ginkgo cranii* sp. nov., based on studies using SEM and LM on well-preserved ovulate organs and associated leaves from the

Upper Paleocene Sentinel Butte Formation of North Dakota, USA. The ovulate organ is of the modern type and pedicel-absent, with two ovules seated in separate collars directly attached to the peduncle, but only one of them is matured. The fully developed ovules are platy-spermic, 12-14 mm long by 11-14 mm wide and about 10-12 mm thick. Stomata with deeply-sunken guard cells and slightly-raised subsidiary cells are sparsely distributed among epidermal cells which are characterized by dome-like, strongly bulging periclinal walls and developed anticlinal wall flanges in integument and collar cuticles. The pollen grain adhered to the cuticle is fusiform with a narrow medium colpus and finely granulate exine. The associated leaves are generally similar to the ovulate organ in cuticular structure, especially in having epidermal cells with more or less bulging periclinal walls and developed periclinal wall flanges. *Ginkgo cranii* is the only Tertiary species of the genus described so far, of which the ovulate organs are known. The study further corroborates the hypothesis that modern *Ginkgo* was evolved from its ancestors by reduction, and is helpful to classify Cenozoic ginkgos in a natural system.

<sup>1</sup>Nanjing Institute of Geology and Palaeontology, Chinese Academy of Sci, Nanjing, 210008, China<sup>2</sup>East Tennessee State University, Department Of Biology, PO Box 70703, Johnson City, TN, 37614-1710, USA

338 QUAN, CHENG\*<sup>1</sup>, LIU, YUSHENG<sup>1</sup>  
and UTESCHER, TORSTEN<sup>2</sup>

### Climatic gradients, distribution and evolution of the East Asian Eocene

Based on 66 floral assemblages from 37 sites, we here reported the first large-scaled quantitative results and discuss the the Eocene East Asian climatic patterns. Our results demonstrate that the seasonal climates were rather evenly distributed through the region, with relatively high mean annual temperatures (MATs, >13.7 °C) and mean annual precipitations (MAPs, >755 mm). The overall latitudinal MAT gradient along the eastern coastal was about 0.1 °C/° latitude, more equably than those of the North America (0.4 °C/1° latitude in west coasts and 0.6 °C/1° latitude in the interior and east coasts) and coeval sea surface temperature (SST). The unexpected shallow latitudinal gradients might result from relatively high temperatures in the north China which were probably caused by the intensified paleo-East Asian monsoon in the Eocene. Latitudinally, the temperatures (both MAT and seasonal temperatures) and precipitations were slightly lower in the middle part than those of south and north, probably because of the cooling effect of the high evaporation in the subtropical high region. The precipitations declined from the west to the central regions, as well as decreased northward in the Tibetan Plateau, further corroborating the immense climatic impact of the collision of India with Asian and then consequent retreat of Tethys and the uplift of the plateau. Moreover, our results indicate that the MAT of

the tropical area decreased stably with an overall cooling trend through the Eocene, from  $18.4 \pm 2.8$  °C, then  $17.6 \pm 6.3$  °C, to  $16.1 \pm 0.3$  °C, largely in consistent with the pattern of the tropical SST. The winter temperature remarkably declined, particularly during the middle to late Eocene interval, but the summer temperature (WMT) remained almost the same throughout the tropical Eocene.

<sup>1</sup>East Tennessee State University, Department Of Biology, PO Box 70703, Johnson City, TN, 37614-1710, USA<sup>2</sup>Bonn University, 4Steinmann Institute, Bonn, 53115, Germany

**339 MILLER, LAUREN<sup>1</sup>, SMITH, SELENA<sup>2</sup>, STROMBERG, CAROLINE\*<sup>3</sup> and SHELDON, NATHAN<sup>1</sup>**

### **A high-resolution record of deep-time vegetation dynamics from the Eocene of Montana**

Reconstructing past vegetation at high resolution is key to understanding ecological dynamics and links with earth processes on geological time scales. Macrofossil floras provide important data on vegetation types, but are limited in terms of geographic and temporal coverage. Phytoliths (plant silica bodies) offer an opportunity to study vegetation in the absence of macrofossils. While phytoliths have previously been used for examining vegetation on broad spatial and temporal scales, we wanted to test the ability of phytoliths and other biosilica (e.g., diatoms) to reconstruct vegetation dynamics on a shorter (<1 million years) time scale for a single locality. In addition, this study represents the first to compare directly phytolith and paleosol data. We examined vegetation patterns inferred from phytoliths from a section of the Renova Formation, Timberhills region, Montana dated to  $39.2 \pm 3$  Ma. The section is composed of Alfisols, Entisols, Inceptisols, and composite paleosols superimposed onto floodplain sediments that were deposited under generally low-energy conditions. Phytoliths from 27 paleosol horizons were extracted to reconstruct a high-resolution vegetation history for this section. Phytolith morphotypes are predominantly from forest plants, confirming the presence of forests in Montana ~40 Ma. Tropical elements such as palms (Arecaceae) and gingers (Zingiberales) are present throughout the section, suggesting this was a paratropical forest. The high-resolution sampling demonstrates vegetation shifts between three main dominant plant types: closed forest, moderately open forest (forest gaps, edges, and woodland; represented by Zingiberales), and grasses. The heterogeneity is likely due to succession and vegetation patchiness. Grasses are interpreted as early-successional and tolerant of relatively drier conditions, but are out-competed by forest vegetation on longer time-scales. At some stratigraphic horizons, there is poor correspondence of paleosol type and phytolith assemblages, reflecting changing vegetation along a soil depth profile. This study demonstrates that high-

resolution sampling and multiple lines of evidence are necessary for capturing vegetation dynamics in time and across microhabitats in deep time.

<sup>1</sup>University of Michigan, Geological Sciences, 2534 CC Little Bldg, 1100 North University Ave, Ann Arbor, MI, 48109-1005, USA<sup>2</sup>University Of Michigan, Department Of Geology, 1100 North University Avenue, 2534 CC Little Building, Ann Arbor, MI, 48109, USA<sup>3</sup>University of Washington, Biology, 24 Kincaid Hall, Box 351800, Seattle, WA, 98195-1800, USA

**340 CHEN, TINA\*<sup>1</sup>, TAING, THANG<sup>1</sup> and MANCHESTER, STEVEN R.<sup>2</sup>**

### **Fossil Pollen from the Wilbanks II Clay Pit of Weakley County, Tennessee**

Fossil fruits with affinities to old world genera of Icacinaceae were recently identified from the Eocene Wilbanks II clay pit in Weakley County, Tennessee. We initiated a study of pollen preserved in the same sediments as the fossil fruits in order to narrow the stratigraphic age of the deposit and to investigate the regional vegetation to which these plants belonged. The pollen was obtained by treating a clay sample in which the icacinaceous fruit was preserved with 47% hydrofluoric acid, followed by centrifugation using 4% Darvan detergent to concentrate the grains in a density gradient. Slides of pollen grains were made and viewed by light microscopy. Commercial clay pits in western Tennessee are well-known for abundance of Eocene fossil leaves and reproductive organs and there is an even higher abundance in the pollen found. Based on preliminary data collection, 10 to 15 types of megafossils were counted in the collection while at least 20 different types of pollen were found in the slides observed thus far. Pollen grain types include those of Fagaceae, *Carya* sp. and Ericaceae. No pollen of Icacinaceae has yet been recovered from the sample. Pollen reviewed so far are consistent to that of Middle or Late Eocene age.

<sup>1</sup>University of Florida, Department of Biology, University of Florida, Gainesville, FL, 32611, USA<sup>2</sup>

## Phycological Section

## POSTERS

**341 ASOKRAJA, ILAVARASI<sup>1</sup>, NOORUDDIN, THAJUDDIN<sup>1</sup> and MUTHUKUMARAN, GUNASEKARAN\*<sup>2</sup>**

***Monoraphidium* sp, HM 768826: A suitable sustainable lipid source for biodiesel production**

Due to diminishing fossil fuel reserves, it is necessary for us to shift for an alternative fuel source that could be sustainable and ecofriendly. Microalgae produce different ratios of lipids, proteins and carbohydrates. Microalgal lipid can potentially be employed for biodiesel production. Our research has demonstrated the total lipid content, fatty acid profile and biodiesel production from a naturally isolated strain of *Monoraphidium* sp. from fresh water pond. In the present study, the total lipid content was found to be 8.9% under normal nutrient conditions whereas it was increased to 23.1% under nitrogen deficiency conditions. The fatty acid profile showed the presence of high level of saturated and monounsaturated fatty acid than polyunsaturated fatty acid, which is optimum for biodiesel application. Biodiesel was produced from extracted algal oil by alkali-catalyzed transesterification. The pH of the produced biodiesel was found to be 8.1 and it was stored for further analysis. Moreover, we have partially characterized the isolate based on 18SrRNA sequence and submitted in GenBank with accession number as *Monoraphidium* sp. HM768826.

<sup>1</sup>Bharathidasan University, Microbiology, School of Life sciences, Tiruchirappali, Tamil Nadu, 620 024, India<sup>2</sup>Fisk University, Biology, 1000 17th Ave North, Nashville, TN, 37208, USA

**342 ROCKWELL, TIMOTHY\*, VITALE, ANGELA and COOK, MARTHA**

**Cell division in the charophycean green alga *Entransia fimbriata***

Differential interference contrast light microscopy and transmission electron microscopy were used to study cell division in *Entransia fimbriata*, a member of the Klebsormidiales. Cells contained a single large vacuole and a single large parietal chloroplast, each of which extended the length of the cell. The nucleus resided next to the chloroplast at the midpoint. The first indication of cell division was cleavage of the chloroplast, which divided completely or almost completely prior to mitosis. Initiation of a septum occurred after chloroplast division and before or during prophase, but the septum did not continue to develop until later. The late prophase nucleus was diamond shaped, and the nucleolus was present until just before metaphase.

Though the telophase nuclei initially formed near the division plane, they had moved to opposite ends of the cell and were no longer aligned with each other during cytokinesis. Septum formation was centripetal. *Entransia*, like *Chlorokybus*, exhibits chloroplast division and septum initiation before prophase. These processes are reported to occur later in *Klebsormidium*. Cell division in *Entransia* is consistent with that in other early divergent charophycean algae.

Illinois State University, School of Biological Sciences, Campus Box 4120, Normal, IL, 61790-4120, USA

**343 DAVOODBASHA, MUBARAKALI<sup>1</sup>, JOHNSON, SHANI<sup>2</sup>, THIYAGARAJAN, SHENBAGAVALLI<sup>1</sup>, THAYALAN, MARI NIVETHA<sup>1</sup>, RAMASAMY, PRAVEENKUMAR<sup>1</sup>, ASOKRAJA, ILAVARASI<sup>1</sup>, ABDULAZEES, PARVEEZ AHAMED<sup>1</sup>, NOORUDDIN, THAJUDDIN<sup>1</sup> and MUTHUKUMARAN, GUNASEKARAN\*<sup>2</sup>**

**Nutritional based optimization of increased lipid content in freshwater microalgae, *Scenedesmus bijugatus* var *bicellularis* for biodiesel feedstock**

Many alternative bio-feedstocks are currently being exploited for biodiesel production, out of that; microalgae have emerged as one of the most promising candidate for biofuels. In the present study, fresh water microalgae, *Scenedesmus bijugatus* var *bicellularis* was isolated, morphologically characterized and subsequently mass cultivated in Bold's basal medium. The cells were harvested during their stationary growth phase and it was re-inoculated in the same medium with different nitrogen concentration (0%, 20%, 40%, 60%, 80% and 100%) to identify the optimal nitrate concentration for lipid production. The total lipid content was estimated at logarithmic and early stationary phases. The maximum lipid content of about 42.3% and minimum of 24.9% were estimated at 60% and 0% of nitrate concentration in dry cell weight respectively. The fatty acid profile of the lipids extracted from the cells, which grown at 60% and 100% (as control) nitrate concentration. The major fatty acids were found to be C18:0, C20:0, C17:1 and C16:0. The obtained data depicted that the cells grown with 60% nitrate deficiency showed higher levels of saturated and monounsaturated fatty acids than the polyunsaturated fatty acids which is important for biodiesel applications. Additionally, the linolenic acid content was also found to be below 12%, which is also advantageous to use this strain as biodiesel feedstock. This is being the first report in utilizing *Scenedesmus bijugatus* var *bicellularis* for its oil content.

<sup>1</sup>Bharathidasan University, Microbiology, School of Life sciences, Tiruchirappali, Tamil Nadu, 620 024, India<sup>2</sup>Fisk University, Biology, 1000 17th Ave North, Nashville, TN, 37208, USA

344 THIYAGARAJAN,  
SHENBAGAVALLI<sup>1</sup>, DUNCAN, KAYLIA<sup>2</sup>,  
DAVOODBASHA, MUBARAKALI<sup>1</sup>,  
RAMASAMY, PRAVEENKUMAR<sup>1</sup>,  
NOORUDDIN, THAJUDDIN<sup>1</sup> and  
MUTHUKUMARAN, GUNASEKARAN<sup>\*2</sup>

**Antimicrobial activities of fatty acid methyl esters (FAME) of *Scenedesmus bijugatus* var. *bicellularis*.**

In our collaborative study, we evaluated the efficiency of microalgal (*Scenedesmus bijugatus* var *bicellularis*) fatty acid methyl esters (FAME) as an antimicrobial agent against *Staphylococcus aureus*, *Escherichia coli* and *Candida albicans*. The FAME analysis by Gas Chromatograph (GC) with Flame Ionization detector (FID) revealed the presence of 30 different methyl esters. Out of these, various pharmacologically active FAME like Stearic acid methyl ester (C18:0) (0.6 % w/w), Oleic acid methyl ester (C18:1) (1% w/w), Linoleic acid methyl ester (C18:2) (1.40% w/w), Linolenic acid methyl ester (C18:3) (6.26%), Eicosapentanoic acid methyl ester (C20:5) (1.13 % w/w), Erucic acid methyl ester (C22:1) (1.03% w/w) and Docosahexenoic acid methyl ester (C22:6) (2.27 % w/w) exhibited both anti-bacterial and anti-candidal activity. To the best of our knowledge, this is the first report on the antimicrobial activity of FAME from microalgae.

<sup>1</sup>Bharathidasan University, Microbiology, School of Life sciences, Tiruchirappali, Tamil Nadu, 620 024, India<sup>2</sup>Fisk University, Biology, 1000 17th Ave North, Nashville, TN, 37208, USA

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**Physiological Section**

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*See also Ecophysiology, Stress Tolerance and Strategies for healing our coast lines: Deepwater Horizon oil spill in the Gulf of Mexico, erosion and urban degradation: progress for the North American future marine macro-plants.*

**ORAL PAPERS**

345 BAILEY, PAMELA

**Sustainable Landscape Designs Utilizing Native Species to Increase Pollinator Habitats**

This LEGACY publication provides the Department of Defense (DoD) with guidance on developing native plantings that provide food sources and shelter for pollinators and the plant lists are inclusive of plantings for all the different groups of pollinators. The main objective of this project is to provide to DoD land managers with tools they can use to provide planting areas for our native pollinator species and increase pollinator interactions. This is meant to be used on Military installations in 10 different parts of the country. DoD installations across CONUS was overlaid on a GIS map of Bailey's Ecoregions, and 10 regions were chosen from 35 ecoregions across the United States. For each ecoregion there is a map, a residential landscape plan, a planting island plan and a seed mix using native plants. The landscape plans are largely focused on the cantonment areas where the base housing, installation buildings and suitable open space for plantings would be found. Habitat information and nesting designs for pollinator species is also included in the document.

US Army Engineer Research and Development Center, 3909 Halls Ferry Road, Vicksburg, MS, 39180

346 THORHAUG, ANITRA

**Healing Biodiversity by Large Scale Seagrass Restoration in Anthropogenic Modified Settings with Resulting Persistent (up to 38 yr) Seagrass Beds including Reassembled Biodiversity**

In the Gulf of Mexico, Atlantic subtropics and tropics series of seagrass meadows were planted under a variety of physiological conditions which will be reviewed and evaluated as long-term persistent meadows despite increasing pollution in the estuaries of their regrowth. These chiefly were within estuaries with moderate to severe anthropogenic effects. The species *Thalassia testudinum* had areas of 587298 m<sup>2</sup> planted in Biscayne Bay Florida in a set of 17 locations some as large as 206780 m<sup>2</sup> by seedling, sprig, plug and machine.

The first planting in 1973 persist today. *Syringodium filiforme* had 708980 m<sup>2</sup> planted chiefly by sprigs and plugs. *Halodule wrightii* 724355 m<sup>2</sup> which expanded rapidly in the majority of sites and persist in meadows today in north Biscayne Bay. All but a small portion of these three species are now persistent and most have expanded well beyond the meters planted. In the Laguna Madre, Texas, the *Halodule wrightii* planted by plug methods in 275361 m<sup>2</sup> restored from propeller scars, scrape down and barren bottoms. *Halophila engelmannii* was planted specimens in close to 30 ha. The remarkable resilience of seagrass's physiological adaptation to increase pollution was the key factor. *Halodule wrightii* and *Syringodium filiforme* in sediments containing former intense sewer outfall grew giant size with extreme sheath elongation which lifted blades into a more intense photiczone which clearly had more red light available. Salinity alterations between extreme high and low as well as a large sediment accretion occurred for the Laguna Madre *Halodule wrightii* which is withstood. Other examples of persistent beds were found in Kingston Harbor where a less than 0.5 ha meadow became multi hectared, although turbidity from the major sewerage outfall, outgoing riverine pollutants, and bay turbidity were major water factors.

Yale University, School of Forestry and Environmental Sciences, 359 Prospect St., New Haven, Ct., 06901, USA

**347 MOLLIK, MD. ARIFUL HAQUE\*<sup>1</sup>, RAHMAN, FOUZIA<sup>2</sup>, AZAM, MD. NUR KABIDUL<sup>1</sup>, FERDAUSI, DILARA<sup>1</sup>, RAHMAN, MD. TAUFIQ-UR<sup>3</sup>, RAHMAN, MD. MAHAFUZUR<sup>1</sup>, JAHAN, ROWNAK<sup>2</sup>, RAHMATULLAH, MOHAMMED<sup>1</sup> and KHATUN, MST. AFSANA<sup>4</sup>**

### Knowledge and use of plants for asthma by the Kavirajes in Khulna district of Bangladesh

Asthma is a common chronic disorder of the airways leading to bronchospasm, airflow obstruction, and underlying inflammation. An incidence of asthma is on the increase in both developing countries and the developed world because of the rise of environmental pollution, particularly the degradation for air quality because of increasing traffic exhausts. It has been estimated that in the developed countries, one out of four children in urban areas may suffer from asthma. The most widely used preventive medications are inhaled glucocorticoids. Long-term use of these medications can lead to serious side-effects. Since the numbers of asthmatic patients are on the rise in Bangladesh, we decided to conduct a survey amongst the traditional medicinal practitioners (Kavirajes) of Khulna district, Bangladesh to learn more about plants used to treat asthma. Since part of the Sunderbans forest region falls within this district Kavirajes have a huge diversity

of plants at their disposal for treatment of various ailments. Interviews were conducted with the help of a semi-structured questionnaire and plant specimens as pointed out by the Kavirajes were collected and identified at the Bangladesh National Herbarium. It was observed during the course of the survey that the Kavirajes are well-aware of asthma and treat the ailment using formulations prepared from a number of plants. Unlike inhalers, these formulations are administered orally. The plants used to treat asthma (with family name given in parenthesis) included *Richardia scabra* L. (Rubiaceae Juss.), *Centella asiatica* (L.) Urb. (Apiaceae Lindl.), *Anisomeles malabarica* (L.) R.Br. ex Sims (Lamiaceae Lindl.), *Justicia candicans* (Nees) L.D.Benson (Acanthaceae Juss.), *Euphorbia antiquorum* L. (Euphorbiaceae Juss.), *Piper cubeba* L.f. (Piperaceae Bercht. & J.Presl), *Cycas revoluta* Thunb. (Cycadaceae Persoon), *Ruellia tuberosa* L. (Acanthaceae Juss.), and *Aloe vera* (L.) Burm.f. (Asparagaceae Juss.). The above-mentioned plants may prove to be good sources for obtaining anti-asthmatic compounds, which has less or no side-effects. It is expected that scientific studies conducted with these plants can lead to discovery of novel drugs.

<sup>1</sup>University of Development Alternative, Biotechnology and Genetic Engineering, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh <sup>2</sup>University of Development Alternative, Molecular Medicine and Bioinformatics, 80 Satmasjid Road, Dhanmondi R/A, Dhaka, 1205, Bangladesh <sup>3</sup>University of Cambridge, Pharmacology, Tennis Court Road, Cambridge, CB2 1PD, UK <sup>4</sup>Lincoln College, Pharmacy, Mayang Plaza, Block A, No 1, Jalan SS 26/2, Taman Mayang Jaya, Petaling Jaya, Selangor Darul Ehsan, Kuala Lumpur, 47301, Malaysia

**348 GANGER, MICHAEL\*, STUREY, TIFFANY and BAHNY, BETH**

### Induction and conversion in *Ceratopteris richardii*, a gender-labile fern: more pieces to the puzzle

*Ceratopteris richardii* is a homosporous fern whose gametophytes may develop into either males or hermaphrodites. Development of an undifferentiated spore into a male, a process called induction, is strongly influenced by the presence of antheridiogen, a gibberellin-like hormone secreted by hermaphrodites. In the absence of antheridiogen or in the presence of both antheridiogen and abscisic acid (ABA), spores are likely to develop into hermaphrodites. Males have been shown to remain male in the continued presence of antheridiogen, but may convert to hermaphrodites with its removal, in a process called conversion. Two experiments will be discussed. The first concerns the determinants of male gametophyte size. Spores of determined sizes from two strains, wild type (*RNWT1*) and highly male (*him1*), were sown onto agar containing 0x, 0.5x, 1x, and 2x strength antheridiogen and allowed to grow for 3 weeks under 24 hour grow lights at 24-28 degrees Celsius. Spore size was positively, though weakly,

related to male gametophyte size, while antheridiogen concentration was negatively related to ultimate male gametophyte size. No difference in size was observed between *C. richardii* strains. These results suggest that antheridiogen may influence gender through slowing growth. Slow growing gametophytes would be expected to bias toward male development, while faster growing gametophytes would develop as hermaphrodites. This would be due to the resource requirements of the hermaphrodite since it supports sporophyte growth. The second experiment concerns the role of ABA in conversion. Three-week old males were exposed to several concentrations of ABA, 0 microM, 1 microM, 10 microM, 100 microM, and 300 microM. Males in low concentrations of ABA were more likely to convert and converted more quickly than those in higher concentrations. While ABA is antagonistic to antheridiogen during early development, it appears to function similarly to antheridiogen during conversion.

Gannon University, Biology, 109 University Square, Erie, PA, 16541,

### 349 THORHAUG, ANITRA\*<sup>1</sup> and BERLYN, GRAEME<sup>2</sup>

#### **The Effect of Green and Blue Light vs. Red Light on the Subtropical/Tropical Western Atlantic Seagrasses *Syringodium filiforme* vs. *Halodule wrightii*'s Spectral Reflectance and Partial Absorpti**

The possible fate of sunlight within a plant are absorbance, reflectance, fluorescence, emission and transmittance. In the physiology of a plant, spectral reflectance and absorbance signatures can illuminate biochemical composition, pigment content, and water content, as well as structural features. Seagrasses bathed in salt water have no stomata and are relatively balanced for water. However, their pigment content except for generalized measurements with extracted pigments has not been analyzed, especially for physiological responses for many factors including light. We compare responses of Eastern Atlantic subtropical/tropical whole living mature *Syringodium filiforme* to *Halodule wrightii* incubated for 6 h (a half a tidal cycle) using a non-destructive, non-invasive spectral reflectance meter to diminishing colored light. Each species was highly activated within the 420-520 nm areas with 10 and 23% light during a 6 h incubation. The xanthophyll plus carotenoid responses to red light were different than their responses to green or blue light, particularly at the diminished levels in each species, but not equivalent between species. These responses will be discussed in detail. However, the yellow light incubations had surprising results, especially for *Syringodium filiforme*. Generally, the red edge was more similar in blue vs. green light than that of red and yellow. The green edge response differed widely among treatments. Peaks of pigment activations were highly pronounced for the accessory xanthophyll and carotenoid

pigments during these treatments especially compared to responses of *Thalassia testudinum* and *Zostera marina*. The implications of this data to life in shallow and deep marine waters will be discussed as well as the synergistic responses of light levels with changes in salinity.

<sup>1</sup>Yale University, School of Forestry and Environmental Sciences, 359 Prospect St., New Haven, Ct., 06901, USA <sup>2</sup>Yale University, School Of Forestry & Environmental Studies, GREELEY LAB-370 PROSPECT ST, NEW HAVEN, CT, 06511, USA

### 350 THORHAUG, ANITRA\*<sup>1</sup> and BERLYN, GRAEME<sup>2</sup>

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<sup>1</sup>Yale University, School of Forestry and Environmental Sciences, 359 Prospect St., New Haven, Ct., 06901, USA <sup>2</sup>Yale University, School Of Forestry & Environmental Studies, GREELEY LAB-370 PROSPECT ST, NEW HAVEN, CT, 06511, USA

351 MOHAMMED, ABDUL\*,  
HOLGATE, LEON and TARPLEY, LEE

**High night temperature and ethylene reception inhibition effects on rice (*Oryza sativa* L.) morphology, phenology and physiology**

Elevated atmospheric greenhouse gases can increase night temperatures (NT) more than day temperatures. Night temperature is one of the major environmental factors influencing plant metabolic processes and increase in NT can decrease rice (*Oryza sativa* L.) seed production and quality. Increase in NT increases ethylene production which in turn can trigger reactive oxygen species production, thus causing damage to the membranes, leading to a decrease in seed production. The objective of this study was to determine the effects of high night temperature (HNT) and an ethylene receptor activity inhibitor (1-methylcyclopropene; 1-MCP) on growth, development, physiology and seed production of rice plants. Plants were subjected to ambient night temperature (ANT) (25 °C) or HNT (30 °C) through use of continuously, precisely controlled infrared heaters, starting from 2000 h until 0600 h, starting 30 day after emergence. The HNT did not affect leaf photosynthetic rates; however, HNT increased respiration rates (20%), relative membrane injury (28%), internal CO<sub>2</sub> concentration (3%), and transpiration (12%) and decreased pollen germination (34%), spikelet fertility (21%) and panicle dry weight (10%). The 1-MCP-treated plants grown under HNT showed decreased respiration (5%) and relative membrane injury (10%) and increased pollen germination (186%), spikelet fertility (28%) and panicle dry weight (4%), compared to untreated plants grown under HNT. Application of 1-MCP increased rice seed production under HNT by decreasing respiration rates and increasing membrane stability, pollen germination and spikelet fertility, providing evidence for a role of ethylene reception in rice response to HNT.

Texas AgriLife Research, 1509 AGGIE DR, BEAUMONT, TX, 77713, USA

352 CAPPA, JENNIFER JOCAROLE\*<sup>1</sup>,  
YETTER, CRYSTAL<sup>2</sup>, FAKRA, SIRINE<sup>3</sup>,  
MARCUS, MATTHEW<sup>2</sup>, SIMMONS, MARK<sup>4</sup>  
and PILON-SMITS, ELIZABETH<sup>1</sup>

**Characterization of selenium uptake and metabolism in *Stanleya* (Brassicaceae)**

Selenium naturally occurs in soils around the globe with extreme variation in its concentration and distribution. Some soils have high concentrations of Se, particularly the western United States, due to the presence of seleniferous Cretaceous shale and chalk sediments. Owing to the similarity of Se to sulfur, most plants readily take up selenate from the environment and assimilate it into organic forms. A few plant genera even accumulate Se to levels typically 100-fold higher than surrounding vegetation on seleniferous soils (0.1-1% of dry weight); these species are called Se hyperaccumulators. *Stanleya pinnata* var. *pinnata* is a Se hyperaccumulator and occurs in most western states, while most of the other six species in *Stanleya* have narrow ranges and are endemic to a specific mountain range or desert. *Stanleya pinnata* var. *pinnata* incorporates Se into the non-protein amino acid methyl-selenocysteine (Me-SeCys), thereby preventing Se incorporation into proteins, and its associated toxicity. Six of the seven species of *Stanleya* were collected in the field. The leaves, siliques and soil from each individual were analyzed for *in situ* Se concentrations. The seeds were germinated and seedlings were tested for Se accumulation and tolerance in hydroponics. Seedlings were also grown in MS agar for analysis at the Advanced Light Source in Berkeley, CA for Se allocation and chemical speciation. Furthermore, four nuclear genes have been amplified in three individuals from differing populations for each species for use in phylogenetic inference. We have evidence of differential metabolism of Se within the genus *Stanleya* based on accumulation, tolerance, chemical speciation and Se sequestration. By combining these data in a phylogenetic context we can formulate hypotheses about the evolution of Se hyperaccumulation in *Stanleya*.

<sup>1</sup>Colorado State University, Biology, Fort Collins, CO, 80523, USA <sup>2</sup>Eastern University, St. Davids, PA, 19087, USA <sup>3</sup>Lawrence Berkeley National Laboratory, Berkeley, CA, 94720, USA <sup>4</sup>Colorado State University, Department Of Biology, FORT COLLINS, CO, 80523-1878, USA

353 MELCHER, PETER\*<sup>1</sup>,  
ZWIENIECKI, MACIEJ<sup>2</sup> and HOLBROOK,  
N. MICHELE<sup>3</sup>

### Functional embolism refilling in red maple (*Acer rubrum* L.)

The goal of this study was to assess the ability of mature trees and saplings of *Acer rubrum* L. to refill artificially embolized vessels in intact branches. Embolism was induced by injecting air (4.5 MPa) into the stem. Following the air-injection treatment, changes in the stems capacity to transport water were determined using grainer-style sap-flow probes inserted into branches located about 1-m distally to the point of air injection. Sap flow was measured continuously over many days following air injection. No measurable effect from air injection on the flow of sap was observed. Air injection also had no effect on stomatal conductance and leaf water potentials. Injecting air at 5.5 MPa pressure into the main stems of potted, three-year-old saplings also had no immediate or prolonged effects on whole plant transpiration. Regression analysis revealed that whole plant transpirational flow rates were either the same, or even greater after air injection than prior to injection treatment. We also measured changes in petiole hydraulic conductivity (Kpet) following air-injection pressures of 0, 3.0 or 5.5 MPa to assess if air-injection treatments resulted in embolisms within petioles. Kpet was found to be reduced to values near zero immediately following air injection into stems (at time zero). However, Kpet completely recovered within 2½ minutes on petioles that had their branches subjected to the 3.0 MPa air injection treatments and it took about 5 to 10 minutes to restore Kpet to 70 % of the initial Kpet values in petioles attached to branches injected with 5.5 MPa of gas pressure. These studies provide further evidence that embolism refilling can occur in tree species when plants are actively transpiring and under negative water potentials. Although we should be aware that the air injection method may cause artificial conditions that do not exist in nature and may result in artifacts that potentially skew our assessment of embolism refilling.

<sup>1</sup>Ithaca College, Biology, 953 Danby Road, Center for Natural Sciences, Ithaca, NY, 14850, United States <sup>2</sup>Arnold Arboretum of Harvard University, Jamaica Plain, MA, 02130, USA <sup>3</sup>Harvard University, Department of Organismic and Evolutionary Biology, 16 Divinity Avenue, Biological Laboratories, Cambridge, MA, 02138, USA

## POSTERS

354 BROUWER, MARIEKE\*, GRIFFIN-NOLAN, ROBERT and MELCHER, PETER

### Investigating the role of green light in photosynthesis in *Coleus* spp

We measured the ability of green light to power photosynthesis in two varieties of *Coleus* spp. (Red Head and Henna) grown under high and low-light conditions (900 and 300 mmol m<sup>-2</sup> s<sup>-1</sup>). These plants were able to sequester CO<sub>2</sub> using only green light energy (λ<sub>max</sub> = 550 nm) and shade adapted plants required only 30 μmol m<sup>-2</sup> s<sup>-1</sup> of green-light energy to reach their photosynthetic compensation points. However, even though the high-light adapted plants of both *Coleus* spp. varieties did sequester CO<sub>2</sub> using green-light energy, these plants could not overcome their higher, sun-leaf respiration requirements and only shade-adapted leaves had positive quantum efficiencies when exposed to green light intensities of c.30 μmol m<sup>-2</sup> s<sup>-1</sup> and above. To determine how various qualities and quantities of light affected electron flow through the photosystems of isolated chloroplasts, we measured the rate of reduction of an artificial electron acceptor 2,6-Dichlorophenol-Indophenol (DPIP) and found that the t<sub>1/2</sub> values of DPIP reduction were the same for chloroplasts exposed to either white, red, blue or green light energy measured at three light intensities of 10, 50 and 500 μmol m<sup>-2</sup> s<sup>-1</sup>. We also observed anatomical variations of anthocyanin accumulation within leaves exposed to the two light treatments. With respect to the location of the chlorophyll layer, we observed that the low-light exposed plants had leaves with only a prominent abaxial anthocyanin layer and sun adapted plants had leaves with both an intense adaxial and abaxial anthocyanin layers. From the fact that anthocyanins absorb green light and that the sun-adapted leaves could not use green light energy to effectively power photosynthesis, we hypothesize that the prominent adaxial anthocyanin layer effectively absorbed, and thus blocked green light from reaching the chloroplast layer. The mechanism of using green light to effectively drive photosynthesis in the shade-adapted leaves is still unclear and under investigation. However, we suspect that carotenoids and xanthophylls are playing a major role in this process.

Ithaca College, Biology, 953 Danby Road, Center for Natural Sciences, Ithaca, NY, 14850, United States

**355 STANFIELD, RYAN\*<sup>1</sup>, EWERS, FRANK<sup>2</sup>, BOBICH, EDWARD<sup>3</sup> and BOZAK, KRISTEN<sup>1</sup>**

### **Methods for Testing the Presence of Cadmium in Cystoliths of *Ruellia tuberosa***

The tropical herb *Ruellia tuberosa* was subjected to various concentrations of cadmium to determine if its calcium carbonate cystoliths are able to sequester heavy metals. Seeds of *R. tuberosa* were grown on standard tissue culture media for two weeks, then transferred to cadmium infused media and left to grow for an additional two weeks. Tissue culture media contained standard nutrient concentrations with the addition of 1mg/l of the cytokinin Benzyl Adenine Purine (BAP) as well as 1mg/ml of the auxin Naphthalene Acetic Acid (NAA). As a control, another set of *R. tuberosa* seeds were transferred to the standard tissue culture media after two weeks of growth, instead of the cadmium media. Cystoliths were then separated from leaves by blending in absolute ethanol, then the blended solution was strained through cheesecloth. The heavier cystoliths descended to the bottom of the collecting flask, which allowed for the removal, by pipette, of the lighter dissolved leaf solution. The captured cystoliths and dissolved leaf solutions were then sent to California State University, Long Beach for qualitative confirmation of cadmium, using Inductively Coupled Plasma Mass Spectrometry (ICP-MS).

<sup>1</sup>California State Polytechnic University, Pomona, Biology, 3801 West Temple Avenue, Pomona, CA, 91768, USA<sup>2</sup>California State Polytechnic University, Pomona, Department Of Plant Biology, 3801 West Temple Avenue, Pomona, CA, 91768, USA<sup>3</sup>California State Polytechnic University, Pomona, 3801 W. Temple AVE, Pomona, CA, 91768, USA

**356 MEHTA, DR. MANJARI\*<sup>1</sup> and SAXENA, DR. O. P.<sup>2</sup>**

### **Evaluation of photosynthetic and yield performance by using presoaking seed treatments of plant growth regulators on two different chick pea cultivars**

Grain legumes are important source of protein. Chick pea (*Cicer arietinum* L.) is one of the most important legume crop of India. The yield of this crop is very poor. The efficiency of assimilation of CO<sub>2</sub> and crop yield is closely related. Photosynthesis is the crucial process involved in plant growth, development and yield of any crop plant. Significant use of Plant Growth Regulators (PGRs) in the form of presoaking seed treatments showed enhanced plant growth and productivity. Different plant growth regulators (PGRs) namely, Gibberellic acid (GA<sub>3</sub>), Caffeic acid (CA), and distilled water (DW) are considered for the experiment. Two

different chick pea cultivars namely, ICCV 4 and Gujarat - 2 were taken as experimental seed material. Different parameters in relation to photosynthesis have been taken into account to estimate the relationship between photosynthesis activity and plant growth regulators under field conditions. The growth and yield data were collected. Plant growth regulators and distilled water showed its influence on both the cultivars. PGRs seed soaking treatments showed improvement in vegetative growth and reproductive growth. The maximum photosynthetic active radiation (PAR) and internal CO<sub>2</sub> were observed at 75 days after sowing in Gujarat - 2 with presoaking treatments of Caffeic acid. ICCV 4 also showed similar trend and resulted in maximum yield.

<sup>1</sup>340, Mill Road, Apt. # 609, Toronto, ON, M9C1Y8, Canada<sup>2</sup>

**357 MEHTA, DR. MANJARI\* and SAXENA, DR. O. P.**

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358 RATNAPRABHA,  
RATNAPRABHA\*<sup>1</sup>, PINSON, SHANNON<sup>2</sup>,  
SALT, DAVID<sup>1</sup> and TARPLEY, LEE<sup>3</sup>

### Comparative ionomes of rice leaves and seeds

The project is investigating the possibility of using the mineral (ionomics) composition of rice (*Oryza sativa* L.) seedling leaves to predict varieties that accumulate large amounts of certain minerals in their seeds. This information will be used for improving our understanding of the mineral physiology of rice and other plants, and for genetically improving the nutritional value of rice grain. In 2007 and 2008, preliminary field trials were conducted on 1600 varieties from the USDA world germplasm collection. These flooded and unflooded trials identified rice varieties with varying levels of seed mineral composition. The objective of the presented study was to establish correlations across varieties between seedling-leaf and seed mineral contents such that leaf data could be used to predict seed content for certain minerals, with an initial emphasis on K, Fe, Zn and Mo. This would greatly accelerate the selection process for desirable seed mineral traits. The 40 varieties selected for their extreme seed mineral composition were grown in an outdoor potted plant study in 2010. All 40 varieties were planted in 7-10 day intervals to provide on a single sampling date, plants of a wide range of developmental stages. Leaf tips (5cm) for ionic analysis were collected from the most recently fully emerged leaf. Rice varieties from Malaysia (GSOR accessions 310354, 310355, 310356, 311643 and 311743) with high seed Mo also displayed high leaf Mo indicating that leaf data can be used to predict seed Mo. However, rice varieties with high seed K, Fe and Zn did not show any such correlation. The high seed and leaf Mo in these Malaysian varieties is hypothesized to be due to a root-localized trait and to be related to an acid-tolerance mechanism as these Malaysian soils are highly acidic (pH 4.7). Future study will quantify growth and physiology of roots and shoots of varieties varying in Mo content when grown under different pH regimes. Funded by NSF DBI 070111.

<sup>1</sup>University of Aberdeen, Institute of Biological & Environmental Sciences, Cruickshank Building, St. Machar Drive, Aberdeen, AB24 3UU, UK<sup>2</sup>U.S.D.A.-A.R.S, 1509 Aggie Drive, Beaumont, Texas, 77713, USA<sup>3</sup>Texas AgriLife Research, 1509 AGGIE DR, BEAUMONT, TX, 77713, USA

359 BORER, CATHERINE\* and SAPP,  
SARAH GRACE

### Phenology of foliar calcium accretion and partitioning in flowering dogwood (*Cornus florida* L.)

Flowering dogwood (*Cornus florida* L.) is an important understory tree species that is thought to enhance ecological calcium (Ca) cycling and soil Ca availability through high foliar Ca content and rapid leaf litter decomposition. Ca is an essential macronutrient in plants, important for stabilizing the structure of cell walls and plasma membranes. It is also a ubiquitous intracellular second messenger, helping plants to sense and physiologically respond to numerous internal and external environmental cues. Previous research demonstrated that analyses of total foliar Ca concentrations in red spruce trees (*Picea rubens* Sarg.) are not always consistent with a plant's true physiological Ca status because they can be dominated by a chemically sequestered form that is not readily available for cellular processes. In contrast, analyses of specific foliar partitions are more closely tied to Ca-dependent processes such as signal transduction. To further develop our mechanistic understanding of the role of flowering dogwood trees in ecological Ca cycling, we investigated the phenological patterns of Ca partitioning and sequestration in the foliage of flowering dogwood. Grab samples of foliage were collected at 2-3 week intervals during an entire growing season, at a forested site in northwest Georgia. Foliage was rinsed, flash-frozen, freeze-dried, ground to a fine powder, and tested for three physiologically relevant pools of foliar Ca, using sequential acidic extractions. We found that flowering dogwood preferentially partitions Ca into the more labile and physiologically accessible pools of foliar Ca as Ca accumulates throughout the growing season, with minimal accumulation of sequestered Ca. This is in contrast to other species, such as red spruce, which sequesters Ca into a physiologically unavailable form once a sufficiency threshold has been reached, and white oak (*Quercus alba* L.), in which much of the foliar Ca is sequestered in a relatively unavailable form. This work helps elucidate a mechanism by which flowering dogwood can enhance Ca cycling in forested systems.

Berry College, Biology, P.O. Box 490430, Mount Berry, GA, 30149,

360 TRAN, CUU BAO CHAU  
FLORENCE and LALIBERTE, SYLVIE\*

**pH<sub>i</sub> changes in larch protoplasts over 33.5h of culture, as analysed with flow cytometry and using *in vitro* and *in situ* calibration of C-SNARF-1**

Many processes are regulated by intracellular pH and SNARF indicators are frequently used for pH<sub>i</sub> determination. Probes have been calibrated *in vitro* and *in situ* for confocal microscopy or spectrofluorometry and shown to behave differently once loaded into cells. This has generally been attributed to interactions with intracellular components generating over- or underestimations of pH<sub>i</sub>. We compared *in situ* and *in vitro* calibrations of C-SNARF-1 AM using flow cytometry. The first was performed with nigericin, while an *in vitro* calibration of the probe embedded in agarose pieces and de-esterified by porcine esterase was devised. Reproducibility was evaluated for both methods. The experimental system consisted of hybrid larch protoplasts, isolated from embryogenic suspensions and analysed at 2-3 days intervals over a 33.5h culture period. The experiment was repeated once and each sampling sequence involved two protoplast isolations. When compared, calibration curves showed pK<sub>a</sub> shifts and *in situ* curves differed more from each other than *in vitro* ones. pH<sub>i</sub> estimations during the first 21h showed a change from 6.26 to 6.89 when *in situ* calibration equation was used while values differed from 0.004 to 0.32 unit with *in vitro* equation. Following this alkalization, pH<sub>i</sub> kept mostly over neutral value and fluctuated slightly; estimates from *in situ* and *in vitro* equations differed from 0.10 to 0.19 unit. As mentioned for other species, initial acidic values could reflect intracellular acidification caused by cell incubation in the digestion medium (pH 5.8) during protoplast preparation, while subsequent alkalization might correspond to gradual pH<sub>i</sub> recovery towards homeostasis. The tendency towards a smaller amplitude in pH<sub>i</sub> changes observed after 23h of culture could be attributable to tighter pH<sub>i</sub> regulation. We cannot ascertain which, of *in situ* or *in vitro* calibration, generated better estimations of real pH<sub>i</sub>. However, the simultaneous use of both approaches allows some evaluation of the representativity of pH<sub>i</sub> values, through the range of variation between estimates from *in situ* and *in vitro* calibrations.

University of Quebec in Montreal, Biological sciences, C.P. 8888, Succ. Centre-Ville, Montreal, Quebec, H3C3P8, Canada

361 JORDON-THADEN, INGRID<sup>1</sup>,  
FACIO VICCINI, LYDERSON<sup>2</sup>, COMBS,  
JOSEPH ANTHONY<sup>\*1</sup>, CHESTER,  
MICHAEL<sup>1</sup>, SOLTIS, DOUGLAS<sup>1</sup> and  
SOLTIS, PAMELA<sup>3</sup>

**Physiological comparisons of two recently formed allotetraploid *Tragopogon* (Asteraceae) species and their diploid parents**

This study seeks to understand how polyploidy affects phenotypic variation in natural and synthetic allotetraploids (*Tragopogon mirus* and *Tragopogon miscellus*) through comparison with their diploid parents (*T. dubius*, *T. pratensis*, and *T. porrifolius*). This system is ideal to study speciation processes, due to the recent formation of these two polyploids. Easily definable phenotypic characteristics, such as plant height (cm), total leaf number, and photosynthetic efficiency, were measured and will be correlated to genetic data from the same set of plants in a parallel study. *Tragopogon* plants (diploid and tetraploid) were placed in a temperature and light controlled growth chamber in randomized blocks. Over a period of a month, several discrete growth measurements were taken. Growth rate data were taken by measuring the longest leaf on a given plant and the number of healthy, green leaves on the plant. Over a period of two weeks, the physiological potential for photosynthesis of each plant was taken with a fluorometer to determine the photosynthetic efficiency of photosystem II. The synthetic and natural allotetraploids appear to have similar growth rates and photosynthetic capacity. The allotetraploids compared to their diploid parents reach maximum height quicker and are more photosynthetically efficient. When compared by maximum leaf growth, the allotetraploids *T. miscellus* and *T. mirus* exhibit a growth pattern comparable to that of the diploid parent *T. pratensis* or *T. porrifolius*, respectively, and are divergent from their shared *T. dubius* parent. These results suggest that allotetraploid species are more robust and vigorous in certain phenotypic traits, such as the ability to perform photosynthesis, than their parents, but in other physical characteristics the allotetraploids tend to exhibit characteristics of a single parent.

<sup>1</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA <sup>2</sup>Instituto de Ciências Biológicas, Universidade Federal de Juiz de Fora, Departamento de Biologia, Juiz de Fora, Minas Gerais, 36036-900, Brazil <sup>3</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA

362 KERR, LILA DALE\*<sup>1</sup> and GRAVATT, DENNIS<sup>2</sup>

### The effects of ultraviolet light on anthocyanin accumulation in the adventitious roots of *Sedum wrightii*.

Several studies have supported the idea that anthocyanin accumulation may be a possible protection mechanism in plants against DNA damage caused by ultraviolet light. The following study explores the accumulation of anthocyanins in the adventitious root tips of *Sedum wrightii* using various treatments of ultraviolet light. The root tips were grown under four separate sets of conditions: UVA, UVA + low UVB, UVA + high UVB, or the control. Afterwards, the anthocyanins were extracted using acidified ethanol and centrifugation. The absorption of the extract was taken using a Beckman spectrophotometer. The values were converted to nanomoles per milligram of fresh weight and then the groups were compared using data analysis software. The results supported the hypothesized differences that occurred between the groups. The anthocyanin concentrations were significantly higher in the UVB treatments than the other groups.

<sup>1</sup>Stephen F. Austin State University, Biology, PO. Box 13003, Nacogdoches, TX, 75962, USA<sup>2</sup>Stephen F. Austin State University, Dept of Biology-Po Box 13003, Nacogdoches, TX, 75961, USA

## ORAL PAPERS

363 NESTER-HUDSON, JOAN

### Spore age as a factor influencing spore viability and gametophyte development in the fern, *Anemia mexicana*

*Anemia mexicana* is a homosporous fern with non-green spores. Nongreen fern spores usually have longer viability than green fern spores. This study investigated spore viability and gametophyte development in this fern using spores collected from seven different years between 1978 (32 years) and 2003 (7 years). Spores had been stored in glass vials at 4C except during transport. Spores were dusted onto the surface of agar-solidified mineral medium in plastic petri dishes and placed under fluorescent lights at room temperature. Percent spore germination was determined with a dissecting microscope after 9 days. A dissecting microscope was used to monitor gametophyte growth and development for 50 days. All ages of spores began germinating at 4-5 days after spore sowing with protrusion of the rhizoid. All spores, including those from 1978, had approximately 75-90% spore germination at 9 days. At nine days, most gametophytes were two-dimensional with an elongate rhizoid. A lateral meristem was initiated by day 14

and this meristem shifted to the terminal position after several days. Unicellular marginal trichomes were produced after development of the meristem. Antheridia began forming at day 22 and were abundant by day 32 on male gametophytes. Archegonia were visible on separate gametophytes at 38 days. Gametophyte growth and development varied within each age of spores but there was essentially no difference in gametophyte growth and development when *Anemia mexicana* spores were 7 to 32 years old and had been stored at 4 C.

SHSU/DEPT OF BIO SCI, PO BOX 2116, HUNTSVILLE, TX, 77341-2116, USA

364 CHAU, MARIAN\*<sup>1</sup>, WALKER, LAWRENCE<sup>2</sup> and MEHLTRETER, KLAUS<sup>3</sup>

### The invasive Australian tree fern alters soil and plant nutrient dynamics in Hawaii

Tree ferns that have higher leaf N and P content than co-occurring plant species have strong potential to influence nutrient cycling. The native *Cibotium glaucum* tree fern, a keystone species in Hawaiian forests, is displaced by *Sphaeropteris cooperi*, the non-native Australian tree fern. *Sphaeropteris cooperi* invades intact forests, producing more leaves that grow faster, contain more N and P, and decompose faster than *C. glaucum* leaves. Our experiment tested the effects of native and non-native tree fern leaf litter addition on the growth and nutrient content of four native angiosperm species in forest (high-fertility) and landslide (low-fertility) soils. Leaf litter of both types inhibited growth initially in all species, but subsequent responses were species-specific. Relative growth rates were higher in the faster-growing *Carex wahuensis* and *Hibiscus arnottianus* with *S. cooperi* litter, especially in landslide soil. Leaf N in *C. wahuensis* was highest with forest soil and *S. cooperi* litter, as expected, but other leaf nutrient responses showed some evidence of nutrient immobilization from litter addition. Several growth measures were highest with forest soil and *S. cooperi* litter, indicating that N availability is the strongest driver of growth. Our results show that *S. cooperi* can alter nutrient cycling in Hawaiian plants, sometimes with positive effects, but in forest environments it eventually out-competes other species by the same means with which it initially facilitates them. Because *S. cooperi* is such a pervasive threat to *Cibotium* and native forests, our results support continued efforts to eradicate this invasive tree fern.

<sup>1</sup>University of Hawaii at Manoa, Department of Botany, 3190 Maile Way, Room 101, Honolulu, HI, 96822, USA<sup>2</sup>University of Nevada Las Vegas, School of Life Sciences, 4505 Maryland Parkway, Las Vegas, NV, 89154, USA<sup>3</sup>Instituto de Ecología, A.C., Red de Ecología Funcional, Carretera antigua a Coatepec No. 351, El Haya, Xalapa, Veracruz, 91070, México

365 MATOS, FERNANDO\*<sup>1</sup>, LABIAK,  
PAULO HENRIQUE<sup>2</sup> and AMORIM,  
ANDRE<sup>3</sup>

### The ferns and lycophytes of a montane tropical forest in southern Bahia, Brazil

The Serra Bonita Mountain Range is located in southern Bahia State, northeastern Brazil, and occupies an area of approximately 7,500 ha. The Serra Bonita Reserve encompasses the last remnants of old-growth forest from that region, protecting about 2,000 ha of land (at 300 to 1,080 m a.s.l.) in the center of this mountain range. A floristic survey of the ferns and lycophytes of this Reserve was carried out from 2005 to 2009 in areas above 600 m, resulting in the collection of 182 species, distributed among 67 genera and 23 families. Ferns comprised 173 species in 64 genera and 21 families, while the lycophytes comprised nine species in three genera and two families. Approximately 25 percent of these species were recorded for the first time in Bahia State or northeastern Brazil (44 new records). Special mention is given to *Asplenium truncorum* (Aspleniaceae), *Megalastrium indusiatum* (Dryopteridaceae), and *Thelypteris beckeriana* (Thelypteridaceae), which were described for the first time from recent collections in the study area. The Serra Bonita Reserve also harbors the only known population of *Terpsichore asplenifolia* (Polypodiaceae) in Brazil.

<sup>1</sup>The New York Botanical Garden, Pfizer Lab., 2900 Southern Blvd., Bronx, NY, 10458-5153, USA<sup>2</sup>Universidade Federal do Paraná, Departamento de Botânica, Curitiba, Paraná, 81531-980, Brazil<sup>3</sup>Universidade Estadual de Santa Cruz, Ciências Biológicas, Ilhéus, Bahia, 45662-900, Brazil

366 LI, FAY-WEI<sup>1</sup>, KUO, LI-YAUNG<sup>2</sup>,  
ROTHFELS, CARL<sup>3</sup>, EBHARA, ASTUSHI<sup>4</sup>,  
CHIOU, WEN-LIANG<sup>5</sup>, WINDHAM,  
MICHAEL<sup>3</sup> and PRYER, KATHLEEN\*<sup>6</sup>

### *rbcl* and *matK* earn a thumbs up as the core DNA barcode for ferns

DNA barcoding will revolutionize our understanding of fern ecology, most especially because the accurate identification of the independent but cryptic gametophyte phase of the fern's life history—an endeavor previously impossible—will finally be feasible. In this study, we assess the discriminatory power of the core plant DNA barcode (*rbcl* and *matK*), as well as alternatively proposed plant barcodes (*trnH-psbA* and *trnL-F*), across all major fern lineages. We also present plastid barcode data for two genera in the hyperdiverse polypod clade—*Deparia* (Woodsiaceae) and the *Cheilanthes marginata* group (in the process of being segregated as a new genus of Pteridaceae)—to further illustrate the resolving power of these loci. Our results

clearly demonstrate the value of *matK* data, previously unavailable in ferns due to a major rearrangement of the chloroplast genome. With its high sequence variation, *matK* complements *rbcl* to provide a two-locus barcode capable of distinguishing most species that have evolved through divergent evolution. With sequence variation comparable to *matK*, *trnL-F* appears to be a suitable alternative barcode region in ferns, and perhaps should be added to the core DNA barcode for plants. In contrast, *trnH-psbA* shows dramatically reduced sequence variation for the majority of ferns. This is likely due to the translocation of this segment of the chloroplast genome into the inverted repeat regions, which are known to have a highly constrained substitution rate. Our study provides the first endorsement of the two-locus barcode (*rbcl* + *matK*) in ferns, and favors *trnL-F* over *trnH-psbA* as a potential back-up locus.

<sup>1</sup>Duke University, Biology, Science Drive, Durham, NC, 27708, USA<sup>2</sup>National Taiwan University, Institute of Ecology and Evolutionary Biology, Taipei, 10617, Taiwan<sup>3</sup>DUKE UNIVERSITY, Department Of Biology, BOX 90338, DURHAM, NC, 27708, USA<sup>4</sup>National Museum of Nature and Science, Department of Botany, Tsukubashi, Ibaraki, Japan<sup>5</sup>Taiwan Forestry Research Institute, Division of Botanical Garden, Taipei, 10066, Taiwan<sup>6</sup>Duke University, Science Drive, Durham, NC, 27708-0338, USA

367 HOOPER, ELISABETH\*<sup>1</sup>,  
YATSKIEVYCH, GEORGE<sup>2</sup>, HUIET,  
LAYNE<sup>3</sup>, WINDHAM, MICHAEL<sup>3</sup> and  
PRYER, KATHLEEN<sup>3</sup>

### Into or out of Africa? What do molecular data reveal about the identity and biogeographic origin of *Aleuritopteris farinosa* (Forssk.) Fee (Pteridaceae)?

*Aleuritopteris farinosa* is the type species of *Aleuritopteris* and yet it has a geographic distribution that is atypical for the genus. Although most of the 40+ species in *Aleuritopteris* have a Sino-Himalayan distribution, *A. farinosa* is found in continental Africa (extending to Yemen, Madagascar, and La Reunion) and the Americas (Mexico to S. America). As part of an ongoing molecular phylogenetic study of *Aleuritopteris* using three plastid gene markers (*rbcl*, *atpA*, and *trnGR*) we have been investigating the relationship between *A. farinosa* and its Asian congeners, as well as the relationship between Old and New World elements within *A. farinosa* itself. Results thus far confirm that *A. farinosa* is nested within a monophyletic group of approximately 14 species informally called the *A. farinosa* complex. At one time this clade was treated as a single, broadly-distributed, heterogeneous species (*A. farinosa* sensu lato), but more recently the Asian elements have been segregated as distinct species and *A. farinosa* sensu stricto has been reserved for the African/American taxon. There has been controversy, however, concerning the true identity of *A. farinosa* s.s. This taxon is morphologically quite variable across its range, leading some to recognize segregate

taxa. Moreover, there are at least two known cytotypes in East Africa (a triploid apomict and a sexual tetraploid), suggesting the occurrence of reticulate evolution in the group. To investigate this situation, we have been evaluating the genetic relationship among Old and New World elements of *A. farinosa* s.s. One surprising early result suggests that New World collections referred to *A. farinosa* are more closely related to certain Asian species than they are to collections of *A. farinosa* from Africa. Here we report the results of additional sampling within *A. farinosa* s.s. and discuss their significance with respect to taxonomic circumscription, phylogenetic position, and biogeographic origin of *A. farinosa*.

<sup>1</sup>Truman State University, Department of Biology, Kirksville, MO, 63501, USA<sup>2</sup>Missouri Botanical Garden, PO Box 299, St. Louis, MO, 63166-0299, USA<sup>3</sup>Duke University, Department of Biology, Durham, NC, 27708, USA

### 368 ZHANG, LI-BING\*<sup>1</sup>, HE, HAI<sup>2</sup> and GAO, XIN-FEN<sup>3</sup>

#### Diversity, Cryptic speciation, and phylogeny of the fern genus *Polystichum* (Dryopteridaceae): A large-scale analysis.

One of the most exciting examples of apparently rapid speciation in ferns is the genus *Polystichum* (Dryopteridaceae). As one of the largest genera of ferns, *Polystichum* contains ca. 400 species. This genus is nearly cosmopolitan, but the species are most numerous in subtropical regions, with the highest diversity clearly in Asia, especially in southwestern China and adjacent regions. While more than half of the ca. 400 species evolved recently as result of fast radiation, little is known about the species of *Polystichum* in limestone areas, especially in karst caves, in southern China. There are two competing hypotheses about the ages of cave species: old relics among different caves vs. young radiation. Molecular data placed cave species in younger lineages suggesting that they are new endemics. Most notably, several morphologically and palynologically different cave species formed well-supported monophyletic groups. These species occur geographically in adjacent areas. Are these hard or soft polytomies? More molecular data will be added to answer this question. Molecular data also help identify some cryptic species unrecognizable using morphological data only.

<sup>1</sup>Missouri Botanical Garden, Science and Conservation, P.O. Box 299, St. Louis, MO, 63166, USA<sup>2</sup>Chongqing Normal University, College of Life Sciences, Shapingba, Chongqing, 400047, China<sup>3</sup>Chengdu Institute of Biology, Chinese Academy of Sciences, The ECORES Lab, P.O. Box 416, Chengdu, Sichuan, 610041, China

### 369 MCHENRY, MONIQUE\*<sup>1</sup> and BARRINGTON, DAVID<sup>2</sup>

#### Investigating morphological diversity of Andean *Polystichum* (Dryopteridaceae): seeking explanations for incongruence between sequence variation and morphological variation

The northern and central Andes represent the third highest center of endemism in the fern genus *Polystichum* (Dryopteridaceae). Previous work on *Polystichum* in South America has circumscribed taxa based on morphological characters alone. We explored patterns of both sequence and morphological variation in two sister subclades of monophyletic Andean *Polystichum*, the *orbiculatum* subclade and the *montevidense* subclade. Our results from phylogenetic analyses based on plastid and nuclear markers suggest an interesting paradox: one subclade exemplifies cryptic speciation with morphologically similar taxa that exhibit high sequence variation, whereas the other subclade exhibits the inverse - low sequence variation with high morphological variation. From these results we conclude that geographically disjunct entities in the *montevidense* subclade exhibit identical morphologies despite significant sequence divergence due to convergent evolution of morphological characters, leading to underdescription of species. In the *orbiculatum* subclade, by contrast, high morphological variation correlates to different ecological and developmental factors, leading to an abundance of names pertaining to a single widespread taxon. With our improved understanding of morphological variation in Andean *Polystichum* we will move on to exploring the patterns of speciation in the northern and central Andes.

<sup>1</sup>University of Vermont, Plant Biology, Jeffords Hall, Burlington, VT, 05405, United States<sup>2</sup>University of Vermont, DEPT OF PLANT BIOLOGY, Burlington, VT, 05405-0086, USA

### 370 RANKER, TOM A.\*<sup>1</sup> and SUNDUE, MICHAEL A.<sup>2</sup>

#### Molecular phylogenetics of grammitid ferns: global biogeographic perspectives

Grammitid ferns comprise a monophyletic group of 900 species of tropical, forest-dwelling epiphytes. One of the long-standing challenges in the study of grammitid ferns has been the circumscription of genera, with some authors recognizing a single genus and others up to 24. Molecular phylogenetic studies have shown that several large genera occurring mostly in the Paleotropics (*Ctenopteris* s.l., *Grammitis* s.l.) or mostly in the Neotropics (*Lellingeria*, *Terpsichore*) were polyphyletic, necessitating nomenclatural innovations at the generic level. Although recent taxonomic and

phylogenetic studies have made significant progress in delineating primarily Neotropical genera, relatively little progress has been made in the Paleotropics, which holds about 2/3 of the diversity of the clade. We have conducted phylogenetic analyses of DNA sequence data on 295 accessions of grammitid ferns representing 253 species. Neotropical species account for 161 of the accessions and Paleotropical account for 134. These analyses were based on the plastid DNA sequences of *rbcl*, *atpB*, and *trnL-trnF* intergenic spacer. There are several important features of our analyses: 1) A Paleotropical clade was supported as monophyletic (posterior probability support of 0.92). This clade is estimated to comprise ~500 species (two-thirds of all grammitids). It is restricted to Asia and the Pacific except for a single dispersal to Southern Chile (*Grammitis magellanica*). African and Madagascan species are not part of this clade, they are all disjunctions from otherwise Neotropical genera (*Alansmia*, *Ceradenia*, *Enterosora*, *Melpomene*, *Stenogrammitis*, and *Zygophlebia*) or from the circum-austral *Grammitis* s.s.; 2) Several Paleotropical genera, as sampled so far, were supported as monophyletic (i.e., *Calymmodon*, *Chrysogrammitis*, *Dasygrammitis*, *Scleroglossum*, and *Xiphopterella*); but, 3) several genera were either clearly not monophyletic (e.g., *Ctenopterella*, *Grammitis*, *Prosaptia*, *Micropolypodium*, *Radiogrammitis*, and *Tomophyllum*) or there was insufficient resolution to infer relationships or circumscriptions (e.g., *Oreogrammitis* and *Themelium*); 4) The three plastid sequences analyzed provided less phylogenetic resolution among Paleotropical taxa than among Neotropical taxa, although some of the lack of resolution may be due to missing data.

<sup>1</sup>University of Hawaii at Manoa, Department of Botany, 3190 Maile Way, Room 101, Honolulu, HI, 96822, USA<sup>2</sup>University of Vermont, Department of Plant Biology, 111 Jeffers Hall, Burlington, VT, 05405, USA

371 TRIPP, ERIN\*<sup>1</sup>, LENDEMER, JAMES<sup>2</sup> and HARRIS, RICHARD<sup>1</sup>

### How known is well-known? Progress in lichenology in Great Smoky Mountains National Park.

The southern Appalachians represent a diversity hotspot for many groups of organisms, including lichens. Although the region, like the rest of eastern North America, has been subjected to considerable anthropological change, a large portion of it has been protected at the federal, state, and local level resulting in contiguous areas of natural habitat that include the largest and most significant tracts of old-growth forest in eastern North America. Lichenological data from our previous studies in the southern Appalachians (e.g., Gorges State Park, NC) indicated that much is yet to be learned in an area of the world that is supposedly "well-known" biologically. As such, we initiated an inventory of the lichens of Great Smoky Mountains National Park

(GSMNP) in 2007. Since then, over the course of only short five collecting trips (2,500 cumulative collections), we have added > 170 new lichen records to the Park's checklist (including several species and two genera new to science). Previous Park checklists were also revised. These new reports collectively expand the known lichen biota of GSMNP to include between 603 and 779 taxa, an increase of ~33-46% from previous checklists, rendering it the most lichenologically diverse National Park in the United States.

<sup>1</sup>New York Botanical Garden, 200th Street and Southern Blvd, Bronx, NY, 10458, USA<sup>2</sup>New York Botanic Garden, 200th Street And Southern Blvd, Bronx, NY, 10458, USA

ORAL PAPERS

372 TUOMINEN, LINDSEY K.\*<sup>1</sup>,  
PAYYAVULA, RAJA S.<sup>2</sup>, HARDING, SCOTT  
A.<sup>1</sup> and TSAI, CHUNG-JUI<sup>3</sup>

**Perturbation of *Populus* Phenylpropanoid  
Metabolism in Suspension Cell Cultures**

*Populus* secondary metabolism is characterized by a diversity of phenylpropanoid compounds that can collectively account for up to 30% of leaf dry mass. The various classes of these compounds are thought to derive from separate, potentially competing biosynthetic branch pathways. To develop a better understanding of phenylpropanoid partitioning and the impact of this pathway on primary metabolic processes, we subjected heterotrophic suspension cell cultures of *P. tremuloides* to a series of feeding experiments. Methyl jasmonate (MeJA) was used as a defense elicitor to stimulate phenylpropanoid metabolism with varying constraints in the core pathway imposed by one of three metabolic inhibitors: piperonylic acid (PIP) for cinnamate-4-hydroxylase,  $\alpha$ -aminooxy- $\beta$ -phenylpropionic acid (AOPP) for phenylalanine ammonia lyase, and methylendioxy-cinnamic acid (MDCA) for 4-coumaroyl:CoA ligase. Cells were sampled 48 h after treatment and analyzed by metabolite profiling using GC-MS and LC-MS, as well as by colorimetric quantification of condensed tannins. Core phenylpropanoid metabolites showed changes broadly consistent with expected enzyme inhibition, with increases in phenylalanine in AOPP-treated cells and cinnamic acid in PIP-treated cells. Interestingly, MDCA-treated cells did not show increases in coumaric acid as expected, but cinnamic acid levels were strongly increased, suggesting a possible feedback mechanism in the pathway. Flavonoid derivatives, including condensed tannins, generally showed additive rather than interactive effects between elicitation and inhibition. Several amino acids also showed strong increases under AOPP treatment, while PIP and MDCA treatments had only subtle impacts. Citric acid cycle metabolites did not appear to be strongly affected by the inhibitors but did respond to elicitation. Overall, the results provide metabolic evidence for possible linkage between phenylpropanoid and amino acid metabolism, supporting previous suggestions of cross-talk between carbon and nitrogen metabolism via phenylalanine-N cycling.

<sup>1</sup>The University of Georgia, Warnell School of Forestry & Natural Resources, 180 E Green St, Athens, GA, 30602, USA<sup>2</sup>Michigan Technological University, School of Forest Resources & Environmental Science, 1400 Townsend Drive, Houghton, MI, 49931, USA<sup>3</sup>The University of Georgia, Department of Genetics/Warnell School of Forestry & Natural Resources, 180 E Green St, Athens, GA, 30602, USA

373 MAJETIC, CASSIE\*<sup>1</sup>, RAGUSO,  
ROBERT A.<sup>2</sup> and LEVIN, DONALD A.<sup>3</sup>

**All in the family: assessing floral pigment-  
floral scent associations in the genus *Phlox***

Floral color and floral scent are two characteristics used by plants to attract pollinators. Until recently, biologists have assumed that color and scent evolved separately to match pollinator preference. However, some scent compounds (benzenoids and phenylpropanoids) are produced by branches of the same biochemical pathways that produce anthocyanin floral pigments, suggesting the potential for pleiotropic associations between them. Other scent compounds, such as terpenes, have no direct biochemical linkage to anthocyanin synthesis and should not co-vary with pigment. We studied six species from the genus *Phlox* (Polemoniaceae) and a related outgroup species (*Polemonium caeruleum*), examining floral scent composition and emission rates from pigmented vs. white (no visible anthocyanin) cultivars for each species. Specifically, we predicted that white and pigmented cultivars should differ significantly in benzenoid/phenylpropanoid production regardless of species, while the production of terpenoids and other scent compounds should show no specific pattern related to color. Our results suggest mixed support for this hypothesis. We do find substantial qualitative and quantitative differences between conspecific color morphs for most species. Relative abundance of such benzenoid/phenylpropanoid compounds as methyl salicylate and 3-hydroxy-4-phenyl-2-butanone account for some of the differences in scent production observed between pigmented and white cultivars of *Phlox stolonifera* and *Phlox bifida*, but these differences were not in the same direction for both species. Moreover, other differences between cultivars for all examined species were attributable to differences in terpenoid abundance, against our predictions. Assessment of emission rates of individual compounds yields a similar pattern - most differences between cultivars showed increased release of some benzenoids or terpenoids with concurrent decreases in other compounds from the same biochemical category. These data suggest that patterns of scent emission in this genus are not primarily governed by tradeoffs with pigmentation; rather, species identity is more important for defining floral scent profiles.

<sup>1</sup>Saint Mary's College, Department of Biology, State Route 933, Notre Dame, IN, 46556, USA<sup>2</sup>Cornell University, Department of Neurobiology and Behavior, Room W355, Seeley G Mudd Hall, 215 Tower Road, Ithaca, NY, 14853, USA<sup>3</sup>The University of Texas at Austin, Section of Integrative Biology, 1 University Station C0930, Austin, TX, 78712, USA

374 ROSE, JANNA

### Isolation of Ellagic acid from the Bioassay-Guided Fractionation of Methanolic Crude Extracts of *Rosa canina* L. Galls

During the spring of 2009, I conducted ethnobotanical fieldwork with Turkish villagers and gathered information on plant-based remedies for diarrheal diseases. After evaluating 15 of the anti-diarrheal plants for bacterial inhibition, the crude methanolic extracts of galls from *Rosa canina* L. (dog rose) showed the lowest MIC's (from 4 to 64ug/ml) against twelve bacterial strains that infect the human intestinal tract. Methanolic extracts of *R. canina* fruits were less potent (from 128 to 512ug/ml). Using an Alamar Blue Cytotoxicity Assay, I tested methanolic gall and fruit extracts for cytotoxic properties and found the extracts to have acceptable viability percentages with liver, prostate, and skin cancer cell lines. Finally, *R. canina* fruit and gall extracts were fractionated by high-performance liquid chromatography (HPLC) and analyzed via bioassay-guided fractionation techniques. Using Mass Spectrometry with ElectroSpray Ionization (MS-ESI) the fraction with activity was shown to contain ellagic acid. I repeated the bioassay with standard ellagic acid and obtained comparable results. Ellagic acid is a known yet under-studied phenolic compound and phytoalexin--a plant defense compound that could be used for human medicines.

Florida International University, Biological Sciences, 11200 SW 8th Street, Owa Ehan 167, Miami, FL, 33199, USA

375 ESPINOSA-MORENO, JUDITH\*<sup>1</sup>, CENTURION-HIDALGO, DORA<sup>2</sup>, BORGES-ARGAES, ROCÍO<sup>3</sup> and MAYO-MOSQUEDA, ALBERTO<sup>1</sup>

### Evaluation of potential antimicrobial activity against *Staphylococcus aureus* of aromatic and medicinal plants essential oils

Food diseases are produced by the consumption of food contaminated with pathogenic bacteria and/or their toxins have been of great interest to public health. *Staphylococcus aureus* is a microorganism particularly virulent that causes a great variety of health conditions including pneumonia, osteomyelitis, endocarditis y bacteremia. Antimicrobial activity of essential oils obtained from dehydrated leaves of seven aromatic and medicinal plants (*Ocimum micranthum*, *Eryngium foetidum* L., *Pimenta dioica* (L.) Merr, *Plectranthus ambonicus* (Lour.) Spreng, *Malvaviscus arboreus* Cav., *Byrsonima crassifolia* (L.) Kunth y *Psidium guajava* L.) was evaluated against *Staphylococcus aureus*. Leaf essential oil was obtained through hidrodestylation in an equipment type Clevenger and the bioautography bioassay carried out in two TLC plaques. One of them was revealed with

fosfomolibdic acid as a reference and contained positive (Amikacine 1%) and negative (hexane) controls. Bacterial presence was observed by intense red coloration and registering the inhibition zone diameters. This chromatographic plaque was compared with the one revealed before for corroborating the presence of compounds with antimicrobial activity. Minimal Inhibitory Concentration (MIC) was determined by visual observation of turbidity presence in the microplaque wells with the addition of 100  $\mu$ L 1% MTT confirming alive bacteria presence by a red coloration. Four essential oils from the evaluated species presented antimicrobial activity against *S. aureus* and the one of *Psidium guajava* L. presented the highest number of active fractions.

<sup>1</sup>Universidad Juarez Autonoma de Tabasco, Division Academica de Ciencias Agropecuarias, Avenida Universidad s/n, Zona de la Cultura, Col. Magisterial, Centro, Villahermosa, Tab, 86040, Mexico  
<sup>2</sup>Universidad Juarez Autonoma de Tabasco, Division Academica de Ciencias Agropecuarias, Avenida Universidad s/n, Zona de la Cultura, Col. Magisterial, Centro, Villahermosa, Tab, 86040, Mexico  
<sup>3</sup>Centro de Investigacion Cientifica de Yucatan, A.C., Calle 43 No. 130, Colonia Chuburna de Hidalgo, Merida, Yuc, 97200, Mexico

376 MEYER, RACHEL\*<sup>1</sup>, WHITAKER, BRUCE<sup>2</sup> and LITT, AMY<sup>1</sup>

### Modifications to the phenolic biosynthesis pathway correlated with domestication in eggplant

Phenolic compounds in fruits and vegetables are well known for having flavorful and health-beneficial properties. Eggplant (*S. melongena* L) contains a wide array of phenolic compounds. In previous analyses, we identified phenolics that differed in their presence/absence or relative amount among fruits of eggplant and related species. Several compounds differed significantly between *S. melongena* and the wild progenitor of eggplant (Asian *S. incanum*/*S. undatum*), and also differed among these and other wild relatives. This study aimed to elucidate how human selection may have modified the complex phenolic biosynthetic pathway to produce different amounts of specific end-products. Fruits from thirty accessions, including Asian eggplant landraces, and representatives of the wild progenitor and wild relatives, were analyzed to determine the relative expression of seven biosynthetic genes in the phenolic pathway using quantitative Real-Time PCR. These data were evaluated for correlations with phenolic profiles generated by high performance liquid chromatography from the same thirty fruits. Key results were the identification of three genes that are coexpressed and whose transcript levels are tightly correlated to the total production of a subset of phenolic compounds, the hydroxycinnamic acid derivatives. This particular group of compounds is of interest because assays have shown that their therapeutic functions align with specific Asian medicinal applications of eggplant. Additionally, several genes were differentially expressed in different species. These results

suggest that gene expression may have been altered as a result of selection for certain medicinal or culinary qualities of eggplant. Results are discussed in the context of early and contemporary uses of eggplant fruits.

<sup>1</sup>The New York Botanical Garden, 200th St and Southern Blvd, Bronx, New York, 10458, USA<sup>2</sup>United States Department of Agriculture, Food Quality Laboratory, 10300 Baltimore Avenue, Bldg 0002, Beltsville, MD, 20705, USA

**377 GUNN, JORDAN\*<sup>1</sup>, ELKINGTON, BETHANY G.<sup>2</sup>, HARTMANN, JOHN F.<sup>3</sup>, SOUTHAVONG, BOUNHONG<sup>4</sup>, SYDARA, KONGMANY<sup>5</sup> and SOEJARTO, DR. DJAJA D.<sup>6</sup>**

### **Preliminary Results of a Hepatotoxicity Literature Screening of Lao Traditional Herbal Medicine**

The indigenous communities of Laos have been using medicine derived from natural sources, primarily plant species, for hundreds if not thousands of years. The continuous use of these species over time is often referenced to be an indication of their safety. However, toxicity remains problematic with herbal medicines. Some herbs may have chronic toxicity that is not noted by common observation, while other toxic herbs may be used in small doses for specific medicinal purposes by experienced practitioners. If herbs of either class become more widely used, without the supervision of experienced practitioners, problems of toxicity may result. In a continuation of studies on the toxicity of Lao traditional medicines, the researchers at the University of Illinois at Chicago's Department of Medicinal Chemistry and Pharmacognosy have critically reviewed a set of over 900 Lao medicinal plant species for hepatotoxicity, as indicated by bioassay and chemotaxonomic analysis using literature and database evaluation techniques. Data on the presence and identity of compounds within plant species which are known to be hepatotoxic, as well as hepatotoxicity studies conducted on these species or related species will be presented.

<sup>1</sup>uc, Medicinal Chemistry and Pharmacognosy, 833 South Wood Street, (M/C 877) Room 325, Chicago, IL, 60612, usa<sup>2</sup>University of Illinois at Chicago, Department of Medicinal Chemistry and Pharmacognosy, 833 South Wood Street (M/C 781), Chicago, IL, 60615, USA<sup>3</sup>Northern Illinois University, Department of Foreign Languages and Literatures, DeKalb, IL, usa<sup>4</sup>Ministry of Health, Institute of Traditional Medicine, Lao pdr, Vientiane, Laos<sup>5</sup>Ministry of Health, Institute of Traditional Medicine, Lao pdr, Vientiane, Laos<sup>6</sup>College of Pharmacy, University of Illinois at Chicago, Chicago, Department of Medicinal Chemistry and Pharmacognosy, 833 S. Wood St., Chicago, IL, 60612, USA

**378 GOYAL, SHAILY\*<sup>1</sup> and RAMAWAT, KISHAN GOPAL<sup>2</sup>**

### **Increased isoflavonoids biosynthesis in cell suspension cultures of a woody legume, *Pueraria tuberosa* grown in shake flasks and bioreactor**

Tubers of *Pueraria tuberosa* (Roxb. ex. Willd.) DC are widely used in various Ayurvedic (ancient Indian system of medicine) formulations, and contain isoflavonoids, viz., puerarin, daidzein, genistein and genistin which are under clinical trials against cancer, osteoporosis and cardiovascular diseases. Plant cell and callus cultures have always been an attractive means for the production of bioactive molecules and attempts have been made to increase their accumulation. The *Pueraria* cell cultures were maintained in MS medium containing 0.1 mg/l 2,4,5-trichlorophenoxyacetic acid (2,4,5-T) and 0.1 mg/l kinetin. The cells were analysed for isoflavonoids content using HPLC. Isoflavonoids accumulation in cell cultures was improved by 48 hours of elicitors' treatment at the stationary phase. Yeast extract, 150 mg/l was optimal for isoflavonoids production yielding 10 mg/l (~11-folds increase) isoflavonoids. Ethrel at 100  $\mu$ M after 48 hours treatment, increased 14-folds (~12 mg/l) of isoflavonoids accumulation. Further, the addition of 1.0 mg/l 6-( $\hat{1}^3, \hat{1}^3$ -Dimethylallylamino) purine(2iP) in maintenance medium resulted in about ~32-folds increase in the production of isoflavonoids. A marked increase in yield of isoflavonoids ~82-folds (80 mg/l) was obtained in cultures grown at 0.1 mg/l morphactin and 5.0 mg/l of 2iP. The cultures were scaled-up to 3L flasks and 2L stirred tank bioreactor. Further, the influence of angiospermic parasite, *Cuscuta reflexa* was studied on isoflavonoids production in cell cultures. The optimized elicitation conditions were used in vessels of varying capacity where maximum yield of ~91 mg/l of isoflavonoids was recorded in a 2 L bioreactor giving productivity of ~4 mg/l/day. The increase in isoflavonoids content was elicitor dose-dependent and can be explored to trigger high yields of isoflavonoids/secondary metabolites in production.

<sup>1</sup>500, Center Grange Road, Apt 74, Monaca, PA, 15061, USA<sup>2</sup>M.L. Sukhadia University, Department of Botany, College of Science, Udaipur, Rajasthan, 313001, India

## POSTERS

## 379 SINKA, BRITTANY\* and MAJETIC, CASSIE

**The effects of fertilizer on floral scent of *Phlox subulata***

Floral scent is one characteristic that has been shown to be important in the survival and reproduction of many plant species, due to its role in manipulating pollinator visitation and behavior. Environmental conditions such as temperature, pollution loads, and humidity have been known to alter floral scent emission patterns; altering floral odor phenotype could potentially change the types of pollinating visitors a plant can attract, and therefore plant reproductive success. However, few studies have explored whether these factors could cause measurable phenotypic plasticity in floral scent emission. This study explores the possibility that floral scent could be plastic in response to fertilization in the species *Phlox subulata*. Fertilizers often contain a significant amount of nitrogen compounds, which are used by plants to synthesize amino acids; benzenoid volatile compounds are derived from one specific amino acid, phenylalanine. Therefore, we predict that plants grown in high soil nitrogen conditions could produce more benzenoid compared to plants grown in low nitrogen conditions. Eight genotypes of *Phlox subulata* were divided into two groups: 4 plants of each genotype were treated with high-nitrogen fertilizer and 4 plants were treated with low-nitrogen fertilizer. Floral scent emission rates for several benzenoid compounds were then examined for evidence of phenotypic plasticity using reaction norm graphs and analysis of variance. *Phlox subulata* genotypes showed some phenotypic plasticity in response to change in soil nutrient levels. These results suggest that if floral scent is plastic in natural settings, changes in soil nitrogen levels could result in altered scent profiles. This could, in turn, alter pollinator visitation patterns and potentially plant fitness.

Saint Mary's College, Department of Biology, State Route 933, Notre Dame, IN, 46556, USA

380 MAHADY, GAIL B\*<sup>1</sup>, LOCKLEAR, TRACIE D<sup>2</sup>, PATEL, UDESHI<sup>2</sup>, ADCOCK, AUDREY F<sup>1</sup> and KROLL, DAVID<sup>1</sup>**Chemopreventative activities of extracts of *Brassica oleracea* (collard greens) from the Lumbee Tribe of North Carolina**

*Brassica oleracea* var. *acephala* L. (Brassicaceae also known as Cruciferae) is the cultivar of *B. oleracea* known as "collard greens" or "collards" is a non-heading form of wild cabbage commonly eaten by populations in southern USA. "Collards" are a staple of Southern

cuisine and are typically eaten year-around. Among the vegetable-containing plant families with proven anti-carcinogenic properties, the genus *Brassica* (cabbage family) has been determined to be effective at reducing the risk of cancer. *Brassica oleracea* var. *acephala* L. (collard greens) were collected in North Carolina and deposited in the Herbarium at Chapel Hill, NC. The leaves (5 kg) were dried, pulverized, and extracted in methanol (MeOH, extracted to exhaustion). The MeOH extract was defatted with dichloromethane (3 L) and partitioned into chloroform, ethyl acetate and butanol. The partitions were dried and tested at 20 mcg/ml in an MCF-7 ERE-SEAP reporter gene assay. The ethyl acetate partition (EtOAc) was the most active in the MCF-7 cells assay and modified the expression of estrogen-dependent reporter genes. Both the methanol extract and the EtOAc partition inhibited the activity of HER-2 tyrosine kinase by 100% at a concentration of 20 mcg/ml. In addition, the EtOAc partition reduced the expression of the HER-2 receptor proteins in SK-BR breast cancer cells. In order to identify the chemical constituents responsible for this activity the EtOAc partition was fractionated using column chromatography (C18 reverse phase silica gel) using increasing concentrations of methanol/water as a solvent (10% MeOH to 100% MeOH), affording 5 fractions (10%, 30%, 50%, 70% and 100% methanol). The fractions were each analyzed by HPLC (Dionex), and the 70% fraction was found to be a single compound. Based on mass (*m/z* 309.1) and UV spectrometry and nuclear magnetic resonance (NMR) fraction 70 appears to be a known phenylpropanoid named hydroxycinnamoyl malate. This compound was previously identified in *Brassica rapa*.

<sup>1</sup>North Carolina Central University, Durham, NC, 20772, USA<sup>2</sup>University of Illinois at Chicago, Pharmacy Practice, 833 S Wood St, Chicago, IL, 60612, USA

## 381 MAHADY, GAIL B\*, SONI, KAPIL K, LOCKLEAR, TRACIE and PATEL, UDESHI

**In vitro and in vivo effects of Ayurvedic traditional medicines for the management of asthma**

The medicinal plants *Bacopa monnieri* (Brahmi, whole plant) and *Boswellia serrata* and *Osimum sanctum* (Holy basil) were collected from Vidisha (M.P.), India based on literature and traditional use in Ayurveda to treat asthma. Materials were dried, pulverized to powder and extracted in methanol to exhaustion. The methanol extracts were tested in three in vitro assays, leukotriene-C<sub>4</sub>-synthase, leukotriene-A<sub>4</sub>-hydroxylase and cyclooxygenase-2. The active extracts were partitioned in dichloromethane (DCM), ethyl acetate (EtOAc) and 50% methanol and each partition was re-tested for activity. Extracts and partitions of the three plant species showed inhibition of all three enzymes in vitro suggesting anti-inflammatory and anti-asthmatic activities. Dried extracts of all three plants were tested in

24 BALB/c mice (6arms, 4 animals per arm) sensitized by intraperitoneal injections of OVA weekly for 3 weeks and then treated by gastric lavage for four days with the extracts at a dose of 100 mg/kg for four days plus intranasal OVA challenge. Control animals were treated with PBS (negative control) or dexamethasone (positive control treatment). Animals were subjected to 2-D in vivo imaging using a Xenogen IVIS 2000 (Caliper Corp) system and lung inflammation was assessed based on the treatments. Animals sensitized and challenged with OVA had significant lung and peritoneal inflammation as compared with the PBS control group. Treatment of the mice with dexamethasone reduced OVA-induced inflammation by 50-60%. Treatment of the mice with the Ayurvedic herbal extracts also reduced inflammation, with the activities of the extracts being in the order of *Ocimum sanctum*>*Boswellia serrata*>*Bacopa monnieri*. These data support the use of these Ayurvedic herbs for the management of the inflammatory symptoms of inflammatory asthma.

University of Illinois at Chicago, Pharmacy Practice, 833 S Wood St, Chicago, IL, 60612, USA

### 382 CUMMINGS, KATE\* and HALL, KAREN

#### Sassafras tea: determining safety and projecting costs (human and natural) associated with harvest

The Eastern Band of Cherokee Indians in Western North Carolina consists of a community that upholds traditions of the Cherokee language and arts and crafts. One craft in particular is the cultivation, harvesting, and processing of the root of the sassafras tree, *Sassafras albidum*, from which they prepare teas and syrups. Sassafras, native to the eastern U.S., is a versatile species known for rapid colonization of disturbed and abandoned sites and as a food source for many woodland species. Sassafras extract was popular as a food extracts until 1960, when the Food and Drug Administration (FDA) banned the presence of safrole in sassafras products (CFR, Sec. 189). Many experiments since then have confirmed the hepatocarcinogenic effects of safrole on rats in the laboratory (Zhou et al. 2007). Though, recent research on safrole-containing species from China, the South Pacific, and Micronesia concluded that when traditional indigenous preparation methods were applied, the level of safrole in the final product dropped to very little or not detectable (Chen, et al., 2009; Farag and Abo-Zeid, 1997; Reynertson et al. 2005). There has been no known chemical analysis of the safrole levels of sassafras products made using traditional indigenous methods. The purpose of the research is twofold: to work directly with the Cherokee Indians to both investigate the toxicity of sassafras products and to ensure a supply of raw material. To investigate the toxicity, we will analyze the potential of traditional preparation method to effectively reduce safrole levels to the FDA standard. We

will also provide a full, long-term cost analysis model of the human and environmental costs associated with its production. To ensure a supply of sassafras root, we will be providing a stand of sassafras trees to the Center for Cherokee Plants as well as developing educational material and a map of the nursery.

Clemson University, Forestry and Natural Resources, 261 Lehotsky Hall, Clemson, SC, 29634, USA

### 383 CENTURION-HIDALGO, DORA\*<sup>1</sup>, ESPINOSA-MORENO, JUDITH<sup>2</sup>, MONTERO-ARIAS, LUIS ALBERTO<sup>1</sup> and MAYO-MOSQUEDA, ALBERTO<sup>1</sup>

#### Antibacterial activity of medicinal plants used against gastrointestinal diseases

Plants have been so important to humanity in all latitudes, that they have been traditionally utilized for all the cultures worldwide. Tea (herbal infusion) consumption has a variety of potential health benefits because they can prevent or lessen the effects of different pathologies, for this reason teas are considered as functional foods. A great number of tropical plants present medicinal properties, some are well known but most of them remain ignored. Return towards natural products in therapeutic use is an actual tendency nowadays. The aim of the present work was to evaluate the antibacterial activity of infusions of *Malvaviscus arboreus* Cav., *Pimenta dioica* (L.) Merr. and *Tradescantia pendula* var. *zebrina* against *Staphylococcus aureus*, *Salmonella typhimurium* and *Bacillus cereus*. Three grams of fresh leaves were soaked in 200 ml of boiling distilled water, let stand for 10 min and filtered. The filtered liquid was lyophilized and stored at 4Å°C. Antibacterial activity was evaluated using the diffusion sensibility test with paper discs and Minimal Inhibitory Concentration was determinate through tube dilution method. The infusion of *Pimenta dioica* was the most effective inhibiting 40% of *B. cereus* growth and 60% of *S. typhimurium* growth in comparison to positive control (Amikasin 1%). Minimal Inhibitory Concentrations varied from 1.7 to 4 mgL<sup>-1</sup> for *Pimenta dioica* infusion in all the bacteria tested. In conclusion, all the herbal infusions used against gastrointestinal diseases presented effective antibacterial activity.

<sup>1</sup>Universidad Juarez Autonoma de Tabasco, Division Academica de Ciencias Agropecuarias, Avenida Universidad s/n, Zona de la Cultura, Col. Magisterial, Centro, Villahermosa, Tab, 86040, Mexico  
<sup>2</sup>Universidad Juarez Autonoma de Tabasco, Division Academica de Ciencias Agropecuarias, Avenida Universidad s/n, Zona de la Cultura, Col. Magisterial, Centro, Villahermosa, Tab, 86040, Mexico

384 RAWLINS, CATHERINE\*<sup>1</sup>, LEIST, BENJAMIN<sup>1</sup>, ABLER, REBECCA<sup>2</sup> and CARLSON, KITRINA<sup>3</sup>

### Characterization of potential therapeutic properties of the Hmong medicinal plant, *Tradescantia zebrina*

Through oral interviews with Hmong elders, *Tradescantia zebrina* (Tz) was identified as a therapeutic plant used in traditional Hmong medicine. In this culture, Tz is used as a poultice on abnormal growths and in the treatment of wounds. Previous research at UW-Stout found that water decoction extracts of Tz leaves were toxic and inhibitory to head and neck cancer cells. To better understand the medicinal properties of Tz, and potentially isolate plant compounds of interest, a more thorough screening of Tz is underway, including the DPPH antioxidant assay, antimicrobial testing, brine shrimp lethality, and zebra fish embryo chemical screens. Tz leaf extracts were prepared from both water decoction as well as methanolic extractions at 50%, 25% and 10%. All samples were evaporated under reduced pressure and reconstituted in either water or 2.5% ocean salt solution. Samples were subsequently filter sterilized. Results from these chemical screens and bioassays will be presented. Current results suggest that some extracts of Tz may increase survivorship in bioassaytest subjects.

In addition to characterizing the medicinal potential of Tz, a fundamental goal of this partnership is to increase STEM retention through mentored research experiences. For this reason, samples were prepared at the UW-Stout campus and some of the bioassays were performed at the UW-Manitowoc campus. This work is part of an NSF STEP grant-funded collaborative research initiative that links 2-year campus students with students working at a 4-year comprehensive campus.

<sup>1</sup>University of Wisconsin - Stout, Biology, Menomonie, WI, 54751, USA<sup>2</sup>University Of Wisconsin - Manitowoc, Biological Sciences, 705 Viebahn St., Manitowoc, WI, 54220, USA<sup>3</sup>University of Wisconsin - Stout, Biology, 334G Jarvis Hall, Menomonie, WI, 54751, USA

385 JONES, TRISTESSE\*<sup>1</sup>, MAHADY, GAIL<sup>2</sup>, LOCKLEAR, TRACIE<sup>2</sup>, PARKER, CHRISTINA<sup>2</sup> and DUNCAN, SARA<sup>2</sup>

### Pharmacological activities of extracts of *Salvia officinalis* L. leaves used by the Lumbee Tribe of North Carolina for the treatment of menopause

Sage (*Salvia officinalis* L; Lamiaceae) is a popular food plant and herb used medicinally by many Native Americans. The Latin genus name "*Salvia*" meaning to cure and the species name "*officinalis*" meaning medicinal, suggests that the plant was widely used to

treat a range of medical conditions. In the Lumbee Tribe of North Carolina and other Native American tribes, *S.officinalis* was used as an anti-transpirant, anti-inflammatory, antibacterial agent and was also used to treat sweats associated with the menopausal transition. As part of an ongoing collaboration with the Lumbee Tribe, we have been investigating medicinal herbs used by the tribe for the management of women's health conditions and menopause. The leaves of *S. officinalis* were collected in North Carolina and deposited in the Herbarium at Chapel Hill, NC. The leaves (5 kg) were dried, pulverized, and extracted in methanol (MeOH, extracted to exhaustion). The MeOH extract was defatted with dichloromethane (3 L) and partitioned into chloroform, ethyl acetate and water. The partitions were dried and tested at 20 ug/ml in an MCF-7 ERE-SEAP reporter gene assay. The ethyl acetate partition (EtOAc) was highly estrogenic in the MCF-7 cell assay and significantly enhanced the expression of estrogen-dependent reporter genes. In order to identify the chemical constituents responsible for this activity, the EtOAc partition was fractionated using column chromatography (C18 reverse phase silica gel) using increasing concentrations of methanol/water as a solvent (20% MeOH to 100% MeOH), affording 5 fractions (20%, 40%, 60%, 80% and 100% methanol). These fractions were tested again in the reporter gene assay and fraction 40% was found to be weakly estrogenic and fraction 80% was found to be an estrogen agonist/antagonist. Rosmarinic acid was isolated as the estrogen agonist/antagonist and carnolic acid was found to be weakly estrogenic in MCF-7 cells and enhance the activity estradiol in the cells. These data support the traditional use of *S. officinalis* for the management of menopause by Native Americans.

<sup>1</sup>University of Illinois at Chicago, Department of Medicinal Chemistry and Pharmacognosy, 833 S Wood Street, Chicago, IL, 60612, USA<sup>2</sup>University of Illinois at Chicago, Department of Pharmacy Practice, 833 S Wood Street, Chicago, IL, 60612, USA

POSTERS

386 JOHNSON, ANNE KATHLEEN<sup>\*1</sup>,  
ROTHFELS, CARL<sup>1</sup>, GRUSZ, AMANDA<sup>2</sup>,  
SIGEL, ERIN<sup>3</sup>, WINDHAM, MICHAEL<sup>1</sup> and  
PRYER, KATHLEEN<sup>4</sup>

**Sporophytes and gametophytes of  
notholaenid ferns (Pteridaceae) show  
correlated presence/absence of farina**

The "notholaenids" comprise a monophyletic group of New World ferns commonly characterized by the presence of farina on the abaxial leaf surfaces of the sporophytes. Farina, a whitish or yellowish waxy exudate produced by glandular hairs, is thought to be an adaptation to xeric habitats. During unusually dry conditions, the leaves of notholaenids curl up to expose their farinose undersides, reducing water loss by increasing reflectivity. All species of the notholaenid clade previously investigated have scattered farina-producing hairs on their gametophytes as well. This has been interpreted as a potential synapomorphy for the genus *Notholaena* because no other ferns display farina in both the sporophytic and gametophytic phases of their life cycle. Recent phylogenetic studies demonstrate that two species with non-farinose sporophytes (*Cheilanthes brachypus* and *Cheilopteron rigidum*) are well-nested within the notholaenids, and a third non-farinose species (*Cheilanthes leucopoda*) is strongly supported as sister to all other notholaenids. This raises the question: are the gametophytes of these three species farinose like those of their close relatives, or are they glabrous? Here, we assay the gametophytes of a broad sample of notholaenids—including all three species with non-farinose sporophytes—to determine if the presence/absence of farina is correlated across the gametophytic and sporophytic phases of the life cycle for notholaenid ferns. Our survey of cultivated gametophytes indicates that species with non-farinose sporophytes also have non-farinose gametophytes. All other notholaenids sampled exhibit farina-producing hairs on the gametophytes. Thus, while farinose gametophytes are not upheld as a synapomorphy for the notholaenid clade, these desert ferns are consistent in their farina production across both phases of their life cycle.

<sup>1</sup>DUKE UNIVERSITY, Department Of Biology, BOX 90338, DURHAM, NC, 27708, USA<sup>2</sup> Duke University, Box 90338, Durham, NC, 27708, USA<sup>3</sup>Duke University, Department Of Botany, Box 90338, Duke University, Durham, NC, 27708, USA<sup>4</sup>Duke University, Science Drive, Durham, NC, 27708-0338, USA

387 METZGAR, JORDAN<sup>1</sup> and ICKERT-BOND, STEFANIE M.<sup>\*2</sup>

**Developing the parsley ferns  
(*Cryptogramma*) as a system for studying  
rapid climate change in seed free plants**

The parsley ferns (*Cryptogramma*) make an excellent candidate for testing hypotheses of colonization following the Last Glacial Maximum (LGM). Thanks to their minute and easily dispersed spores, these rock-loving ferns could have utilized refugia to rapidly and repeatedly colonize deglaciated landscapes, or they could have survived in situ on nunataks. Herbarium specimens indicate that *Cryptogramma* survives today on nunataks, but cannot answer whether this was the sole recolonization source used following the LGM or if recolonization from refugia also played a complementary or dominant role. By first generating well-resolved and robustly supported hypotheses of species relationships of the genus, we place the North American taxa in a phylogenetic context and answer lingering questions regarding (1) the origin of allopolyploid taxa and (2) if these taxa were formed when previous climate conditions forced currently allopatric parental taxa into close proximity. Field work throughout northwestern North America sampled numerous populations and haplotype network analyses of these specimens reveal the contributions and locations of glacial refugia for *Cryptogramma* during the LGM. Ecological niche modeling will allow us to project these future range shifts under a variety of climate scenarios and determine if polyploid species possess a lower extinction probability than diploid species.

<sup>1</sup>University Of Alaska Fairbanks, Museum Of The North, 907 Yukon Drive, Fairbanks, AK, 99775, USA<sup>2</sup>University of Alaska, UA Museum of the North Herbarium & Dept. of Biology and Wildlife, 907 Yukon Dr., Fairbanks, Alaska, 99775, USA

388 BRETZMAN, JAYNA<sup>1</sup>, DIAMOND, HOPE<sup>2</sup> and SWATZELL, LUCINDA<sup>\*1</sup>

**Changes in PIP1 Aquaporin Expression  
Following Rehydration of *Cheilanthes  
lanosa* Gametophytes**

*Cheilanthes lanosa* is a xerophytic fern that exhibits desiccation tolerance. The gametophyte can dry completely and return to full volume within minutes upon rehydration. Clearly, the dehydrated fern possesses aquaporins that allow this rapid influx, but there are many unanswered questions about the type of aquaporin and quantity maintained during desiccation. In this study, dehydrated gametophytes were examined for the presence and quantity of PIP1 aquaporins. This was compared to the presence and quantity of PIP1 aquaporin in rehydrated gametophytes for up to 24 hr.

Gametophytes rehydrated for only 1 hr contain similar amounts of PIP1. However, gametophytes that had been rehydrated for 24 hr contained significantly less PIP1. Results suggest a molecular memory or a change in aquaporin type following rehydration.

<sup>1</sup>Southeast Missouri State University, Biology, Mail Stop 6200, One University Plaza, Cape Girardeau, MO, 63701, USA<sup>2</sup>University of North Texas, Risk Management Services, 1155 Union Circle #310950, Denton, TX, 76203-5017, USA

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## Systematics Section/ASPT

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### ORAL PAPERS

**389 LIU, YANG<sup>1</sup>, BUDKE, JESSICA\*<sup>2</sup>  
and GOFFINET, BERNARD<sup>3</sup>**

#### **Phylogenetic inference rejects sporophyte-based classification of the Funariaceae (Bryophyta): a rapid radiation suggests rampant homoplasy in sporophyte evolution**

The Funariaceae, which include the model organisms *Physcomitrella patens* and *Funaria hygrometrica*, comprise 15 genera, three of which accommodate approximately 95% of the 250-400 species. Historically, generic concepts are based on the morphological complexity of the moss sporophyte. The boundary between two of the major genera, *Entosthodon* and *Funaria*, has fluctuated with authors emphasizing alternate diagnostic characters. We sampled ten loci across the three genomic compartments to reconstruct the relationships within the Funariaceae and assess whether supraspecific taxa defined by traits of the sporophyte represented monophyletic lineages. The sporophyte-based circumscription of two of the speciose genera of the Funariaceae is rejected. *Entosthodon* and *Physcomitrium*, as well as some of their subgenera, are resolved as polyphyletic, and even the three species of *Physcomitrella* are confirmed to have diverged from distinct ancestors. By contrast, exemplars of *Funaria*, that are morphologically diagnosed by a compound annulus, comprise a single clade. Each of these hypotheses is robust, withstanding a series of tests for monophyly of the genera. These observations suggest that sporophytic features alone, often considered to be more conserved and hence phylogenetically more informative than vegetative traits can also be highly homoplastic. Within the Funariaceae, none of the novel clades seem a priori to be defined by a uniquely derived character state, when considering the characters historically used to distinguish lineages. The core clade of the Funariaceae (i.e., Funarioideae minus *Funaria*), which may ultimately include much of the species diversity, is estimated to have diversified rapidly in the Miocene. The combination of polyphyly of supraspecific taxa defined by sporophytic traits, rampant homoplasy of these traits and the rapid radiation of the core Funariaceae, reveals that characters of the sporophyte, such as the peristome architecture, length of the seta, and symmetry of the capsule are phylogenetically labile and that the genetic networks underlying their expression may have been under a rather loose control.

<sup>1</sup>University Of Connecticut, Ecology & Evolutionary Biology, 75 North Eagleville Road, Storrs, CT, 06269-3043, USA<sup>2</sup>University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Rd. U-3043, Storrs, CT, 06269, USA<sup>3</sup>University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Road, U-3043, STORRS, CT, 06269-3043, USA

390 ROTHFELS, CARL\*<sup>1</sup>, LARSSON, ANDERS<sup>2</sup>, KUO, LI-YAUNG<sup>3</sup>, KORALL, PETRA<sup>4</sup>, CHIOU, WEN-LIANG<sup>5</sup> and PRYER, KATHLEEN<sup>6</sup>

### Ancient, rapid, yet resolvable: The backbone phylogeny of the eupolypod II radiation

The eupolypod II clade comprises nearly a third of extant fern species, including such well-known groups as the spleenworts (*Asplenium*), the ladyferns (*Athyrium*), and the marshferns (*Thelypteris*). While this clade is frequently recovered with strong support in phylogenetic analyses, the relationships within it have resisted elucidation by both molecular and morphological data, and classifications have correspondingly varied wildly. Earlier results suggest that the perennial difficulty in resolving the backbone relationships in the Eupolypods II is due to three factors: 1) the ancient rapid radiation of this group (the phylogeny is characterized by long ingroup branches among a series of very short backbone internodes); 2) the absence of a closely related outgroup; and 3) the presence of strongly heterogeneous lineage-specific rates of evolution within the ingroup. We assembled a five-locus dataset (*atpA*, *atpB*, *matK*, *rbcl*, *trnG-R*) from 81 accessions selected to capture the deepest divergences in Eupolypods II, and evaluated the resulting phylogenetic hypothesis against potential artifacts including those induced by the ancient rapid radiation model, highly divergent outgroups, lineage-specific rate heterogeneity, and the failure of some implementations of Bayesian inference to account for the possibility of polytomies in the option set (the "star-tree paradox" artifact). The backbone internodes (seven out of eight of which were highly supported under both maximum likelihood and Bayesian inference) proved robust to our evaluations, which nonetheless revealed unexpected behavior of our methods on these data, including model-mediated impacts of outgroup composition and strongly divergent effects of two methods intended to avoid the Bayesian star-tree paradox artifact. This study is one of the few investigations of these methods with empirical data, and provides a template for those wishing to resolve ancient rapid radiations (or other challenging phylogenetic problems) with moderate amounts of data. Among the significant phylogenetic results are the strongly supported eupolypod II backbone, the demonstrated paraphyly of Woodsiaceae as currently circumscribed, and the well-supported placement of the enigmatic genera

*Homaliosorus*, *Diplaziosis* and *Woodsia*.

<sup>1</sup>DUKE UNIVERSITY, Department Of Biology, BOX 90338, DURHAM, NC, 27708, USA<sup>2</sup>Uppsala University, Systematic Biology, Evolutionary Biology Centre, Norbyv. 18D, Uppsala, SE-752 36, Sweden<sup>3</sup>National Taiwan University, Institute of Ecology and Evolutionary Biology, No. 1, Sec 4, Roosevelt Road, Taipei, 10617, Taiwan-<sup>4</sup>Uppsala University, PHANEROGAMIC BOTANY, Norbyv. 18D, Uppsala, SE-752 36, Sweden<sup>5</sup>TAIWAN FORESTRY RESEARCH INST, 53 NAN-HAI RD, TAIPEI, 100, Taiwan<sup>6</sup>Duke University, Science Drive, Durham, NC, 27708-0338, USA

391 LARSON, JASON\* and BALLARD JR, HARVEY

### A Re-evaluation of Great Lakes Taxa in North American *Lycopodiella* (Lycopodiaceae)

Six species of *Lycopodiella* (Lycopodiaceae) have been recognized to date from North America: *Lycopodiella alopecurooides*, *L. appressa*, *L. inundata*, *L. margueritiae*, *L. prostrata* and *L. subappressa*. Interspecific hybridization and substantial variation have been documented in this region, and the taxa represent diploids (most taxa), tetraploids (two Great Lakes taxa, potentially endemic, their hybrids, and reportedly, eastern *L. appressa*), and triploids (hybrids between diploids and tetraploids). Jim Bruce documented the existence of two tetraploids, possibly Great Lakes endemics, in his 1975 dissertation and reported hybrids between them and with the frequently co-occurring *L. inundata*. Unpublished phenetic studies by the second author, conducted in 1986 on mass collections from 17 southwestern Michigan *Lycopodiella* sites, confirmed and elaborated on Bruce's taxonomic concepts, re-identifying many herbarium specimens and Heritage Program reports of the three taxa and clarifying their distributional status. Fifteen years later (1991), Bruce, Wagner and Beitel published names for the two Great Lakes species, *L. margueritiae* (for Bruce's "appressed inundata") and *L. subappressa* ("northern appressa"), in advance of their "Flora of North America" generic treatment. However, scrutiny of the keys, protologues and specimen citations of that publication are highly heterogeneous and do not conform consistently to Bruce's original species concepts of dissertation data. Moreover, type specimens of both names disagree in diagnostic features with Bruce's original taxa and appear to represent endpoints on the continuum of variation recently detected in "robust" *L. inundata*, an unrecognized taxon frequent in Great Lakes coastal sites. New investigations by the first author, utilizing previous field collections and new ones made in 2010, and several major herbarium collections, are re-examining the genus in the Great Lakes and in eastern North America. We will present evidence to clarify diagnostic features, variation patterns and interspecific hybridization in the Great Lakes taxa and will contrast our taxon concepts against those currently

manifested in the literature and herbarium collections.

Ohio University, Environmental And Plant Biology, Porter Hall 315, Richland Ave., Athens, OH, 45701, USA

**392 SHARMA, PRABHA\*<sup>1</sup>, UNIYAL, P.L.<sup>1</sup>, TRIPATHI, S.B.<sup>2</sup>, NEGI, M.S.<sup>2</sup> and SCHWEKENDIEK, A.<sup>3</sup>**

### The identity reveal: Four new morpho-molecular species within Section Pseudobaccatae of the genus *Ephedra* in Western Himalaya

A review of *Ephedra* species of the Western Himalayan region led to the discovery of Four new species and a variety (*E. yurtungensis* Sharma & Uniyal sp. nov., *E. yurtungensis* var. *lutea* Sharma & Uniyal comb. nov. *E. Lamayuruensis* Sharma & Uniyal sp. nov., *E. sheyensis* Sharma & Uniyal sp. nov., *E. khardongensis* Sharma & Uniyal sp. nov.). The most distinctive characters observed are shape and size of male strobilus, number of bracts, length of synangiophore with synangia, shape and size of female strobilus, number of bracts, size and color of seeds, and several features of the micropyle for morphological analysis including AFLP diagnosis at the molecular level. These species are most similar to *E. intermedia* and *E. regeliana*. The present study also emphasize Sympatric speciation highlighting conserved morphological reproductive character states answering evo-devo mechanism in the case of *Ephedra*.

<sup>1</sup>university of delhi, botany, lab no. 311 b, new delhi, 110 007, India<sup>2</sup>The Energy Research Institute, Biotechnology and Management of Bioresources Division, Darbari Seth Block India Habitat Centre, Lodhi Road New Delhi- 110003<sup>3</sup>University of Northern Iowa, Department of Biology, Cedar Falls, IA 50614

**393 HOLMAN, GARTH\*<sup>1</sup>, DEL TREDICI, PETER<sup>2</sup>, HAVILL, NATHAN<sup>3</sup> and CAMPBELL, CHRISTOPHER<sup>4</sup>**

### Affinities of a new species of *Tsuga* (Pinaceae) from Ullueung island, South Korea

*Tsuga* plants from Ulleung island in South Korea are distinct from other species of hemlocks based on molecular, morphological, and ecological evidence. Ulleung island has 30 endemic species of angiosperms, but no endemic gymnosperms have been described. Ulleung hemlocks have previously been treated as *T. sieboldii*, based on their hairless twigs and geographic proximity. DNA sequences from nearly complete chloroplast genomes and nuclear genes of the Ulleung hemlock, *T. chinensis*, *T. diversifolia*, and *T. sieboldii* show the Ulleung hemlock is more divergent from its closest relative, *T. diversifolia*, than *T. chinensis* is from its close relative, *T. sieboldii*. Based on three seasons of phenological data for Ulleung hemlocks and eight other species

of *Tsuga* grown in a common garden experiment, Ulleung hemlock is most similar to *T. chinensis*. Both species have an early season bud break and a long growing period, which may be adaptations to a warm-temperate coastal environment. The sterile bracts at the base of the ovulate cone of the Ulleung hemlock have broad, membranous denticulate margins and a more woody, bidentate mucro that is distinct from other hemlock species. Although chloroplast sequences coalesce for all species, all four sampled plants of *T. diversifolia* possess divergent copies of ITS that are strongly supported either as sister to the Ulleung hemlock or as part of a clade with *T. chinensis* and *T. sieboldii*. This incongruence between chloroplast and nuclear phylogenies suggests that *T. diversifolia* may be of hybrid origin, with the chloroplast (which is paternally inherited in Pinaceae) coming from Ulleung hemlock and either *T. chinensis* or *T. sieboldii* as the ovulate parent. Our findings support treatment of the Ulleung hemlock as a species that is sister to *T. diversifolia*.

<sup>1</sup>University Of Maine, School Of Biology And Ecology, 5735 Hitchner Hall, Orono, ME, 04469, USA<sup>2</sup>ARNOLD ARBORETUM, 125 ARBORWAY, JAMAICA PLAIN, MA, 02130-3519, USA<sup>3</sup>USDA Forest Service, Northern Research Station, 51 Mill Pond Rd., Hamden, CT, 06514, USA<sup>4</sup>University Of Maine, Department Of Biological Sciences, 261 HITCHNER HALL, ORONO, ME, 04469-5735, USA

**394 SALAZAR, JACKELINE\*<sup>1</sup>, LITTLE, DAMON P.<sup>2</sup>, JARAMILLO, M. ALEJANDRA<sup>3</sup> and NIXON, KEVIN<sup>4</sup>**

### New Genus of Canellaceae From The Greater Antilles

Six genera worldwide have been described in Canellaceae: *Cinnamosma*, *Warburgia*, *Capsicodendron*, *Canella*, *Cinnamodendron*, and *Pleodendron*. Three of these genera - *Cinnamodendron*, *Canella*, and *Pleodendron* - and approximately seven species have been reported for the Antilles. A complete cladistic analysis of genera within Canellaceae was conducted using molecular and morphological data. An analysis using nrITS, *matK*, *rbcL*, *trnD*<sup>GUC-trnT</sup><sup>GGU</sup>, and *trnL-trnF* data in combination with 49 informative morphological characters was performed to test the monophyly of the family and evaluate the placement and monophyly of the genera. *Cinnamodendron* was recovered as a polyphyletic group with the Antillean and South American species present in two different clades. The Antillean species form a clade sister to *Pleodendron macranthum*. The priority of the name is given to the South American *Cinnamodendron* since the type of the genus is the Brazilian *C. axillare* Endl. ex Walp. A new genus of Canellaceae is proposed based on *Cinnamodendron corticosum* Miers, for the Antillean clade. The newly proposed genus, exclusive to the Greater Antilles, is present in Cuba, Hispaniola, and Jamaica. It differs from other genera in the family in having tetramerous flowers with eight pet-

als, eight stamens, four carpels, and four placentae. Its members are found mainly in humid forests on limestone.

<sup>1</sup>Universidad Autónoma de Santo Domingo (UASD), Escuela de Biología, Zona Universitaria, Santo Domingo, DN, República Dominicana <sup>2</sup>The New York Botanical Garden, Lewis B. and Dorothy Cullman Program for Molecular Systematics, NY, 10458 USA <sup>3</sup>Universidad Icesi, Biological Sciences, Calle 18 # 122-135, Cali, VA, Colombia <sup>4</sup>Cornell University, L. H. BAILEY HORTORIUM, 408 MANN LIBRARY, ITHACA, NY, 14853-4301, USA

### 395 JABBOUR, FLORIAN\*, ROJAS, ALFONSO and RENNER, SUSANNE

#### A phylogeny of the Delphinieae (Ranunculaceae) reveals that *Aconitum* is embedded in *Delphinium*: Implications for flower evolution

The Delphinieae comprise the mostly holarctic genera *Aconitum* L. and *Delphinium* L., with c. 350 species each, and the small *Consolida* and *Aconitella*, which recent work has shown to be part of *Delphinium* (Jabbour and Renner, in review). Monkshoods and larkspurs have complex bee-adapted flowers, with bi-symmetry (creating bee working platforms), hidden nectar, a petaloid outermost whorl of tepals, and a reduced innermost one. A characteristic feature of Delphinieae flowers is the presence of nectar-leaves nested inside the dorsal tepal (either hooded or spurred) of the outermost flower whorl. The mutual monophyly of *Aconitum* and *Delphinium* has long gone unquestioned, but extensive species sampling (using plastid and nuclear DNA sequences) reveals that *Aconitum* is embedded in *Delphinium*. *Delphinium* subgenus *Staphisagria*, with three species endemic to Mediterranean islands, is sister to all remaining Delphinieae. Using a Bayesian relaxed molecular clock and maximum likelihood ancestral area reconstruction we inferred the migration routes and times of the Delphinieae expansion to the Mediterranean, tropical African mountains (a single event c. 12.9 Mya), and North America. Since the sister clade of the Delphinieae is uncertain, the region of origin cannot be inferred; the eastern Himalaya and southwestern China are richest in endemic species. The newly revealed relationships imply an evolutionary increase in spur length and homoplastic reduction in the innermost tepal whorl. The synorganization of nectar-leaves evolved once in the ancestor of the most derived lineage, *Aconitella/Consolida*. To achieve monophyletic genera in the Delphinieae one could resurrect *Staphisagria* J. Hill (1756) and transfer the 52 species of *Aconitella* and *Delphinium*, which would involve only seven name changes because most were placed in *Delphinium* at some time. Developmental genetic studies of flower evolution in the Delphinieae will benefit from the new

phylogeny.

Systematic Botany and Mycology, Department of Biology, University of Munich (LMU), Munich, 80638, Germany

### 396 EMERSON, JOHN\* and HOOT, SARA B.

#### Phylogeny and Phylogeography of *Anemone* L. sect. *Omalocarpus* DC. (Ranunculaceae)

*Anemone* L. sect. *Omalocarpus* DC. have a circumpolar distribution throughout the Northern Hemisphere, with alpine regions of Western China exhibiting the highest species diversity. Due to essentially continuous morphological variation, previous attempts at phylogeny reconstruction have proven difficult and species delimitations are fluid. Using combined nuclear (ITS) and chloroplast (*trnL-F* spacer, *rpl16*, *atpB-rbcL* spacer) data, a phylogeny of *Anemone* sect. *Omalocarpus* is presented, including suggestions for reclassification. Two subsections are recognized within section *Omalocarpus*: *Omalocarpus* (circumpolar, montane regions in Eurasia and America) and *Himalayicae* (China, Nepal, Bhutan, India). *Anemone polycarpa*, previously included in subsect. *Himalayicae*, is moved to subsect. *Omalocarpus*. *Anemone imbricata*, a taxonomically difficult species, is included within subsect. *Omalocarpus*. Individuals recently assigned to *Anemone geum* ssp. *ovalifolia* should instead be retained in *A. obtusiloba* ssp. *ovalifolia*. Additionally, the relationship between three distinct species (*A. demissa*, *A. obtusiloba* and *A. coelestina*) and Asian alpine regions will be discussed in the context of morphology, geography, climatic influences and historical geologic events.

University Of Wisconsin, Dept Of Biol Sci/Lapham Hall, Po Box 413, Milwaukee, WI 53201, USA

### 397 SCHUSTER, TANJA\*, REVEAL, JAMES<sup>2</sup> and KRON, KATHLEEN<sup>1</sup>

#### Evolutionary relationships within tribe Polygoneae Rchb. (Polygoneae)

Several genera included in tribe Polygoneae are investigated using a molecular framework. These genera include *Atraphaxis*, *Duma*, *Fallopia*, *Muehlenbeckia*, *Polygonella*, *Polygonum*, *Oxygonum* and *Reynoutria*. Morphological data have been used to recognize three sections in *Polygonum* (*Duravia*, *Polygonum* and *Pseudomollia*) and to support the inclusion of *Polygonella* within *Polygonum* based on similarities to members of sect. *Duravia*. *Oxygonum* has been considered a member of Polygoneae based on morphology but it has not been included in any molecular analysis to date. The evolutionary relationships among genera of Polygoneae were addressed with Maximum Likelihood and Maximum Parsimony methods using sequence data from

one nuclear (nrITS) and three chloroplast (*matK*, *ndhF* and *trnL-trnF*) markers. The results of this study indicate that tribe Polygoneae is composed of three clades with *Knorringia* sister to all other taxa within Polygoneae. A second clade is formed by *Reynoutria* and *Fallopia* + *Muehlenbeckia* and the third by their sister clade comprising *Atraphaxis*, *Duma* and *Polygonum* (including *Polygonella*). The currently accepted sections within *Polygonum* were also recovered with these molecular data and show that *Polygonum* sect. *Duravia* including subsection *Polygonella* is sister to a clade formed by the sects. *Polygonum* and *Pseudomollia*. Within the strongly supported subsection *Polygonella*, *Polygonella robusta* is sister to all other species sampled. Finally, *Oxygonum* was shown not to be included in Polygoneae and branches between Persicarieae and Fagopyreae, but with weak bootstrap support.

<sup>1</sup>Wake Forest University, Department of Biology, Reynolda Station, P.O. Box 7325, Winston-Salem, NC, 27109, USA<sup>2</sup>L.H. Bailey Hortorium, Department of Plant Biology, 412 Mann Building, Cornell University, Ithaca, NY, 14853, USA

**398 MOORE, MICHAEL<sup>\*1</sup>, BRUENN, RIVA<sup>1</sup>, DRUMMOND, CHLOE<sup>1</sup>, JOFFE, JONAH<sup>1</sup>, MOSTOW, REBECCA<sup>1</sup>, STALBERG, GABRIEL<sup>1</sup>, DOUGLAS, NORMAN<sup>2</sup> and BROCKINGTON, SAMUEL<sup>3</sup>**

### The age of gypsum endemism and arid-adapted plants within Nyctaginaceae inferred using extensive taxon sampling in Caryophyllales

Morphological, distributional, and genetic evidence suggests that gypsum endemic plant clades in southwestern North America predate the Pleistocene, and consequently survived the climatic fluctuations of the last two million years. We test this hypothesis in Nyctaginaceae tribe Nyctagineae, which contains multiple clades of gypsum endemics, using a molecular dating approach. Sequences were generated for the three most variable plastid protein-coding genes (*ycf1*, *ndhF*, and *matK*) for an extensive sampling of Nyctaginaceae and surrounding families, as well as exemplar taxa throughout Caryophyllales. In addition, all available Caryophyllales sequences of these genes were downloaded from GenBank and included in gene-specific analyses to examine the influence of taxon and gene sampling on age estimates. Molecular dating analyses include constraints based on the best available fossils for Caryophyllales, including Eocene and late Cretaceous pollen of Amaranthaceae s.l. We address the implications of our results for the origins of both gypsum endemism and arid adaptations within Nyctagineae, in light

of other recent studies.

<sup>1</sup>Oberlin College, Department of Biology, 119 Woodland St., Oberlin, OH, 44074, USA<sup>2</sup>North Carolina State University, Department Of Biology, Campus Box 7612, Raleigh, NC, 27695, USA<sup>3</sup>University of Cambridge, Department of Plant Sciences, Downing Street, Cambridge, CB2 3EA, UK

**399 SAUNDERS, N.<sup>\*1</sup> and SIPES, SEDONIA<sup>2</sup>**

### A Molecular Phylogeny of *Abronia* Juss. and *Tripterocalyx* (Torr.) Hook (Nyctaginaceae) with notes on the generic revision

*Abronia* Juss. is a genus of 20 sand and gypsum specialists found in maritime, montane and desert habitats of western North America. *Tripterocalyx* (Torr.) Hook includes four species limited to the Great Basin Desert. All are characterized by small population sizes, adaptation to a highly specific and uncommon habitat, and tolerance of environmental extremes. The genera are thought to have only recently radiated into the North American deserts, and many taxa are thought to be actively speciating. Modern treatments rely on highly variable morphological characters, soil preferences, or geographic location for species delineation, resulting in an unstable taxonomy. Treatments have variously collapsed *Tripterocalyx* within *Abronia* with others holding them distinct. Although generic hybrids are unknown, many *Abronia* readily hybridize in sympatry. We sampled 116 populations, representing 20 recognized *Abronia*, four *Tripterocalyx* and four outgroup species from within the Nyctaginaceae. We sequenced the nuclear ribosomal intergenic spacer, using primers ITS1 and ITS4, as well as three chloroplast regions (trnS-trnG-trnC, trnF-trnDT, and rpoB-trnCR) and performed a phylogenetic analysis to produce a maximum likelihood-bootstrap tree. Our analysis supports the monophyly of *Abronia* and *Tripterocalyx*. Within *Abronia*, there are two well supported maritime clades, with *Abronia latifolia* distinct from the other maritime species with which it grows in sympatry and *Abronia alpina* sister to all other *Abronia*. The third clade includes desert and montane species, and our data supports a cold desert and a hot desert grouping. We provide preliminary information on a taxonomic revision of the genera and include information about a species within *Abronia*, believed to be new to science.

<sup>1</sup>Southern Illinois University, Plant Biology, 1125 Lincoln Drive, Suite 420, Carbondale, IL, 62901-6509, USA<sup>2</sup>Southern Illinois University, 1125 Lincoln Drive, Mail Code 6509, Carbondale, IL, 62901, USA

400 BARBA MONTOYA, JOSE ANTONIO<sup>\*1</sup>, MAGALLON PUEBLA, SUSANA<sup>2</sup> and TREJO SALAZAR, ROBERT<sup>1</sup>

### Understanding arid Neotropical biodiversity: the timing and diversification rate of tribe Pachycereeae (Cactaceae, Caryophyllales).

Arid Neotropical biomes encompass an exceptionally rich biological diversity. To provide insights about some of the diversification dynamics underlying their species richness, we consider tribe Pachycereeae (Cactoideae), corresponding to the North American columnar cacti, including emblematic forms such as the saguaro (*Carnegiea gigantea*) and the Old Man (*Cephalocereus senilis*). We conducted a Bayesian phylogenetic analysis on a sample of 86 species, representing all the genera in Pachycereeae, plus two outgroups, using sequences of the cp *rpl16* intergenic spacer. The resulting phylogeny was used to estimate the age and phylogenetic diversification rate of the tribe and its main lineages. Age estimation was conducted with an uncorrelated lognormal relaxed molecular clock, implementing a secondary calibration derived from a Cactaceae-wide study. The onset of diversification of Pachycereeae was estimated at 8.52 Ma (late Miocene). Diversification rates were calculated on the basis of the age and standing diversity of clades, using an estimator that accounts for the possibility of extinction. The diversification rate of Pachycereeae as a whole ranged between 0.595 and 0.380 speciation events/Ma, which is very high, in comparison with a variety of angiosperm lineages. Nevertheless, diversification rate heterogeneity was detected within the group. The recent onset and high rate of Pachycereeae diversification suggest that the group probably represents a rapid radiation that took place recently, possibly as a consequence of global and regional aridification trends. The causal relationship of Pachycereeae diversification and its pollination syndrome will be explored.

<sup>1</sup>Instituto de Ecología, UNAM, Ecología Evolutiva, Circuito exterior s/n anexo al Jardín Botánico Exterior Apartado Postal 70-275 Ciudad Universitaria, UNAM 04510 México, D.F., Mexico City, Distrito Federal, 04510, Mexico <sup>2</sup>Instituto de Biología, UNAM, Botánica, Circuito Exterior s/n, Ciudad Universitaria, Copilco, Coyoacán A.P. 70-367 México, Distrito Federal. C.P. 04510, Mexico City, Distrito Federal, 04510, Mexico

401 MAJURE, LUCAS<sup>\*1</sup>, JUDD, WALTER<sup>2</sup>, SOLTIS, PAMELA<sup>3</sup> and SOLTIS, DOUGLAS<sup>4</sup>

### Searching for needles in a stack of needles: diploids in *Opuntia* s.s. and what they tell us about the evolutionary history of the clade

The widespread American clade *Opuntia* s.s. is well known for consisting of a very high percentage of polyploid species. In general, polyploids are typically more widespread and apparently more successful than the geographically restricted and therefore less common diploids. We wanted to know 1) the geographical delineation of diploids and polyploids in a subclade of *Opuntia* s.s., the *Humifusa* clade, and 2) what the diploid phylogeny can tell us about the origin of the clade and polyploid taxa within the clade. We analyzed 15 taxa of the *Humifusa* clade with individuals sampled from across the United States, using cytological (including 250 new counts) and phylogenetic data (5 plastid and 2 nuclear loci) to answer these questions. Diploid species are confined to the southeastern United States and two locations in the southwestern United States. Our phylogenetic results suggest that the *Humifusa* clade originated in the southeastern United States and allopolyploid formation resulted from contact with divergent members of its own clade and possibly its sister clade (the *Macrocentra* clade), as the *Humifusa* clade spread north and west from the southeastern United States. Drastic fluctuations in sea level likely were a factor in the union of evolutionarily divergent species that led to the formation of polyploid taxa, since geographic boundaries of certain diploid and polyploid taxa follow the predictions of sea level changes during previous interglacial events of the late Miocene and Pleistocene epochs.

<sup>1</sup>University Of Florida, Florida Museum Of Natural History, PO. Box 117800, Gainesville, FL, 32611, USA <sup>2</sup>University of Florida, Department of Biology, Po Box 118526, Gainesville, FL, 32611, USA <sup>3</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA <sup>4</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA

402 FRANCK, ALAN

### Phylogeny, biogeography, & subgeneric classification of *Harrisia*

Based on sequences of taxa within Cereeae sensu Nyffeler & Eggli from two nuclear and two plastid loci, *Harrisia* is a well supported monophyletic genus. The molecular analyses also found high support for four groups within *Harrisia*, which are treated as subgenera and morphologically interpreted. A dated phylogeny was produced, calibrated on the possible origin of a Plio-Pleistocene caatinga (*H. adscendens*) and a Plio-

cene subandean Chaco (*H. tetraacantha*). Caribbean (subg. *Harrisia*) and chaco species (subg. *Eriocereus*) of *Harrisia* were nearly identical for the four loci and are subtly separable morphologically. *Harrisia* is biogeographically interpreted as originating near the Bolivian Andes, spreading into the chaco and caatinga, and from the caatinga dispersing into the Caribbean.

University of South Florida, CMMB, BSF 218, 4202 E. Fowler Ave., Tampa, Fl, 34241, USA

#### 403 PRINCE, LINDA

##### *Franklinia alatamaha* or *Gordonia alatamaha*: molecular, morphological, and anatomical evidence

The Ben Franklin tree, *Franklinia alatamaha*, known from a single locality along the Altamaha River near Ft. Barrington, Georgia, is presumed to be extinct in the wild. Last seen in the 1803, it persists through cultivation. It was originally described as a species of *Gordonia* but most 20th century researchers maintain it as a monotypic genus closely related to *Gordonia* and *Schima*. Recent cladistic analyses of a diversity of morphological characters suggest it might better be included within *Gordonia*, as originally described. A number of nucleic acid sequence data sets from both the chloroplast and nuclear genomes were analyzed using parsimony and Bayesian methods to test this hypothesis. Anatomical and morphological characters were also analyzed. Results do not support the inclusion of *Franklinia* within *Gordonia*. These data do support the recognition of *Gordonia* as narrowly defined (*G. lasianthus* + *G. brandegeei*) to the exclusion of *Laplacea* and *Polyspora*.

Rancho Santa Ana Botanic Garden, 1500 N College Avenue, Claremont, CA, 91711-3157, USA

#### 404 PORTER, J. MARK

##### Phylogeny of *Loeselia* (Polemoniaceae): Diversification of a self-compatible lineage

*Loeselia* L. is an obscure lineage in Polemoniaceae that incorporates a genus of approximately 17 species in two subgenera, *Loeselia* and *Glumiselia*. *Loeselia* ranges from Colombia and Venezuela to southern Arizona, U.S.A., but its greatest diversity is in México. It has played a central role in hypotheses concerning the origin and diversification of Polemoniaceae in the temperate New World. Grant (1959, 1998a, 1998b) has suggested that *Loeselia*, with its putatively ancestral features (woodiness, simple leaves, tropical distribution) represents the common ancestor of temperate genera such as *Eriastrum* Woot. & Standl., *Gilia* Ruiz & Pav., *Ipomopsis* Michx., *Langloisia* Greene, and *Loeseliastrum* (Benth.) Timbrook. Discussions concerning the phylogenetic

relationships of *Loeselia*, as with those concerning the phylogeny of Polemoniaceae as a whole, reflects the tension between more traditional approaches to classification, (use of a classifications for developing an understanding of phylogeny; see Grant 1998), and classification as an outcome of explicit phylogenetic hypothesis development, based on repeatable and philosophically justifiable methods such as parsimony, maximum likelihood or Bayesian analyses. Here I examine phylogenetic relationships of *Loeselia*, using chloroplast and nuclear DNA sequences, analyzed using maximum likelihood analysis and Bayesian inference. Phylogenetic inferences contradict both subgeneric classification and the reputed central role for *Loeselia* in the origin of *Gilia* and other genera. However, these inferences support two independent origins of hummingbird pollination in an otherwise self-compatible lineage.

Rancho Santa Ana Botanic Garden and Claremont Graduate University, Research: Program in Botany, 1500 N. College Ave., Claremont, CA, 91711, USA

#### 405 FELDENKRIS, EMILY<sup>1</sup>, BROE, MICHAEL<sup>2</sup> and FREUDENSTEIN, JOHN<sup>\*1</sup>

##### A mitochondrial DNA and combined evidence analysis of relationships at the base of Ericaceae

As part of a comprehensive study to resolve relationships among the earliest diverging lineages at the base of Ericaceae, sequences from introns in two mitochondrial NADH dehydrogenase gene subunits, *nad1* and *nad5*, were analyzed using parsimony and likelihood approaches. These loci were analyzed individually and combined, as well as in combination with nuclear ITS-26S sequences and morphology. The pyroloids, monotropoids, and arbutoids are each resolved as monophyletic groups. Monotropoids and arbutoids are resolved as sisters, with the majority of Ericaceae sister to them. Pyroloids are then sister to that assemblage, with *Enkianthus* falling at the base of the tree. This analysis lends further support to the dissociation of monotropoids and pyroloids into their own subfamilies and suggests that the tendency toward extreme mycotrophy found in these groups and indicated by their highly reduced seeds, has evolved in parallel. Substantial structure is present within each of these clades, elucidating character evolution and suggesting a basis for taxonomic revision in particular among monotropoids.

<sup>1</sup>The Ohio State University Herbarium, Evolution, Ecology and Organismal Biology, 1315 Kinnear Rd., Columbus, OH, 43212, USA <sup>2</sup>The Ohio State University Herbarium, Evolution, Ecology and Organismal Biology, 1315 Kinnear Rd., Columbus, OH, 43212, USA

406 BROE, MICHAEL\* and  
FREUDENSTEIN, JOHN

### ***Monotropa hypopithys* L. (Ericaceae) is a distinct genus with well-defined species segregates at the molecular level**

The Monotropoideae are a herbaceous, achlorophyllous subfamily of the Ericaceae, within which 12 species in 10 genera are currently recognized. Most species are endemic to North America, however two *Monotropa uniflora* L. and *Monotropa hypopithys* L.---have a much wider distribution in the Americas and Eurasia. We performed an extensive sampling of monotropoids across N. America, and here present molecular evidence for a revised treatment of this group based on ITS1, ITS2 and 26S (approx. 1200 bp). While the two *Monotropa* have long been recognized as a single genus, the phylogeny we present strongly supports the recognition of two distinct genera. *Hypopithys* (*M. hypopithys*) forms a monophyletic group with *Pityopus*, while *Monotropa sensu stricto* (*M. uniflora*) forms a monophyletic assemblage with *Monotropis* and *Monotropastrum* (Asia). *Hypopithys* and *Monotropa* are further separated by the intervening genera *Allotropa* and *Hemitomes*. Within *Hypopithys* itself species and sub-species have been erected and subsequently synonymized to a remarkable degree. Small recognized five species in N. America, while in the most recent monograph Wallace rejected all such distinctions, choosing to synonymize some 80 putative species, subspecies and varieties in the Americas and Europe, noting 'there are no segregates that yet warrant taxonomic recognition'. Our analysis reveals five geographically circumscribed clades of *Hypopithys* in N. America alone---although the pattern is only partially congruent with Small's analysis---as well as a distinct Eurasian clade. This contrasts markedly with *Monotropa*, which exhibits no such structure in N. America at this level of phylogenetic resolution.

The Ohio State University Herbarium, Evolution, Ecology and Organismal Biology, 1315 Kinnear Rd, Columbus, OH, 43212, USA

407 ROSE, JEFFREY\*<sup>1</sup> and  
FREUDENSTEIN, JOHN<sup>2</sup>

### **A Tale of Two Pygmy Pipes: Quantifying Variation in *Monotropis* (Ericaceae)**

*Monotropis* is a genus of uncommon mycoheterotrophic plants endemic to the southeastern United States. Most recent taxonomic treatments treat the genus as monotypic, but past authors have recognized up to three species, based on variation in floral characters and differences in flowering time. No explicit quantitative analyses have previously been performed to assess this variation. We examined morphological and

molecular variation across the range of the genus and conclude that while entities that were defined based on differences in phenology are not distinct, there is a significant pattern of variation to warrant recognition of two species, *M. odorata* Schwein., found in the Appalachian Mountains from Maryland to northern Georgia, and *M. reynoldsiae* (A. Gray) Heller, restricted to north-central Florida. Recognition of the latter, which is a very uncommon species, has conservation implications.

<sup>1</sup>The Ohio State University, Evolution, Ecology And Organismal Biology, Museum Of Biological Diversity, Herbarium, 1315 Kinnear Rd., Columbus, OH, 43212, USA<sup>2</sup>Ohio State University, MUSEUM OF BIOLOGICAL DIVERSITY, 1315 KINNEAR RD, COLUMBUS, OH, 43212-1157, USA

408 JUDD, WALTER<sup>1</sup>, BUSH, CATHERINE<sup>2</sup>, FRITSCH, PETER<sup>3</sup> and  
KRON, KATHLEEN\*<sup>4</sup>

### **Phylogenetic relationships and morphological evolution in the Gaultherieae: combined molecular and morphological data**

The wintergreen group (Gaultherieae) previously has been shown to be monophyletic and include the currently recognized genera: *Chamaedaphne*, *Diplycosia*, *Eubotrys*, *Gaultheria*, *Leucothoe* and *Tepuia*. This clade can be characterized by the combined possession of pedicels articulated with the flower, usually axillary inflorescences, flowers on the shoots of the previous season and anthers often with 4 apical appendages. In this study 57 morphological characters of 65 species of *Gaultheria* representing all sections (10) and series (22) currently recognized, three species of *Diplycosia* and two species of *Tepuia* were analyzed with maximum parsimony (MP; PAUP 4.0). Sequence data from the chloroplast genes *matK* and *ndhF*, and the nuclear ribosomal ITS were analyzed using MP and maximum likelihood criteria (ML; RAxML). Combined morphology and molecular data were analyzed using MP. *Eubotrys racemosa* and *Leucothoe fontanesiana* were used as outgroups. Analysis of the morphological data alone resulted in a highly unresolved tree with most species in a large polytomy. Results of the combined molecular and morphological data resulted in a well-resolved tree that indicates *Gaultheria* as currently recognized is paraphyletic. *Diplycosia* and *Tepuia* are each monophyletic but are nested within a clade that also includes species of *Gaultheria*. *Diplycosia* is sister to *G. procumbens* and *Tepuia* is sister to the *G. hispidula* and *G. suborbicularis* pair. A potential synapomorphy for this clade is the presence of connate bracteoles. Although most morphological characters show homoplasy, some clades can be characterized by a combination of characters, e.g., the *G. ulei* to *G. thymifolia* clade with small leaves, inflorescences in fascicles and apical bracteoles. Based on the results a new classification of the Gaultherieae is proposed

that includes *Diplycosia* and *Tepuia* within *Gaultheria*.

<sup>1</sup>University of Florida, Department of Biology, Po Box 118526, Gainesville, FL, 32611, USA<sup>2</sup>Valdosta State University, Biology, 1500 N. Patterson St., Valdosta, GA, 31698, USA<sup>3</sup>California Academy Of Sciences, 55 Music Concourse Drive, SAN FRANCISCO, CA, 94118-4503, USA<sup>4</sup>Wake Forest University, Department Of Biology, 1834 Wake Forest Road, WINSTON-SALEM, NC, 27106, USA

**409 BUSH, CATHERINE\*<sup>1</sup>, FRITSCH, PETER<sup>2</sup> and KRON, KATHLEEN<sup>3</sup>**

### **A taxonomic revision of the genus *Gaultheria* (Ericaceae) in Australia and New Zealand.**

**A** taxonomic revision of the genus *Gaultheria* in Australia and New Zealand is presented. A total of 31 quantitative and 33 qualitative characters are documented for 17 taxa recognized in the region. Analyses include 23 box plots on the quantitative data and multiple PCAs performed on different combinations of vegetative and reproductive characters. The results indicate that ten taxa should be recognized. A recently described taxon, *G. viridicarpa*, is maintained as a distinct species. Varietal status in *G. depressa* is rejected. Several species have been synonymized: *G. parvula* (= *G. tasmanica*); *G. colensoi*, *G. crassa* and *G. paniculata* (= *G. rupestris*). Two previously named taxa are determined to be of hybrid status (*G. fluviatilis* = *G. antipoda* x *G. macrostigma*; *G. nubicola* = *G. depressa* x *G. tasmanica*). The treatment includes a key to the species, descriptions, distributions, molecular phylogenetic references and specimen citations.

<sup>1</sup>Valdosta State University, Biology, 1500 N. Patterson St., Valdosta, GA, 31698, USA<sup>2</sup>California Academy Of Sciences, 55 Music Concourse Drive, SAN FRANCISCO, CA, 94118-4503, USA<sup>3</sup>Wake Forest University, Department Of Biology, 1834 Wake Forest Road, WINSTON-SALEM, NC, 27106, USA

**410 POWELL, ELIZABETH\*<sup>1</sup>, DURCHHOLZ, ELAINE<sup>1</sup>, WILLIAMS, MALLORY<sup>1</sup>, GILLESPIE, EMILY<sup>2</sup>, EVANS, RODGER<sup>3</sup>, POLASHOCK, JAMES<sup>4</sup> and ROWLAND, JEANNIE<sup>5</sup>**

### **Evolutionary relationships of *Vaccinium* section *Cyanococcus* with a focus on the highbush blueberries**

**V***vaccinium* section *Cyanococcus* includes the ecologically and economically important blueberry species, *Vaccinium corymbosum* (highbush blueberry), *Vaccinium angustifolium* (lowbush blueberry), and *Vaccinium myrtilloides* (velvet-leaf blueberry). Species in section *Cyanococcus* are found from northern Canada, south to Florida and as far west as Illinois and are an ecologically important component of the shrub

community in acidic bogs, swamps, and heathlands throughout eastern North America. The evolutionary relationships of the blueberries from section *Cyanococcus* have been the subject of much debate but have not been adequately assessed using DNA sequence data. This study examines the evolutionary relationships of section *Cyanococcus* using the nuclear DNA region granule bound starch synthase (*waxy*). For this study we amplified *waxy* from all currently recognized species from section *Cyanococcus*, 17 other blueberry species from the blueberry tribe, and one outgroup (*Gaultheria*) and we analyzed the data using maximum parsimony, maximum likelihood, and Bayesian algorithms. Results indicate that section *Cyanococcus* is monophyletic and closely related to *V. stamineum* and *V. arboreum*. Results also show that the highbush blueberry species are found in several lineages within section *Cyanococcus*. A robust and resolved phylogeny of section *Cyanococcus* will provide critical information about the closest relatives of the economically important blueberry species and will provide a strong foundation for breeding and crop enhancement programs.

<sup>1</sup>University of Evansville, Biology, 1800 Lincoln Ave., Evansville, IN, 47722, USA<sup>2</sup>Wake Forest University, 226 Winston Hall, Wake Forest University, Winston-Salem, NC, 27109, USA<sup>3</sup>Acadia University, BIOLOGY DEPARTMENT, 33 Westwood Avenue, WOLFVILLE, NS, B4P 2R6, Canada<sup>4</sup>United States Department of Agriculture - ARS, GIVFL, Marucci Center for Blueberry and Cranberry Research & Extension, 125A Lake Oswego Rd., Chatsworth, NJ, 08019, USA<sup>5</sup>United States Department of Agriculture - ARS, GIVFL, Genetic Improvement of Fruits and Vegetables Lab, BARC-West, 10300 Baltimore Ave., Beltsville, MD, 20705, USA

**411 NAZAIRE, MARE\*<sup>1</sup> and HUFFORD, LARRY<sup>2</sup>**

### **A broad phylogenetic analysis of Boraginaceae: implications for the relationships of *Mertensia***

**M***Mertensia* (Boraginaceae) comprises approximately 45 species in both Asia and North America. The phylogenetic relationships of *Mertensia* are uncertain, and taxonomists have placed it in various tribes of subfamily Boraginoideae, with the most recent placement in Trigonotideae. The present study applies molecular phylogenetic methods to test the monophyly and closest relatives of *Mertensia*. We used DNA sequence data from the nuclear ribosomal internal transcribed spacer (nr-ITS) region and four chloroplast (cp) regions (*matK*, *ndhF*, *rbcl*, *trnL-trnF*) to examine the placement of over 70 new accessions representing over 25 species of *Mertensia* and accessions from approximately 70% of Boraginaceae genera obtained from GenBank. Preliminary phylogenetic reconstructions using maximum parsimony and maximum likelihood analyses show a topology largely congruent with previous molecular phylogenetic analyses of Boraginaceae, which had used

far fewer taxa. We recovered *Mertensia* as monophyletic and among its closest relatives was a clade consisting of *Myosotidium* and *Omphalodes*. Results from our broad sampling of the Boraginaceae provide insights on the major clades of the family and have important ramifications for the taxonomy of subfamily Boraginoideae.

<sup>1</sup>Washington State University, School of Biological Sciences, 312 Abelson Hall, P.O. Box 644236, Pullman, WA, 99164-4236, USA-

<sup>2</sup>Washington State University, SCHOOL OF BIOLOGICAL SCIENCES, 312 Abelson Hall, PULLMAN, WA, 99164-4236, USA

## 412 COHEN, JIM

### **A phylogenetic analysis of morphological and molecular characters of Boraginaceae: Taxonomic reevaluations and character evolution**

**B**oraginaceae, a family that includes ca. 112 genera and 1600 species, is one of the largest plant families without a comprehensive and critical phylogeny. Multiple generic- and tribal-level phylogenetic studies have provided evidence that the current taxonomy of the family is not aligned with modern practices; therefore, a family-wide phylogeny would be useful in the reevaluation of the taxonomy of Boraginaceae. To this end, a matrix of 23 morphological characters and multiple chloroplast DNA regions was constructed for approximately half of the genera of the family. The results of the phylogenetic analyses of this matrix recover four well supported, monophyletic tribes: Boragineae, Cynoglosseae, Echiochileae, and Lithospermeae. Among these tribes, Cynoglosseae exhibits greater variation in fruit morphology, while Lithospermeae shows more diversity in floral morphology. Among all members of the family, some characters, including cleistogamy and heterostyly, originated multiple times, whereas others, such as leaf venation and the presence/absence of floral bracts, are less variable, and tend to characterize larger clades. An understanding of the patterns of character evolution in the family will allow for the identification of characters or suites of characters that diagnose tribes and groups of genera.

Texas A&M International University, Biology and Chemistry, 5201 University Blvd, Laredo, TX, 78041, USA

## 413 BRESOWAR, GERALD EDWARD\*<sup>1</sup> and MCGLAUGHLIN, MITCHELL E<sup>2</sup>

### **Phylogenetics of the genus *Cryptantha* subgenus *Oreocarya* (Boraginaceae): A western North American endemic taxon**

**T**he Colorado Plateau/Great Basin flora contains a large number of taxa with rare and/or endemic species. The genus *Cryptantha* subgenus *Oreocarya* (Boraginaceae) is one such taxon. The Colorado Plateau of the Western U.S. is the center of diversity for the subgenus.

Geographic distributions and occurrence patterns within the subgenus vary from widespread and common, to narrowly endemic and rare. A phylogenetic study of the genus *Cryptantha* subgenus *Oreocarya* (Boraginaceae) is being conducted using the nDNA region *ITS* and the cpDNA regions *trnL-T*, *trnT-F*, and *trnQ-rps16*. The data indicate non-congruence between the cpDNA and nDNA phylogenies, with *ITS* data suggesting polyploidy in multiple species. Statistical support for topological structure is significant, though resolution is low. Tree topologies suggest a recent species radiation. This study is relevant to the understanding of evolutionary relatedness in a warm-desert plant taxon.

<sup>1</sup>University of Northern Colorado, Biology, 501 20th St., Greeley, CO, 80639, United States<sup>2</sup>University of Northern Colorado, Biology, 501 20th St, Greeley, CO, 80639, USA

## 414 GUILLIAMS, C. MATT\*<sup>1</sup> and BALDWIN, BRUCE G.<sup>2</sup>

### **Memoirs of a Frequent Flier - Molecular Phylogenetic Evidence for Multiple Long-Distance Dispersals of Popcorn Flowers (*Plagiobothrys*, Boraginaceae) Between North America and South America**

**P**lagiobothrys (Boraginaceae) is a predominantly New World genus of annual and perennial herbs, with approximately 55 minimal-rank taxa occurring in western North America and approximately 29 in temperate South America. Fruit morphology of *Plagiobothrys*, critically important in most taxonomic treatments, has been studied extensively but evolution in the genus has only recently been examined using molecular techniques. Here we present further results of molecular phylogenetic study of *Plagiobothrys*, analyses that are based on DNA sequence data from five non-coding regions (*ITS*, *ETS*, *trnL-trnF* intergenic spacer, *rps16* intron, and 3' *trnL* intron). With sampling of nearly all currently recognized taxa in *Plagiobothrys* and additional taxa in subtribe *Cryptanthinae*, we find continued support for the non-monophyly of both *Plagiobothrys* and *Cryptantha*. Three of five recognized sections within *Plagiobothrys* are recovered as monophyletic groups with strong support, including the predominantly vernal pool group, sect. *Allocarya*. Biogeographic analyses of *Plagiobothrys* and close relatives show a relatively large number of long-distance dispersal events from North America to South America by comparison with estimated dispersal histories for other amphitropically-distributed New World plant taxa.

<sup>1</sup>University of California, Berkeley, University and Jepson Herbaria, Department of Integrative Biology, 1001 Valley Life Sciences Building #2465, Berkeley, CA, 94720, USA<sup>2</sup>University Of California Berkeley, JEPSON HERB & DEPT INTEGR BIOL, 1001 Valley Life Sciences Building, MC 2465, Berkeley, CA, 94720-2465, USA

415 SCHORI, MELANIE

**Fruit Morphology and Anatomy in Aquifoliales**

**F**ruit morphology and anatomy are often neglected as sources of phylogenetically informative data for assessing patterns of evolution. A detailed comparative study of fruit structure in the eudicot order Aquifoliales (20 genera in five families) highlights the range of diversity present at the generic level in this basal campanulid clade. Four main fruit types are present: *Ilex* and *Helwingia* have a drupe with several pyrenes, *Phyllonoma* has a few-seeded berry, *Cardiopteris* has a symmetrically winged samara with one seed, and the other 16 genera all produce drupes with a single seed. Several unusual fruit morphologies occur, including a lateral fleshy appendage in seven genera of Stemonuraceae, and an accrescent terminal appendage in *Cardiopteris*. *Cantleya* and *Citronella* both exhibit invaginated endocarps. The fruits are also diverse anatomically, with two kinds of mucilage cells, several combinations of crystal types, tannin cells in three genera, abundant xylem fibers in Stemonuraceae, and gelatinized cell walls in *Gonocaryum*. Parthenocarpic fruits, examined from dioecious genera in three different families, differ anatomically from seed-bearing fruits. This diversity of fruit structure provides important new data for understanding relationships among members of Aquifoliales.

Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AG, UK

416 SCHORI, MELANIE\* and FURNESS, CAROL FURNESS

**Pollen Diversity in Aquifoliales**

**T**he order Aquifoliales, as currently circumscribed, includes 20 genera in five families, three of which are monogeneric. Pollen was obtained from 19 genera and examined with light and scanning electron microscopy. Shape varies from prolate to oblate, circular or triangular in polar view, with the latter angulaperturate. Pollen grains tend to be quite small, with many genera less than 25 µm along the longest axis. Although pollen generally does not vary substantially within a genus, pollen types within the order are relatively diverse. *Ilex*, *Helwingia*, *Phyllonoma*, and *Citronella* are tricolporate, *Gonocaryum* is cryptoporate, and the other genera are (1-)3(-6)-porate. Exine patterns range from psilate (*Leptaulus*) to echinate (*Discophora*, *Medusanthera*), reticulate (*Citronella*), striato-reticulate (*Whitmorea*), rugulate (*Gomphandra*), clavate (*Ilex*) and perforate (*Pseudobotrys*). Several interesting exine features are associated with apertures in certain genera. *Ilex* has colpi with a margo, *Pseudobotrys* has vestibulate pores, and *Cardiopteris* characterized by a ridge around each mesocopial face. This diversity indicates that pollen will

provide useful characters in future phylogenetic analyses of the order.

Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AG, UK

417 AHMAD PUAD, AIDA SHAFREENA\* and BARKMAN, TODD J

**Phylogenetics relationship of the genus *Schefflera* (Araliaceae) in Borneo, Malaysia inferred from chloroplast and nuclear DNA sequences**

**T**he molecular phylogeny of *Schefflera* in Borneo based on chloroplast DNA and nuclear ribosomal DNA was estimated to test the monophyly of *Schefflera* in Borneo and determine species relationships to the Asian clade. Based on study conducted in the past, the genus *Schefflera* comprises five unrelated clades distributed throughout all the major lineages of Araliaceae that correspond closely to geographic distribution: *Scheffleras.str.*, Neotropical *Schefflera*, Pacific *Schefflera*, African-Malagasy *Schefflera* and Asian *Schefflera*. Although Borneo is part of the Asian region, not a single species from Borneo was included in previous studies. To study the phylogenetic relationship of the genus *Schefflera* in Borneo we sequenced three noncoding cpDNA (*accD-psaI*, *psbA-trnH*, *trnL-trnF*) and the nrDNA ITS and 3'ETS regions. The analyses from maximum likelihood suggested that *Schefflera* in Borneo falls within the Asian clade. *Scheffleras* in Borneo are not monophyletic but rather are comprised of eight lineages from within the Asian clade. Some of the taxa are more closely related to Indonesian (West Papua) and New Guinea species while others are more closely related to Chinese species.

Western Michigan University, Biological Sciences, 3437 Wood Hall, 1903 W. Michigan Ave., Kalamazoo, MI, 49008, USA

418 ZAPATA, FELIPE

**Diversification in the mountains of South America: Phylogenetics and species limits in *Escallonia* (Escalloniaceae)**

**D**etailed knowledge of the evolutionary history and the species boundaries of organisms occurring in hotspots of biodiversity may provide valuable insights for unravelling the patterns and process underpinning biodiversity. *Escallonia* (Escalloniaceae), a morphologically and ecologically diverse genus with 39 species found throughout the Andes and the highlands of southeastern Brazil, provides an ideal opportunity to study the diversification of a group of woody plants from the biodiverse mountains of South America. Based on a comprehensive taxonomic and geographic sampling (35 species), I analyzed patterns of variation in molecular (3 unlinked markers; 100 accessions),

phenotypic (40 characters; 680 specimens) and bioclimatic (19 variables; 680 unique localities) variables to reconstruct the evolutionary history of *Escallonia* and evaluate species boundaries within this genus. Molecular phylogenetic analyses revealed i) that *Escallonia* is monophyletic, ii) a remarkable level of geographical phylogenetic structure, and iii) a widespread absence of species-level monophyly (22 species). These results are consistent with the hypothesis that geography played an important role early in the history of *Escallonia* by separating populations, which later diversified rapidly and/or recently in isolation. Morpho-geographic multivariate analyses showed evidence for morphological discontinuities supporting seven hypothesized species boundaries, suggesting that in this group neutral molecular variation and phenotypic variation may not be evolving in concert. Multivariate analyses of bioclimatic variables indicated that 12 hypothesized species differed in their bioclimatic niche, suggesting that these species, some sympatric, display differences in their present day selective regimes. Interpreting these three operational species criteria in the light of the General Lineage Species Concept (GLSC) suggests that most species (71%) within *Escallonia* represent distinct evolutionary lineages on independent evolutionary trajectories. Taken together, these results illustrate a powerful multidimensional approach to studying the diversification of a plant clade, emphasizing the collection and integration of a variety of biological data to illuminate our understanding on the origin and evolution of plant species.

University Of California, Department Of Integrative Biology, 3060 Valley Life Sciences Bldg. #3140, Berkeley, CA, 94720-3140, USA

419 CELLINESE, NICO\*, MAVRODIEV, EVGENY and CROWL, ANDY

### The phylogenetic utility of low-copy nuclear genes in Campanuloideae (Campanulaceae) with special focus on the evolution of NW Alpine *Campanula* endemics

The Campanuloideae comprise approximately 50 traditionally circumscribed genera and 1050 species. Although cosmopolitan, about 96% of taxa occur in the Old World, especially Eurasia and the Mediterranean basin. The majority of traditional genera are polyphyletic, including *Campanula* and *Wahlenbergia*. We will show the utility of recently developed low-copy markers in resolving low-level relationships within the Campanuloideae, especially in *Campanula*. We present a phylogeny that includes a small radiation of NW Alpine endemic taxa and compare resolution obtained using chloroplast genes alone.

University of Florida, Florida Museum of Natural History, Gainesville, FL, 32611, USA

420 GONZALEZ, FAVIO\*, GARZON, JAVIER and VELEZ, JORGE

### *Burmeistera* (Campanulaceae) revisited: A taxonomic account based on the Colombian species

After the cosmopolitan *Lobelia* L. (c 405 species), and the neotropical *Siphocampylus* Pohl (c 231 species) and *Centropogon* C. Presl. (c 212 spp.), *Burmeistera* (c 100 spp.) is the fourth largest genus of the Lobelioideae (Campanulaceae). The genus was erected by J. J. Triana in 1854, based on *B. ibaguensis*. Molecular and morphological characters indicate that *Burmeistera* is monophyletic, unlike the related *Centropogon*, *Lobelia*, and *Siphocampylus*, which have shown to be polyphyletic. The only infrageneric classification of *Burmeistera*, based on the presence or absence of a tuft of hairs on the ventral anthers, is in conflict with molecular data. The species of *Burmeistera* are herbs, subshrubs or sometimes shrubs up to 5 m tall, with whitish to yellow (sometimes red) bat-pollinated flowers. Most species have restricted distribution in low to high elevation (200 to 3000 m) cloud forests in Honduras, Costa Rica, Panama, Colombia, Venezuela, Peru and Ecuador. We revisited the taxonomy of the genus based on the study of the 47 Colombian species, thirty of which are exclusive to this country. Most Colombian species (c 80%) are restricted to the Western and the Central cordilleras, which could be related to a preference for volcanic soils. We described six new species, proposed twelve new synonyms, and clarified the nomenclatural and taxonomic issues related to the type species of the genus. Furthermore, we designated lectotypes for *B. ceratocarpa* Zahlbr., *B. ibaguensis*, and *B. rivina* E. Wimm., as well as a neotype for *B. mutisiana* (Kunth) E. Wimm. A careful examination of the hair tuft in the ventral anthers during floral development shows that this diagnostic character needs to be studied in preanthesis, as these hairs shrivel during anthesis. The presence of this hair tuft in the ventral anthers could be plesiomorphic in *Burmeistera*, as it is also present in the related genera *Centropogon*, *Lobelia*, and *Siphocampylus*. We propose the ebracteate peduncle as a potentially phylogenetically informative character within *Burmeistera*.

National University of Colombia, Institute of Natural Sciences, Apartado 7495, Bogota, Colombia

421 SIMMONS, MARK\*<sup>1</sup>, MCKENNA, MILES J.<sup>1</sup>, BACON, CHRISTINE D.<sup>1</sup>, YAKOBSON, KENDRA<sup>1</sup>, CAPP, JENNIFER J.<sup>1</sup>, ARCHER, ROBERT H.<sup>2</sup> and FORD, ANDREW J.<sup>3</sup>

### Phylogeny of Celastraceae tribe Euonymyae inferred from morphological characters and nuclear and plastid genes

The phylogeny of Celastraceae tribe Euonymyae (~230 species in eight genera in both the Old and New Worlds) was inferred using morphological characters together with plastid (*matK*, *trnL-F*) and nuclear (ITS and 26S rDNA) genes. Tribe Euonymyae has been defined as those Celastraceae genera with generally opposite leaves, isomeric carpels, loculicidally dehiscent capsules, and arillate seeds (except *Microtropis*). *Euonymus* is the most diverse (129 species) and widely cultivated genus in the tribe. We infer that tribe Euonymyae consists of at least six separate lineages within Celastraceae and that a revised natural classification of the family is needed. *Microtropis* and *Quetzalia* are inferred to be distinct sister groups that together are sister to *Zinowiewia*. The endangered *Monimopetalum chinense* is an isolated and early derived lineage of Celastraceae that represents an important component of phylogenetic diversity within the family. *Hedraianthera* is sister to *Brassiantha*, and we describe a second species (*Brassiantha hedraiantheroides* A.J.Ford) that represents the first reported occurrence of this genus in Australia. *Euonymus globularis*, from eastern Australia, is sister to *Menepetalum*, which is endemic to New Caledonia, and we erect a new genus (*Dinghousia* R.H.Archer) for it. The Madagascan species of *Euonymus* are sister to *Pleurostyliya* and recognized as a distinct genus (*Astrocassine* ined.). *Glyptopetalum*, *Torrallbasia*, and *Xylonymus* are all closely related to *Euonymus* sensu stricto, and questionably distinct from it. Current intrageneric classifications of *Euonymus* are not completely natural and require revision.

<sup>1</sup>Colorado State University, Department Of Biology, FORT COLLINS, CO, 80523-1878, USA<sup>2</sup>South African National Biodiversity Institute, National Herbarium, Pretoria, Republic of South Africa<sup>3</sup>Cairo, Ecosystem Sciences, Atherton, Queensland, Australia

422 SAMARAKOON, THARANGAMALA\*<sup>1</sup> and ALFORD, MAC<sup>2</sup>

### Taxonomic Revision of *Casearia* Species in South-Central Asia

*Casearia* Jacq. is the largest genus of the flowering plant family Samydeaceae. It is found throughout the tropics and consists of about 200 species of small to medium sized trees. Within Samydeaceae, *Casearia* are distinguished from other genera by having her-

maphroditic flowers with a single series of staminodes (=disk glands) and a well-developed style. Taxonomic revisions have covered all *Casearia* species throughout the world except the species present in south central Asia including Pakistan east to Burma and south to Sri Lanka. This investigation mainly aims to resolve the taxonomic problems of *Casearia* species present in south central Asia, to prepare detailed descriptions of the taxa with illustrations, to infer their relationships to other species and biogeographical areas, and to build a robust taxonomic key to identify them. Different taxonomists have described as many as 15 species and as few as 6 species in south central Asia. Some of these species are doubtful due to misleading morphological characters such as variable leaf morphology and pubescence, lack of ample sampling and nomenclatural conflict. A thorough investigation of morphological and phenological characters combined with geographical distribution support the delineation of 13 *Casearia* species in south central Asia, namely: *C. andamanica*, *C. bourdillonii*, *C. glomerata*, *C. graveolens*, *C. grewiiifolia*, *C. kurzii*, *C. rubescens*, *C. sikkimensis*, *C. thwaitesii*, *C. tomentosa*, *C. vareca*, *C. wynnadensis* and *C. zeylanica*. This revision includes nomenclatural justification, taxonomic description, and geographical distribution of each species.

<sup>1</sup>University Of Southern Mississippi, Department Of Biological Sciences, Alford Lab, 118 College Drive #5018, Hattiesburg, MS, 39406, USA<sup>2</sup>University Of Southern Mississippi, Department Of Biological Sciences, 118 COLLEGE DRIVE #5018, HATTIESBURG, MS, 39406-0001, USA

423 VELA DIAZ, DILYS

### *Calophyllum* L. (Calophyllaceae) in South America: the utility of anatomical characters combined with multivariate analyses.

Opposite leaves, secondary parallel venation, and yellow resin are characters that distinguish *Calophyllum*, a tropical tree, among other Calophyllaceae. Overlapping floral and vegetative characters at intra- and inter-species level has made delimitation of *Calophyllum* species challenging. Eight species have been recognized in South America, but the last revision of the genus there is over a century old. A detailed study of South American species is needed to understand patterns of variation there, especially within *C. brasiliense*, the most variable species. Multivariate analyses and anatomical characters have been useful in disentangling species complexes. Multivariate analyses of morphological and anatomical characters were performed at three different geographic levels for *Calophyllum*. At the general level, all specimens were included; at the regional level, different ecological regions were the foci; and at the local level, political divisions (e.g. countries) were the units used. In total, thirteen preliminary morphogroups were identified using 32 morphological characters of the leaf, flower and fruit, taken from 400 specimens, and 18 ana-

tomical leaf characters observed on 45 specimens. Principal Component Analyses (PCA) and Discriminant Analyses (DA) were performed, DA being used only for those PCAs that showed potential groups. Only five species were supported by both multivariate analyses and morphological and anatomical characters. Key characters included leaf blade length and width and anatomical characters like presence/absence of hypodermis, amount of sclerenchymatous tissue associated with resin canal, and orientation of resin canals at the leaf margin. This study is the first to integrate both morphological and anatomical characters in a multivariate framework for *Calophyllum* species. Taxonomic treatment of South American *Calophyllum* species based on the results of this study will be discussed; two new species need to be described, including one from Central America.

University Of Missouri - St. Louis, Department Biology, 223 Research Building, One University Blvd., Saint Louis, MO, 63121-4499, USA

#### 424 BALLARD JR, HARVEY

### Delineating taxon boundaries in two confusing species complexes of Mesoamerican *Hybanthus* (Violaceae)

Two confusing species complexes with morphologically overlapping taxa reside under *Hybanthus*. Neither has been adequately studied to date but collectively represent a considerable percentage of Mesoamerican hybanthoid specimens in herbaria. To clarify taxonomic boundaries in each complex, we used traditional herbarium methods, phenetic analysis and pollen stainability as evidence for decisions. The *Hybanthus thiemei* complex, with long filiform pedicels and petioles and strongly zygomorphic corollas, consists of *H. longipes* and *H. thiemei*, putatively differing in pedicel length and capsule pubescence. After assigning specimens to glabrous versus puberulent capsules, features of stem, petiole and leaf blade, and mature flowers, were measured and subjected to canonical variates analysis. The capsule pubescence phenotypes were fully intergradient, with highly variable petiole and pedicel length, and no feature besides capsule pubescence provided separation, suggesting that *H. longipes* should be synonymized under *H. thiemei*. The *Hybanthus elatus* complex, with beaked capsules and elliptical to lanceolate leaves, consists of *H. elatus* in western Guatemala, *H. potosinus* in northern Mexico, *H. verbenaceus* in central and southern Mexico, and *H. brevis* in Chiapas and western Guatemala. The last has mostly been ignored since description or synonymized under *H. elatus*. Distinctive pubescence type and distribution were used to assign specimens to taxa. Canonical variates analysis largely separated specimens based on leaf shape and blade margin, and it consistently placed *H. brevis* between specimens of lower-elevation *H. verbenaceus* and higher-elevation *H. elatus*. Analysis of floral and fruit features further distinguished all four taxa. Pollen

stainability was high (>86%) in *H. elatus*, *H. potosinus* and *H. verbenaceus* but statistically lower (52-77%) in *H. brevis*. Morphological intermediacy, intermediate montane slope position, monospecific populations, and depressed fertility but substantial seed production raise the possibility that *H. brevis* is a partially stabilized hybrid derivative of *H. elatus* and *H. verbenaceus*.

Ohio University, ENVIR & PLANT BIOLOGY-PORTER H, 315 Porter Hall, Athens, OH, 45701-2979, USA

#### 425 FLICKER, BEN\*<sup>1</sup> and BALLARD JR, HARVEY<sup>2</sup>

### Molecular phylogeny of *Hybanthus enneaspermus* (L.) F. Muell. (Violaceae) species complex from the Old World Tropics

The *Hybanthus enneaspermus* species complex (Violaceae) in the old world tropics is a group consisting of about 20 species of mostly herbs and subshrubs. *Hybanthus enneaspermus sensu stricto* is a vegetatively polymorphic herb that is widespread throughout the group's range in the paleotropics. The other taxa are mostly woody subshrubs with narrow distributions scattered around Africa, Madagascar, Southeast Asia, and northern Australia. Representatives of the narrow endemics as well as representatives of *H. enneaspermus* s.s. from all over its range were sampled for DNA sequencing. Analysis of both nuclear (ITS) and chloroplast (trnL-F) markers indicate that the woody shrubs and subshrubs are the basal taxa within the complex and that *H. enneaspermus* is polyphyletic with other herbaceous endemics nested within. Phylogenetic results and inferred biogeographic histories are presented and discussed.

<sup>1</sup>Ohio University, Environmental and Plant Biology, Porter Hall Rm. 317, Athens, OH, 45701, USA <sup>2</sup>Ohio University, Environmental & Plant Biology, 315 Porter Hall, Athens, OH, 45701, USA

#### 426 PORTER-UTLEY, KRISTEN\*<sup>1</sup>, KROSINICK, SHAWN<sup>2</sup>, MCDADE, LUCINDA<sup>3</sup>, JOLLES, DIANA<sup>4</sup>, JØRGENSEN, PETER M.<sup>5</sup> and MACDOUGAL, JOHN M.<sup>6</sup>

### Untangling the passionflower vines: insights on the phylogeny of *Passiflora* subg. *Decaloba* based upon cytGS, ITS, ncpGS, ndhF, and trnL-F sequences

*Passiflora* is a large genus of ca. 550 species of vines, lianas, and trees known for its incredible morphological diversity and stunningly beautiful flowers. The genus is currently recognized with five subgenera: *Astrophea*, *Decaloba*, *Deidamioides*, *Passiflora*, and *Tetrapatheia*. The largest and most diverse subgenera are *Passiflora* and *Decaloba*, each consisting of ca. 235 spe-

cies. Due to its economic significance, subg. *Passiflora* has been the focus of most recent scientific study. The equally fascinating and species-rich subg. *Decaloba* has been largely ignored, yet this group displays equivalent morphological and ecological variation. Moreover, it consists of many species that are currently recognized as threatened or endangered and has special biogeographic significance in that it is the only clade in the genus with species naturally present in both the New and Old World. Subgenus *Decaloba* contains eight supersections, of which only two, *Disemma* and *Cieca*, have been tested for monophyly. Thus, we present here a preliminary phylogenetic analysis of subg. *Decaloba*-based on *cytGS*, *ncpGS*, *ndhF*, *ITS*, and *trnL-F* data and including taxa that represent all supersections in subgenus *Decaloba*. These data support the monophyly of supersections *Auriculata*, *Bryonioides*, *Cieca*, *Decaloba*, *Disemma*, *Hahniopathanthus*, and *Pterosperma*, but suggest that *Multiflora* is polyphyletic as currently defined. Morphological and molecular synapomorphies for the monophyletic lineages are provided. We also use the molecular dataset to explore rates of diversification across the subgenus. Recent analyses with limited sample sizes have suggested that rates of nucleotide substitution have been relatively constant across *Decaloba*. Given the morphological variability observed in this clade, these conclusions are revisited and possible explanations for this diversity are considered. This is the third presentation stemming from NSF 0717084 to PIs P.M. Jorgensen, S. Krosnick, J.M. MacDougal, L. McDade, and K. Porter-Utley.

<sup>1</sup>Keene State College, Biology, 229 Main St., MS-2001, Keene, NH, 03435, United States <sup>2</sup>Southern Arkansas University, Biology, 100 E. University, P.O. Box 9222, Magnolia, AR, 71753, USA <sup>3</sup>Rancho Santa Ana Botanic Garden, Department Of Botany, 1500 N. College Avenue, Claremont, CA, 91711, USA <sup>4</sup>Rancho Santa Ana Botanic Garden, Claremont Graduate University, 1500 North College Avenue, Claremont, CA, 91711, USA <sup>5</sup>Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166, USA <sup>6</sup>Harris-Stowe State University, Math and Sciences, 3026 Laclede Avenue, St. Louis, MO, 63103, USA

**427 GARDNER, ANDREW\*<sup>1</sup>,  
EMSHWILLER, EVE<sup>2</sup>, VAIO,  
MAGDALENA<sup>3</sup>, GUERRA FILHO,  
MARCELO<sup>3</sup>, OBERLANDER, KENNETH<sup>4</sup>,  
DREYER, LEANNE<sup>5</sup> and HEIBL,  
CHRISTOPH<sup>6</sup>**

**From woody shrubs to weedy, succulent,  
and bulb-bearing herbs: an updated  
phylogeny for *Oxalis***

The genus *Oxalis* (Oxalidaceae) is extremely diverse in morphology, habitat, and geographic range. Among the 500+ species, there are woody shrubs inhabiting the Atlantic rainforests of Brazil, succulent Andean tuber crops, cosmopolitan weedy annuals, and bulb-bearers in southern Africa and many regions of the

Americas. Leaves are not only trifoliate, but also unifoliate and pinnately or palmately-compound. Breeding systems include tristylly, distylly, and (semi-) homostylly. Earlier taxonomic and recent phylogenetic work has addressed groups within this complex genus, but never *Oxalis* as a whole. A representative phylogeny for the entire genus will be crucial for our understanding of the evolutionary transitions that have led to the incredible diversity we see in the extant species of *Oxalis*. We present our most recent phylogenetic inference for the genus based on plastid and nrITS sequence data, using the phylogeny to reconstruct its morphological and geographical diversification. Among our key inferences are transitions from woody morphology to diverse storage morphologies, from pinnately-compound to unifoliate and palmately-compound leaves, from tristylly to several other forms of heterostylly, and from exclusively South American to African, North American, and cosmopolitan distributions.

<sup>1</sup>University Of Wisconsin-Madison, Botany, 430 Lincoln Dr., Madison, WI, 53706, USA <sup>2</sup>University Of Wisconsin-Madison, Botany Dept, 321 Birge Hall, 430 Lincoln Drive, Madison, WI, 53706-1313, USA <sup>3</sup>Federal University of Pernambuco, Botany, Rua Nelson Chaves s/n, Recife, PE, 50670-420, Brazil <sup>4</sup>Stellenbosch University, Conservation Ecology and Entomology, Private Bag X1, Matieland, 7602, South Africa <sup>5</sup>Stellenbosch University, Botany And Zoology, Private Bag X1, Matieland, 7602, South Africa <sup>6</sup>University Of Munich, Biology

**428 BABINEAU, MARELLE\*<sup>1</sup> and  
BRUNEAU, ANNE<sup>2</sup>**

**Systematics of three closely related and  
endangered Legume genera (*Delonix*,  
*Colvillea* and *Lemuropisum*): implications  
for Malagasy-African dispersion during  
the Tertiary.**

The genus *Delonix* comprises eleven species: nine are endemic to Madagascar and the two others occur in East Africa. *Delonix* is considered to be paraphyletic with regards to its closest relatives, two monospecific genera endemic to Madagascar: *Colvillea* and *Lemuropisum*. All of the above species are endangered despite being important ecological trees of local and worldwide economic interest. However, to argue for their protection it is essential to account for the genetic uniqueness of each and to establish their past and present evolutionary relationships. This study aims to clarify phylogenetic relationships within this trigenic clade and to estimate divergence times, geographical origin and dispersal patterns. Parsimony and Bayesian analyses, based on four chloroplast (*matK*, *trnL-F*, *trnD-T*, *rps16*) and three nuclear (*ITS*, *Leafy*, *tRALS*) markers, strongly refute the monophyly of *Delonix* with *Lemuropisum* occurring as nested within it. *Colvillea* is a unique lineage sister to *Delonix*. Our analyses suggest rapid speciation of *Delonix*, with species showing numerous morphological, ecolog-

ical and pollination differences, but low genomic variation. Seven clades are found which are congruent with morphological classifications, except that the two African species generally do not group together. A biogeographical analysis, together with a penalized likelihood fossil-calibrated method, shows at least one clear event of dispersal from Madagascar to East Africa around 30 Ma. This could have been facilitated by the presence of a land bridge from 25–40Ma in the Mozambique canal. Our analyses support recent studies indicating that the flora of Madagascar is not necessarily derived from African ancestors. The geographical pattern also indicates a spatial tendency where southern xerophytic woodland lineages are derived relative to northern deciduous forest species. Based on our studies, conservation efforts and classification should 1) consider *Colvillea* as an evolutionary and morphologically unique genus, 2) treat *Lemuropisum* as a specialised species within *Delonix*, and 3) emphasise protection of the three diversity centers observed for *Delonix*, which presently are poorly covered by national parks.

<sup>1</sup>Centre sur la Biodiversité, Institut de Recherche en biologie végétale, 4101 rue Sherbrooke est, Montreal, Qc, H1X 2B2, Canada<sup>2</sup>Université de Montréal, Institut de Recherche en Biologie Végétale, 4101 Sherbrooke Est, Montreal, Qc, H1X 2B2, Canada

**429 FOUQ»RE-DANEZAN, MARIE<sup>1</sup>, ZHANG, LI-BING\*<sup>2</sup>, JOLY, SIMON<sup>3</sup>, BRUNEAU, ANNE<sup>4</sup> and GAO, XIN-FEN<sup>5</sup>**

### **Phylogenetic relationships in the genus *Rosa* as inferred from chloroplast and nuclear markers**

Roses are of worldwide economic importance as ornamental shrubs, cut flowers, for perfumes, scents industry and pharmaceutical research. However, despite substantial recent efforts, little is known on the evolution of roses to date. There are about 150 to 200 species of roses widely distributed throughout the temperate and subtropical habitats of the northern hemisphere of which 95 (65 endemic) occur in China. The Chinese roses have been to date constantly undersampled and understudied. Considering that China gathers almost half of the wild species of roses in the world and that several of these species have been hypothesized to have made major contributions to the modern commercial rose it is of great importance to study wild Chinese species. The most frequently used classification (Rehder 1940) divides the genus *Rosa* into four subgenera (*Eurosa*, *Hesperhodos*, *Hulthemia*, and *Platyrhodon*) and the subgenus *Eurosa* into ten sections (*Banksianae*, *Bracteatae*, *Caninae*, *Carolinae*, *Cinnamomae*, *Gallicanae*, *Indicae*, *Laevigatae*, *Pimpinellifolia*, and *Synstyliae*). We use both chloroplast (*trnL* intron, *trnL-F* spacer, *psbA-trnH* spacer) and nuclear markers (*GAPDH*) to resolve the relationships among wild roses of the world with a particular emphasis on Chinese roses. Our results strengthen previous findings that most of the subdivi-

sions of Rehder are not monophyletic but reveal that some clades are roughly consistent with some of them. Several hybridization events are also revealed by comparison of chloroplast and nuclear phylogenies. The genetic database obtained will be used to solve the origin of some of the cultivars of this genus.

<sup>1</sup>Chengdu Institute of Biology, Chinese Academy of Sciences, The ECORES Lab, P.O. Box 416, Chengdu, Sichuan, 610041, China<sup>2</sup>Missouri Botanical Garden, Science and Conservation, P.O. Box 299, St. Louis, MO, 63166, USA<sup>3</sup>McGill University, Biology Department, 1205 Docteur Penfield, Montréal, Québec, H3A 1B1, Canada<sup>4</sup>Université de Montréal, Institut de Recherche en Biologie Végétale, Sherbrooke Est 4101, Montréal, Québec, H1X 2B2, Canada<sup>5</sup>Chengdu Institute of Biology, Chinese Academy of Sciences, The ECORES Lab, Chengdu, Sichuan, 610041, China

**430 DICKINSON, TIM\*<sup>1</sup>, ZARREI, MEHDI<sup>1</sup>, KUZMINA, MARIA<sup>2</sup> and STEFANOVIC, SASA<sup>3</sup>**

### **Mixed success with DNA barcoding of hawthorns (*Crataegus* L., Rosaceae)**

The genus *Crataegus* is one in which the promises of DNA barcoding make this technology extremely attractive. *Crataegus* species can be notoriously hard to identify on the basis of morphology. Both flowering and fruiting specimens from a given individual may be needed for a definitive identification, in addition to field observations of features that are not preserved in herbarium material (e.g. color of the undehiscent anther, time course of fruit color development). We have drawn on a reference collection of voucher specimens and field-collected silica gel dried tissue of North American and Eurasian *Crataegus* taxa representing 50 species, and have used two standard barcode loci (*rbcl* and *matK*) and two supplementary markers (*ITS2* and *psbA-trnH*) that have been proposed for plants. Our results suggest that routine DNA barcoding may have limited utility in *Crataegus*, and possibly also within Rosaceae subtribe Pyrinae (equivalently, the fleshy-fruited members of subfamily Maloideae). We were unable to get sequences of *matK*, but succeeded with *psbA-trnH*, *rbclA*, and *ITS2*. Despite earlier successes using *psbA-trnH* together with three other cpDNA spacer regions in phylogenetic studies, *psbA-trnH* by itself (185 sequences for 49 species) yielded an NJ tree with virtually no resolution. Greater resolution was obtained using *rbclA* (189 sequences for 49 species), as four species (18 accessions) were resolved in the NJ tree. These results with cpDNA loci are not surprising in view of how poorly these loci resolve genera in the Pyrinae, to say nothing of species in *Crataegus*. Fewer sequences (118, for 40 species) were obtained with *ITS2* amplified from genomic DNA. Nevertheless, with *ITS2* at least nine species were resolved as monophyletic, and other clades comprised members of a single series or section of the genus. However, one diploid species and a polyploid species complex were each polyphyletic on the NJ tree, suggesting

the amplification of more than one ITS2 paralog.

<sup>1</sup>Royal Ontario Museum, Natural History, Green Plant Herbarium (TRT), 100 Queen's Park, Toronto, ON, M5S 2C6, Canada<sup>2</sup>Biodiversity Institute of Ontario, University of Guelph, 50 Stone Rd East, Guelph, ON, N1G 2W1, Canada<sup>3</sup>University Of Toronto At Mississauga, Department Of Biology, 3359 Mississauga Rd N, Mississauga, ON, L5L 1C6, Canada

#### 431 WHITTEMORE, ALAN

##### Ploidy races in *Ulmus americana*

American elm (*Ulmus americana*) is a widespread canopy tree of eastern North America. Once common in horticulture and in the wild, it has been heavily impacted by Dutch elm disease, caused by an Asian fungus. Long considered the sole tetraploid in the otherwise diploid genus *Ulmus*, *U. americana* includes both diploid and tetraploid populations, with tetraploids being more widespread. Diploids and tetraploids may co-occur in the same area, sometimes in the same stand. The genetic relationship between the two ploidy levels is being clarified by further investigation of the geographical distribution of different ploidies within and among stands, and investigation of plants of known ploidy using SSR markers.

UNITED STATES NATIONAL ARBORETUM, 3501 NEW YORK AVENUE, WASHINGTON, DC, 20002-1958, USA

#### 432 OCAMPO, GILBERTO\* and ALMEDA, FRANK

##### Systematic and phylogenetic significance of seed micromorphology in the tribe Miconieae (Melastomataceae): Preliminary results

The Melastomataceae are among the most diverse families of flowering plants with more than 5,000 species. Within the family, the tribe Miconieae (restricted to the Neotropics) displays the largest radiation, with over 1,800 described taxa. Previous studies have shown that the tribe is highly variable in seed micromorphology. Some of this seed diversity is of potential use in identifying synapomorphies for certain clades. The present work shows preliminary results derived from the study of seeds of more than 200 species (ca. 10% of the diversity of the tribe), sampled across the Miconieae. Seeds were examined with scanning electron microscopy (SEM) to study their micromorphological details. As a result, a series of characters to describe the seed morphological diversity in the tribe are proposed. In addition, characters were coded in a data matrix and subject to ancestral character reconstruction. An interactive identification key using SEM images and the proposed characters is under development and will be available to the public through the Planetary Biodiversity Inventory in Miconieae website (<http://sweetgum.nybg.org/melastomataceae/>).

<http://sweetgum.nybg.org/melastomataceae/>).

California Academy of Sciences, Botany, 55 Music Concourse Drive, Golden Gate Park, San Francisco, CA, 94118, USA

#### 433 KRIEBEL, RICARDO\*<sup>1</sup> and MICHELANGELI, FABIÁN ARMANDO<sup>2</sup>

##### Phylogeny of *Conostegia* (Melastomataceae) reveals multiple losses of herkogamy

*Conostegia* is a genus within the exclusively Neotropical and berry fruited tribe Miconieae, and consists of about 42 species concentrated in Northern South America, Central America and the Caribbean. Traditionally *Conostegia* has been defined by the combination of having a calyprate calyx that dehisces at anthesis, and pleiostemonous flowers (having more than double the number of stamens than petals). To test the monophyly of *Conostegia*, we gathered sequence data from two nuclear loci (*nrITS* and *nrETS*) and four chloroplast spacers (*accD-psaI*, *atpF-H*, *psbKL*, *trnS-G*) for thirty of the forty two recognized species. Our results corroborate previous molecular phylogenetic studies which demonstrated that *Conostegia* is paraphyletic and includes several species currently in *Clidemia* and *Miconia*, although not *Leandra subulata* and *Tococa spadiciflora* as had been found in previous analyses. The calyprate calyx has evolved at least three times independently in the *Conostegia* clade and was lost at least once. The degree of pleiostemony appears to be correlated to the type of herkogamy present. Four types of herkogamy were observed in the *Conostegia* clade, approach herkogamous flowers in which the style is exerted well beyond the anthers, a second type of approach herkogamous flowers similar to the first but with the style also bending to one side of the flower, a third type of approach herkogamous flowers with the style the same length as the stamens but deflected in opposite direction to them, and blossoms with giant stigmas which are hypothesized to be large pollen receivers. The latter four types of herkogamy help to diagnose subclades within *Conostegia*. In addition, herkogamy has been lost at least three times within the *Conostegia* clade. Only species within two of the non herkogamous subclades have reached the Caribbean islands. Our data in addition to published observations of self-compatibility in non herkogamous *Conostegia montana* lead us to hypothesize that the loss of herkogamy is a pre-adaptation for long distance dispersal and successful colonization.

<sup>1</sup>The New York Botanical Garden / Graduate Center, CUNY, 2900 Southern Blvd., Bronx, NY, 10458, USA<sup>2</sup>The New York Botanical Garden, Institute Of Systematic Botany, 2900 Southern Blvd., Bronx, NY, 10458, USA

434 CADDAH, MAYARA KRASINSKI\*<sup>1</sup>,  
MICHELANGELI, FABIÁN ARMANDO<sup>2</sup> and  
GOLDENBERG, RENATO<sup>3</sup>

**Taxonomic and phylogenetic studies  
on *Miconia* sect. *Glossocentrum*  
(Melastomataceae)**

Melastomataceae is one of the most diverse families of flowering plants. *Miconia* is its biggest genus, comprising about 1070 species and along with other 17 related genera it comprises the tribe Miconieae, reaching over than 1800 species. The most recent revision of the family was conducted by Cogniaux over than a century ago, when *Miconia* was composed of less than half of the species currently known. Recent phylogenetic insights advocate for a new approach for the infrafamilial classification, suggesting that *Miconia* is a complex polyphyletic genus, with other large genera such as *Leandra*, *Clidemia*, *Ossaea*, *Tococa*, *Conostegia*, and several others embedded within it. Similarly, recent analyses show a lack of support for the infrageneric classification of *Miconia*. *Miconia* sect. *Glossocentrum* has about 90 species, distributed from Central America and Caribbean Islands to Southern Brazil, Argentina and Paraguay. The section is characterized by short and linear stamens, 1-porate, with innapendiculate or just dorsally appendiculate connectives. Here we present a phylogenetic study of *Miconia* sect. *Glossocentrum* using four plastidial (*trnS-G*, *accD-psaI*, *psbI-K* and *atpF-H*) and two nuclear (ETS and ITS) loci. These analyses reveal that the section is highly polyphyletic, but about half of the species form a well-supported clade, the *Miconia discolor* group. This group can be morphologically characterized by its glomerulate or scorpioid inflorescences, stamens without conspicuous appendices in the connectives, leaves with the abaxial surface moderately to densely covered by branched hairs, and a distribution restricted to the Atlantic Forest and associated biomes. However, no specific morphological character or character combination is able to completely circumscribe the clade, mirroring the problematic morphological circumscriptions of most genera and sections within tribe. The species of section *Glossocentrum* with regular inflorescences, glabrous leaves, and/or wide distribution are resolved far away from the *Miconia discolor* group, and do not form a cohesive group.

<sup>1</sup>State University of Campinas, Plant Biology, Rua Monteiro Lobato, 255, Cidade Universitária Zeferino Vaz, Campinas, SP, 13083970, Brazil<sup>2</sup>The New York Botanical Garden, Institute Of Systematic Botany, 2900 Southern Blvd., Bronx, NY, 10458, USA<sup>3</sup>Universidade Federal do Paraná, Botânica, Campus Politécnico, Jardim das Américas, Curitiba, PR, 81531970, Brazil

435 DE-NOVA, ARTURO\*<sup>1</sup>,  
MAGALLON, SUSANA<sup>2</sup>, MEDINA,  
ROSALINDA<sup>3</sup>, MONTERO, JUAN CARLOS<sup>3</sup>,  
WEEKS, ANDREA<sup>4</sup>, ROSELL, JULIETA<sup>5</sup>,  
OLSON, MARK<sup>6</sup> and EGUIARTE, LUIS<sup>7</sup>

**Evolutionary Diversification in Species-  
Rich Mesoamerican Seasonally Dry  
Tropical Forests: *Bursera* (Burseraceae,  
Sapindales) as a Case Study**

Mesoamerican arid biomes epitomize Neotropical rich and complex biodiversity. To document some of the processes underlying the vast species richness of Mesoamerican Seasonally Dry Tropical Forests (SDTFs), and to evaluate specific predictions about the age, geographical structure and niche conservatism of SDTF-centered woody plant lineages, we consider the genus *Bursera* as a case study. Using a nearly complete species-level phylogeny from nuclear and plastid genomic markers, we estimate divergence times, test for phylogenetic and temporal diversification heterogeneity, test for geographical structure, and reconstruct habitat shifts. *Bursera* split from *Commiphora* in the earliest Eocene, and by the middle Eocene, its major lineages were distinct. Most living species of *Bursera* originated during independent early Miocene consecutive radiations that took place in SDTFs, uncoupled from habitat shifts. The late Miocene average age of *Bursera* species, their geographical structure and strong conservatism to SDTFs conform to expectations derived from South American SDTF-centered lineages. Nevertheless, *Bursera*'s geographical structure is comparatively weak, suggesting that SDTF attributes that shape the evolution of SDTF-centered lineages are relaxed in Mesoamerica. The Miocene diversifications of *Bursera* are congruent with enhanced aridity in Mesoamerica resulting from global cooling and rain shadows caused by increased orogeny.

<sup>1</sup>Universidad del Mar, Puerto Escondido, Instituto de Genética, Ciudad Universitaria Km. 3.5, Carr. Puerto Escondido-Sola de Vega, Distrito de San Pedro Mixtepec, Puerto Escondido, Oaxaca, 71980, Mexico<sup>2</sup>Instituto De Biología, Universidad Nacional Autónoma De México, 3er Circuito De Ciudad Universitaria, Del. Coyoacan, A.P. 70-233, Mexico City, Mexico D.F., N/A, 04510, Mexico<sup>3</sup>Universidad Nacional Autónoma de México, Instituto de Biología, 3er Circuito de Ciudad Universitaria, Del. Coyoacan, Mexico City, Mexico D.F., 04510, Mexico<sup>4</sup>George Mason University, 4400 University Drive MSN 5F2, Fairfax, VA, 22030, USA<sup>5</sup>Club America 8-1, Villa Lazaro Cardenas, Mexico, D.F., 14370, México<sup>6</sup>5084 Santa Susana Place, Santa Barbara, CA, 93111, USA<sup>7</sup>Instituto De Ecología, UNAM, Apartado Postal 70-275, C.U., Coyoacán, México, C.P.04510, Mexico

**436 ADEYEMI, TEMITOPE OLABISI\*,  
OGUNDIPE, OLUWATOYIN TEMITAYO  
and OLOWOKUDEJO, JAMES DELE**

**Epidermal Morphology of African  
Sapindaceae**

**S**apindaceae is one of the most important plant families in the tropics particularly in Africa most widely known for their use in medicine. Foliar epidermal studies were carried out on some representative members of the family sapindaceae in Africa. Fifty (50) taxa representing a total of fifteen (15) genera were studied and illustrated with scanning electron microscopy (SEM). This revealed that the family exhibits a diverse range of characters, with no one feature being diagnostic. Most members of the family are hypostomatic. They exhibit anomocytic or paracytic stomata types; simple, nonglandular, glandular or stellate trichomes and straight, wavy or curved anticlinal wall patterns. Papillae are present in some members while others possess striae. A brief description of the epidermis of all genera studied is given, and character combinations are discussed which may allow the identification of these taxa.

University of Lagos, Botany, University of Lagos, Akoka, Yaba, Lagos, LAGOS, 23401, Nigeria

**437 NEUBIG, KURT\*<sup>1</sup>, BLANCHARD,  
ORLAND<sup>2</sup>, SCHWARTZ, EMILY<sup>1</sup> and  
MCDANIEL, STUART<sup>1</sup>**

**Molecular phylogenetics of *Kosteletzkya*  
(Malvaceae, Hibisceae) reveals multiple  
polyploid speciation events**

**K***osteletzkya* (Malvaceae) is a genus of over 20 species found in the New World, Africa, Madagascar, and southeast Asia. We generated both nuclear (*CesA1* & *A1341*) and plastid (*matK*, *trnL-F*, *rpl32-trnL*, & *ycf1*) loci for most of the species of *Kosteletzkya* (60 accessions belonging to 15 species of ingroup taxa) as well as some outgroup taxa of Hibisceae. Phylogenetic analysis of these data shows that the African and New World species form a monophyletic group. However, the Malagasy species are very distantly related to the rest. The African species form a paraphyletic grade relative to a New World clade. Recent studies of chromosome counts using pollen mother cells revealed diploid, tetraploid, and hexaploid species. These analyses demonstrate that polyploidy has only occurred in and between some African species, at different times and between different parental constituents. These data support the relatively ancient formation of a putative autotetraploid species (*K. semota*), one recent allotetraploid species (*K. borkouana*), two relatively ancient, all tetraploid species (*K. begoniifolia* and *K. rotundalata*), and one recent all

ohexaploid species (*K. racemosa*). These data underscore the importance of analysis of multiple DNA loci from plastid and nuclear genomes to understand reticulate evolution.

<sup>1</sup>University of Florida, Department of Biology, Po Box 118526, Gainesville, FL, 32611, USA <sup>2</sup>University of Florida, Florida Museum of Natural History, PO Box 117800, Gainesville, FL, 32611, USA

**438 DONNELL, ALIYA\*, BALLARD JR,  
HARVEY and CANTINO, PHILIP**

***Callianthe*: A new genus of Malvaceae**

**T**he boundaries between the genera *Bakeridesia* and *Abutilon* have long been debated. Results from recent phylogenetic studies of the Internal Transcribed Spacer (*ITS*) in tribe Malveae strongly suggest that these two genera as currently delimited are not monophyletic. Species previously included in each genus form a well-supported clade that is phylogenetically removed from both *Bakeridesia* and *Abutilon*. The congruence of morphological and karyological distinctions with this molecular evidence provides compelling support for recognition of the clade as a new genus, to be called *Callianthe*. Thus far, 40 species have been placed in *Callianthe*, based on the *ITS* data (including a molecular synapomorphy of a 25-bp deletion in the *ITS2*) and/or morphological evidence, including four or more ovules per mericarp, serrate leaves (versus entire leaves in *Bakeridesia*), heavily veined petals, and large, showy flowers (versus smaller flowers in *Abutilon*). In addition, species of *Callianthe* share a base chromosome number of  $x = 8$  (versus 7 in *Abutilon* and 15 in *Bakeridesia*). Not only is *Callianthe* phylogenetically removed from both *Bakeridesia* and *Abutilon*, but it is also morphologically distinct from its closest phylogenetic relative, *Gaya*, which has a base chromosome number of  $x = 6$ . *Callianthe* has a neotropical distribution with a center of diversity in eastern Brazil. It includes all of *Bakeridesia* subg. *Dipteron* and several species previously assigned to *Abutilon*.

Ohio University, ENVIRONMENTAL & PLANT BIOLOGY, Porter Hall, Richland Ave., Athens, OH, 45701-2979, USA

439 WINDHAM, MICHAEL\*<sup>1</sup>, BECK, JAMES<sup>2</sup>, ALEXANDER, PATRICK<sup>3</sup>, ALLPHIN, LOREEN<sup>4</sup>, BAILEY, C. DONOVAN<sup>5</sup>, CALL, CHRISTINA<sup>4</sup>, LI, FAY-WEI<sup>6</sup>, RUSHWORTH, CATHERINE<sup>7</sup> and AL-SHEHBAZ, IHSAN<sup>8</sup>

### Is the glass half-empty or half-full?: the current state of *Boechera* (Brassicaceae) systematics

With upwards of 60 sexual diploid species originating within the last four million years, *Boechera* (Brassicaceae) is among the most rapidly diversifying genera of flowering plants. Pre-zygotic reproductive isolating mechanisms have failed to keep pace with diversification in the group, and recurrent hybridization among geographically proximate species has given rise to hundreds of hybrid lineages that persist and reproduce through polyploidy and/or apomixis. This makes *Boechera* (formerly *Arabis*) one of the most intractable species complexes in North America, with patterns of morphological variability that monographer Reed Rollins conceded "nearly defy taxonomic resolution." In the past few years, significant progress has been made toward understanding the systematics of *Boechera* by focusing on the sexual diploids that lie at the heart of the complex. Implementation of this "diploids-first" approach in *Boechera* is facilitated by pollen differences between sexual diploids and polyploids/apomicts observable using a dissecting microscope. A critical re-examination of overall morphology has shown that the 60+ sexual diploids are rather easily distinguished from one another, and a newly developed 15-locus microsatellite data set provides critical genetic markers for each of these diploid genomes. The microsatellite data set currently comprises ca. 2400 samples, including nearly every sexual diploid *Boechera* recognized in the recently published *Flora of North America* treatment. Range-wide sampling of many species has been facilitated by extracting DNA from herbarium specimens, which provided more than 95% of the data. Microsatellites provide an effective barcode allowing determination of the genomic make-up (and usually the ploidy level and reproductive mode) of almost any *Boechera* specimen collected within the last 125 years. These successes are tempered by the discovery that the taxonomy of *Boechera* is even more complex than previously thought. The great diversity of apomictic triploids in the genus have been interpreted as either autopolyploids or digenomic hybrids (e.g., AAB or ABB). Instead, the majority appear to be trigenomic (ABC) hybrids that are much

more difficult to diagnose morphologically.

<sup>1</sup>DUKE UNIVERSITY, Department Of Biology, BOX 90338, DURHAM, NC, 27708, USA<sup>2</sup>University Of Wisconsin, Milwaukee, Lapham Hall S394, P.O. Box 413, Milwaukee, WI, 53201-0413, USA<sup>3</sup>New Mexico State University, Biology Department, 248 Foster Hall, Las Cruces, NM, 88003, USA<sup>4</sup>Brigham Young University, Department of Plant and Wildlife Sciences, Provo, UT, 84602, USA<sup>5</sup>New Mexico State University, Department Of Plant Sciences, P.O. Box 30001 Msc 3AF, Las Cruces, NM, 88003, USA<sup>6</sup>Duke University, Department of Biology, Durham, NC, 27708, USA<sup>7</sup>Duke University, PO Box 90338, Durham, NC, 27708, USA<sup>8</sup>Missouri Botanical Garden, Department of Asian Botany, P.O. Box 299, St. Louis, MO, 63166, USA

440 BORJA, GUADALUPE\*<sup>1</sup> and DOUST, ANDREW<sup>2</sup>

### Distinguishing incomplete lineage sorting and gene flow to infer the evolution of the Southeastern bladderpods (*Paysonia* spp.): a preliminary phylogenetic analysis

Two main problems that complicate phylogenetic analyses are incomplete lineage sorting and hybridization. One genus in which these phenomena are manifested is *Paysonia*, a small genus of mustards (Brassicaceae) with an unusual distribution pattern that divides the group into two distinct geographic areas, the Southeast and the Southwest. These eight species were originally positioned under the larger genus *Lesquerella* but were recently recognized as a monophyletic group based on morphological characters and chloroplast sequence data. Preliminary phylogenetic analyses utilizing the nuclear marker *ITS* reveals that the Southwestern *Paysonia* are well resolved, but the clade containing the five Southeastern species forms a complex species group. To address the problem of incomplete lineage sorting, three non-coding loci from the chloroplast genome, the *ndhF-rpl32*; the *trnDGGU-trnTGGU*; and the *psbD-trnTGGU*spacers, were directly sequenced from three individuals of each of the eight *Paysonia* species, including 2 outgroup species from the sister genus *Physaria*. Likelihood and Bayesian phylogenetic methods are being used to infer the evolutionary relationships among species, and we propose to add sequences of two nuclear genes (*Phytochrome A* and *Atmyb2*) and an independent empirical estimate of gene flow from microsatellite data to further resolve these complex evolutionary patterns.

<sup>1</sup>Oklahoma State University, Botany Department, 106 Life Sciences East, Stillwater, OK, 74078-3013, USA<sup>2</sup>Oklahoma State University, Botany, 104 Life Sciences East, Stillwater, OK, 74078, USA

441 ARIAS, TATIANA\*<sup>1</sup> and PIRES, JOSEPH

### A phylogenomic approach to resolving the evolutionary relationships among Brassica crops and their wild relatives (Brassicaceae, Brassicaceae)

**B**rassica crops and their wild relatives (tribe Brassiceae) belong to the mustard family (Brassicaceae) and contain more agriculturally and horticulturally important crops than any other family of flowering plants. They are native to Western Europe, the Mediterranean, and temperate regions of Asia. Mustard plants are most diverse in the Mediterranean region where their evolutionary history has been shaped by geological activity, climate change, and human activity. The Brassiceae is a monophyletic group with 54 genera and approximately 240 species. Relationships among, and circumscription of, its subtribes have been a matter of debate for many years. This research focuses on recovering a robust phylogeny for the tribe using traditional phylogenetic and new phylogenomic approaches. First, we sequenced four highly variable and phylogenetically informative chloroplast intergenic regions for 120 species. Our phylogeny recovers seven well-supported clades: *Nigra*, *Crambe*, *Oleracea*, *Cakile*, *Vella*, *Zilla* and a new African clade comprised of genera that have not been previously sampled. Relationships among these seven main clades are weakly supported in this phylogeny, and there is a lack of resolution among the seven subtribes. The monophyly of the tribe is confirmed with *Vella* and *Zilla* as the outer clades. This phylogeny challenges the evolutionary relationships and phylogenetic position of several genera previously defined using classical taxonomy. Second, we reconstructed a whole chloroplast and whole mitochondrial phylogeny for 26 taxa representing eight main clades in the tribe. The whole chloroplast phylogeny recovered eight clades with 100% bootstrap values for most nodes in the phylogeny. The *Oleracea* clade is sister to *Savignia*, and this clade is sister to *Crambe* + *Nigra*. *Cakile* is sister to these four clades followed by the sister group *Vella*. The outer group sister to all the other clades in the tribe is *Zilla*. These results are complementary to the four-chloroplast markers phylogeny. The whole mitochondrial phylogeny recovered two of the seven main clades identified with the whole chloroplast phylogeny, *Oleracea* and *Cakile*.

<sup>1</sup>University of Missouri, Biological Sciences, 311 Life Sciences Center, Columbia, MO, 65211, USA <sup>2</sup>University Of Missouri, 371 B Life Sciences Center, 1201 Rollins Street, Columbia, MO, 65211-7310, USA

442 KATES, HEATHER ROSE\*<sup>1</sup>, WEINMANN, SOPHIA<sup>1</sup>, CHARBONEAU, JOSEPH<sup>2</sup>, PLUMB, RACHEL<sup>1</sup>, SANDERS, JEFFREY<sup>1</sup> and MOORE, MICHAEL<sup>3</sup>

### Expanding the Study of the Phylogeny and biogeography in a Chihuahuan Desert gypsum endemic, *Nerisyrenia* (Brassicaceae), through the use of low copy nuclear markers and increased population sampling.

*Nerisyrenia* Greene (Brassicaceae) is a small genus of 11 arid-adapted species endemic to the Chihuahuan Desert of southwestern North America and Mexico. With the exception of the widespread *N. camporum* (A. Gray) Greene, all species within *Nerisyrenia* are endemic to gypsum deposits and soils that are scattered in an island-like fashion throughout the Chihuahuan Desert. While early research postulated a recent origin for modern North American arid-adapted taxa, patterns of morphology, phylogeny, and biogeography within other Chihuahuan Desert gypsum endemics suggest an age of several million years. As part of a larger effort to understand the age and origins of Chihuahuan Desert gypsum endemics, we initiated a phylogenetic and phylogeographic study of *Nerisyrenia* to address: (1) How many times has gypsum endemism evolved within the genus?; (2) Is gypsum endemism the ancestral character state?; and (3) Is there a strong correlation between biogeographic distribution and genetic diversity both within and between gypsum endemic species of *Nerisyrenia*? We constructed a 5 chloroplast spacer region gene tree and an ITS gene tree using initial sampling of all species, including numerous populations of the North American species, *N. camporum* and *N. linearifolia* (S. Wats.) Greene, from across their geographic ranges. Our phylogeny revealed high levels of diversity within *Nerisyrenia* and indicated that the widespread gypsum endemic *N. linearifolia* has a significant amount of geographically-correlated variation, while non-gypsum endemic *N. camporum* shares chloroplast haplotypes with several other species. To better elucidate this complex evolutionary history, we have identified and sequenced two useful low copy nuclear markers (alcohol dehydrogenase and *pistllata*) and increased sampling across the 9 Mexican taxa. In addition to improving resolution within our phylogeny, expanded geographic sampling of *Nerisyrenia* may reveal greater diversity in Mexican population than in northern populations, as has been found in several other gypsum-endemics.

<sup>1</sup>Oberlin College, Biology, Science Center K123, 119 Woodland St. Oberlin, OH, 44074, USA <sup>2</sup>University of Wyoming, Botany, 1000 E. University Ave., University of Wyoming, Laramie, WY, 82071, USA <sup>3</sup>Oberlin College, Department of Biology, 119 Woodland St., Oberlin, OH, 44074, USA

443 PAUDYAL, SUSHIL\*<sup>1</sup>, DELPRETE, PIERO<sup>2</sup> and MOTLEY, TIMOTHY<sup>1</sup>

**In out, in out: using total evidence to support treating *Strumpfia maritima* as a monotypic tribe in the Cinchonoideae (Rubiaceae)**

*Strumpfia maritima* Jacq. is a morphologically distinctive species and the only member in the genus *Strumpfia*. It is a dwarf shrub with ericoid, broom-like branches, and occurring in littoral habitats in the Caribbean region ranging from South Florida to the Antilles and North Venezuela and from Yucatan peninsula of Mexico to the Bahamas. Various molecular studies have placed *Strumpfia* related to the genera of the tribes Chiococceae, Catesbaeeae, and some former members of the tribes Condamineae and Cinchoneae of the Rubiaceae. The most recent tribal delimitation of the subfamily Cinchonoideae, based on molecular phylogenetic analyses, placed *Strumpfia* sister to the rest of the tribe and included it in the tribe while earlier studies had found similar phylogenetic relationships, but were reluctant to include *Strumpfia* in the Chiococceae. The earlier authors noted significant morphological differences between *Strumpfia* and the other genera of the tribe. Some scientists argue against creating monotypic tribes. Because including *Strumpfia* in the Chiococceae creates a group of genera no longer supported by a single synapomorphy, we decided to revisit the inclusion of *Strumpfia* in the Chiococceae *sensu* Manns and Bremer. We examined genetic divergences among the tribes of the subfamily Cinchonoideae using trnL-F data analyzed using both Maximum Parsimony and Bayesian Inference. Results from the present molecular data and morphology provide strong evidence for treating *Strumpfia* as a monotypic tribe.

<sup>1</sup>Old Dominion University, Biological Sciences, 110 Mills Godwin Building, 45th Street W, Norfolk, VA, 23529, USA<sup>2</sup>IRD - UMR AMAR, Herbar de Guyane, Boite Postale 165, 97323 Cayenne Cedex, Cayenne, French Guiana

444 WHITLOCK, BARBARA A.\*, GUNATHILAKE, ANURADHA and GROFF, PAULA.

**Intraspecific geographic variation of DNA barcodes within *Gentiana affinis*, *Swertia perennis*, and western North American *Gentianopsis* (Gentianaceae)**

Several markers have been proposed as DNA barcodes for identification of plant species; however, an important question is the extent to which these markers vary within species and whether that variation is geographically structured. We present examples

of intraspecific geographic variation in three proposed plant DNA barcodes in *Gentiana affinis*, *Swertia perennis*, and species of *Gentianopsis* from western North America. Across the ranges of co-distributed species, we find some commonalities in the patterns of geographic structure. These geographic patterns have implications for hypotheses of historical biogeography and of community migration and assembly, as well as for the design of DNA barcoding studies.

University of Miami, Department of Biology, Coral Gables, FL, 33124, USA

445 MATHEWS, KATHERINE\*<sup>1</sup>, RUIGROK, MICHELLE<sup>2</sup> and MANSION, GUILHEM<sup>3</sup>

**Phylogeny and trait evolution in *Sabatia* (Gentianaceae) and uneven diversification rates in subtribe Chironiinae**

*Sabatia* (Gentianaceae, subtribe Chironiinae) is an herbaceous, eastern U.S., primarily coastal plain group of flowering plants. Previous phylogenetic analyses within *Sabatia* employing three chloroplast noncoding regions and one nuclear rDNA region resolved five well-supported clades, but relationships among these clades were not resolved. The addition of a fourth noncoding cpDNA region and a new species suspected of being an early-evolving lineage greatly increases resolution at the base of the phylogeny. We find evidence for single origins of both stable floral polymery and white corollas from the ancestral conditions of pentamerous flowers and pink corollas, respectively. Autogamy has evolved twice in this primarily outcrossing genus and appears unrelated to ploidy, but rather to adaptation to ephemeral habitats. *Sabatia* is characterized by high levels of aneuploidy, which may be responsible for speciation, along with geographical isolation and ecological specialization. The most ancestral species, *S. arenicola* and *S. campetris*, have the lowest chromosome numbers in the genus, and ploidy increases throughout the genus. *Sabatia* (20 species) shows greater species richness than its sister genera, *Gyrandra* (5 species) and *Eustoma* (3 species). We explore shifts in diversification rates in subtribe Chironiinae with respect to trait evolution in the group.

<sup>1</sup>Western Carolina University, 132 NATURAL SCIENCE BUILDING, CULLOWHEE, NC, 28723, USA<sup>2</sup>Highlands Biological Station, 265 N. Sixth Street, Highlands, NC, 28741, USA<sup>3</sup>Botanischer Garten und Botanisches Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6 - 8, 14195 Berlin, Germany

446 DOFFITT, CHRIS\*<sup>1</sup> and WALLACE, LISA<sup>2</sup>

**Phylogenetic relationships within the genus *Amsonia* (Apocynaceae) in North America based on chloroplast and nuclear markers**

*Amsonia* is one of the few genera in the Apocynaceae with a primarily holarctic distribution. The approximately 20 species are found in four geographic regions: southeastern and southwestern North America, the Mediterranean, and Japan. This distribution represents a disjunct pattern that is also observed in many other taxonomic groups. Currently the genus is recognized as having four sub-genera *Euamsonia* (includes species from the southeastern U.S. and Japan), *Articularia*, *Longiflora*, and *Spinctosiphon* (all from the Southwestern U.S.). The groups of species found in southeastern and southwestern North America appear to be complexes of closely related species, several of which are rare or of conservation concern. This work examines the relationships of the species within southeastern and southwestern North America with an emphasis on the members of the sub-genus *Euamsonia*. In addition, it examines the relationship of *Amsonia orientalis* (Mediterranean) and *Amsonia elliptica* (Japan) to the North American members of the genus based on phylogenetic analyses of cpDNA sequences derived from *trnH-psbA*, *trnD-trnT*, *rpl14-rpl36* intergenic spacers, and nuclear sequences of the ribosomal DNA Internal Transcribed Spacer (ITS) region. The resulting phylogenies suggest that *Amsonia* is not monophyletic if *A. orientalis* and *A. elliptica* are included in the genus. Additionally, *A. ciliata*, a southeastern U.S. species, is closely related to the southwestern species, which suggests that the sub-genus *Euamsonia* is not monophyletic. Also, some southeastern taxa are nested within a clade containing the wide-ranging species *A. tabernaemontana*, providing evidence that *A. tabernaemontana* is not monophyletic and is perhaps a wide-ranging polymorphic species. The morphology and apparent affinity of *A. ciliata* with the southwestern U.S. taxa seem to suggest aridification has provided a selective pressure that has influenced speciation. It is likely that similar abiotic influences have shaped morphological features in the southeastern species, with the species occurring on drier sites tending to have narrower leaves and more trichomes.

<sup>1</sup>Mississippi State University, Department Of Biological Sciences, PO Box GY, Mississippi State, MS, 39762-5759, USA <sup>2</sup>Mississippi State University, PO Box GY, Mississippi State, MS, 39762, USA

447 REIN, ANGELA\* and FISHBEIN, MARK

**Evaluating the Utility of COSII Markers for Phylogenetic Analysis of Non-Twining Milkweed Vines (Apocynaceae, *Matelea* subgenus *Chthamalia*)**

Though often common in their range throughout the Americas, the evolution, classification, and phylogeny of milkweed vines in subtribe Gonolobinae (Apocynaceae) are poorly understood, and have never received comprehensive systematic or phylogenetic study. Gonolobinae has a tropical origin, but many species exist in subtropical and temperate North America, making it an ideal group for ecological and phylogenetic study of grassland flora. Species of *Matelea* subgenus *Chthamalia* are of particular interest due to variation in floral morphology and especially growth habit. It is likely that one or more losses of a climbing habit have evolved in this subgenus. Conserved Orthologous Set (COS) markers have been developed from comparative genomic data and suggested as phylogenetically useful nuclear loci. "Universal" asterid loci were screened across Apocynaceae, and milkweed specific primer sets were developed. Thirteen species of *Matelea* subgenus *Chthamalia* have been screened with three COS markers, and the resulting fragments have been sequenced, aligned, and analyzed. COS markers show at least twice as much sequence divergence when compared to chloroplast data for the same species. Preliminary phylogenetic trees that estimate relationships within the subgenus are presented. COS markers appear to have phylogenetic utility because they are more variable than plastid loci, but individual loci may not resolve many relationships. In the future, multiple unlinked loci, including COS markers, have the potential to further resolve phylogenetic relationships in Gonolobinae.

Oklahoma State University, Dept Of Botany, 104 Life Sciences East, Stillwater, OK, 74078, USA

448 SHARBER, WYATT\* and FISHBEIN, MARK

**Morphometric and molecular phylogenetic investigations of the *Asclepias pringlei* complex**

No abstract available.

Oklahoma State University, Botany, 104 Life Sciences East, Stillwater, OK, 74078, USA

449 BYE, ROBERT<sup>\*1</sup>, LUNA-CAVAZOS, MARIO<sup>2</sup> and SOSA, VICTORIA<sup>1</sup>

### **Enbotany, geography, and systematics of *Datura* (Solanaceae) in MegaMexico**

*Datura* is one of 5 genera of the Solanaceae that is endemic to MegaMexico (sensu Rzedowski). The ethnobotany is based upon the employment of specific chemical active principles (i.e., alkaloids). Various tropane alkaloids which provoke delirium have been incorporated in prehispanic rituals that persist to present-day. Medicinally, jimsonweed (or "toloache") uses are associated with its anti-inflammatory and antiseptic properties. An overdose can produce death while a sublethal dosis can induce a temporary disorientation or, if permanent, a condition referred to as "en limbo" or "entolochado" or "zombi". *Datura metel* was domesticated as an ornamental. Some species (such as *D. ferox* y *D. stramonium*) are weedy and found on most of the continents with considerable variation. New cultural evidence has been interpreted to support pre-Columbian dispersal of 2 species to the Old World. Geographic analysis indicates that the species are distributed naturally in the arid regions of southwestern USA to northern Central America. The majority of the species are concentrated in 3 of the 19 Mexican Biogeographic Provinces: Altiplano Norte, Altiplano Sur, and Sierra Madre Occidental. The latitude, the precipitation of the driest trimester, and the altitude predict the distribution of *Datura* in Mexico. Conventional taxonomy recognizes 14 species divided among 3 sections established by Bernhardt (1833): 1) *Datura* (o *Stramonium*), 2) *Dutra*, and 3) *Ceratocaulis*. Though originally considered a fourth section, *Brugmansia* (tree datura) is the sister genus based upon morphological and molecular characters. Based upon phenetic and phylogenetic analyses of data derived from morphometry, isozymes, and cDNA, we propose that the section *Dutra* be divided into 2 sections.

<sup>1</sup>Instituto de Ecología, A. C., Biología Evolutiva, Xalapa, Veracruz, Mexico <sup>2</sup>Colegio de Postgraduados, Botánica, Montecillo, Mexico, Mexico

450 CROAT, THOMAS

### **Phytogeography of the Araceae in the Guianas**

The Araceae of the Guianas number fewer species (23 genera and 165 taxa) than comparable areas of similar size in the western Andes but they are comparably rich in endemics with 50% of the species endemic to the Guianas and 70% endemic to eastern South America. The Guianas share with the Andes most of the same genera with only *Chlorospatha* absent among the widespread genera. In comparison to western South America, species diversity is much lower in the Guianas.

*Philodendron* with 65 species (42% endemic) is the largest genus. A subset of 14 species are in subgenus *Pteromischum*. *Anthurium*, with 22 species (68% endemic to eastern South America) is the second largest genus. The genus *Caladium* is unusually rich in the Guianas with 4 species, three of which are endemic to the region. *Diefenbachia* has 9 species (55% endemic to the Guianas). *Dracontium* has 3 species, two of which occur only in Eastern South America. *Heteropsis* with 6 species is also primarily endemic to eastern South America. *Monstera* with 6 species in the Guianas has only one species endemic. *Rhodospatha* has 4 species with no endemics. *Spathiphyllum* has 6 species, four of which are endemic to Eastern South America and *Stenospermation* has 5 species, 4 of which are endemic to Eastern South America. *Syngonium* has 2 rather widespread species and *Xanthosoma* has 13 species, 8 of which are endemic to the Region of the Guianas.

The distribution of Araceae within the Guianas is uneven with fewer species in Guyana (78) and in Suriname (100) than in French Guiana (129). This may be due the presence of large areas of savanna vegetation in Suriname and Guyana where aroids are scarce as well by the fact that French Guiana is both more heavily forested and has a larger percentage of Amazonian species while still retaining a substantial percentage of species endemic to the Guianas.

Missouri Botanical Garden, Department Of Botany, P.O. Box 299, St. Louis, MO, 63166-0299, USA

451 CARLSEN, MONICA

### **Understanding the tempo and mode of evolution of the genus *Anthurium* Schott (Araceae) using a molecular phylogeny**

*Anthurium* is the richest genus in Araceae, with ca. 1000 species distributed throughout the Neotropics. It is also among the most basal lineages in the family, and in comparison with other early divergent taxa in Araceae, it shows an extremely wide range of morphological diversity. In this study, a molecular phylogeny based on combined chloroplast (*trnG* intron, *trnH-psbA* and *trnC-ycf6* intergenic spacers) and nuclear (second intron of *CHS*) DNA datasets was used to understand the timing and pattern of diversification within the genus. Molecular evidence reveals that the initial divergence between *Anthurium* and its sister genus *Pothos* is quite old, but it was much later in time that *Anthurium* itself diversified explosively. A molecular signature of very low DNA sequence differentiation among species and increased diversification rate when compared to its sister genus, suggests that a rapid radiation gave rise to most of the species within *Anthurium*. On the other hand, there is a high rate of morphological differentiation among species, with highly homoplasious leaf shape, venation and texture characteristics, and more stable inflorescence and fruit characters. The pattern of rapid diversification is also coupled with ge-

ography, where species in close geographic proximity are more closely related to each other, even if they differ in terms of vegetative morphology.

Missouri Botanical Garden, PO Box 299, St. Louis, MO, 63166, USA

**452 LOPEZ PEREDO, ELENA\*<sup>1</sup>, LES, DONALD<sup>1</sup>, BENOIT, LORI<sup>1</sup> and TIPPERY, NICHOLAS<sup>2</sup>**

### **Cryptic speciation in *Najas marina* L. (Hydrocharitaceae)**

*Najas marina* is a cosmopolitan aquatic monocot currently viewed as comprising 12 subspecies with six varieties. This is the only dioecious species in an otherwise monoecious group of annual hydrophiles and resolves phylogenetically as the sister to the remainder of the genus. Three distinct karyotypes have been reported for *N. marina*, including one autotetraploid ('BB') and two diploid ('A', 'B') races. The A and B karyotypes differ extensively by rearrangements resulting from the breakage and reunion of chromosomal segments. Previous studies have associated these rearrangements with high infertility, which is manifest by extreme genetic divergence between the diploid karyotypes (e.g., no allozyme alleles shared at 23 loci surveyed). As part of an ongoing systematic study of *Najas*, we are evaluating the intraspecific taxonomy of *N. marina* using DNA sequence analysis. In contrast to the currently proposed taxonomy, an analysis of DNA sequence data for 22 globally distributed populations resolves only two distinct lineages within *N. marina*, which arguably correspond to the two fundamental karyotypes. Our results confirm that these karyotypes rarely are interfertile as indicated by their substantial level of DNA sequence divergence at both cpDNA and nuclear regions. Unexpectedly, all Eurasian material analyzed (China, Czech Republic, Latvia) presumably corresponds to the A karyotype (i.e., subsp. *marina*) despite the known occurrence of B karyotypes in this region. Conversely, all North American material (ostensibly karyotype B; subsp. *intermedia*) is essentially identical to plants from Australia, thereby supporting an earlier hypothesis that New World plants represent a recent introduction. Our inability to detect B karyotypes from other regions is curious and we are expanding our geographical survey to resolve this discrepancy. Except for minor seed characters (which differ between the two karyotypes), we cannot detect any consistent pattern of morphological variation to support those infraspecific taxa delimited previously. Rather, we regard *N. marina* as an aggregate taxon of two cryptic species, which are effectively isolated reproductively by their extensively rearranged genomes.

<sup>1</sup>University Of Connecticut, Ecology & Evolutionary Biology, 75 N. Eagleville Road, Unit 3043, Storrs, CT, 06269-3043, USA<sup>2</sup>University Of Wisconsin-Whitewater, Department of Biological Sciences, 800 W Main St, Whitewater, WI, 53190

**453 LES, DONALD\*<sup>1</sup>, BENOIT, LORI<sup>1</sup>, LOPEZ PEREDO, ELENA<sup>1</sup> and KING, URSULA<sup>2</sup>**

### **"Now *that's not Najas!*" A genetic marker for the water sprites (*Najas*; Hydrocharitaceae)**

Increasingly, procedures to facilitate plant identification have become sought after, especially as the level of botanical expertise dwindles while infestations of invasive species multiply. Aquatic plants are particularly difficult to identify, even to genus, as they often are found in vegetative condition where few distinctive characteristics are apparent to the casual observer. In such cases, the identification of individual species using a characteristic 'DNA barcode' region has been offered as one potential solution, but has been the subject of some debate, particularly with respect to providing the most effective and distinctive genetic region for analysis. At best, identifications using DNA barcodes still involve a somewhat lengthy sequencing protocol and the availability of expensive technical equipment. As we evaluated next-generation (454) genomic DNA sequence data for *Najas flexilis*, we discovered one cpDNA region, which differed by a simple 3 bp (AGA) insert relative to a large number (>100) of angiosperm family sequences deposited in GenBank, including one from the closely-related Araceae. The insert occurs within the LSC region of the chloroplast genome within a relatively conserved 28 bp spacer between the *psaA* and *psaB* genes. To evaluate the phylogenetic potential of this marker, we developed a PCR/RFLP method, which enabled us to characterize more explicitly the extent of the insert by rapidly surveying nine other *Najas* species as well as a representative sample of 24 other alismatid genera from 10 families: Alismataceae (*Alisma*, *Astonia*, *Sagittaria*), Aponogetonaceae (*Aponogeton*), Butomaceae (*Butomus*), Cymodoceaceae (*Halodule*, *Syringodium*, *Thalassodendron*), Hydrocharitaceae (*Blyxa*, *Egeria*, *Elodea*, *Enhalus*, *Hydrilla*, *Hydrocharis*, *Ottelia*, *Stratiotes*, *Thalassia*, *Vallisneria*), Juncaginaceae (*Triglochin*), Posidoniaceae (*Posidonia*), Potamogetonaceae (*Potamogeton*), Ruppiaceae (*Ruppia*) and Zosteraceae (*Phyllospadix*, *Zostera*). Our survey indicated that this genetic marker was not unique to *Najas flexilis*; however, it was restricted to the *Najas* species analyzed. Thus, this coincidental discovery from 454 sequence data has provided a simple, rapid, PCR-based technique that confidently separates *Najas* species from superficially similar genera such as *Egeria*, *Elodea*, *Hydrilla*, and *Potamogeton*.

<sup>1</sup>University Of Connecticut, Ecology & Evolutionary Biology, 75 N. Eagleville Road, Unit 3043, Storrs, CT, 06269-3043, USA<sup>2</sup>Trinity College Dublin, Biology, Dublin, Ireland

454 BENOIT, LORI\*<sup>1</sup> and LES,  
DONALD<sup>2</sup>

**Phylogenetic structure in the  
cosmopolitan aquatic angiosperm  
*Hydrilla verticillata* (L.f.) Royle  
(Hydrocharitaceae): evidence for cryptic  
speciation in a monotypic genus?**

*Hydrilla verticillata* (L.f.) Royle (Hydrocharitaceae), a submersed, cosmopolitan aquatic plant, currently is recognized as the only species of a monotypic genus. Presumably, its native range includes Australia, India and Southeast Asia; it is invasive in the United States, with two introduced biotypes (dioecious; monoecious). These biotypes are similar morphologically, with much of their vegetative variation attributed to phenotypic plasticity. Here we evaluate phylogenetic and nonparametric network methods to reconstruct complex gene genealogies, determine origins of introduced populations, and identify clades that might be significant taxonomically. Nuclear (nrITS; cloned nrITS; phytoene desaturase - PDS; cloned PDS), and plastid (*trnL* intron/*trnL-F* spacer) sequences were evaluated. Maximum parsimony analyses resolved four clades (PDS) or three clades (ITS; *trnL/trnL-F*). The clades recovered for PDS had greater support than those for ITS, but the topologies were congruent overall. Clades I and II (ITS; PDS) contained 'US dioecious' haplotypes as well as genomic sequences and haplotypes from Burundi, China, India, and Nepal. Accessions from Europe, Japan, and Korea comprised a third clade that was well-supported in all trees. A fourth, broadly Indo-Pacific clade (Australia, Indonesia and Malaysia), was not well-supported in the nuclear gene trees. 'US monoecious' haplotypes were found in clades II and IV in PDS, but only in clade IV in ITS. Plastid data placed the US monoecious haplotype with an uncommon Korean haplotype; neither was part of clade III, which contained the most commonly found Korean nuclear gene sequences. All data indicated that US dioecious plants originated from India, a result consistent with previously published phenetic analyses. Cloned nuclear gene sequences revealed a complex, somewhat reticulate gene history, which for some accessions and relationships was better visualized using network rather than tree-based methods. Phylogeographic patterns indicated genetic divergence over large spatial scales, but additional data will be required to assess whether the clades described here deserve taxonomic recognition, perhaps as cryptic species. Morphological character analyses also are underway for this purpose.

<sup>1</sup>University Of Connecticut, Ecology & Evolutionary Biology, 75 N. Eagleville Road, Unit 3043, Storrs, CT, 06269-3043, USA <sup>2</sup>University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Road, Unit 3043, Storrs, CT, 06269-3043, USA

455 LEE, CHANG SHOOK<sup>1</sup>, LEE,  
BO RA<sup>2</sup>, KIM, SEUNG-CHUL\*<sup>3</sup> and LEE,  
NAMSOOK<sup>2</sup>

**Phylogeny of genus *Lilium* (Liliaceae)  
based on nrDNA ITS and cpDNA *matK*  
sequences, with special emphasis on  
Korean species**

The genus *Lilium* L. includes approximately 100 species and is distributed mainly in temperate regions. About 11 taxa, three of which are endemic (*L. hansonii*, *L. amabile*, and *L. callosum* var. *flavum*), are widely distributed in the Korean peninsula. Infrageneric classification of the genus has been problematic and thus has been subject of considerable investigations. Previous molecular phylogenetic studies provided several insights into understanding infrageneric classification of the genus. These earlier studies, however, either focused on some sections (e.g., *Liriotypus* and *Sinomartagon*) or have limited sampling for the phylogeny of the entire genus. Using ITS sequences of nrDNA, we conducted most comprehensive phylogenetic analysis of *Lilium* based on 196 accessions (83 species and 14 varieties) and evaluated infrageneric classification. The ITS data showed that only one section, *Martagon*, is monophyletic. Three sections, *Archelirion*, *Liriotypus*, and *Pseudolirium* are not monophyletic because two, one, and two species in each section were placed in other lineage, respectively. Two major lineages of section *Leucolirion* were confirmed in this study, and section *Sinomartagon* is highly polyphyletic. The origin of *Lilium hansonii*, a Korean endemic to Ulleung Island, is perplexing given the fact that it has ribotype of *Martagon*, while its cpDNA haplotype is similar to *Sinomartagon*. The origin of another endemic, *L. amabile*, is equally elusive. We determined that *L. callosum* var. *flavum* originated from *L. callosum* in southern Korea. We sequenced *matK* region of cpDNA, as an independent source of phylogenetic information, and reevaluated infrageneric classification of *Lilium*. The 50% bootstrap consensus tree is moderately resolved among major groups, while within each group is highly unresolved. Three major lineages within *Lilium* were identified based on *matK* sequences, but the origins of three Korean endemic species were not assessed due to lack of enough resolutions. Major lineages of *Lilium* and origins of Korean endemic species and comparisons between nrDNA and cpDNA *matK* gene tree will be discussed in details.

<sup>1</sup>Ewha Womans University, Institute of Eco Science, Seoul, 120-750, KOREA <sup>2</sup>Ewha Womans University, Life Sciences, Seoul, 120-750, KOREA <sup>3</sup>Sunkyunkwan University, Biological Sciences, 300 Cheoncheon Dong, Suwon, Gyeonggi-do, 440-746, KOREA

456 HEANEY, JAMES\*<sup>1</sup>, COOPER, HILLARY<sup>2</sup>, RUIZ-SANCHEZ, EDUARDO<sup>3</sup>, SPECHT, CHELSEA<sup>3</sup>, SOLTIS, DOUGLAS<sup>4</sup> and SOLTIS, PAMELA<sup>5</sup>

### Systematics of *Nolina* (Nolineae, Rusceae)

*Nolina* is taxonomically complex and badly in need of molecular phylogenetic analysis. Recent studies of Nolineae have focused on either *Beaucarnea* or *Dasyliirion*. Relationships in *Nolina* and the relationship of the genus to other genera of the Rusceae remain unclear. We used a large plastid data set (5607 bp), as well as ITS, for 41 taxa (22 in *Nolina*) to elucidate relationships among *Nolina* species and between *Nolina* and its closest relatives. Support for the monophyly of the tribe is strong. Unlike in previous analyses with significantly smaller sample sizes, all three genera are consistently resolved as monophyletic. *Beaucarnea* (including *Calibanus*) is sister to *Dasyliirion*, and these two groups form a strongly supported clade sister to *Nolina*. However, few morphological synapomorphies for *Nolina* are apparent. The pronounced secondary thickening at the stem base, as occurs in *Beaucarnea*, is absent in *Nolina*, except in *N. interrata*. Serrations on the leaf margins are minute, as opposed to pronounced in *Dasyliirion*, and inflorescences are typically open panicles unlike the closely packed panicles in *Dasyliirion*. Nonetheless, exceptions do occur in *Dasyliirion*, and minutely serrated leaf margins and open inflorescences also characterize *Beaucarnea*. This has led to the lumping of *Beaucarnea* with *Nolina* in some previous treatments. Relationships within *Nolina* will be discussed in the context of the classification by Trelease into four sections, although these groups generally appear to be artificial in preliminary results.

<sup>1</sup>University Of Florida, Dickinson Hall, Museum Road, Gainesville, FL, 32611-7800, USA<sup>2</sup>Northern Arizona University, Department of Biological Sciences, P.O. Box 5640, Flagstaff, AZ, 86011, USA<sup>3</sup>University of California, Berkeley, Department of Plant and Microbial Biology, 111 Koshland Hall, MC 3102, Berkeley, CA, 94720, USA<sup>4</sup>University Of Florida, Department Of Botany, 220 BARTRAM HALL, Gainesville, FL, 32611, USA<sup>5</sup>University Of Florida, Florida Museum Of Natural History, Dickinson Hall, Gainesville, FL, 32611-7800, USA

457 WILSON, CAROL

### Progress toward a new subgeneric classification for *Iris*

Previous systematic treatments for the approximately 300 species of *Iris* recognized six subgenera and two to five segregated genera based on characters such as sepal beards and/or crests, seed arils, and the type of geophytic organ present. Recent phylogenetic studies have shown that several of these subgenera are not

monophyletic and that most of the characters used in earlier classifications are homoplastic across the genus. Phylogenetic relationships among the six *Iris* subgenera were reconstructed based on chloroplast sequence data using maximum likelihood and Bayesian inference methods. A preliminary classification is presented that recognizes 10 subgenera and one unresolved clade. Leaf, floral and geophytic morphology and structure are examined in light of the new information on evolutionary relationships. Lineages not fully sampled and those that are not considered stable are also discussed.

Rancho Santa Ana Botanic Garden, 1500 North College Avenue, Claremont, CA, 91711-3157, USA

458 GUO, JINYAN\*<sup>1</sup> and WILSON, CAROL<sup>2</sup>

### Are sepal crests phylogenetically informative in *Iris*

Crested irises account for more than one fifth of the approximately 270 species in the genus *Iris* and are distributed across three subgenera, *Limniris*, *Nepalensis*, and *Scorpiris*. An elaborated ridge that is parallel and perpendicular to the lamina of the sepal distinguishes crested species. In these species, crests are morphologically diverse, mostly because of ridge elaborations. Subgenus *Limniris* section *Lophiris* species were historically grouped together and called the "crested iris" based on their shared characters of a sepal crest that is often relatively large, conspicuous, and brightly colored and the presence of rhizomes. All of the crested species in subgenera *Nepalensis* and *Limniris* and about 30% of the species in *Scorpiris* were sampled. Phylogenetic analyses were based on *matK*, *trnK*, *trnL-trnF*, *rpoB-trnC*, *psbJ-petA* and *rpl32-trnL* sequence data and structural studies used light and SEM microscopy. Our preliminary results show that section *Lophiris* is not monophyletic and that crests evolved independently at least six times in *Iris*. A core crested clade was resolved, which consists of two eastern Asian section *Lophiris* lineages and species from subgenera *Scorpiris* and *Nepalensis*. Five species currently assigned to section *Lophiris* represent three additional independent lineages while two species within subgenus *Limniris* section *Limniris* series *Chinensis* represent the other two independent crest origins. Although the presence of a sepal crest is homoplastic and has multiple independent origins in *Iris*, macro- and micro-morphological studies of mature sepal crests from each lineage showed that this character is phylogenetically informative.

<sup>1</sup>Rancho Santa Ana Botanic Garden/Claremont Graduate University, Botany, 1500 North College Ave., Claremont, CA, 91711, USA  
<sup>2</sup>Rancho Santa Ana Botanic Garden, 1500 North College Avenue, Claremont, CA, 91711-3157, USA

459 HONG-WA, CYNTHIA\*<sup>1</sup> and  
BESNARD, GUILLAUME<sup>2</sup>

### Phylogeny of the genus *Noronhia* (Oleaceae) and relatives: inferences from nuclear and chloroplast sequence data

*Noronhia* (Oleaceae) currently comprises 45 species, all of which are endemic to the Malagasy floristic region (43 species in Madagascar and 2 in the Comoro Islands). *Noronhia* is a morphologically and ecologically very diverse group, whose close relationship with the three Malagasy species of *Chionanthus* (previously included in *Linociera*) has long been suggested. Recent molecular phylogenies indicate unresolved relationships within subtribe Oleinae, which includes *Noronhia*, *Chionanthus*, *Olea* and nine other extant and extinct genera. In this study, the phylogenetic utility of chloroplast (trnLF, trnTL, trnSG, matK) and nuclear (nrITS, Tpi) DNA markers in identifying relationships within subtribe Oleinae is assessed, the monophyly of *Noronhia* is investigated, and relationships among its species are examined. Nine of the twelve genera within Oleinae were sampled and preliminary results show improved resolution of phylogenetic relationships among them. *Noronhia* and *Chionanthus* from the Malagasy floristic region form a monophyletic group, sister to an African clade of *Chionanthus* (formerly *Linociera*). A near-complete species-level phylogeny of *Noronhia* shows an unexpected lack of genetic variation among species to allow meaningful reconstruction of infra-generic relationships, and suggests a rapid and/or recent radiation within Madagascar or slow molecular evolution. Results also suggest several cases of para- or polyphyly within Oleinae; these, with previous studies, call for a comprehensive taxonomic revision within the family.

<sup>1</sup>University of Missouri-St. Louis, Biology, One University Blvd, St. Louis, MO, 63121, USA<sup>2</sup>CNRS UMR 5174-Université Paul Sabatier, Laboratoire EDB, 118 Rue de Narbonne, Toulouse, 31062, France

460 KEENE, JEREMY\*<sup>1</sup> and BALLARD  
JR, HARVEY<sup>2</sup>

### An examination of the species limits within the *Monopyle sodiroana* complex (Gesneriaceae)

The *Monopyle sodiroana* complex in the Gesneriaceae ranges from central Colombia through northern Peru. It is composed of both terrestrial and epiphytic plants. This taxon was originally described as having lacinate calyx margins and a terminal inflorescence. Subsequent treatments, ignoring these particular diagnostic characters, have led to some confusion as to what defines the species and separates it from relatives. Interpretation of inflorescence structure (e.g., terminal versus axillary inflorescence type) from specimens has

proven challenging and confusing to lay taxonomists and specialists alike. Moreover, the lack of a designated type and inclusion of a mixed collection by Sodiro have exacerbated the problem of its proper circumscription and fostered an overall misunderstanding of the morphology of this taxon. The goal of this study is to precisely circumscribe *M. sodiroana* morphologically in a narrow sense, designate an appropriate lectotype for the name *M. sodiroana*, and then describe the several new species currently passing under that name and related morphologically to it. Thus far, nine morphologically distinctive species have been segregated from this polymorphic complex. These vary by indument, calyx shape, and consistent characters of leaves. The taxa are also geographically separate, narrowly endemic, and only occupy moist montane forest habitats.

<sup>1</sup>Ohio University, Environmental & Plant Biology, Porter Hall 317, Athens, OH, 45701, USA<sup>2</sup>Ohio University, Environmental & Plant Biology, 315 Porter Hall, Athens, OH, 45701, USA

461 MORA, M. MARCELA\*<sup>1</sup> and  
CLARK, JOHN L.<sup>2</sup>

### A preliminary phylogeny of the Neotropical plant genus *Paradrymonia* (Gesneriaceae) based on chloroplast and nuclear markers

*Paradrymonia* (Gesneriaceae) is a genus of facultative epiphytic herbs with 38 currently recognized species. It occurs throughout the Neotropics except for SE Brazil and the Caribbean with centers of diversity in Colombia and Ecuador. Monophyly of *Paradrymonia* and species relationships within the genus and closely related genera were evaluated based on molecular sequence data from the nuclear ribosomal (nrDNA) internal and external transcribed spacer regions (ITS and ETS), and the chloroplast (cpDNA) *trnH-psbA* intergenic spacer. Analyses utilizing parsimony, maximum likelihood and Bayesian inference methods were used to assess phylogenetic relationships among the 22 species of *Paradrymonia* and closely related genera. A preliminary analysis strongly supports that *Paradrymonia*, as currently circumscribed, is polyphyletic and includes taxa in three different clades. The clade that contains the type species is described as *Paradrymonia* sensu stricto (s.s.) and includes three species: *Paradrymonia ciliosa*, *P. decurrens* and *P. campostyla*. The *Paradrymonia* s.s. clade is sister to a clade that includes species of *Nautilocalyx*, *Chrysothemis* and other species traditionally recognized as *Paradrymonia*. Another clade including *Paradrymonia longifolia* and *P. anisophylla* nest within a paraphyletic *Drymonia*. Our results support a re-circumscription of *Paradrymonia* and the resurrection of a previously recognized genus name, *Trichodrymonia*, in order to accommodate the remaining ex-*Paradrymonia* species. Morphological characters such as bearded anthers, rosette habit, and anisophylly are discussed as potential

characters for circumscribing generic boundaries.

<sup>1</sup>The University of Alabama, Department of Biological Sciences, Tuscaloosa, AL, 35487-0345, USA<sup>2</sup>The University of Alabama, Department of Biological Sciences, Box 870345, Tuscaloosa, AL, 35487, USA

462 SCHULTE, LACIE J.<sup>\*1</sup>, OOI, MAGGIE T.<sup>2</sup>, JEFFRIES, SHANDRA K.<sup>2</sup>, CLARK, JOHN L.<sup>3</sup>, AMAYA MARQUEZ, MARISOL<sup>4</sup> and SMITH, JAMES<sup>5</sup>

### Phylogeny and climatic and morphological adaptation in the angustata clade of *Columnnea* (Gesneriaceae)

To better recognize and appreciate the mechanisms of speciation we must first understand the patterns and processes of important evolutionary/ecological forces that drive the process. The tropical plant family Gesneriaceae offers researchers insight into the speciation process. Until recently phylogenetic resolution of the family Gesneriaceae has proven difficult based on morphological characteristics alone. Molecular data have begun to shed light on the evolutionary relationships of the family, specifically focusing on the genus *Columnnea*. Previous morphological data had placed the species of *Columnnea* into a single genus (*Columnnea*) divided into five sections. The most recent molecular data is beginning to break down this previous classification system and shows support for seven clades within the genus. One of the well-supported monophyletic groups, the angustata clade, needs to be investigated further. Species found within the angustata clade are epiphytes with small (< 5cm), slightly ventricose corollas, short pedicels (< 2cm), and inflorescences of 3-12 flowers. This study uses seven gene regions (5 cpDNA regions, ITS, and ETS) to determine which species belong within the angustata clade and to place those species in a well supported phylogenetic tree. This tree will then be used to map both morphological characteristics and climate variables to study correlations among sister species within the clade to infer evolutionary patterns and processes.

<sup>1</sup>Boise State University, Biological Sciences, 1910 University Drive, Boise, ID, 83725-1515, USA<sup>2</sup>Boise State University, Biological Sciences, 1910 University Drive, Boise, ID<sup>3</sup>University of Alabama, Biological Sciences, Box 870345, Tuscaloosa, AL, 35487, USA<sup>4</sup>Universidad Nacional de Colombia, Instituto de Ciencias Naturales, Aptdo. Aereo 7495, Bogota, Colombia<sup>5</sup>BOISE STATE UNIVERSITY, Biology Department, 1910 UNIVERSITY DRIVE, Boise, ID, 83725-1515, USA

463 KIEL, CARRIE<sup>\*1</sup>, MCDADE, LUCINDA<sup>2</sup> and DANIEL, THOMAS<sup>3</sup>

### Unraveling Relationships Among the Morphologically Diverse and Taxonomically Complex New World Justicioids

The diverse justicioid lineage (ca. 1000 species) is part of the large, pantropical tribe Justicieae (Acanthaceae). Many justicioids share a number of morphological characteristics, notably, (1) the presence of a rugula: a channel-like structure formed by parallel ridges of corolla tissue that partially enclose the style, and (2) 'anther complexity' (i.e., expanded connective, reduced, highly modified, or sterile theca). Comprising the majority of this monophyletic lineage are members of *Justicia* from the Old World (OW) and New World (NW). *Justicia* is both species rich, particularly in the New World tropics, and taxonomically problematic. Our phylogenetic data show that *Justicia* is highly polyphyletic and contradict the most recent infra-generic classification. All NW *Justicia* and five smaller NW genera (collectively "NW justicioids") form a strongly supported clade, with significant resolution for major subclades but with moderate to low support for relationships among them. OW *Justicia*, however, is grossly paraphyletic. Interestingly, the species-rich Diclipterinae embedded within justicioids putatively have lost the morphological traits that mark justicioids and thus have not previously been associated with them. Here we present our recent phylogenetic work from nuclear *PHOT1-2*, nrITS and chloroplast *trnS-G*, *trnT-L*, *rps16*, *rpL16*, *trnL*<sub>(<sup>uag</sup>)</sub>, *-ndhF*, *ndhA* genes with a focus on the species rich NW justicioid lineage. In addition, we re-evaluate characters traditionally used in taxonomy classifications of *Justicia* in particular, pollen, androecium, and inflorescence characters, and discuss morphological evidence that support the hypothesized phylogenetic relationships among NW justicioids.

<sup>1</sup>Rancho Santa Ana Botanic Garden, 1500 North College Ave., Claremont, CA, 91711, USA<sup>2</sup>Rancho Santa Ana Botanic Garden, Department Of Botany, 1500 N. College Avenue, Claremont, CA, 91711, USA<sup>3</sup>California Academy of Sciences, Department of Botany, 55 Music Concourse Drive, Golden Gate Park, San Francisco, CA, 94118, USA

464 MCDADE, LUCINDA\*<sup>1</sup>, DANIEL, THOMAS<sup>2</sup> and KIEL, CARRIE<sup>3</sup>

### Making sense of massive polyphyly of the genus *Carlowrightia* (Acanthaceae: Justiceae: *Tetramerium* Lineage)

In our first paper on phylogenetic relationships among members of the *Tetramerium* lineage (Acanthaceae: Justiceae; Daniel et al. 2008. Syst Bot 33: 416–436), we reported a number of results that were not congruent with existing taxonomic treatments of these plants. This was especially true of New World plants among which only a single non-monospecific genus was shown to be monophyletic with strong support (i.e., *Tetramerium*). Even in this context, *Carlowrightia*, a genus of 26 species (12 sampled for the earlier study) was noteworthy, with species placed in three different clades. More recently, with the goal of understanding the evolutionary history of the genus as a whole, we have added six additional species (carefully chosen to encompass morphological diversity and the geographic range of the genus). Analysis of a data set of nearly 4500 bps confirms results for the 12 previously sampled taxa and places some of those newly sampled as expected based on morphological characters. In contrast, three of the newly sampled taxa are placed in two new clades. Argentinian *C.sulcata* is part of a clade referred to as the South American *Anisacanthus* clade in our earlier paper, adding support to the notion of a geographic signal among these plants. Two Chihuahuan desert species, *C. parvifolia* and *C. albiflora* are placed with monospecific *Gypsacanthus* which shares the same habitat. Plants of species of *Carlowrightia* vary markedly in corolla morphology (from subactinomorphic to pseudopapilionaceous) and also in seed morphology; patterns of variation in these traits are mostly congruent with our new phylogenetic results albeit with some notable exceptions.

<sup>1</sup>Rancho Santa Ana Botanic Garden, Department Of Botany, 1500 N. College Avenue, Claremont, CA, 91711, USA<sup>2</sup>California Academy of Sciences, Department of Botany, 55 Music Concourse Drive, Golden Gate Park, San Francisco, CA, 94118, USA<sup>3</sup>Rancho Santa Ana Botanic Garden, 1500 North College Ave., Claremont, CA, 91711, USA

465 TRIPP, ERIN\*<sup>1</sup>, MCDADE, LUCINDA<sup>2</sup>, ISA, SITI FATIMAH<sup>3</sup> and DARBYSHIRE, IAIN<sup>1</sup>

### *Physacanthus* (Acanthaceae): a heteroplasmic, intergeneric, interlineage hybrid?

Taxonomic affinities of the genus *Physacanthus* (Acanthaceae) have been in question for well over a century. Different authors have classified the genus into one of two distantly related lineages in the family: tribes Acantheae or Ruellieae. Morphological features (e.g., presence/absence of cystoliths, monotheous vs. bitheous anthers, open or ascending cochlear vs. contort corolla aestivation) support the phylogenetic distinctiveness of Acantheae and Ruellieae, and analyses of molecular data indicate that the two clades are not sister taxa. Thus, it is curious that researchers have struggled to classify this genus based on its phenotype. To ascertain which lineage *Physacanthus* is allied to, we re-evaluated morphology of the genus and generated nuclear and chloroplast sequence data for 18 accessions representing all three species in the genus. Unexpectedly, in multiple instances, cloning led to the retrieval of both Acantheae- and Ruellieae-like chloroplast genotypes from single accessions of *Physacanthus*, indicating that plants are heteroplasmic. Although our limited nuclear data (here, only ITS) do not support the hybrid hypothesis, morphology does: species of *Physacanthus* possess some traits characteristic of Acantheae, but others characteristic of Ruellieae.

<sup>1</sup>Royal Botanic Gardens, Kew, Herbarium, Tw9 3ab, Richmond, Surrey, UK<sup>2</sup>Rancho Santa Ana Botanic Garden, Department Of Botany, 1500 N. College Avenue, Claremont, CA, 91711, USA<sup>3</sup>Rancho Santa Ana Botanic Garden, 1500 N College Ave, Claremont, CA, 91711, USA

466 FRAGA, NAOMI

### Examining diversity in Western *Mimulus* (Phrymaceae): Evidence from morphological and molecular data reveals hidden species

At least 66 species of *Mimulus* are currently listed by U.S. government agencies and native plant societies as sensitive, rare, or endangered, making *Mimulus* a group of conservation concern. However, species delimitation and taxonomic relationships in *Mimulus* remain unclear, with 90 to 150 species recognized. In many recent regional treatments of the group, some previously recognized rare species with limited distributions have been lumped with more common species. Taxonomic confusion in *Mimulus* persists in part because diagnostic floral characters are often obscured when plants are pressed and dried. These easily ob-

scured characters are informative in understanding species diversity and delimiting species boundaries within the genus. A primary objective of this study is to resolve taxonomic issues and identify taxa that are in need of conservation. Because previous taxonomic treatments in *Mimulus* have been based primarily on study of herbarium specimens, more field studies are needed. Over the course of my work I have conducted extensive field research, photographing and collecting data and plant material from more than 60 populations. As a result I have identified five undescribed species of *Mimulus*. In this study I expand previous sampling, and utilize sequences from three non-coding regions from the chloroplast genome (*petA-psbJ*, *psbD-trnT*, *rpl32-trnL*) to examine species limits and monophyly. Preliminary results and taxonomic implications of these data will be discussed.

Rancho Santa Ana Botanic Garden, 1500 North College Avenue, Claremont, CA, 91711, USA

#### 467 CHAU, JOHN<sup>\*1</sup>, CRAIG, BAILEY<sup>2</sup> and OLMSTEAD, RICHARD<sup>3</sup>

### Phylogeny and biogeography of *Buddleja* (Scrophulariaceae): a preliminary study on a widely-distributed genus of showy shrubs and trees

No Abstract Available.

<sup>1</sup>University of Washington, Department of Biology, Campus Box 351800, Seattle, WA, 98195, USA<sup>2</sup>University of Washington, Department of Biology, Seattle, WA, 98195, USA<sup>3</sup>University of Washington, Department of Biology, CAMPUS BOX 355325, SEATTLE, WA, 98195-5325, USA

#### 468 LATVIS, MARIBETH<sup>\*1</sup>, SOUZA, VINICIUS C.<sup>2</sup>, SOLTIS, PAMELA<sup>3</sup> and SOLTIS, DOUGLAS<sup>4</sup>

### Phylogenetic Relationships and Divergence Time Analysis in *Agalinis* (Orobanchaceae)

*Agalinis* (Orobanchaceae) is a hemiparasitic genus of approximately 60 species, with a geographical distribution extending from Nova Scotia, Canada, to Argentina and Chile. Intrageneric relationships between the two continents are unknown, and the South American species appear to have a fascinating history of character evolution, including woody growth forms and changes in floral form involving new pollinator syndromes. While the North American species have been the focus of recent study, the South and Central American species of *Agalinis* are poorly understood and have not been included in phylogenetic studies until now. Approximately half of the South American species

occur in southeastern Brazil, with several species endemic to the region, in addition to *Esterhazyia*, a closely allied genus whose distinction from *Agalinis* has been questioned. Most of the remaining taxa occur in the Andean puna communities of Peru and Bolivia above 3000 meters. Thus, the two South American population centers of *Agalinis* are disjunct from one another. These disjunctions within South America, and between North and South America, provide intriguing questions regarding migration and diversification. By combining data sets from the North American taxa with data for newly collected taxa from Brazil, the Andes, and Central America, we have produced a molecular phylogeny of *Agalinis* and four outgroup genera (*Brachystigma*, *Dasistoma*, *Aureolaria* and *Esterhazyia*) using seven chloroplast and four nuclear loci. Dates for nodes within the tree were obtained by expanding sampling into the Lamiales and calibrating the phylogeny using lamiid fossils (e.g. *Fraxinus*, Bignoniaceae) using Penalized Likelihood in r8s. These results will be discussed, along with implications for future studies of biogeography and character evolution within this clade.

<sup>1</sup>Florida Museum Of Natural History, Florida Museum Of Natural History, Dickinson Hall, Museum Rd., Gainesville, FL, 32611, USA<sup>2</sup>Universidade de São Paulo, Escola Superior de Agricultura Luiz de Quei, Departamento de Ciências Biológicas, Avenida Pádua Dias, 11 - Caixa Postal 9 Agronomia, Piracicaba, SP, 13418-900, Brazil<sup>3</sup>University of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA<sup>4</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA

#### 469 RODRIGUES, ANUAR<sup>\*1</sup>, COLWELL, ALISON<sup>2</sup> and STEFANOVIC, SASA<sup>3</sup>

### Phylogeny of the parasitic genus *Conopholis* (Orobanchaceae): Evidence from plastid and nuclear DNA sequences

Little is known of the evolutionary relationships among populations and species of *Conopholis*, a small holoparasitic genus with reduced vegetative morphology. In the most recent taxonomic classification of this genus, *Conopholis* is described as having two species, *C. americana* and *C. alpina*. This classification is based on a combination of presence/absence of characters along with a number of quantitative traits. We conducted the first phylogenetic study of *Conopholis* designed to develop a resolved and well-supported multi-locus phylogenetic hypothesis for this genus. We analyzed plastid (*trnM-E* intergenic spacer and *clpP* gene/introns) and nuclear (*phyA* intron 1) nucleotide sequence data using the neighbor-net, Bayesian, and parsimony approaches in addition to conducting tests of alternative hypotheses. Our data set contained populations from a wide taxonomic sampling covering its entire geographical range in North America. The results indicate that regardless of the data set used or phylogenetic methodology employed, none of our analyses lend

support for the strict subdivision of the genus into the two currently recognized species. Instead, three distinct genetic clusters were recovered and indicates that reciprocal monophyly between the two currently accepted species has not yet been achieved. *Conopholis alpina* is paraphyletic and shows evidence of belonging to at least two separate lineages. The monophyly of *C. americana* was also not recovered; however, this possibility could not be rejected with confidence. These analyses recovered three distinct lineages indicating that there could be a minimum of three species within the genus. We anticipate that a fine-scale morphometric analysis of morphological features within *Conopholis* may reveal shared features that could further corroborate our molecular results.

<sup>1</sup>University of Toronto Mississauga, Biology, 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada<sup>2</sup>Division of Biological Resources, Yosemite National Park, El Portal, CA, 95318, USA<sup>3</sup>UNIVERSITY OF TORONTO, Department Of Botany, 3359 MISSISSAUGA RD N, MISSISSAUGA, ON, L5L 1C6, Canada

**470 WOLFE, ANDREA\* and HOUSE, JOSHUA**

### **Assessing the host range of *Hyobanche* L. (Orobanchaceae) using DNA forensics**

*Hyobanche* L. is a small genus of holoparasitic plants distributed across southern Africa. It is found in a variety of ecosystems ranging from coastal sand dunes to fynbos biomes, the Little and Great Karoos, and into the highlands Lesotho. *Hyobanche* is a root parasite with a unique system of secondary haustoria formed on the leaf bracts of the rhizomes, which can be quite an extensive system underground. Proximity to other plants is not a good indicator of the actual host plant being parasitized. To determine the host range for species of *Hyobanche* ca. 400 host roots attached to haustoria were collected and their DNA extracted. Accessions with amplifiable DNA were sequenced and matched to sequences deposited into Genbank or to sequences obtained from potential host plants collected in proximity to parasitic plants collected in the field. *Hyobanche* parasitizes a wide range of plant genera from Asteraceae, Goodeniaceae, Poaceae, and Thymelaeaceae, and multiple plant genera may be parasitized at the same time.

Ohio State University, Department of Evolution, Ecology, and Organismal Biology, 318 W. 12th Avenue, Columbus, OH, 43210-1293, USA

**471 WENZEL, AARON\*<sup>1</sup>, WOLFE, ANDREA<sup>1</sup>, ENGLISH, CAROL<sup>2</sup> and BRUEDERLE, LEO<sup>3</sup>**

### **Reproductive biology and genetic diversity in *Penstemon degeneri* (Plantaginaceae), a rare species endemic to Colorado.**

*Penstemon degeneri* Crosswhite (Plantaginaceae), otherwise known as Degener's Beardtongue, is a rare Colorado endemic that is reported to be restricted in distribution to Custer and Fremont Counties, and has a reported chromosome number of  $n = 8$ . It is considered imperiled at the state level (S2), as well as globally (G2). Fieldwork addressing the reproductive biology of this species revealed that *P. degeneri* sets fruit involving outcrossing effected by a variety of insect visitors coupled with a small amount of self-pollination in the absence of pollinators. Effective pollinators determined from visitor frequency, behavior, body pollen, and fidelity revealed that effective pollinators included *Osmia* and *Bombus* bees, as well as *Pseudomasaris vespoidea*, an oligolectic pollen wasp. A population genetics study was conducted using eight microsatellite loci revealing allelic variation among populations and a genetic profile consistent with polyploidy rather than diploidy.

<sup>1</sup>Ohio State University, Department of Evolution, Ecology, and Organismal Biology, 318 W. 12th Avenue, Columbus, OH, 43210-1293, USA<sup>2</sup>University Of Colorado Denver, PO Box 281, Morrison, CO, 80465, USA<sup>3</sup>University Of Colorado Denver, CB171, PO. 173364, DENVER, CO, 80217-3364, USA

**472 GODDEN, GRANT\*<sup>1</sup>, BURLEIGH, GORDON<sup>2</sup>, SOLTIS, PAMELA<sup>3</sup> and SOLTIS, DOUGLAS<sup>4</sup>**

### **Out of the Bushes and Into the Trees: Interpreting Complex Patterns in Mint Phylogeny**

The mint family (Lamiaceae) is species rich and morphologically complex, with a dynamic and contentious taxonomic history. Phylogenetic analyses of closely related mints based on molecular data often yield few well-supported clades. Although these patterns do not resolve taxonomic questions, they may represent important evolutionary events and processes. For example, phylogenetic inference may be greatly complicated by incomplete lineage sorting, gene duplications, and heterogeneous processes of molecular evolution across loci and lineages. Furthermore, systematic error—including alignment error, unrecognized paralogy, inadequate taxonomic sampling, and model misspecification—also might be misleading the phylogenetic analyses. We assembled the available DNA sequence data from Lamiaceae along with new sequences for New World Menthaeae in order to examine relationships throughout Lamiaceae

and to investigate potential factors complicating phylogenetic inference. This analysis produced the most comprehensive family-wide phylogeny for Lamiaceae, representing a synthesis of current molecular data. We also used fossil evidence for Lamiaceae (and Lamiales) and phylogenetic dating techniques to estimate the first divergence dates and evolutionary rates for the family. We discuss the implications of our analysis on mint systematics as well as promising future directions for resolving relationships throughout Lamiaceae.

<sup>1</sup>University of Florida, Department of Biology, Florida Museum of Natural History, 357 Dickinson Hall, Gainesville, FL, 32611-7800, USA<sup>2</sup>University of Florida, Department of Biology, 220 Bartram Hall, Gainesville, FL, 32611, USA<sup>3</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA<sup>4</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA

**473 WICKETT, NORMAN J<sup>\*1</sup>, DUARTE, JILL<sup>2</sup>, WAFULA, ERIC<sup>3</sup>, LEEBENS-MACK, JIM<sup>3</sup> and DE PAMPHILIS, CLAUDE W<sup>4</sup>**

### Reconstructing plant phylogenies using the cDNA sequences of over 900 low copy nuclear genes

The recent advances in Next Generation Sequencing technologies have led to a dramatic increase in the availability of plant transcriptomes that, in addition to their utility in detecting patterns of gene expression, can be mined for phylogenetically informative markers. A scaffold of orthologous gene clusters was created using orthoMCL to cluster the inferred protein sequences of 10 sequenced plant genomes; from this scaffold we identified 970 genes that are single copy in each of seven angiosperm genomes. We sorted both publicly available and newly sequenced transcriptomes, and recently sequence plant genomes into this scaffold and identified putative homologs of these 970 genes. The resultant super matrix consisted of over two million aligned sites and over 800,000 parsimony informative characters. Here, we discuss the phylogenetic hypotheses that result from using the cDNA sequences of these low copy nuclear genes with multiple sets of both taxa and genes.

<sup>1</sup>Penn State University, Biology, 403 Life Sciences Building, University Park, PA, 16802, USA<sup>2</sup>Penn State University, 403 Life Sciences Building, University Park, PA, 16802, USA<sup>3</sup>University Of Georgia, 4503 Miller Plant Sciences, Athens, GA, 30602, USA<sup>4</sup>Pennsylvania State University, Department Of Biology, 101 LIFE SCIENCES BUILDING, UNIVERSITY PARK, PA, 16802, USA

**474 HILU, KHIDIR<sup>\*</sup> and MOUKARZEL, KEENAN**

### MatK is a pseudogene in many angiosperms: Is it really?

Due to its high proportion of phylogenetic signal, the plastid *matK* gene has become one of the most utilized genomic regions in plant molecular phylogenetics. The *matK* gene is known for its considerably high rate of substitution at the nucleotide level, but more so at the amino acid level due to near equity in rates of mutations across the three codon positions. These high rates of substitutions, in particular the rate of amino acid substitutions, raised question on whether this group II intron maturase is a pseudogene since conserved amino acid substitution is a prerequisite for maintaining structural and functional integrity of any transcribed protein product. Some studies have explicitly noted that *matK* is a pseudogene because of either a lack of an apparent start codon or the presence of one or more premature stop codons that could result in a truncated protein. Further, GenBank also contains a number of *matK* sequences that are described as "*matK*-like" or "pseudogene". Using empirical data, we will address issues concerning the definition of *matK* open reading frame, patterns of substitutions in functional genes vs. pseudogenes, and the impact of gene functionality on phylogenetic reconstruction. Our findings question several of the published contentions regarding *matK* as a pseudogene.

Virginia Tech, Department of Biological Sciences, 2119 Derring Hall, Blacksburg, VA, 24061, USA

**475 STEELE, PAMELA<sup>\*1</sup> and PIRES, JOSEPH<sup>2</sup>**

### Reciprocal Illumination: Combining Morphological and Genomic Characters for Species Identification

Accurate identification of organisms is fundamental to science and industry. Traditionally, taxonomists have used morphological, geographical, chemical, reproductive, and anatomical characteristics to delineate species. However, in many cases, species identifications remain unclear. DNA barcoding is a modern method of identifying organisms using portions of their genetic sequence analyzed from a small amount of tissue. DNA barcoding has been used to identify native and exotic organisms, illegally imported organisms at ports and borders, undesirable plant and animal substances in processed foodstuffs, pathogens or vectors of pathogens, ancient DNA samples, museum fragments, organisms and tissues at crime scenes, and to assess biodiversity in an ecosystem. However, current DNA barcoding methods are limited to a small

number of PCR-amplified markers, and as a result, no genomic markers have yet been discovered that can correctly identify all species tested. We propose a species identification tool that combines classical taxonomy and genome sequencing and takes advantage of recent advances in high-throughput sequencing technology. Current sequencing technologies make it easier and more cost effective to sequence entire plant chloroplast and animal mitochondrial genomes than to sequence a few genes individually. These technologies also make available sequence data from the nuclear and mitochondrial genomes that can provide further support for species identification. We present results of a pilot study designed to test this strategy in an endangered tallgrass prairie ecosystem in Missouri that focused on the three largest and most economically important plant families found in the prairie - Poaceae (grasses), Fabaceae (legumes), and Asteraceae (sunflowers). We compared nuclear ribosomal genes, several mitochondrial genes, and whole chloroplast genomes, genes, and noncoding regions at all taxonomic levels, including investigations between species and across angiosperms. We compared these results with traditional DNA barcoding methods and present our findings.

<sup>1</sup>University Of Missouri, 371 B Life Sciences Center, 1201 Rollins Street, Columbia, MO, 65211-7310, USA<sup>2</sup>University Of Missouri, 371 B Life Sciences Center, 1201 Rollins Street, Columbia, MO, 65211, USA

**476 SIMMONS, MARK\*<sup>1</sup> and FREUDENSTEIN, JOHN<sup>2</sup>**

### **Spurious 99% bootstrap and jackknife support for unsupported clades**

Quantifying branch support using the bootstrap and/or jackknife is generally considered to be an essential component of rigorous parsimony and maximum likelihood phylogenetic analyses. Previous authors have described how application of the frequency-within-replicates approach to treating multiple equally optimal trees found in a given bootstrap pseudoreplicate can provide apparent support for otherwise unsupported clades. We demonstrate how a similar problem may occur when a non-representative subset of equally optimal trees are held per pseudoreplicate, which we term the *undersampling-within-replicates* artifact. We illustrate the frequency-within-replicates and undersampling-within-replicates bootstrap and jackknife artifacts using both contrived and empirical examples, demonstrate that the artifacts can occur in both parsimony and likelihood analyses, and show that the artifacts occur in outputs from multiple different phylogenetic-inference programs. Based on our results, we make the following five recommendations, which are particularly relevant to supermatrix analyses, but apply to all phylogenetic analyses. First, when two or more optimal trees are found in a given pseudoreplicate they should be summarized using the strict-consensus rather than frequency-within-replicates approach. Second jack-

knife resampling should be used rather than bootstrap resampling. Third, multiple tree searches while holding multiple trees per search should be conducted in each pseudoreplicate rather than conducting only a single search and holding only a single tree. Fourth, branches with a minimum possible optimized length of zero should be collapsed within each tree search rather than collapsing branches only if their maximum possible optimized length is zero. Fifth, resampling values should be mapped onto the strict consensus of all optimal trees found rather than simply presenting the  $\geq 50\%$  bootstrap or jackknife tree or mapping the resampling values onto a single optimal tree.

<sup>1</sup>Colorado State University, Department Of Biology, FORT COLLINS, CO, 80523-1878, USA<sup>2</sup>Ohio State University, MUSEUM OF BIOLOGICAL DIVERSITY, 1315 KINNEAR RD, COLUMBUS, OH, 43212-1157, USA

**477 RANDLE, CHRISTOPHER\*<sup>1</sup> and FREUDENSTEIN, JOHN<sup>2</sup>**

### **The effect of within-replicate search strategies on jackknife support of clades of different size**

Empirical phylogenetic studies demonstrate a correlation between clade size and Bayesian clade support, with large and small clades often receiving greater support than clades of intermediate size. This is not surprising in that a non-uniform prior on topologies induces just such a relationship on the prior probabilities of component clades. What is surprising is that the same relationship exists for parsimony jackknife, though no such prior on topologies is explicitly included in their estimation. This surprising correlation may be due in large part to homoplasy; theoretically, jackknife values should be uniform on clades of any size supported by the same number of uncontraverted synapomorphies. Within-replicate search strategy may have substantial effects on the inference of jackknife support. In general, less thorough within-replicate search strategies yield lower jackknife support values because suboptimal trees sampled from these replicates will be randomized in respect to each other. This randomization of inferred topologies across replicates should mirror the effect on clade support induced by the uniform topology in Bayesian inference. In this study we investigate the effect of within-replicate search strategy on jackknife support across clades of different size, using two well-characterized empirical data sets. Search strategies differed in 1) the number of random addition searches per replicate, 2) the number of trees held during searching, 3) the number of trees retained from each replicate, 4) the branch-swapping algorithm used, and 5) how trees were summarized across replicates.

<sup>1</sup>Sam Houston State University, Department of Biological Sciences, 1900 Avenue I, Huntsville, TX, 77340, USA<sup>2</sup>Ohio State University, MUSEUM OF BIOLOGICAL DIVERSITY, 1315 KINNEAR RD, COLUMBUS, OH, 43212-1157, USA

478 SMITH, STACEY D.

**Traits shaping trees: Detecting character-state dependent diversification**

Although traits are commonly portrayed as evolving along branches of phylogenetic trees, it is clear that many traits actually affect the shape of the tree by changing the probability that a lineage will speciate or go extinct. Recently developed likelihood and Bayesian methods now allow rigorous tests of character-state dependent diversification, and have revealed some surprising shifts from previous notions about directionality in trait evolution. I will discuss these empirical examples and the anticipated impact of these new approaches on the field of comparative methods.

University of Nebraska-Lincoln, School of Biological Sciences, 1104 T St, 314 Manter Hall, Lincoln, NE, 68588-0118, USA

479 VELA DIAZ, DILYS\*<sup>1</sup> and JIMÉNEZ, IVÁN<sup>2</sup>**Species delimitation: identifying the most relevant dimensions to infer gaps in morphology**

Although species are considered important biodiversity units, methods to define their limits have been contentious. Multivariate ordination techniques have been widely used to delimit species based on discontinuities (gaps) in morphological variation. Often only the first few ordination axes are used to visually inspect morphological variation, under the unwarranted assumption that axes capturing most variation across all specimens are the most relevant for species delimitation. Here we show that a recently developed method to measure morphological discontinuities, based on analyses of multivariate normal mixtures, can be extended to identify the dimensions of morphological variation that are most informative for species delimitation. Hence, this method can help to measure the strength of the evidence for the existence of a morphological gap between two hypothesized species. We examine the performance of the approach under various sample sizes using simulated taxonomic samples based on Edgar Anderson's Iris flower dataset.

<sup>1</sup>University Of Missouri - St. Louis, Department Biology, 223 Research Building, One University Blvd., Saint Louis, MO, 63121-4499, USA <sup>2</sup>Missouri Botanical Garden, Center for Conservation and Sustainable Development, Saint Louis, MO, 63166-0299, USA

480 GRASS PHYLOGENY WORKING GROUP II,

**Relationships among the subfamilies of grasses (Poaceae)**

The phylogeny of the grass family has received a great deal of attention, and published data to date have supported twelve well-supported clades that are named as subfamilies. The three smallest subfamilies are consistently supported as successive sisters to the remainder, which are divided into the BEP clade (Bambusoideae, Ehrhartoideae and Pooideae) and the PACMAD clade (Panicoideae, Arundinoideae, Chloridoideae, Micrairoideae, Aristidoideae and Danthonioideae). Although both the BEP clade and the PACMAD clade are strongly supported, relationships among their respective subfamilies are unresolved. Phylogenetic analyses using one or two genes have found almost all possible relationships among the subfamilies, and the results are often highly sensitive to taxon sampling. The PACMAD clade is of particular interest here because it contains at least 17 origins (and possible reversals) of  $C_4$  photosynthesis; however, determining the precise number and phylogenetic position of these changes requires a resolved and robust phylogeny. The GPWGII was formed in 2010 specifically to resolve the PACMAD phylogeny as a crucial step towards investigating  $C_4$  evolution. By using data available in NCBI and supplementing it with extensive unpublished data from each of our lab groups, we were able to assemble a dataset of 540 taxa with sequences from the chloroplast loci *rbcL*, *ndhF* and *matK*. Additional sequences were then produced to fill in gaps in the matrix and reduce missing data to only 7%. Within the PACMAD clade, our data support the position of Aristidoideae as sister to the other subfamilies, and Panicoideae as the next diverging clade. The remaining four clades have the relationship ((chloridoid, danthonioid), (arundinoid, micrairoid)). Although not a focus of this particular project, we also resolved the BEP clade as ((bambusoid, pooid), oryzoid). Our taxon sampling focused particularly on Panicoideae, for which we included nearly all currently recognized genera. Our results are consistent with previous single-gene studies, but with better resolution and stronger support.

NESCent, 2024 W. Main Street, Suite A200, Durham, NC, 27705-4667, USA

481 CHOKTHAWEEPANICH,  
HATHAIRAT\*<sup>1</sup>, FISHER, AMANDA<sup>2</sup>,  
DRANSFIELD, SOEJATMI<sup>3</sup>, WIDJAJA,  
ELIZABETH<sup>4</sup>, WONG, KHOON MENG<sup>5</sup>,  
RATTAMANEE, CHAKKRAPONG<sup>6</sup> and  
CLARK, LYNN<sup>1</sup>

**Phylogeny and classification of the  
paleotropical woody bamboos (Poaceae:  
Bambusoideae: Bambuseae)**

The paleotropical woody bamboo clade consists of ca. 460 species, or approximately a third of total bamboo diversity, and is widely distributed in Asia, Africa, Australia, India, Sri Lanka, and Madagascar. These bamboos are important and even dominant elements in many paleotropical forest habitats and have a multitude of uses for humans. Despite the important ecological and economic roles of these bamboos, the phylogenetic relationships of their major lineages have remained obscure. Our objectives were to test the monophyly of the four currently recognized subtribes of paleotropical woody bamboos and examine their phylogenetic relationships. Sixty-five species of the Bambusinae (18 genera; 36 spp.), Melocanninae (7 genera; 15 spp.), Hickeliinae (9 genera; 11 spp.), and Racemobambosinae (2 genera; 3 spp.), two species of *Incertae Sedis*, and six outgroup species of Neotropical woody bamboos were sequenced for both non-coding (*trnD-trnT*, *rpl16* intron, *rps16* intron) and coding (*ndhF3*, *matK*) chloroplast DNA regions. Phylogenetic analyses supported subtribe Melocanninae as monophyletic and sister to all other paleotropical woody bamboos, consistent with previous analyses. The other three subtribes were resolved as paraphyletic or polyphyletic, with relatively poor resolution and support within the diverse Bambusinae. The taxa of subtribe Hickeliinae from Madagascar, however, did form a monophyletic group with strong support. The evolution of selected morphological characters including vegetative branching, synflorescence architecture and fruit type is examined using the phylogeny.

<sup>1</sup>Iowa State University, Department Of Ecology, Evolution, And Organismal Biology, 253 Bessey Hall, Ames, IA, 50011-1020, USA, <sup>2</sup>Idaho State University, Department of Biological Sciences, 921 South 8th Avenue, Stop 8007, Pocatello, ID, 83209-8007, USA-<sup>3</sup>Herbarium, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AB, UK<sup>4</sup>Herbarium Bogoriense, Puslitbang Biologi LIPI, Bogor, INDONESIA<sup>5</sup>Singapore Botanic Gardens, 1 Cluny Road, 259569, Singapore<sup>6</sup>Kasetsart University, Department of Horticulture, Faculty of Agriculture, 50 Phahon Yothin Rd, Chatuchak, Bangkok, 10900, THAILAND

482 TRIPLETT, JIMMY\*<sup>1</sup>, CLARK,  
LYNN<sup>2</sup>, WEN, JUN<sup>3</sup> and PETERSON, PAUL<sup>4</sup>

**Polyploid speciation on a grand scale: the  
evolution of the temperate bamboos**

The temperate bamboos encompass 500+ species in Asia, Africa, and North America and are among the most problematic plants from a taxonomic perspective. Recent molecular evidence suggested that the temperate bamboos provide a large-scale example of speciation at the polyploid level. In the current investigation, low-copy nuclear genes (including an endo-1,4- $\beta$  glucanase and a poly-A binding protein) were used to reconstruct phylogenetic relationships within the woody bamboos in order to examine the origin of polyploidy in the temperate clade. These data suggest that all 500+ species of temperate bamboos are descended from a single allotetraploid ancestor that was derived from two divergent parents. Subsequent diversification has produced species that are genetically, morphologically, and ecologically distinct, yet retain both parental genomes. Moreover, new species have been produced by ongoing hybridization at the tetraploid level. This new evidence, combined with previous studies using chloroplast DNA and AFLP data, reveal that hybridization and polyploidy have had important and recurrent roles in the evolution of the temperate bamboos.

<sup>1</sup>Jacksonville State University, 700 Pelham Road North, Jacksonville, AL, 36265, USA<sup>2</sup>Iowa State University, Department of Ecology, Evolution and Organismal Biology, 253 Bessey, Ames, IA, 50011-1020, USA<sup>3</sup>Smithsonian Institution, Botany, MRC-166 National Museum Of Natural History, 10th St. & Constitution Ave., NW, MRC 166, Washington/DC, N/A, 20013-7012, USA<sup>4</sup>Smithsonian Institution, Botany, MRC-166 National Museum Of Natural History, PO Box 37012, WASHINGTON, DC, 20013-7012, USA

483 ATTIGALA, LAKSHMI\*<sup>1</sup>,  
TRIPLETT, JIMMY<sup>2</sup> and CLARK, LYNN<sup>3</sup>

**A new major lineage of the Arundinarieae  
(Poaceae: Bambusoideae) based on a  
multi-locus plastid phylogeny**

The temperate woody bamboo tribe Arundinarieae is a morphologically diverse and taxonomically complex group within the Bambusoideae (Poaceae). Arundinarieae includes over 500 species and is broadly distributed in temperate or subtropical regions in North America and Eastern Asia and at higher elevations in Africa, Madagascar, Sri Lanka, India and the Philippines. Monophyly of the temperate clade is well supported in many previous molecular studies. The most recent phylogenetic analyses based on chloroplast DNA reveal ten major lineages, but without resolution among them. This study included all the native Sri Lankan *Arundinaria* species along with representatives from

all ten main lineages of the temperate bamboo clade to reconstruct the phylogeny based on four chloroplast DNA noncoding regions (rpoB-trnC, rps16-trnQ, trnD/T, and trnT/L intergenic spacers). Our objectives were to place the Sri Lankan *Arundinaria* species in the correct genus or genera and understand the interrelationships of the major clades within Arundinarieae. Phylogenetic analyses fully supported the monophyly of the Sri Lankan *Arundinaria* species, but failed to resolve the position of this clade relative to the other ten clades. These species therefore represent the eleventh lineage of the temperate bamboo clade. We discuss these results and propose the recognition of a new genus to accommodate the Sri Lankan clade. Key morphological characters including rhizome morphology, culm leaves, vegetative branching pattern, and synflorescence structure are compared among the Sri Lankan clade and *Arundinaria*, *Yushania*, and *Thamnochalamus*, the genera in which the Sri Lankan species have been classified.

<sup>1</sup>Iowa State University, Department of Ecology Evolution and Organismal Biology, 253 Bessey Hall, Ames, IA, 50011-1020, USA

<sup>2</sup>Jacksonville State University, 700 Pelham Road North, Jacksonville, AL, 36265, USA <sup>3</sup>Iowa State University, Department Of Ecology, Evolution, And Organismal Biology, 253 Bessey Hall, Ames, IA, 50011-1020, USA

#### 484 RUIZ-SANCHEZ, EDUARDO<sup>\*1</sup>, SOSA, VICTORIA<sup>2</sup> and MEJIA-SAULES, TERESA<sup>3</sup>

##### New insights into the phylogeny and taxonomy of the Mesoamerican bamboo genera *Olmecca-Otatea* (Poaceae: Bambusoideae: Bambuseae)

A synthesis of the most recent molecular and morphological phylogenetic studies in the monophyletic sister bamboo genera *Olmecca* and *Otatea* is here presented. A new species in *Olmecca* and four new species in *Otatea* have been recently described. The molecular phylogenetic analysis based in nuclear and plastid DNA regions retrieved unresolved trees at species level in both genera, contrary to the morphological phylogenetic analysis. These bamboos are found in habitats from tropical dry forests to tropical rainforests and cloud forests with two kinds of fruits (fleshy and dry caryopsis). The molecular dating reveals an age of 4.3 Ma for the most common ancestor of these genera and the ancestral area reconstruction indicates a Mesoamerican origin with dispersal to South America. Molecular and morphological phylogenetic analyses retrieved trees with conflicting topologies. These conflicts could be explained due to incomplete lineage sorting with retention of ancestral polymorphism correlated to the recent origin of these Mesoamerican bamboos. The results of phylogenetic analyses of *Olmecca* and *Otatea* and taxa in the subtribe Guaduinae resulted in a new classification

of the group.

<sup>1</sup>University of California, Berkeley, Plant and Microbial Biology, 431 Koshland Hall, Berkeley, California, 94720, USA <sup>2</sup>ISTITUTO DE ECOLOGIA A.C., APDO POSTAL 63, XALAPA, Veracruz, N/A, 91000, Mexico <sup>3</sup>Instituto de Ecología AC, Biología Evolutiva, Apartado Postal 63, Xalapa, Veracruz, 91000, Mexico

#### 485 VOSHELL, STEPHANIE<sup>\*1</sup>, BALDINI, RICCARDO<sup>2</sup>, KUMAR, ROHIT<sup>1</sup>, TATALOVICH, NICHOLAS<sup>1</sup> and HILU, KHIDIR<sup>3</sup>

##### *Phalaris* (Canary Grasses, Poaceae): Elucidating trends in floret evolution and polyploidy using molecular phylogenetics

The 21 species of *Phalaris* L. (Poaceae, *Aveneae*) are distributed in temperate areas and tropical mountains of Africa and in South America. The genus contains annual and perennial diploids based on  $x=6$  and 7 and polyploids based on  $x=7$ , with the  $x=6$  displaying less species diversification. The multi-continent and varied patterns of distribution, notable variation in morphological traits, and the evident role of polyploidy in its evolution rendered *Phalaris* as a potentially valuable case study for speciation in conjunction with chromosomal evolution and biogeography in Poaceae. We reconstructed the first phylogenetic tree for the genus using nuclear ITS and plastid *trnT-F* sequences to assess species relationships and map trends in floret differentiation and patterns of polyploid evolution. The study demonstrated the single origin of  $x=6$  chromosome number and revealed the sister group relationship of this lineage to the monophyletic  $x=7$  lineage. Clades recovered in the phylogenetic analyses reflect geographic affinities and show diploid-polyploid associations. A trend in sterile lemma reduction is evident from sister genera in respective Pooideae clades to terminal lineages of the ingroup, with members of the early diverging  $x=6$  lineage displaying relatively large lanceolate morphotypes followed by gradual reduction in size, culminating in almost obsolete sterile lemmas in one of the terminal  $x=7$  clades.

<sup>1</sup>Virginia Tech, Biological Sciences, Derring Hall, Blacksburg, VA, 24061, USA <sup>2</sup>Università degli Studi, Dipartimento di Biologia Evoluzionistica, Via G. La Pira 4, Firenze, 50121, Italy <sup>3</sup>VIRGINIA TECH, Department Of Biology, 2119 Derring Hall, BLACKSBURG, VA, 24061-0406, USA

486 BARKWORTH, MARY\* and  
BUSHMAN, SHAUN

### North American *Meliceae* (*Poaceae*): morphology, geography, and phylogeny

The *Meliceae*, a basal pooid tribe, are represented in North America by four of its eight genera: *Melica*, *Glyceria*, *Pleuropogon*, and *Schizachne*. *Melica* grows in dry to moist sites but the other three genera grow in moist to wet habitats. *Melica* also differs from the other three genera in having a chromosome base number of 9 rather than 10. Six of the 36 North American species in the four genera extend across the northern part of the continent: *G. borealis*, *G. grandis*, *G. striata*, *M. smithii*, *P. sabinei*, and *S. purpurascens*. The remainder are either western or eastern in their distribution. There is also a marked morphological distinction between the western and eastern species of *Melica* but not *Glyceria*. *Melica* is also the only one of the four genera to be well represented in South America. Our preliminary work on the phylogeny of the tribe indicates that *Glyceria* is basal to the other three genera and that *Pleuropogon* is derived from it. *Pleuropogon sabinei* was sister to *P. oregonus* on both the ITS and cpDNA trees but relationships among other members of the genus differ between the two trees. *Schizachne* and *Melica* form a separate clade, with *Schizachne* basal to *Melica*. There is little molecular differentiation within North American members of *Melica* but the western and eastern species are in separate clades on the ITS tree and the eastern species appear to be more closely related to South American species than to the Asian or western North American species. Relationships on the chloroplast tree are unresolved. We plan to extend this work to other members of the tribe so that, in collaboration with others, relationships at the base of the *Poideae* are clarified and a strong foundation developed for elucidating the genetic basis of the subfamily's success.

487 REID, CHRISTOPHER

### Molecular Systematics of *Cyperus* L. (*Cyperaceae*): A Preliminary Analysis of Nuclear ITS Sequences

*Cyperus* (flat sedges) has perhaps 700 species worldwide. Generic limits and infrageneric taxonomy of *Cyperus* are unclear. This study presents the results of an analysis of 50 ingroup OTUs, most of which were field collected during the growing season of 2010. In addition to *Cyperus* s.s., the ingroup included members of *Kyllinga*, *Lipocarpha*, *Pycneus*, and *Queenslandiella*. Previous molecular studies of *Cyperus* and tribe Cyperaceae have analyzed chloroplast markers using maximum parsimony. This study explores phylogenetic relationships

within *Cyperus* s.l. using Bayesian analysis of nuclear ribosomal Internal Transcribed Spacer (ITS) sequences. The ITS tree, while not completely resolved, offers some interesting insights. *Cyperus* s.l. formed a well-supported clade, within which *Kyllinga*, *Lipocarpha*, *Pycneus*, and *Queenslandiella* were embedded. Within *Cyperus* s.l., two major clades corresponding to photosynthetic pathway ( $C_3$  and  $C_4$ ) were resolved. This  $C_3/C_4$  split is consistent with previous cladistic analyses of chloroplast sequences. The  $C_3$  clade consisted of a polytomy involving three clades, one of which corresponding to the *Luzulae* group. Genus/subgenus *Pycneus*, diagnosed by lenticular achenes which are oriented edge-wise to the rachis of the spikelet, was polyphyletic in this analysis. The position of subgenus *Dididium* within the tree suggests that the rank of section may be more appropriate. Future work will involve sequencing the ITS region for additional taxa. Other molecular markers such as *matK* will be sequenced and analyzed. Markers used by other workers will be sequenced in more New World taxa to enable a collaborative analysis of a larger taxon sample.

Louisiana State University, Biological Sciences, Life Science Annex Building, Rm. A257, Baton Rouge, LA, 70803, USA

488 MONFILS, ANNA\*<sup>1</sup>, FLEMING,  
SAMANTHA<sup>2</sup>, LICHTENWALD,  
SAMANTHA<sup>2</sup>, SHIELS, DEREK<sup>2</sup> and BLUM,  
MICHAEL<sup>3</sup>

### Evolution and diversity in the *Schoenoplectus pungens* species complex (*Cyperaceae*)

The *Schoenoplectus pungens* species complex is characterized with a high level of morphological similarity among species and frequent hybridization. Descriptions of species and varieties in the complex overlap in character states, confounding practical identification. Hybridization, prevalent in the group, has led previous authors to question the integrity of individual species and variety descriptions. The study presented here undertook a comprehensive molecular and morphological investigation of species and varieties in the *S. pungens* species complex (including *S. americanus*, *S. deltarum*, *S. pungens* var. *pungens*, *S. pungens* var. *badius*, and *S. pungens* var. *longispicatus*) to evaluate diacritical characters for species and variety boundaries, determine integrity of species and variety descriptions, and resolve the origin of *S. deltarum*. We assessed potential diacritical morphological characters including awn length and coloration, culm morphology and diameter, bract length, stigma lobe number, distal leaf blade length and spikelet number from 36 populations and up to 1000 specimens from throughout North America. DNA sequence variation of the nuclear ITS and chloroplast trn $TLF$  regions were analyzed for all species, varieties and potential hybrid combinations. Additional studies of genotypic differentiation were assessed within and among *S. pun-*

*gens*, *S. americanus* and *S. deltarum* using microsatellite data. Awn length, stigma lobe number, distal leaf blade length, culm diameter and morphology, and spikelet number were identified as key morphological features for species and hybrid identification. Awn coloration delineated *S. pungens* var. *badius* from other varieties. Molecular sequence data indicated clear genotypic differences between *S. americanus* and all other members of the complex. Microsatellite data indicated *S. deltarum* is a distinct entity in comparison to *S. pungens* and *S. americanus*, and *S. deltarum* and *S. pungens* are more closely related to one another than either is to *S. americanus*. Results from these analyses provide clear characters and molecular evidence for species differentiation, help resolve the origin of *S. deltarum*, and facilitate the examination of the varietal status within *S. pungens*.

<sup>1</sup>Central Michigan University, Biology Department, 180 Brooks Hall, Mount Pleasant, MI, 48858, USA<sup>2</sup>Central Michigan University, Biology Department, 217 Brooks Hall, Mount Pleasant, MI, 48858, USA<sup>3</sup>Tulane University, Dept of Ecology & Evolutionary Biology, New Orleans, LA, 70118, USA

#### 489 HINCHLIFF, CODY\*<sup>1</sup> and ROALSON, ERIC<sup>2</sup>

#### A supermatrix of sedges: results from a large combined analysis of Cyperaceae

The highly diverse sedge family Cyperaceae has long been a topic of interest to plant systematists. Numerous molecular phylogenetic studies have been conducted on the family in recent decades, which have led to the inclusion of a broad spectrum of sedge diversity in public genetic sequence databases such as GenBank. We mined GenBank for targeted sequence data to generate the largest sedge phylogeny yet constructed, which consists of over 1,000 species and is based on genetic data from over 20 nuclear and chloroplast loci (counting cpDNA loci individually). We also generated novel sequence data to fill in gaps in the alignment and to add taxonomic diversity to underrepresented clades. The resulting phylogenetic hypotheses provide better taxonomic coverage than any sedge phylogeny yet produced, and represent a major advancement toward a highly resolved sedge tree of life. We will present these phylogenetic results and discuss their implications for sedge systematics, and we will briefly explore some of the challenges and advantages of the supermatrix approach to phylogenetics.

<sup>1</sup>Washington State University, School of Biological Sciences, 239C Abelson Hall, Pullman, WA, 99164-4236, USA<sup>2</sup>Washington State University, School of Biological Sciences, 332 Abelson Hall, Pullman, WA, 99164-4236, USA

#### 490 FADEN, ROBERT\*<sup>3</sup>, LAYTON, DANIEL J.<sup>1</sup>, BURNS, JEAN H.<sup>2</sup> and WURDACK, KENNETH J.<sup>3</sup>

#### Diversity and Relationships in *Commelina* (Commelinaceae)

With an estimated 170 species, the nearly cosmopolitan *Commelina* is the largest and most widespread genus of Commelinaceae. Its center of diversity is tropical Africa, with about 100 species, but smaller radiations have also occurred in Madagascar, North and South America, tropical Asia and Australia. With a conservative bauplan - leafy bracts (spathes) enclosing small numbers of monosymmetric flowers -- and usually mediocre herbarium specimens, due to poor flower preservation, the frequent absence of capsules and seeds, and inadequate collectors' notes, *Commelina* is very difficult to study without access to living plants and spirit collections. Long term research and recent floristic treatments have revealed: 1) large numbers of new species and infraspecific taxa, particularly in Africa; 2) cryptic species that have been long overlooked, even in well-collected areas; 3) variation in common, widespread species that is resistant to formal classification; and 4) a suite of new characters that is useful for distinguishing taxa and evaluating relationships among them. Characters that can be used to separate species include: spathe and floral morphology; flower color; capsule dehiscence; adaptations for animal dispersal of seeds; leaf anatomy; types of trichomes present and their distributions on vegetation and reproductive organs; and basic chromosome number and ploidy. The only infrageneric classification of *Commelina* is that of Clarke (1881), who recognized two subgenera, based on ovule number per locule, and three sections in each subgenus, based on capsule locule numbers and dehiscence. Preliminary phylogenetic studies, including Burns et al. (in press), do not support Clarke's classification, but they are not yet far enough advanced to propose an alternative system.

<sup>1</sup>University of Missouri-St. Louis, Biology, 223 Research Bldg. One University Blvd. St. Louis, MO 63121, USA<sup>2</sup>Case Western Reserve University, Biology, 2080 Adelbert Road, 307 DeGrace Hall, Cleveland, OH, 44106-7080, USA<sup>3</sup>Smithsonian Institution, Botany, MRC-166 National Museum Of Natural History, PO Box 37012, WASHINGTON, DC, 20013-7012, USA

491 AGUIRRE-SANTORO, JULIAN\*<sup>1</sup>,  
BETANCUR, JULIO<sup>2</sup>, BROWN, GREGORY<sup>3</sup>  
and WENDT, TANIA<sup>4</sup>

### Phylogeny and Delimitation of the Disjunct Genus *Ronnbergia* (Bromelioideae:Bromeliaceae) Based on Morphology and Molecular Data

Recent phylogenetic studies on Bromelioideae (Bromeliaceae) suggested that the reported geographic disjunctions within the most derived groups of this subfamily (also called core Bromelioideae) may be the result of erroneous generic and infrageneric boundaries. In order to test the disjunct distribution and monophyly of one of these genera, a phylogenetic study of *Ronnbergia* including its more likely related genera was developed using plastid DNA regions (*matK*, *trnL-trnF*, and *psbA-trnH*) and morphology. As the events of speciation within the core Bromelioideae may correspond to a recent rapid radiation, our results based on independent analyses of morphological and molecular data provided unresolved and poorly supported trees. Analyses using combined data provided stronger results, showing *Ronnbergia* as a non-monophyletic group with its species distributed in three clades. The four species endemic to the Atlantic Forest are grouped in one clade with species of the *Aechmea lingulata* complex. The remaining ten species from Northwestern South America and Central America are distributed in the other two clades. The first clade, *Ronnbergia* sensu stricto, contains only *Ronnbergia* species of the Choco biogeographical region, whereas the second clade is formed by *Ronnbergia* species grouped with species of *Aechmea* subgenus *Pothuava* also from this Neotropical biome. Taxonomic changes based on these results will be suggested as a contribution for the reorganization of the core Bromelioideae. This study provides further evidence showing that geographic proximity in groups of recent and rapid speciation is more likely than disjunction, a factor that has to be considered for future taxonomic restructuring of the core Bromelioideae.

<sup>1</sup>The New York Botanical Garden, The Graduate Center/Lehman College-CUNY, Plant Sciences, 2900 Southern Boulevard, New York Botanical Garden, Pfizer Plant Research I, Bronx, NY, 10458-5126, USA<sup>2</sup>Universidad Nacional de Colombia, Instituto de Ciencias Naturales, Apartado 7495, Bogotá, Colombia<sup>3</sup>UNIVERSITY OF WYOMING, Department Of Botany, BOX 3165, LARAMIE, WY, 82071-3165, USA<sup>4</sup>UNIVERSIDADE FEDERAL DO RIO DE JANEIRO, DEPT DE BOTANICA CCS JB, Av. Brigadeiro Trompowsky, S/n, Rio De Janeiro, N/A, 21941-5900, Brazil

492 BENEDICT, JOHN

### Using fruit and seeds of Zingiberales to understand character evolution and phylogeny

The Zingiberales are a diverse group of monocots that inhabit the understory of tropical and subtropical forests across the globe. Phylogenetic studies based on combined morphology and molecules have established the validity of the eight recognized families, and confirmed the monophyly of the order. Typically, floral and vegetative characters are incorporated into datasets to assess phylogenetic relationships, however fruit and seed characters are less frequently used. In conjunction with my study of the fossil record of zingiberalean fruits and seeds, a survey of extant forms reveals over a dozen characters of potential phylogenetic significance. For example, fruits in the order vary in locule number (1-3), placentation, and type, from mostly berries (Musaceae) or loculicidal capsules (Cannaceae, Costaceae, Strelitziaceae, Lowiaceae) to drupe-like fruits (Heliconiaceae), with some families having several different fruit types (Marantaceae, Zingiberaceae). Anatomical details of fruit pericarps throughout the order are not well known. Seeds are also quite variable. Characters such as the aril, embryo shape, seed coat, micropylar collar, and chalazal chamber promise additional data for testing phylogenetic hypotheses. Together, extant fruit and seed characters can be compared to their fossil counterparts to enhance our understanding about both character evolution and the phylogeny of the Zingiberales.

Arizona State University, School Of Life Sciences, PO Box 4601, Tempe, AZ, 85287-4601, USA

493 STAPAY, TARA\*<sup>1</sup>, ESSELMAN,  
ELIZABETH<sup>2</sup>, SMITH, MARIAN<sup>3</sup> and  
MCKENZIE, PAUL<sup>4</sup>

### Evidence for hybridization between *Schoenoplectushallii* and *S. saximontanus* (Cyperaceae) using ISSR markers

*Schoenoplectus hallii*, or Hall's bulrush, belongs to *Schoenoplectus* section *Supini* (Chern.) J. Raynal in the family Cyperaceae. This annual species is confined to wetland habitats with variable water levels. The species is of conservation concern wherever it occurs, partially due to its vast population losses over the past 25 years. A contributing factor to its decline could be the hybridization with a closely related species, *S. saximontanus*. These two species differ in their ranges and chromosome numbers; however, past morphological studies suggest that hybridization is possible. This study provided molecular evidence of hybridization using inter-simple sequence repeat (ISSR) DNA markers. A total of 260 plants were examined from 17 populations across

4 states. Seven species-specific markers were found for *S. saximontanus*, and 4 were found for *S. hallii*. These markers were found in the proposed hybrids, supporting the hypothesis that hybridization is occurring. The ISSR data was also used to examine the genetic diversity within and among populations. The lowest levels of diversity were found in Missouri and Illinois, and the highest levels were found in Oklahoma where the two species co-occur. Higher diversity in plants at this site could be due to hybridization between the species. The isolated sites in the Midwest are valuable since they are hybrid free. However, poor reporting and habitat degradation due to agricultural development threatens *S. hallii*'s continued survival. Conservation efforts are needed to preserve the extant populations.

<sup>1</sup>Southern Illinois University Edwardsville, Biological Sciences, Edwardsville, IL, 62026, USA <sup>2</sup>Southern Illinois University, Department Of Biology, RM 3330 SCIENCE BLDG, EDWARDSVILLE, IL, 62026-1651, USA <sup>3</sup>Department Of Biological Sciences, 1222 Chancellor Drive, EDWARDSVILLE, IL, 62025, USA <sup>4</sup>

494 TIPPERY, NICHOLAS\*<sup>1</sup> and LES, DONALD<sup>2</sup>

**Evidence for natural hybridization between two dioecious North American *Nymphoides* species (*N. aquatica* and *N. cordata*; Menyanthaceae)**

Outcrossing in the floating-leaved aquatic plant genus *Nymphoides* (about 50 species) is promoted by various sexual conditions including dimorphic heterostyly (most species) and dioecy (four species). The eastern North American *N. aquatica* and *N. cordata* are dioecious sibling species that differ by relatively minor morphological traits including adventitious root form, leaf texture, and overall size. Although these features distinguish the majority of individuals, the existence of morphological intermediates within broadly overlapping ranges confounds the identification of some specimens. In addition, similar floral morphology, reliance on outcrossing, and broadly overlapping ranges contribute to the likelihood of pollen transfer between *N. aquatica* and *N. cordata*. We undertook a molecular phylogenetic study using nuclear (ITS) and chloroplast (*matK/trnK*) sequence data obtained from individuals collected across the ranges of both species, in order to ascertain the distinctness of *N. aquatica* and *N. cordata* and to investigate their potential for hybridization. Our results indicated that most individuals of *N. aquatica* and *N. cordata* were readily identifiable to one or the other species, and these corresponded to reciprocally monophyletic groups. However, some individuals collected within the sympatric range of *N. aquatica* and *N. cordata* were revealed by molecular cloning to be interspecific hybrids. These data are consistent with the existence of two North American *Nymphoides* species that are predominantly distinct morphologically but nonetheless occasionally produce genetically intermedi-

ate hybrids.

<sup>1</sup>University Of Wisconsin-Whitewater, Department of Biological Sciences, 800 W Main St, Whitewater, WI, 53190 <sup>2</sup>University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Road, Unit 3043, Storrs, CT, 06269-3043, USA

495 CLAY, DANIELLE\*, SMITH, JAMES, NOVAK, STEPHEN and SERPE, MARCELO

**Homoploid hybrid speciation in a rare endemic *Castilleja* from Idaho**

Interspecific hybridization has played a pivotal role driving both extinctions and speciation events within angiosperms. The combination of interspecific hybridization and allopolyploidy has significantly contributed to the evolution of the genus *Castilleja*. The diploid *Castilleja christii* is a highly fertile rare endemic species, and widespread on 200 acres at the summit of Mt. Harrison, ID. We provide evidence for the homoploid hybrid speciation of *Castilleja christii* between congeneric diploids *Castilleja miniata* and *C. linariifolia*, using molecular and morphological analyses. Some individuals of *Castilleja christii* that were initially thought to be hybrids between *C. christii* and either *C. miniata* or *C. linariifolia* were found to be transgressive for several morphological traits based on ANOVA analyses and Cochran-Mantel-Haenszel test statistics. Using the single copy nuclear gene *waxy*, all *Castilleja christii* individuals were found to share the genomes of *C. miniata* and *C. linariifolia*. All individuals of *Castilleja christii* and *C. linariifolia* sampled from Mt. Harrison were identified as diploids using chromosome squashes. Most individuals of *C. miniata* were also diploid with the exception of one subpopulation that was octoploid. This study is the first to report homoploid hybrid speciation in the genus *Castilleja*, adding to the understanding of the complex evolutionary history in this group. Further, this research will assist land managers with conservation strategies that may contribute to the species protection of *Castilleja christii*, which to date has not been explored scientifically.

Boise State University, Biological Sciences, 1910 University Drive, Boise, ID, 83725-1515, USA

496 TANK, DAVID\*<sup>1</sup> and EASTMAN, JONATHAN<sup>2</sup>

**Diversification rates, life history shifts, and chromosomal evolution in *Castilleja* and relatives (Castillejinae, Orobanchaceae)**

<sup>1</sup>University of Idaho, Stillinger Herbarium, PO Box 441133, Moscow, ID, 83844-1133, USA<sup>2</sup>University of Idaho, Biological Sciences, PO Box 443051, Moscow, ID, 83844-3051, USA

497 DOUCETTE, ERIC\*<sup>1</sup>, BURGESS, MICHAEL<sup>2</sup>, CUSHMAN, KEVIN<sup>3</sup>, FRYE, CHRISTOPHER<sup>4</sup> and CAMPBELL, CHRISTOPHER<sup>1</sup>

**What is *Amelanchier laevis*?**

*Amelanchier laevis* Wieg. as currently circumscribed occurs from northern Georgia to Newfoundland and west to the Great Lakes ecoregion. This species is part of a clade with *A. arborea* (Michx. f.) Fern. and *A. canadensis* (L.) Medik. that is strongly supported by DNA sequence data. Members of this clade have many flowered elongate inflorescences, normally glabrous ovary summits, and (at least in some individuals) an arborescent habit. *Amelanchier laevis* is morphologically diagnosable by the character suite of anthocyanic and glabrescent emerging foliage, long petals, and long lowest pedicel. Our fieldwork revealed diploid and tetraploid individuals conforming to this morphology. The diploid form, which we refer to as diploid *A. laevis*, occurs only at higher elevations in the southern Appalachians, with polyploids occupying the remainder of the sampled range. Based on the location of the type specimen (Massachusetts), Wiegand described the polyploid taxon. In phylogenetic trees based on nuclear regions ETS and ITS, some clones of all our tetraploid *A. laevis* individuals are linked to diploid *A. laevis*, and other clones, depending upon the individual plant, nest with *A. canadensis* or have unresolved relationships with other clade B members. These trees suggest that tetraploid *A. laevis* is an assemblage of genetically heterogeneous allotetraploids of multiple origins whose ancestry is wholly within clade B. Morphologically, *A. laevis* is closest to *A. arborea*, and hybrids between them can be difficult to detect. Hence, ETS sequences revealed a southern Appalachian diploid to be a morphologically cryptic hybrid between these two species. Inflorescence and leaf characters may separate the two ploidy levels, although this potential difference needs to be assessed with greater sampling. We plan to obtain additional samples to explore the relationship between the two ploidy levels with *A. laevis* morphology and to investi-

gate the taxonomic status of the diploid.

<sup>1</sup>University Of Maine, Department Of Biological Sciences, 261 HITCHNER HALL, ORONO, ME, 04469-5735, USA<sup>2</sup>University of Pennsylvania, USA<sup>3</sup>P.O. Box 143, Levant, ME, 04456, USA<sup>4</sup>Maryland Wildlife And Heritage Service, 909 Wye Mills Road, PO Box 68, Wye Mills, MD, 21679, USA

498 CUSHMAN, KEVIN\*<sup>1</sup>, DOUCETTE, ERIC<sup>2</sup>, BURGESS, MICHAEL<sup>3</sup>, FRYE, CHRISTOPHER<sup>4</sup> and CAMPBELL, CHRISTOPHER<sup>2</sup>

**Morphological and molecular relationships of Nantucket shadbush (*Amelanchier nantucketensis*, Rosaceae)**

*Amelanchier nantucketensis* Bickn. was named in 1911 based on plants from Nantucket Island, Massachusetts. This species is the only taxon in the genus with andropetal: the presence of microsporangia on small spatulate petals. The expression of this feature varies greatly, but almost all plants of this taxon have some andropetal. This shrub is known only as a tetraploid and usually grows on acidic sands and rock outcrops from the southeastern United States through much of New England and southern Nova Scotia. The origin of Nantucket shadbush is unclear. Weigand, in his 1912 treatment of Eastern North American *Amelanchier*, considered this taxon to be a hybrid of *A. canadensis* (L.) Medic. var. *oblongifolia* Michx. and *A. spicata* (Lamarck) K. Koch. In his 1946 monograph of North American *Amelanchier*, Jones lumped *A. nantucketensis* with *A. humilis* Wiegand, a diploid, and *A. spicata*, a taxonomically complex tetraploid. Distinguishing non-flowering *A. nantucketensis* and *A. spicata* is difficult. All polyploid *Amelanchier* studied are aposporous, pseudogamous apomicts capable of creating morphologically discrete microspecies. Hybridization and occasional sex within some microspecies have spawned a bewildering array of forms and, over time, generated loosely connected, morphologically similar, and widely dispersed species complexes. *Amelanchier nantucketensis* is morphologically rather uniform, but unlike many microspecies that we have observed in the genus, it has a relatively broad distribution. Sequence data from nrDNA ETS and ITS show that Nantucket shadbush is strongly tied to *A. canadensis* and weakly linked to a clade that includes *A. arborea* (Michx. f.) Fern., *A. canadensis*, *A. laevis* Wiegand, and *A. bartramiana* (Tausch) M. Roemer. An ITS pseudogene shared by Nantucket shadbush and taxa related to *A. humilis*, but not *A. humilis* itself, suggests a member of the clade that includes *A. humilis* was an ancestor of *A. nantucketensis*. It appears that *A. nantucketensis* has had a complex history that has partially obscured its diploid progenitors.

<sup>1</sup>University of Maine, School of Biology and Ecology, 5751 Murray Hall, Orono, Me, 04469, USA<sup>2</sup>University Of Maine, Department Of Biological Sciences, 261 HITCHNER HALL, ORONO, ME, 04469-5735, USA<sup>3</sup>Maryland Wildlife And Heritage Service, 909 Wye Mills Road, PO Box 68, Wye Mills, MD, 21679, USA

499 FINCH, KRISTEN<sup>\*1</sup>, MEYERS, STEPHEN<sup>2</sup> and WILLYARD, ANN<sup>1</sup>

### How distinct are the geographically isolated coastal populations of ponderosa pines in the Willamette Valley of Oregon and Fort Lewis, Washington?

Incomplete lineage sorting and the potential for interspecific hybridization in the genus *Pinus* make it challenging to determine recent biogeography and perhaps even to delimit some species. We studied isolated natural stands of ponderosa pines in the Willamette Valley of Oregon and on the Fort Lewis military base near the Puget Sound in Washington. Several researchers have reported that one or both of these pine populations have unique characteristics such as the timing of spring growth, wood density, and biochemistry. These populations are geographically distant from the ponderosa pines of coastal California (*P. benthamiana* Hartw.), but grow in a very different climate than the nearer populations of ponderosa in eastern Oregon and eastern Washington (*P. ponderosa*, North Plateau Race). We sampled 14 populations (ca. 350 individuals) from the Willamette Valley, the Puget Sound, *P. benthamiana* in California, and the North Plateau Race from eastern Washington, western Idaho, and central Oregon. Multi-locus nuclear and chloroplast genotypes from microsatellite loci (SSRs) provided useful length variation in regions of the genome that harbor SSRs because individuals of the same species have diverse numbers of SSR repeats. We analyzed these data in several frameworks to reveal relationships within and among populations. Considering the large geographic distance between these populations and their apparent sister populations, we tested whether the ponderosa populations from the Willamette Valley and the Puget Sound are more closely related to each other than they are to other populations and whether each population shares a more recent history with *P. benthamiana* or with *P. ponderosa*.

<sup>1</sup>Hendrix College, Biology Dept, 1600 Washington Ave, Conway, AR, 72032, USA <sup>2</sup>Oregon State University, Botany and Plant Pathology, Cordley 2082, Corvallis, OR, 97331, USA

500 SHELTON, GLENN W.K.

### Sympatry without intergradation: an evaluation of the *Trifolium longipes* complex in northern California

The *Trifolium longipes* complex comprises about 12 infraspecific taxa endemic to vernal wet meadows on serpentine substrates in the western United States, from Montana to New Mexico and west to the Pacific States. Some of these taxa clearly intergrade, but others differ strongly by a combination of traits including plant height, peduncle length, leaflet and calyx shape, corolla

color, and the extent to which the pedicels reflex with age. Some of the more distinct taxa have been regarded as separate species in the past, but the prevailing view is that they are linked by intergradation and are best considered one species. Current study focuses on two pairs of significantly distinct subspecies occurring sympatrically in northern California: subspecies *hansenii* (Greene) J.M. Gillett with ssp. *oreganum* (Howell) J.M. Gillett in Humboldt and Trinity Counties, and ssp. *elmeri* (Greene) J.M. Gillett with ssp. *shastense* (House) J.M. Gillett in Shasta County. In both cases, the subspecies occur in the same meadows, bloom concurrently, and maintain their morphological distinction without intergradation, although the differences between ssp. *hansenii* and ssp. *oreganum* are less striking than those separating ssp. *elmeri* and ssp. *shastense*. Herbarium data are being used to locate additional instances of sympatry. Field observations are particularly critical in this group because traits such as corolla color and the degree to which the pedicels reflex can be difficult to interpret on herbarium specimens. If additional field reconnaissance reveals clear distinction across a broad geographic range, the recognition of separate species will be strongly encouraged. Conversely, an unanticipated significant intergradation will warrant a study of reinforcement of reproductive isolation in areas of sympatry without intergradation. The ultimate goal of this evaluation is a comprehensive revision of *T. longipes* in northern California and adjacent Oregon including updated ranges and descriptions of some of the taxa.

Humboldt State University, Department of Biological Sciences, 1 Harpst Street, Arcata, CA, 95521, USA

501 COMER, JASON R<sup>\*1</sup>, ZOMLEFER, WENDY<sup>2</sup>, MATTE SANTOS, ALEXANDRE<sup>1</sup> and LEEBENS-MACK, JIM<sup>3</sup>

### A preliminary study of the genetic diversity in Georgia and Florida populations of *Veratrum woodii* (Liliales: Melanthiaceae)

*Veratrum woodii* grows in moist deciduous forests predominately on north- and east-facing slopes, ranging from as far south as northern Florida northward into Ohio, reaching its western range edge in Missouri-Iowa down to eastern Oklahoma. However, most states have only a few isolated populations, where *V. woodii* is ranked endangered, rare, or threatened. The species is locally common only in Missouri, where it occurs in most of the eastern half of the state. *Veratrum woodii* is a long-lived rhizomatous perennial species with maroon flowers with large adaxial perigonal nectaries and is insect pollinated. Based on this pollination syndrome, this species is considered to be outcrossing. The purpose of this preliminary study is to assess the genetic diversity of populations of *V. woodii* in Georgia and Florida. Leaf tissue was collected from seven populations from

Georgia and three in Florida for Amplified Fragment Length Polymorphism (AFLP) analyses. Amplified Fragment Length Polymorphisms were selected for this study because they do not require previous knowledge of the genome, and the data represent samples of the entire genome. Populations ranged in size from more than 600 to as few as five individuals. Thirty individuals were sampled from each population whenever possible. Three primer combinations were selected, and the fragments generated were analyzed using GenAlix software. The results show that *Veratrum woodii* has a mean expected heterozygosity comparable to other rare long-lived perennials. While most of the genetic variation is within populations, the phi pt value indicates that *V. woodii* has been undergoing some inbreeding, as well.

<sup>1</sup>University of Georgia, Plant Biology, 2502 Miller Plant Sciences, Athens, GA, 30602, USA<sup>2</sup>University of Georgia, Department of Plant Biology, 2052 Miller Plant Sciences Building, 120 Carlton Street, Athens, GA, 30602, USA<sup>3</sup>University of Georgia, 4503 Miller Plant Sciences, Athens, GA, 30602, USA

## 502 KIRCHOFF, BRUCE

### A New Type of Paper Visual Key (to the Fagaceae of the Southeastern United States)

Standard keys are terminology-based tools for plant identification, which are often supplemented with images. Visual keys are identification tools that are primarily visual, supplemented by some text. Traditional, terminology-based keys do not take advantage of the forte of visual experts, pattern recognition. Visual keys, on the other hand, are primarily image-based, and take advantage of these abilities. Characters in these types of keys are visually, not verbally defined. In this paper a set of paper visual keys to the Fagaceae of the southeastern United States are presented. Photographs of the Fagaceae were obtained from internet databases, or were taken specifically for this project. The images were printed, and then sorted into hierarchical groups. These hierarchical groups of images were used to create the "couplets" of the keys. A reciprocal process of key creation and testing was used to produce the final keys. Four keys were created, one for each of the following plant parts -leaves, buds, fruits, and bark. Species description pages consisting of multiple images were also created for each of the covered species. Creation and testing of the key has resulted in a list of best practices for image use in visual keys.

University of North Carolina At Greensboro, Department of Biology, PO BOX 26170, GREENSBORO, NC, 27402-6170, USA

## 503 DIAZGRANADOS, MAURICIO\*<sup>1</sup>, NICOLAS, RODRIGUEZ<sup>2</sup> and BARBER, JANET<sup>1</sup>

### Interactive Digital Key for the frailejones (Espeletiinae Cuatrec., Asteraceae) of the South American paramos

The paramos of the Northern Andes are largely dominated by a group of composite species known as frailejones. These plants comprise a neotropical monophyletic assemblage and are found between 1,800-4,700 m in elevation in Colombia (ca. 81 spp.), Venezuela (ca. 69 spp.) and Ecuador (1 sp.). The group is widely recognized as a classic example of rapid radiation in the tropics due to its remarkable diversity. The nearly 143 named species are classified into eight genera: *Carramboa* (5 spp.), *Coespeletia* (6 spp.), *Espeletia* (68 spp.), *Espeletiopsis* (27 spp.), *Libanothamnus* (11 spp.), *Paramiflos* (1 sp.), *Ruilopezia* (24 spp.) and *Tamania* (1 sp.). Unfortunately, only one published key (1996) exists for a single genus, and one extremely incomplete treatment for *Espeletia* published in 1935 that includes only 20% of the currently recognized species. Cuatrecasas' monograph of the subtribe remains unpublished. This monograph does not include more than ten recently discovered species and describes only seven of the eight genera (excluding *Espeletiopsis*); furthermore, its dichotomous keys are particularly difficult to follow due to the large number of overlapping continuous characters. We have constructed an interactive digital key for the Espeletiinae, using the software Lucid3 v.3.5. The key includes all currently known species and incorporates 566 features (=character states), scored using seven conditions (absent, common, rare, uncertain, common and misinterpreted, rare and misinterpreted, and not scoped), in addition to numeric variables representing normal ranges and extreme values. The lack of consistency between species descriptions was a challenge, and often required careful re-examination of specimens. Performance of the key was tested repeatedly. On average, 69 features distinguish any two randomly chosen species, and 23 distinguish the most similar species. By using the wizard tool of the key to choose the best diagnostic characters, users can identify any species in only a few steps. The key includes photographs and illustrations for species and morphological characters, glossaries and distribution maps. It is available online at <http://www.espeletia.org/>.

<sup>1</sup>Saint Louis University, Biology, 3507 Laclede Ave., St. Louis, MO, 63103, USA<sup>2</sup>Universidad de los Andes, Departamento de Ciencias Biológicas, Apartado Aéreo 4976, Bogotá, D.C., Colombia

504 SWADEK, REBECCA

### The Vascular Flora of the North Central Texas Walnut Formation

Political boundaries most frequently define local floras. This floristic project takes a geological approach inspired by *Dalea reverchonii* (Comanche Peak Prairie Clover), which is endemic to glades of the Walnut Formation. The Walnut Formation (Comanchean) lies on the drier westernmost edge of the Fort Worth Prairie. Its shallow limestone soils, formed from alternating layers of hard limestone and clayey marl, support a wide variety of habitats. Glades of barren limestone typically appear on ridgetops, grassland savannas form on eroding hillslopes, and seeps support a variety of hyper-seasonal vegetation. Preliminary results indicate floristic affinities to Limestone Cedar Glades of Tennessee and Kentucky and to calcareous Apacherian Savannas of Southwestern North America.

Texas Christian University, Environmental Science, Fort Worth, TX, 76129

505 SHIPUNOV, ALEXEY

### Flora of North Dakota project

North Dakota first plant inventory started in 1890s with the establishment of North Dakota Agricultural College and was reported independently by H.F. Bergman in 1918 and J. Lunell in 1915. They list approximately 960 plant species. Next (and unfortunately the last) inventory of North Dakota flora was published in 1950 (with some additions in 1963) by O.A. Stevens, making the total number of North Dakota plant species over 1200. In 1970-80s, E. DeKeyser (NDSU) organized a systematic research of North Dakota flora, but state inventory was not fully implemented: only part of North Dakota (mostly counties from Missouri Plains) was covered. The other ongoing effort is the online database for plants of Missouri plains (project of M.L. Gabel from Black Hills State University, SD). The project covers, however, only a half of state. In all, contemporary plant inventory is highly desirable for North Dakota. Such an inventory will not only list plants in traditional way, but also incorporate "non-classic" methods including plant barcoding. We plan also to create on-line database which will provide information both for scientists and for local communities; it will include data about local and native plant uses and determination keys. Other proposed outcomes are: training students in floristic research; expanding MSU herbarium collection and making virtual herbarium; tracing invasive plants across the state; clarifying the state endangered and rare plant list; and performing a pilot research in patterns of heavy metal distribution in soils in accordance with floristic composition of plant communities across the state.

Minot State University, Biology, 500 University Ave, Minot, ND, 58707, USA

506 SAADEDDIN, RAJA

### An Illustrated Guide to Wild Plants from Karak Province and Some Areas in south Jordan

Southern Jordan is rich in flora due to the great variations in habitat, which include mountain areas, characterized by a *Mediterranean* climate, with high rainfall and fertile soils; Dead Sea areas, which are depressions with very low altitudes, distinguished by *Sodanian* or *Tropical* environmental conditions exhibit very high temperatures in summer, and medium in winter, that could be become below zero degrees in some seasons, with variable types of soil, from fertile to highly saline soils where salt tolerant plants (halophytes) grow heavily in salt marshes; and Desert areas, represents *saharo arabian* regions, with very hot summer, very cold winter and very low rainfall. The vegetation is rich in many salt tolerant, and drought tolerant plants, including trees and shrubs as *Atriplex*. Also annual and perennial herbaceous plants, some of which are grazed by animals, while others are used as medicinal plants. These plants could be used in future as source of germ plasm for valuable salt and drought tolerant crops. During spring, a number of wild plants grow in different parts of southern Jordan were photographed by a cannon camera, either in their natural habitat or after they have been collected for the herbarium, while they were still fresh. Two hundred and twelve plants belong to 45 plant families and 147 genera were identified according to their morphological features and their medical uses have been recorded.

Attila East, Muhammed Sayel Alhusban St. 19, P.O. Box: 954016, Amman, 11954, Jordan

### POSTERS

507 MAVRODIEV, EVGENY\*<sup>1</sup>,  
LAKTIONOV, A. P.<sup>2</sup> and ALEXEEV, YU. E.<sup>3</sup>

### On the new species *Salix fursaevii* Mavrodiev in context of the old question about rapid speciation in river plains

We propose that *Salix serotina*, an endemic of the Lower Volga region discovered by Peter Simon Pallas (1741-1811), must be excluded from synonymy of the widely circumscribed *S. viminalis* L. and should be accepted at the rank of species. We also describe as a new species *Salix fursaevii* Mavrodiev sp. nova, another putative endemic of the Lower Volga region. In the past both *Salix serotina* and *S. fursaevii* were widely treated as a "late-flood-plain-ecotypes" of *S. viminalis* L. s. l. and *S. triandra* L. s. l. respectively. Due to different flowering times, the Lower Volga plain populations of *S. fursaevii* and *S. serotina* are reproductively isolated form sympat-

ric, morphologically different non-plain populations of *S. viminalis* s. str. and *S. triandra* s. str. Here, *Salix fursaevii* and *S. serotina* are presented as an example of the process of rapid speciation in river plains. Based on detailed study of the Lower Volga plain flora and vegetation the Russian botanist A. D. Fursajew originally demonstrated this phenomenon more than 70 years ago but the last one was not investigated further by others since that time. Due to the presumed high levels of endemism, the Lower Volga plain proposed here as a useful natural model system for modern evolutionary studies.

<sup>1</sup>University of Florida, Florida Museum of Natural History, Gainesville, FL, 32611, USA<sup>2</sup>Astrakhan State University, Department of Biology, Astrakhan, 414056, Russia<sup>3</sup>Moscow State University, Department of Geobotany, Biological Faculty, 119899 Moscow, Russia

## 508 ZANDER, RICHARD

### Theory-based Alternative to Axiomatic Structuralism in Systematics

**1.** Phylogenetics attempts an axiomatic quasi-mathematical foundation: (a) cladogram as fundamental pattern in nature (structuralism), (b) all non-data-set information mapped (relegated) to cladogram, (c) strict monophyly (a principle) eliminates non-axiomatic theory aspects of macroevolution, (d) explanation of paraphyly and polyphyly as "convergence" is the only explanation if analysis is axiomatic. **2.** Phylogenetics as discovery process fails through inconsistency between analyses: (a) morphology and molecular analyses, (b) paraphyly and polyphyly on molecular cladograms, (c) classifications from synchronic and diachronic relationships. **3.** Evolutionary theory allows consistency with only apparent loss in precision: (a) Alpha taxonomy based on informal genetic algorithms providing heuristic initial theory of relationships, (b) Morphological phylogenetic analyses provide natural keys (based on conservative homologous traits whose similarity implies close evolutionary relationships), (c) Molecular phylogenetic analyses provide genetic continuity and isolation events but not necessarily speciation, (d) Heterophyly within molecular and between morphological and molecular cladograms is informative of deep ancestral taxa, and (e) Dollo's Law and biosystematics provide additional data to help judge theoretical diachronic direction of evolution. **4.** The phylogenetic tree of life is a set of commonly well-supported nested parentheses but lacking scientific realism among the nodes. The evolutionary tree of life is a combination of Besseyan cactus and cladogram, being an approximation combining synchronic phylogenetic pattern and diachronic causalistic inferences through both deduction and induction. Examples are given.

Missouri Botanical Garden, Science and Conservation, PO Box 299, St. Louis, MO, 63166, USA

## 509 MAYFIELD, DUSTIN\*<sup>1</sup>, SMELSER, WOODSON<sup>2</sup>, NEWTON, KATHLEEN<sup>2</sup> and PIRES, JOSEPH<sup>3</sup>

### Organellar genome sequence assembly of maize lines and grass relatives using Illumina sequence data

**T**he scale and economy of next-generation sequencing is greatly improving researchers' ability to investigate organellar genomes. Here, we assemble and analyze the organellar genomes of rice, sorghum, two teosintes, and other maize lines from genomic or isolated mitochondrial DNA. In the case of maize, it is thought that the species was derived from *Z. mays parviglumis* and that greater than ten percent of its genome was introgressed by *Z. mays mexicana*. Here, we show variation among these teosinte organellar genomes, along with other lines with or without expression of cytoplasmic male sterility (CMS) phenotypes. This variation may explain the molecular basis of CMS in maize. Our results demonstrate the degree that eukaryotic plant organellar genomes can be accurately assembled from shallow Illumina sequencing.

<sup>1</sup>University of Missouri-Columbia, Division of Biological Sciences, 311 Life Sciences Center, 1201 Rollins Street, Columbia, MO, 65211, USA<sup>2</sup>University of Missouri-Columbia, Division of Biological Sciences, 324 Tucker Hall, Columbia, MO, 65211, USA<sup>3</sup>University Of Missouri, 371 B Life Sciences Center, 1201 Rollins Street, Columbia, MO, 65211-7310, USA

## 510 KAONONGBUA, WITTAYA\*<sup>1</sup> and BEVER, JAMES<sup>2</sup>

### *Xerospora xerophila* gen. et sp. nov., a new arbuscular mycorrhizal fungus from a semi-arid region of North America

**W**hile investigating the biodiversity of arbuscular mycorrhizal (AM) fungi in the US grasslands, we encountered a previously undescribed species of AM fungi in desert grassland from New Mexico. Both morphological and molecular data strongly support the hypothesis that this AM fungus is an undescribed species and a member of a distinct genus within the family *Diversisporaceae* (*Glomeromycota*). Therefore, we erect a new genus, *Xerospora* gen. nov., to accommodate the new species, *Xerospora xerophila* sp. nov. Spores of *X. xerophila* are globose, subglobose or occasionally oblong; 231.2-206.4 µm in average dimensions; dark yellow, pale brown, brown or dark reddish brown and frequently with adhering debris and soil particles. Each spore comprises of a single spore wall with 2 layers. The composite thickness of the spore wall is approximately 25 µm. The outer layer (L1) is yellow, pale brown or brown, 5-20 µm thick with the mean of 11.9 µm and laminated. Some of the outer-most sub-layers of this

may degrade over time and start attracting soil particles. The inner layer (L2) is hyaline, 5–20  $\mu\text{m}$  thick with the mean of 12.4  $\mu\text{m}$  and both laminated and semi-flexible. The inner-most sub-layers of this may be mistaken for an additional spore wall layer. To date, *X. xerophila* has only been reported from the type locality.

<sup>1</sup>Indiana University, Biology, 1001 E. 3rd St., Jordan Hall 142, Bloomington, IN, 47405, USA <sup>2</sup>Indiana University, Department Of Biology, Jordan Hall, 1001 East Third Street, Bloomington, IN, 47405, USA

**511 VASUDEVAN, HARI\*<sup>1</sup>, TELEWSKI, FRANK<sup>2</sup>, MARQUARDT, PAULA<sup>3</sup> and WILLYARD, ANN<sup>1</sup>**

**How genetically distinct are the isolated ponderosa pines of southern Arizona?**

We studied isolated populations of ponderosa pines in southern Arizona in relation to the continuously distributed pines of the southern Rockies. We also investigated potential hybrid zones between ponderosa pine and *Pinus arizonica* in the Chiricahuas and on Mt. Lemmon where these two species grow in close proximity and where trees with intermediate morphologies have been reported. Length variation in nuclear and chloroplast multi-locus microsatellites and mitochondrial minisatellites was used to reveal genetic relationships within and among populations. SSRs newly developed for ponderosa pine and an expanded use of mitochondrial haplotypes aided our investigation. Genetic data from biparentally inherited (nuclear), paternally inherited (chloroplast in pines), and maternally inherited (mitochondrial) helped us detect hybridization and determine the direction of gene flow. In current treatments, *Pinus ponderosa* is defined to cover an enormous range of geographic and morphological variation. In light of our current understanding of genetic relationships, we discuss how the name *Pinus brachyptera* (published by George Engelmann from collections made by Friedrich Adolph Wislizenus in 1846 near Santa Fe, New Mexico) fits with the name *Pinus ponderosa* (collected by David Douglas in 1826 near present-day Spokane, Washington).

<sup>1</sup>Hendrix College, Biology, 1600 Washington Ave, Conway, AR, 72032, USA <sup>2</sup>Michigan State University, Department of Plant Biology, East Lansing, MI, 48824-1312, USA <sup>3</sup>USDA Forest Service, Institute for Applied Ecosystem Studies, 5985 Hwy. K, Rhinelander, WI, 54501, USA

**512 FINNEY, JACK\* and WILLYARD, ANN**

**The taxonomic status and relation of the sand hill pines of Santa Cruz County, California to *Pinus ponderosa* Douglas ex Loudon and to *P. benthamiana* Hartweg**

Outlying populations of ponderosa pine on "sand hills" soils of coastal California have long been recognized as representing an unusual habitat for the species. These pine populations are surrounded by redwood-mixed conifer forests, a highly unusual location for ponderosa pine. Some researchers have also suggested that morphological and biochemical features of the sand hill populations may differ from typical ponderosa. We used multi-locus nuclear and plastid microsatellite (SSR) genotypes and a mitochondrial haplotype from more than 200 individuals to observe variability within and among populations. We compared two populations of sand hill pines from Santa Cruz County, California with nearby samples from the Santa Lucia Mountains in Monterey County and Pine Ridge in Santa Clara County. These coastal populations were then analyzed in relation to samples from inland Northern California (Pacific Race of *P. ponderosa* var. *ponderosa*), and with populations representing *P. scopulorum*, the ponderosa pines of the southern Rockies, and the isolated ponderosa pines of Southern Arizona. We used our results to address the question of whether Hartweg's 1847 collection of *P. benthamiana* in Santa Cruz County: i) is best used to support just the sand hill pines; ii) is best used to typify the entire range of pines currently treated as the Pacific Race of *P. ponderosa*; or iii) should remain subsumed within *P. ponderosa* as currently treated in the *Flora of North America*.

Hendrix College, Biology Dept, 1600 Washington Ave, Conway, AR, 72032, USA

**513 SALAZAR, JACKELINE\*<sup>1</sup> and BARROS, FABIO DE<sup>2</sup>**

***Cinnamodendron brasiliense* J. Salazar & F. Barros (Canellaceae), a new species from Brazil**

A new species of the genus *Cinnamodendron* (Canellaceae) is described and illustrated as *Cinnamodendron brasiliense* J. Salazar & F. Barros. This species is a shrub or treelet (up to 3 m) with 1 or 2 flowers per inflorescence, and a fruit up to 2 cm long and obovoid. *C. brasiliense* is similar to *C. ochionii* F. Barros & J. Salazar, but this second species is a tree (8–20 m tall), with up to 4 or 5 flowers per inflorescence, and the fruits are smaller (up to 1.5 cm long) and globose. *C. brasiliense* is known from areas of Atlantic Forest in the State of São Paulo (Southeastern Brazil), in coastal

areas at sea level, growing in wetlands of the Picinguaba River and associated to mangroves. The specific epithet refers to the country where the species was found, Brazil.

<sup>1</sup>Universidad Autónoma de Santo Domingo (UASD), Escuela de Biología, Zona Universitaria, Santo Domingo, DN, República Dominicana <sup>2</sup>Instituto de Botânica, Núcleo de Pesquisa Orquidário do Estado, Caixa Postal 3005, São Paulo, SP, 01061-970, Brazil

514 PENAGOS ZULUAGA, JUAN CARLOS\*<sup>1</sup> and VAN DER WERF, HENK<sup>2</sup>

### Evaluation of the relationship of *Aiouea* with *Cinnamomum*, *Ocotea* and *Mocinnodaphne* (Lauraceae) using stomatal and cuticular leaf characters

In a previous molecular study, *Aiouea* was found in two quite separate clades. The first clade relates species of *Aiouea* with the species of the *Ocotea insularis* group. The second clade relates species of *Aiouea* with neotropical species of *Cinnamomum* and *Mocinnodaphne*. This grouping is also supported by floral characters. Methods: Cuticle and stomatal characters of forty species were examined under light microscopy and scanning electron microscopy, and characters were measured from digital images. Samples were taken from herbarium collection of the Missouri Botanical Garden. Variables with high loadings from a principal component analysis were considered as the most important and evaluated separately to determine their utility from a taxonomic perspective. Multilevel analysis was then used to determine the relationship between environmental variables and these characters, taking into account species-level characteristics. Results: Three groups were recognized in the PCA. The three most important characters were stomatal rim width, stomata and aperture length. The first group has a wide stomatal rim and includes all the species of *Aiouea* from South America, neotropical species of *Cinnamomum*, and *Mocinnodaphne*. The second group has a narrow stomatal rim and includes all the species of *Aiouea* from Central America and northwest South America and the species of *O. insularis* group from Central America. A third group includes two species (*A. uatematicensis* and *A. inconspicua*) without a stomatal rim. These two species are the northern distribution range of *Aiouea* and the lack of molecular information does not allow further inference about relationship with other groups in the family. Preliminary results from multilevel analyses show a correlation between environmental variables and stomata length vary at species-level, and are do not suggest that they are conservative characters within the different clades. Conclusion: Results show that some cuticular characters are still useful in taxonomy being conservative characters in clades. Conversely, stomatal length can vary as a specific response to environmental variation and

should be treated more carefully in taxonomy.

<sup>1</sup>University of Missouri - Saint Louis, Department of Biology, One University Boulevard, R223 Research Building, St. Louis, MO, 63121-4400, USA <sup>2</sup>Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166-0299, USA

515 STULL, GREGORYW\*<sup>1</sup>, JOHNSON, DAVID<sup>2</sup> and SOLTIS, PAMELA<sup>3</sup>

### A preliminary molecular phylogeny of the pantropical genus *Xylopia* (Annonaceae): implications for character evolution and historical biogeography

The Annonaceae, a pantropical family of trees, shrubs, and lianas within the Magnoliales, are an ecologically important and diverse constituent of wet lowland tropical forests. Although molecular studies over the past 10 years have made considerable progress in resolving broad-scale phylogenetic patterns within the family, several large clades within the family remain poorly understood in terms of their phylogenetic relationships. For example, *Xylopia*, the second largest genus in the family (with approximately 180 spp), is a phylogenetically poorly understood group despite its biogeographic significance as the only pantropical genus within the family. Here we present a preliminary phylogeny of *Xylopia* based on the chloroplast genes *ndhF*, *psbA-trnH*, *trnL-F* and *ycf1*. These data confirm that *Xylopia* is monophyletic and sister to *Artabotrys*, as has been suggested by previous analyses. A new hypothesis presented here is that the ancestors of the genus likely possessed stilt roots and occurred in swamp or riverine habitats. Additional implications for historical biogeography and character evolution are discussed.

<sup>1</sup>University of Florida, Florida Museum of Natural History, Dickinson Hall, Gainesville, FL, 32611, USA <sup>2</sup>OHIO WESLEYAN UNIVERSITY, DEPT OF BOTANY-MICROBIOLOGY, Department Of Botany Microbiology, DELAWARE, OH, 43015, USA <sup>3</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA

516 SERNA, MARCELA  
Magnolias of the Neotropics

Magnoliaceae family comprises over 230 species of trees and shrubs distributed in temperate and tropical zones from southeast and east of Asia, North America, West Indies, Central America and South America, included Colombia, Venezuela, Ecuador, Peru, Bolivia and Brazil. Species belonging to this family are very appreciated because of their wood, floral scents, and pharmaceutical and horticultural uses. This group has been object of many studies, especially on taxonomy, evolution and conservation. One of the latest publications about conservation is the Red List of Magnoliaceae, published in 2007, in which 110 species

from many countries are included. On the other hand, the latest synopsis of neotropical Magnoliaceae, with 45 species, was published in 1994. Since then, there has been extensive field work and research leading to several publications on conservation, taxonomy, systematics, genetic variability; also several new species of Magnoliaceae from South America have been described. The goal of this project is to update the review of the Neotropical species of Magnoliaceae, including morphological descriptions, information about ecology and conservation and detailed distribution of the species. A complete up to date account on the Neotropical species of Magnoliaceae would be a vital tool for both Colombian and International conservation groups in assessing conservation status and goals for all neotropics species of Magnolia. This project is supported by the Elizabeth E. Bascom Fellowship program.

Tecnológico de Antioquia, Medellín, Antioquia, 05001000, Colombia

**517 ORTIZ, ROSA\*<sup>1</sup>, SORIANO, SARA FUENTES<sup>1</sup> and JACQUES, FRÉDÉRIC, M.B.<sup>2</sup>**

**Evaluating the phylogenetic signal and mode of evolution of continuous traits in Menispermaceae (Ranunculales): an example using endocarp size**

With about 520 species, the Menispermaceae is considered a medium-size family among Ranunculales. The moonseed-shaped endocarps that characterize many of the genera in the family are easily recognized, are very diverse, and have therefore historically played an important role in the classification of extant as well as in the identification of fossil taxa in Menispermaceae. Recent studies using DNA sequence data have greatly improved our understanding of the relationships within the Menispermaceae, and several morphological traits, treated as discrete characters, have been evaluated and their ancestral state hypothesized. Here we present preliminary results of the ancestral endocarp size estimation in Menispermaceae, with size treated as a continuous character. Measurements of endocarp length and width, a phylogeny of 77 taxa for a combined analysis of three chloroplast markers, and available divergence time estimates for the family and major clades were analyzed using a Bayesian approach. The evolutionary dynamics of endocarp size within the Menispermaceae was evaluated by calculating levels of phylogenetic signal of endocarp size. The best-fitting models of evolution and tests for directional evolutionary change were evaluated prior to ancestral endocarp size estimations.

<sup>1</sup>Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166, USA<sup>2</sup>Nanjing Institute of Geology and Palaeontology, CAS Department of Palaeobotany and Palynology, 39 East Beijing Road, Nanjing 210008 Jiangsu, PR China

**518 OLFELT, JOEL\*<sup>1</sup> and HANDZIC, NIZAR<sup>2</sup>**

**A new species of North American *Rhodiola* (Crassulaceae)**

Recent studies of the North American *Rhodiola* (Crassulaceae) indicate that the group's most widely used taxonomic treatment does not accurately reflect its evolutionary history. This is of especial concern because one of the currently defined taxa, *Rhodiola integrifolia* ssp. *leedyi* (Leedy's roseroot) is on the New York and Minnesota endangered, and the U. S. federal threatened species lists. The taxon is described by some authorities as indistinguishable from *R. rosea*. To more accurately represent the phylogenetic relationships we examined both newly obtained and previously published morphological, molecular, and geographical data. We sequenced the Internal Transcribed Spacer (ITS) regions I and II from 54 individuals representing all of the described North American *Rhodiola* taxa. Four of the five known Leedy's roseroot populations were each represented by six individuals, and each of the other five described *Rhodiola* taxa were represented by six individuals. We evaluated the phylogenetic relationships using Maximum Parsimony (MP) analysis. To test the relationships of the North American *Rhodiola* with their Asian counterparts we used MP analysis on a combined dataset of published ITS sequences from 21 Asian *Rhodiola* taxa and the newly obtained sequence data. Preliminary analyses of the North American taxa yields a single tree with strong (98%) bootstrap support for Leedy's roseroot as a distinct clade. Four of the North American taxa, including Leedy's roseroot, are in a clade with the eastern Asian species *R. algida*. The taxon *R. rosea*, which is native to North America, Asia, and Europe, is more closely related to the Asian *Rhodiola* taxa *R. heterodonta* and *R. ishidae* than to any of the North American *Rhodiola* species. The molecular, morphological, and geographical data combine to demonstrate that Leedy's roseroot is distinct from *R. integrifolia* and *R. rosea*, and should be elevated to species status (*R. leedyi*). Furthermore two subspecific taxa (subsp. *leedyi* and subsp. *senecana*) should be recognized within *R. leedyi*.

<sup>1</sup>Northeastern Illinois University, Biology, 5500 North St. Louis Ave, Chicago, IL, 60625, USA<sup>2</sup>Northwestern University, Physiology, 1918 Sheridan Road, Evanston, Evanston, IL, 60208-4020, USA

519 MOURA, TÂNIA MARIA DE\*<sup>1</sup>,  
MANSANO, VIDAL DE FREITAS<sup>2</sup>, SOUZA,  
ANETE PEREIRA DE<sup>1</sup> and TOZZI, ANA  
MARIA GOULART DE AZEVEDO<sup>1</sup>

**Evidence of non-monophyly within  
*Mucuna* Adans. (Leguminosae -  
Papilionoideae) as inferred from  
phylogenetic analysis**

*Mucuna* Adans. (Leguminosae, Papilionoideae, Phaseoleae) has about 100 species and a pantropical distribution. The highest diversity of the genus is in the Old World, with only about 16-20 species in the Americas. These latter species are remarkable for their morphological diversity and different pollination syndromes. Two subgenera are recognized, *Mucuna* subg. *Stizolobium* (P. Browne) Bauer and *Mucuna* subg. *Mucuna*. The representatives of *Mucuna* subg. *Stizolobium* differ substantially from members of the typical subgenus, mainly in relation to fruit and seed morphology. Additionally, *Mucuna bennetti* F. Muell. has a strict morphological relationship with *Strongylocodon macrobotrys* A. Gray. However, phylogenetic relationships of *Mucuna* representatives have not been investigated yet. The phylogenetic relationships between the representatives of the Old and New World are also unknown. This study aimed to test the monophyly of *Mucuna* and verify the phylogenetic relationships between *M. bennetti* and *S. macrobotrys*. For that, we sampled individuals of *Mucuna* from the New and Old World of both subgenera. *S. macrobotrys*, *Desmodium cajanifolium* (Kunth) DC., *Erythrina fusca* Lour. and *E. speciosa* Andrews were used as outgroups. The phylogenetic analysis was carried out using the ITS spacer region (17-26SE). Trees were obtained by maximum parsimony and likelihood methods. The results showed that *Mucuna* is not monophyletic because, as predicted, *M. pruriens* is grouped in a polytomy with the genus *Erythrina* and apart the rest of *Mucuna*. The results also suggest the monophyly of *Mucuna* subg. *Mucuna*, once all specimens of this subgenus sampled were grouped together into a single clade. Despite the reduced number of species sampled in our study we included as much morphological variation as was possible as a way to have the whole genus represented. The variation included species with the following morphological variation: inflorescence nodose and umbellate; fruit without ornamentation and ornamented; different pollination syndromes and representatives of the Old and the New World. Our results showed no phylogenetic relationship between *M. bennetti* and *S. macrobotrys*.

<sup>1</sup>State University of Campinas, Vegetal Biology, Biology Institute, postal box 6109, Campinas, SP, 13083-970, Brazil; <sup>2</sup>Jardim Botânico do Rio de Janeiro, Rua Pacheco Leão, 915., Rio de Janeiro, RJ, 22460-030, Brazil

520 FORTUNA PEREZ, ANA PAULA\*<sup>1</sup>  
and TOZZI, ANA MARIA GOULART DE  
AZEVEDO<sup>2</sup>

**Morphological analysis of fruit of  
the Brazilians species of *Zornia* J.F.  
Gmel. (Leguminosae, Papilionoideae,  
Dalbergieae) and its systematic  
significance**

*Zornia* comprises 80 species with a pantropical distribution, arranged in two subgenera (*Myriadena* and *Zornia*) and three sections (*Zornia*, *Isophylla* and *Anisophylla*). The genus is a member of the informal *Adesmia* group of the pantropical Dalbergioideae. It is most closely related to the predominantly South American genera *Poiretia* and *Amicia*. *Zornia* is characterized mainly by its flowers arranged in a spiciform inflorescence, with paired peltate bracteoles protecting each flower, and stipules that resemble the bracteoles. This work aimed to a morphological analysis of fruit of the species of *Zornia* that occur in Brazil, and a systematic evaluation of its meaning. The analyses were made by scanning electron microscopy and stereomicroscopy (XL 30-ESEM). During the revision, in which 36 species of *Zornia* from Brazil were recognized, more than 3,000 accessions were analyzed through the visits to European and Brazilian herbaria and loans from elsewhere, as well as field plants. In relation to morphological studies of the fruit, loment type, it is shown that the detailed analysis of the articles provides excellent taxonomic characters to distinguish among the Brazilian taxa. In this study were found both smooth and ornamented surfaces, with or without indument, bristles and glands. This study corroborated with hypotheses of co-identification, such as *Zornia gemella* Willd. ex Vogel and *Z. curvata* Mohlenbr., where the surface of the articles did not show any difference. However, in cases of recognition of distinct species, such as *Z. reticulata* Sm. and *Z. glabra* Desv., species often confused, the surface of the articles showed differences, such as the presence of indument and absence of glands on the surface of *Z. reticulata* and glabrous surface with glands in *Z. glabra*. The species of the subgenus *Myriadena* have unique type of trichomes: *Z. myriadena* Benth. showed stellate trichomes in the surface of the article, while *Z. echinocarpa* Moric. presented echinate trichomes. An identification key, descriptions and comments on similarities in morphology, botanical illustrations and SEM photographs of fruit of species of *Zornia* are provided.

<sup>1</sup>Universidade Estadual de Campinas, Biologia Vegetal, Monteiro Lobato, 970 - Barão Geraldo - , Campinas, São Paulo, 6109, Brazil-

<sup>2</sup>Universidade Estadual de Campinas, Biologia Vegetal, Monteiro Lobato, 970, Cidade Universitária - Barão Geraldo, Campinas, São Paulo, 6109, Brazil

521 FREIRE-FIERRO, ALINA\*<sup>1</sup>,  
SPOTILA, JAMES, R.<sup>2</sup>, RUSSELL, JACOB  
A.<sup>2</sup>, DORR, LAURENCE J.<sup>3</sup>, SCHUYLER,  
ALFRED E.<sup>1</sup>, KILHAM, SUSAN S.<sup>2</sup> and BIEN,  
WALTER, F.<sup>2</sup>

### Systematics of *Monnina* (Polygalaceae)

*Monnina* (Polygalaceae) is a monophyletic genus with unknown phylogenetic origins. The ca. 230 species within the genus are morphologically diverse and are an important element of the Neotropical montane flora. The goal of this research is to use morphological and molecular approaches to determine the phylogenetic relationships within the genus and between *Monnina* and its related genera. This research will address these questions using morphological and molecular approaches. The study and analysis of the already selected 100 morphological characters from about 200 borrowed herbarium specimens (~95 species) will provide information regarding the morphological variability in the genus, while phylogenetic analyses with nuclear and chloroplast genes will provide us with information about the timing and order of evolution in this group. Material from previously hypothesized sister genera (e.g. *Polygala*, *Comesperma*, and *Securidaca*), together with specimens from *Monnina* from Costa Rica, Mexico and the rest of Central America and South America will be sampled. The markers *trnL-trnF*, *matK*, and *ndhF-rpl32* have been successfully used with Polygalaceae. Nuclear genes (low copy and/or ITS) will be tested if cpDNA markers are not informative at the infrageneric level. The phylogenies will be inferred through parsimony and Bayesian statistics. Further taxonomic and ecological studies could provide valuable data regarding the distribution and conservation status of *Monnina*.

<sup>1</sup>Academy of Natural Sciences, Botany, 1900 Benjamin Franklin Parkway, Philadelphia, PA, 19103, USA<sup>2</sup>Drexel University, Biology, 3141 Chestnut St., Philadelphia, PA, 19104, USA<sup>3</sup>Smithsonian Institution, Botany, 10th St. and Constitution Av., NW, Washington, D.C., 20560, USA

522 STEELE, KELLY\*<sup>1</sup>, ELLINGBO,  
AARON<sup>1</sup> and WOJCIECHOWSKI, M<sup>2</sup>

### Phylogenetic analyses of *Medicago* using plastid and nuclear-encoded molecular markers: key to understanding chromosomal and morphological evolution within the genus

Phylogenetic analyses of the genus *Medicago* using a five molecular marker data set of both plastid and nuclear-encoded molecular markers (plastid *trnK/matK* region, nuclear encoded GA3 oxidase gene, nrDNA ITS, CNGC5, and b-cop-likegene) are used to

develop a robust phylogeny to consider hypotheses of chromosomal and morphological evolution within the genus. Results of Bayesian analyses of these data support the hypothesis of a sister group relationship between the section *Medicago* clade that includes alfalfa, *M. sativa*, and a subsection *Pachyspireae* clade that includes the modellegume, *M. truncatula*. A data set comprised of nrDNA ITS sequences from more than 150 samples including multiple accessions of most species was analyzed separately. Results of Bayesian analyses of those data support the hypothesis that the putative parents of two polyploid taxa, *M. scutellata* and *M. rugosa* (2n=30), both thought to be the result of hybridization of a 2n=14 parent and a 2n=16 parent (the ancestral condition), are within the subsection *Pachyspireae* clade and may have at least one parent in common.

<sup>1</sup>Arizona State University, School of Life Sciences, Tempe, AZ, 85287-4501, USA<sup>2</sup>Arizona State University, PO Box 874501, Tempe, AZ, 85287-4501, USA

523 RICE, JACQUELINE\*<sup>1</sup>, HEANEY,  
JAMES<sup>2</sup>, JUDD, WALTER<sup>3</sup>, SOLTIS,  
DOUGLAS<sup>1</sup> and SOLTIS, PAMELA<sup>4</sup>

### Systematics of *Myrica cerifera* L.

This study focuses on the currently unresolved systematics of *Myrica cerifera* L. (wax myrtle) and *Myrica cerifera* var. *pumila* Michaux (dwarf wax myrtle). The two entities are treated as the same species by many researchers. However, because their morphologies are noticeably different (*M. cerifera* is a large shrub, *M. cerifera* var. *pumila* is a small understory subshrub), others have proposed that these plants are actually two distinct species, *M. cerifera* and *M. pumila* (Michaux) Small. The two entities have been observed to have consistent morphological differences, although it is unknown whether or not these morphological differences stem from genetic differences, or if they are simply a response to the habitat in which the plants occur. Using DNA sequences from samples across the southeastern United States, phylogenetic analyses show small but consistent differences between the two in both nuclear ribosomal ITS and plastid regions (*psbA-trnH*, *trnG-trnS*, *trnG-trnG*, *psbM-ycf6*, *petA-psbJ*, *rpl32-trnL*) of DNA. Specifically, results of this study show three polymorphic sites between *M. cerifera* and *M. cerifera* var. *pumila* in ITS. These results suggest that *M. cerifera* and *M. cerifera* var. *pumila* could indeed be distinct from one another at the species level.

<sup>1</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA<sup>2</sup>University Of Florida, Dickinson Hall, Museum Road, Gainesville, FL, 32611-7800, USA<sup>3</sup>University of Florida, Department of Biology, Po Box 118526, Gainesville, FL, 32611, USA<sup>4</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA

524 KIM, CHAN-SOO\*<sup>1</sup>, MOON, MYUNG-OK<sup>2</sup> and KIM, SOO-YOUNG<sup>3</sup>

### A new species of *Rubus* (Rosaceae) from Korea

*Rubus jejuensis*, a new species of Rosaceae from Korea is described. It is morphologically related to *R. croceacanthus* and *R. sumatranus* because of the presence of stout and elongate stems, and pinnate leaves. But *Rubus jejuensis* can be distinguished from *R. croceacanthus* and *R. sumatranus* by the presence of unarmed evergreen arching stems, slender pedicels, and glabrous leaves and rachis. Chromosome data are presented.

<sup>1</sup>Korea Forest Research Institute, Warm-temperate Forest Research Center, Seogwipo, Jeju, 697-050, ROK<sup>2</sup>Jeju National Univ, Research Institute for Basic Science, Jeju, Jeju, ROK<sup>3</sup>National Institute of Biological Resources, Wildlife Genetic Resources Center, Incheon, 404-708

525 NELSON, GRETCHEN\*<sup>1</sup>, BURGESS, MICHAEL<sup>1</sup>, CUSHMAN, KEVIN<sup>2</sup>, DOUCETTE, ERIC<sup>3</sup> and CAMPBELL, CHRISTOPHER<sup>3</sup>

### Morphological and phylogenetic relationships of an unusual species, *Amelanchier bartramiana* (Rosaceae)

*Amelanchier bartramiana* (Tausch) M. Roemer is the most distinctive species of this genus in eastern North America. Its few-flowered inflorescences, imbricate leaf arrangement in bud, tapering ovary summit, and capacity to grow in alpine habitats are unique to this species in eastern North America. Diploid *A. bartramiana* carries two variants of the LEAFY gene that are far more divergent from one another than different variants of this gene are with any other diploid species in the genus. The relationships of these presumed gene copies to sequences of this gene in other diploid species are striking. One copy occurs in the eastern North American diploids *A. arborea* (Michx. f.) Fern., *A. canadensis* (L.) Medik., and *A. laevis* Wiegand that comprise what we call clade T and in all Old World diploids. The other copy found in *A. bartramiana* is also present in another eastern North American diploid, *A. humilis* Wiegand, and all western North American diploids. Our sampling of *A. bartramiana* has uncovered diploids at high elevation from Maine to West Virginia and polyploids at lower elevations from New England to the Great Lakes. These two groups differ more or less markedly in petiole length, petal size, and leaf shape. Sequences from the ETS region from *A. bartramiana* tetraploids either nest within a clade comprised only of *A. bartramiana* diploid individuals or are weakly supported as sister to the strongly supported clade that contains *A. bartramiana* plus clade T. This topological pattern is consistent

with allopolyploidy, with diploid *A. bartramiana* as one parent. The other parent was most likely *A. humilis*, the range of which overlaps a large part of the range of *A. bartramiana*. One triploid *A. bartramiana* plant is apparently the only autopolyploid among scores of polyploids that we have studied in the genus.

<sup>1</sup>University of Pennsylvania, The Morris Arboretum, 100 E. North-western Avenue, Philadelphia, PA, 19118<sup>2</sup>P.O. Box 143, Levant, ME, 04456, USA<sup>3</sup>University Of Maine, Department Of Biological Sciences, 261 HITCHNER HALL, ORONO, ME, 04469-5735, USA

526 HEO, KYEONG-IN<sup>1</sup>, LEE, SANGTAE\*<sup>2</sup> and KIM, SEUNG-CHUL<sup>1</sup>

### Systematic studies of the genus *Potentilla* s.l. (Rosaceae) in Korea

The phylogeny of Korean *Potentilla* s.l. was studied based on nrDNA ITS sequences as well as morphology and palynology. For the ITS phylogeny, we analyzed a total of 19 species and one variety of Korean *Potentilla* s.l., and additional species from GenBank database were included in this study. The ITS phylogeny suggests that *Potentilla* s.l. is monophyletic, and two major clades were identified. One clade includes taxa treated as segregate genera (i.e., *Comarum*, *Argentina*, *Dasiphora*; *Potentilla* sunsu Wolf, 1908) as well as *Fragaria*. The other clade includes species of *Potentilla* s.s. and *Duchesnea* (Hutchinson, 1964). *Potentilla anserina* which has been treated as *Argentina* is included in the former clade, but in pollen and leaf surface characters it has similar characters to taxa of *Potentilla* s.s. *Fragaria* and *Dasiphora* are diverged within the former clade. The pollen characters and the style shape support a close relationship between two genera. However, *P. bifurca* var. *major* of ser. *Bifurcae* (*Dasiphora*) and *Fragaria* x *ananassa* have pollen characteristics of *Potentilla* s.s. The taxa of *Duchesnea*, which often has been treated as independent genus, are part of *Potentilla* s.s. clade. In addition, the pollen morphology suggests inclusion of *Duchesnea* in *Potentilla* s.s. These results are congruent with the two clades recognized by Erisson et al. (2003). The former and latter clade corresponds to *Fragariinae* and *Potentilla* s.s., respectively. However, these molecular, palynological, and morphological results support that taxa treated as independent genera, *Comarum*, *Argentina*, *Dasiphora*, *Duchesnea*, and *Fragaria*, should be included in *Potentilla* s.l. The monophyly of sections of *Potentilla* s.l. is not supported, but series are monophyletic except for *P. centigrana* of ser. *Kleinianae* of sect. *Conostylae*, which is deeply nested within ser. *Eriocar-pae* of sect. *Nematostylae*.

<sup>1</sup>Sungkyunkwan University, Department Of Biological Sciences, 300 Cheoncheon-Dong, Jangan-Gu, Suwon, N/A, 440-746, Korea-

<sup>2</sup>Sungkyunkwan University, Biological Science, Cheoncheon Dong 300, Jangan Gu, Suwon, Gyeonggi, 440-746, South Korea

527 TOLL, KATHERINE\*<sup>1</sup> and  
WHITLOCK, BARBARA A.<sup>2</sup>

**A molecular phylogeny of *Micromelum*  
(Rutaceae: Aurantioideae) and  
observations on floral morphology using a  
historical plant anatomy resource**

*Micromelum* includes nine species of shrubs and small trees in the citrus subfamily (Aurantioideae) of Rutaceae. It has the largest geographic range of any genus in Aurantioideae, extending from South and Southeast Asia to Australia and Oceania, with both widely distributed species and narrow endemics. At least some species of *Micromelum* have the unusual character of convoluted locules caused by the twisting of the radial walls of the ovary. Although twisted ovaries are often described as a generic character, it is unclear if all species of *Micromelum* have them. We constructed a phylogeny of *Micromelum* using non-coding cpDNA sequences and made observations on floral morphology using the historical Swingle Plant Anatomy Reference Collection to test the following hypotheses: (1) the widely distributed species *M. minutum* is monophyletic, (2) species with limited geographic ranges (e.g., *M. ceylanicum*) are genetically distinct from their more widely distributed relatives (e.g. *M. minutum*), (3) all species of *Micromelum* have twisted ovaries, and if not, (4) species with twisted ovaries form a monophyletic group. Relationships among specimens of *M. minutum* sampled are unresolved, so it is uncertain whether it is monophyletic. The narrow endemic *M. ceylanicum* found only in dry lowland forests of Sri Lanka appears to be genetically distinct from all other species sampled. Although twisted ovaries are often described as a defining trait of *Micromelum*, we observed them in only three of eight species represented in the Swingle Collection, suggesting their occurrence may be more limited than what is currently thought. Alternatively, twisting may occur in some species at later developmental stages than those observed. We compare these results to observations on two other characters important in defining *Micromelum*: valvate petal aestivation and oil glands at the tip of each locule.

<sup>1</sup>University of Miami, Department of Biology, Coral Gables, FL, 33124, USA <sup>2</sup>University Of Miami, Department Of Biology, P.O. Box 249118, CORAL GABLES, FL, 33124-0421, USA

528 LAURON-MOREAU, AURELIEN\*,  
PITRE, FREDERIC, E., LABRECQUE,  
MICHEL and BROUILLET, LUC

**Molecular phylogeny of *Salix* (Salicaceae)  
in order to characterize the origin of  
native *S.eriocephala* : a new perspective for  
biomass production**

Fast growing willows (*Salix* sp.) are increasingly used in Europe and North America for biomass production and other environmental applications. However, the phylogeny of willows is incomplete, which slows down the selection of suitable native species and the development of improvement programs. *Salix* includes around 500 species worldwide, mainly in temperate and cold regions of the Northern Hemisphere, and more than 100 species are found in North America. A phylogeny including introduced species already in usage along with native species could help uncover clades with suitable native species for biomass production, such as *S.eriocephala*. We gathered leaf material from ca. 50 native diploid willows and introduced cultivated species. We sequenced the chloroplastic gene *matK*, the ITS region, and the nuclear gene *calcineurin-likephosphoesterase*. Phylogenetic analyses were carried out using parsimony and Bayesian approaches and *Populus* was used as the outgroup. A first analysis used *matK* and ITS to identify clades in the genus. Two major clades were found in the analyses, one of which included the species of interest. We then focused on those clades where cultivated introduced species and *S. eriocephala* were included for a second analysis using *calcineurin-likephosphoesterase*. The phylogenetic tree indicates that species of interest might have an evolutionary relationship. Polyploid willows will eventually be added to the analysis as they are also potentially useful in environmental applications. More nuclear markers must also be developed to increase the resolution of our analysis.

Universite de Montreal, Institut de recherche en biologie vegetale, 4101 rue Sherbrooke Est, Montreal, QC, H1X 2B2, Canada

529 KING, COLIN\* and BALLARD JR,  
HARVEY

**Investigating the *LEAFY* Gene for  
Phylogenetic Analysis in the Violet Family  
(Violaceae)**

The *LEAFY* gene has recently gained attention as a marker for phylogenetic studies of vascular plants. However, of the two dozen published studies using *LEAFY*, few have focused on families of Rosids. These studies generally have shown *LEAFY* to be variable and phylogenetically informative, especially at the species level. Given documented problems with the

Internal Transcribed Spacer region of nrDNA to infer interspecific relationships, we are investigating *LEAFY* for its phylogenetic utility in the Violet family. Primers were designed for use with the Violet family and potentially other families in the Rosids, by first aligning complete sequences of the gene from GenBank for *Arabidopsis thaliana* (Brassicaceae), *Chenopodium rubrum* (Amaranthaceae), *Ricinus communis* (Euphorbiaceae), *Populus balsamifera* (Salicaceae), and *Viola pubescens* (2 sequences, Violaceae). A consensus sequence from the aligned sequences was submitted to Primer 3 online, and primers were identified in conserved areas of exons 2 and 3. A primer pair successfully amplified five genera distributed across the Violaceae: *Rinorea crenata*, *Gloeospermum diversipetalum*, *Allexis cauliflora*, *Hybanthus linearifolius*, and *Viola pubescens*. Products sequenced satisfactorily using the PCR primers, but polymorphic sequence in some taxa suggests the presence of two copies (confirmed previously in *Viola pubescens*). Although the coding regions were very conserved, intron 2 showed extreme numbers of nucleotide substitutions and indels. These preliminary results suggest that the gene will most likely be particularly useful among species within a genus or closely related genera. Imminent future studies will isolate duplicated loci of *LEAFY* and develop locus-specific primers, and will apply these to representatives of *Viola* to better assess species-level variation and phylogenetic utility. Our *LEAFY* primers deserve further investigation for potential use in other Rosid families.

Ohio University, Environmental & Plant Biology, 315 Porter Hall, Athens, OH, 45701, USA

**530 JOHNSON, CHRIS\*<sup>1</sup>, FLICKER, BEN<sup>1</sup> and BALLARD JR, HARVEY<sup>2</sup>**

### **Numerical Phenetic Analysis of the Polymorphic species *Hybanthus enneaspermus* (L.) F. Muell. in Tropical East Africa**

*Hybanthus enneaspermus* (L.) F. Muell. (Violaceae) is a small, polymorphic herb, commonly found on roadsides and other disturbed areas throughout much of the Old World Tropics. Because of its high degree of morphological variation, previous circumscriptions of species complex have presented a single, morphologically plastic species. Results of numerical phenetic analysis of morphological variation within *H. enneaspermus sensu lato* support 8 distinct taxa recognizable by vegetative, floral, and fruiting characters. Results of cononical variates analysis and charts of characters used in the data matrix will be presented.

<sup>1</sup>Ohio University, Environmental and Plant Biology, Porter Hall Rm. 317, Athens, OH, 45701, USA<sup>2</sup>Ohio University, Environmental & Plant Biology, 315 Porter Hall, Athens, OH, 45701, USA

**531 DERESIENSKI, TESS\*<sup>1</sup> and PORTER-UTLEY, KRISTEN<sup>2</sup>**

### **A New Molecular Phylogeny for *Passiflora* Subgenus *Decaloba* Supersection *Cieca* (Passifloraceae)**

A new molecular phylogeny of the closely related species of *Passiflora* subgenus *Decaloba* supersection *Cieca* (Passifloraceae) is presented. Supersection *Cieca* is a monophyletic group of herbaceous to woody climbers found in subtropical and tropical regions of the world. The 19 species, including two subspecies, recognized here are primarily distributed in the southern United States, Mexico, Central America, South America, and the Caribbean. The species of the supersection are recognized by their small, apetalous, usually greenish flowers with the filaments of the corona mostly in two series. The supersection contains two problematic species complexes, *P. suberosa* and *P. coriacea*. Phylogenetic relationships within supersection *Cieca* have been investigated by means of cladistic analyses of morphological (external morphology) and molecular (ITS) characters. Though many clades within the supersection are well-resolved in the analyses of these data, several relationships are poorly resolved. Additional genes, *cytGS*, *npcGS*, and *trnL-Fare* used as additional data sources to further resolve the evolutionary relationships within the supersection. The gene datasets are analyzed independently and combined with the ITS data to produce a more well-resolved phylogeny of the supersection. The morphological phylogeny is compared to the individual and combined molecular phylogenies.

<sup>1</sup>Keene State College, Biology, 229 Main St., Keene, NH, 03435, USA<sup>2</sup>Keene State College, Biology, 229 Main St., MS-2001, Keene, NH, 03435, United States

**532 GAHAGEN, BENJAMIN\*<sup>1</sup> and BALLARD JR, HARVEY<sup>2</sup>**

### **A Preliminary Morphological Study of *Tovomita weddelliana* Planch. & Triana (Clusiaceae)**

*Tovomita* is one of 27 genera in the family Clusiaceae and reportedly includes approximately 45 species distributed throughout Central America and the Amazonian region of South America. The genus is characterized by 1 ovule per carpel, distinct styloids, 2 outer sepals enveloping the bud, moderately excavated petiole bases, and a vascularized ariloid structure visible when the fruit dehisces. Within this genus are several species complexes, one of which is the problematic and variable *Tovomita weddelliana* complex. The complex is distinctive in the genus in many traits, including leaves clustered near branch tips; (sub)sessile oblanceolate blades with distinctly pale or glaucous lower surface;

ovate-suborbicular sepals; numerous stamens with linear-subulate filaments; and an oblong obtuse glabrous ovary with four locules. Examination of herbarium collections suggests several taxa presently subsumed under the name *T. weddelliana*, which is exceedingly well represented in herbarium collections. The present study reexamines the *T. weddelliana* species complex morphologically, uncovering correlated patterns of variation in many characteristics of branch, leaf phyllotaxy, leaf shape, petiole development and leaf decurrence, lateral veins, margin, and lamina surface; inflorescence, sepals and petals; and fruit anatomy, shape, indument, and locules. Preliminary investigation has delimited at least nine distinct morphological species including *T. weddelliana* sensu stricto. Imminent future research will examine molecular phylogenetic relationships among these and other members of *Tovomitia*.

<sup>1</sup>Ohio University, Environmental and Plant Biology, Porter Hall 315, Athens, OH, 45701, USA<sup>2</sup>Ohio University, ENVIR & PLANT BIOLOGY-PORTER H, 315 Porter Hall, Athens, OH, 45701-2979,

**533 SCHWARTZ, EMILY\*<sup>1</sup>, NEUBIG, KURT<sup>1</sup>, JUDD, WALTER<sup>1</sup> and BLANCHARD, ORLAND<sup>2</sup>**

**Molecular and morphological phylogenetic study of species delimitation in *Kosteletzkya depressa* and *K. hispidula* (Malvaceae, Hibisceae)**

Ongoing phylogenetic studies of the genus *Kosteletzkya* have revealed unresolved phylogenetic relationships among *K. depressa* and *K. hispidula*. In this study, multiple population accessions from throughout the two species distributions were sampled in order to run analyses using molecular and morphological data. Two plastid loci (*trnL-F* and *rpl32-trnL*) and two nuclear loci (*GBSSI* and *CesA1*) were sequenced for all accessions of *K. depressa* and *K. hispidula*. Eleven morphological characters were chosen for analysis and character states were scored for each accession. In the combined analysis of all four gene regions, *K. hispidula* is strongly supported as a monophyletic clade. *Kosteletzkya depressa* appears as a paraphyletic group relative to the *K. hispidula* clade, and, according to DNA data alone, *K. hispidula* is sister to the NW Mexican *K. depressa* clade. In a combined analysis of the four gene regions and morphology, the *K. hispidula* clade is reinforced as a strong monophyletic group. However, a clade consisting of *K. hispidula* and *K. ramosa* appears to be sister to *K. depressa*, the populations of which also form a clade. This discrepancy could be explained by introgressive hybridization between *K. hispidula* and *K. depressa* resulting in a chloroplast capture event. A shared plastid haplotype, seen in *rpl32-trnL*, may be a molecular remnant of a chloroplast donation from *K. hispidula* to NW *K. depressa* populations (or vice versa) in the sympatric region of northwest Mexico, and is an

incomplete and misleading representation of their true phylogenetic relationship. The results of the study exhibit the need for further research, with additional gene loci (both nuclear and plastid), in order to increase our confidence in the evolutionary history of these plants.

<sup>1</sup>University of Florida, Department of Biology, Po Box 118526, Gainesville, FL, 32611, USA<sup>2</sup>University of Florida, Florida Museum of Natural History, PO Box 117800, Gainesville, FL, 32611, USA

**534 JEFFRIES, SHANDRA K.\*<sup>1</sup>, SCHULTE, LACIE J.<sup>2</sup>, CLARK, JOHN L.<sup>3</sup>, AMAYA MARQUEZ, MARISOL<sup>4</sup> and SMITH, JAMES<sup>5</sup>**

**Using selected gene regions to find rapidly evolving DNA sequences of closely related species of the genus *Columnnea***

Knowing evolutionary relationships among species can improve our understanding of many biological functions. Within the past thirty years, molecular data has changed how these evolutionary relationships are determined and made molecular phylogenetics an important discipline in biology. The standard in phylogenetic research has been to use DNA sequences to compare genetic variation in gene regions. When attempting to resolve phylogenetic relationships between species, common gene regions known to show variation are the nuclear ribosomal ITS regions and the chloroplast DNA regions, *rpl32-trnL*, and *psbA-trnH* spacers. Unfortunately, in the genus *Columnnea* these gene regions have not given sufficient variation to resolve relationships between and among closely related species. Certain low copy gene regions have been shown to rapidly evolve and provide supportive variation in other genera. In this study, we examined the feasibility of four low-copy nuclear gene regions and one chloroplast region for phylogenetic comparison across six species using PCR, gel analysis, and DNA sequencing. The utility of these gene regions on phylogenetic analyses was assessed and compared to the results for the aforementioned regions by pairwise percent differences and percent phylogenetically informative characters. The results of these comparisons will minimize time and resources needed to resolve phylogenetic relationships in the genus *Columnnea*.

<sup>1</sup>Boise State University, Biological Sciences, 1910 University Drive, Boise, ID, 83725-1515, USA<sup>2</sup>Boise State University, Biological Sciences, 1910 University Drive, Boise, ID<sup>3</sup>University of Alabama, Biological Sciences, Box 870345, Tuscaloosa, AL, 35487, USA<sup>4</sup>Universidad Nacional de Colombia, Instituto de Ciencias Naturales, Aptdo. Aereo 7495, Bogota, Colombia<sup>5</sup>BOISE STATE UNIVERSITY, Biology Department, 1910 UNIVERSITY DRIVE, Boise, ID, 83725-1515, USA

535 OOI, MAGGIE T.\*<sup>1</sup>, CLARK, JOHN L.<sup>2</sup>, AMAYA MARQUEZ, MARISOL<sup>3</sup> and SMITH, JAMES<sup>4</sup>

### Distinguishing Species with DNA Sequencing in the *Columnnea strigosa* Complex

Historically, identifying species boundaries has depended on morphology. However, morphology alone is often challenging because of convergent evolution, phenotypic plasticity, and intra-specific variation. New methods like molecular phylogenetics, which is the analysis of DNA sequences to determine evolutionary lineages, has become essential to modern day systematic biology since 1981. Molecular data are less prone to the challenges that are found in morphology since DNA sequences can be used to define species boundaries when species are defined as evolutionary lineages. Determining species boundaries within the widespread Neotropical genus *Columnnea* has been complicated based on morphology alone due to all of the problems mentioned above. The *Columnnea strigosa* complex is one particular case. This complex has been delimited from one to six species over the past 150 years. Here we examine molecular data of individuals from throughout the geographical and morphological range of the complex. DNA regions used were nuclear regions ITS and three chloroplast regions (*rpl16x1-trnQ5* spacer, *rpl32-trnL* spacer, and *rps16* intron). Sequences were then analyzed to assess relationships between species within the complex.

<sup>1</sup>Boise State University, Biological Sciences, 1910 University Drive, Boise, ID<sup>2</sup>University of Alabama, Biological Sciences, Box 870345, Tuscaloosa, AL, 35487, USA<sup>3</sup>Universidad Nacional de Colombia, Instituto de Ciencias Naturales, Aptdo. Aereo 7495, Bogota, Colombia<sup>4</sup>BOISE STATE UNIVERSITY, Biology Department, 1910 UNIVERSITY DRIVE, Boise, ID, 83725-1515, USA

536 ROBERT, BRUCE\*, GORE, RAHUL and POLICICCHIO, BEN

### Phylogeny and Biogeography of *Pedicularis* (Orobanchaceae) in North America

*Pedicularis* is an arctic/alpine plant genus consisting of 40 species in North America out of an estimated 600-800 species worldwide. ITS and matK DNA regions have been sequenced from 32 North American species. We included an additional 124 ITS sequences obtained from GenBank in our analysis. Utilizing PAUP, MrBayes, BEAST, sDIVA, and associated programs, we have inferred the evolutionary history, biogeography, and chronology of *Pedicularis* in North America relative to *Pedicularis* species in Asia. Two distinct North American clades were resolved, each with an ancestral

area in Asia. Our molecular clock estimation for entry of both clades into North America overlaps the Miocene (14-10 Myr) epoch, a time when the Bering Land Bridge was open for migration of boreal taxa. In one clade, subsequent divergence into North America also includes divergence into the Japanese archipelago. Once in North America, this clade displays a divergence route that converges into the southern Rocky Mountains by two different pathways, one by an earlier direct passage from the northern Rocky Mountains and the other by way of the Southern Cascade and Sierra Nevada ranges. The Furbish Lousewort (*P. furbishiae*) is an eastern North American relic disjunct member of this clade. The second clade, on the other hand, shows widespread divergence across most North American mountain ranges and into eastern North America via multiple routes. This clade also includes three European species in which North America is inferred as the ancestral area.

University of Pittsburgh at Johnstown, Biology, 450 Schoolhouse Road, Johnstown, PA, 15904

537 MARTINEZ, NIRZKA\*<sup>1</sup>, SANTIAGO, EUGENIO<sup>1</sup>, SALAZAR, JACKELINE<sup>2</sup> and MATEO, AMELIA<sup>2</sup>

### A preliminary phylogenetic analysis of Caribbean *Tabebuia* based on nuclear (ITS) and chloroplast (*psbD-trnT* and *rpl32-trnL*) molecular regions

*Tabebuia* Gomes ex DC. (Bignoniaceae) is an extraordinarily diverse plant genus that comprises species of economical importance. Traditionally, the genus circumscribed ca. 100 Neotropical species (Gentry, 1992), with many (ca. 60 species) confined to the Greater Antilles, especially to the islands of Cuba and Hispaniola. The genus exhibits great morphological variability and adaptations to a great diversity of ecological conditions (dry coastal scrubs, moist subtropical forest, cloud forest, among others). These characteristics make *Tabebuia* an interesting case to assess plant radiation in the Caribbean islands. Recent molecular studies based on chloroplast data indicate that the genus is paraphyletic (Grose and Olmstead, 2007a), supporting a taxonomic revision that has separated the "traditional *Tabebuia*" or "*Tabebuia* sensu lato" into three genera: *Handroanthus*, *Roseodendron* and *Tabebuia* (Grose and Olmstead, 2007b). Still, the relationships between the many species in the Caribbean have not been elucidated. The purpose of the study is to test the monophyly of the Caribbean species of *Tabebuia*, and to evaluate their evolutionary relationships, diversification, and biogeography. A preliminary phylogeny has been established based on nuclear (ITS) and chloroplast (*psbD-trnT*, *rpl32-trnL*) DNA sequences. The position in the phylogeny of members of Crescentieae and the genus *Spirotecoma* and *Ekmanianthe* included in the analysis further supports the hypothesis that the "traditional" ge-

nus *Tabebuia* is paraphyletic. Furthermore, the results suggest that the Caribbean group is monophyletic, with a close relationship to predominantly continental species *T. rosea* and *T. aurea*. Although additional sampling and molecular analyses are currently underway, the preliminary results clearly show the complexity of the taxa under study. Financial support: University of Puerto Rico (NSF-CREST Program, Biology Department-Rio Piedras campus and UPR Botanical Garden Herbarium); Ministerio de Educación Superior, Ciencia y Tecnología de República Dominicana (MESCyT).

<sup>1</sup>University of Puerto Rico - Rio Piedras, Biology Department, PO Box 23360, San Juan, PR, 00931, USA<sup>2</sup>Universidad Autónoma de Santo Domingo (UASD), Escuela de Biología, Zona Universitaria, Santo Domingo, DN, República Dominicana

**538 SALAZAR, JACKELINE<sup>1</sup>, SANTIAGO, EUGENIO<sup>2</sup>, MARTINEZ-MILLAN, MARCELA<sup>3</sup>, MARTINEZ, NIRZKA<sup>2</sup> and MATEO, AMELIA<sup>1</sup>**

### Leaf epidermis of *Tabebuia* alliance (Bignoniaceae) and its systematics significance

*Tabebuia* alliance is a Neotropical clade in the Bignoniaceae family with 14 genera and around 147 species, most found in the genus *Tabebuia* Gomes ex DC. In order to help assess patterns of morphological evolution of epidermal characters and its systematic significance, a survey of epidermal trichomes and stomata in *Tabebuia* alliance has been performed. These characters were evaluated using Scanning Electron Microscopy (SEM) and light microscopy with epidermal peeling maceration following the Gifford technique. The epidermal characters were mapped on the molecular phylogeny of the group published by Grose & Olmstead (2007). The analysis indicates that the general characteristics of the *Tabebuia* alliance include leaves that are hypostomatic as most of the species in Bignoniaceae, as well as glandular and eglandular trichomes. In addition, the clade has anomocytic type of stomata, a character that is also present in members of the Paleotropical clade, Bignoniaceae, and *Jacaranda*. The genus *Sparattosperma* at the base of the clade presents anomocytic stomata, peltate scales glandular and eglandular, and simple uniseriate trichomes. Although *Tabebuia* group plus *Ekmanianthe* mainly have glandular and eglandular scale peltate trichomes, a few species (e.g., Hispaniolan *T. bullata*) have acicular and filiform hairs. *Spirotecoma* and tribe *Crescentieae* are also groups characterized with scale peltate trichomes. On the other hand, *Tabebuia* group II, now genus *Handroanthus* (Grose & Olmstead, 2007), presents mainly branched hairs either dendritic or stellate or both, acicular or filiform, and glandular scale peltate trichomes. Thus, trichomes are important for defining two genera, *Tabebuia* and *Handroanthus*. However, a better resolved phylogeny is necessary to do the assessment of

epidermal characters within these two genera.

<sup>1</sup>Universidad Autónoma de Santo Domingo (UASD), Escuela de Biología, Zona Universitaria, Santo Domingo, DN, República Dominicana<sup>2</sup>University of Puerto Rico - Rio Piedras, Biology Department, PO Box 23360, San Juan, PR, 00931, USA<sup>3</sup>6622 130th Ave NE Apt D203, Kirkland, WA, 98033, USA

**539 ISA, SITI FATIMAH<sup>\*1</sup>, TRIPP, ERIN<sup>1</sup> and MCDADE, LUCINDA<sup>2</sup>**

### Comparative anatomy and morphology of the genus *Satanocrater* (Acanthaceae)

The aromatic and ethnobotanically important genus *Satanocrater* (Acanthaceae) from arid northern Africa has been little studied. Here, we examine morphology, phylogeny, anatomy, and ecology of all four species in the genus. All four share features that suggest adaptations to xeric environments (e.g., the possession of a thick-walled epidermis, thick waxy cuticle, abundant glandular trichomes, and/ or dense, gland-like scales). Two of the species were also observed to have sunken stomata while massive trichomes and/ or glands on the other two species obscured the stomatal structure. Interestingly, plants of *S. paradoxus* possess bundle sheath cells indicative of Kranz anatomy. If confirmed, *Satanocrater* will represent the second known occurrence of C4 photosynthesis in the family. This study is the first to document pollen and seed morphology in the genus; traits pertaining to both support its placement in the Ruelliae lineage. Within Ruelliae, pollen morphology of *Satanocrater* is somewhat transitional between two major lineages, and phylogenetic data are consistent with this "transitional" hypothesis.

<sup>1</sup>Rancho Santa Ana Botanic Garden, 1500 N College Ave, Claremont, CA, 91711, USA<sup>2</sup>Rancho Santa Ana Botanic Garden, Department Of Botany, 1500 N. College Avenue, Claremont, CA, 91711, USA

**540 SORIANO, SARA FUENTES**

### Patterns of trait evolution within the tribe Physarieae (Brassicaceae): changes in morphology

The mustard family (Brassicaceae) is economically important but the evolution of its morphology is not well understood. Here I re-evaluated patterns of morphological evolution in Brassicaceae and estimated ancestral trait values of eleven continuous morphological traits using the tribe Physarieae as a model system. A three-locus data set for the tribe gathered from chloroplast and nuclear data and new methods to model directional change were used to identify the best-fitting models of evolution before ancestral character values were reconstructed using Bayesian analyses. The analyses included traits traditionally used in the systematics of Brassicaceae, such as fruits and seeds, as well as other

characters frequently neglected in the study of the family, such as style length, and pollen size. Results show rather unexpectedly that levels of morphological homoplasy, as defined by values of trait phylogenetic signal, within Brassicaceae vary from being very obvious to almost absent. Modes of trait evolution were mostly consistent with a gradual model, but a few characters fit best with models of punctuated evolution (fruit width, replum shape, pollen size). Historically, rates of trait evolution were mostly constant, except for the rapid and recent evolution of replum shape, seed number, and pollen size. Fruit evolution within Physarieae reflected changes of individual components as inferred by the different rates and modes of individual trait evolution. Change in pollen size and seed number were predominantly directional. These results not only highlighted the phylogenetic potential of using continuous traits in the systematics of Brassicaceae, but also suggested that the individual components of single organs, such as fruit or seeds (e.g. length, width, size, number of parts) can evolve at different rates and modes. These results are especially relevant to understanding morphology and variation of the fruits, which is one of the most diverse and traditionally used characters in the systematics of the family.

Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166, USA

#### 541 NUNEZ, OSCAR TORO\*<sup>1</sup> and MORT, MARK<sup>2</sup>

##### Phylogenetic relationships of *Mathewsia* and *Schizopetalon* (Brassicaceae) based on two nrDNA and cpDNA regions

*Schizopetalon* (10 spp) and *Mathewsia* (9 spp) are two small genera of Brassicaceae endemic from southern Peru to northern Chile. These genera are characterized by their contrasting habits; *Schizopetalon* comprising annuals, whereas *Mathewsia* is entirely perennial. Most of their species occur along the southern Atacama Desert with species disjunct between the coast and the Andes. These characteristics make them suitable for evolutionary studies of adaptation and diversification in extremely arid environments. Broad studies of Brassicaceae support the monophyly of both genera and place them as sister taxa; however, there has been no focused phylogenetic study of either genus. We performed phylogenetic analyses of separate and combined nuclear (i.e. nrDNA ITS and ETS) and cpDNA (i.e. *psbA-trnH* and *rps16* introns) data sets, from a total of 22 individuals representing 13 species (~70% of total taxa), to assess the monophyly and elucidate the phylogenetic relationships within each genus. Our results suggest that *Schizopetalon* is monophyletic but relationships among species are only weakly supported. In contrast, *Mathewsia* is not resolved as monophyletic because a species from the high Andes, *M. nivea*, is sister to a *Mathewsia* + *Schizopetalon* clade. In both genera, species were placed in groups representing the northern

(southern Peru and Atacama) and southern (central Chile) areas of distribution. Also, analyses showed *S. bipinnatifidum* and *M. biennis* as polyphyletic.

<sup>1</sup>University of Kansas, Department of Ecology and Evolutionary Biology, Natural History Museum and Biodiversity Research Center, 1200 Sunnyside Avenue, Lawrence, Kansas, 66045, USA <sup>2</sup>University of Kansas, Department of Ecology and Evolutionary Biology, Natural History Museum and Biodiversity Research Center, 1200 Sunnyside Avenue, Lawrence, Kansas, 66046, USA

#### 542 ROLFSMEIER, SUSAN\*<sup>1</sup> and FERGUSON, CAROLYN<sup>2</sup>

##### Phylogeny and taxonomy of North American *Lappula* (Boraginaceae) in the context of Eurasian diversity

The genus *Lappula* (Boraginaceae) includes approximately 67 species of annual and biennial herbs. Diversity is concentrated in Asiatic Russia and Central Asia. In the late nineteenth and early twentieth century, over twenty species were described from western North America. These have, at various times, been treated as synonymous with (or as varieties of) particular Eurasian species. The North American specimens with a single row of spines have variously been referred to the Eurasian *L. redowskii* (Hornem.) Greene, and those with multiple rows of spines to the Eurasian *L. squarrosa* (Retz.) Dumort (which has been introduced and naturalized in North America). DNA sequence data from the internal transcribed spacer (ITS) region of the nuclear ribosomal DNA suggest that the native North American taxa represent a monophyletic group, distinct from the Eurasian taxa; preliminary data from chloroplast intergenic spacers also support this finding. *Lappula redowskii* is sister to the North American clade, while *L. squarrosa* (including samples from Siberia and from naturalized populations in North America) is more distantly related. An overview of phylogenetic findings is presented, along with discussion of taxonomic implications.

<sup>1</sup>Kansas State University, Division Of Biology, Ackert 115, Manhattan, KS, 66506, USA <sup>2</sup>Kansas State University, Division of Biology, Ackert Hall, Manhattan, KS, 66506, USA

543 CROWL, ANDY\*<sup>2</sup>, MANSION, GUILHEM<sup>1</sup> and CELLINESE, NICO<sup>2</sup>

**Evolution and biogeography of endemic taxa within the *Roucela* aggregate (Campanulaceae: Campanuloideae) in the Eastern Mediterranean region**

The Campanuloideae (Campanulaceae) are a highly diverse group in the Mediterranean region and include the polyphyletic *Campanula* with approximately 120 species found in Greece alone and an exceptionally high degree of endemism (ca. 60 endemic species). One group of particular interest is the putatively monophyletic *Roucela* complex, which includes approximately 12 species traditionally included in *Campanula*. This taxonomically complex group is primarily distributed within the eastern Mediterranean basin, with many of the taxa restricted to a single or a few islands. This work examines the phylogenetic relationship and biogeography of *Roucela* within the Campanuloideae based on chloroplast and low-copy nuclear markers.

<sup>1</sup>Botanischer Garten und Botanisches Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6 - 8, 14195 Berlin, Germany<sup>2</sup>University of Florida, Florida Museum of Natural History, Gainesville, FL, 32611, USA

544 TED, KIM

**Variation of Inter-Simple Sequence Repeat (ISSR) Markers among the woody *Sonchus* alliance (Asteraceae: Sonchinae) in Madeira Variation of Inter-Simple Sequence Repeat (ISSR)**

For many years, plants systematics was rely on morphological characters. These days, many molecular markers are available for phylogenetic study. Since PCR (Polymerase Chain Reaction) has been invented, the window of using molecular markers in phylogenetic study has been widely opened. There are many well-known and well-established molecular markers, such as chloroplast DNA or nuclear DNA markers. Sequence data from those markers are indubitable but often variations are not sufficient enough to resolve phylogenetic relationships among closely related species or recently radiated groups. In this case, other types of markers, such as Inter-Simple Sequence Repeat Marker (ISSR) can provide further resolutions. In this research, we investigated the woody *Sonchus* alliance in Madeira to resolve phylogenetic relationships among taxa as well as to determine patterns of colonization within each taxon. Five taxa (including one undescribed species) are widely distributed in Madeira. Madeira is a group of young islands, located in eastern Atlantic Ocean and the estimated age of the oldest island is 20 million year.

The absolute age estimation of most recent common ancestor of five taxa in Madeira is approximately 3 million years old. We estimated ISSR variations among five taxa of the woody *Sonchus* alliance in Madeira. Of 10 surveyed primers, we found three primers that gave us most variations and repeatable banding patterns. And from those ISSR variations, we determined phylogenetic relationship among the woody *Sonchus* alliance in Madeira. We included three outgroup taxa from the Canary Islands: *Sonchus acaulis*, *Sonchus congestus*, and *Sonchus canariensis*. The ISSR variations among five tax and their phylogenetic relationships will be presented in details. In addition, the colonization patterns of *Sonchus ustulatus* ssp. *ustulatus* and ssp. *maderense* will be discussed.

Sung Kyun Kwan Univ, Biology, 300 cheoncheon dong , 440746, South Korea

545 NEUBIG, KURT\*<sup>1</sup>, TALLEY, SHARON<sup>2</sup>, ABBOTT, J. RICHARD<sup>3</sup>, GERMAIN-AUBREY, CHARLOTTE<sup>4</sup> and WHITTEN, W. MARK<sup>5</sup>

**Phylogenetics and population genetics of the *Mikania micrantha* complex (Asteraceae)**

Using DNA sequences from nrITS, various plastid loci, and 16 microsatellite loci, this project aims to help elucidate the phylogenetic relationships and population genetics of the invasive species *Mikania micrantha* recently discovered in south Florida. The goals are to help delimit species within this species complex (which includes the native *M. scandens*), to develop the molecular tools to identify exotic material and, potentially, to locate the point of origin of exotic material in Florida. Preliminary phylogenetic results show that taxonomic delimitation in this species complex is very poor and that *M. micrantha* is not a monophyletic species. Nonetheless, there exists strong and distinct biogeographic signal among haplotypes, not only in this species, but also its closest relatives. *Mikania micrantha* is a significant invasive plant in Asia and it could also pose a significant threat to the flora of south Florida because of its aggressive growth rate; therefore, it is important to adequately understand the taxonomic circumscription for accurate identification and subsequent control.

<sup>1</sup>University of Florida, Department of Biology, Po Box 118526, Gainesville, FL, 32611, USA<sup>2</sup>USDA-APHIS-PPQ, Center for Plant Health Science and Technology, 2301 Research Blvd., Suite 108, Fort Collins, CO, 80526, USA<sup>3</sup>University of Florida, Florida Museum of Natural History, PO Box 117800, Gainesville, FL, 32611, USA<sup>4</sup>University Of Florida, Florida Museum Of Natural History, Soltis Lab, Dickinson Hall . Museum Road, Gainesville, FL, 32611, USA<sup>5</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA

546 MOSBY, LISA A.\*<sup>1</sup>, ALBRECHT, MATTHEW<sup>2</sup>, ESSELMAN, ELIZABETH<sup>3</sup>, CLAWITTER, HELEN<sup>3</sup> and RHODES, MATT<sup>5</sup>

### Determination of Seed Viability in a Rare Species: The Tennessee Coneflower

The Tennessee purple coneflower (*Echinacea tenesseeensis*) (Beadle) Small [Asteraceae] is a federal and state endangered species naturally found in cedar glades in middle Tennessee. A loss of habitat and a naturally restrictive geographic range contributed to this coneflower being listed as endangered. Conservation efforts have been made, new populations of Tennessee coneflower have been established, and a move to delist certain populations is currently under way. However, few studies have examined how the demography and genetics of restored populations compare to natural populations. The purpose of this study is to examine reproductive success in natural and introduced populations of the Tennessee purple coneflower. We compared seed production, seed viability and seed mass in twenty-one and nineteen restored and natural populations, respectively. For most demographic variables, restored populations were just as or more successful than natural populations. Our data highlights the importance of comparing demographic traits in natural and introduced populations for determining success rates in rare plant restoration projects. Future work on this coneflower includes germination studies to determine germination rates and percentages of germination success. Successfully germinated plants will be grown in a greenhouse and leaf tissues will be used for future DNA analysis of genetic diversity.

<sup>1</sup>Southern Illinois University Edwardsville, Biological Sciences, Room 3330 Science Building, Edwardsville, IL, 62026, USA<sup>2</sup>Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166, USA

<sup>3</sup>Southern Illinois University, Department Of Biology, RM 3330 SCIENCE BLDG, EDWARDSVILLE, IL, 62026-1651, USA<sup>4</sup>Washington University, One Brookings Drive, St. Louis, MO, 63130, USA

<sup>5</sup>Center for Conservation and Sustainable Development, Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166, USA

547 ZULUAGA, ALEJANDRO\*<sup>1</sup> and CAMERON, KENNETH<sup>2</sup>

### A preliminary phylogeny of *Monstera*, Araceae

*Monstera* is a medium-sized genus of the family Araceae, and a very important hemiepiphytic component of montane and lowland tropical rainforests. It is exclusively Neotropical, and has two principal centers of diversity: Costa Rica-Panama and the Colombian Andes. *Monstera* is a poorly known genus, and its taxonomy historically has been problematic due to relatively small but overlapping morphological variation, the great amount of existing names, incorrect use of them, and a noticeable deficiency of herbarium col-

lections. The last revision for the genus in 1977 included 22 species, and four sections were proposed based on morphological characters. The delimitation of the species classified within the largest section, *Monstera* sect. *Monstera*, is especially challenging due to the morphological intergradation of the species across their geographical distribution. Today 38 species are recognized, and as many as 10-15 remain undescribed. Recent phylogenetic analyses of Araceae by different authors, but including only 1-3 species of *Monstera*, suggest that the genus is monophyletic and closely related to the *Amydrium-Epipennum* clade. A detailed morphological study is underway, and this is being generated together with a phylogenetic reconstruction for *Monstera* based on chloroplast *trnL-F* and other loci. Species from each of the four sections, as well as individuals representing several populations of the most variable species, are included.

<sup>1</sup>University Of Wisconsin-Madison, 430 Lincoln Drive, UW Wisconsin-Department Of Botany, Madison, WI, 53706, USA<sup>2</sup>Wisconsin State Herbarium, Department Of Botany, 154 Birge Hall, 450 Lincoln Drive, Madison, WI, 53706, USA

548 NEUBIG, KURT\*<sup>1</sup>, WHITTEN, W. MARK<sup>2</sup>, WILLIAMS, NORRIS<sup>2</sup>, CHASE, MARK<sup>3</sup>, BLANCO, MARIO<sup>1</sup>, ENDARA, LORENA<sup>1</sup>, BURLEIGH, GORDON<sup>1</sup>, SILVERA, KATIA<sup>4</sup> and CUSHMAN, JOHN<sup>5</sup>

### Generic recircumscriptions of Oncidiinae (Orchidaceae: Cymbidieae) based on combined molecular data sets

Phylogenetic relationships within the orchid subtribe Oncidiinae sensu Chase were inferred using maximum likelihood analyses of individual and combined sequence alignments of nrITS DNA and three plastid regions (*matK*, *trnH-psbA* spacer, two portions of *ycf1*) for 738 individuals representing ca. 590 species plus 7 outgroup taxa. Based on the highly supported bootstrap consensus, we recognize 61 genera in Oncidiinae. Previous classifications emphasized homoplasious *Oncidium*-type floral features, phylogenetically intercalated with many other variable floral syndromes, resulting in non-monophyletic genera. Batesian and Mullerian mimicry of oil-secreting Malpighiaceae (and other oil-secreting flowering plant groups) may be responsible for convergence in floral features across the subtribe. This classification based on monophyly will facilitate focused monographs and will clarify the evolution of morphological and biochemical traits of interest within this subtribe.

<sup>1</sup>University of Florida, Department of Biology, 220 Bartram Hall, Gainesville, FL, 32611-8526, USA<sup>2</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA<sup>3</sup>Royal Botanic Gardens - Kew, Jodrell Laboratory, Kew Road, Richmond, N/A, TW9 3DS, United Kingdom<sup>4</sup>University Of Nevada Reno, 3141 Terrace Dr, Riverside, CA, 92507, USA<sup>5</sup>University of Nevada Reno, Department of Biochemistry, Reno, NV, 89557-0014, USA

549 SALAZAR, GERARDO\*<sup>1</sup>, CABRERA, LIDIA I.<sup>1</sup>, VAN DEN BERG, CASSIO<sup>2</sup>, SMIDT, ERIC C.<sup>3</sup>, BATISTA, JOAO A. N.<sup>4</sup>, FRAGA, CLAUDIO N.<sup>5</sup>, BORBA, EDUARDO L.<sup>6</sup> and CHASE, MARK<sup>7</sup>

**Assessment of generic limits and floral evolution in subtribe Spiranthinae (Orchidoideae, Cranichideae) based on phylogenetic analysis of plastid and nuclear DNA sequences**

**S**piranthinae comprise about 400 species of terrestrial orchids largely restricted to the Neotropics, representing one of the major radiations of subfamily Orchidoideae in the New World. Phylogenetic relationships in the subtribe were inferred using parsimony and Bayesian inference of over 5000 bp of combined DNA sequences (nuclear ribosomal ITS region, plastid *matK/trnK* and *trnL/trnF* regions) for ca. 200 individuals representing 165 species of Spiranthinae and suitable outgroup taxa. Our data show that morphologically distinctive, monotypic genus *Discyphus* does not belong to Spiranthinae and recovers *Cotylolabium* as sister to a strongly supported group that includes four main lineages, namely the *Stenorrhynchos*, *Pelexia*, *Eurystyles*, and *Spiranthes* clades. Our results reveal instances of generic polyphyly associated with convergence in floral morphology, either as a result of independent adaptation to a same pollinator group (e.g. hummingbirds in *Stenorrhynchos* s.l.) or of structural simplification due to a reduction in flower size (e.g. *Brachystele*). The recent proliferation of new genera based on single floral characters or character combinations is for the most part incompatible with strongly supported clades in our molecular trees and results in many genera becoming paraphyletic. This problem is particularly critical in the *Pelexia* clade, with no less than four "genera" embedded in *Cyclopogon* and three in *Pelexia*. Floral features associated with hummingbird pollination, such as a showily colored floral tube and a hard, pointed rostellum are reconstructed as plesiomorphic in the subtribe but this syndrome evolved secondarily in bee-pollinated lineages at least two additional times. Our study confirms previous suggestions of evolutionary lability in floral characters directly involved in pollination and provides a firm ground for a revised generic classification of Spiranthinae

<sup>1</sup>Instituto de Biología, Universidad Nacional Autónoma de México, Departamento de Botánica, Mexico City, Distrito Federal, Mexico <sup>2</sup>Universidade Estadual de Feira de Santana, Departamento de Ciências Biológicas, Feira de Santana, Bahia, Brazil <sup>3</sup>Centro Politécnico, Universidade Federal do Paraná, Departamento de Botânica, Setor de Ciências Biológicas, Curitiba, Paraná, Brazil <sup>4</sup>Universidade Federal de Minas Gerais, Departamento de Botânica, Belo Horizonte, Minas Gerais, Brazil <sup>5</sup>Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Rio de Janeiro, Brazil <sup>6</sup>Universidade Federal do ABC, Centro de Ciências Naturais e Humanas, Santo André, São Paulo, Brazil <sup>7</sup>Royal Botanic Gardens, Kew, Jodrell Laboratory, Richmond, Surrey, UK

550 ENDARA, LORENA\*<sup>1</sup>, WHITTEN, W. MARK<sup>2</sup> and WILLIAMS, NORRIS<sup>2</sup>

**The preliminary phylogeny of *Scaphosepalum* (Orchidoideae) suggests speciation patterns strongly influenced by the Andes**

**T**he neotropical orchid genus *Scaphosepalum* (Pleurothallidinae) encompasses 49 species and reaches its diversity peak in the montane forests of the northern Andes. *Scaphosepalum* is an ideal system to explore speciation patterns and the effects of the Andes as a dispersal barrier since it is common to find several narrow endemic species living in sympatry. The objective of this research project is to reconstruct a phylogeny using molecular and morphological characters, and use it as a phylogenetic framework to evaluate if the current distribution of the species is the result of sympatric speciation or allopatric speciation followed by secondary contact. The phylogeny of *Scaphosepalum* was obtained from the amplification and sequencing of the nuclear regions ITS, *pgiC*, *xdh* and the plastid regions *trnL-F*, *matK*, and *ycf1*. The congruence of the data sets corresponding to different gene regions was evaluated previously been combined. The single and combined data sets were analyzed under Maximum Parsimony, Maximum Likelihood, and Bayesian approaches and all obtained similar results. The results of the molecular phylogeny suggest a prevalence of allopatric speciation in the system and a strong geographic structure that reaffirms the importance of the Andes as a dispersal barrier since two almost identical clades were recovered by all the approaches: a mainly Central American-Northwestern Ecuador clade and Eastern Andes-Guyana Shield clade. The morphological dataset is currently being generated using 366 herbarium specimens and preliminary morphological information coincides with the molecular phylogeny reconstruction. Funding: American Orchid Society, San Diego County Orchid Society, International Association of Plant Taxonomists, National Science Foundation, American Society of Plant Taxonomists.

<sup>1</sup>University of Florida, Department of Botany / Florida Museum of Natural History, Dickinson - FLNHN, Gainesville, FL, 32611, USA <sup>2</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA

**Geo-ecological patterns of distribution among the varieties of scentbottle orchids, *Platantheradilatata*, based on GIS**

**E**colological analyses provide a complementary means of studying evolutionary responses to landscape variation. In this study, we examined environmental variation across populations of *Platantheradilatata* (Orchidaceae) identified from herbarium records and field collections using niche models based on numerous environmental variables to understand if divergence within this species is associated with ecological factors. *Platanthera dilatata* comprises three varieties, *dilatata*, *albiflora* and *leucostachys*, which are recognized based on differences in floral morphology and geographic range. Genetic studies have also indicated recent and active divergence in this species. If the varieties are geographically isolated, then allopatric divergence could be a leading cause of the genetic and morphological divergence we see in this species. Here, we test the hypothesis that the varieties are ecologically distinct in western North America. Niche models predicted similarly suitable areas for vars. *dilatata* and *leucostachys* in some areas, and models for vars. *dilatata* and *leucostachys* suggest similar environmental variables are responsible for the populations we examined in western North America. Relatively few populations of var. *dilatata* occur in the coastal ranges of the Pacific Northwest, which suggests that the dry habitat between the Rocky Mountains and Pacific Coastal ranges could have limited westward colonization from the Rockies and fragmented coastal populations, thereby stimulating localized divergence of these varieties. Some of the variables predicted from niche models suggest different environmental variables are important to var. *albiflora*. This taxon is common in the southern Rockies, absent from coastal areas of the Pacific Northwest, and occurs in coastal areas of Canada and Alaska. Although it has been suggested that var. *albiflora* maybe limited to higher elevations than either of the other varieties, we did not find this variable to be of great importance in niche models for this taxon. These analyses will be helpful for identifying areas to target for population sampling to better understand genetic patterns of divergence and the underlying causes of evolutionary divergence in *P.dilatata*.

Mississippi State University, PO Box GY, Mississippi State, MS, 39762, USA

**Phylogenetic Structure In Amaryllidaceae Tribe Hippeastreae (Asparagales) Gains Resolution With An Expanded ITS Tree**

**A**maryllidaceae tribe Hippeastreae constitutes a horticulturally valuable group of petaloid monocots; however, its taxonomy at the generic level has been controversial, with several segregates proposed during the last 40 years. Previous phylogenetic analyses of the nrDNA ITS/5.8S region showed that certain genera are not monophyletic, but lacked good representation of Chilean-Argentinean groups. The hypothesis of possible early lineage reticulation in the tribe was suggested. We have expanded the taxon sampling for this data set by including members of the Chilean endemic genera and additional species of Habranthus, Rhodophiala, Rhodolirium, Sprekelia, and Zephyranthes. A total of approximately 110 species corresponds to more than 60% of the tribe's species-level diversity. The tribe comprises two major clades: a) Traubia, Placea, Phycella, Rhodolirium, and Famatina maulensis, characterized by n = 8, lack of polyploidy, and a capitate stigma, and b) Rhodophiala, Habranthus, Hippeastrum, Sprekelia, Zephyranthes, and the remainder of Famatina, characterized by several basic chromosome numbers ranging between n = 6 - 11, and frequent polyploidy and aneuploidy. No clear morphological features diagnose the latter clade. The first group appears to be composed of three main subclades, each with high bootstrap support (≥99%). The other major clade appears to be composed of four lineages with unresolved relationships, as shown in previous studies based on ITS and plastid regions, even though the latter have been poorly sampled in terms of taxa. Certain species within Hippeastrum, Rhodophiala, Placea, and Phycella have identical or almost identical sequences to others, implying interspecific nrDNA concerted evolution and/or perhaps rapid radiations within these groups. We are currently working with low-copy nuclear genes and several plastid regions to test further this ITS-based phylogenetic hypothesis. A robust phylogenetic framework will serve as a basis for reclassification of the group and for study of its chromosomal evolution, and will facilitate several tests of the ancient inter-clade reticulation hypothesis in Hippeastreae.

<sup>1</sup>University Of Florida, Florida Museum Of Natural History, Dickinson Hall, Gainesville, FL, 32611, USA<sup>2</sup>USDA-ARS-SHRS, UNITED STATES DEPARTMENT OF AGRICULTURE, 13601 Old Cutler Road, Miami, FL, 33158, USA<sup>3</sup>University of Florida, Florida Museum of Natural History, Gainesville, FL, 32611, USA<sup>4</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA

553 MASHAYEKHI, SAEIDEH\*<sup>1</sup> and COLUMBUS, J.<sup>2</sup>

**Leaf anatomy of *Allium* (Alliaceae) subgenus *Amerallium* with a focus on the North American species**

The genus *Allium* (Alliaceae) is distributed over mid-latitude regions from the dry subtropics to the boreal zone. It includes ca. 850 species total, with 84 species in North America. The main center of diversity extends from the Mediterranean Basin to central Asia and Pakistan. A second center of diversity occurs in western North America. Thirteen subgenera are recognized. Subgenus *Amerallium* is divided into two clades: New World and Old World. Most of the New World species are in subgen. *Amerallium* and occur in California (ca. 50 species) and Texas (ca. 14 species). New World species have been placed into eight alliances based on morphological similarities. Characteristics of subgen. *Amerallium* include one-nerved tepals, one row of vascular bundles in the leaf, absence of leaf palisade parenchyma (if present, secondarily evolved from spongy mesophyll), and the presence of subepidermal leaf laticifers. Thus far we have sampled 70 New World and Old World species for transectional leaf anatomy. Permanent slides of sections from the middle of the blade were examined. The sections reveal a surprising amount of variation in both round and flat leaves in terms of arrangement of mesophyll cells and vascular bundles. A separate ongoing study involves the molecular phylogenetics of New World *Allium*. The anatomical variants of the leaves will be discussed in context of the phylogeny.

<sup>1</sup>Rancho Santa Ana Botanic Garden, 1500 N. College Ave., Claremont, CA, 91711-3157, USA <sup>2</sup>Rancho Santa Ana Botanic Garden, 1500 North College Avenue, Claremont, CA, 91711-3157, USA

554 RYAN, SEAN\* and SIMPSON, MICHAEL G.

**Molecular Phylogenetic Relationships and Character Evolution of *Fritillaria* subgenus *Liliorhiza***

*Fritillaria* subgenus *Liliorhiza* (Liliaceae) is an attractive group of mostly North American geophytes whose evolutionary history has not been fully explored. Abundant synonymy and inconsistent species delimitation need to be addressed in order to make appropriate conservation decisions regarding rare taxa in the group. The most extensive molecular phylogenetic study (Ronssted et al. 2005) included only 12 of the approximately 20-25 species in the subgenus. Recent morphology-based classifications (Santana, 1984; Rix, 2001) are in conflict and may be resolved by further morphological and molecular study. My study aims to determine phylogenetic relationships of all described taxa in the

group, to evaluate taxonomic classifications (including questionable species and varieties), and to explore morphological character evolution. To accomplish these goals, I will collect several specimens per taxon, sequence two chloroplast regions (rpl16 and matK) and nuclear ribosomal ITS and ETS, and study morphological characters offlowers, pollen, fruits, seeds, leaves, and bulbs. Preliminary results of molecular phylogenetic analyses and ancestral character state reconstructions will be presented. Previously hypothesized subdivisions based on morphology are partially supported in the molecular analysis, but a complete molecular dataset must be obtained before any definitive reclassification can be made. One moderately supported clade (pp=0.73) corresponds with Subsection *Affines* of Santana (1984) and Section B1 of Rix (2001) with a few exceptions. Another clade, though not supported, corresponds with Subsection *Liliorhiza* of Santana (1984) and Section B2 of Rix (2001). With regard to character evolution, "rice-grain bulblets" appear to be the ancestral state for the group, and have been lost once in a weakly supported clade of four species; whorled leaf arrangement appears to be the ancestral state for the group, and appears to have changed to alternate leaf arrangement a minimum of three times, with one reversal.

San Diego State University, Biology, Evolutionary Biology Program, 5500 Campanile Drive, San Diego, CA, 92182, USA

555 CELIS PACHECO, MARCELA<sup>1</sup> and SORIANO, SARA FUENTES\*<sup>2</sup>

**Pollen diversity and evolution in Tigridaeae (Iridaceae) in the context of recent molecular phylogenetic findings**

Tigridaeae, a diverse tribe of ca. 15 genera and 170 species, is restricted to the Americas. Although vegetatively uniform, the group exhibits sizeable variation in floral morphology, and differences in tepal orientation, color patterning, type of nectar produced, and structure of the stamens and style branches. In Tigridaeae the number of pollen apertures has been used to delimit the two subtribes (Tigridiinae, 2 sulci vs. Cipurinae, 1 sulcus). In this study we expanded the phylogenetic and palynological analyses of the South American Tigridaeae by studying for the first time the genus *Cardenanthus* and increasing the sampling of *Calydorea*, *Cypella*, *Herbertia* and South American *Tigridia*; making it the largest sampling of the tribe to date. The phylogenetic utility of pollen number of sulci and other palynological characters (e. g. pollen size, aperture size, pattern of pollen ornamentation, and lumina and muri size) was carefully evaluated within the tribe. Pollen evolution was studied in light of new molecular phylogenies based on the nuclear ribosomal internal transcribed spacer (nrITS) and five plastid DNA regions -- the non-coding *trnL-trnF*, the *trnL* intron, the non-coding *trnH-psbA* intergenic spacer, the *matK* gene, and the *trnK3* gene. Molecular phylogenetic and statistical analyses of the new palyno-

logical data suggested that differences in number of sulci, lumina size, muri size, and patterns of ornamentation are taxonomically and phylogenetically informative and can be used to distinguish some taxa and clades in Tigridae. The number of pollen apertures (i.e. two sulci) did not support the recognition of subtribe Tigridiinae as traditionally circumscribed, however bi-sulcate pollen supported the expansion of *Tigridia* to include seven other genera (*Ainea*, *Cardiostigma*, *Cobana*, *Colima*, *Fosteria*, *Rigidella*, *Sessilanthera*). Pollen number of apertures and ornamentation supported the recognition of the polyphyletic *Cypella* lineages. Our preliminary results indicate that pollen morphology is potentially useful for understanding phylogenetic relationships within the tribe Tigridae and should be further investigated.

<sup>1</sup>Universidad Nacional de Colombia, Apartado 7495, Bogotá, Colombia<sup>2</sup>Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166, USA

## 556 GRANADOS, CAROLINA<sup>1</sup> and SALAZAR, GERARDO<sup>\*2</sup>

### Phylogenetic relationships of the *Tillandsia erubescens* group (Bromeliaceae) based on plastid DNA sequences and morphology

We assessed monophyly and interspecific relationships of the *Tillandsia erubescens* species group of subgenus *Tillandsia* using separate and combined parsimony analyses of DNA sequences of three regions of the plastid genome (*matK-trnK*, *trnH-psbA* and *trnD-trnT*) and 26 morphological characters. We analysed exemplars of 32 species, including 8 ingroup taxa, representatives of various other lineages of *Tillandsia* and one species each of *Vriesea* and *Catopsis* as outgroups. The combined analysis of all plastid and structural data support the monophyly of the group and provide enough resolution to discern the phylogenetic relations among its species. Monophyly of the *T. erubescens* group is supported by two morphological synapomorphies: absence of floral bracts and descending flowers. Two species of the ingroup are new to science and were discovered during this study. Our results recovered morphologically distinctive *T. achyrostachis* as sister to the *T. erubescens* group and the clade [*T. prodigiosa*-*T. carlos-hankii*-*T. bourgaei*] is their next closest relative. The evolution and taxonomic value of selected reproductive characters is discussed

<sup>1</sup>Research Group Spermatophytes, Department of Biology, Ghent University, Ghent, Belgium<sup>2</sup>Instituto de Biología, Universidad Nacional Autónoma de México, Departamento de Botánica, Mexico City, Distrito Federal, Mexico

## 557 LICHTENWALD, SAMANTHA<sup>\*1</sup>, FLEMING, SAMANTHA<sup>1</sup>, SHIELS, DEREK<sup>2</sup> and MONFILS, ANNA<sup>3</sup>

### A phylogenetic analysis of North American *Schoenoplectus* and *Schoenoplectiella* (Cyperaceae)

*Schoenoplectus sensu lato* (Cyperaceae) is a genus of annual and perennial monocots with a cosmopolitan distribution, predominantly occurring in wetlands. Species in the group are notoriously difficult to describe; species are defined based on few cryptic characters and hybridization is rampant. Recent taxonomic revision in the group has resulted in a more narrow circumscription of *Schoenoplectus* and the erection of a new genus *Schoenoplectiella*. In North America there are 23 species and varieties of *Schoenoplectus* or *Schoenoplectiella*, many of these still require taxonomic revision to determine and designate generic status. To investigate diversity, resolve generic status and elucidate relationships among taxa and genera in North American *Schoenoplectus sensu lato*, we conducted a molecular phylogenetic analysis of the nuclear ribosome ITS region and a second independent DNA dataset from the *trnTLF* chloroplast regions. Phylogenetic evidence was examined relative to morphological data from field collections and voucher specimens from across North America. The resulting phylogenetic analysis including North America's *Schoenoplectus sensu lato* species and all GenBank accessions will be presented representing the largest study of *Schoenoplectus sensu lato* diversity yet conducted. This data will be presented relative to proposed taxonomic revisions in North American species and species complexes and a global re-circumscription of the genera.

<sup>1</sup>Central Michigan University; Biology, 217 Brooks Hall, Mount Pleasant, MI, 48858, USA<sup>2</sup>Central Michigan University, Biology Department, 217 Brooks Hall, Mount Pleasant, MI, 48858, USA<sup>3</sup>Central Michigan University, 180 Brooks Hall, Mount Pleasant, MI, 48859, USA

## 558 SHIELS, DEREK<sup>\*1</sup> and MONFILS, ANNA<sup>2</sup>

### A global re-circumscription and definition of *Schoenoplectiella* (Cyperaceae)

*Schoenoplectiella* Lye, is a recently segregated, cosmopolitan genus currently defined with 31 species formerly recognized as *Schoenoplectus*. *Schoenoplectiella* species were initially separated from *Schoenoplectus* based on their mostly annual habit, amphicarpic flowers and closer genetic relationship to species in *Eleocharis* than *Schoenoplectus*. Additional phylogenetic studies sampling more genes and taxa and morphological analysis of achenes and pollen by later authors further

supported the paraphyletic nature of *Schoenoplectus sensu lato* and the need for systematic revision. The data from these studies reveals two major groups that fall along the same line separating two of the four *Schoenoplectus sensu lato* sections (Sections *Schoenoplectus* and *Malacogeton*) from sections *Actaeogeton* and *Supini*. There are eight species of section *Actaeogeton* that remain classified as part of *Schoenoplectus sensu stricto* and key diagnostic morphological characters have not been defined to fully delineate *Schoenoplectiella* and *Schoenoplectus sensu stricto*. Additionally, there are 14 *Schoenoplectus sensu stricto* species from Africa that have not been given sectional designations and appear to conform to sections *Actaeogeton* and *Supini*. Data from a phylogenetic study of 23 North American *Schoenoplectus sensu lato* taxa, taxonomic literature and herbaria specimens have been studied to (1) propose a global re-circumscription of *Schoenoplectiella* and (2) define the boundaries and key diagnostic morphological characters of *Schoenoplectiella*, *Schoenoplectus sensu stricto*, and sections within each genus. A preliminary re-circumscription will be presented.

<sup>1</sup>Central Michigan University, Biology Department, 217 Brooks Hall, Mount Pleasant, MI, 48858, USA<sup>2</sup>Central Michigan University, 180 Brooks Hall, Mount Pleasant, MI, 48859, USA

559 JUNG, JONGDUK\* and CHOI, HONG-KEUN

### A Preliminary Study for Phylogeny Inference within Cyperaceae Based on a Low Copy Sequence, Low Silicon Mutant Gene 2

Phylogenetic relationship within Cyperaceae is not clear yet although molecular phylogenetic analyses based on the several kinds of sequences, such as nuclear ribosomal internal transcribed spacer (ITS), large subunit of ribulose biphosphate carboxylase gene (*rbcL*), and chloroplast *trnL* intron and *trnL-F* intergenic spacer (*trnL-F*). The three sequences are reasonable to infer phylogenies of many vascular plants. In contrast, phylogenetic tree of Cyperaceae using *rbcL* has insufficient resolution and aligned sequences of non-coding regions (e.g. ITS or *trnL-F*) frequently have ambiguity due to large inserts/deletions. Rapid concerted evolution was reported from high copy sequences (e.g. ITS) and often generate misleading trees. To improve low resolution or to inhibit erroneous interpretation, nuclear single or low copy sequences (e.g. *LEAFY*) have been used in phylogenetic analyses of flowering plants and are very effective to investigate reticulate evolution or detail relationships. Suitable gene or region is strongly needed to infer phylogeny of Cyperaceae, which has unclear phylogenetic relationship, reported numerous polyploidy, and hybrid. Low silicon mutant gene 2 (*Lsi2*), related to transport of silica, was chosen as candidate of the suitable gene because silica accumulation is higher than

other flowering plants and silica bodies are observed frequently in Cyperaceae. Primer pairs were designed based on rice *Lsi2* and sequences of 48 types were determined from 23 Cyperaceae species. Sequences of *Lsi2* first exon have small variance (852-861 bp) in length while length of ITS and *trnL-F* sequences varied from 538 bp to 658 bp and from 784 bp to 1,050 bp respectively. Length of *rbcL* sequences from all species examined was constant (1,293 bp). Portion of parsimony informative characters in aligned sequences of *Lsi2* first exon are 24.4% while 33.8%, 4.8%, and 25.1% of aligned ITS, *rbcL* and *trnL-F* are parsimony informative respectively. Low length variation (i.e. small inserts/deletions) and high proportion of parsimony informative characters shown in this study support that first exon of *Lsi2* are suitable for phylogenetic analysis of Cyperaceae.

Ajou University, Department of Biological Science, San 5, Woncheon-dong, Suwon, Gyeonggi-do, 443-749, South Korea

560 GARRETT, PATRICK C. \* and INGRAM, AMANDA L.

### The utility of the plastid *trnC-rpoB* locus in resolving phylogenetic relationships in *Eragrostis* (Poaceae)

*Eragrostis* Wolf is a genus of approximately 400 morphologically and anatomically diverse grasses distributed throughout the world's tropical and subtropical regions. DNA sequence data from nuclear GBSSI (*waxy*) and the plastid regions *rps16* and *trnL-F* have improved our understanding of *Eragrostis* evolution: all regions have provided insight into the circumscription of the genus, and GBSSI data produce a well-resolved phylogeny within *Eragrostis*. Cladistic analyses of the plastid loci, however, fail to resolve a large polytomy at the base of a clade encompassing the vast majority of *Eragrostis* species. Resolving these relationships is essential for understanding the ways in which allopolyploidy has influenced character evolution, so this study seeks to explore the potential of the *trnC-rpoB* locus in elucidating the evolutionary history of the genus. Sequences were obtained for a broad sample of *Eragrostis* species and were analyzed alone and in combination with *rps16* and *trnL-F*. *trnC-rpoB* alone did not vary sufficiently for resolving the divergence of core *Eragrostis*, but the combined analysis did show improved resolution.

Wabash College, Biology Department, PO Box 352, Crawfordsville, IN, 47933, USA

561 ESTEP, MATT C.\*<sup>1</sup>, VELA DIAZ, DILYS<sup>2</sup> and KELLOGG, ELIZABETH<sup>3</sup>

### Harvesting the cereals in search of phylogenetic signal

Some phylogenetic problems are difficult to resolve. Often adding more data can solve the problem, but which markers should be chosen remains as a critical question. While next generation sequencing and whole chloroplast genomes are being used increasingly, in some groups, particularly the grasses, chloroplast data is not sufficient to resolve complex patterns of polyploidy or rapid radiations. Alternatives to whole chloroplast genome sequencing are nuclear encoded loci, which have historically been difficult and expensive to identify and amplify. Over the last decade, extensive genetic and genomic resources have been developed to study agriculturally important plants. Teams of plant scientists have dissected many molecular pathways that influence plant architecture using the most sophisticated forward and reverse genetic screens. As a result, there is a plethora of nuclear encoded genes with known mutant phenotypes, many of which resemble the diverse morphological variation observed in natural groups of species and are the focus of our current research. In order to reduce the hurdles of employing nuclear loci in hard phylogenetic problems, we have developed a fast primer design methodology using Phytozome and Primacle and have converted the amplification, cloning, and transformation steps to a 96-well format. In less than 6 months, we have developed primers and successfully amplified 10 novel nuclear encoded loci and are working to sequence these from ~120 species in the grass tribe Andropogoneae.

<sup>1</sup>University of Missouri-St. Louis, Department of Biology, R223 Research building, St. Louis, MO, 63121, USA<sup>2</sup>University Of Missouri - St. Louis, Biology, 223 Research Building, One University Blvd., Saint Louis, MO, 63121-4499, USA<sup>3</sup>University Of Missouri - St. Louis, Department Of Biology, One University Boulevard, St. Louis, MO, 63121-4499, USA

562 CARSKADDON, JILL R.\*<sup>1</sup>, SPANGLER, SARA B.<sup>1</sup>, RICHARDS, TAMARA C.<sup>1</sup>, FISHER, AMANDA<sup>1</sup>, DENTON, AMYL<sup>2</sup> and KELCHNER, SCOTA<sup>1</sup>

### Three introns corroborate a first estimate of bamboo chloroplast phylogeny

Bamboos (Poaceae: Bambusoideae) include between 1,200 and 1,400 species, and are found in tropical to temperate areas worldwide. The evolutionary history of bamboos has been difficult to infer with comparative sequence analysis: problems include rapid radiation events, relatively slow rates of sequence evolution, limited variation in trialed nuclear loci, and lack of convinc-

ing resolution at key nodes in gene topologies. Although some researchers advocate a phylogenomic approach for problematic taxa like bamboos, a reasonable (and inexpensive) alternative might be to target loci that are strong phylogenetic performers. Three such introns were recently identified by the authors using multilocus comparisons with a corroborated chloroplast topology of 14 bamboo species. In the present study, we resample the taxon set of the Bamboo Phylogeny Group (BPG) and estimate a chloroplast phylogeny using sequence data from the *atpF*, *trnG*, and *petB* introns. Although our combined data set is only one third the size of the BPG alignment, it recovers all but two of the supported branches in the BPG estimation. Our analysis provides the first independent corroboration of the BPG chloroplast phylogeny for bamboos, and suggests that these three introns could be more widely used for phylogenetic inference in the grasses.

<sup>1</sup>Idaho State University, Department of Biological Sciences, 921 South 8th Avenue, Stop 8007, Pocatello, ID, 83209-8007, USA<sup>2</sup>California State University Channel Islands, Department of Biology, One University Drive, Camarillo, CA, 93012, USA

563 ATIA EISA, ATIA M.\*<sup>1</sup> and HILU, KHIDIR<sup>2</sup>

### Phylogeny of *Phleum*L. (Poaceae, timothy grass): species and polyploid evolution

*Phleum* L. (Poaceae, timothy grass) comprises about 15 species of worldwide distribution. It includes annual and perennial species with diploid and polyploid cytotypes based on  $x=7$ . The species are morphologically quite variable, contributing to difficulties in the assessment of species boundaries. A comprehensive systematic study for the genus is lacking. We present the first molecular phylogeny for the entire genus using the nuclear internal transcribed spacer (ITS) and the plastid *trnL-F* and *psbJ-petA* sequences to assess species relationships. Three major clades were recovered that coincide with the morphology-based sectional classification. The fourth clade consists of two morphologically different species, tetraploid *P. paniculatum* and diploid *P. nodosum*. These two species are traditionally placed in different sections, and lack morphological synapomorphies. Polyploidy appear to have evolved in one of the three major clade/sections, whereas the other two remain diploid. We also conducted a detailed morphological study of a number of vegetative and reproductive characters for all the species. Floret features are mapped on the tree to discern character evolution and their potential implication in the taxonomy of *Phleum*.

<sup>1</sup>Desert Research Center, Ecology and Range mangment, 1 mathaf Elmatariya st., Cairo, Egypt<sup>2</sup>VIRGINIA TECH, Department Of Biology, 2119 Derring Hall, BLACKSBURG, VA, 24061-0406, USA

564 DRUMWRIGHT, ABBY<sup>1</sup>, ALLEN, BRIAN<sup>2</sup>, RITCHEY, PATRICIA<sup>3</sup>, HUFF, KRISTA<sup>4</sup> and CAHOON, AUBREY\*<sup>3</sup>

### Survey and DNA Barcoding of Poaceae in Flat Rock Cedar Glades and Barrens State Natural Area, Murfreesboro, TN

A survey of grass species from the Flat Rock Cedar Glades and Barrens State Natural Area in Murfreesboro, TN was undertaken during the 2008 growing season with the goal of creating a comprehensive list of grass species living in a single glade environment. Twenty four different species were identified during the survey. All species had been previously recorded in Tennessee but two had not been noted in cedar glades, *Sporobolus clandestinus* and *Elymus hystrix*, and one, *Dichanthelium scoparium*, had not been collected in Rutherford County. The survey also provides information on species distribution within the glade, amount of sunlight exposure, and flowering time within the growing season. The plastid *matK* and *rbcl* genes and the *trnH-psbA* intergenic spacer region were sequenced from the specimens and are catalogued in GenBank. Variance analysis of each sequenced locus was conducted with the sequences produced in this study as well as GenBank archived sequences from other grasses. Our data conservatively suggest that the CBOL recommended loci, *matK* and *rbcl*, should enable Poaceae species identification with 95% accuracy.

<sup>1</sup>Pope John Paul II High School, 117 Caldwell Dr, Hendersonville, TN, 37075, USA<sup>2</sup>Siegel High School, 3300 Siegel Dr., Murfreesboro, TN, 37129, USA<sup>3</sup>Middle Tennessee State University, Biology, 1301 E. Main St., Box 60, Murfreesboro, TN, 37132<sup>4</sup>Middle Tennessee State University, Biology, 1301 E. Main St., Box 60, Murfreesboro, TN, 37132, USA

565 JONES, KATY\*<sup>1</sup>, HISCOCK, SIMON<sup>2</sup> and CARINE, MARK<sup>1</sup>

### What explains the Azores diversity enigma?

Macaronesia comprises the volcanic archipelagos of the Azores, Madeira, Canary Islands, Salvage Islands and the Cape Verdes, in the North Atlantic Ocean. Based on current taxonomic concepts, the Azores angiosperm flora is distinctive in that there are very few endemic taxa (c. 60 taxa) and of those, only a small proportion are Single Island Endemics (SIEs; 4%). In contrast, the Canary Islands have an extremely rich endemic flora of c. 607 species with a large proportion of SIEs. Island age, lineage age and habitat diversity alone do not provide satisfactory explanations for these differences. Several new hypotheses have been put forward to explain the differences observed; (i) high levels of undocumented extinctions in the Azores flora, (ii)

high dispersal ability of Azorean taxa, (iii) differences in climate across the Macaronesian archipelagos and (iv) inadequacies in the level of taxonomic knowledge of the Azores flora. Molecular analyses of several endemic lineages suggest that there may be a considerable amount of previously undocumented diversity in the flora. This poster presents a preliminary analysis of herbarium collections of Azorean taxa worldwide which suggest that hypothesis (iv) may help to explain the differences in the diversity patterns of endemic taxa between the Azores and the Canary Islands. Future plans for investigations to help resolve the 'Azores diversity enigma' are also outlined.

<sup>1</sup>The Natural History Museum, Department Of Botany, Cromwell Road, London, SW7 5BD, United Kingdom<sup>2</sup>Bristol University, Biological Sciences, University of Bristol, Woodland Road, Bristol, Oval, BS8 1UG, UK

566 DIGGS, JR., GEORGE M.<sup>1</sup>, LIPSCOMB, BARNEY<sup>2</sup> and BYERLEY, M. BROOKE\*<sup>2</sup>

### Ferns and lycophytes of Texas: a 55-year update

The last statewide treatment of Texas pteridophytes was published in 1956 by Donovan Stewart Correll. Since that time much has changed in taxonomy. By investigating the current literature and herbarium collections around the state, we have compiled a much-needed update for this region. We show that Texas now hosts 146 total native and naturalized pteridophyte taxa representing 138 species, a 28% increase in species richness. Of these species, 127 are native, more than any other state in the continental United States. Texas has representatives from seven of the 11 current fern orders (Equisetales, Ophioglossales, Osmundales, Polypodiales, Psilotales, Salviniiales, and Schizazeales) and 19 different fern families. Also present are members from all three extant lycophyte families, including the endemic *Isoetes lithophila*. Biogeographic patterns show the vast majority of Texas pteridophytes are concentrated in three vegetational regions: the deciduous forests of East Texas, the Edwards Plateau region of Central Texas, and the Trans-Pecos region of West Texas. We propose that the high species richness in Texas is due predominantly to latitudinal gradient, proximity to source floras in eastern U.S. and Mexico, and high habitat diversity. Additional GIS analysis is forthcoming pending the completion of current herbarium collection georeferencing projects.

<sup>1</sup>Austin College, Department of Biology and Center for Environmental Studies, Sherman, TX, 75090, USA<sup>2</sup>Botanical Research Institute of Texas, 1700 University Drive, Fort Worth, TX, 76107, USA

567 DEAN, ELLEN<sup>\*1</sup>, THOMSEN,  
CRAIG<sup>2</sup> and HARRINGTON, GORDON<sup>1</sup>

### **Initial Floristic Prospecting in the BLM Cache Creek Wilderness, Lake County, CA**

The Bureau of Land Management's Cache Creek Wilderness is a roadless natural area in Lake County with unexplored botanical resources. The Wilderness and the adjacent Bear Creek Ranch together form the BLM Cache Creek Natural Area. In 2010, with funding from the National Landscape Conservation System, preliminary surveys for special-status plants were conducted during eight visits to the Wilderness. We mapped eight California Rare Plant Rank list 1B and five California Rare Plant Rank list 4 plants in the Wilderness and encountered many rare plant communities and fascinating landscapes. Most of the special-status plants that we mapped were on serpentine-influenced substrates. A large serpentine barren with waterfalls and serpentine riparian vegetation is present near the southern border of the Wilderness, one of many areas in the Wilderness that need further exploration. Herbarium specimen vouchers from this study were incorporated into the herbarium at the UC Davis Center for Plant Diversity. The plant species recorded during this study were added to the existing plant list of the adjacent BLM Bear Creek Ranch to create a joint plant list for the Cache Creek Natural Area.

<sup>1</sup>UC Davis Center for Plant Diversity, Plant Sciences, m.s. 7, One Shields Ave., Davis, CA, 95616, USA<sup>2</sup>UC Davis, Plant Sciences, m.s. 1, One Shields Ave., Davis, CA, 95616, USA

568 BOBICH, EDWARD GEORGE<sup>\*1</sup>  
and EWERS, FRANK<sup>2</sup>

### **Resurrecting, Reorganizing, and Refocusing the Cal Poly Pomona Herbarium: Creating an Active Learning Environment While Maintaining a Trading Herbarium in LA County**

The Cal Poly Pomona (California) Herbarium had built an extensive synoptic and teaching collection up until the year 2000, when much of the collection was donated to other local herbaria and the specimens that remained were moved to several different locations on campus. By the late 2000s the fate of the herbarium was uncertain due to a lack of funding, maintenance, and interest. In spring of 2008 it was decided, at the urging of several bright, diligent, and eager students who were taking California Flora (BOT 343) at Cal Poly Pomona, to save the herbarium and refocus the collection on the flora of the San Jose Hills, which are part of the important wildlife corridor that connects the San Gabriel Mountains of the Transverse Ranges to the Santa Ana Mountains of the Peninsular Ranges. Since 2008, nine students have devoted their time to restoring and cata-

logging the specimens that were collected on the natural lands of the current campus and at the original Voorhis campus in San Dimas, California. The students have also collected new specimens, including five species previously undocumented in the area. The actively trading herbarium (Index Herbariorum acronym CSPU), has 763 specimens representing 244 species. In addition to being an excellent teaching tool where students learn how to do curatorial work, properly collect specimens, and learn about the many uses of herbaria, the herbarium will bring more attention to the need to preserve the natural areas of the San Jose Hills, which have been greatly reduced in the last two decades due to urbanization.

<sup>1</sup>California State Polytechnic University, Pomona, Biological Sciences, 3801 W. Temple Ave., Pomona, CA, 91768, USA<sup>2</sup>California State Polytechnic University, Pomona, Department of Plant Biology, 3801 West Temple Avenue, Pomona, CA, 91768, USA

569 APPLEQUIST, WENDY L.<sup>\*1</sup>,  
KUHLMAN, ALYSE R.<sup>1</sup>, SOLOMON, JAMES  
C.<sup>2</sup>, LOWRY II, PORTER P.<sup>2</sup>, BUSSMANN,  
RAINER<sup>1</sup> and MAGILL, ROBERT E.<sup>2</sup>

### **The Missouri Botanical Garden's DNA Bank: Expanding opportunities to serve the American systematics community**

The Missouri Botanical Garden's William L. Brown Center maintains a repository of leaf samples preserved in silica gel that are made available to support molecular studies of plant systematics and evolution. This collection comprises over 11,000 accessioned samples, collected from 55 countries and representing 368 families and 2502 genera. About 1600 samples have been distributed, the majority to US-based researchers. Fifteen countries are represented by more than 100 samples (the top four being the United States, Madagascar, New Caledonia, and Bolivia), as are seventeen angiosperm families (by far the most strongly represented being Asteraceae, with over 2200 samples). Over 400 bryophyte samples are also available. The collection therefore has great potential to facilitate the efficient and affordable conduct of molecular systematic studies. The distribution of samples reflects the Garden's international partnerships and collectors' interests; since such biases are probably inevitable, a national network of DNA banks is essential to provide comprehensive support to the botanical research community. We describe briefly the Missouri Botanical Garden's approach to the practical, legal, and ethical challenges associated with running a DNA bank and discuss options for further development. In particular, encouraging and facilitating sample contributions to DNA banks from collectors at institutions without DNA banks has the potential to increase both the scientific value and the utilization of these collections.

<sup>1</sup>Missouri Botanical Garden, William L. Brown Center, PO Box 299, St. Louis, MO, 63166-0299, USA<sup>2</sup>Missouri Botanical Garden, P. O. Box 299, St. Louis, MO, 63166-0299, USA

570 NARRO, MARTHA\*<sup>1</sup>, BOYLE, BRAD<sup>2</sup>, LU, JERRY<sup>3</sup>, HOPKINS, NICOLE<sup>1</sup>, PIEL, WILLIAM<sup>4</sup>, RAYGOZA GARAY, JUAN ANTONIO<sup>1</sup>, LOWRY, SONYA<sup>1</sup>, MATASCI, NAIM<sup>1</sup>, FREELAND, CHRIS<sup>5</sup>, MCKAY, SHELDON<sup>1</sup> and ENQUIST, BRIAN<sup>2</sup>

### The TNRS: a Taxonomic Name Resolution Service for Plants

Correcting and standardizing taxonomic names is a major challenge for virtually every field of plant biology. Even large organismal databases such as GBIF, SpeciesLink, VegBank, SALVIAS, TraitNet, GenBank and TreeBASE suffer from taxonomic error and uncertainty, with up to 30% of taxon-author strings unmatched to a validly-published name, and 5-20% of published names synonymous. Despite the growing availability of digitized sources of names<sup>1,2,3,4</sup>, identifiers<sup>2,4</sup> and taxonomic opinion<sup>3,5</sup>, the task of correcting taxonomy within existing data sets remains a time-consuming and largely ad hoc process. The need for tools for automated standardization of taxonomic names has never been greater. The TNRS, or Taxonomic Name Resolution Service<sup>6</sup> is an online tool for automated and user-assisted standardization of taxonomic names of plants. The result of collaboration between the iPlant Tree of Life project (iPToL), the Botanical Information and Ecology Network (BIEN), the Missouri Botanical Garden (MOBOT) and many others, the TNRS builds upon and extends existing open source solutions such as the GNI name parser and the Taxamatch fuzzy matching algorithm. The primary source of reference names and synonymy used by the TNRS is MOBOT's Tropicos database with additional sources to be added in the near future. Features include batch parsing and correction of misspelled names and authorities, extraction of embedded botanical annotations and morphospecies strings, conversion of synonyms to accepted names, flagging of inherently ambiguous names (e.g. pro parte synonyms) and the standardization of higher taxonomic categories such as family. Currently accessible as a publicly-accessible stand-alone version<sup>6</sup>, the TNRS will soon be available within the feature-rich iPlant Discovery Environment. A RESTful web service will provide additional functionality, such as the ability to discover and correct names of internal nodes of phylogenies. References:[1] [www.ipni.org](http://www.ipni.org), [2] [www.globalnames.org](http://www.globalnames.org) [3] [www.tropicos.org](http://www.tropicos.org) [4] [www.ubio.org](http://www.ubio.org) [5] [www.theplantlist.org](http://www.theplantlist.org) [6] <http://tnrs.iplantcollaborative.org>

<sup>1</sup>Plant Collaborative, University of Arizona<sup>2</sup>University of Arizona, Ecology and Evolutionary Biology<sup>3</sup>Cold Spring Harbor Laboratory, Plant Biology<sup>4</sup>Yale University, Peabody Museum of Natural History<sup>5</sup>Missouri Botanical Garden, Center for Biodiversity Informatics

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## Teaching Section

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*See also Grab that Research Baton and Teach: Bessey Award Winners and The fruitful outcome of graduate student-designed curricula: research modules, publishing opportunities, and outreach inspired by the NSF's Graduate STEM Fellows in K-12 Education (GK-12) Program.*

## ORAL PAPERS

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571 GOODWILLIE, CAROL

### Ecology, evolution and undergraduate education: pulling it all together in a long-term field experiment

A long-term study that addresses classic questions for undergraduates to participate in field research carried out at a large spatial and temporal scale. Since 2003, undergraduate researchers at East Carolina University have investigated the effects of fertilizer and mowing on the plant community at a wetland site. In seven years of sampling the plant community, we have observed significant effects of the two treatments on species diversity and composition, abundance of obligate wetland species, and relative dominance of forbs, grasses and woody plants. We are currently expanding the study to investigate effects of the disturbance on genetic diversity of several dominant focal species and to test for adaptation to experimental treatments. Undergraduate biology courses associated with the site train students in field methods, data management and analysis and hypothesis testing.

EAST CAROLINA UNIVERSITY, Department Of Biology, Mail Stop 551, GREENVILLE, NC, 27858, USA

572 HENDERSON, FLOR\*<sup>1</sup>, VANDEBROEK, INA<sup>2</sup>, BALICK, MICHAEL<sup>3</sup> and KENNELLY, EDWARD<sup>4</sup>

### Creating botanical-cultural awareness in urban Community College students

Botanical education is a field of great importance to contemporary society. With population increase in urban areas there is a need to explore strategies to enhance opportunities for botanical teaching and learning. The City University of New York (CUNY) is one of the nation's largest urban universities, it includes twenty-three colleges, six of which are community colleges. Among these, Hostos Community College (HCC), the smallest, is located in the South Bronx. HCC serves a large Hispanic population, predominantly first or second generation Dominican immigrants. We devised a project to involve Dominican students in botanical education by incorporating their traditional cultural heri-

tage, and increase their cultural sensitivity. Dominicans comprise one of the largest Hispanic groups in New York City and have a rich tradition in botanically based health care. The pedagogical goals of the project were to provide students an opportunity to gain scientific research experience and build their cultural and language skills. This experience was part of a large scale project conducted by the Institute of Economic Botany at the New York Botanical Garden, whose focus was on gathering and studying medicinal plant knowledge of Dominicans living in New York City and the Dominican Republic. Students were trained to conduct interviews in Spanish, learn basic plant identification, and collect plant samples in the field. In addition they were introduced to phytochemical laboratory techniques for plant extraction in the phytochemistry lab of the Department of Biological Sciences at Lehman College. The students demonstrated great competence in their involvement in the project. Their social and language skills were extremely useful with social norms and with language regionalisms. Engaging students from underrepresented minorities in fields of science in collaboration with leading research institutions provides unique opportunities to reinforce skills such as critical and analytical thinking, interpersonal relations, communication, cultural awareness and validation of traditional knowledge, all necessary talents for academic performance and professional success in our contemporary multicultural global society.

<sup>1</sup>Hostos Community College, CUNY, Natural Sciences Department, 500 Grand Concourse, A107G, Bronx, New York, 10451, USA<sup>2</sup>New York Botanical Garden, 2900 Southern Boulevard, Bronx, NY, 10548, USA<sup>3</sup>New York Botanical Garden, 200th St And Southern Blvd., Bronx, NY, 10458, USA<sup>4</sup>Lehman College, CUNY, Department of Biological Sciences, 250 Bedford Park Blvd. West, Bronx, NY, 10468, USA

**573 MICHEL, JOANNA\*<sup>1</sup>, KELLEY, MICHELE<sup>2</sup>, MAHADY, GAIL<sup>3</sup>, CACERES, ARMANDO<sup>4</sup> and SOEJARTO, DR. DJAJA D.<sup>5</sup>**

### **Ethnobotany and Youth Action Research: From the rainforest of Guatemala to the Urban Streets of Chicago**

This project reports both study results and applied action outcomes of a community collaborative inquiry to document cultural, environmental, and social factors associated with health beliefs and practices among the Q'eqchi Maya of Guatemala. Participant observation, interviews, and focus groups with midwives, *curanderos*, and community members revealed relationships between community member status, plant species used, and the location where collected. All healers expressed concern about the loss of medicinal species, the degradation of traditional knowledge and lack of interest among youth. Consequently, youth-oriented participatory action curricula were developed. These curricula, informed by ethnobotany, empowered youth

with the knowledge and skills to collect and preserve their own cultural heritage related to health. The curriculum includes field manuals, ethnomedical flash cards, a botany lab, a solar herb dryer, and plans for a rural herbarium. Implications for the adaptation of such curriculum to urban, immigrant Latino populations in the US are also discussed.

<sup>1</sup>University of Illinois at Chicago College of Medicine, Medical Education, 808 South Wood Street, Chicago, IL, 60612, USA<sup>2</sup>University of Illinois at Chicago School of Public Health, Community Health Sciences, 1603 W Taylor Street, Chicago, IL, 60612, USA<sup>3</sup>University of Illinois at Chicago College of Pharmacy, Pharmacy Practice, 833 South Wood, Chicago, IL, 60612, USA<sup>4</sup>Universidad de San Carlos, Facultad de Ciencias Químicas y Farmacia, Edificio T-10. Ap. Postal 1160, Zona 12, Guatemala City, 1160, Guatemala<sup>5</sup>College of Pharmacy, University of Illinois at Chicago, Chicago, Department of Medicinal Chemistry and Pharmacognosy, 833 S. Wood St., Chicago, IL, 60612, USA

**574 SHIPMAN, J\*<sup>1</sup> and KAPLAN, MONTY<sup>2</sup>**

### **The Effect of Higher Order Thinking Skills on Student Behavior and Classroom Management in the Urban Classroom**

Teaching higher order thinking skills is essential to an educated public in a democratic society. Public schools are encouraged to teach higher order thinking while also teaching content. Science teaching is no exception. Classroom experience has shown that as tasks requiring higher order thinking are implemented, aversive classroom behaviors may increase and positive behaviors may decrease. This paper will present data on science classroom activities involving higher order thinking and behaviors occurring. It also looks at the tasks of science education, and how they relate to higher order thinking, in terms of the resulting behaviors in an urban classroom setting.

<sup>1</sup>MAKTAG School, Www.read-about-it.blogspot.com, 54 Bryon Road-1, Chestnut Hill, MA, 1860 Rt 211 East, Middletown, NY, 10941, USA<sup>2</sup>Emerson College, Boston, MA, USA

**575 RYBCZYNSKI, STEPHEN M.\*<sup>1</sup> and SCHUSSLER, ELISABETH E.<sup>2</sup>**

### **Effects of inquiry vs. direct instruction on student attitude towards biology lab**

Scientific inquiry is a method of instruction thought to increase student attitude, however, conflicting results have been reported. An undergraduate introductory biology course (34 sections; 17 teaching assistants (TAs)) was delivered in two treatments, each with two levels: inquiry vs. direct instruction and explicit/reflective (ER) discussions vs. no ER (to foster nature of science understanding). Three modified subscales (12 Likert questions each) of the Fennema-Sherman Math-

ematics Attitude Scale were administered pre and post semester to assess student confidence, perception of usefulness, and effectance motivation. Participant pre- and post-semester scores ( $N = 357$ ) were summed and relative changes in attitudes were calculated. All subscales were reliable as measured by Cronbach's- $\alpha$  (0.95, 0.91, and 0.90 respectively). There were no significant differences among treatments or their interactions for confidence ( $p=0.50$ ), usefulness ( $p=0.37$ ), or motivation ( $p=0.95$ ) using a mixed-model ANOVA with treatment and interactions as a fixed effects and demographic variables within treatment as random effects. One-way ANOVA revealed significant differences among lab sections for confidence ( $p>0.000$ ) and motivation ( $p=0.02$ ) but not for gender, background, or career plans. Confidence was correlated with average section grades (Pearson's  $r=0.48$ ). These results indicate TAs and grades influence attitude more than instructional strategy and underscore the importance of TA training when undertaking curriculum reforms.

<sup>1</sup>Miami University, Botany, 700 East High Street, Oxford, OH, 45056, USA<sup>2</sup>University Of Tennessee, Department Of Ecology And Evolutionary Biology, 569 Dabney Hall, Knoxville, TN, 37996, USA

## 576 RICE, STANLEY

### Root Foraging: A General Botany Project that Demonstrates Plant Behavior

Many students think that plants are passive. The root foraging project is a way of demonstrating that plants have behavior. In this project, the students put alternating layers of potting soil (high nutrients) and perlite (low nutrients) into clear glass cylinders, then plant seeds at the top and maintain the plants for several weeks. As the roots grow into the alternating substrate layers, students can see and measure the proliferation of roots in soil vs. perlite. They measure root length and root weight in each layer. When the students used bean seedlings, they found that the roots had no difference between soil and perlite. They noticed root nodules. They concluded that roots of large-seeded plants, especially legumes, do not prefer rich soil. When the students used sunflower seeds instead, they found that the roots had a clear preference for rich soil. This project allowed the students to figure out how to avoid problems with experimental setup (how to water the plants without disturbing the layers) and design (how to avoid bias due to the sequence effect).

SOUTHEASTERN OKLAHOMA STATE UNIVERSITY, 1405 N. FOURTH, BOX 4027, DURANT, OK, 74701-0609, USA

## 577 STUESSY, CAROL\* and PETERSON, CHERYL ANN

### Behind the Scenes of the Virtual *PlantingScience* Learning Environment

Within the *Planting Science* learning environment, sponsored by the Botanical Society of America, scientist-mentors engage online with small groups of middle and high school students who think and act like scientists as they perform hands-on plant investigations in their classrooms. Students use the online platform to post scientific questions, observations, hypotheses, methods, and results. Scientist-mentors use the platform to review students' work and respond to students' posts with questions, comments, and encouragement. Both students and scientist-mentors engage in dialogues that vary in length, depth, and frequency. This presentation explains "what goes on" behind the scenes of the virtual online platform. We take our audience into the actual classrooms of three experienced science teachers. First we present a pedagogical model for the effective orchestration of the actual and virtual *PlantingScience* learning environment. The model is based on teachers' classroom enactments that focus on students' opportunities to engage in three sense-making strategies: (1) "practicing" science, (2) reflective discourse, and (3) representational fluency. To find support for the model, we observed at least two inquiry-based lessons (IBLs) in the classrooms of three *PlantingScience* teachers, which were videotaped and analyzed for evidence of the three sense-making strategies. We also analyzed online use of the *PlantingScience* platform, which revealed differences in students' engagement in the platform that corresponded with differences in teachers' classroom implementations. Results revealed associations of the three features proposed in the pedagogical model with students' engagement in the *PlantingScience* platform. Also associated with students' patterns of platform use and teachers' IBLs were teachers' beliefs; prior classroom experiences with inquiry, plants, and technology; and perceptions of support from school administrators and other teachers.

Texas A&M University, College Station, Teaching, Learning, and Culture, Mail Stop 4232, College Station, TX, 77840, USA

## 578 BARKWORTH, MARY\*<sup>1</sup> and GILBERT, EDWARD<sup>2</sup>

### SYMBIOTA: Providing tools for public engagement with collection information

Herbarium digitization enables increased access, visibility, and value for individual collections in addition to greater operating efficiency. It also offers new opportunities for engaging the public, k-12 teachers, and students with plants and collections but devel-

oping tools for such outreach takes time and money. SYMBIOTA is open source, community developed portal software that includes several outreach tools. These can be used with any group of organisms but their greatest use has been by herbaria. Because the software draws on resources provided by multiple collections and individuals, the task of generating functional versions of tools for a region is greatly reduced. These tools include generation of dynamic checklists and identification keys based on specimen data and management and publication of checklists generated from floristic research. The checklists themselves can be viewed either as lists of names (scientific or English), or with names supplemented by images. The images can be of living plants or of specimens, depending on the resources made available by contributors. Checklists can be used to generate flashcard quizzes and as the basis for games of "hangman". Species Profile pages can be generated by clicking on a scientific name at any stage. These pages include descriptions ( (currently from the *Flora of North America* and/or the Vascular Plants of Arizona project), images (of specimens and/or living plants), a dynamic distribution map, the English name, and resource links. Each component on these pages is linked to the underlying resource, enabling more detailed examination. The ability to create personal field guides from such pages is in development. Clearly, the value of such tools depends on the resources that contributors make available but the impact of each contribution is multiplied by SYMBIOTA, software created and managed by the scientific community but presenting information in a manner that is useful to a wide range of users, including novice botanists, students, teachers, and the general public.

<sup>1</sup>Utah State University, Department Of Biology, 5305 OLD MAIN HILL, Logan, UT, 84322-5305, USA<sup>2</sup>Arizona State University, Global Institute Of Sustainability, 2831 E. 18th St, Tucson, AZ, 85716, USA

## 579 SCHULZ, KATJA

### Encyclopedia of Life Version 2: A Preview of New Features and a Vision for a Global Collaborative Project

The Encyclopedia of Life (EOL, eol.org) is an unprecedented partnership between the scientific community and the public. Our goal is to build a freely accessible, reusable online collection of descriptive information about all species known to science. In its early phase, the project has focused on aggregating and indexing large amounts of materials from data partners ranging from natural history museums and international research consortia to members of popular sites like Flickr and Wikipedia. Growing and transforming this rich and diverse compilation into a comprehensive, coherent, and authoritative resource for research, teaching, and learning is a monumental task that can only be accomplished through the participation of many volunteer contributors, reviewers, and editors. To foster this

community, we will launch EOL version 2 in late summer/early fall 2011. Along with a more user-friendly site design, the new EOL will introduce tools and interactive technologies to facilitate collaborative knowledge discovery, content creation, and data management. In order to fulfill EOL's promise as a global project, we will also greatly improve our support for content and user interfaces in many different languages. To this end, we are working with organizations and institutions on five continents to establish global EOL partner sites focusing on content development for the flora and fauna of their particular region.

National Museum of Natural History, Encyclopedia of Life, 10th St. & Constitution Ave. NW, Washington, DC, 20560, USA

## 580 POULTON, JENNIFER

### Evaluating the accuracy of image search engines as potential learning tools for plant recognition

Image search engines provide easy access to an almost endless array of digital images on the internet. These search engines have the potential to act as powerful tools for learning sight recognition of plants. However, their usefulness as learning aids depends on their accuracy. The images retrieved must be high quality, relevant images, if they are to be useful in species recognition. In 2011, I challenged my students to learn to recognize 50 common wildflowers of the tallgrass prairie in hopes of increasing their awareness and appreciation of the plants living in their local environment (thereby reducing plant blindness). This species list was used to evaluate three popular image search engines: Google Images, Bing Images, and Picsearch. Using different search strategies and settings, I performed multiple searches for each plant species. The first 40 image results in each search were classified as useful, marginally useful, or not useful for species recognition. This study indicates that image search engines may be effective tools for learning sight recognition of plants if recommended search strategies are followed. Whereas most field guides only provide one or a few images of each plant species, image search engines produce many images, illustrating natural variation within species and different life stages. This approach may better prepare students for plant identification in the field.

Graceland University, Division of Science and Math, 1 University Place, Lamoni, IA, 50140, USA

581 PETERSON, CHERYL ANN\*<sup>1</sup> and STUESSY, CAROL<sup>2</sup>

### Comparing Students' Online Interactions: Does Teacher Workshop Attendance Make a Difference?

Inquiry-based learning (IBL) encourages students to think and act like scientists. The online IBL platform, *PlantingScience* (PS), developed by the Botanical Society of America, facilitates IBL interactions among students and scientist-mentors. We developed the Online Elements of Inquiry Checklist (OEIC; inter-rater reliability of 92.1%) to assess students' online IBL performance. In this exploratory study we compared IBL performance of two groups of students differing in their teachers' preparation. One group had teachers who were engaged in a PS-sponsored summer workshop; the other had teachers without the advantage of the workshop. We used the OEIC to compare IBL performance of 263 randomly selected groups of students who used either *Wonder of Seeds* and *Power of Sunlight* PS modules in Fall 2008 to Fall 2009 PS sessions. Randomization involved implicit sorting of groups by grade level and then selection by explicit variables of module, workshop teacher, and mentoring experience. *Wonder of Seeds* participants consisted of 214 teams (74 middle school), 41 teachers (9 workshop attendees), and 144 scientist-mentors. Participants using *Power of Sunlight* consisted of 49 teams (one middle school), 13 teachers (5 workshop attendees), and 42 scientist-mentors. Results indicate similar IBL performance in both groups. Students typically used the platform to discuss research questions, predictions, and design, but rarely discussed other IBL elements in detail. Students either rarely posted or had a tendency to engage in lengthy discussion. By individual sections of the OEIC, scientist-mentors posted less often than students, with the exception of experimental design and procedures sections, and rarely discussed other elements. Our online results are similar to previous investigations examining students' inquiry performance in face-to-face settings, which leads to questions about pedagogy for IBL. We suggest that teachers and scientist-mentors familiarize themselves with the OEIC and use it as a prompt to engage students' IBL. Students should be encouraged to examine other students' work posted on the PS website, as our results indicate underutilization of this valuable resource.

<sup>1</sup>Texas A&M University, College Station, Teaching, Learning, and Culture, Mail Stop 4232, College Station, TX, 77840, USA<sup>2</sup>Texas A&M University, TAMU 4232, Harrington Tower 443, College Station, TX, 77843-4232, USA

582 SHIPMAN, J

### Patterns of Internet Use on the Science Education and Science Literacy Website: [www.read-about-it.com](http://www.read-about-it.com)

Science education plays a role in effective, "Healing of the Planet." People "wired or wireless," to the internet, are reachable by science educators. Gathering data on this use informs our e-teaching. Developing/improving e-teaching needs data: how we use internet science sources. Data from 2004-2010 of internet use and reaction to the science literacy and education website, [www.read-about-it.blogspot.com](http://www.read-about-it.blogspot.com) are analyzed. Data presented will include: Countries of people frequenting the site, outreach links used most often, popular topics, and how botany topics compare to other topics. Since science outreach programs are available from numerous sources, including, but not limited to, the Botanical Society of America, NASA, and Plants Cafe, the site [www.read-about-it.blogspot.com](http://www.read-about-it.blogspot.com) links users to these and other outreach sites. In addition, it provides discussions and tools both to encourage informal science education, botany and other sciences in the curriculum, science literacy. Such tools, provided here conveniently, foster a knowledgeable public that can act wisely to prevent/alleviate environmental problems.

MAKTAG School, [www.read-about-it.blogspot.com](http://www.read-about-it.blogspot.com), 54 Bryon Road-1, Chestnut Hill, MA, 1860 Rt 211 East, Middletown, NY, 10941, USA

## POSTERS

583 GIBSON, J. PHIL\* and HOEFNAGELS, MARIELLE

### Tree-Thinking in Introductory Biology Evolution Education

Introductory-level biology majors are often overwhelmed by the amount of data supporting evolution that is typically condensed into only a few lectures "on evolution" during the semester. We are testing whether a curriculum based on Tree-thinking improves understanding and acceptance of evolution. Tree-thinking is an approach to evolution education based on the idea that there is a link between learning evolutionary theory and understanding how evolution is represented in phylogenetic diagrams. This curriculum infuses evolution throughout the semester, presents evolution as a topic for hypothesis testing and experimentation, and gives students experiences they can use to construct their own conceptual understanding of the topic. We present results of the first four semesters of the study, which indicate success with our curriculum, as well as preliminary data from a study of non-majors.

University of Oklahoma, Department of Botany and Microbiology  
Department of Zoology, Norman, OK, 73019, USA

### The Neotropical Ethnobotany Field School on Ometepe Island, Nicaragua

The 3 ½-week Neotropical Ethnobotany field school will be taught this summer through the Maderas Rainforest Conservancy on Ometepe Island, Nicaragua from July 22-August 16, 2011. The course instructors are Dr. Mark Merlin and Laura Shiels, Msc Botany and Herbalist. The course will focus on ethnobotany -- how people interact with ecosystems, and medical ethnobotany -- how people interact with medicinal plants. Students will learn from a combination of classroom-style lectures and hands-on activities. Students may also have the opportunity to conduct original ethnobotanical research. We will engage in several outdoor excursions and hikes in the attractive and diverse environments of Ometepe as part of the class. Major topics include the following:

Overview of the science of ethnobotany-Natural history, volcanism, botany, and ecology of Ometepe, a world heritage site- Comparison of natural history and ecology of the "old" and "new" world tropics-Land management, the environment, and health-Ethnobotanical research ethics, methods/techniques, and project design -Different perspectives from which to explore the relationship between people and plants-Botanical history of medicine-How plant medicines work in the body-Herbal medicine making and medicinal specimen collecting workshops-The food-medicine-poison continuum and food/herb-drug interactions-Conduct original ethnobotanical research in a unique cultural and ecological environment  
Course Objectives: - Gain a deeper knowledge and appreciation for the relationship between people and plants, and diverse cultures and ecosystems.-Learn how plants have contributed to society as we know it and how our relationship with plants shapes the future to come.-Learn how and why people have utilized plants as medicine, for material culture, for spiritual enlightenment.-Learn how people shape environments and the associated consequences for health and the environment.-Learn to conduct ethnobotanical research/improve research skills.-Contribute beneficially to the community and environment of Ometepe.-Develop meaningful friendships with people with similar interests.-Optional: Publish original research results.

University Of Hawaii At Manoa, Botany, 3190 Maile Way, St. John 101, Honolulu, Hawaii, 96822, USA

### Establishing a campus Arboretum: benefits and challenges

An Arboretum is being established at Delaware State University as a component of the educational programs of the Claude E. Phillips Herbarium (DOV). In 2006, a Campus Tree Walk was initiated, comprising 87 species of established mature campus trees which were labeled, and mapped on a brochure. These trees are used in teaching undergraduate and graduate courses, and in the Herbarium's outreach programs. Mortality of these labeled mature trees was 16% (14 trees), over the five year period from 2006 to 2011. Since other individuals of some of these species existed elsewhere on campus, total loss of species was 7%. The greatest cause of mortality was building construction (57%, 8 trees), followed by storm damage (21%, 3 trees), too large/too close to adjacent building (14%, 2 trees), and unknown causes (7%, 1 tree). Mortality of mature campus trees could be reduced by incorporating tree plantings into the campus master plan, and selecting appropriate species for mature tree size to plant near buildings. In 2010, an additional 57 young trees were planted to further increase tree diversity on campus. Mortality of the young trees planted last year was 5% (3 trees): 1 because of heat/drought, 1 broken, and 1 dying on arrival. These newly-planted trees were selected for their educational and ecological value; 61% were native to Delaware, and 39% non-native. Natives include American chestnut (*Castanea dentata*), hazelnut (*Corylus americanus*), American persimmon (*Diospyros virginiana*), butternut (*Juglans cinerea*), American crabapple (*Malus coronaria*), red mulberry (*Morus rubra*), American plum (*Prunus americana*), beach plum (*Prunus maritima*), chestnut oak (*Quercus prinus*), American linden (*Tilia americana*), American elm (*Ulmus americana*), and slippery elm (*Ulmus rubra*). Non-natives planted include horse-chestnut (*Aesculus carnea*), monkey-puzzle tree (*Araucaria araucana*), dove-tree (*Davidia involucrata*), and franklinia (*Franklinia alatamaha*). The University's curricula and community outreach are enriched by developing the campus trees into an Arboretum, with tree labels, brochure, map, and the planting of new tree species.

Delaware State University, Claude E. Phillips Herbarium, Department of Agriculture & Natural Resources, 1200 North Dupont Highway, Dover, DE, 19901, USA

586 ROBINSON, DAVE\* and LAU, JOANN

### Involvement of Your Botany Students In Biomedical Research: Join *The Ambrosia Project*.

Up to 20% of the human population develops hay fever in response to exposure to the pollen of Ragweed. It has been estimated that over one billion dollars is spent in the U.S. each year on the treatment of hay fever, causing millions of people to miss school or work. Pollen biology, therefore, is an excellent way to link plant science with medicine. A major source of allergenic pollen is Giant Ragweed (*Ambrosia trifida* L.), a common weedy plant. In spite of the huge public-health impact of this plant there are currently only seven nuclear DNA sequences from *A. trifida* in the NCBI nucleotide database (as of April, 2011). To examine gene expression in Giant Ragweed pollen we constructed a cDNA library using mRNA isolated from dehiscent male flowers. Our Botany students have been characterizing this library as one of their laboratory exercises for the past four years. *The Ambrosia Project* is a collaborative effort by which students randomly select cDNA colonies for plasmid purification, and perform restriction digestion and gel electrophoresis and then send the plasmids out for sequencing. Once sequenced, the students distinguish cDNA from vector and predict the translation product. Students do BLAST searches, learn about the gene product, and speculate on its function in plants. Already students have isolated cDNAs that are homologous to metallothionein, germin, osmotic-stress protein kinase, auxin response factor-2, and a sweet-tasting thaumatin-like protein. Numerous genes for allergenic proteins have also been identified, including lipid transfer proteins and pectate lyase. Students appear to enjoy the prospect of discovering unique genes in this uncharacterized species, and like seeing their names published in the NCBI EST database. At the same time they learn important molecular techniques and concepts that are applicable to other biological disciplines. We have already published 529 accessions in the NCBI EST database and are looking for instructors at other colleges and universities to collaborate with us in characterizing this library.

Bellarmine University, Biology, 2001 Newburg Road, Louisville, KY, 40205, USA

587 HARLEY, SUZANNE

### Using Case Studies in an Introductory Plant Form and Function Class

Case studies provide a way to introduce students to research design and the primary literature. In particular, the interrupted case study method described by Herreid in 2005 (*Journal of College Science Teaching* 35[2]: 4-5) allows for the stepwise presentation of back-

ground information, experimental design, data collection, and data analysis from a published paper. Pausing between each of these elements gives students time to work through the investigation as the authors did. I have incorporated several interrupted case studies into my Plant Form and Function class. This class is the introductory course for Botany majors and minors at Weber State University, an open enrollment, regional comprehensive institution in Ogden, UT. I will present cases that I have developed on mimicry-based defense against herbivory, autumn leaf coloration, and possible adaptations for interactions with birds that are now extinct.

Weber State University, Botany, 2504 University Circle, Ogden, UT, 84408-2504, USA

588 ICKERT-BOND, STEFANIE M.\*<sup>1</sup>,  
CICERO, CARLA C.<sup>2</sup>, COOK, JOSEPH A.<sup>3</sup>,  
EDWARDS, SCOTT V.<sup>4</sup> and LACEY, EILEENA.<sup>2</sup>

### AIM-UP! A research coordinating network to increase the use of museum collections in undergraduate education

Natural history collections provide invaluable resources for numerous aspects of undergraduate education, including instruction in evolution, biodiversity, and conservation. The value of these resources as educational tools, however, is often poorly understood, even at colleges and universities that maintain such collections. AIM-UP! is an NSF-funded Research Coordination Network (RCN) developed to increase awareness of natural history collections as critical resources for undergraduate instruction. Specific goals of the network include (1) training undergraduates in museum-based research, (2) developing instructional tools based on freely-accessible online museum databases, (3) informing educators at non-museum institutions regarding the instructional power of museum collections, and (4) interacting with the public to increase awareness of the educational importance of natural history museums. Each year of the initial 5-year project will emphasize a different conceptual theme: during our first year, the network has focused on developing integrated strategies for collecting and analyzing data from multiple taxonomic groups, each of which has distinct research and curatorial traditions. Starting with a seminar on this theme held at UNM (and attended electronically by network participants from other institutions), the network has developed an initial set of educational modules that draw upon the publicly-accessible ARCTOS database to provide students with hypothesis-driven, inquiry-based learning opportunities rooted in natural history collections data. Educators from all institutions- those with museums and those without- are encouraged to visit our website ([www.aim-up.org](http://www.aim-up.org)) and to consider partici-

pating in the network.

<sup>1</sup>University of Alaska, UA Museum of the North Herbarium & Dept. of Biology and Wildlife, 907 Yukon Dr., Fairbanks, Alaska, 99775, USA<sup>2</sup>Museum of Vertebrate Zoology, University of California Berkeley, Department of Integrative Biology, 3101 Valley Life Sciences Building, Berkeley, CA, 94820, USA<sup>3</sup>Museum of Southwestern Biology, University of New Mexico, Department of Biology, Albuquerque, New Mexico, 87131-0001, USA<sup>4</sup>Museum of Comparative Zoology, Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, MA, 02138, USA

**589 LAU, JOANN\* and ROBINSON, DAVE**

### **A six-week laboratory project in plant molecular biology and bioinformatics with subsequent publication in the NCBI GenBank.**

This project introduces molecular and bioinformatics techniques to students by having them isolate and characterize a housekeeping gene from uncharacterized plant species. The gene encodes Glyceraldehyde3-Phosphate Dehydrogenase (GAPDH), a pivotal enzyme of glycolysis. We have partnered with Bio-Rad Laboratories in the development of a complete kit for this project, called the "Cloning and Sequencing Explorer Series" (#166-5000EDU). Students start the project by extracting genomic DNA from a plant species, or cultivar, whose GAPDH has not been previously published. PCR is used to amplify a major portion of the GAPDH gene, which is then ligated to a vector for bacterial transformation. Once screened, putative clones are examined by restriction digestion and then sent off for sequencing. Once sequenced, students analyze the resulting DNA chromatograms using iFinch™ software made available by Geospiza, Inc. through purchase of this kit. This software allows students to assess the quality of their cloned-DNA sequence, distinguish between vector and GAPDH sequence, and compare it to already-published GAPDH sequences from other plants. Students can also determine gene structure, such as introns and exons. Student achievement was evaluated using pre-, mid-, and final-test assessments, as well as with a survey to assess student perceptions about the project. Student confidence about basic laboratory techniques and knowledge of bioinformatics tools was significantly increased upon completion of this exercise. This project differs from other biology lab exercises in that the final data can be published in the National Center for Biotechnology Information (NCBI) GenBank. This exercise has already resulted in the publication of at least 22 unique plant GAPDH sequences generated by students at high schools, colleges and universities throughout the country and includes species like begonia, coriander, thyme and spinach. The exercise can be repeated year after year, each time with a different plant species, or cultivar. This makes the project worthwhile for both students and instructors, and contributes

significantly to the study of GAPDH biochemistry and phylogenetics.

Bellarmine University, Biology, 2001 Newburg Road, Louisville, KY, 40205, USA

**590 SCHULZ, KATJA\*, HAMMOCK, JENNIFER, DEWEY, TANYA and PARR, CYNTHIA**

### **Encyclopedia of Life: Current Content Status and Plans for the Future**

Since its launch in February 2008 with 30,000 founding species pages, the Encyclopedia of Life (EOL, eol.org) has continuously expanded and enriched its content. On the EOL site, text and data from multiple sources are integrated and complemented by photographs, video, maps, etc. Expert curators ensure the quality of the core collection by authenticating materials submitted by diverse projects and individual contributors. Now in its fourth year, EOL has engaged well over one hundred data partners. Content is available for over 500,000 taxa, and more than 400,000 taxon pages feature materials that have been vetted by experts. Also, there are over one million taxon pages with links to literature, made available through the Biodiversity Heritage Library (BHL). Using topical or taxon-focused themes, we seek to galvanize communities to achieve specific content development goals. In addition, we are working with international institutions to establish region-specific encyclopedias, which will serve materials in their own languages and share local content with the rest of the world through the EOL main site. We always seek new collaborators, and we are continually adapting our policies and practices to meet user needs. We are confident that our approach will scale to meet increasing demands for biodiversity information, and we hope that increased access to online knowledge about taxa and biological systems will transform the science of biology and the public's understanding of life on Earth.

National Museum of Natural History, Encyclopedia of Life, 10th St. & Constitution Ave. NW, Washington, DC, 20560, USA

**591 MCCONNELL, JAMES**

### **Experiences Developing Plant Biology as an On-line Lab Course in Moodle**

The experiences of developing an on-line course in Plant Biology are presented. This course was originally delivered face-to-face. Over the last two years the course has evolved from face-to-face, to being a hybrid course, to being fully on-line, including the lab activities. Currently, the lab activities are done by students at home using a commercial lab kit which is supplemented with on-line images and discussion using Moodle.

University of Guam, College of Natural and Applied Sciences, Division of Agriculture and Life Sciences, Mangilao, GU, 96923, USA

592 MALLCHOK, MALIA<sup>1</sup> and THOMAS, MICHAEL\*<sup>2</sup>

### Applications of Mobile Cell Phone and QR Code Technologies for Botanical Education

An educational self-guided botanical audio tour was developed to evaluate two new technologies: Quick Response (QR) codes and mobile cell phone technology. The tour was implemented in a University of Hawai'i at Manoa campus botanical garden. Fifteen Polynesian introduced plants, commonly referred to as Canoe Plants, were selected for the self-guided audio tour. Introductory botanical, ethnobotanical, taxonomic, and historical narratives were authored for each species. Narratives were recorded and limited to about one minute per plant. Audio recordings were created using Audacity - a free, open-source software and saved as MP3 files. The audio tour was created using commercial audio tour service which provides online content management. The QR code tour utilized two-dimensional barcodes linked to a unique Uniform Resource Locator (URL). QR codes were generated using a free online QR code generator, Kaywa ([qrcode.kaywa.com](http://qrcode.kaywa.com)). Content for the QR code tour was hosted on a free online web hosting site ([www.weebly.com](http://www.weebly.com)). Each plant was labeled with its Hawaiian, common, scientific, and family names. In addition, the audio tour phone number, prompt number and a QR code were printed on each label. Thirty students participated in the 20 minute self-guided audio tour and participants completed a 17 question online survey. Results of the survey indicated the students responded positively to both tours and enjoyed using the technologies. A large majority (87%) agreed or strongly agreed that the technologies were easy to use and 86% agreed or strongly agreed that they would be interested in using these technologies again in similar environments. The length of the audio recordings were considered to be 'Just Right' by 87% of participants with 10% reporting that they were too long and 3% stating that they were too short. The project successfully developed a self-guided audio tour which has potential to be incorporated into undergraduate curricula as a laboratory assignment as well as to serve as a methodology to inform visitors about plants in the campus landscape.

<sup>1</sup>University of Hawai'i at Manoa, Technology & Distance Programs, Honolulu, HI, 96822, USA <sup>2</sup>University of Hawai'i at Manoa, Botany Department, 3190 Maile Way, Room 101, Honolulu, HI, 96822, USA

593 BAKER, STOKES\*<sup>1</sup> and SELBY, KAREN<sup>2</sup>

### Small fluorescent microarrays for use in undergraduate instruction

One of the goals stated by the National Research Council in Bio2010: Transforming Undergraduate Education for Future Research Biologists is undergraduate biology instruction should build greater expertise in mathematics and computer technologies. To support these goals, this project is developing affordable small microarrays to allow students to conduct hands-on experiments with fluorescent microarrays. An instrument is being developed that allow students to view and digitally record microarray fluorescence with dissecting microscopes. The first set of instructional materials will involve students assessing changes in *Saccharomyces cerevisiae* gene expression when growth conditions are altered. The instructional effectiveness of integrating digital imaging analysis and statistics into the student's laboratory instruction will be assessed by a combination of content tests and focus group interviews.

<sup>1</sup>University of Detroit Mercy, Biology Department, 4001 W. McNichols Rd., Detroit, MI, 48221 <sup>2</sup>University of Detroit Mercy, Department of Education, 4001 W. McNichols Rd., Detroit, MI, 48221,

594 OSTRIN, ZVI\*, TRACHMAN, JULIE and GILLEN, JOHN

### Student-driven Urban Fieldwork in Lichenology

Organismic biology fieldwork by urban community college students is subject to several constraints, including budgetary issues, travel time, and the limited science and natural history backgrounds of students, and is particularly problematical in the multilingual and predominantly minority student population at Hostos Community College, located in the South Bronx. We developed and have piloted a student-driven environmental field study that addresses these issues; the study involves mapping macrolichen populations in several areas of New York City and correlating differing levels of urban pollution with lichen species distribution and abundance. Initial implementation of this project has been successful, and the project will be expanded this summer. The pedagogical advantages of this study are manifold. Students involved in the project see the natural world in a new way: they learn that nature is all around, that patterns of ecological interaction are as close as the trees outside the college or their apartment building, and that societal choices have direct impact on the environment and human health. They learn to identify trees and lichens, and learn about symbiotic relationships among plants, fungi, and algae. They also learn in a practical hands-on way about experimental design,

close observation of organisms, statistical analysis, and the craft of writing a scientific paper. Costs involved in carrying out this study are minimal, making it ideal for biology departments constrained by limits on travel, equipment, and materials. Depending on the desired emphasis, the project can focus on the algal/fungal or plant/lichen symbiosis, or on the effect of environmental factors on lichen success and species distribution.

Hostos Community College, Natural Sciences, 475 Grand Concourse, Bronx, NY, 10451, USA

## 595 BUTTERWORTH, KARA

### Showcase of Student PlantingScience Projects

The PlantingScience program has provided students a unique opportunity to design their own research projects with the help of professionals in plant science. I had the pleasure of attending the PlantingScience Summer Institute in June 2010 and my students took part in the program during the 2010-2011 school year. A collection of student projects will be displayed.

Combs High School, 2505 E Germann Rd, San Tan Valley, AZ, 85140, USA

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## Tropical Biology Section

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### ORAL PAPERS

## 596 LUMER, CECILE

### Pollination of *Blakea purpusii* (Melastomataceae) by birds in Mexico

Pollination of *Blakea purpusii* (Melastomataceae) by birds in Mexico. The genus *Blakea* in the tropical family Melastomataceae is represented in Central America by two floral types. The most common are showy, open dish-shaped, pink and white flowers with a sweet scent. These flowers are buzz pollinated by several species of bees. However, the genus also contains species in which the flowers are green, lack scent, are cryptic, and hang below and within the foliage. Several of the green flowered species in Costa Rica are pollinated by small rats and mice. The most northern green-flowered species, *B. purpusii*, is found in Guatemala and Chiapas, Mexico on the sides of Volcan Tacana, adjacent to Guatemala. *B. purpusii* has several characters in common with the other green-flowered *Blakea* species. However, there is one important character which sets *B. purpusii* apart and which points to a difference in pollinators. The anthers of the rodent pollinated species are maroon, whereas the anthers of *B. purpusii* are yellow and the base of the inside of the petals is deep rose pink. *B. purpusii* is visited and pollinated by several bird species, including migratory birds. All species of *Blakea* studied were found to be self compatible. To date the evidence indicates that while birds may be involved in selfing, little autogamy occurs in *B. purpusii*.

Cochise County Herbarium, 1140 N Colombo Ave, Sierra Vista, AZ, 85635, United States

## 597 TERDAL, ERIK\* and TERDAL-VANDEVUSSE, RHEA

### Achioté (*Bixa orellano* L.) cultivation and preparation by Maya women in Belize, Central America

Annatto (*Bixa orellano* L.) is a neotropical shrub cultivated world-wide in tropical regions as a source of a natural food colorant. In Belize, annatto is known by the indigenous name achioté. We present preliminary data on the cultivation, harvest, processing, sale, distribution and use of achioté in the Cayo District. Our data was gathered as part of an ongoing study of medicinal plant use by the Maya in this area of Belize. Achioté-specific data for this presentation was gathered by semi-structured interviews in January, 2009, and March, 2010. We met with 15 people involved in the production and sale of achioté in one town and three villages. Cultivation is primarily by Maya-speakers and

entirely by women. The number of shrubs per household ranged from one to seven. Harvest and processing is done by women as seasonal work. Achioté is used in traditional stews for color and flavor as well as for perceived health benefits.

Terdal Farm, 15310 S Harvard Ave, Bixby, OK, 74008, USA

**598 LAGOMARSINO, LAURA\*<sup>1</sup>,  
ANTONELLI, ALEXANDRE <sup>2</sup> and DAVIS,  
CHARLES C.<sup>3</sup>**

### **Molecular Systematics of the Lobelioideae (Campanulaceae), with an Emphasis on the Primarily Neotropical CBS Clade**

The Lobelioideae is the largest subfamily within the Campanulaceae. It includes approximately 1,200 primarily tropical species. Nearly half of the species in the Lobelioideae fall within the single well-supported clade including the Neotropical genera *Centropogon*, *Burmeistera*, and *Siphocampylus* (the CBS clade<sup>2</sup>). Relationships within the largely Andean CBS clade are poorly understood: less than 7% of the species in this clade have been sampled, and existing phylogenies are not well supported. We present a phylogeny of the CBS clade inferred from four rapidly evolving plastid gene regions (ndhF-rpl32, rpl32-trnL, trnS-trnG-trnG and rps16-trnK) sampled from ~150 species. Our preliminary results indicate that two of the three genera, *Centropogon* and *Siphocampylus*, are not monophyletic. This increased phylogenetic resolution has important implications for their classification, biogeography, and pollination biology.

<sup>1</sup>Harvard University, Organismic And Evolutionary Biology, 22 Divinity Ave., Cambridge, MA, 02138-2625, USA<sup>2</sup>Gothenburg Botanical Garden, Carl Skottsbergs gata 22A, SE-413 19, Göteborg, Sweden<sup>3</sup>Harvard University, Organismic and Evolutionary Biology, 22 Divinity Ave, Cambridge, MA, 02138, United States of America

**599 AREVALO BURBANO, RAFAEL\*  
and CAMERON, KENNETH**

### **Phylogenetic relationships of *Mormolyca* Fenzl (Orchidaceae) based on chloroplast genes and ITS**

The genus *Mormolyca* Fenzl belongs to the subtribe Maxillariinae, which is one of the most conspicuous and diverse groups of Neotropical orchids. Distributed from southern Mexico to Peru and northwestern Brazil, the recently expanded circumscription of *Mormolyca* comprises ca. 25 species. With new species remaining to be described and questionable species boundaries to be clarified, this new concept of *Mormolyca* represents a challenge to the plant systematist concerned with taxonomy and nomenclature of Neotropical orchids. This genus is also especially ideal for studying broader phe-

nomena of biology, since many of the species are distinguishable by their unique floral fragrance and micro-morphology, characters assumed to play an important role in their insect pollination, through compensation or deceit. To further understand the structure, evolution, and species delimitation of *Mormolyca*, we construct a phylogenetic hypothesis using sequence data from five chloroplast regions (rpoC1, matK gene and flanking trnK intron, atpB-rbcL intergenic spacer, and the 3' portion of ycf1) and the internal transcribed spacer (ITS). Phylogenetic analyses support a monophyletic *Mormolyca*, even though relationships within the clade are at odds with current taxonomic classification. The obtained phylogeny also suggestst hat species found mostly in Central America are a monophyletic radiation derived from exclusively South American taxa. We are taking advantage of these phylogenetic hypotheses to address questions concerning the evolution of vegetative characters, floral fragrance profiles, and pollination mechanisms within *Mormolyca*.

**600 BENAVIDES, JUAN C.\*<sup>1</sup>,  
CRANDALL-STOTLER, BARBARA<sup>2</sup> and  
STOTLER, RAY<sup>3</sup>**

### ***Fossombronia peruviana* and Allied Species in Latin America - A Systematic Puzzle**

The northern Andean *Fossombronia peruviana* Gottsche & Hampe is the only Latin American taxon included by Schuster in the genus *Austrofossombronia* R. M. Schust. This segregate was differentiated from *Fossombronia* by large plant size, elongate rather than spheroidal capsules, capsule walls 3 or more cell layers in thickness, and its unique wetland habitat. In molecular phylogenies the species of *Austrofossombronia* have been resolved in multiple clades of *Fossombronia*, providing little justification for its recognition. Our recent expanded molecular analyses, coupled with comprehensive studies of living and herbarium specimens from throughout the Andean chain provide evidence for the recognition of more than one species in the *F. peruviana* clade. Populations that are morphologically referable to *F. peruviana* are widely distributed in wet, high elevation sites from Venezuela to Bolivia. Within the range of *F. peruviana*, we have discovered a second, as yet undescribed, genetically distinct sister species from several localities in Venezuela, which is, in turn, closely related to a third morphologically distinct element from Toluca Volcano, Mexico. Both gametophyte and sporophyte characters clearly differentiate the Mexican element from *F. peruviana*, and the Venezuelan element differs from both *F. peruviana* and the Mexican population in leaf insertion and antheridial anatomy. In the absence of female plants and sporophytes from the Venezuelan element, however, its relationship to the Mexican popu-

lation is equivocal. A single collection of a similar, large *Fossombronia* made by J. B. Hatcher in Feugia, which was identified as *F. naumannii* Schiffn. by Evans (1898. Bull. Torrey Bot. Club 25: 415), is not referable to that species, but appears to be, on the basis of morphology, aligned with the Venezuelan element. Although combined molecular and morphological data provide indisputable evidence of species level divergence between *F. peruviana* and allied elements in Mexico, Venezuela and Feugia, determining how the latter are related to each other requires more extensive sampling of high elevation Fossombronias along the Cordilleras of Latin America.

<sup>1</sup>Southern Illinois University, Department of Plant Biology, 1125 Lincoln Dr, LSII Bld Room 420, Carbondale, IL, 62, USA<sup>2</sup>Southern Illinois University, Department Of Plant Biology, 1125 Lincoln Avenue, CARBONDALE, IL, 62901-6509, USA<sup>3</sup>Southern Illinois University, Department Of Plant Biology, 1125 Lincoln Drive, CARBONDALE, IL, 62901-6509, USA

## POSTERS

### 601 GARWOOD, NANCY

#### Neotropical seedlings: The current state of our knowledge of this important stage in the life cycle and ways to improve it

I published a review of published information on Neotropical seedlings in my book, *Seedlings of Barro Colorado Island and the Neotropics* in 2009. At that time I did not calculate the percentage of Neotropical taxa for which seedlings have been identified because obtaining good estimates of the number of species in Neotropical families and genera was difficult when that part of the manuscript was prepared. Better estimates of Neotropical diversity are now available. Here I present data on that percentage by family, genus and species. Not surprisingly, the percent of taxa with at least one species with an identified seedling is high at the family level but lower at the generic level. Seedlings are known from only a small percentage of the more than 75,000 Neotropical angiosperm species. I also contrast seedling knowledge in families differing in number of genera and species and those that are primarily woody versus herbaceous. Lastly, I discuss strategies to improve seedling knowledge in the Neotropics.

Southern Illinois University, Life Science II, Mailcode 6509, Life Science II, Mailcode 6509, 1125 Lincoln Ave., Carbondale, IL, 62901, USA

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## Biogeography

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### ORAL PAPERS

#### 602 SHETH, SEEMA<sup>1</sup>, LOHMANN, LUCIA<sup>2</sup>, TRISH, DISTLER<sup>3</sup> and JIMENEZ, IVAN<sup>\*4</sup>

#### The Wallacean shortfall: bias in estimates of geographic range size

Geographic range size is an important variable in biogeography, ecology and conservation biology. Unfortunately, the geographic distribution of many species is poorly known (the Wallacean shortfall). Despite the widespread use of estimates of species' geographic distributions derived from natural history museum and herbarium specimens, little is known about how bias in these estimates of range size are related to geographic range size itself. Is this bias more severe for widely or narrowly distributed species? To answer this question we developed the working hypothesis that the relationship between range size, measured as area of occupancy (AOO), and bias in estimates of range size is approximately described by the central limit theorem. Three predictions follow from this hypothesis: the expected value of bias is independent of AOO, the variance of bias decreases as AOO increases, and the skewness of bias becomes less negative as AOO increases. To test these predictions we used computer simulations based on a dataset of herbarium specimen records of Bignoniaceae species (Bignoniaceae). The results supported all three predictions and imply that, despite a similar expected value, bias in estimates of AOO differs between narrowly and widely distributed species. For most narrowly distributed species bias in estimates of AOO was particularly high. Indeed, many of these species were not represented by any museum/herbarium specimen, and thus were unknown to science. Yet, bias was exceptionally low for a small proportion of narrowly distributed species, and the geographic distributions of these species were better known than that of any other (narrowly or widely distributed) species. In contrast, for widely distributed species bias in estimates of AOO was unlikely to be as extreme as for narrowly distributed species, so that most widely distributed species were represented by museum/herbarium specimens but their ranges were not particularly well known.

<sup>1</sup>Colorado State University, Department Of Biology, Colorado State University, Fort Collins, CO, 80523-1878, USA<sup>2</sup>Universidade De Sao Paulo, Insituto De Biociências, Departamento E Botânica, Rua Do Matao, 277, Sao Paulo, N/A, 05508-090, Brazil<sup>3</sup>Missouri Botanical Garden, Center for Conservation and Sustainable Development, P.O. Box 299, St. Louis, MO, 63166, USA<sup>4</sup>Missouri Botanical Garden, Center for Conservation and Sustainable Development, P.O. Box 299, St. Louis, MO, 63166

603 MAVRODIEV, EVGENY<sup>1</sup>,  
LAKTIONOV, A. P.<sup>2</sup> and CELLINESE,  
NICO\*<sup>1</sup>

### How floristic data can inform historical biogeography: an example from the Caucasian monocot, gymnosperm, and pteridophyte flora

The Caucasus is a distinct floristic area that includes 42 well-defined sub-regions characterized by the presence of over 950 monocot and pteridophyte native taxa. We constructed a presence-absence taxon matrix that we investigated using a Parsimony Analysis of Endemicity (PAE) approach modified by analyzing the dataset in a Maximum Likelihood framework using a simple Mk model and Gamma distribution rates of heterogeneity. We present results based on both parsimony and maximum likelihood. We used the resulting taxon-area cladogram as the basis for stochastic key species reconstruction to suggest that taxon distribution may actually convey a substantial amount of historical information.

<sup>1</sup>University of Florida, Florida Museum of Natural History, Gainesville, FL, 32611, USA<sup>2</sup>Astrakhan State University, Department of Biology, Astrakhan, 414056, Russia

604 FISHER, AMANDA\*<sup>1</sup>, CLARK,  
LYNN<sup>2</sup> and KELCHNER, SCOT A.<sup>1</sup>

### Andean radiation of the genus *Chusquea* (Poaceae: Bambusoideae: Bambuseae)

A recent phylogeny estimation of the woody bamboo genus *Chusquea* recovered four major, well supported clades: *Neurolepis* I, *Neurolepis* II, *Rettbergia*, and *Euchusquea*. Subsequent analysis focused on the *Euchusquea* clade and found unexpectedly low genetic variation across multiple loci (both plastid and nuclear) and was unable to convincingly resolve relationships in this species rich lineage. *Chusquea* contains approximately 160 described species and has a wide distribution in the neotropics. All four lineages have radiated into montane habitats in the Northern Andes, Central America, Mexico, or the Austral Andes, and there have been multiple introductions to southeastern Brazil. At least forty *Chusquea* species in the *Neurolepis* I, *Neurolepis* II and *Euchusquea* clades are found in open habitats, including high elevation paramos, *campos de altitud*e and *campo rupestre*. In several cases, montane taxa may have subsequently given rise to low elevation radiations. BEAST estimates of divergence times place *Chusquea* lineage crown nodes in the early Pliocene or late Miocene, coincident with uplift events in the Northern Andes. The large number of described Andean *Chusquea*, coupled with an inferred recent origin of the group, results in an exceptional speciation rate. *Chusquea* bam-

boos are unusual in comparison to other recent Andean plant radiations (e.g., *Espeletia*, *Fuchsia*, *Halenia*, *Jamaconia*, *Lupinus*, and *Macrocarpaea*) in that *Chusquea* is anemophilous and a majority of species experience long generation times.

<sup>1</sup>Idaho State University, Department of Biological Sciences, 921 South 8th Avenue, Stop 8007, Pocatello, ID, 83209-8007, USA<sup>2</sup>Iowa State University, Department of Ecology, Evolution and Organismal Biology, 253 Bessey, Ames, IA, 50011-1020, USA

605 GILLESPIE, EMILY\*<sup>1</sup> and KRON,  
KATHLEEN<sup>2</sup>

### Phylogeny and historical biogeography of the small, intercontinentally disjunct genera *Epigaea* and *Rhodothamnus*

Within the tribe Phyllodoceae (Ericaceae: Ericoideae), a strongly-supported clade comprised of *Epigaea* and *Rhodothamnus* occurs. *Epigaea* includes three species: *Epigaea repens* occurs in Eastern North America, *E. gaultherioides* occurs in the Caucasus, and *E. asiatica* occurs primarily in Japan. *Rhodothamnus* includes two species, *R. sessilifolius* and *R. chamaecistus*, which are found in the Alps and Caucasus. A phylogeny was generated within the context of the broader Phyllodoceae using Bayesian, Maximum Likelihood and Maximum Parsimony analyses. An examination of the historical biogeography of the group was conducted using multiple approaches, including a newly available program, RASP (Reconstruct Ancestral State in Phylogenies) using the Bayesian phylogeny.

<sup>1</sup>Wake Forest University, 226 Winston Hall, Wake Forest University, Winston-Salem, NC, 27109, USA<sup>2</sup>Wake Forest University, Department of Biology, Reynolda Station, P.O. Box 7325, Winston-Salem, NC, 27109, USA

606 CLARK, JOHN\*<sup>1</sup>, BRAMLEY,  
GEMMA<sup>2</sup>, ATKINS, HANNAH<sup>3</sup> and  
WAGNER, WARREN<sup>4</sup>

### Towards a comprehensive phylogeny, biogeographic hypothesis, and revised taxonomy for *Cyrtandra* (Gesneriaceae): recent progress and continuing challenges

The paleotropical-Pacific angiosperm genus *Cyrtandra* (Gesneriaceae), with over 600 species, has proven a challenge for botanists since its discovery in 1776. Recent phylogenetic studies indicate that rapid lineage radiations and potentially in situ hybridization complicate efforts to understand this genus. A robust, genus-wide phylogenetic and biogeographic hypothesis is required to better understand speciation and to revise existing, inadequate taxonomy. To this end, a multi-institutional collaboration has been formed to pool resources, fieldwork, and expertise in completing this

goal. Broad scale sampling across Southeast Asia and the Pacific has been conducted with moderate to high species sampling in Indonesia, Solomon Islands, Vanuatu, Fiji, Samoa, Tonga, Niue, Micronesia, Marquesas, and Hawaii. Relatively few samples have been collected from New Guinea and the Philippines posing serious challenges in completing a genus-wide evolutionary hypothesis. Current phylogenetic hypotheses are presented based on ITS, ETS and *psbA-trnH* genic sequence data. Ongoing and future efforts are also discussed.

<sup>1</sup>Catalina Island Conservancy, PO Box 2739, Avalon, CA, 90704, USA<sup>2</sup>Royal Botanical Gardens Kew, UK<sup>3</sup>Royal Botanical Gardens Edinburgh, UK<sup>4</sup>Smithsonian Institution, Botany, MRC-166 National Museum Of Natural History, PO Box 37012, WASHINGTON, DC, 20013-7012, USA

**607 WILSON, ANDREW\*<sup>1</sup>, BINDER, MANFRED<sup>2</sup> and HIBBETT, DAVID<sup>2</sup>**

### **Evolution and biogeography of ectomycorrhizal associations in and enigmatic group of fungi, the Sclerodermatineae (Boletales, Basidiomycota)**

The Sclerodermatineae is an enigmatic lineage of ectomycorrhizal fungi whose members are known to associate with a diverse range of plant hosts. Species from Sclerodermatineae genera such as *Pisolithus* and *Scleroderma* have been studied for their ability to form ectomycorrhizal relationships with a broad diversity of plant hosts, making them good subjects for re-forestation practices. However, related genera such as *Calostoma* appear to have developed a narrower range of host associations. Describing the evolution of host association in the group would generate a better understanding of host specificity vs. host generality in this group and, in general, help evaluate the ability of plant and fungal symbionts to diversify their ectomycorrhizal associations.

For this study, phylogenetic analysis of multi-gene datasets was used to study the history of ectomycorrhizal associations in the Sclerodermatineae by correlating associations through biogeographic distribution and evolutionary co-occurrence. A supermatrix of nrRNA and protein sequences consisting of 168 taxa was produced for molecular dating using BEAST. The first step involved analysis of 17 Agaricomycetideae taxa, performed using fossils to calibrate the Suillineae and mycenoid lineages. The second step used dates from the first analysis to calibrate a more inclusive Sclerodermatineae dataset and to estimate the ages for internal lineages. The BEAST tree from the dating analysis was used as input for LaGrange to reconstruct the biogeographic history of the group.

The preliminary results suggest that the basal Sclerodermatineae diversified about 100 MYA while the Core Sclerodermatineae diversified between 40-50 MYA.

This corresponds with previous analyses and indicates that the Sclerodermatineae is young enough to have cultivated associations in both Angiosperms and Gymnosperms. At the time of this abstract analysis to finalize dates for the internal nodes in the Sclerodermatineae and to describe the biogeographic history for the group are still ongoing. The results of these will be shared in the presentation, and will be used to reconstruct the evolution of ectomycorrhizal host associations in the Sclerodermatineae.

<sup>1</sup>Chicago Botanic Garden, Plant Conservation Science: Soil Science, 1000 Lake Cook Rd, Glencoe, IL, 60022<sup>2</sup>CLARK UNIVERSITY, Department Of Biology, WORCESTER, MA, 01610-1477, USA

**608 MARTIN, GRACIE\*<sup>1</sup>, KRESS, W<sup>2</sup>, SPECHT, CHELSEA<sup>3</sup>, DRISCOLL, HEATHER<sup>4</sup>, LOPEZ, IDA<sup>5</sup>, FRALEY, SARA<sup>1</sup> and GUPTA, SHALIKA<sup>3</sup>**

### **An analysis of speciation modes within Heliconiaceae: a biogeographical approach**

Heliconiaceae (Zingiberales) containing the single genus *Heliconia*, is a family of rhizomatous herbs with most species occurring in Central and South American tropics and a few species native to Southeast Asian tropics. Heliconiaceae is a recently diverging lineage inclusive of some 215 extant species, and as such provides a rapidly radiating group from which to study modes of speciation and the processes that govern distribution and variation. Based on a recently completed 7-marker molecular phylogeny of *Heliconia* we compare distributions and ecological niches of sister species belonging to recently established Central American clades hypothesized to have arrived in this location as a result of two different distribution routes and at two different times. This information matched with ancestral distributions generated by dispersal-vicariance analyses (DIVA), molecular dating and Spatial Evolutionary and Ecological Vicariance Analysis (SEEVA) for *Heliconia* are then used to test hypotheses on modes of speciation within *Heliconia*. The results of these analyses provide a unique insight into the role of niche conservatism versus niche divergence in speciation within Heliconiaceae. This study relies on newly available digitalized herbaria collections and the resources available at the Smithsonian, Botany Department paired with newly developed analytical methods.

<sup>1</sup>University of California, Berkeley, Plant and Molecular Biology, College of Natural Resources, 111 Koshland Hall, Berkeley, CA, 94720, USA<sup>2</sup>Smithsonian Institution, Botany, MRC-166 National Museum Of Natural History, PO Box 37012, WASHINGTON, DC, 20013-7012, USA<sup>3</sup>University of California, Berkeley, Plant and Molecular Biology, College of Natural Resources, 431 Koshland Hall, Berkeley, CA, 94720, USA<sup>4</sup>Department Of Botany, 572 Dwight Place, Berkeley, CA, 94704, USA<sup>5</sup>Smithsonian Institution, National Museum of Natural History, Botany, 1400 Constitution Ave NW, Washington, DC, 20013, USA

609 ANGELO, COURTNEY\* and  
DAEHLER, CURTIS

### Impacts of future climates on fire-promoting invasive grass distributions in the Hawaiian Islands.

Climate warming in the tropics has been documented during the past century. Warming has been predicted to increase invasions in tropical montane environments more so than in temperate montane environments, however, current research has primarily addressed the influence of climate change on plant distributions in temperate ecosystems. Invasive  $C_4$  and few  $C_3$  grasses are known to change fire-frequencies, alter ecosystem processes and displace native species in the tropics; these species are of particular concern. To predict changes in invasive  $C_4$  grass distributions in response to a warming climate in the Hawaiian Islands, climate niche models were developed for four fire-promoting invasive  $C_4$  grasses using Maxent. Average minimum temperature during January, annual precipitation, and driest quarter were the environmental variables used to build the models. For future projections, we increased the average minimum temperature for January by 1.35 degrees Celsius based on expected warming trends for the Hawaiian Islands for the year 2050. We found that *Urochloa maxima* and *Schizachyrium condensatum* ranges increased in area by 4% and 6%, respectively, while, *Melinis minutiflora* and *Cenchrus ciliaris* ranges decreased 7% and less than 1% respectively. *Cenchrus ciliaris* was primarily limited by rainfall rather than by temperature, thus its distribution was not projected to change with an increase in temperature. Although our study failed to find conclusive evidence for an overall expansion of  $C_4$  grasses, we did find that  $C_4$  grass distributions are likely to shift with a warming climate. Similar patterns are expected for ecosystems elsewhere in the tropics, where invasion by fire adapted grasses at lower elevations is already well documented.

University of Hawaii at Manoa, Department of Botany, 3190 Māile Way, St. John Rm 101, Honolulu, HI, 96822, USA

610 RUIZ-SANCHEZ, EDUARDO\* and  
SPECHT, CHELSEA

### Phylogeography and ecological niche modeling of the Mexican endemic shrub *Nolina parviflora* (Nolinoideae: Asparagaceae)

*Nolina parviflora* is a Mexican endemic rosette-leaved shrub to tree-like monocot, which ranges along of the Transmexican Volcanic Belt. Its populations extend from Veracruz in the East to Jalisco in the west, with the most northern plants reaching Queretaro

and the southern populations extending into Oaxaca. The species inhabits dry tropical and oak forests at its western distribution, but is mostly found in xerophytic scrub, pine-juniper, and pine-oak forests in the central and eastern part of its range. Based upon response to Pleistocene climate change, we formulated the following questions: Do the current populations share haplotypes despite their wide geographical distribution? Does gene flow still exist between eastern and western populations of *Nolina parviflora* despite their distance, and between the northern and southern populations currently separated by the Transmexican Volcanic Belt? How have populations survived past ecological niche changes? To answer these questions, we collected 25 populations and more than 200 individuals along the geographical distribution and sequenced the *trnH-psbA* and *trnL-F* chloroplast spacers from these individuals. Using Bayesian, likelihood and parsimony analysis, we found two clades that have geographic correspondence to the central/eastern and western populations. The northern and the southern populations present unique haplotypes that appear to be related to the central/eastern clade. The current ecological niche models based on these two clades shows overprediction in the western clade and excellent prediction for the eastern clade. Predictions using past climate models showed similar patterns to those of the present. The molecular and ecological results indicate limited gene flow between populations across long distances and across the Transmexican Volcanic Belt.

University of California, Berkeley, Plant and Microbial Biology, 111 Koshland Hall, Berkeley, CA, 94720, USA

611 SARKINEN, TIINA\*<sup>1</sup>, SIMON, MARCELO<sup>2</sup>, PENNINGTON, R.TOBY<sup>3</sup>, LAVIN, MATT<sup>4</sup> and HUGHES, COLIN<sup>1</sup>

### Evolutionary islands in the Andes: persistence, isolation and endemism in Andean dry tropical forests

The relative contribution of biome history and geological setting to species richness in biodiversity hotspots remains poorly understood. The tropical Andes is one of the world's top biodiversity hotspots, and with its diverse biomes and the relatively recent but dramatic mountain uplift, the Andes offers a setting to study the importance of biome stability and geological history in species rich biomes. Using densely-sampled time-calibrated molecular phylogenies for a set of Andean tropical dry forest plant lineages (*Mimosa*, *Amicia*, *Cyathostegia*, *Poissonia* and *Coursetia*, Leguminosae), we show that the high levels of endemism in these forests have resulted from a long history of biome stasis and dispersal limitation. Deep divergences between sister species and geographically structured clades of inter-Andean valley endemics suggest that dispersal between these dry forests has been limited over the past c. 19 million years of Andean uplift. Such prolonged dry forest stasis is in line with Miocene fossils from Ecuador closely resembling

extant dry forest plants. The contrasting evolutionary timescales of older dry forest and very recent paramo plant diversification suggest that the exceptional biodiversity found in the Andes is the outcome of a complex set of different patterns of historical species assembly.

<sup>1</sup>University of Zurich, Institute for Systematic Botany, Zollikerstrasse 107, Zurich, 8008, Switzerland<sup>2</sup>Embrapa, Recursos Genéticos e Biotecnologia, PqEB, Caixa Postal 02372, Brasília, DF, 70770-917, Brazil<sup>3</sup>Royal Botanic Gardens, 20A INVERLEITH ROW, EDINBURGH, N/A, EH3 5LR, United Kingdom<sup>4</sup>Montana State University, Plant Sciences and Plant Pathology, Bozeman, Montana, 59717, USA

## 612 WALLACE, LISA\* and DOFFITT, CHRISTOPHER

### Phylogeographic patterns of *Trillium cuneatum* and *Trillium stamineum* within the Black Belt and Jackson Prairie Regions of Mississippi and Alabama

It has been hypothesized that the high levels of diversity noted for the Southeast are related to the restriction of species' ranges and subsequent migrations during and after the last glacial period. Numerous refugia have been proposed in the Southeast, and many of these have been supported by empirical phylogeographic studies of plants and animals. *Trillium* (Melanthiaceae), a highly diverse genus in the Southeast, includes many species that are locally endemic. Given this pattern, it has been hypothesized that vicariance associated with the restriction of populations in pockets of suitable habitat in association with local adaptation have been leading causes of evolutionary diversification within *Trillium*. In this study, we examined DNA sequence variation within two *Trillium* species, *T. cuneatum* and *T. stamineum*, in eastern Mississippi and western Alabama to evaluate the potential for local differentiation. Forested regions where these species occur are separated by the regions of the Black Belt and Jackson Prairies, which are not considered to contain suitable habitats for *Trillium*. We hypothesized that *T. cuneatum* and *T. stamineum* would exhibit similar patterns of genetic structure and that populations separated by the prairie patches would be most divergent. Based on variation in the *trnL* intron and *trnL-trnF* intergenic spacer region of the chloroplast genome we identified a high level of haplotypic diversity in both species - five and four haplotypes in *T. cuneatum* and *T. stamineum*, respectively. Additionally, there is strong regional structure for both species with very little polymorphism within populations, suggesting that gene flow by seed dispersal is quite limited in both of these species. This pattern of structure was not wholly consistent with the historical extent of the prairies. Other landscape features, such as rivers, may have served as additional barriers to dispersal. These results corroborate previous studies and further point to survival in multiple refugia, possibly located in southern Alabama and/or southern Mississippi prior to recolonization of

present-day populations.

Mississippi State University, Biological Sciences, 295 Lee Blvd., Mississippi State, MS, 39762, USA

## 613 MCCARTHY, DIANE\*<sup>1</sup> and MASON-GAMER, ROBERTA<sup>2</sup>

### Phylogeography of the American basswood

Many North American tree species are widely distributed and morphologically variable, but little is known about the processes underlying their distribution and variation. Fortunately, new techniques and sources of data allow us to investigate patterns within taxa that result from cryptic processes occurring over space and time. *Tilia americana*, the American basswood, is an excellent candidate for such a study. Its range covers the eastern half of North America from Canada to Mexico, and though it is now hypothesized to be a single species, it has been divided into as many as 15 species based on morphological variation. We sequenced the non-coding chloroplast DNA marker *rpL32-trnL* from 425 individuals in 75 natural populations of *Tilia americana* across its range and detected 25 haplotypes. While we failed to detect a concordance between haplotype and species *sensu stricto*, the distribution of haplotypes across the continent showed clear structure. Phylogeographic tools allow us to investigate the relationship between intraspecific genetic variation, geography, and history more precisely. Using a niche modeling approach, we conduct a phylogeographic study of American basswood in order to identify evolutionary and geographic sources of genetic structure and to assess the hypothesis that there is only one basswood species in North America.

<sup>1</sup>University of Illinois at Chicago, Department of Biological Sciences, 845 W. Taylor, MC 066, Chicago, IL, 60607, USA<sup>2</sup>University of Illinois Chicago, DEPT. OF BIOLOGICAL SCIENCES (M/C.066), 845 W. TAYLOR ST., CHICAGO, IL, 60607, USA

## POSTERS

## 614 KHOURY, COLIN\*<sup>1</sup>, GREENE, STEPHANIE<sup>2</sup> and CASTAÑEDA ALVAREZ, NORA PATRICIA<sup>1</sup>

### Initial Steps toward a National Conservation Strategy for Crop Wild Relatives of the United States

An effective strategy for conservation of biodiversity worldwide requires a spectrum of actions enacted from the global to the local level. Agricultural biodiversity is no exception, and the wild relatives of crops (CWR), as important genetic resources for crop improvement, represent a dual challenge of requiring conservation as well as access for use. In many regions

these resources are threatened by habitat modification, land use changes, and other factors, requiring their urgent collection and long-term availability for research and breeding from *ex situ* genebank collections, as well as their adequate protection *in situ* in order to support an evolving gene pool for the uses of the future. CWR resources are often globally important, yet their management is dependent upon national policy and interests. We suggest that an effective national approach toward the conservation of CWR entails the systematic coverage of this diversity in a network of genetic reserves, with samples of this diversity safeguarded in national genebanks. We present the work to date on planning for a national effort to conserve CWR and economically important taxa that are native or naturalized in the United States. We are developing a national inventory of taxa that represent CWR of the world's crops, or are directly used for food, fiber, forage, forestry, industrial, medicinal, ornamental, and restoration purposes, which currently contains close to 3,000 taxa. We have also developed a methodology for identification of the gene pools of the world's important crops. Especially species-rich native gene pools of important crops include *Allium* (onion), *Carya* (pecan), *Fragaria* (strawberry), *Helianthus* (sunflower), *Hordeum* (barley), *Ipomoea* (sweet potato), *Lactuca* (lettuce), *Nicotiana* (tobacco), *Phaseolus* (bean), *Prunus* (cherry, almond, peach), *Ribes* (currant), *Rubus* (raspberry), *Vaccinium* (blueberry, cranberry), and *Vitis* (grape), and many additional genera are also represented. We conclude by discussing our next steps for developing a national conservation strategy for crop wild relatives: prioritizing taxa by relatedness to crop species, assessing the coverage of CWR in genebanks and in protected areas, and making recommendations for conservation actions.

<sup>1</sup>International Center for Tropical Agriculture (CIAT), Decision and Policy Analysis Program, Km 17, Recta Cali-Palmira, Apartado Aéreo 6713, Cali, Colombia<sup>2</sup>United States Department of Agriculture, Agricultural Research Service, National Temperate Forage Legume Germplasm Resources Unit, 24106 North Bunn Road, Prosser, WA, 99350, USA

**615 HOCH, PETER\*<sup>1</sup>, BARBER, JANET<sup>2</sup> and DIAZGRANADOS, MAURICIO<sup>2</sup>**

### Phylogeny and biogeography of *Ludwigia* (Onagraceae)

*Ludwigia* is a diverse widespread genus of 82 species currently divided into 23 sections. Fourteen of the sections are monotypic, and only three have more than five species. The genus exhibits a complex biogeographical pattern, with 10 sections endemic to or centered in South/Central America, three in North America, four in Africa, three in Asia, two in the Paleotropics, and two are cosmopolitan. Polyploidy is widespread, with gametic chromosome numbers from  $n = 8$  to  $n = 64$ . Strong molecular and morphological data place *Ludwigia* as sister to the rest of the Onagraceae, so under-

standing its phylogeny is crucial to understanding the family. The family appears to have originated about 93 Ma, and *Ludwigia* arose between 93 and 80 Ma. No molecular phylogeny is available for *Ludwigia*, and the considerable age of the clade makes interpretation of the morphology particularly challenging, so we have undertaken a comprehensive phylogenetic analysis of *Ludwigia* in order to assess the validity of this highly fragmented classification, test relationships among sections and species, and elucidate the complex biogeographical history of the genus, especially as it relates to the origin of the family. Preliminary data (cpDNA and nDNA sequences from 24 taxa) show good resolution of strong monophyly of the genus and of at least some groups (sect. *Oligospermum*, and the North American sections), although it appears that the chromosomally complex North American sections *Isnardia* and *Microcarpum* may be paraphyletic. Substantial additional sampling is needed, particularly in the South American sections. Recent explosive invasions, particularly by *L. hexapetala* and relatives in wUSA, Australia, and southern Europe, highlight the need for a comprehensive modern revision and phylogeny in order to identify and possibly control these invasives.

<sup>1</sup>Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166-0299, USA<sup>2</sup>Saint Louis University, Biology, 3507 Laclede Ave., St. Louis, MO, 63103, USA

**616 LIMA, JACIRA RABELO\*<sup>1</sup>, TOZZI, ANA MARIA GOULART DE AZEVEDO<sup>2</sup> and MANSANO, VIDAL DE FREITAS<sup>1</sup>**

### Phylogenetic structure of Leguminosae assemblages in South America

Leguminosae is found in various vegetation types in South America, occurring from seasonal to humid vegetation. The most severe conditions (higher temperatures and less precipitation) of the seasonal vegetation, when compared with the humid vegetation, can act as strong environmental filters for the species present there. Environments where the structuring forces are abiotic filters tend to present species with similar niches, and thus more phylogenetically related than expected by chance (clumped). Once the seasonal vegetation present in South America represents a more stressful environment compared to areas of humid vegetation, it is expected that these areas have a clumped phylogenetic structure. We carried out a survey of tree and shrub species of Leguminosae present in different vegetation in South America based on published works. A phylogenetic tree was calculated using the software package phylogenetic Phylom. The richness, diversity and phylogenetic structure (Phylogenetic Species Variability - PSV; Average Taxonomic Distinctness - ATD and Net Relatedness Index - NRI) were calculated using PAM software. Our revision included 328 areas studied, resulting in 124 genera and 780 species. The driest areas present, in general, higher species richness and a clumped

phylogenetic structure. This result suggests that, in these dry areas, the environmental filters are probably more important in structuring the community. For some areas of humid vegetation, the main structuring force is competition, which leads to an increase in the number of taxa of different lineages and a consequent over-dispersion phylogenetic structure.

<sup>1</sup>Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rua: Pacheco Leão, 915, Jardim Botânico, Rio de Janeiro, Rio de Janeiro, 22460-030, Brazil<sup>2</sup>Universidade Estadual de Campinas, Departamento de Biologia Vegetal, Rua: Monteiro Lobato, 255, Cidade Universitária "Zeferino Vaz", Campinas, São Paulo, 13083-970, Brazil

## 617 WELLARD, BLAKE

### Relict Populations of *Quercus x pauciloba* Rydb. (prosp.) [gambelii x turbinella] in Northern Utah

*Quercus x pauciloba* Rydb. (pro sp.) [gambelii x turbinella] is a common hybrid oak in the American Southwest where parents co-occur. In 1954 Rudy Drobnick found relict clones of this hybrid in Northern Utah by; an area thought to be exclusive to *Quercus gambelii*. The nearest *Quercus turbinella* is found roughly 300 miles to the south. The origin of the relict clones is still debated, but the most commonly accepted hypothesis is that the parents migrated north during the Holocene Climatic Optimum and hybridized along the way. Until recently these hybrids typically occurred as one to few clones but on October 22, 2010, a hybrid swarm was found near Salt Lake City, Utah. To understand how this hybrid swarm has persisted, the population dynamics need to be documented. This is being done by collecting basic habitat characteristics (e.g. soil, slope, elevation, aspect), and sclerophylly index (leaf dry weight / leaf area). Isozyme analysis will be used as one method to distinguish clones from individuals. On March 18, 2011, another hybrid was discovered at perhaps the lowest elevation yet documented near Ogden, Utah. This site will serve as a comparison to the hybrid swarm. The data on these relict hybrids from various sites in northern Utah may provide additional clues to this regions climatic and floristic past.

Weber State University, Botany, Department of Botany, Weber State University, 2504 University Circle, Ogden, UT, 84408-2504, USA

## 618 QIU, YINGXIONG<sup>1</sup>, SUN, YI<sup>\*1</sup>, FU, CHENGXIN<sup>1</sup> and COMES, HANS<sup>2</sup>

### Molecular phylogeography of East Asian *Kirengeshoma* (Hydrangeaceae) in relation to Quaternary climate change and landbridge configurations

*Kirengeshoma* comprises two species inhabiting warm temperate-deciduous forests in eastern China/ southern Japan (*Kirengeshoma palmata*) and South Korea (*Kirengeshoma koreana*) (CJK region). A survey of chloroplast (cp) DNA, inter-simple sequence repeats (ISSRs) and microsatellites (SSRs) variation in *Kirengeshoma* was carried out to determine the population history of a plant taxon around the East China Sea (ECS). CpDNA, ISSRs and SSR revealed lower genetic divergence between China and Japan relative to the other contrasts, in line with intrageneric classification. Molecular dating suggests that *K. koreana* diverged at the Plio-Pleistocene boundary from the Japanese populations, whereas the latter migrated into China during the early to mid Pleistocene via the ECS basin. Vicariant segregation of Chinese and Japanese populations likely occurred during the mid-Pleistocene. Mismatch distributions and neutrality tests indicated that Chinese populations expanded their range during the Late Pleistocene, probably during a cold period, whereas those from Japan showed no significant population growth. Recent immigrants, detected by assignment tests, tend to decrease from the grandparent generation to the current generation, suggesting the potentially highly restricted current gene flow among fragments may render the fragmented populations of *K. palmata* at a higher risk of local extinction several generations after fragmentation. We conclude that the current distribution and differentiation of components of presently isolated warm temperate-deciduous forests in China, Japan and Korea likely resulted from a combination of relatively ancient vicariant and immigration events, and those from Japan were particularly sensitive to range fragmentation and long-term refugial isolation throughout the Late Pleistocene. This study can not only provide information useful for developing recovery plans that can meaningfully sample and preserve genetic diversity, but also provide the theoretic basis for successful propagation and management of endangered species. Additionally, this study will provide methodological guidelines for studying on the conservation genetics and phylogeography of other endangered species in the CJK region.

<sup>1</sup>College of Life Sciences, Zhejiang University, Key Laboratory of Conservation Biology for Endangered Wildlife, Ministry of Education, 338 Yuhangtang Road, Zijingang Campus, Hangzhou, Zhejiang, 310058, China<sup>2</sup>Department of Organismic Biology, Salzburg University, Salzburg, A-5020, Austria

619 GERMAIN-AUBREY,  
CHARLOTTE\*<sup>1</sup>, SOLTIS, PAMELA<sup>2</sup>,  
NEUBIG, KURT<sup>3</sup>, THURSTON, TAYLOR<sup>1</sup>,  
SOLTIS, DOUGLAS<sup>4</sup> and GITZENDANNER,  
MATTHEW<sup>5</sup>

**Testing hypotheses in a comparative  
phylogeography study: the case of four  
plants endemic to the central Florida  
scrub**

The highly threatened central Florida scrub encompasses an exceptional proportion of endemic species, making it a biodiversity hotspot in North America. However, the origins of this unique community are poorly understood. To study phylogeographic patterns, we used available sequence data, along with our own, to place four endemic plant (*Prunus geniculata*, *Persea humilis*, *Ilex opaca* var. *arenicola* and *Polygala lewtonii*) in their respective generic-level phylogenies. The four phylogenetic trees provided tests of the monophyly of each taxon and identified their sister species, shedding light on the geographic origins of the central Florida scrub. The origin of the central Florida scrub has been debated, but never tested in a phylogeographic context. Here, we take the two most widely accepted hypotheses and build simulations of topologies for each scenario, for each of the species. The first scenario argues for a fragmentation of the Pliocene xeric belt extending from Florida to Texas and the southwestern US, with subsequent speciation leading to the sister species of the Florida endemics having a western distribution. The second hypothesis focuses on the Pleistocene glacial cycles leading temperate species to take refuge in Florida, including the scrub, resulting in the endemic species being most closely related to widespread species distributed in eastern and northeastern North America. Statistically testing the departure of each observed phylogeny from the simulated ones, we reject the western hypothesis in three cases, while the fourth phylogeny fails to reject both hypotheses. These results provide an initial view of the geographical origins of the species that shape the central Florida scrub and support a single major migration event rather than several smaller ones. The implications of our findings for the conservation of this community are briefly discussed.

<sup>1</sup>University of Florida, Department of Horticultural Sciences, Gainesville, FL, 32611, United States<sup>2</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, Gainesville, FL, 32611-7800, USA<sup>3</sup>University of Florida, Department of Biology, Po Box 118526, Gainesville, FL, 32611, USA<sup>4</sup>University of Florida, Department of Biology, Gainesville, FL, 32611, USA<sup>5</sup>University Of Florida, Florida Museum Of Natural History, PO BOX 117800, GAINSVILLE, FL, 32611-7800, USA

620 LIU, QING

**Climatic-niche structure of grasses  
(Poaceae) in China's nature reserves**

Explaining climate-niche structure for grasses over broad geographic scales is a central issue of biogeography and macroecology. We document climate-niche structure for grasses in China's nature reserves and discuss their formation mechanisms using grass richness data combined with climatic, physiological and phylogenetic data. Our results suggest that climatic-niche structure of grasses is phylogenetically conservative for BEP and PACCMAD clades along temperature gradients and phylogenetically conservative for Chloridoideae and Panicoideae along precipitation gradients. At the national scale, the divergence patterns of climatic-niches between two major clades were more distinguishable than the difference between C<sub>3</sub> and C<sub>4</sub> grasses. High rates of climatic-niche evolution of C<sub>4</sub> grasses is shown in the nodes of the subtropical forest region. There appears to be a strong association between elevation gradients and grass diversity where specific environmental condition (e.g. energy) and rapid shifts among climatic regimes drive high grass diversity. Evolutionary conservatism of climatic-niches may be influenced by species interactions within nodes of each C<sub>4</sub> variant besides physiological tolerances. These results have important implications for explaining continental (eastern Asia) scale of grass richness patterns, and imply that adaptations to major climate changes readily will be accomplished in C<sub>4</sub> grass nodes of high rates climatic-niche evolution in China's nature reserves.

South China Botanical Garden, Chinese Academy Of Sciences, Herbarium, So China Botanical Garden, Xingke Road 723#, Tianhe District, Guangzhou, N/A, 510650, China

621 HUANG, PU\* and SCHAAL,  
BARBARA

**Phylogeography of Asian wild rice, *Oryza  
rufipogon*: a genome-wide view**

Asian wild rice (*Oryza rufipogon*) which ranges widely across the eastern and southern part of Asia is widely recognized as the direct ancestor of the cultivated Asian rice (*O. sativa*). Studies of the geographical structure of *O. rufipogon*, based on chloroplast and low-copy nuclear markers, reveal a possible phylogeographic signal of subdivision in *O. rufipogon* populations. However, this signal of geographical differentiation is not consistently observed among different markers and studies. Additionally, theoretical studies point out that inadequate geographic sampling, or incomplete lineage sorting due to the small number of markers, could potentially bias the detection of a phylogeographic signal. To more precisely characterize the phylogeography of *O. rufipogon* populations, a

genome-wide survey of unlinked markers, intensively sampled from across the entire distribution range is critical. In this study, we surveyed sequence variation at 42 genome-wide sequence tagged sites (STS) in 96 *O. rufipogon* accessions from throughout the native range of the species. Using Bayesian clustering, principal component analysis and AMOVA, we conclude that there are two genetically distinct *O. rufipogon* groups, Ruf-I and Ruf-II. The two groups exhibit a clinal variation generally from northeast to southwest. Different from some earlier studies, Ruf-I which is found mainly in China and Indochinese peninsula, showed genetic similarity with one major cultivated rice variety, *O. sativa indica*. Whereas Ruf-II, mainly from South Asia and Indochinese peninsula, is not found within any cultivated rice varieties. Additional analysis using diffusion approximation suggests potential historical gene flow from cultivated rice into the *O. rufipogon* populations.

Washington University, Department Of Biology, CAMPUS BOX 1137, 1 Brookings Drive, St. Louis, MO, 63130-4899, USA

**622 KHOURY, COLIN<sup>\*1</sup>, CASTAÑEDA ALVAREZ, NORA PATRICIA<sup>1</sup>, VINCENT, HOLLY<sup>2</sup>, JARVIS, ANDY<sup>1</sup>, MAXTED, NIGEL<sup>2</sup>, EASTWOOD, RUTH<sup>3</sup> and GUARINO, LUIGI<sup>4</sup>**

### **Planning for Collecting the Crop Wild Relatives of the World's Major Crops**

The wild plant species related to the world's major crops are playing an ever increasing role in providing traits of value to crop improvement programs, as techniques for utilization improve and as breeders survey ever wider diversity in order to increase agricultural production. Adaptation of agriculture to the more variable and extreme climates of the future is likely to rely substantially upon the genetic resources found within crop wild relatives (CWR). Like many plant species, CWR are exposed to increasing pressures from habitat modification, and climate change is projected to further stress populations in many areas. As the representation of CWR diversity in *ex situ* conservation (genebanks) is far from comprehensive, the genetic resources that are vitally important for crop adaptation are in danger of being lost, limiting the options available to future agriculture. It is becoming increasingly feasible to formulate a global plan for the efficient and effective collection of CWR diversity due to 1) the taxonomic relationships between species increasingly clarified, 2) better knowledge and tools for modelling and mapping the distribution of plant species through Geographic Information Systems, and 3) a new International Treaty on Plant Genetic Resources for Food and Agriculture which facilitates international collection and conservation efforts. We document the progress to date on planning for a major new global initiative for the collection and conservation of CWR, the results and products of which will be available to the global community. The gene pools of 80 of

the major crops of the world are listed, with the closely related species given prioritization. Ecogeographic data for these species, gathered via collaborations with herbaria, genebanks, and researchers, is utilized to model species distributions and to expose gaps in the coverage of these populations in *ex situ* collections. We discuss the next steps in planning for collecting trips worldwide, and invite the research community to collaborate in this global project through data provision and validation of results.

<sup>1</sup>International Center for Tropical Agriculture (CIAT), Decision and Policy Analysis Program, Km 17, Recta Cali-Palmira, Apartado Aéreo 6713, Cali, Colombia<sup>2</sup>University Of Birmingham, School of Biosciences, Edgbaston, Birmingham, B15 2TT, UK<sup>3</sup>Royal Botanic Gardens, Kew, Millennium Seed Bank Partnership, Seed Conservation Department, Wakehurst Place, Ardingly, West Sussex, RH17 6TN, UK<sup>4</sup>Global Crop Diversity Trust, c/o Food and Agriculture Organization (FAO) of the United Nations, Viale delle Terme di Caracalla 1, Rome, 00153, Italy

ORAL PAPERS

623 PALMQUIST, EMILY\*<sup>1</sup>, AYERS, TINA<sup>2</sup> and SPENCE, JOHN<sup>3</sup>

**Phylogeny and Evolutionary History of *Anticlea vaginata* Rydb. (Melanthiaceae): A Hanging Garden Endemic**

This study examines the taxonomic status, population genetics, and evolutionary history of the rare, endemic plant species, *Anticlea vaginata* (Melanthiaceae). Doubts about its distinctness as a species have been raised, which has implications for its status as a rare species. Morphological differences between *A. vaginata* and its closest relative, *Anticlea elegans*, were assessed using Principle Components Analysis, Canonical Discriminant Functions analysis, and one-way analyses of variance. Genetic variability and population structure were assessed using the AFLP technique. Non-metric Multidimensional Scaling, Analysis of Molecular Variance, cluster analyses, gene diversity estimates, and Structure 2.2 were used to determine the levels of genetic differentiation. *Anticlea vaginata* and *A. elegans* exhibit large amounts of overlap in morphological and genetic variability. Despite this overlap, there are indications of ongoing diversification. *Anticlea vaginata* populations exhibit genetic structuring and do not group as a species. Populations of *A. vaginata* show genetic patterns consistent with those expected for relictual populations. We conclude that since there are no consistent distinguishing characteristics between *A. vaginata* and *A. elegans*, *A. vaginata* should be treated as a subspecies of *Anticlea elegans*. It is likely that there is little gene flow between the populations of subsp. *vaginata* and subsp. *elegans*, and the populations of *A. elegans* subsp. *vaginata* may be on their own evolutionary trajectories.

<sup>1</sup>Northern Arizona University, Biological Sciences, PO Box 5640, Flagstaff, AZ, 86011, USA<sup>2</sup>Northern Arizona University, Department Of Biological Sciences, PO Box 5640, Flagstaff, AZ, 86011-5640, USA<sup>3</sup>Glen Canyon National Recreation Area, Natural Resources, PO Box 1507, Page, AZ, 86040, USA

624 KROISS, STEVE\* and KNIGHT, TIFFANY

**What limits the occupancy of rare plant species in restored habitats? A trait comparison between rare and widespread species in restored Missouri glades**

Understanding factors that limit species presence within restored habitats has been a longstanding goal of restoration ecology, especially in terms of factors that govern differences in the relative rarity and commonness between species. While some species are widespread and abundant, others are locally abundant, but regionally rare. These differences in occupancy rates may be heavily influenced by species traits since species traits may determine whether or not the species could persist locally when the habitat became degraded, and whether or not the species could recolonize when the habitat was restored. Traits important for allowing species to persist locally or disperse into restored habitats may include: wide habitat tolerances, clonality, perennality, self-compatibility, wind dispersal, and small seed size. To determine if plant traits related to persistence or dispersal ability explain species occupancy patterns, I surveyed 32 restored glades in Missouri. I used a step-wise multiple regression analysis and AIC model selection to assess the extent to which the variance in species occupancy and abundance could be explained by a composite of the aforementioned species traits. The multiple regression analysis indicated that the traits most important for explaining species occupancy in restored glades were dispersal mechanism, habitat association, and life-form (R-squared: 0.32, p=0.03). The results of this study provide several important implications for the future of restoration efforts. First, our results serve to indicate species that may be in need of active seeding efforts in restored areas such as species with annual or biennial life-forms, gravity dispersed seeds, and specialization on early successional habitats. Conversely, species with perennial life-forms, wind dispersed seeds, and habitat associations that include mid-successional habitats are likely to become widespread after restoration on their own. Second, our results may also aid in the prioritizing of habitat conservation. For example, habitats that are diverse in species with poor dispersal and persistence traits should be prioritized for conservation as they could serve as seed sources for other restored areas.

Washington University, DEPARTMENT OF ZOOLOGY, One Brookings Drive, Box 1137, St. Louis, MO, 63130, USA

625 PATE, SARAH\*, GODSMARK,  
GEORGE and MURRELL, ZACK

### Phylogeography and Mating System of *Spiraea virginiana* Britton

*Spiraea virginiana* Britton is a threatened shrub endemic to second and third order drainages in the southern Appalachians and Cumberland Plateau. Because little is known about the species, characterization of its mating system, potential for sexual reproduction, and evolutionary relationships within the species could lead to improved conservation management. In order to examine genetic structure across the species' range, we conducted a phylogeographic study using a multi-locus approach. A phylogenetic analysis based on maximum parsimony of Inter Simple Sequence Repeats (ISSRs) revealed similarity within drainages, as well as monophyly of the species. To assess maternal relationships within the species, three regions of non-coding chloroplast DNA were sequenced, and a Bayesian phylogenetic analysis was conducted. Mapping of a haplotype network and the major clades identified in the Bayesian analysis revealed little structure within drainages and potential relatedness across elevational gradients. These conflicting genetic signatures are difficult to interpret, but studies of the species' reproductive biology provide some clues. Pollination treatments were conducted in a common garden setting and in three wild populations along the New River in Ashe County, NC. Results from these treatments tentatively suggest the species has a mixed mating system, and can reproduce sexually, contrary to prior observations. However, seed size, seed weight, and fruit set were variable among populations and germination rates were low. Based on our observations and the patterns revealed by the phylogeography, sexual reproduction in the species may be more possible than previously thought and seed may be wind-dispersed.

Appalachian State University, Biology, 572 Rivers Street, Boone, NC, 28608-2027, USA

626 CHI, KATHERINE\* and MOLANO-FLORES, BRENDA

### Environmental and demographic effects on reproduction in the rare species *Besseyia bullii* (Plantaginaceae)

*Besseyia bullii* (Plantaginaceae) is a prairie-savanna forb endemic to the Midwestern United States, where it is considered rare throughout its range. During species assessments in the 1980s, woody encroachment was frequently cited as a potential cause of *B. bullii*'s decline. In addition, declining populations of *B. bullii* may be subject to problems associated with demographic factors (i.e., Allee effects). The objective of this study was

to determine if environmental (i.e., shading) and demographic (i.e., number of flowering individuals) factors affect reproduction in this species and contribute to its rarity. Sites were selected from across the range of *B. bullii*, resulting in 25 populations that were then assigned to one of the following habitat categories: open, semi-shaded, and shaded. Populations were visited from April to June, and data was collected on population size and the percent of flowering individuals. At each population, 20 infructescences were randomly collected to estimate fruit and seed set. The mean percent of flowering individuals was highest in open habitats and lowest for shaded habitats, with many shaded sites having completely sterile populations. Seed set was found to correlate positively with increasing population size, and increase in open habitats compared to shaded habitats. These results show that woody encroachment has a negative effect on reproduction in *B. bullii*, and confirm traditional conservation theory regarding the importance of maintaining large population sizes.

University of Illinois, Illinois Natural History Survey, 1816 S. Oak St., Champaign, IL, 61820, USA

627 MOURA, TÂNIA MARIA DE\*<sup>1</sup> and MARTINS, KARINA<sup>2</sup>

### Genetic divergence in populations of *Solanum lycocarpum* A. St.-Hil, in the Brazilian Cerrado

In common species that are widely distributed and with long-distance seed and pollen dispersal agents, it is expected that there is connectivity and no strong genetic divergence among populations. Understanding genetic divergence among populations of species with these characteristics may prove valuable in developing appropriate conservation strategies. Based on this, the present study evaluated the genetic divergence among six populations of *Solanum lycocarpum* separated by distances between 19 and 128 km. This species is endemic, common, widely distributed in the Brazilian Cerrado, is mostly pollinated by large bees (*Xylocopa* sp) and the seed mostly dispersed by the maned wolf (*Chrysocyon brachyurus*). Both promote gene flow over long distances. For this study, 60 sampled individuals in each population were genotyped with five polymorphic microsatellite loci (SSR). The population with the highest number of alleles was the only population located in a conservation area with the largest continuous area of preserved native vegetation. This may indicate the importance of protected areas for conservation of genetic diversity. Inbreeding was not observed within populations ( $f = -0.002$ , 95% CI -0.122 to 0.127). The test of isolation by distance showed a moderate negative but significant correlation between the logarithms of gene flow and geographic distances between pairs of populations ( $r = -0.745$ ,  $P = 0.011$ ) showing a trend of isolation through distance. The population located in the disturbed area differed the most. The genetic diver-

gence among populations ( $teta-p = 0.068$ , 95% CI 0.039 to 0.097) was significant (G test,  $P < 0.01$ ), and this may be due to the restriction of gene flow and genetic drift. Our results show the effect of habitat fragmentation on populations of plant species from the Cerrado, suggesting that the removal of native vegetation due to agricultural expansion is negatively impacting on pollen and seed dispersers and thus promoting genetic isolation of fragmented populations.

<sup>1</sup>State University of Campinas, Vegetal Biology, Biology Institute, postal box 6109, Campinas, SP, 13083-970, Brazil <sup>2</sup>Federal University of São Carlos (Ufscar), Biology, road 'João Leme dos Santos', Km110, Sorocaba, SP, 18052-780, Brazil

**628 CROFT, GENEVIEVE<sup>\*1</sup>,  
YATSKIEVYCH, GEORGE<sup>2</sup> and SCHAAL,  
BARBARA<sup>3</sup>**

***Claytonia ozarkensis* (Montiaceae):  
genetic variation in a rare Spring Beauty  
endemic to the Ozarks and its relatives**

In a 2006 taxonomic monograph of the genus *Claytonia*, J.M. Miller and K.L. Chambers recognized a wide-leaved *Claytonia* located only in the Ozark Highlands of Arkansas, Missouri and Oklahoma. They remarked that *C. ozarkensis*, known from only nine localities, is deserving of protection under the Endangered Species Act. These plants had been previously determined as *C. caroliniana*, a species otherwise absent in these states. Miller and Chambers described the new species, *C. ozarkensis*, in this monograph and provided two key morphological characters distinguishing it from the more common, eastern, species: petal color and bract number. A third species, *C. virginica*, has a broad range that includes the distributions of both *C. caroliniana* and *C. ozarkensis*, but is narrow-leaved and otherwise morphologically dissimilar. Fieldwork revealed a notable ecological difference between *C. ozarkensis* and *C. caroliniana*. Whereas *C. caroliniana* is ground-dwelling, *C. ozarkensis* inhabits cliffs. Recent field expeditions have been unable to locate extant populations in Oklahoma or Missouri. For this study, *C. ozarkensis* was obtained from three localities in Arkansas. We analyzed variation at three neutrally evolving loci to assess levels of genetic diversity within these populations. We compared these sequences to those of *C. caroliniana* and *C. virginica* from the eastern and Mid-western United States to determine whether Arkansas has one or two species of wide-leaved *Claytonia*, and to compare population-level genetic diversity among these three groups. If the data support three separate taxa, *Claytonia ozarkensis* is a rare endemic species known only from three extant metapopulations in Arkansas, and a species of conservation concern.

<sup>1</sup>Washington University, Biology, 1 Brookings Drive, Campus Box 1137, St. Louis, MO, 63130, USA <sup>2</sup>Missouri Botanical Garden, PO Box 299, St. Louis, MO, 63166-0299, USA <sup>3</sup>Washington University, Department Of Biology, CAMPUS BOX 1137, 1 Brookings Drive, St. Louis, MO, 63130-4899, USA

**629 JOLLS, CLAUDIA L.<sup>\*1</sup>, MARIK,  
JULIE<sup>1</sup>, BELL, TIMOTHY S.<sup>2</sup>, HAVENS,  
KAYRI<sup>3</sup>, FANT, JEREMIE<sup>3</sup>, VITT, PATT<sup>3</sup>,  
MCEACHERN, A. KATHRYN<sup>4</sup>, PAVLOVIC,  
NOEL B.<sup>5</sup> and BOWLES, MARLIN L.<sup>6</sup>**

**Persistence vs. extirpation of *Cirsium  
pitcher*, Pitcher's thistle, a rare sand dune  
endemic of the upper Great Lakes**

*Cirsium pitcheri*, Pitcher's thistle, is a threatened monocarp of dunes and shorelines of the Great Lakes. Since 2005, we have collaborated to bring together demographic data on more than 12,700 plants at 27 sites, spanning two years to more than two decades. Our goal is to better understand how factors contributing to local demography and genetic composition interact to influence persistence at the population- and regional-levels. Detailed demographic monitoring shows most natural populations are below replacement, including for 9 of the 11 years at one northern MI site (stochastic  $\lambda = 0.9101 \pm 0.0017$ ). We used these long-term data to construct transition matrices and model population viability in the face of demographic stochasticity, inbreeding and catastrophes. The inclusion of inbreeding had the greatest effect on projected population size, not surprising given inbreeding reduces fecundity to ~25% of outcrossed plants. Our experimental and empirical work demonstrates that size, microsite (light, litter), water availability and invasive plants (e.g., baby's breath, *Gypsophila paniculata*) and insects (biocontrol weevil, *Rhinocyllus conicus*) can affect survival and fecundity. How these plant responses scale-up to population-level impacts, i.e., weather, drought and even climate change, is less clear. We decomposed elasticity matrices to evaluate plant growth, stasis (persistence) and fecundity on population growth. *Cirsium pitcheri* populations may be as sensitive to the success of vegetative individuals as to seedling recruitment. Still, the most effective management option for increasing population persistence and viability of Pitcher's thistle is enhanced seedling recruitment. Although populations at the southern end of the range have been extirpated and extant ones may be in decline, restorations appear highly successful in the short term. Given its dependence on long-term (historic Holocene events that formed the Great Lakes shorelines) as well as short-term dynamics of lake-level, *Cirsium pitcheri* may be a "flash-in-the-pan" Pleistocene relict bound for extinction in a major portion of its range, exacerbated by anthropogenic change.

<sup>1</sup>East Carolina University, Department Of Biology, Howell Science Complex Mail Stop 551, Greenville, NC, 27858-4353, USA <sup>2</sup>Chicago State University, Department Of Biological Sciences, 9501 South King Drive, Chicago, IL, 60628-1598, USA <sup>3</sup>Chicago Botanic Garden, CONS SCI DEPT, 1000 Lake Cook Road, Glencoe, IL, 60022, USA <sup>4</sup>US Geological Survey, Western Ecological Research Center, Channell Islands Field Station, 1901 Spinnaker Dr., Venture, CA, 93001, USA <sup>5</sup>US Geological Survey Great Lakes Science Center, Western Basin Ecosystems Branch, Public Lands Ecology Section, Lake Michigan Ecological Research Station, 1100 North Mineral Springs Road, Porter, IN, 46304, USA <sup>6</sup>Morton Arboretum, Research Department, Rt. 53, Lisle, IL, 60532, USA

630 VEDIYA, DR. SANJAY D.

### Study of Plant Diversity in Jamgadth area of Meghraj Range Forest District Sabarkantha, North Gujarat, India

**B**iodiversity conservation is major problem of the day. We are trying to establishment of natural habitate for plant. Meghraj forest is the part of Arravali Mountains so it is unique example from floristic point of view. In present study a total of 186 species belonging to 84 families have been recorded from Meghraj range forest in particular zone Jamgadth of district Sabarkantha, North Gujarat, during December 2009. The investigation also reveals the ecological balance is being upset due to rapid rise of human population and their increased demand for more utilization of natural resources.

Sir P. T. Science College, P.G. Centre in Botany, Biology Department, College Campus, Modasa, Gujarat, 383315, INDIA

631 VASUT, RADIM\* and SOCHOR, MICHAL

### Are the populations of *Salix daphnoides* in the Western Carpathians (Czech Republic) natural?

**S***alix daphnoides* Vill. is distributed from southern Europe to Scandinavia. Its natural distribution in Central Europe is confined to mountain regions of the Alps and the Carpathians. The Carpathian Mts. extends to the Czech Republic only in its easternmost part (Beskydy Mts.) and the species is naturally occurring only in this part of the country. From the ecological point of view, we can divide Carpathian populations of *S. daphnoides* into three groups: *i*) occurring on river gravel banks; *ii*) Wet *Cirsium* meadows; and *iii*) Ash-alder alluvial forests. Populations from the first biotope are ecologically similar to those ones from the Alps and High Carpathians, they are rich in number of individuals and they are age-structured. Whereas populations from the second and third biotope are spatially limited and age structure is not well differentiated even in larger populations. We therefore hypothesize that at least some population of the Western Carpathians (Beskydy Mts.) are not natural, but of (older) human origin. *Salix daphnoides* serves as a honey-bearing tree. We therefore address the question whether or not populations on biotopes *ii*) and *iii*) might represent spontaneously and clonally reproducing willows for past hundred years. To test this hypothesis, we study population dynamics, mode of reproduction and genetic diversity of these Czech populations. We characterize populations in the field (age structure, vegetation, spatial structure of populations) and consequently analyze their genetic diversity

using microsatellites (SSR, simple sequence repeats). So far, we found that populations from biotope *i*) are genetically diverted, however population have significant heterozygote deficit. Population from the biotope *ii*) and *iii*) are confirmed to be formed by one or two genotypes only suggesting their anthropogenic origin.

Palacky University Olomouc, Faculty of Science, Department of Botany, Slechtitelu 11, Olomouc, CZ, 78371

632 ABDULHASAN, NABEEL

### The Restoration of Mesopotamian Marshlands in Southern Iraq- Botanical Perspective

**H**istorically, the Mesopotamian marshlands covered approximately 20,000 km<sup>2</sup>, extended over three provinces of southern Iraq, and presented in three major marshes, (Hawaiza, Hammar, and Central Marshes). The mass desiccation of Mesopotamian marshlands during the 1990s, resulted in the disappearance of many aquatic and semi aquatic plants. The re-flooding of 2003 brought exceptional, significant, and rapid environmental restoration in just a short time. By 2007, maximum restoration of the marshlands was attained, with 58% of the original flooded area restored. Regarding plant cover, more than 50 species were observed during field surveys between 2003 and 2010; totaling 50% restoration of aquatic plants historically recorded in the marshlands. In 2005, *Utricularia australis* and *Nymphoides indica* were listed as non-restored plants, but after 2006 they were observed for the first time in the Hawaiza and Central Marshes respectively. There was one invasive species *Hydrilla verticillata*, which was recorded in all the restored marshes. The "Iraqi Marshlands Habitat Classification System" has been developed to inventory vegetation types of the habitats in these marshlands and to develop a methodology for application elsewhere in Iraq. Climate change, increase of upstream agricultural activities, urban development and dam building continue to threaten these important wetlands with repeat drought. Some actions, such as modifying the water regime and building regulators at the outlets of these marshlands, were made by Iraq's government as part of the conservation activities.

Nature Iraq, Nature Iraq, Sulimaniya, NA, Iraq

633 MOODY, MICHAEL

### Deep divergence within a rare species complex (*Myriophyllum petraeum*) of geographically disjunct granite "islands" in the arid landscape of the Biodiversity Hotspot of southwest Australia

The international biodiversity hotspot of southwest Australia has an ancient landscape, above sea level and devoid of glaciations for over 200 million years. The region has also lacked major geological events such as volcanism and mountain uplifting. This has led to distinctive patterns of evolution at the landscape scale with a very high rate of local endemism and rarity with often geographically disjunct species distribution patterns. While the region has seen major advances over the past decade in taxonomic discovery and description, an estimated relatively high proportion of the flora is yet to be formally described (>15% of the WA flora) and species level phylogeographic studies are still rare. *Myriophyllum petraeum* is a species of conservation concern in southwest WA with its 20 known population distributed over a 300 km<sup>2</sup> region overlapping five recognized bio-regions. Populations are found in small ephemeral pools (< 10 m<sup>2</sup>) on granite outcrops scattered across the region well known for their particularly unique floras, acting as islands in an often arid landscape. The level of geographic isolation of *M. petraeum* populations would predict a potential for low gene flow at an ancient time scale, as onset of aridity dates > 4 m.a. Species level DNA sequence markers (nrDNA ITS and cpDNA *trnL-rpl32*) were utilized to determine level of divergence among populations within this complex. Deep divergence was found at a geographic scale among population with 9 unique ITS genotypes and 10 unique cpDNA haplotypes recognized from 12 sampled populations. The level of sequence diversity among populations is comparable to that found among many well defined morphological species pairs in the genus. Nodal divergence among populations is estimated as high as 1.8 m.a., near the beginning of the Pleistocene.

University of Western Australia, Plant Biology, 35 Stirling Highway, Crawley, WA, 6009, Australia

634 MILLER, CHRISTOPHER

### Population Dynamics and Restoration of *Mauritia flexuosa* palm swamps (aguajales) in the Peruvian Amazon

*Mauritia flexuosa* (aguaje) is a dioecious palm species found throughout in the Amazon Basin and can form dense mono-dominant stands in wetlands (aguajales). This species is widely harvested for its economically important fruits in the Peruvian Amazon, which are widely eaten by many forest mammals and

birds. In recent decades the widespread destructive harvesting of aguaje has resulted in little or no regeneration of the aguajal ecosystem. The absence of *Mauritia* in these wetlands has resulted in an apparent Allee effect; in turn, this causes a widespread change in ecological succession. This study examines recent efforts to restore these aguajales along the Tahuayo River in Loreto Province, Peru and a study on the population dynamics of this species.

Saint Leo University, Science, P.O. Box 6665 MC 2127, Saint Leo, FL, 33576, USA

635 MCKINNEY, HELEN K.\*<sup>1</sup>, HUIISH, RYAN DAVID<sup>1</sup> and MATEBOTO, JOSEYA<sup>2</sup>

### Broadening implications of ethnobotany and conservation: How human influence over the past millennia may have saved a rare tree species in the South Pacific

Community-mediated management strategies for indigenous resources, employed by various communities, have shown success on local levels despite overall trends of resource decline. While the history of sandalwood trade in the South Pacific is rife with over exploitation, ancient cultural practices and modern management techniques for native *Santalum yasi* by Fijian and Tongan communities may have actually enabled *S. yasi*'s survival despite the continuing threat of over harvesting and habitat destruction. Remaining wild *S. yasi* stands lack genetic insularity typical of island populations, suggesting significant migratory events, such as the pre-historic movement of seeds and seedlings across and between Tonga and Fiji via trade, and marriage practices as documented by early explorers to these regions. Furthermore, current strategies employed by a Fijian village in the management of *S. yasi* reveal foundational principles that can guide the development of effective management of other endangered economic resources and curtail common problems of implementation. Existing local leadership within the community oversee caretaking responsibilities, ensure contract guidelines are followed, and see that compensation is appropriately earmarked towards village improvements and community benefits. The inclusion of all community members, in the benefits and responsibilities of resource tenure and stewardship, enables better prevention of poaching, and fiscal community interests. Further research and application of these, and similar practices in other areas, may help resolve current management challenges to the preservation of culturally and economically valuable species around the world.

<sup>1</sup>Hollins University, Biology, 7916 Williamson Rd., Roanoke, VA, 24020, USA <sup>2</sup>Fiji Forestry Department, Kadavu Island, Fiji

636 JENSEN, HELEN<sup>\*1</sup>, DREISEITL, ANTONIN<sup>2</sup>, SADIKI, MOHAMMED<sup>3</sup> and SCHOEN, DANIEL J.<sup>1</sup>

### The evolution of pathogen resistance in traditional varieties of barley (*Hordeum vulgare*) conserved on-farm versus in seed bank collections.

Traditional varieties of crop plants are often conserved in seed banks (*ex situ* conservation). It may, however, be preferable to conserve them in their native environment (*in situ* conservation), to ensure continued adaptation to evolving pathogen virulence. We tested if collections of a traditional variety of barley (*Hordeum vulgare* ssp. *vulgare*) collected in Morocco and conserved *ex situ* for 23 years show a decline in resistance to an endemic fungal foliar pathogen, *Blumeria graminis* f.sp.*hordei* (*Bgh*), compared with *in situ* collections that have been continuously cultivated in the region. We measured the qualitative and quantitative resistance to *Bgh* of these collections using detached leaf assays and field trials. *Ex situ* collections did not show a significant decline in qualitative resistance to eight specific isolates of powdery mildew, compared to *in situ* collections. In field trials, however, where plants were exposed to naturally occurring powdery mildew inocula, there were both increases and decreases in quantitative resistance in *ex situ* versus *in situ* collections. Overall, in this study system, *in situ* conservation resulted in both adaptive and maladaptive changes in the quantitative resistance of the crop germplasm, depending on the collection tested. This challenges the assumption that *in situ* conservation consistently results in improved adaptation to pathogen virulence and suggests a more complex scenario, consistent with examples of plant-pathogen co-evolution in wild systems. We discuss these findings with regards to resistance evolution and crop germplasm conservation.

<sup>1</sup>McGill University, Department of Biology, 1205 Dr. Penfield Avenue, Montreal, QC, H3A 1B1, Canada<sup>2</sup>Agricultural Research Institute Kromeriz, Department of Plant Protection, 2787 Havlickova, Kromeriz, 76701, Czech Republic<sup>3</sup>Institut Agronomique et Vétérinaire Hassan II, Département d'Agronomie et d'Amélioration des Plantes, B.P. 6202 Rabat-Instituts, Rabat, Morocco

637 DIAZGRANADOS, MAURICIO, WAHIDI, LILA, VINZON, PAOLO and BARBER, JANET<sup>\*</sup>

### Predicting impacts of climate change on future distributions of Macaronesian *Sideritis*

Macaronesian *Sideritis* L. comprises an endemic clade of 23 species of suffrutescent to woody perennials. The species are restricted to the Atlantic archipelagoes of the Canary Islands and Madeira and represent one of the most spectacular Macaronesian plant radiations. The insular *Sideritis* clade – indeed the entire native Macaronesian flora – survives in a precarious state, threatened by land use practices and climate change. Only four species are found on more than one island and populations in general are small and narrowly restricted to specific ecological zones. Several species are considered threatened or endangered. The goal of this project is to generate working hypotheses to predict how these plants will respond to climate change. We databased all herbarium collections of *Sideritis* from nine herbaria and from published literature, a total of 222 collections; of these, 208 are georeferenced. Modeling was performed with Maxent 3.3.3a and ArcMap 10, using layers of climate (19 bioclim layers) and elevation with a resolution of 30 arc-seconds available through the Worldclim database ([www.worldclim.org](http://www.worldclim.org)). Predictions were inferred using thirty different scenarios of climate change for the years 2020-2080 and employing different models (CCCMA-CGCM3.1, CSIRO-MK30, IPSL-CM4, MPI-ECHAM5, UKMO-HADCM3, NCAR-CCSM30) for two emission scenarios (A1b and dB2a). Outcomes vary depending on individual species, years and scenarios. In general, most scenarios predict a decrease in distribution area for most species, with 1-8 species predicted to become extinct by 2080. Unexpectedly, some models predict an increase in the distribution area for 2-7 species, coupled with a displacement or concentration of suitable areas. One caveat to these predictions is that the models do not incorporate impacts of land use practices. Overall, our results suggest an active, ongoing dynamic for species of Macaronesian *Sideritis*. These results provide an unprecedented opportunity to test biogeographic processes and responses to climate change and should lead to a better understanding of the specific variables contributing to species distributions in this diverse and threatened clade.

Saint Louis University, Department Of Biology, 3507 Laclede Avenue, St. Louis, MO, 63103, USA

638 SAAR, DAYLE

**Red and White Mulberries (*Morus rubra* and *M. alba*: Moraceae) and Their Interspecific Hybrids: the "Real" Red Mulberry is not as Previously Thought**

*Morus rubra* (Red Mulberry) is the only mulberry native to eastern North America; only two species are native to this continent. *M. alba* (White Mulberry) is naturalized from Asia and is widespread throughout the United States, as a result of escapes from cultivation, both as a street planting and from unsuccessful attempts to establish a silk industry in this country (leaves used to feed larvae of the silkworm, *Bombyx mori*). Both species produce leaves of similar size and shape, and fruits are often the same color. For well over a century, plant keys and other literature have distinguished the two species based almost exclusively on the abundance (or lack of) and location leaf pubescence. The two species readily hybridize, and the fairly common trait of intermediate pubescence has been the presumed result. Results of this study with DNA-identified individuals demonstrate that leaf pubescence is not a reliable character for field identification of these two species. Further, hybrids are quite common and are often cryptic when judged on pubescence. *M. alba* and interspecific hybrids have been located in relatively undisturbed habitats, misidentified by current morphological criteria, but confirmed by molecular data. *M. alba* appears to be more cold-hardy, and this trait has been imparted on the hybrids. Based on our preliminary data, present maps show an inflated geographic range for *M. rubra*, including states where the "true" *M. rubra* probably does not exist. In at least one of these states, it appears that individuals of *M. alba*, misidentified as *M. rubra*, have been declared "threatened" in that state. Currently, DNA identifications are being compared with trees in an effort to discover more reliable morphological characters for field identification. Leaf vein patterns appear to be much more reliable than pubescence, and more testing is underway to confirm this. Reliable identifications based on morphology are imperative for field botanists and conservation personnel, particularly where *M. rubra* is an imperiled species.

Murray State University, Department of Biological Sciences, Biology Building 1112D, Murray, KY, 42071, USA

639 VANDERWEIDE, BENJAMIN\*, SANDERCOCK, BRETT and FERGUSON, CAROLYN

**Mark-recapture analysis of herbarium data from the northern Flint Hills of Kansas, USA**

Data from herbarium specimens are frequently used to track changes in flora, including range shifts, extinctions, and species introductions. However, the detection probability of a plant species in a flora is often less than one and is not constant across space, time, or taxa. As a result, studies of regional species richness may report patterns where there are none or miss patterns that exist. Furthermore, the number of species in regional flora may often be grossly underestimated. Capture-mark-recapture (CMR) tools are widely used to account for such problems in the study of demographic patterns in plant and animal populations and communities, and may be useful for the analysis of herbarium data. We obtained data representing herbarium specimens collected between 1892-2005 from seven counties of the northern Flint Hills of Kansas, USA, from the Kansas State University Herbarium (KSC) and the University of Kansas R. L. McGregor Herbarium (KANU) in October 2010. Robust design model was used to perform the initial analysis. This model combines open and closed population modeling to estimate population size (the number of species in the flora), apparent survival ( $\phi$ ), and the detection probability ( $p$ ), among other parameters. Four periods of peak collection were used as the primary sampling occasions: the first from 1892-1897, the second from 1924-1929, the third from 1972-1977, and the fourth from 2000-2005. The initial analysis indicates that many parameters, including estimates of species richness and detection probability, are dependent on collecting effort. Furthermore, compared to analysis of the raw data, the robust design analysis indicated a significant linear increase in introduced species richness in the regional flora over time. Despite limitations of herbarium data, these initial analyses suggest that capture-mark-recapture methods may be used to account for these problems, providing better estimates of changes in regional flora over space and time and valuable insights into collection patterns.

Kansas State University, Division of Biology, Ackert Hall, Manhattan, KS, 66506, USA

640 FRANCES, ANNE\*<sup>1</sup>, CORDEIRO, JAY<sup>2</sup>, KABAY, EDWARD<sup>3</sup>, OLIVER, LEAH<sup>1</sup>, YOUNG, SUZANNE<sup>1</sup> and YOUNG, BRUCE<sup>1</sup>

### Assessing Chihuahuan Desert Cacti for Vulnerability to Climate Change

We assessed 28 Chihuahuan Desert cactus species for their vulnerability to climate change using the Climate Change Vulnerability Index. Most cactus species were vulnerable to climate change: 43% were moderately vulnerable, 21% were highly vulnerable, and 4% were extremely vulnerable. None of the cactus species assessed was predicted to increase with climate change, although 4% of species were predicted to be stable. Five percent of species could not be evaluated due to insufficient evidence. The Index assesses a species' exposure and sensitivity to climate change by evaluating several factors, which are then combined to determine a categorical vulnerability score. Exposure to temperature and moisture (both historical and predicted) were quantified within the cactus species' U.S. ranges using GIS analysis. To assess a species' sensitivity to climate change, we evaluated several natural and life history characteristics. For the cactus species that were vulnerable to climate change, no single factor fully explained the increased vulnerability. However, key vulnerability factors included the potential disruption of interspecific interactions, limited hydrological niches, and likely impacts from mitigation-related land use changes in response to climate change. Many of the cactus species assessed depend on other species for pollination, to generate habit (nurse plants), and for protection from herbivory (ants). Changes in climate may result in asynchronous phenological changes or range shifts between cacti and other species upon which the cacti depend, likely increasing vulnerability. Several cactus species assessed are restricted to desert regions and depend on summer rainfall for growth and reproduction. Predicted changes in seasonal precipitation patterns coupled with increased drying resulted in increased vulnerability for these species. Species rarity was not a consistent predictor of vulnerability. The result of insufficient evidence for some species highlights the need for continued research on their basic biology, genetic diversity, and measured phenological responses to climate change. The results of this study can be used to better inform management plans and conservation activities in the Chihuahuan Desert region.

<sup>1</sup>NatureServe, 1101 Wilson Blvd., 15th Floor, Arlington, VA, 22209, USA<sup>2</sup>NatureServe, c/o University of Massachusetts Boston Biology Department, 100 Morrissey Boulevard, Boston, MA, 02125, USA<sup>3</sup>University of Maryland, College Park, Conservation Biology, 0105 Cole Field House, College Park, MD, 20742, USA

## POSTERS

641 ORTIZ, VIVIAN NEGRON

### Reproductive ecology and conservation of a federally threatened Florida Panhandle species, *Euphorbia telephioides* Chapman (Euphorbiaceae).

Conservation of imperiled plant species requires an understanding of demography and reproductive biology, including breeding system and seed ecology. *Euphorbia telephioides* Chapman (telephus spurge) is a federally threatened herbaceous species primarily endemic to xeric and mesic pine flatwoods in three counties of northwest Florida. Plants are long-lived and individuals flower and fruit profusely, but seedling recruitment is rare or absent. As part of a long-term study to understand the conservation requirements of *E. telephioides*, I am investigating the growth and reproductive biology. In 2010 I established study sites throughout this species' range and monitored plant growth (number and length of stems) and reproduction (inflorescence length, gender, fruit and seed production) monthly. Plant emergence typically occurs in April, but was dramatically delayed for two months due to cold weather in 2010. Individuals in the Bay and Gulf County populations averaged 1.3 stems whereas Franklin County population plants averaged 2.3 stems. On average the Gulf County plants had larger stems than plants in the other populations, with more vegetative growth early in the season. *Euphorbia telephioides* is diclinous with separate staminate and pistillate flowers either on the same plant or on different plants. Populations averaged more reproductive plants than sterile (mean 74 % reproductive), with more females (mean 40%) than males (mean 28 %); only one plant was found with both male and female flowers. Stem height differed significantly among the sexes, with females averaging 15.7 cm, males 13.9 cm, and steriles 11.7 cm ( $F = 3.9$ ,  $p < 0.02$ ). On average, fruit and seed production per female were higher for the Franklin population (means = 3.2 fruits, 9 seeds) than for the Bay (2.7, 8.2) and Gulf (2.3, 6.8) populations. Plants are permanently marked, enabling me to investigate growth and gender change relationships across years. Germination studies, which will be initiated in spring 2011, and conservation implications, will be discussed.

U.S. Fish and Wildlife Service, 1601 Balboa Avenue, Panama City, FL, 32405, USA

642 SCHWABE, ANNA\*<sup>1</sup>, NEALE,  
JENNIFER<sup>2</sup> and MCGLAUGHLIN,  
MITCHELL E<sup>1</sup>

**Analysis of nuclear DNA from *S. glaucus* and *S. parviflorus* to determine the level of directionality and hybridization between these two species**

*Sclerocactus glaucus* (Cactaceae), the Colorado Hookless cactus is an endangered plant species endemic to Colorado. Presently there is concern that *S. glaucus* is hybridizing with the closely related and more common *S. parviflorus*. If there is extensive hybridization between these two species it is possible that *S. glaucus* will effectively become extinct. *Sclerocactus glaucus* is found in western Colorado and historic estimations place the numbers of individuals at about 10,000. Current estimates of individuals predict much lower numbers as many of the sites have not been visited for over ten years. The purpose of this project is to examine the genetic structure within and among *Sclerocactus* populations to explore the extent of gene flow from *S. parviflorus* potentially threatening the continued existence of *S. glaucus*. Collaborators at the Denver Botanic Garden have collected floral tissue from about 800 individuals from both species in 35 distinct populations. The genetic data collected from nuclear microsatellite markers in these individuals will be used to determine the level of diversity between and among *S. glaucus* populations as well as the level of hybridization between *S. glaucus* and *S. parviflorus*. The DNA analysis will include development of a microsatellite library that will be used to develop 15 loci for genotyping individuals. Additionally, the genetic data will be used to assess the possibility that *S. glaucus* and *S. parviflorus* are converging to form one species or if there are two distinct and separate species. It is our expectation that these two species are hybridizing in many areas but there may still be some populations of *S. glaucus* which are isolated and are not hybridizing with *S. parviflorus*. If there are pristine populations of *S. glaucus* they can be identified and managed so this rare Colorado native cactus can be preserved.

<sup>1</sup>University of Northern Colorado, Biology, 501 20th St, Box 92, Greeley, CO, 80639, USA<sup>2</sup>Denver Botanic Gardens, University of Colorado Museum, 909 York Street, Denver, CO, 80206, USA

643 CRANDALL, RAELENE\*<sup>1</sup> and  
MASTERS, RONALD<sup>2</sup>

**Effects of timber and fire management on the understory plant community in a mixed-pine hardwood forest**

Low intensity fires were historically recurrent in mixed-pine hardwood habitats in North America. In the absence of fire, open savannas and prairies were converted to closed-canopy forests with low understory plant diversity. The Pushmataha Forest Habitat Research Area was established in the Ouachita Mountains of Oklahoma to test an array of forest management and prescribed fire regimes for large-scale application in restoration of fire-suppressed habitats. This study examined the effectiveness of these restoration efforts 17 and 18 years post-treatment by measuring understory plant community composition and species richness. Eight treatments were replicated three times in a randomized block design and sampled using 0.1 ha plots. The treatments were: (1) control; (2) four-year interval, late dormant season, rough-reduction burn; (3) harvest pine only and annual burn; and (4) five harvest pine and thin hardwood treatments with no burn, or four-, three-, two-, or one-year burn intervals. Regardless of timber harvesting, burned and unburned treatments differed in species composition and richness. Timber management alone had no effect on understory species composition or richness as compared to controls. Species richness was significantly higher in burned than unburned treatments. One- and two-year burn intervals prevented the establishment of woody species in the canopy and resulted in prairie habitat. Three-year burn intervals created savanna habitat with patchy and clumped establishment of woody species. In the four-year burn intervals, open woodlands appear to be forming at a higher density. We conclude that restoration of species richness in fire-suppressed, mixed-pine hardwood forests is possible with prescribed fire alone after extended periods of time. However, restoration of structure and function in the short term for species of special concern (i.e., woodland-grassland obligate songbirds) will require alteration of stand structure through thinning to open the canopy and restore these habitats to their historical state. Although a three-year burn interval appears to be a threshold, shifting community structure from herbaceous to woody dominated, we recommend a variable frequent fire regime.

<sup>1</sup>Washington University - St. Louis, Department Of Biology And Tyson Research Center, Box 1137, St. Louis, MO, 63130, USA<sup>2</sup>Oklahoma State University, Department of Natural Resource Ecology and Management, Stillwater, OK, 74078, USA

644 PALMER, COREY\*<sup>1</sup>,  
RICHARDSON, SARAH C.<sup>1</sup>, MIDDLETON,  
ELIZABETH<sup>2</sup>, BEVER, JAMES<sup>3</sup>, SCHULTZ,  
PEGGY A.<sup>4</sup> and YERMAKOV, ZHANNA<sup>5</sup>

### Investigating the outward spread of benefit from vesicular-arbuscular mycorrhizal fungi of varying origins into an urban prairie restoration

**B**ackground: Previous research highlights the importance of integrating soil ecological knowledge into restoration practices. There is evidence that Vesicular-arbuscular mycorrhizal (AM) fungi benefit certain plant species in prairie restorations, and may increase the rate of succession from plants of predominantly low conservation values to those of higher conservation values. Current research is addressing the effects of AM fungi on an urban prairie installation along Chicago's southern Lake Shore Drive. This study aims to quantify the maximum distance uninoculated plants can receive benefit from plants inoculated with either commercial or native fungi. Methods: Four prairie plant species were used as nurse plants, and inoculated with a mix of either commercially produced fungi of unknown ecotype or fungi species native to Chicago region prairies. The inoculated nurse plants were transplanted down the centerline of 27 study plots. Uninoculated seedlings of *Sporobolus heterolepus*, a grass shown to benefit from mycorrhizal symbiosis, were transplanted into the plots at 0.5, 1.0, and 1.5 meters from the nurse plants. Growth of *S. heterolepis* was considered an indirect measure for the outward spread of fungi from the nurse. Results: *S. heterolepis* grown in plots with native fungi nurses grew best at the 0.5 and 1 meter distances. Test plants associated with commercial fungi nurses did not grow or survive as well as those with native fungi nurse plants. Implications: Results suggest that prairie plants can access AM fungal benefit up to one meter away from an inoculation point in the first growing season. Response was strongest with native prairie fungi, suggesting there are benefits to prairie plant growth and survival when using coevolved fungi instead of fungi from an unknown ecosystem. Investigation will quantify further spread of AM fungal benefit throughout the second growing season. Future study may seek direct evidence of AM fungal spread, and explore other sources of benefit associated with the fungi that may precede actual colonization.

<sup>1</sup>DePaul University, Environmental Science, 2325 N. Clifton Ave, #1F, Chicago, IL, 60614, United States<sup>2</sup>Indiana University, 1001 E Third Street, Bloomington, IN, 47405, USA<sup>3</sup>Indiana University, Department Of Biology, Jordan Hall, 1001 East Third Street, Bloomington, IN, 47405, USA<sup>4</sup>Indiana University, Department of Biology, Jordan Hall, 1001 East Third Street, Bloomington, IN, 47405, USA<sup>5</sup>Chicago Park District, 541 N. Fairbanks, Chicago, IL, 60611, United States

645 KUTCHMAN, ROBERT R.\*<sup>1</sup>,  
BROSI, SUNSHINE<sup>2</sup> and HOWELL, JAMES<sup>1</sup>

### The impact of artificial shade cloth and substrate on the establishment success of cultivated *Actaea racemosa* L. in western Maryland, USA

**B**lack cohosh, *Actaea racemosa* L., has been popularized as an herbal treatment for symptoms associated with menopause. *Et situ* conservation efforts and commercial cultivation are uncommon with this species to date. As demand increases it is essential to determine optimal conditions for survival, growth, and production of active constituents. Limited information exists, however, on effective methods of cultivation (Fischer et al. 2006). Previous studies have shown increasing gactein and deoxyactein concentrations under increasing light using 78% artificial shade and forested areas (McCoy et al. 2007). Questions remain of the ideal shade cloth percentage for production in non-forested areas. Rhizomes from two sources were transplanted under 50, 60, 70, and 80% artificial shade. First year mortality rate under shade conditions was 35.3%. The full sun plots suffered 67% mortality. This contrasts a previous study, under irrigated conditions, which correlated successful growth in full sun (Persons and Davis 2005). One of the main factors affecting emergence and survival for this study was initial rhizome weight. Rhizomes with an initial weight of less than 10g experienced 90% mortality, while rhizomes weighing above 50g had over 50% survival. Initial rhizome size was significantly correlated with plant height ( $r^2=0.13$ ,  $p=0.0446$ ), but not diameter ( $r^2=0.07$ ,  $p=0.2653$ ). Between artificial shade percentages there were no significant differences in survival, height, or diameter ( $p > 0.05$ ). Future studies include evaluating the material for active constituents. This research will aid in identifying factors for *et situ* conservation and cultivation for this important medicinal herb. Fischer, J., M. Berti, R. Wilckens and A. Del Pozo. 2006. Development of vegetative propagation for *Actaea racemosa* Nutt. Industrial Crops and Products. 24, 244-252. McCoy, J., J.M. Davis, N.D. Camper, I. Khan, and A. Bharathi. 2007. Influence of rhizome propagule size on yields and triterpene glycoside concentrations of black cohosh. [*Actaea racemosa* L. syn *Cimicifuga racemosa* (L.) Nuttall]. HortScience 42:61-64. Persons, W.S. and J.M. Davis. 2005. Growing and marketing ginseng, goldenseal, & other wood-land medicinals. Bright Mountain Books, Inc., Fairview, N.C. 466pp.

<sup>1</sup>Allegheny College of Maryland, Science, 12401 Willowbrook Road, Cumberland, MD, 21502, USA<sup>2</sup>Frostburg State University, Biology, 101 Braddock Road, Frostburg, MD, 21532, USA

646 ZANDER, RICHARD

### Epistemological Extinction Threatens Rare and Endangered Taxa

Phylogenetic analysis is problematic, being axiomatic, and long touted as a theory-free, discovery process. The cladogram is considered a discoverable fundamental pattern in nature, following the rationale of structuralism in other fields. All non-phylogenetically informative information is "mapped" or otherwise relegated to the cladogram by phylogeneticists. Because the axiomatic quasi-mathematical method deals only with synchronic (present-day) relationships, the model of one taxon being derived from another taxon of the same or lower taxonomic rank is wrongly not considered, macroevolution being considered nonaxiomatic scientific theory thus mere narrative. Microevolution (descent with modification of traits) substitutes in cladograms for macroevolution (descent with evolution of taxa). Strict phylogenetic monophyly ensures that macroevolution is never modeled in cladograms through taxonomic recognition of paraphyletic groups. The result is that some taxa that are paraphyletic or apophyletic on molecular trees are threatened with (1) complete loss of their scientific names (underlexicalization), (2) downgrading of rank to force them into taxonomically and evolutionarily different ancestral or derived groups, or (3) burial among a proliferation of molecularly distinguishable "cryptic" taxa (overlexicalization). Some of these threatened taxa are rare and endangered and all are evolutionarily distinctive by expressed traits. Loss of names stymies conservation efforts by hiding or masking important taxa, or eliminating them entirely from consideration. Examples are given.

Missouri Botanical Garden, Science and Conservation, PO Box 299, St. Louis, MO, 63166, USA

647 SAVO, VALENTINA\*<sup>1</sup>, CANEVA, GIULIA<sup>2</sup> and GUARRERA, PAOLO MARIA<sup>3</sup>

### Food for body and mind: the evolution of the idea related to traditional food in the Tolfa area (Central Italy)

In Europe, the fast changing socio-economic conditions, especially the lack of time and the disconnection between older and younger generations, threaten the persistence of the remained knowledge about wild plants. In industrialized countries there is a considerable rise in expenditure for convenience food, but also a renewed interest for local or traditional food, since it is considered natural and healthy. The landscape of the Tolfa area (central Italy) is characterized by a mosaic of pastures, cultivated land and woodland. The area has been inhabited since the end of the Bronze Age (9th-8th centuries B.C.). The aim of this study, developed

in a wider research project, was to assess the amount of wild and cultivated plants used for traditional food preparations and to define the people idea or perception related to them. A total of 45 semi-structured interviews were carried out in the research area between Spring 2010 and Spring 2011. Data on wild plants, traditional food preparations and perception were collected. Wild species used to prepare traditional dishes are about 50: they are consumed raw or cooked, especially to prepare soups (as for example the *acquacotta*) or as side dishes. Few species are used to prepare alcoholic beverages. Most species are still consumed by inhabitants of the area and the main part of uses is still present, a little percentage of uses is disappearing or already disappeared. Some informants reported the widespread use of traditional food to attract tourists in new food festivals, wild plants are no more famine food, but used as a sort of brand idea. Traditional food is still consumed by local families: generally during Feasts and celebrations but rarely in the everyday life. On the other hand, it is often served in local restaurants and during food festivals, which have been recently created, as a tourist attraction.

<sup>1</sup>University Roma Tre, Environmental Biology, Viale Marconi, 446, Rome, RM, 00146, Italy <sup>2</sup>University Roma Tre, Environmental Biology Dept, Viale Marconi, 446, Rome, RM, 04014, Italy <sup>3</sup>Istituto Centrale per la Demoetnoantropologia, Piazza G. Marconi 8, Rome, RM, 00144, Italy

648 BROECKER, LAUREN\*<sup>1</sup>, ALBRECHT, MATTHEW<sup>2</sup>, ROMERO HERNANDEZ, CAROLINA<sup>3</sup> and MILLER, ALLISON<sup>4</sup>

### Conservation Genetics of *Geocarpon minimum*

Intraspecific genetic variation provides the foundation for species to respond to changes in the environment, and empirical studies have shown that decreased levels of intraspecific genetic variation are correlated with greater extinction risk. *Geocarpon minimum*, an endangered plant species native to the central Midwest (Arkansas, Louisiana, Missouri, and Texas), is listed under the Endangered Species Act. As the only species in the genus, *G. minimum* is considered a relict species, one that was once widespread in North America but whose distribution has become smaller over time due to changing climate and habitat. In this study, we characterized the amount and structure of genetic variation in 14 *G. minimum* populations using amplified fragment length polymorphisms (aflps). Three primer pairs yielded 237 fragments which were used to estimate genetic variation within and among populations. The resulting data revealed that *G. minimum* populations harbor low levels of genetic variation. The three most genetically depauperate populations were collected on Bona Glade MO (MOBG), Halltown Glade MO (MOHG), and Truman Lake MO (MOTL). Further, *G. minimum* populations exhibited substantial population structure ( $G_{ST-B} =$

0.43). These data will be used by the United States Fish and Wildlife Service to refine conservation strategies for *G. minimum*.

<sup>1</sup>Saint Louis University, Biology, 3507 Laclede Avenue, St. Louis, MO, 63103, USA<sup>2</sup>Missouri Botanical Garden, P.O. Box 299, St. Louis, MO, 63166, USA<sup>3</sup>PhD Student-Saint Louis University, Biology, 2118A Cleveland Pl., Saint Louis, MO, 63110, USA<sup>4</sup>Saint Louis University, Department Of Biology, 3507 Laclede Avenue, St. Louis, MO, 63103, USA

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## Ecophysiology

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### ORAL PAPERS

649 CAUDLE, KERI\* and MARICLE, BRIAN

#### Responses of respiration and photosynthesis to spilled oil in coastal wetland grasses

The presence of petroleum hydrocarbon can affect plants in several ways, including toxicity to cells, disruption of plant nutrient uptake, and reduced exchange of oxygen between the plant and environment. The objective for this project was to study the effects of spilled oil on photosynthesis and respiration in several important members of the Gulf Coast plant community. Native smooth cordgrass (*Spartina alterniflora*), introduced reed canarygrass (*Phalaris arundinacea*), and introduced common reed (*Phragmites australis*) were exposed to 6 L m<sup>-2</sup> oil for six weeks in greenhouse experiments. Photosynthesis and anaerobic respiration were measured following exposure to oil in sediments. Maximum photosynthesis rates were 50% higher in C<sub>4</sub> *S. alterniflora* compared to C<sub>3</sub> *P. arundinacea* and *P. australis*. However, photosynthesis was not influenced by oil in any of the three species. Root alcohol dehydrogenase (ADH) activities indicated oxygen deficiency in roots of *P. arundinacea*, but not in *S. alterniflora* or *P. australis*. Root ADH activities increased ten-fold in flooded *P. arundinacea*. By contrast, root ADH activities remained low and unchanged in flooded *S. alterniflora* and *P. australis*. Tolerance to spilled oil in soil relates to tolerance of anaerobic conditions in submerged tissues. The highly flooding-tolerant *S. alterniflora* and *P. australis* were better able to tolerate limited gas exchange in roots compared to the relatively flooding-sensitive *P. arundinacea*, which became oxygen stressed by the oil treatment. Therefore, oil spills could lead to opportunities for invasion by highly flood-tolerant nonnative species in coastal marshes. Understanding physiological responses to environmental stress, such as an oil spill, could lead to ecological awareness and preservation of wetland habitats.

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Fort Hays State University, Department Of Biological Sciences, 600 Park St., Hays, KS, 67601-4099, USA

650 DRENOVSKY, REBECCA<sup>\*1</sup>,  
KOEHLER, CATHERINE<sup>2</sup>, SKELLY,  
KATHRYN<sup>1</sup> and RICHARDS, JAMES<sup>3</sup>

### Nutrient resorption plasticity in California chaparral woody species

Nutrient conservation mechanisms play key roles in plant adaptation to low nutrient availability. Resorption (the recycling of nutrients from senescing tissues) is considered one of the most important traits plants have to retain nutrients, but its relationship to soil nutrient availability is unclear. We proposed that phylogenetic relationships and various environmental factors may obscure relationships between soil nutrient availability and plant nutrient resorption. For six years, we collected senesced leaf tissue from community dominants and congener pairs found on and off serpentine (low nutrient) soils. In year five we collected soils under the target congener pairs. We hypothesized that serpentine species would be more proficient at N and P resorption, due to low nutrient availability on these soils. Both serpentine and non-serpentine soils were low in nitrogen availability, with non-serpentine soils having lower total soil N ( $P=0.001$ ) and serpentine soils have higher soil C:N ( $P<0.0001$ ). Extractable soil P was 1.9-fold higher on non-serpentine compared to serpentine soils ( $P=0.0002$ ). Non-serpentine and serpentine species were equally proficient at N resorption ( $P>0.05$ ), but serpentine species were more proficient at P resorption ( $P<0.0001$ ). Large interannual variability was observed in resorption proficiency in all species studied, but this variability was not strongly related to either seasonal or annual variability in temperature or precipitation. Our data suggest that controlling for phylogeny can aid in interpretation of resorption patterns. More importantly, our study clearly shows that resorption patterns can only be discerned through long-term datasets, of which few exist in the literature.

<sup>1</sup>John Carroll University, Biology, 20700 North Park Blvd, University Heights, OH, 44118, USA<sup>2</sup>University of California, Davis, Donald and Sylvia McLaughlin Natural Reserve, 26775 Morgan Valley Road, Lower Lake, CA, 95457, USA<sup>3</sup>University Of California Davis, Land, Air And Water Resources, One Shields Avenue, Davis, CA, 95616-8627, USA

651 EBBS, STEPHEN<sup>\*1</sup>, WHANKAEW,  
SUKHUMAN<sup>2</sup>, RHANOR, THOMAS<sup>1</sup> and  
TRIWITAYAKORN, KANAKPORN<sup>2</sup>

### Utilization of cyanide as a supplemental source of nitrogen by plants under nitrogen replete conditions and nitrogen starvation

Cyanide is generally perceived as a metabolic poison both for plants and animals. Nevertheless, ongoing studies are revealing that at the sub-toxic concentrations more commonly encountered in the natural environment, plants transport and assimilate cyanide as an alternate source of nitrogen, even in the presence of nominal concentrations of ammonium and nitrate. Hydroponic studies using wheat, sorghum, and other plants have shown that exposure to cyanide (labeled with the stable isotope  $^{15}\text{N}$ ) results in a highly significant enrichment in  $^{15}\text{N}$  without a corresponding increase in total plant N, mediated by the assimilatory activity of the  $^{\text{P}}\text{-cyanoalanine}$  pathway. Moreover, under nitrogen starvation, cyanide assimilation by this pathway increases commensurate with an increase in activity of the principal enzyme,  $^{\text{P}}\text{-cyanoalanine synthase}$ . These results indicate that assimilation of cyanide allows the cyanogenic N atom to be incorporated into primary metabolism, ostensibly as an alternate source of ammonium. Single nitrogen source growth experiments conducted with these species showed that when presented at the same concentration, plant growth was similar when nitrate, ammonium, or cyanide was the source of nitrogen, although the relative growth rate of plants grown under the cyanide regime was less than that for nitrate or ammonium. The results suggest that when cyanide is present in the soil environment, the nitrogen from this molecule can serve as a supplement to plant nitrogen metabolism, particularly when other nitrogen sources may be limiting or absent. Cyanide at non-toxic concentration may therefore be benefit to plant mineral nutrition when present in the rhizosphere.

<sup>1</sup>Southern Illinois University Carbondale, Plant Biology, 420 Life Science II, 1125 Lincoln Dr., Carbondale, IL, 62901-6509, USA<sup>2</sup>Mahidol University, Institute of Molecular Biosciences, 25/25 Phuttamonthon 4 Road, Salaya, Nakhon Pathom , 73170, Thailand

**Xylem transport of CO<sub>2</sub> derived from root respiration indicates that tree root respiration has been substantially underestimated.**

We measured the quantity of CO<sub>2</sub> released from root respiration that moved internally in xylem sap in nine *Populus deltoides* trees throughout a growing season. We compared that CO<sub>2</sub> flux with the CO<sub>2</sub> efflux from the soil surface, which is generally considered to measure soil (autotrophic plus heterotrophic) respiration. The internal transport of root-derived CO<sub>2</sub> was calculated from measurements of sap flow and dissolved CO<sub>2</sub> concentration ([CO<sub>2</sub>]) in the xylem at the base of the stem. Soil CO<sub>2</sub> efflux was measured using the [CO<sub>2</sub>] gradient approach. We found that on a daily basis the amount of CO<sub>2</sub> that fluxes upward from tree root systems into stems via the xylem stream rivals the amount of CO<sub>2</sub> diffusing from the soil surface. Over the growing season, the internal transport of root-derived CO<sub>2</sub> increased total belowground respiration by 33%. This indicates that autotrophic respiration was substantially higher than previously estimated, and also higher than heterotrophic soil respiration. The quantity of internally transported CO<sub>2</sub> was influenced by both seasonal and daily environmental factors that influenced sap flow rates. We observed high concentrations of CO<sub>2</sub> in xylem sap, ranging from 1% to 20% [CO<sub>2</sub>] among and within individual trees through time. Our results provide evidence that belowground autotrophic respiration consumes a larger amount, and stem respiration consumes a smaller amount, of carbohydrates than previously realized. Our findings have important implications for our understanding of the physiological functioning of trees and carbon cycling in forests. Our observations of an alternative pathway for root-derived CO<sub>2</sub> flux highlights the inadequacy of using CO<sub>2</sub> efflux to the atmosphere alone to measure root respiration. We suggest the internal transport of root-derived CO<sub>2</sub> should be measured concurrently with CO<sub>2</sub> efflux to the atmosphere to more fully understand rates of respiration of trees.

University of Georgia, Forestry and Natural Resources, 180 E Green Street, Athens, GA, 30602, USA

**Desert shrub responses to seasonal timing of precipitation are contingent on soil depth: long-term experimental evidence, from leaves to populations.**

Climate change is predicted to alter the variability of precipitation and soil water storage in arid environments. We examined how 17 years of experimental changes in precipitation seasonality affected cover, crown and canopy volume, population density, and ecophysiology of big sagebrush (*Artemisia tridentata*) relative to soil water content, in plots with shallow or deep soils. We hypothesized that supplemental winter precipitation (WIN) would favor shrub growth at organism and population scales via increased soil water storage, relative to ambient (AMB) and supplemental summer (SUM) precipitation. WIN increased volumetric soil water content 4-8 percentage points (i.e., 18% to 22%) relative to AMB, resulting in abundant and uniformly distributed soil water through July in most years. WIN resulted in greater shrub cover, crown and canopy size (volume), and density (individuals/m<sup>2</sup>) relative to both SUM and AMB in deep-soil plots, but WIN reduced shrub cover and size in plots with shallow soils (1 m depth). SUM increased water content of the top 40 cm of soil by 2-4 percentage points, but did not increase shrub size and cover. These treatment effects suggest a strong role for deep soil water, yet AIC modeling analysis showed that water in both the shallowest (0-20 cm) and deepest (>1 m) soil depths were important predictors of shrub growth. Instantaneous photosynthetic gas exchange and plant water potentials were similar among the treatments throughout the growing season, but more negative δ<sup>13</sup>C of sagebrush shoots in WIN indicated decreased water-use efficiency throughout the growing season. Our experimental results suggest that the seasonal timing of precipitation has equal or greater effects compared to the amount of annual precipitation on this dominant and widespread shrub species. However, strong and predictable soil-depth contingencies on the effects of precipitation seasonality presage a landscape mosaic of changes in shrub abundance due to climate change.

Idaho State University, Biology, Pocatello, ID, 83209, USA

654 EILTS, J. ALEXANDER

**An early look at the transport of mineral resources in the clonal forb *Fragaria vesca* L**

The movement of resources within plants is critical to their growth, competition and herbivore responses. In clonal plants the movement of resources between ramets can facilitate the persistence of ramets and whole clones in otherwise unfavorable conditions. Though this movement or sharing of resources between ramets has been shown to provide numerous benefits for survival, little is known about which tissues act as the pathways of long distance transport under varying resource availabilities. To better understand the responses in resource sharing between ramets I have made a preliminary exploration of the tissues through which mineral resources are transported in the clonal forb *Fragaria vesca*. I conducted two experiments to address whether xylem or phloem predominates in inter-ramet movement of mineral resources. The first experiment measured gas exchange in two-ramet, clonal fragments under varying experimental resource availabilities seeking a signal of water transport regulation. The second experiment utilized a radio isotope of phosphorus to examine phosphorus uptake and retention in two-ramet, clonal fragments under manipulated resource availability conditions in addition to a phloem girdling treatment applied to the connecting stolon. Contrary to expectations, transpiration was greatest in ramets receiving fertilizer connected to an unfertilized partner. The specific activity from the radio isotope of phosphorus was higher only in the unfertilized, labeled ramets with the girdling treatment applied suggesting accumulation was reduced when phloem could act to export the phosphorus. Though both experiments are preliminary in their findings, they suggest that phloem, not xylem, dominates as the transport tissue for mineral resource sharing in this species. This finding contradicts preconceived expectations about resource sharing in clonal plants. The implications of phloem versus xylem transport of mineral resources in clonal plants will be discussed along with future directions of this work.

University Of Minnesota, Ecology, Evolution & Behavior, 1987 Upper Buford Circle, 100 Ecology, St. Paul, MN, 55108, USA

655 OLSEN, JACOB\*<sup>1</sup>, TETREAU, HANNAH<sup>2</sup>, GOAD, RACHEL<sup>3</sup>, MENDOLA, MEREDITH<sup>3</sup>, JOHNSON, LORETTA<sup>2</sup>, BAER, SARA<sup>3</sup> and MARICLE, BRIAN<sup>4</sup>**Photosynthetic variation of big bluestem and sand bluestem influenced by ecotype and precipitation**

Big bluestem is a perennial, warm-season, C<sub>4</sub> grass that dominates tallgrass prairies in North America. It has high variation of phenotypes among its ecotypes across the Great Plains. No attempt has been made previously to study ecotypes of big bluestem over a large precipitation gradient. Four ecotypes of big bluestem, including a common cultivar Kaw, and one ecotype of sand bluestem were reciprocally transplanted in four locations across the east-west precipitation gradient of the Great Plains. Source populations for the native ecotypes, collected from pristine prairies in central and eastern KS, and southern IL, were planted across the precipitation gradient (400 mm/yr to 1200 mm/yr) in Colby, Hays, and Manhattan, KS and Carbondale, IL. Photosynthetic measurements were taken on each plant during times early, middle, and late in the growing season. Sand bluestem exhibited photosynthetic rates 23% higher across sites than big bluestem, possibly through development of lower water potentials or through structural adaptations of leaves. The Hays ecotype exhibited photosynthetic rates 15% higher across all sites than Kaw, the closest rival of the big bluestem ecotypes, showing the Hays ecotype has adapted to dry conditions, but can take advantage of high rainfall when available. Differences between ecotypes became especially pronounced at drier sites, where putative drought adaptations of the Hays ecotype were particularly advantageous. The results of this project give knowledge on the potential fate of the Great Plains ecosystem in the face of impending climate change.

<sup>1</sup>Fort Hays State University, Department of Biological Sciences <sup>2</sup>Kansas State University, Division of Biology <sup>3</sup>Southern Illinois University, Department of Plant Biology <sup>4</sup>Fort Hays State University, Department of Biological Sciences, 600 Park Street, Hays, Kansas, 67601, USA

656 CARTER, JACOB\*<sup>1</sup> and NIPPERT, JESSE<sup>2</sup>**The maintenance of physiological functioning by *Tamarix ramosissima* across a broad soil salinity gradient**

Developments of dams, stream diversions, and groundwater pumping have altered stream flow regimes in riparian ecosystems of western North America. These alterations have decreased periodic overbank flooding, which has led to salinization and lowered water

table height in riparian ecosystems. These factors have subsequently contributed to the decline of native mesic tree species. As hydrologic processes have changed over the past century, the exotic, invasive plant species *Tamarix ramosissima* has increased in range, abundance and cover in riparian ecosystems. Understanding how changes in riparian salinization impact *Tamarix* physiology may facilitate predictions of *Tamarix* responses in the future. In this study, we investigated the response of *Tamarix* leaf-level and whole-plant physiology to increasing salinity using both field and controlled environment studies. To measure the impacts of soil salinity on *Tamarix* physiology in the field, we measured leaf-level responses across a broad range of salinity concentrations at two sites in western Kansas. Light saturated photosynthesis ( $A_{sat}$ ), stomatal conductance to water ( $g_s$ ), intracellular  $[CO_2]$  ( $C_i$ ), leaf  $\delta^{13}C$ , and leaf water potential ( $\psi_w$ ) were relatively constant over a range of soil salinities (0.5 to 17.65 mmhos/cm). Leaf-level responses were also assessed by canopy position (bottom, middle, or top of tree), but a salinity\*position response was not significant ( $p > 0.05$ ) for leaf-level physiological responses and  $\delta^{13}C$ . To increase the range of soil salinities (0.22, 54 mmhos/cm), *Tamarix* cuttings from both field sites were grown in a controlled environment. *Tamarix* leaf-level physiology was consistently lower at the highest salinity (54 mmhos/cm). Results from this study also suggest that acclimation to high salinity occurs quickly over time as reflected by leaf-level physiology and dark-adapted chlorophyll fluorescence ( $F_v/F_m$ ). This data illustrates the robust physiological functioning of *Tamarix* in response to increasing salinity. Our results suggest that the physiological tolerance of *Tamarix* to a range of soil salinities is one mechanism facilitating range expansion and persistence in riparian ecosystems.

<sup>1</sup>University of Kansas, Ecology and Evolutionary Biology, 1200 Sunnyside Ave., Lawrence, KS, 66045, USA <sup>2</sup>Kansas State University, Biology, 116 Ackert Hall, Manhattan, KS, 66506, USA

**657 GEVAERT, SCOTT\*<sup>1</sup> and DONOVAN, LISA<sup>2</sup>**

### **Spatial and temporal variation in drought induced mortality for the rock outcrop annual sunflower, *Helianthus porteri***

**P**lant communities which occur in depressions on granite outcrops in the southeastern United States have been used to demonstrate the role of drought stress in shaping community structure by driving species zonation. Here we ask whether drought may additionally be an agent of selection driving adaptive differentiation for geographically isolated populations. We focused on an endemic annual species that has to persist through hot, dry summer conditions in order to reproduce in the fall, *Helianthus porteri*. We followed plant performance (height and survival to flowering) and water status of *H. porteri* plants in three populations (CMR, PM, HR) that

spanned its range in GA, and in relatively wet and dry habitats within each population. The three year study encompassed a regional drought year (2008), a relatively wet year (2009) and a year with approximately average precipitation (2010). Population differences in plant growth and survival depended on year, with the fewest differences apparent during the wettest year, and the greatest differences in the drought year when all plants at HR died before flowering. There was also variation within populations, with sites initially identified as relatively dry having lower growth and survival whenever habitats differed. Survival to flowering was correlated with soil water availability estimated by plant predawn water potentials. The range of predawn water potentials for *H. porteri* was similar to those reported for other mesic plants, suggesting that it is not drought tolerant. However, the spatial variation in plant performance of *H. porteri* related to water availability could drive adaptive differentiation in drought avoidance traits among the isolated populations. Common garden comparisons are being conducted to assess genetic differentiation among populations for traits that might be related to drought avoidance.

<sup>1</sup>University of Georgia, Plant Biology, 2502 Miller Plant Sciences, Athens, GA, 30602, United States <sup>2</sup>University Of Georgia, PLANT BIOLOGY DEPT, 2052 MILLER PLANT SCIENCES, Athens, GA, 30602-7271, USA

**658 JOHNSON, DANIEL M\*<sup>1</sup>, MCCULLOH, KATHERINE<sup>2</sup>, MEINZER, FREDERICK<sup>3</sup> and WOODRUFF, DAVID<sup>3</sup>**

### **Xylem embolism is a primary factor in drought-induced declines in leaf hydraulic conductance**

**H**draulic conductance of leaves ( $K_{leaf}$ ) typically decreases with increasing water stress and recent studies have produced conflicting results as to the mechanisms responsible for decreasing  $K_{leaf}$ . We measured  $K_{leaf}$  concurrently with ultrasonic acoustic emissions (UAE) in dehydrating leaves of several species to determine whether declining  $K_{leaf}$  was associated with xylem embolism. In addition, we performed experiments in which the surface tension of water in the leaf xylem was reduced by allowing excised leaves to take up a surfactant solution. Finally, we compared the hydraulic vulnerability of entire leaves to the leaf lamina in one species.

**L**eam hydraulic vulnerability based on rehydration kinetics and acoustic emission was very similar, except in *Quercus garryana*. However, the water potentials corresponding to the initial decline in  $K_{leaf}$  and the onset of UAE in *Q. garryana* were similar. Midvein embolism in this species started near the center of the vascular bundle and moved outward radially. In all three species tested, a surfactant-induced decline in the surface tension of water caused  $K_{leaf}$  to decline at less negative water potentials compared to leaves supplied with

water, suggesting embolism as the primary mechanism for  $K_{\text{leaf}}$  decline. Microscopy images revealed that as the fraction of embolized xylem increased,  $K_{\text{leaf}}$  declined sharply for *Q. garryana*. Measurements on *Q. garryana* leaf disks revealed that relative reductions in lamina hydraulic conductance with decreasing water potential were not as great as those observed in intact leaves, suggesting that vein embolism was the primary mechanism for reductions in  $K_{\text{leaf}}$  during dehydration.

<sup>1</sup>Ohio University, Environmental and Plant Biology, 309A Porter Hall, Athens, OH, 45701, USA<sup>2</sup>Oregon State University, Wood Science and Engineering, Richardson Hall, Corvallis, OR, 97331, USA<sup>3</sup>USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR, 97331, USA

## POSTERS

659 **KHASANOVA, ALBINA<sup>\*1</sup>, JAMES, JEREMY<sup>2</sup> and DRENOVSKY, REBECCA<sup>3</sup>**

### Impacts of drought on mineral nutrition of grasses and forbs in the Intermountain West

**D**rought decreases plant growth and limits their ability to access soil nutrients. However, it is unclear how drought impacts plant nutrient budgets, resource use efficiency and internal nutrient recycling (resorption), important components of whole plant performance. We hypothesized that drought may result in higher green leaf N (due to its negative effects on growth) but decreased photosynthetic nitrogen use efficiency and resorption. For this experiment the perennial grasses, *Elymus elymoides*, *Festuca idahoensis*, and *Pseudogegneria spicata*; the native forbs, *Achillea millefolium* and *Sphaeralcea munroana*; and the non-native forbs *Centaurea stoebe* and *Linaria dalmatica*, were grown under high and low water availability. Droughted plants had higher green leaf nitrogen concentrations ( $P < 0.0001$ ) but lower photosynthetic nitrogen use efficiency ( $P < 0.0001$ ). In response to drought, senesced leaf nitrogen concentration (a measure of resorption) was species specific ( $P < 0.0001$ ). In *Achillea millefolium*, *Centaurea stoebe*, *Linaria dalmatica*, *Festuca idahoensis*, *Pseudogegneria spicata* senesced leaf nitrogen increased with lower water availability. However, *Sphaeralcea munroana* showed no differences between control and drought plants while *Elymus elymoides* had lower senesced leaf nitrogen under drought. There was a significant species by water interaction for senesced leaf C:N ratio ( $P = 0.002$ ), with most species having a higher C:N ratio under drought ( $P = 0.0001$ ) while two species (*Linaria dalmatica*, *Pseudogegneria spicata*) did not show such effect. Higher senesced leaf C:N could have potential negative impacts on soil nutrient cycling. Future experiments should focus on the impact of drought on mineral nutrition in more closely related species (i.e., congener pairs) to account for potential phylogenetic

effects on plant nutrient resorption.

<sup>1</sup>John Carroll University, Biology Department, 20700 North Park Blvd, University Heights, OH, 44118, USA<sup>2</sup>USDA-ARS, 67826A Hwy 205, Burns, OR, 97720, USA<sup>3</sup>John Carroll University, Biology, 20700 North Park Blvd, University Heights, OH, 44118, USA

660 **WATRUD, LIDIA<sup>\*1</sup>, BOLLMAN, MICHAEL<sup>1</sup>, LEE, E. HENRY<sup>1</sup> and KING, GEORGE<sup>2</sup>**

### Sudangrass reproductive biomass responses under climate change scenarios in oak savannah and mesic prairie mesocosm communities

**P**otential climate change effects include shifts in the distribution of plant species and changes in reproductive output. We tested the hypothesis that environmental stressors such as elevated temperature and drought that are associated with climate change would increase the reproductive output of feral biofuel crop species that became established within native plant communities. Sunlit mesocosms were planted with five herbaceous native plant species found in either oak savannah or wet prairie communities in the Willamette Valley in western Oregon. A subset of the mesocosms had sudangrass (*Sorghum bicolor* [Piper]) which has been proposed as a biofuel species, planted at the same density as the native species. Three climate change scenarios were imposed on the two types of plant communities, drought (20% lower soil moisture levels), elevated temperature (+ 2° C) in the summer months, and a combination of elevated temperature and drought and tested relative to the control scenario for temperature and water. Soil moisture levels in the control mesocosms for each plant community followed seasonal patterns as measured in nearby local native oak savannah and mesic prairie communities respectively. In the oak savannah mesocosms each of the three climate change conditions resulted, as hypothesized, in an increased proportion of sudangrass reproductive biomass relative to total aboveground biomass ( $P = 0.06$ ). Interestingly, a corresponding shift of sudangrass reproductive:total biomass was not observed in the wet prairie mesocosms.

<sup>1</sup>US Environmental Protection Agency, 200 SW 35th Street, Corvallis, OR, 97333<sup>2</sup>Dynamac Corporation, 200 SW 35th Street, Corvallis, OR, 97333

661 MILLAN, PAMELA\*<sup>1</sup>, MELCHER, PETER<sup>1</sup> and SACK, LAWREN<sup>2</sup>

### Intracanopy leaf plasticity and the impact of light versus height on carbon and nitrogen isotope discrimination for five temperate deciduous tree species

The goal of this study was to determine how intracanopy microclimate impacts leaf-level traits. Many leaf traits are known to vary within canopies, such as leaf thickness, leaf area, stomatal conductance and leaf water status, and this suggests potentially strong variation in leaf nutrient composition and carbon isotope discrimination ( $\Delta$ ). We determined the impact of light and height on  $\Delta$ , nitrogen (N) and carbon (C) concentrations as well as other anatomical and morphological leaf traits. We collected leaves using an aerial lift from three crown positions, top-exposed (TE), basal-exposed (BE), and basal-interior (BI) from five common mature temperate tree species. The  $\Delta$  related to both height and light with light having a stronger signal in  $\Delta$  than height for *Betula alleghaniensis* (birch), *Ginkgo biloba* (ginkgo) and *Quercus rubra* (red oak), and height having a stronger signal on  $\Delta$  for *Liriodendron tulipifera* (tuliptree) and *Sassifras albidum* (sassafras). We also found correlations of carbon and nitrogen concentrations measured on a leaf area basis with canopy irradiance and height ( $r = 0.51-0.73$ ,  $0.29-0.33$  and  $0.50-0.73$  respectively;  $P < 0.05$ ). However, when analyzed on a leaf mass basis the N and C concentrations and N:C ratios were independent of irradiance and height ( $r = 0.009-0.16$ ;  $P > 0.10$ ). These relationships were supported using an Akaike Information Criterion (AIC) analysis of models indicating that both irradiance and height played an important role in determining  $\Delta$ ; a model based on both factors was selected above models based on either factor alone. By contrast, for  $C_{area}$ , a model based on height alone was selected and for  $N_{area}$ , the model based on irradiance alone was selected. This variation indicates species-differences in the modulation of carbon uptake and water loss across the canopy.

<sup>1</sup>Ithaca College, Biology, 953 Danby Road, Center for Natural Sciences, Ithaca, NY, 14850, United States <sup>2</sup>UCLA, 621 Charles E. Young Drive South, Los Angeles, CA, 90095, USA

662 CARINGELLA, MARISSA\*<sup>1</sup>, BOBICH, EDWARD<sup>2</sup> and EWERS, FRANK<sup>3</sup>

### Seasonal nighttime transpiration in adults and resprouts of southern California black walnut and coast live oak

Nighttime transpiration has been reported in many species, but the seasonal patterns, which may provide insight as to the mechanisms and function, have been little studied. We examined day and nighttime transpiration in two species with differing leaf habit, the deciduous southern California black walnut (*Juglans californica*) and evergreen coast live oak (*Quercus agrifolia*). For each species two growth forms were examined, adults and 2-year post-fire basal resprouts. Daytime (12pm-4pm) and nighttime (12am-4am) stomatal conductance was measured in order to determine if nighttime transpiration was occurring, and to compare the levels of occurrence between species and growth forms. Results showed consistent nighttime stomatal conductance for both species, although at a greater percentage of the daytime rate in *Q. agrifolia*. Mean day and nighttime stomatal conductance were also significantly higher in *Q. agrifolia* (day  $89.5 \text{ mmol m}^{-2}\text{s}^{-1}$ ; night  $53.5 \text{ mmol m}^{-2}\text{s}^{-1}$ ) as compared to *J. californica* (day  $49.3 \text{ mmol m}^{-2}\text{s}^{-1}$ ; night  $22.4 \text{ mmol m}^{-2}\text{s}^{-1}$ ). Within both species the resprouts had greater mean day and nighttime stomatal conductance as compared to the adults. Day and nighttime water potential measurements showed a slight increase in stomatal conductance as leaf water potential increased across both species and growth forms. No correlation was shown between stomatal conductance and percent relative humidity. The level of nighttime stomatal conductance in *Q. agrifolia* suggests an unseen benefit to nighttime transpiration in this species that outweighs the cost of transpirational water loss even in a water-limited Mediterranean-type climate.

<sup>1</sup>California State Polytechnic University, Pomona, Biological Sciences, 3801 West Temple Avenue, Pomona, CA, 91768, USA <sup>2</sup>California State Polytechnic University, Pomona, 3801 W. Temple AVE, Pomona, CA, 91768, USA <sup>3</sup>California State Polytechnic University, Pomona, Department Of Plant Biology, 3801 West Temple Avenue, Pomona, CA, 91768, USA

663 HESCHEL, M. SHANE\*<sup>1</sup>, BOWEN, C.<sup>2</sup>, EVANKOW, A.<sup>2</sup>, BIBEE, K.<sup>2</sup>, GROSSCUP, V.<sup>2</sup> and GIBSON, J.<sup>2</sup>

### Disturbance, physiological performance, and fitness of *Tamarix*.

Water relations in riparian systems of the southwestern United States can influence plant community structure. Water use has been examined in relation to *Tamarix*, *Populus*, and *Salix* abundance and distribution; however, the strength of selection on transpiration rates and stomatal conductance has rarely been investigated in this system. Here, we measured stomatal conductance and reproductive fitness of *Tamarix ramosissima* plants of different ages in an open sandbar habitat in southeastern Colorado. We also performed selection analyses to quantify direct and indirect sources of natural selection on water use in *Tamarix*. We detected weak and inconsistent selection on stomatal conductance across two seasons indicating that water use might not have a strong role in fecundity and community interactions.

<sup>1</sup>Colorado College, Biology, 14 E. Cache La Poudre St., Colorado Springs, CO, 80903, USA<sup>2</sup>Colorado College, Biology

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## Evolutionary Developmental Biology (Evo-Devo)

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### ORAL PAPERS

664 WHIPPLE, CLINTON\*<sup>1</sup>, BYBEE, SETH<sup>1</sup> and JACKSON, DAVID<sup>2</sup>

### Evolution of a bract suppression mechanism in the grass family

Leaf growth is often suppressed after the transition from vegetative to reproductive growth. Inflorescence leaves are called bracts, and bract suppression has evolved several times in the angiosperms. We have begun a genetic characterization of the bract suppression pathway in the grass family. Several maize mutants with de-repressed bract growth, known as *tasselsheath* (*tsh*), have been isolated. The genes responsible for two of these mutants, *tsh1* and *tsh4*, have been cloned. Interestingly, the *Tsh1* and *Tsh4* orthologs in *Arabidopsis* do not have a bract suppression function and it appears that distinct bract suppression mechanisms have evolved in the Brassicaceae and the Poaceae. The genetic mechanism of bract suppression is conserved in distantly related grasses as the barley *third outer glume* (*trd*) and the rice *neck leaf1* (*nl1*) mutants both have a similar bract growth phenotype and are caused by mutations *Tsh1* orthologs. We are currently investigating the evolution of *NL1/Tsh1/TRD* (*NTT*) genes in grasses and bracteate outgroups. Our phylogenetic analysis indicates that there are three paralogous clades of *NTT* genes in the grasses created by sequential duplication events. Interestingly, the lineage containing the bract suppression genes *Tsh1*, *NL1* and *TRD* arose before the evolution of bract suppression at the base of the grass family. When expressed in lateral organs of transgenic *Arabidopsis*, both *HAN* and *Tsh1* are capable of suppressing outgrowth, suggesting that grass bract suppression involved evolution of a novel expression domain in the *NTT* lineage. We are testing for this by examining the expression domains of *NTT* and related genes in grasses and outgroups.

<sup>1</sup>Brigham Young University, Biology, 401 Widb. Provo, UT, 84604, USA<sup>2</sup>Cold Spring Harbor Laboratory, 1 Bungtown Rd., Cold Spring Harbor, NY, 11724, USA

665 XIANG, QIUYUN (JENNY)\*<sup>1</sup>,  
FENG, CHUNMIAO<sup>2</sup>, LIU, XIANG<sup>3</sup>, YU, YI<sup>3</sup>  
and FRANKS, ROBERT<sup>1</sup>

### Post-gene-duplication alteration in selection, co-evolution, expression, and post-transcription regulation of MADS-box B-class genes in dogwoods (*Cornus*, Cornaceae) - Deciphering the genetic links to bract petaloidy evolution

The MADS-box B-class genes have duplicated repeatedly during angiosperm evolution. It is hypothesized that the extensive duplication of B-class genes accounts for the floral diversification observed in angiosperm and is responsible for the heterotopic petaloidy via ectopic expression (Homeoheterotopy). However, the molecular and evolutionary mechanisms underlying the hypothesis has not been well understood. The two B-class genes *PI* and *AP3* homologs were derived from an ancient gene duplication event, and are known to form obligate heterodimers in regulating petal development in the model plants. This predicts co-evolution of gene sequences and co-expression of *AP3* and *PI* homologs in petals and petaloid organs, according to Homeoheterotopy. We test this hypothesis by analyses of sequence co-evolution, comparative gene expression and analysis of floral and bract development for six species of *Cornus* that are divergent in inflorescence architecture and bract morphology. Our preliminary results showed that *PI* and *AP3* homologs in *Cornus* have co-evolved. They are co-expressed in floral development. However, in bract development, alteration in selection, co-evolution partnership, and expression pattern have occurred following *PI* duplication, which have likely contributed to the evolution of petaloidy in the flowering dogwood *C. florida*. Our results further suggest that bract petaloidy probably evolved independently in the bunchberry *C. canadensis*, via a different molecular mechanism that may not involve *PI*. The data raise a possibility of *AP3* functioning by forming homodimers. Finally, we report the expression of petal specific *AP3* splice isoforms not detected in the petaloid bracts that are predicted to encode truncated *AP3* proteins, suggesting deviation of the molecular mechanism in bract petaloidy from that of petals.

<sup>1</sup>North Carolina State University, Genetics, Raleigh, NC, 27695, USA  
<sup>2</sup>North Carolina State University, 2214-A Gardner Hall, Campus Box 7612, Raleigh, NC, 27695-7612, USA  
<sup>3</sup>North Carolina State University, Plant Biology, Gardner Hall 2115, Campus Box 7612, Raleigh, NC, 27695, USA

666 PUHR, ROSEMARY\*<sup>1</sup> and  
MALCOMBER, SIMON<sup>2</sup>

### Evolution of the flavin monooxygenase/ *YUCCA SPARSE INFLORESCENCE1* lineage in grasses

The *YUCCA* gene family catalyzes a broadly conserved pathway for production of the growth hormone indole acetic acid (IAA), the predominant form of auxin in plants. *YUCCA* genes function in the tryptophan-dependent pathway where they catalyze the conversion of tryptamine (TAM) intermediate to N-hydroxyl TAM. *YUCCA* genes are functionally redundant in *Arabidopsis* but have non-redundant roles in grasses and petunia. One *YUCCA* gene in maize, *SPARSE INFLORESCENCE1* (*SPI1*), has a non-redundant role during reproductive development, but no inflorescence phenotype is reported in RNAi knockdowns of the *SPI1* ortholog in rice (*Oryza*). These data suggest *SPI1* function and the extent of *YUCCA* gene redundancy may have changed during the diversification of the grass family. Phylogenetic and comparative genomic analyses show that *SPI1* orthologs are restricted to monocots and reside in syntenic chromosomal regions within grasses. RT-PCR expression analyses indicate *SPI1* and orthologs are expressed broadly throughout various organs within the plant, though to varying degrees and in a stage-dependent manner. *In situ* hybridization analyses in diverse grasses demonstrate that *SPI1* genes have largely overlapping, localized expression patterns that coincide with sites of local auxin biosynthesis associated with lateral branching. These data suggest that the apparent *SPI1* functional diversification is not explained by differing expression patterns and that gene knockdown studies are needed to further characterize the evolution of *SPI1* in grasses.

<sup>1</sup>California State Univ. - Long Beach, Biological Sciences, 1250 Bellflower Blvd, Long Beach, CA, 90840, USA  
<sup>2</sup>CSU - Long Beach, 1250 Bellflower Blvd, Long Beach, CA, 90840, USA

667 ZHONG, JINSHUN

### Molecular evolution of flower symmetry patterning genes *CYCLOIDEA2* within Lamiales

*CYCLOIDEA2* (*CYC2*) specifies flower symmetry and has undergone repeated duplications that are presumed to be important for the evolution of floral form and plant diversification. The *CYC2*-regulated pathway has been recruited multiple times in the evolution of the core eudicots. Our preliminary phylogenetic analysis within Lamiaceae shows that the family has two copies of *CYC2*. In addition, the duplication that gave rise to two *CYC2* paralogs in the family is independent of the ones that occurred in Gesneriaceae and

Plantaginaceae (Antirrhineae). This study focuses on (1) determining when the duplication of *CYC2* occurred in Lamiales, (2) testing whether paralogous of *CYC2* experienced any selective pressure, and (3) testing whether selection on the paralogs correlates with transformation in floral form. Preliminary phylogenetic analysis of *CYC2* within the Lamiales shows that there are at least four independent duplication events within the order, in Oleaceae, Gesneriaceae, Plantaginaceae and other core Lamiales, respectively. The duplication after the divergence between Plantaginaceae and other core Lamiales correlates with the duplication events of two other flower patterning genes *FLO/LFY* and *DEF/AP3* that indicated an ancient whole genome duplication event within the Lamiales.

Department Of Biology, Research BLDG 223, One University Blvd, Saint Louis, MO, 63121, USA

668 PRESTON, JILL\*<sup>1</sup> and HILEMAN, LENA<sup>2</sup>

### Candidate gene expression provides insights into the evolution of Commelinaceae inner tepal symmetry

Flower bilateral symmetry has evolved multiple times independently across angiosperms, and is correlated with increased pollinator specialization and speciation rates. Functional analyses in distantly related core eudicots implicate independent recruitment of class II TCP genes in the evolution of flower bilateral symmetry. By contrast, available evidence suggests that monocot flower bilateral symmetry might have evolved through changes in B-class homeotic MADS-box gene function. In order to test the non-exclusive hypotheses that changes in TCP and B-class gene function underlie flower symmetry evolution in the monocot family Commelinaceae, we compared expression patterns of *TEOSINTE BRANCHED1* (*TB1*)-like, *DEFICIENS* (*DEF*)-like, and *GLOBOSA* (*GLO*)-like genes in morphologically distinct bilaterally symmetrical flowers of *Commelina communis* and *C. dianthifolia*, and radially symmetrical flowers of *Tradescantia pallida*. Expression data demonstrate that both *TB1*-like and *DEF*-like genes are asymmetrically expressed in inner tepals of *C. communis*. However, similar data for *C. dianthifolia* and *T. pallida* indicate that only *DEF*-like gene expression is strongly correlated with differentiation of the ventral inner tepal. Together with other studies, this suggests parallel recruitment of B-class genes in the independent evolution of petal bilateral symmetry in monocots, and a complex history of *CYC/TB1*-like gene evolution across angiosperms.

<sup>1</sup>University of Kansas, Ecology and Evolutionary Biology, 1200 Sunnyside Avenue, Lawrence, KS, 66045, USA

669 LAYTON, DANIEL J.\*<sup>1</sup> and FADEN, ROBERT<sup>2</sup>

### Stamen evolution in the Commelinaceae

The dayflower family (Commelinaceae) is a nearly cosmopolitan monocot lineage representing about 650 species. The family is characterized by short flowering periods of only a few hours per day, a lack of nectar, and presenting only pollen as a reward for pollinators. It has been suggested that these inherited limitations have led to the evolution of accentuated male reproductive organs in order to attract floral visitors, often resulting in the "deception" of pollinators with exaggerated rewards. Indeed, modifications to the male reproductive organs are responsible for much of the family's floral variation. Nearly half of the genera have two or three morphologically distinct types of stamens, and in turn about half of these have stamens in which producing male gametes is no longer the apparent primary function. The remaining genera have six equal stamens with fertile pollen, these being no less diverse in ornamentation. Staminodes have arisen independently in the family at least seven times, each representing a novel morphology. Depending on the taxon, staminodes may contain reduced quantities of fertile pollen, sterile pollen, no pollen, no pollen sacs, or no anthers. Several stamen morphologies found in the Commelinaceae resemble loss of function mutant phenotypes known from model organisms. Investigations are underway in order to simultaneously clarify the evolutionary history of the family and better understand stamen evolution in particular by isolating orthologs of stamen development genes identified in *Arabidopsis*. Observations of floral development using an SEM will complement these data.

<sup>1</sup>University of Missouri-St. Louis, Biology, 223 Research Bldg. One University Blvd. St. Louis, MO 63121, USA <sup>2</sup>Smithsonian Institution, Botany, MRC-166 National Museum Of Natural History, PO Box 37012, WASHINGTON, DC, 20013-7012, USA

670 BARTLETT, MADELAINE\* and WHIPPLE, CLINTON

### The evolution of DEF-GLO heterodimerization in the grasses

The B class MADS box genes *DEFICIENS/APETALA3* (*DEF/AP3*) and *GLOBOSA/PISTILLATA* (*GLO/PI*) play key roles in specifying second and third whorl floral organ identity. *DEF* and *GLO* are transcription factors that, like other floral organ identity genes, bind DNA as part of multimeric protein complexes. *GLO* and *DEF* orthologs from the grasses *Oryza* and *Zea*, as well as from the eudicots *Antirrhinum*, *Arabidopsis*, *Petunia*, *Papaver*, and *Aquilegia*, bind DNA as obligate heterodimers in vitro. In a number of earlier diverging monocots, however, B class homodimers were found to be capable of bind-

ing DNA. In *Lilium*, GLO homologs form functional homodimers while in *Phalaenopsis* both DEF-like and GLO-like homodimers are capable of binding DNA in vitro. Additionally, a GLO ortholog from the close grass relative *Joinvillea* can bind DNA both as a homodimer and as part of a DEF-GLO heterodimer. In addition, it has been demonstrated that B class proteins from the gymnosperm *Gnetum* form homodimers capable of binding DNA. Taken together, these results imply that the obligate DEF-GLO heterodimerization relationship evolved separately in the eudicots and in the monocots from ancestral homodimerization. We present results from experiments exploring the convergent evolution of this protein-protein interaction in the grasses.

Brigham Young University, 401 WIDB, Provo, UT, 84602, USA

**671 PABON-MORA, NATALIA<sup>1</sup>, MEYER, RACHEL<sup>2</sup> and LITT, AMY\*<sup>1</sup>**

### **The role of a *FRUITFULL* ortholog in the development of berries (tomato) and capsules (flowering tobacco) in Solanaceae**

**S**olanaceae provides an excellent system for studies of the evolution of morphology and underlying developmental genetic mechanisms; among other features, the family includes extensive morphological variation and is amenable to genetic manipulation. As part of an ongoing study aimed at identifying the genes that distinguish between dry dehiscent and fleshy fruits in Solanaceae, we have begun functional studies of candidate genes. Our previous studies had identified four common stages in the development of both fruits, based on previously described stages in tomato development: (1) ovary development; (2) cell division triggered by fertilization; (3) cessation of cell division; (4) maturation. Based on microarray and Illumina sequencing transcriptome analyses of fruits of *Nicotiana sylvestris* (flowering tobacco) and *Solanum lycopersicum* cv Micro-Tom (tomato) at stage 2 (initiation of cell proliferation), we selected 12 differentially expressed genes for further investigation. qRT-PCR studies on a subset of 7 of these showed that expression patterns of all were significantly different between the two species; transcript levels differed at individual developmental stages and dynamically across the four developmental stages. To determine the function of these candidate genes, we have initiated Virus Induced Gene Silencing (VIGS) analyses with an ortholog of the Arabidopsis gene *FRUITFULL* (*FUL*). Preliminary results from VIGS-treated tomato plants show a range of abnormalities including increased branching of the plants, defects in sepal, stamen, and ovary formation, and fruit defects in size, shape, and coloration. Some of these phenotypes are consistent with previously recorded functions of *FUL* and orthologs, but others may be novel.

<sup>1</sup>The New York Botanical Garden, 200th St and Southern Blvd, Bronx, New York, 10458, USA <sup>2</sup>New York Botanical Garden, 111 E 125th Street, Apt 4E, New York, NY, 10035, USA

**672 GLEISSBERG, STEFAN\*, HIDALGO, ORIANE and BARTHOLMES, CONNY**

### **Roles of a leaf polarity gene in dissected leaf development**

**D**issected leaves produce lateral structures such as leaflets from a marginal blastozone during primary morphogenesis. These primordial margins form along a contact layer of adaxial and abaxial identities, hence leaf dissection relies on the proper establishment of bifacial leaf structure. Medio-lateral expansion of leaf blades and tissue maturation during secondary morphogenesis also occur along this boundary of adaxial and abaxial domains. Studies in species with dissected leaves have revealed several important genetic components of leaf dissection, whereas polarity establishment has been studied mostly separately in species with simple leaves. Here, we investigate the disruption of a leaf polarity pathway in the context of dissected leaf development, using virus-induced gene silencing (VIGS) in *Eschscholzia californica*. We have characterized five *YABBY* genes in *Eschscholzia* that belong to three angiosperm-wide gene clades known to act in leaf development downstream of leaf polarity pathways. We show that *Eschscholzia YABBY* gene expression is associated with leaflets, and that VIGS-mediated downregulation results in defects in leaf polarity and primordial margin establishment, impacting bifaciality, leaflet initiation, and leaf architecture.

Ohio University, Environmental and Plant Biology, Porter Hall 500, Athens, Ohio, 45701, USA

**673 BAKER, ROBERT\*<sup>1</sup> and DIGGLE, PAMELA<sup>2</sup>**

### **Making branches in *Mimulus*: intraspecific developmental variation in shoot architecture**

**S**hoot architecture is a fundamentally developmental aspect of plant biology with important implications for plant form, function, reproduction, and life history evolution. *Mimulus guttatus* is morphologically diverse and fast becoming a model species for evolutionary biology and ecology. Shoot architecture, however, has never been examined from a developmental perspective in *M. guttatus*. We examined the development of branches and flowers over the course of ontogeny in plants from two locally adapted populations of *M. guttatus* with contrasting flowering times, life histories, and branch numbers. We find no evidence for direct trade-offs between flowers and branches, and flowering and branching are not limited by meristem number. All branches occur at the first four nodes in plants from both populations. Heterochronic processes are responsible for dif-

ferences in branching and flowering at the 3<sup>rd</sup> and more distal nodes while differences in the frequency of branch outgrowth at the two basal most nodes are primarily responsible for population level differences in branch number. Histological and scanning electron microscope analyses demonstrate that plants from both populations initiate axillary meristems in similar numbers, and at similar locations and developmental stages. At the two basal most nodes, population level differences in branch number are most likely controlled by node-specific mechanisms governing meristem outgrowth.

<sup>1</sup>University Of Colorado, Boulder, Ecology And Evolutionary Biology, Ramaley N122, Campus Box 334, University Of Colorado, Boulder, Boulder, CO, 80309, USA<sup>2</sup>University Of Colorado, Department Of Ecology And Evolutionary Biology, CAMPUS BOX 334, University Of Colorado, Boulder, CO, 80309-0334, USA

**674 DIGGLE, PAMELA\*<sup>1</sup>, DI STILIO, VERONICA<sup>2</sup>, GSCHWEND, ANDREA<sup>3</sup>, GOLENBERG, EDWARD<sup>4</sup>, MOORE, RICHARD<sup>5</sup>, RUSSELL, JOHN<sup>6</sup> and SINCLAIR, JORDAN<sup>1</sup>**

### Multiple developmental processes underlie flower sex differentiation in angiosperms

The production of unisexual flowers has evolved numerous times in dioecious and monoecious taxa. Based on repeated evolutionary origins, a great variety of developmental and genetic mechanisms underlying unisexual flower development is predicted. We comprehensively review the modes of development of unisexual flowers, and ask: When during development, and by what process, does loss of reproductive organ function occur? Is organ abortion more common at certain stages and are some developmental mechanisms of abortion more prevalent than others? Does organ abortion vary according to sexual system or among male and female flowers within the same species? We recognized four stages of organ abortion in 292 angiosperm taxa. Among these taxa, loss of sexual organ function occurs with equal frequency at each of the four developmental stages in both male and female flowers, and in monoecious and dioecious taxa. Arrest of development does not tend to occur preferentially at any particular stage, suggesting that there are no key stages of androecial or gynoecial development that are affected repeatedly upon the evolutionary origin of unisexual flowers. Even among closely related taxa, there is no evidence that loss of organ function tends to occur at the same stage. Surprisingly, we found that stage of organ abortion in male and female flowers is temporally correlated within species. Review of developmental processes that terminate organ development found that no process predominates and several may contribute to sterility of the same organ. Changes in the timing of otherwise "normal" developmental processes (cell death, senescence,

termination of cell division) often contribute to organ abortion. Clearly, diverse modifications of development underlie the termination of organ development in unisexual flowers.

<sup>1</sup>Wayne State University, Department of Biological Sciences, Detroit, MI, USA<sup>2</sup>University Of Washington, Kincaid Hall 24, PO BOX 351800, SEATTLE, WA, 98115-1800, USA<sup>3</sup>University of Illinois, Department of Plant Biology, Champaign, IL, USA<sup>4</sup> Wayne State University, Department of Biological Sciences, Detroit, MI, USA<sup>5</sup> Miami University, Botany, 316 Pearson Hall, Oxford, OH, 45056, USA<sup>6</sup>University of Oxford, Department of Plant Sciences, Oxford, UK

**675 HEARN, DAVID**

### Coevolutionary interactions among plant anatomical characters are modular, yet selection pressure for modularity remains elusive

Modularity is pervasive throughout biological systems ranging from molecular to ecosystem scales. Despite the ubiquity of modularity, selection pressures responsible for the evolution of modularity are still debated. A consensus, however, is that modularity can improve system robustness in the face of a changing environment either by limiting the propagation of disturbances to within a module, or by focusing system change through one or a few network hubs. Plant anatomical features provide new light on the evolution of modularity. Previous ecological-anatomical studies illustrate a tight association between climate and anatomical morphology. Using an extensive dataset consisting of over 65,000 anatomical measurements from 52 species of *Adenia* (Passifloraceae), in conjunction with molecular phylogenetic analysis of these species, I tested for modular structure among evolutionary changes in anatomical state. Phylogenetically-informed analyses that took phylogenetic uncertainty into account reconstructed a weighted network of evolutionary interactions among 42 morphological characters. This network was more modular than randomized networks ( $P < 0.001$ ), implying that evolutionary cascades of morphological change are, themselves, modular. Next, associations between climate and morphology were analyzed using modified phylogenetically independent contrasts. Although several expected correlations between climate change and morphological evolution were detected, modules in the morphological network neither limited propagation of impacts of climate change, nor were effects of climate change on anatomical state focused through network hubs. This lack of association between modular structure and climate change suggests that underlying evolutionary pressures on modular structure may have more to do with pleiotropy or developmental constraint than to impacts of external environmental change.

Towson University, 8000 York Road, Towson, MD, 21252, USA

676 FRIEDMAN, WILLIAM\*<sup>1</sup> and DIGGLE, PAMELA<sup>2</sup>

### Charles Darwin and the origins of plant evolutionary developmental biology

Much has been written of the early history of comparative "embryology" and its influence on the emergence of an evolutionary developmental perspective. However, this literature, which dates back nearly a century, has been focused on metazoans, without acknowledgement of the contributions of comparative plant morphologists to the creation of a developmental view of biodiversity. We trace the origin of comparative plant developmental morphology from its inception in the eighteenth century works of Wolff and Goethe, through the mid nineteenth century discoveries of the general principles of leaf and floral organ morphogenesis. Much like the stimulus that vonBaer provided as a non-evolutionary comparative embryologist to the creation of an evolutionary developmental viewpoint, the comparative developmental studies of plant morphologists were the basis for the first articulation of the concept that plant (namely floral) evolution results from successive modifications of ontogeny. Perhaps most surprisingly, we show that the first person to carefully read and internalize the remarkable advances in the understanding of plant morphogenesis in the 1840s and 1850s is none other than Charles Darwin, whose notebooks, correspondence, and (then) unpublished manuscripts clearly demonstrate that he had discovered the developmental basis for the evolutionary transformation of plant form.

<sup>1</sup>Harvard University and Arnold Arboretum, Organismic and Evolutionary Biology, Cambridge, MA, USA<sup>2</sup>University Of Colorado, Department Of Ecology And Evolutionary Biology, CAMPUS BOX 334, University Of Colorado, Boulder, CO, 80309-0334, USA

## POSTERS

677 VAZQUEZ, JESSICA\*<sup>1</sup> and MALCOMBER, SIMON<sup>2</sup>

### Genomic and expression analyses of *THI1*-like genes in plants

Thiamine derivatives are involved in diverse biochemical pathways in plants including the Calvin cycle, citric acid cycle and glycolysis. The thiamine biosynthetic enzyme (*THI1*) catalyzes the condensation of thiozole and pyrimidines during the synthesis of thiamine and mutations to the *Arabidopsis* *THI1* gene (*At5g54770*) lead to the production of albino leaves and premature plant death. Maize *thi1*-like mutants (*Zmthi2/bladekiller1-R*) have smaller inflorescences and leaf blade defects, but the role of *THI1*-like genes in other plants has yet to be investigated. A Bayesian phy-

logenetic analysis of 34 *THI1*-like genes in taxa spanning the plant clade estimates well-supported vascular plant (0.99 posterior probability [PP]), grass (1.00 PP), and eudicot (0.99 PP) clades that are generally consistent with estimated organismal relationships. *THI1*-like paralogs in *Glycine max*, *Mimulus guttatus*, *Manihotesculentum*, *Zea mays* and *Sorghumbicolor* all appear to be the product of recent polyploidization events. Genomic analyses on *Medicago truncatula*, *Carica papaya*, *Oryza sativa*, *Brachypodium distachyon*, and *Selaginellamoellendorffii* estimate *THI1*-like co-orthologs reside in syntenic genomic regions. Expression analyses in *Medicago truncatula*, *Carica papaya*, *Oryza sativa*, and *Brachypodium distachyon* estimate *THI1*-like gene localization in vascular tissue. Together these data demonstrate the broad occurrence of *THI1*-like genes in plants and estimate a generally conserved role for the genes during vegetative and inflorescence development.

<sup>1</sup>California State University, Long Beach, Biological Sciences, 1250 Bellflower Blvd, Long Beach, CA, 90840, USA<sup>2</sup> CSU - Long Beach, 1250 Bellflower Blvd, Long Beach, CA, 90840, USA

678 AVINO, MARIANO\*<sup>1</sup>, MANKOWSKI, PETER J.<sup>2</sup>, BERNARD, KELSEY C.<sup>2</sup>, HAMMEL, ALEX J.<sup>2</sup>, SULLIVAN, SIERRA L.<sup>2</sup> and HALL, JOCELYN C.<sup>2</sup>

### Evo-devo studies on fruit reveal insights in the genetic mechanism patterning dehiscence in Brassiceae

Evo-devo studies in plants have dramatically increased in the last decade showing how phenotypes have been modified via development. Interestingly most studies have focused on floral evolution, while fruit morphology has been largely overlooked. However, differences in fruit morphology greatly impact seed dispersal, which is ecologically important. The tribe Brassiceae is ideal to investigate mechanisms underlying fruit variation as it displays significant differences in fruit morphology. Some members have dehiscent siliques, similar to *Arabidopsis*, whereas many members have segmented fruits laterally transversely by a joint. This segmentation, referred to as heteroarthrocarpy, is accompanied by variation in dehiscent capabilities. For example, *Cakile lanceolata* has fruits with two indehiscent segments, which disperse independently via separation of the joint at maturity. In contrast, fruits of closely related *Erucaria erucarioides* have a dehiscent proximal segment and an indehiscent distal segment. Three MADS-box transcription factor (*SHATTERPROOF1/2* and *FRUITFULL*), two bHLH genes-like (*INDEHISCENT* and *ALCATRAZ*) and a BEL gene-like (*REPLUMLESS*) regulate the genetic pathway determining proper dehiscence in *Arabidopsis*. Our gene expression studies show partial conservation in this pathway between *Arabidopsis* and the dehiscent segment of *Erucaria*. In contrast,

the indehiscent segments of *Erucaria* and *Cakile* are characterized by lack of expression of these genes. The novel anatomical feature of the joint is also characterized by lack of gene expression despite anatomical similarities between joint abscission and silique dehiscence. Functional analysis, such as virus induced gene silencing, are aimed to down-regulate genes of interest to test in which way they might affect the development and morphology of heteroarthrocarpy.

<sup>1</sup>University of Alberta, Biological Sciences, B602B, Biological Sciences University of Alberta, Edmonton, AB, T6G 2E9, Canada<sup>2</sup>University of Alberta, Biological Sciences, CW405, Biological Sciences University of Alberta, Edmonton, AB, T6G 2E9, Canada

679 MAZIE, ABIGAIL\*<sup>1</sup> and BAUM, DAVID<sup>2</sup>

### Comparative Development of Physariae (Brassicaceae) Trichomes

A primary goal of evolutionary biology is to understand the molecular genetic basis of adaptive morphological features. Comparative analyses of the evolution of developmental pathway genes may shed light on the genetic processes that underlie morphological diversity between species. Plant trichomes are epidermal outgrowths that may play an adaptive role in herbivore defense and/or desiccation resistance. The single-celled, non-glandular leaf trichomes of the mustard family, Brassicaceae, are a good model system for tackling evolutionary questions. Trichome form is highly variable across the family, and trichome development is well characterized in the model species, *Arabidopsis thaliana*. As trichome cells grow away from the leaf surface, their primary axis (or stalk) may branch in numerous patterns. The tribe Physariae (Brassicaceae) includes species with some of the most elaborate branching patterns in the family. These stellate (star-like) trichomes appear to have evolved from dendritic (tree-like) ancestors. An important difference between these patterns is the number of branches that emerge from the central trichome stalk. While 1-2 branches typically emerge from the central stalk of dendritic trichomes, as many as 30 branches may emerge in stellate trichomes. To understand the evolution of stellate trichomes in Physariae, we are exploring the roles of two candidate genes that have been identified to be important for trichome branch initiation in *A. thaliana* - *STICHEL* (*STI*) and *BRANCHLESS TRICHOME* (*BLT*). The results of a comparative scanning electron microscope (SEM) analysis of dendritic and stellate trichome development across members of Physariae will be presented. This comparative data will be analyzed within the context of a phylogenetic tree of Physariae estimated from sequences of *STI* and *BLT*. These studies will allow for comparisons to be made with the known developmental pattern of *A. thaliana* and may provide insight into regions of these two genes that are candidates for selection associated with the evolution of stellate trichomes.

lution of stellate trichomes.

<sup>1</sup>University Of Wisconsin - Madison, Botany, 220 Birge Hall, 430 Lincoln Drive, Madison, WI, 53706, USA<sup>2</sup>University Of Wisconsin, Department Of Botany, Birge Hall, 430 Lincoln Drive, Madison, WI, 53706, USA

680 BOYDEN, GERALDINE\*<sup>1</sup>, HARDEJ, DIANE<sup>2</sup>, LITT, AMY<sup>3</sup> and HOWARTH, DIANELLA<sup>1</sup>

### CYCLOIDEA-like genes are implicated in development and floral patterning in *Fedia cornucopiae* (Valerianaceae)

Angiosperm diversification has been facilitated in part by the independent evolution of bilateral symmetry (zygomorphy, monosymmetry) from actinomorphic ancestors in many groups of flowering plants. Recent breakthroughs point to the role of *CYCLOIDEA*-like (*CYC*-like) genes in floral symmetry and their repeated co-option in developmental patterning in independent lineages. The *CYC*-like genes belong to the ECE clade of class II TCP family of transcription factors and have been shown to function similarly in *Antirrhinum*, *Gerbera*, *Lotus*, and *Pisum*. Recently, studies in *Opithandra* (Gesneriaceae) address the role of *CYC* in establishing stamen number. In this study, the virus-induced gene silencing (VIGS) strategy is used to investigate the role of *CYC*-like genes in *Fedia cornucopiae* (Valerianaceae). Various copies of *CYC*-like genes (*CYC1*, *CYC2A*, *CYC2B*, *CYC3A*, *CYC3B*) and their combinations will be analyzed to provide clues for their role in development, establishing floral patterns in petals and their possible interactions among the other gene copies (paralogs) within the lineage. The relative levels of gene expression will be analyzed by quantitative real-time (RT)-PCR and phenotypic analyses by light and electron microscopy. Preliminary data have shown marked variations in development of *CYC2A* and *CYC2B* mutants compared to wildtype. Flower buds of these mutants were opened prematurely (while green) displaying prominent underdeveloped stamens and the petals acquired the customary pink coloration during the later stages of development. Flowers of the mutants were predominantly actinomorphic with more petals compared to the normal pentapetalae form. In addition, at least one or two commonly aborted stamens were restored. Data from these analyses will allow us to explore how duplications of *CYC*-like genes correlate to evolutionary changes within Dipsacales and on a broader scale, how this phenomenon leads to novel phenotypic traits in core eudicots.

<sup>1</sup>St. John's University, Biological Sciences, 8000 Utopia Parkway, Jamaica, Queens, NY, 11439, USA<sup>2</sup>St. John's University, Pharmaceutical Sciences, 8000 Utopia Parkway, Jamaica, Queens, NY, 11439, USA<sup>3</sup>The New York Botanical Garden, 200th St and Southern Blvd, Bronx, New York, 10458, USA

681 LIU, JUAN\*<sup>1</sup>, FENG, CHUNMIAO<sup>1</sup>,  
LIU, XIANG<sup>1</sup>, FRANKS, ROBERT<sup>2</sup> and  
XIANG, QIUYUN (JENNY)<sup>1</sup>

### Comparative analyses of gene expression and sequences of *LFY* in *Cornus* (Cornaceae) - activities in floral development and inflorescence evolution

Species of Dogwood (*Cornus* L.) exhibits a wide variation in inflorescence structure, including heads, umbels, dichasium, and compound cymes. The genus offers us a unique opportunity to investigate the molecular mechanisms underlying the evolutionary divergence of inflorescence architectures. Studies of *Arabidopsis* identified the gene *LFY* to be a key regulator of the pathways controlling inflorescence development, by acting on floral organ identity genes. Its activity in controlling flowering time and initiation of individual flower have also been reported in a number of other species. In this study, we investigate *LFY* activity in floral and inflorescence development in six dogwood species (*Cornus controversa*, *C. sanguinea*, *C. macrophylla*, *C. officinalis*, *C. florida*, and *C. canadensis*) by examining gene expressions at different developmental stages. Our preliminary results showed that *LFY* is expressed during the initiation and early development of inflorescences and flowers, but the expression ceased during the blooming stage in all species examined. Temporal differences of the gene expression and inter-specific sequence divergence involving both site mutations and small indels were observed in all domains (the N, I, and C) among species. Phylogenetic analyses of the cDNA sequences resulted in species relationships concordant with those inferred from other genes. The results support that the idea that activity of *LFY* in floral and inflorescence development is conserved in dogwood species. The pattern and rate of molecular evolution and underlying evolutionary forces are investigated using a phylogenetic framework. Correlation between molecular changes and inflorescence evolution is evaluated.

<sup>1</sup>North Carolina State University, Plant Biology, Gardner Hall 2115, Raleigh, NC, 27695, USA <sup>2</sup>North Carolina State University, Department of Genetics, Raleigh, NC, 27695, USA

682 LOPEZ, CHRISTOPHER\*<sup>1</sup> and  
MALCOMBER, SIMON<sup>2</sup>

### Phylogenomic analyses of the *VANISHING TASSEL2* in grasses

The *VANISHING TASSEL2* gene in maize is essential for vegetative development and axillary meristem formation during inflorescence development. Phylogenetic analysis indicate that *VT2* is co-orthologous to the *Arabidopsis* TRYPTOPHAN AMINOTRANSFERASE (*AtTAA1*), which catalyzes the conversion of Trp

to indole-3-pyruvic acid in one of four hypothesized Trp-dependent biosynthesis pathways for production of the plant growth hormone indole acetic acid (IAA). Bayesian phylogenetic analysis reveals a well-supported *VT2/VT2L* clade comprised of grasses from both the *BEP* and *PACCMAD* lineages suggesting an origin of the clade at least near the base of the grass family and potentially deeper within monocots. *VT2* is estimated have been produced from a gene duplication within andropogonoid grasses, but phylogenetic and genomic analyses indicate *VT2* orthologs are restricted to maize. Genome analyses reveal a high degree of synteny among *VT2L* genes in *Brachypodium*, rice and sorghum, but only limited evidence of synteny among these taxa and the maize *VT2* and *VT2L* genes. RT-PCR expression analyses indicate *VT2L* and *TAR3/4L* genes are expressed broadly, to varying degrees, in leaves, stems and inflorescence material, however the *Sorghum* *SbVT2L2* and *Brachypodium* *BdVT2L2* were not detected within stem tissue and were only weakly expressed in leaf and inflorescence material. Similar to mRNA in situ expression analyses of maize *ZmVT2*, *Sorghum* *SbVT2L* was localized to the epidermal layer in developing inflorescence tissue and was most pronounced in areas with initiating lateral meristems. Together these data suggest a general role of TAA-like genes in regulating plant growth and development in plants, but also point to a complex evolutionary history of *VT2* and *VT2L* genes in grasses.

<sup>1</sup>California State University, Long Beach, Biological Sciences, 1250 Bellflower Blvd., Long Beach, Ca, 90840, USA <sup>2</sup>CSU - Long Beach, 1250 Bellflower Blvd, Long Beach, CA, 90840, USA

**POSTERS**

**683 GRASSA, CHRIS\*, ANDREW, ROSE, KANE, NOLAN C and RIESEBERG, LOREN**

**Linkage disequilibrium in natural populations of *Helianthus petiolaris***

We used Restriction site Associated DNA (RAD) sequencing to infer genotypes at more than 70,000 loci in one hundred *H. petiolaris* individuals from twenty subpopulations across dune and non-dune habitats in Colorado's Great Sand Dune National Park, ten additional *H. petiolaris* individuals from across the species range, and ten *H. annuus* individuals from across the species range. We aligned RAD sequences to the draft *H. annuus* genome to identify marker loci and estimate the physical distance between them. We calculated measures of linkage disequilibrium for each pair of loci common to subpopulation, population, species, and interspecific groupings. This analysis has enabled the discovery of genomic regions that may differ in structure between *H. annuus* and *H. petiolaris* due to micro-chromosomal rearrangements. Additionally, RAD markers that could not be placed on the draft *H. annuus* genome could be tentatively located in the *H. petiolaris* genome based on patterns of linkage disequilibrium. Despite rapid decay of linkage disequilibrium, RAD sequencing provides a sufficient density of markers for informative analysis.

University Of British Columbia, Department Of Botany, 6270 University Blvd, Vancouver, BC, V6T 1Z4, Canada

**684 WILLIAMS, TANISHA M.\*<sup>1</sup>, FISHER, KIRSTEN<sup>1</sup>, ISABEL, NATHALIE<sup>2</sup> and THOMPSON, STACEY<sup>2</sup>**

**Identification of *Populus* species and hybrids through morphological analyses and single nucleotide polymorphism genotyping in the American southwest**

Poplar is a model tree with applications in biotechnology, and understanding interspecific gene flow in *Populus* can clarify the consequences of hybridization on native systems. Thirty years ago, a morphological analysis diagnosed hybrids between two native species (*Populus fremontii* and *P. trichocarpa*) and one European exotic (*P. nigra*) throughout sympatric zones in California and Nevada. These eight hybrid zones will be revisited, and the 480 samples genotyped using a 42 single nucleotide polymorphism (SNP) assay. The genotypic data will be used to assess the frequency of

each species, hybrids and backcrosses, and the direction of gene flow. In addition, I will collect leaf samples and statistically analyze a series of eight measurements to determine if leaf morphology can identify *Populus* species and hybrids. The identities of samples based on molecular and morphological data will be compared, with the genomic identity taken as indicative. I will evaluate whether morphological characteristics of hybrids are intermediate between the pure parental species, and whether advanced generation hybrids can be identified by leaf morphology. The results of this study may increase our knowledge of the causes and consequences of gene flow in American southwest *Populus*, and can help focus conservation efforts to maintain biodiversity.

<sup>1</sup>California State University Los Angeles, Department of Biological Sciences, 5151 State University Drive, 350 La Kretz Building, Los Angeles, CA, 90032, USA<sup>2</sup>Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, 1055 rue du P.E.P.S., C.P. 10380 succ. Sainte-Foy, Québec, Québec, G1V 4C7, Canada

**685 RINEHART, TIMOTHY\*<sup>1</sup>, SCHEFFLER, BRIAN<sup>2</sup> and REED, SANDRA<sup>1</sup>**

**Transcriptome sequencing of *Hydrangea macrophylla*, a non-model woody plant and specialty crop**

Transcriptome sequencing is a useful first step in functional genomic studies, microarray and gene expression studies, single nucleotide polymorphism (SNP) surveys, quantitative trait loci (QTL) mapping, and genomic scans of diversity. Massively parallel pyrosequencing technology has been used extensively on agronomic crop and model plants. Here we describe annotation and sequence comparison of a normalized EST library from a non-model crop, *Hydrangea macrophylla*, which is grown as a woody landscape ornamental plant, forced greenhouse floral crop, and for cut flowers. Transcriptome sequences were generated using 454 GS-FLX Titanium sequencing of a single normalized EST library made from leaf, bud, stem, and flower tissue. Median sequence length was 431 base pairs and sequencing generated 1.1 million high-quality reads. Assembled data include 46,673 contigs that break down into 42,664 isotigs and 24,201 isogroups. BLAST2Go was used for sequence annotation. Transcriptome data was screened for microsatellites regions, which produced primer pairs for 3500 new SSR markers to saturate linkage map for *Hydrangea macrophylla*. SNP discovery is underway as well. Here we provide a list of candidate genes that could be utilized in future experiments to increase flowering, resist powdery mildew, and enhance floral characteristics.

<sup>1</sup>USDA, Agricultural Research Service, Floral and Nursery Plants Research Unit, TSU Nursery Crop Research Station, McMinnville, Tennessee, 37110, USA<sup>2</sup>USDA, Agricultural Research Service, Genomics and Bioinformatics Research Unit, 141 Experiment Station Road, Stoneville, Mississippi, 38776, USA

**De novo assembly and analysis of transcriptome of a mangrove associate *Hibiscus tiliaceus* L. sequenced by Illumina technology**

*Hibiscus tiliaceus*, a mangrove associate, has two different ecotypes inhabiting in intertidal and inland environments, respectively. It may represent a good example of differential adaptation to heterogeneous habitats. The advent of next-generation sequencing technology such as 454 and Illumina make it possible to analyze the genome or transcriptome in shorter time with less cost and time. We used Illumina sequencing technology to obtain transcriptome data for genomic and evolutionary researches in future. In this study, more than 30 million 75-nt paired-end reads were assembled into 43,899 contigs with an average length of 710 nt by using a short-read assembler ABySS, and all the contigs have the average depth 54.8 x. Of the 43,899 contigs, 32,313 were successfully annotated using Gene Ontology (GO) terms and 5,897 were successfully annotated using the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. This study will help us to find new genes in *Hibiscus*, which has many important garden plants but little transcriptome information. Most importantly, we can conduct evolutionary analysis with other closely related species to learn more about adaptive evolution and codon usage bias of this mangrove species.

Sun Yat-sen University, College of Life Science, xingangxilu 135, Guangzhou, Guangdong, Guangzhou, GD, 510275, China

POSTERS

687 PRINCE, LINDA

**Plastid Primers for Phylogenetics**

The availability of PCR primers for numerous plastid introns or intergenic spacer regions has increased dramatically over the past ten years, yet many botanists are still unable to confidently resolve relationships within their study group. Additionally, structural rearrangements in the chloroplast genome limit the utility of some primer combinations. The goal of the current study was to develop additional plastid markers for phylogenetic reconstruction among closely related flowering plant taxa, ideally between sister species and among subspecies. Primers were designed for 32 non-coding portions of the large single copy region of the chloroplast genome based on the complete chloroplast genomes of sixteen flowering plant species. The utility of the primers was also assessed for a variety of non-flowering land plants. Most primer pairs were tested on at least two non-model angiosperms, *Monardella viminea* (Lamiaceae) and *Agave shawii* (Agavaceae). Primer sequences, taxon specific match, and approximate amplicon size is available for review and download via the [www](http://www.rancho-santa-ana-botanic-garden.org).

Rancho Santa Ana Botanic Garden, 1500 N College Avenue, Claremont, CA, 91711-3157, USA

688 PANES, VIVIAN

**Identification and Cloning of Ribosome Inactivating Protein (RIP) Genes in Selected Species of the Euphorbiaceae**

Ribosome-inactivating proteins (RIP) inhibit protein synthesis in eukaryotic cells by catalytically damaging ribosomes. They have been proven to have an antiviral and antitumour activity because RIPs can truncate the translation of viral coat proteins. The presence of RIP genes in the 13 selected Euphorbiaceae species was screened through genomic DNA PCR using 5 sets of primers. The selected plants included *Acalypha hispida* Burm., *Codiaeum variegatum* L. Bl., *Euphorbia hirta*, *Euphorbia lactea* Haw., *Euphorbia milii*, *Euphorbia pulcherrima* Willd., *Euphorbia tirucalli* L., *Euphorbia trigona* Haw., *Exoecaria cochinchinensis* var. *purpurascens*, *Jatropha pandorifolia* Andr., *Jatropha podagrica* Hook, *Manihot esculenta* Crantz and *Pedialanthus tithymaloides* L. (*Jatropha curcas* L. was used as the control because it has already a known RIP gene as determined by Lin *et al.* 2003b). The genomic DNA sequences obtained were analyzed through BLASTs and ClustaW of MEGA4. PCR products were also cloned and sequenced. RIP primers generated PCR products

for only three plants. These are *J. podagrica*, *J. pandurifolia* and *J. curcas*. Sequence analysis and alignment through BLAST showed 87%-90% homology of *J. pandurifolia*'s RIP gene sequence to *J. curcas* precursor gene and mRNA, while 87%-89% homology of *J. podagrica*'s RIP gene sequence to *J. curcas*' curcin precursor mRNA and gene. Nucleotide sequence and deduced amino acid sequence through Clustal W revealed possible ORFs in *J. podagrica* and *J. pandurifolia*'s genomic DNA PCR products and cloned PCR products. Alignment of the deduced amino acid of the cloned genomic DNA PCR products of *J. podagrica* and *J. pandurifolia* to *J. curcas*' curcin and other RIPs revealed the presence of RIP's conserved regions such as SYFF, ALD and EAA which are the putative active sites. Genomic DNA PCR products of *J. podagrica* and *J. pandurifolia* are 674-678 bp. and 555-590 bp. respectively. Identification of the RIP genes in *J. pandurifolia* and *J. podagrica* will shed light on the medicinal properties of the ribosomal inactivating proteins (RIPs) of these plants.

Ateneo De Manila University, Department of Biology, School of Science and Engineering, Quezon City, 1108, Philippines

**689 ALVES, FÁBIO DE MATOS<sup>1</sup>, SFORÇA, DANILO AUGUSTO<sup>1</sup>, FORTUNA PEREZ, ANA PAULA\*<sup>2</sup>, SARTORI, ÂNGELA LÚCIA BAGNATORI<sup>3</sup> and SOUZA, ANETE PEREIRA DE<sup>1</sup>**

### **Development and characterization of a DNA library enriched on Microsatellite (SSR) of *Prosopis ruscifolia* Griseb**

**M**icrosatellites or simple sequence repeats (SSR) markers are a valuable tool in genetic mapping, genotyping, analysis of paternity, gene flow and marker-assisted selection in breeding due to their characterization of co-dominant loci, high allelic variation and be easily used by PCR. Data on microsatellite abundance comes preferentially from microsatellite enriched libraries and DNA sequence databases. This study aimed to develop and characterize a microsatellite-enriched genomic library of *Prosopis ruscifolia* Griseb. and subsequent synthesis and evaluation of primers. The construction of this library enriched of SSR was done using leaves from one individual of *P. ruscifolia*, collected in Porto Murтинho, Mato Grosso do Sul, Brazil. As a consequence, 95 clones were generated and subsequently sequenced, resulting in 31 sequences among contigs and singlets; besides 38 perfect and imperfect microsatellites were sampled. In this study, 18 motifs dinucleotides, 9 motifs AC/AC, 8 motifs GT/TG, one motif GA, one motif trinucleotide (CTT), and one motif tetranucleotide (GCTT) were totalized. The remaining sequences presented motifs with compounds microsatellites. The primers designed of this library are in the process of synthesis and it will generate data for biodiversity stud-

ies of *Prosopis ruscifolia*.

<sup>1</sup>Universidade Estadual de Campinas, Centro de Biologia Molecular e Engenharia Genética, Av. Cândido Rondon, 400, Barão Geraldo, Campinas, São Paulo, 13083-875, Brazil <sup>2</sup>Universidade Estadual de Campinas, Biologia Vegetal, Monteiro Lobato, 970 - Barão Geraldo - , Campinas, São Paulo, 6109, Brazil <sup>3</sup>Universidade Federal de Mato Grosso do Sul, CCBS, Botânica, Cidade Universitária, Campo Grande, Mato Grosso do Sul, 549, Brazil

## ORAL PAPERS

690 HSU, SHIH-CHUNG\*, OLSEN, KENNETH, PUSADEE, TONAPHA and SCHAAL, BARBARA

**Global evidence suggests separate crop origins of weedy rice (*Oryza sativa* L.)**

Several hypotheses for the origin of weedy rice, the conspecific weed of cultivated rice (*Oryza sativa* L.), have been proposed, including derivation from its wild progenitor (*O. rufipogon* Griff.), introgression between wild and cultivated rice, hybridization between distinct cultivars or de-domestication from the crop. We have used genome-wide sequence tagged site (STS) loci and the pericarp color gene *Rc* to infer the genetic structure and origin of weedy rice by comparing sequences with both cultivated rice and *O. rufipogon*. We found for weedy rice from Japan, South Korea, Thailand and Portugal lower sequence polymorphism at STS loci than in cultivated rice. Moreover, there is usually close genetic similarity to locally grown cultivars. Weedy rice that is similar to *temperate japonica* rice was found in Japan, S. Korea and Portugal, countries which cultivate *japonica* rice, whereas in Thailand, which cultivates *indica* rice, the weedy rice is genetically similar to *indica* cultivars. We also found *indica* type of weedy rice in S. Korea, which once cultivated *indica* rice. Interestingly, both *temperate japonica* and *indica* types of weedy rice were found in a single field in S. Korea. In contrast, US weedy rice has genetic similarities to *indica* and *aus* cultivars that have never been commercially grown in the US. Our results suggest that weedy rice has arisen multiple times across rice growing regions of the world, both within and outside the range of its wild progenitor. At least in some areas, weedy rice may have developed through independent origins from local cultivated rice. The low sequence polymorphisms detected at STS loci imply that either strong selection by weed management practices or founder effects may have shaped the genetic structure of weedy rice. Analysis of *Rc* gene haplotypes suggests that some weedy rice may have an origin via de-domestication or possibly by parallel evolution of a specific *Rc* haplotype. We conclude that weedy rice may originate from cultivated rice by diverse mechanisms.

Washington University, Biology, 1 Brookings Drive, Campus Box 1137, St. Louis, MO, 63130, USA

691 THURBER, CARRIE\*<sup>1</sup>, OLSEN, KENNETH<sup>2</sup>, JIA, YULIN<sup>3</sup> and CAICEDO, ANA<sup>4</sup>

**Molecular evolution of flowering time loci in U.S. weedy rice**

Weedy rice is a persistent weed of cultivated rice (*Oryza sativa*) fields worldwide, which competes with the crop and drastically reduces rice yields. Within the US, two main populations of genetically differentiated weedy rice exist, the straw-hulled (SH) group and the black-hulled/dawned (BHA) group. Current research suggests that both groups are derived from Asian cultivated rice, such that SH weeds are most closely related to a rice variety called *indica*, while the BHA-group is more closely related to a variety known as *aus*. However, the weeds differ from the cultivated groups in various morphological traits. Flowering time is one trait where consistent differences are seen between weedy rice and cultivated rice, and timing of flowering is expected to be important for persistence of weeds in the field. Recently, it has been suggested that the coding region of *hd1* and the promoter of *hd3a* are two of the three most important determinants of flowering time in cultivated rice. In order to determine whether these genes have been mutated in weedy rice so as to cause aberrant flowering phenotypes we took a phenotypic and candidate gene approach. We measured flowering time in cultivated, weedy and wild rice grown in a growth chamber under day neutral conditions, and we sequenced the entirety of the *hd1* gene along with the promoter of the *hd3a* gene. We show that SH weeds flower significantly earlier than cultivated rice while BHA weeds flower slightly later than most cultivated rice. All later flowering BHA samples share a 2 base pair (bp) deletion in exon 2 of the *hd1* coding region that is common in *tropical japonica* and *aus* cultivars, yet is also found in some *indica* cultivars. While the 2 bp deletion differentiates BHA from SH weeds, it does not differentiate the weeds from their putative progenitors. Additionally, nearly all SH and BHA weeds share *hd3a* promoter haplotypes with their respective progenitors, *indica* and *aus* cultivars.

<sup>1</sup>University Of Massachusetts Amherst, 611 North Pleasant Street, Morrill Science Center Room 221, Amherst, MA, 01003, USA-

<sup>2</sup>Washington University, BIOLOGY DEPT, BOX 1137, 1 BROOKINGS DRIVE, St. Louis, MO, 63130-4899, USA <sup>3</sup>USDA-ARS Dale Bumpers National Rice Research Center, 2890 HWY 130 East, 2890 HWY 130 East, AR, 72160, USA <sup>4</sup>University Of Massachusetts, 221 Morrill Science Center, 611 North Pleasant St., Amherst, MA, 01003, USA

692 SHERMAN, NATASHA\*<sup>1</sup>, MUIR, CHRISTOPHER<sup>1</sup>, JOSEPHS, EMILY<sup>2</sup> and MOYLE, LEONIE<sup>1</sup>

### Population variation for reproductive isolating QTL in *Solanum*

The strength of isolation between species can vary greatly depending upon the specific source populations used in interspecific crosses. This is because geographically separated populations that experience different selective forces or stochastic events can fix alternative genetic variants; these, in turn, can have very different pleiotropic consequences for species barriers. Under this scenario, local processes are more important in fixing alleles contributing to species barriers than forces acting throughout the entire species range. Therefore, the dynamics driving the evolution of isolating genes that are fixed (invariant within species) versus polymorphic (intraspecifically varying) are expected to be quite different. To understand the extent and genetic basis of within-species variation in reproductive isolating loci, we simultaneously mapped QTL in two independent populations (Rilpop1 & Rilpop2) of recombinant inbred lines (RILs) generated from two independent crosses between the wild species *Solanum pimpinellifolium* and the domesticated tomato *S. lycopersicum*. Parental *Solanum pimpinellifolium* accessions for each population were from geographically distant (>380km), ecologically differentiated ends of the wild species range. For pollen sterility barriers, we identified three and five QTL in Rilpop1 and Rilpop2, respectively. Only one QTL, on the top of linkage group twelve, was detected in both populations. Our results suggest that intraspecific variation for genetically-based species barriers is extensive. No QTL for seed sterility were identified in either population. To assess whether our pollen sterility QTL are associated with potentially selected differences between *S. pimpinellifolium* source populations, we are also mapping morphological and physiological QTL in each RIL population, and assessing the degree of association between these loci and our polymorphic sterility QTL.

<sup>1</sup>Indiana University, Department of Biology, Jordan Hall 325, 1001 E. Third St., Bloomington, IN, 47405-3700, USA<sup>2</sup>University of Toronto, Department of Ecology & Evolutionary Biology, University of Toronto, 25 Willcocks Street, Toronto, Ontario, M5S3B2, Canada

693 UFFENBECK, MICHAEL\*<sup>1</sup>, LARSON, KATHERINE<sup>1</sup> and NOYES, RICHARD<sup>2</sup>

### Seedling establishment versus clonal spread in the exotic, *Lonicera japonica*

Japanese honeysuckle (*Lonicera japonica*) is a persistent invader in natural areas capable of negatively impacting native species. Previous studies in Arkansas have found low seed levels and pollination rates. These traits suggest vegetative growth may be the pathway Japanese Honeysuckles uses to spread into natural areas. We sought to reconstruct and quantify the colonization pathway of Japanese Honeysuckle within a natural area. Amplified Length Polymorphism (AFLP) was used to identify genotypes in a riparian area and an upland site at Woolly Hollow State Park Greenbrier, Arkansas. Clones were assigned based upon Jaccard's similarity values where the clone threshold was based upon replicated samples. We found a high level of genetic diversity within our study population where the overall average Jaccard similarity was 0.6805 and the Simpson's clonal diversity index was 0.9369 in the upland site and 0.9206 in the lowland site. The G/N ratio was similar in both upland and riparian habitats where it was 0.4444 in the upland site and 0.5278 in the riparian site. The average clonal unit length along the transects was 7.1 meters. In addition, we measured the rate of spread of three genotypes and found one genotype was no more invasive than the native Coral Honeysuckle *Lonicera sempervirens*. Although seed set is rare in Japanese Honeysuckle these results indicate sexual reproduction is still the most important colonization pathway within riparian and upland habitats.

<sup>1</sup>University of Central Arkansas, Biology, Department of Biology, Lewis Science Center 180, Conway, Arkansas, 72035, USA<sup>2</sup>University Of Central Arkansas, Department Of Biology, Lewis Science Center 180, CONWAY, AR, 72035, USA

694 LAPORT, ROBERT\*, MINCKLEY, ROBERT and RAMSEY, JUSTIN

### The Biology of Speciation in the North American Polyploid Complex, *Larrea tridentata* (Zygophyllaceae)

The relative importance of ecological and non-ecological reproductive barriers is widely disputed, even for taxa classically identified as examples of non-ecological speciation. Genome duplication (polyploidy) is a common form of chromosome evolution that causes hybrid inviability (triploid block) and strong reproductive isolation in plants. However, because polyploids are often geographically, morphologically, and physiologically, divergent from diploids, some evolutionists have argued that speciation in polyploids depends upon

ecological adaptation. One widely cited example of polyploid speciation is the creosote bush (*Larrea tridentata*, Zygophyllaceae), a dominant species of the North American desert flora comprised of three geographically isolated chromosome races (diploids ( $2n=2x=26$ ) occur in the Chihuahuan Desert, tetraploids ( $2n=4x=52$ ) occur in the Sonoran Desert, and hexaploids ( $2n=6x=78$ ) occur in the Mojave Desert). Yet, it remains unclear if the chromosome races of *L. tridentata* represent distinct taxonomic units, not only because of uncertainty over the strength of reproductive isolation, but also due to uncertainty over the degree to which they have diverged ecologically, morphologically, and physiologically. Here, we use a combination of DNA molecular analyses and field observations to estimate the strength of pre- and post-zygotic reproductive isolation within the *L. tridentata* polyploid complex; determine morphological and physiological divergence among the cytotypes; and test the hypothesis that gene flow is reduced between the cytotypes. We find that the three cytotypes of North American creosote bush exhibit strong intercytotype reproductive isolation mediated by largely allopatric distributions, divergent flowering phenology, and hybrid inviability/sterility. Furthermore, the allopatric ranges are distinct in climatic and edaphic features, as well as floristic elements. The cytotypes differ slightly in morphological features and display differences in water use efficiency as measured by carbon isotope analyses. Finally, DNA molecular data indicates little evidence for intercytotype gene flow. Taken together, these results suggest ecological isolation may play a significant role in establishing reproductive isolation between the cytotypes.

University Of Rochester, Department Of Biology, RIVER CAMPUS BOX 270211, HUTCHISON HALL, ROCHESTER, NY, 14627, USA

**695 BECK, JAMES<sup>\*1</sup>, ALEXANDER, PATRICK<sup>2</sup>, ALLPHIN, LOREEN<sup>3</sup>, RUSHWORTH, CATHERINE<sup>4</sup>, BAILEY, C. DONOVAN<sup>5</sup> and WINDHAM, MICHAEL<sup>6</sup>**

### **Does hybridization drive the transition to asexuality in diploid *Boechea*?**

Gametophytic apomixis is a common form of asexual reproduction in plants. Virtually all gametophytic apomicts are polyploids, and some view polyploidy as a necessary prerequisite for the transition to apomixis. However, any causal link between apomixis and polyploidy is complicated by the fact that most apomictic polyploids are allopolyploids, leading some to speculate that hybridization, rather than polyploidy, is the primary cause of apomixis. Diploid apomicts present a rare opportunity to isolate the role of hybridization, and a number of these have been documented in the genus *Boechea* (Brassicaceae). Here we present the results of a microsatellite study of 1400 morphologically and geographically diverse diploid individuals, evaluat-

ing the hypothesis that diploid *Boechea* apomicts are hybrids. With few exceptions, diploid apomicts exhibit extraordinarily high levels of heterozygosity resulting from the combination of disparate genomes. This strongly suggests that the genomic consequences of hybridization allow for the transition to gametophytic apomixis in *Boechea*.

<sup>1</sup>University Of Wisconsin, Milwaukee, Lapham Hall S394, P.O. Box 413, Milwaukee, WI, 53201-0413, USA<sup>2</sup>New Mexico State University, Biology Department, 248 Foster Hall, Las Cruces, NM, 88003, USA<sup>3</sup>Brigham Young University, DEPT INTEGRATIVE BIOLOGY, 275 WIDB, Provo, UT, 84602, USA<sup>4</sup>Duke University, PO Box 90338, Durham, NC, 27708, USA<sup>5</sup>New Mexico State University, Department Of Plant Sciences, P.O. Box 30001 Msc 3AE, Las Cruces, NM, 88003, USA<sup>6</sup>DUKE UNIVERSITY, Department Of Biology, BOX 90338, DURHAM, NC, 27708, USA

**696 PUPPO, PAMELA<sup>\*1</sup>, CURTO, MANUEL<sup>1</sup>, PEREZ DE PAZ, PEDRO LUIS<sup>2</sup> and MEIMBERG, HARALD<sup>1</sup>**

### **The role of secondary contact between previously isolated species: the genus *Micromeria* (Lamiaceae) on Tenerife**

Tenerife is the largest and highest island of the Canary Archipelago and has a complex geological history. Tenerife originated from three islands: Teno, Anaga, and Roque del Conde (4 to 12 myo) that got secondarily connected by a successive uprising of volcanoes forming its current outline 200 000 years ago. Interestingly, many of the older parts of the island contain distinct endemic species presumably remnants of an extinct flora. Genus *Micromeria* (Lamiaceae) is represented by 17 species in the Canaries, of which eight occur on Tenerife. Three endemic species are restricted to the palaeo-island of Anaga and adjacent areas and one to Teno. In the geologically younger central part of the island five morphologically similar species grow with a wider distribution. It is quite likely that the younger parts of the island have been colonized from species coming from the old parts. As such, the central part of the island constitutes a secondary contact zone between the species and hybridization is regularly occurring between most of the species, as indicated by the presence of morphological hybrids. We investigate the mechanisms that maintain the morphological differences between the species in the face of introgression. Post-zygotic barriers could impede gene flow despite hybridization. Alternatively, following the hybrid zone theory, parts of the genome could be stabilized by selection while neutral markers could be exchanged between the gene pools. Distinguishing between markers under purifying selection (length polymorphisms between alleles of coding genes) and presumably neutral microsatellite markers, we test for genetic differentiation between the species. The first results indicate little between-species differentiation and a surprisingly high genetic diversity of the restricted species. We hypothesize that introgressive hybridiza-

tion homogenizes some parts of the genomes of these endemics, but that selection on genes important for local adaptation are responsible for maintaining the morphological differences.

<sup>1</sup>University of Porto, Research Center in Biodiversity and Genetic Resources (CIBIO), Rua Padre Armando Quintas, Vairao, 4485-661, Portugal<sup>2</sup>Universidad de La Laguna, Facultad de Farmacia, Av. Astrofísico Francisco Sánchez s/n, La Laguna, Tenerife, E-38200, Spain

697 YONGMEI, CHEN\*, RENCHAO, ZHOU and SUHUA, SHI

### Diversifying selection in a mangrove species *Rhizophora apiculata* revealed by population sequencing

Mangroves live in extreme intertidal environments and are expected to undergo intense selection pressures. Population genetics approach has the potential to identify genes under selection. In this study, we examined DNA polymorphism and population differentiation in three populations of *Rhizophora apiculata* from Hainan, China, by sequencing 78 nuclear genes using Illumina technology and the Sanger method. Thirty individuals were pooled for each population and Illumina sequencing called 81, 109 and 77 SNPs, respectively, from these populations. The average  $\theta_w$  and  $\theta_{pi}$  of the three populations were 0.000261, 0.000341, 0.000242, and 0.000302, 0.000372, 0.000262 respectively, which showed the extremely low level of DNA polymorphism within each population. Most genes showed no or low genetic differentiation, while 46 sites from 28 genes exhibited strong differentiation ( $F_{st} > 0.15$ ). Tajima's D values of 7 genes were significantly larger than zero at the 95% confidence level. We further used Sanger sequencing to obtain haplotypes of about 20 individuals in each population. In Sanya River population, two divergent haplotypes at three genes were found while there was obvious deficiency of heterozygotes. Both genetic bottleneck and population admixture model could not account for the observed patterns, and we suggested that these genes may be affected by diversifying selection. This may be associated with the heterogeneous environments in Sanya River. Our study provides a probable scenario of plant adaptation to extreme and heterogeneous environments by diversifying selection in some specific genes. The candidate genes underlying selection are worth studying further at the physiological and ecological levels.

Sun Yat-sen University, College of Life Science, xingangxilu 135, Guangzhou, Guangdong, Guangzhou, GD, 510275, China

698 RISER, JAMES<sup>\*1</sup> and ROALSON, ERIC<sup>2</sup>

### Phylogenetics of the dwarf milkweed group (*Asclepias eastwoodiana-ruthiae-sanjuanensis-uncialis*, Asclepiadoideae: Apocynaceae)

The dwarf milkweed group comprises four diminutive species of early-flowering milkweeds (*Asclepias eastwoodiana*, *ruthiae*, *sanjuanensis*, and *uncialis*) native to xeric habitats of the western United States. Three of the four species have been treated as infraspecific taxa of *Asclepias uncialis*; however, significant morphological differences exist between these putative species. Additionally, their distributions are essentially allopatric in all but one case. We are using chloroplast DNA markers to reconstruct a phylogeny of these four taxa. A robust phylogeny for this group will allow us to examine the validity of current taxonomic treatments, the potential hybrid origin of *A. sanjuanensis*, and the evolutionary history of the dwarf-milkweed group. This phylogeny will also allow us to test phylogeographic hypotheses related to this group of interesting western plants.

<sup>1</sup>Washington State University, School of Biological Sciences, Abelson, Room 339, PO Box 644236, Pullman, WA, 99164-4236, USA-

<sup>2</sup>Washington State University, School Of Biological Sciences, Abelson Hall 339, Pullman, WA, 99164-4236, USA

699 GRADY, BEN R.\*<sup>1</sup> and SYTSMA, KENNETH<sup>2</sup>

### Sorting out relationships in the 'capitate clade' of *Eriogonum* (Polygonaceae): Evolution in the Great Basin and beyond

Species-level phylogenetic inference in plants can be complicated by many issues (e.g. introgression, incomplete lineage sorting, polyploidy); the causes of genealogical discordance have been well documented. Many of these processes are apparent in the evolutionary history of *Eriogonum* (Polygonaceae). Here we demonstrate incongruent genealogical histories within the 'capitate clade' of *Eriogonum*. Extensive ingroup sampling reveals signatures of a recent, rapid radiation. Few species within this group exhibit reciprocal monophyly based on our chloroplast and nuclear gene trees, although the Genealogical Sorting Index (GSI) is used to test the extent of non-monophyly of species. Specific cases of discordance are highlighted with examples from both rare and widespread species in this clade. For example, *Eriogonum shockleyi*, a widespread member of the 'capitate clade', shows patterns of recent hybridization with other species in this group. Chloroplast capture is evident from plastid intron sequences, and nuclear regions show similar patterns with *E. shockleyi*. Certain sub-clades within this radiation show strong geographic clustering within floristic sections of

the Intermountain Region of the western United States. Spatial and temporal patterns of current species distributions are investigated in a phylogenetic framework, to illuminate the biogeographic history of this group.

<sup>1</sup>University Of Wisconsin-Madison, Botany, 430 Lincoln Dr., Madison, WI, 53706, USA <sup>2</sup>University of Wisconsin-Madison, Department of Botany, 430 Lincoln Dr., Madison, WI, 53706, USA

700 ZAPATA, FELIPE\* and FINE, PAUL

### A molecular perspective on plant chemical defense evolution: Molecular evolution of monoterpene synthases in *Protium* (Burseraceae)

The coevolutionary arms race hypothesis (CARH) states that the selective pressure of herbivores on plant species is largely responsible for the vast diversity of plant secondary metabolites, and thus it predicts that variation of plant chemical defenses should be under diversifying selection, and associated with plant speciation events. Although some studies have analyzed the evolution of plant defense chemistry in relation to herbivore phylogenies, none has evaluated variation in plant chemistry and the genes underlying this variation at the genus level. In the tropical tree genus *Protium* (Burseraceae), terpenes are a major component in the blend of diverse secondary metabolites that likely contribute to resistance against insect herbivores. For a set of species from across the *Protium* phylogeny, we characterized terpene chemical profiles and variation in monoterpene synthases (TPSb), the genes controlling a fundamental step in monoterpene biosynthesis. Preliminary analyses reveal i) considerable interspecific variation in composition and concentration of leaf terpenes, ii) evidence for excess of nonsynonymous substitutions on TPSb genes concentrated in few codons, and iii) variable selection levels along the TPSb phylogeny, with support for positive selection along few branches representing different species or speciation events. These initial results are partially consistent with the predictions of the CARH. We believe that our results, in conjunction with common garden experiments, transcription profiling, heterologous expression, and genomic scans will be a powerful approach to fully elucidate the mechanistic basis underpinning the co-evolutionary processes driving species diversification.

University Of California, Department Of Integrative Biology, 3060 Valley Life Sciences Bldg. #3140, Berkeley, CA, 94720-3140, USA

## POSTERS

701 MAJESKY, LUBOS\*, VASUT, RADIM, TRAVNICEK, BOHUMIL and KITNER, MILOSLAV

### Genetic variability in apomictic clones of common dandelion (*Taraxacum*; Asteraceae).

Clonal reproduction through seeds i.e. apomixis can be significant advantage for plants. Producing high number of seeds of genetically homogeneous plants temporarily increases the success in geographical spread. Apomictic microspecies can spread over larger regions as it is known for e.g. *Rubus*, *Hieracium* or *Taraxacum*. However, the absence of sex leads to mutation accumulation, decreased genetic variability of species etc. Therefore apomictic plants are considered to be blind evolutionary ends. The only source of genetic variation is through gaining the new mutations. These mutations are then inherited by the offspring in consequent lineages only. Genus *Taraxacum*, which consists of apomictic polyploids and diploid sexuals is represented by 2000+ taxons around the world. These facts make the genus ideal study object to address the question, whether apomictic clones are widely distributed or have just the local spread. We selected 9 morphologically uniform accessions (microspecies) and have done genotyping of 188 individuals of *Taraxacum* sect. *Ruderalia*. We used six microsatellite loci together with three AFLP primer combinations. Analyses revealed the presence of genetic differences among and the homogeneity within closely related apomictic microspecies. Low intraspecific genetic variability of apomictic microspecies as well as high interspecific genetic variability suggests that *Taraxacum* microspecies can be considered as clones. We showed that these clones can spread over large regions of Europe. Detected high genetic similarity between morphologically similar microspecies (*T. amplum* agg.) may indicate microevolutionary process of splitting the clone into novel lineages by gaining mutations.

Palacky University Olomouc, Faculty of Science, Department of Botany, Slechtitelu 11, Olomouc, CZ, 783 71, Czech Republic

702 VON WETTBERG, ERIC J BISHOP\*<sup>1</sup>, MORIUCHI, KEN<sup>2</sup>, FRIESEN, MAREN<sup>3</sup>, FOTINOS, TONYA<sup>4</sup>, CORDIERO, MATILDE<sup>5</sup>, VU, WENDY<sup>3</sup>, MUKHERJEE, JAYANTI<sup>6</sup> and BADRI, MOUNAWER<sup>1</sup>

### Maternal Environmental Effects on salt tolerance in *Medicago truncatula*

Through allocation of resources to pods and seeds, maternal plants have the capacity to affect the ability of their offspring to tolerate abiotic stress. If abiotic stress is predictable, perhaps due maternal experience of stress and the likelihood of offspring encountering similar conditions, maternal plants can allocate preferentially to offspring to increase stress tolerance. We tested for maternal environmental effects on stress tolerance in *Medicago truncatula* by growing 40 genotypes under high and low salinity conditions to generate contrasting maternal environments. Seed germination rate was tested at seven salinity levels, and plants were grown to maturity at two salinity levels. Results show that maternal environmental effects are substantial, particularly at early life stages, and that effects are genotype specific.

<sup>1</sup>Centre for Biotechnology Borj Cedria, Legume Ecophysiology, Hamman Lief, Tunis, Tunisia<sup>2</sup>2128 DELTA BLVD, Tallahassee, FL, 32303, USA<sup>3</sup>University of Southern California<sup>4</sup>8771 SW 214th Terrace, Cutler Bay, FL, 33189, USA<sup>5</sup>University of California Davis<sup>6</sup>Florida International University, Biological Sciences, 11200 SW 8th St, Biological Sciences OE 167, Miami, FL, 33199-0001, United States

703 WHEELER, GREGORY L\*<sup>1</sup>, MCGLAUGHLIN, MITCHELL E<sup>2</sup>, HELENURM, KAIUS<sup>3</sup> and WALLACE, LISA<sup>2</sup>

### A comparison of nucleotide and microsatellite diversity for understanding intraspecific evolutionary patterns in two California-endemic *Lotus* species

The Channel Islands, an archipelago of eight oceanic islands off the coast of California, comprise a geographically unique system with a high level of plant endemism. It is not known whether the plant taxa found on the Islands are relicts of species that once existed throughout mainland California and the Channel Islands or if the unique taxa evolved into new niches on the islands. To address this question, it is necessary to have an understanding of phylogenetic relationships within species on the islands and between island and mainland species. In this study, we examined phylogenetic relationships in *Lotus dendroideus*, an endemic species, and *L. argophyllus*, a species with both island-endemic and mainland varieties, using DNA sequences from three chloroplast regions and genotypic data from seven chloroplast microsatellite loci. We compared the information content of these two data sets for recon-

structing intraspecific evolutionary patterns, and tested the hypothesis that the microsatellites would provide more phylogenetically informative characters relative to effort compared to DNA sequencing without an increase in homoplasy. Additionally, we used the combined data set to evaluate intraspecific taxonomy for both species and to identify the most genetically similar mainland species. While the microsatellite loci assayed through fragment-based genotyping methods did provide additional phylogenetic characters with less effort than DNA sequencing, length variation in these loci did not always correspond to variation in the repeat region. Thus, care must be taken to ensure homology of fragment sizes when using the information at microsatellite loci for phylogenetic inference. Neither data set provided strong support for all of the morphologically-determined varieties in either species. Additionally, neither island species was monophyletic relative to mainland relatives. These findings suggest the retention of ancestral polymorphism throughout these taxa, which could make reconstructing a maternal phylogeny difficult. Nevertheless, these data do allow for robust estimation of population-specific patterns within the islands.

<sup>1</sup>Mississippi State University, Biological Sciences, 295 Lee Blvd, Mississippi State, MS, 38762, USA<sup>2</sup>University of Northern Colorado, Biological Sciences, 501 20th Street, Ross Hall 1560, Greeley, CO, 80639, USA<sup>3</sup>University Of South Dakota, Department Of Biology, Vermillion, SD, 57069, USA

704 WARSCHEFSKY, EMILY\*<sup>1</sup>, JESTROW, BRETT<sup>2</sup> and VON WETTBERG, ERIC J BISHOP<sup>1</sup>

### Patterns of genetic variation in the *Chamaecrista* species of South Florida

The legume family is the third largest plant family and includes species important to agriculture as well as ecological function. However, most previous research has focused only on members of the subfamily Papilionoideae, with less emphasis on the other clades. *Chamaecrista fasciculata*, a member of the subfamily Caesalpinioideae has recently emerged as a new model species for evolutionary and ecological studies. The genus *Chamaecrista*, while tropical in origin, also includes species found in temperate climates. South Florida's unique subtropical climate and geographical location provide habitat for both temperate and tropical species at the southern and northern limits of their respective ranges, including five native species and varieties as well as the naturalization of one exotic species. Due to their geographic isolation, it is hypothesized that these populations demonstrate genetic differences from conspecific Caribbean or temperate North American populations. To investigate patterns of population genetic variance found in *Chamaecrista* in South Florida, samples from multiple populations of *C. fasciculata*, *C. nictitans* var. *aspera*, and *C. lineata* were collected. The sequences of seven single copy nuclear

genes were compared within and between populations to determine inbreeding coefficients, Hardy Weinberg allele frequencies, fixation indices, Bayesian clustering, and analysis of molecular variance. The results of these analyses revealed a variety of patterns of population genetic variation in *Chamaecrista* species in South Florida. Most importantly, our results shed light on the limited conservation options available for the rare South Florida *Chamaecrista lineata*, a federal candidate species for endangered species listing that is restricted to low-lying land in the Florida Keys. With little habitat at elevations above expected sea level rise, conservation will have to occur beyond the current range.

<sup>1</sup>Florida International University, Department of Biological Science, 11200 SW 8th Street, Miami, FL, 33199, USA<sup>2</sup>Fairchild Tropical Botanic Garden, Center for Tropical Plant Conservation, 11935 Old Cutler Road, Miami, FL, 33156, USA

**705 LI, XINNIAN\*, RENCHAO, ZHOU and SUHUA, SHI**

### Population genetic variation of a mangrove species *Avicennia marina* in Hainan Island revealed by high-throughput sequencing

Mangroves are woody trees or shrubs inhabiting coastal intertidal zone in tropical and subtropical regions. They adapt to their specific habitats with special properties such as vivipary, salt secretion and aerial roots. Previous studies reported low level of polymorphisms and strong population structure in many mangroves. The advent of next generation sequencing technologies makes population genomics studies feasible in non-model organisms like mangroves. In this study, we used Illumina platform to sequence 91 genes in two natural populations (Wenchang and Sanya) of *Avicennia marina*, a mangrove species. 100 individuals were pooled for each population and our results showed that no single nucleotide polymorphisms (SNPs) were detected in 64 genes for both populations, while 67 SNPs were distributed in the remaining 27 genes. Strong genetic differentiation ( $F_{st} > 0.25$ ) was revealed between the two populations in 3 genes. By using computer simulation, the pattern observed in this species could not be explained by sole demographic factors and we suggested that some genes might experience divergent selection in the two populations of *A. marina* in Hainan Island.

Sun Yat-sen University, Life Science School, Guangzhou, Guangdong, P.R.China

**706 LONGWICH, ADAM\*<sup>1</sup>, CONDON, MARTY<sup>2</sup> and SWENSEN, SUSAN<sup>1</sup>**

### Neotropical Cucumbers: Molecular Phylogenetic Reconstruction of the Genus *Gurania*

*Gurania* are a genus of monoecious flowering vines that are native to Central and South America. Early in their life, vines produce male flowers and climb into the rainforest canopy. Once they reach a certain size, male vines begin to produce female flowers in pendulous inflorescences. *Gurania* serve as hosts to fruit flies in the genus *Blepharoneura* where as many as seven different species of flies may parasitize a single species of *Gurania*. Currently, there is no clear picture of species relationships within *Gurania*. Taxonomic revision based on morphology is currently underway, but geographical variation within species has led to difficulties in species definitions and no phylogenetic analysis has been completed. Our work is aimed at reconstructing a phylogeny of *Gurania* using molecular data. Preliminary comparison of chloroplast DNA regions has indicated little divergence suggesting that *Gurania* species are closely related. As a result, phylogenetic reconstructions require the analysis of multiple, rapidly evolving gene regions. We have identified useful gene regions for phylogenetic reconstruction in *Gurania* based on chloroplast intergenic spacer regions used in phylogenetic reconstruction of *Psiguria*, the sister genus of *Gurania*. Using leaf samples collected in the field, we have extracted, amplified, and sequenced six chloroplast intergenic spacers: *rpoB-trnC*, *trnS-trnG*, *ndhF-rpl32*, *psbE-petL*, *psbM-trnD*, and *ndhC-trnV*. Pairwise comparisons of these sequences reveal 0.22-2.26% sequence divergence among the *Gurania* species suggesting that while *Gurania* are closely related, sufficient sequence variation exists for phylogeny reconstruction. Parsimony and maximum likelihood-based phylogenetic analysis of multiple species of *Gurania* will be presented and used to interpret morphology and biogeography.

<sup>1</sup>Ithaca College, Biology, 953 Danby Road, Ithaca, NY, 14850, USA-<sup>2</sup>Cornell College, Biology, 600 First Street SW, Mount Vernon, IA, 52314, USA

**707 SCOTT, ALISON DAWN\* and BAUM, DAVID**

### Evolutionary history and origin of polyploidy in *Sequoia sempervirens*

The majestic coast redwood (*Sequoia sempervirens*, Cupressaceae) is one of the few polyploid conifers, and the only hexaploid ( $2n=6x=66$ ). Coast redwoods are long-lived trees (some over 2,000 years) and are among the very tallest tree species in the world (up to 115 meters). Their geographical range is limited to the coast of central and northern California, but the fossil record suggests a broader historical distribution.

The origin of hexaploidy in *S. sempervirens* has been a source of speculation; various mechanisms of polyploidization and putative ancestral genome donors have been suggested. The closest living relatives of *S. sempervirens* are the dawn redwood, *Metasequoia glyptostroboides*, native to China, and the giant redwood, *Sequoiadendron giganteum*, endemic to interior central California. South American alerce, *Fitzroya cupressoides*, is another Cupressaceae tetraploid ( $2n=4x=44$ ) and is morphologically similar to the redwoods. Several low-copy nuclear genes have been amplified in *S. sempervirens* and its close relatives and molecular sequence analysis is being used to unravel the ancient polyploid origin of coast redwood.

University Of Wisconsin, Department Of Botany, Birge Hall, 430 Lincoln Drive, Madison, WI, 53706, USA

708 LI, PAN<sup>\*</sup>, WAN, YING<sup>1</sup>, CAMERON, KENNETH<sup>2</sup> and FU, CHENGXIN<sup>1</sup>

### Phylogeography of the North American Herbaceous *Smilax* (Smilacaceae)

The herbaceous *Smilax* (sect. *Nemexia*) exhibit a classic East Asian-North American phylogeographic disjunction. While the two East Asian species are well defined by morphological and molecular evidence, the North American species are more taxonomically confused and treated as 1 to 9 species by different authors. Recent studies of chloroplast and nuclear DNA have shown that North American herbaceous *Smilax* are monophyletic, but failed to resolve the phylogenetic relationships among them. To elucidate these relationships, we reconstructed a phylogeny of *Smilax* sect. *Nemexia* using amplified fragment length polymorphism (AFLP) data. 325 individuals from 49 populations of all the nine North American species + the two East Asian species were sampled across the whole geographic range. Individuals of *S. jamesii* from western North America formed a cluster distinct from the eastern North American species. Within the eastern clade, a population of "*S. biltmoreana*" from the southern Appalachians formed a basal clade. The remaining samples showed a pattern related to geography rather than morphology or taxonomy. To supplement these data we also sequenced three plastid loci (*ycf6*, *trnG* and *rpoC1*). The cpDNA and AFLP results both support our former hypothesis that herbaceous *Smilax* first arrived into western North America via the Bering land bridge, and then spread eastwards, followed by isolation between them. Eastern herbaceous *Smilax* may have localized in glacial refugia in southern Appalachia, then expanded rapidly to the north in order to achieve their present distribution.

<sup>1</sup>Zhejiang University, College Of Life Sciences, 388 Yuhangtang Road, Hangzhou, Zhejiang, 310058, China<sup>2</sup>Wisconsin State Herbarium, Department Of Botany, 154 Birge Hall, 450 Lincoln Drive, Madison, WI, 53706, USA

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## Pollination Biology

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### ORAL PAPERS

710 COLEMAN, CASSANDRA<sup>\*</sup> and CLARK, JOHN L.

### A revised phylogeny and study of pollinator shifts and floral traits in the neotropical genus *Gasteranthus* (Gesneriaceae)

The genus *Gasteranthus*, with 40 currently described species, occurs in Central and South America. Species of *Gasteranthus* have two morphologically different corolla shapes, which are suggestive of specific pollinators. The flower shapes are either hypocyrtoid with an inflated ventral pouch or funnel form and non-pouched. Previous molecular phylogenies of *Gasteranthus* were equivocal of whether or not hypocyrtoid flowers were an apomorphy or plesiomorphy. Molecular sequence data generated from nrDNA (ITS and ETS) and cpDNA (*matKR* and *trnLF*) were generated for 80 taxa representing 25 taxa of *Gasteranthus* and 55 taxa from closely related genera. Our data strongly supports that funnelform flowers associated with euglossine bee pollination are symplesiomorphic and that bee pollination has evolved at least three times in *Gasteranthus*. Pollen presentation and nectar reading schedules, as well as pollinator identification and videography were utilized to better understand the role of pollinators on the species of *Gasteranthus*.

The University of Alabama, Department of Biological Sciences, Box 870345, Tuscaloosa, AL, 35487, USA

710 MEIER, RETHA

### Breeding Systems, Pollination Ecology and Fragrances of *Thelymitra* (Orchidoideae)

The purpose of our study was to investigate the breeding system, pollination ecology and fragrances of *Thelymitra crinita* (blue lady) and *Thelymitra macrophylla* (scented sun orchid). Green house experiments showed that both orchid "parent species" were self-compatible but did not self-pollinate mechanically. We also found that native bees infrequently visit *T. macrophylla* and *T. crinita*. As the orchids' flowering periods and distribution overlapped broadly at one of our field sites in Western Australia, we wanted to know if these blue sun orchids could be mimicking *Orthrosanthos* (Iridaceae) and/or *Leschenaultia* (Tachinidae). To address this research interest, fragrances were collected from all four species and sent to Dr. Robert Raguso at Cornell University for analyses. We found that *T. macrophylla* may

be mimicking *Orthrosanthos* in color (blue) as well as fragrance (both emit 2-phenylethanol). *T. macrophylla* and *Orthrosanthos* smell alike but *T. crinita* does not smell like either of them.

Saint Louis University, Education, 3500 Lindell Blvd, St. Louis, MO, 63103, USA

**711 ICKERT-BOND, STEFANIE M.\*<sup>1</sup>, RYDBERG, ANDERS<sup>2</sup>, BOLINDER, KRISTINA<sup>2</sup>, HAN, JUN<sup>3</sup>, JESSE, SUSANNAH<sup>6</sup>, LITTLE, STEFAN<sup>4</sup>, LOERA CARRIZALES, ISRAEL<sup>5</sup>, RYDIN, CATARINA<sup>2</sup> and VON ADERKAS, PATRICK<sup>6</sup>**

### **Chemical composition of pollination drops in *Ephedra* - safe sex and other oddities.**

**A**lthough pollination drop mechanisms are known from several extinct seed plants, within extant gymnosperms it is restricted to four clades: conifers, *Ginkgo*, cycads and Gnetales. Within conifers pollination mechanisms are highly variable due to varied orientations of the ovule during pollination, presence, modification or absence of the pollination drop mechanism, and whether the pollen is saccate or non-saccate. In Gnetales the ovules are orthotropous and produce pollination drops to capture non-saccate pollen. The pollination drop then retracts, carrying the pollen into the ovule. *Ephedra* pollination drops are produced via nucellar secretion and are presented at the tip of a long micropylar tube, an extension of the integument. Analysis of the chemical composition of pollination drops might give clues to understanding plant-insect associations involving gymnosperms and their nectarivores, pollinivores and pollinators. While most gymnosperm pollination drops contain low concentrations of sucrose (5-10 %), in *Ephedra helvetica* sucrose is not only the predominant sugar, but it is found at high concentrations (~ 25 %). This goes in concert with the lack of invertases in the pollination drop of *Ephedra*. As is typical of other gymnosperms, the protein composition of pollination drops in *Ephedra* includes several defense-related proteins. Since *Ephedra* ovules are exposed to the environment and vulnerable to potential pathogens during the time of pollen receptivity, a potential role of these proteins would be to protect the young ovule from airborne microbes - it's a safe sex mechanism. Based on a proteomic evaluation of pollination droplet proteins in several species of *Ephedra* we discuss implications for

the evolution of pollination biology in *Ephedra*.

<sup>1</sup>University of Alaska, UA Museum of the North Herbarium & Dept. of Biology and Wildlife, 907 Yukon Dr, Fairbanks, Alaska, 99775, USA<sup>2</sup>Uppsala University, Evolutionary Biology Centre, Norbyvägen 18D, SE-75236 Uppsala, Sweden<sup>3</sup>University of Victoria, Genome BC Proteomics Centre, Vancouver Island Technology Park, #3101-4464 Markham St, Victoria, BC, V8Z 7X8, Canada<sup>4</sup>University Of California Davis, Department Of Plant Sciences, Davis, CA, 95616-8515, USA<sup>5</sup>Instituto De Ecologia, A. C., Biología Evolutiva, Apartado Postal 63, Xalapa, Veracruz, 91000, Mexico<sup>6</sup>University of Victoria, Graduate Centre for Forest Biology, Department of Biology, P.O. Box 3020, Station CSC, Victoria, BC, V8W 3N5, Canada

**712 CLARK, JOHN L.\*<sup>1</sup>, COLEMAN, CASSANDRA<sup>1</sup>, CLAVIJO, LAURA<sup>1</sup>, MORA, MARCELA<sup>1</sup> and MUCHHALA, NATHAN<sup>2</sup>**

### **Evolution of anti-bee pollination mechanisms in the Neotropical plant genus *Drymonia* (Gesneriaceae)**

**T**he Neotropical plant genus *Drymonia* is exemplified by a remarkable diversity of flower shapes and colors. The classification of *Drymonia* and closely related genera is still in flux because of the convergence of floral forms. Data from pollen presentation, videography, and molecular-based phylogenetic analyses suggest that multiple shifts from bee to bird pollination have occurred. Two distinctive corolla forms associated with bird pollination have multiple independent origins in *Drymonia*: laterally compressed corollas and hypocyrtoid ('pouched') corollas. Species of *Drymonia* with either of these corolla shapes occasionally retain features of euglossine bee pollination such as poricidal anther dehiscence. Our data suggests that shifts to bird pollination in *Drymonia* area accompanied with the evolution of 'anti-bee' mechanisms, such as narrow flower openings and red coloration, that serve to reduce visits by euglossine bees.

<sup>1</sup>The University of Alabama, Department of Biological Sciences, Box 870345, Tuscaloosa, AL, 35487, USA<sup>2</sup>University of Nebraska Lincoln

**713 COWDEN, NANCY\* and GANNICOTT, PRISCILLA**

### **We talk to the bees: *Cypripedium parviflorum* var. *pubescens* pollination biology insights**

**C***yripedium parviflorum* var. *pubescens* (large yellow lady's-slipper) presents no discernable reward to pollinators, but observations in Virginia indicate that certain plants consistently succeed in setting fruits while other plants experience reduced abilities attracting pollinators. Because fruit set requires vector-mediated pollen transfer, we are confident that resident bees discriminate among *C. parviflorum* var. *pubescens*

individuals. We propose that floral fragrance variations account, at least in part, for uneven reproductive success in large yellow lady's-slippers. During each growing season from 2008 - 2011, we obtained fragrance samples from two *C. parviflorum* var. *pubescens* populations using non-destructive, static headspace solid-phase microextraction (SHS-SPME) employing SPME portable field samplers exposed to the floral headspace and subsequently desorbed in the injection port of a Thermo-Scientific Focus GC/DSQ MS. We also captured and identified to species insects observed within the labella of our tagged plants, enabling us to correlate floral scent characteristics with particular visitors. Nonanal, phenylacetaldehyde, and phenylethyl alcohol occur as major constituents in the *C. parviflorum* var. *pubescens* samples analyzed, and flowers ranging in age from two to seven days produce fragrances detectable by our methods while younger and older flowers do not. Our recovered fauna generally agrees with the diversity encountered by previous researchers, and bee visitations correspond with elevated scent production. While the specific effect of fragrance on bees' behavior remains unknown, evidence suggests large yellow lady's-slippers' perfumes factor in reproductive success.

714 MITCHELL, RANDALL\*<sup>1</sup> and KARRON, JEFFREY<sup>2</sup>

### Influence of pollinator visitation patterns on multiple paternity in *Mimulus ringens*

Animal-pollinated Angiosperms cannot directly control gamete receipt or export. Instead, these plants depend on movements of pollinators whose foraging behaviors often fail to optimize the quantity or quality of pollen deposited on stigmas. Furthermore, the stochastic nature of pollinator visits often leads to striking among-flower differences in mating patterns. One factor likely to contribute to this among-flower variation is the timing and composition of sequential pollen loads deposited on each stigma. Each pollen load may differ markedly in sire representation, especially if successive pollinators approach a flower from distinct compass directions and carry pollen from different donors. Although pollen deposited during an initial floral visit may have a siring advantage due to priority, pollen grains deposited during later visits may also compete successfully for access to ovules. This multiple mating is likely to increase the genetic diversity in a sibship, which may influence competitive interactions among developing seeds within fruits and among seedlings in the field. We experimentally tested the hypothesis that sequential pollinator visits contribute to the exceptionally high levels of multiple paternity in fruits of *Mimulus ringens* (Phrymaceae), a wetland perennial native to North America. We documented all bee visits to individual flowers, quantified resulting seed set, and determined paternity for 20 seeds per fruit. Most (76%) flowers

received multiple visits, and the interval between visits was usually < 30 min. Flowers visited multiple times produced 44% more seeds than flowers visited once. All fruits were multiply sired. Flowers receiving a single visit averaged 3.12 outcross sires per fruit, indicating that single visits deposit pollen from several donors. Multiple paternity was even greater following three or more visits (4.92 outcross sires), demonstrating that sequential visits bring pollen from donors not represented in the initial visit.

<sup>1</sup>UNIVERSITY OF AKRON, Department Of Biology, Department Of Biology, AKRON, OH, 44325-3908, USA <sup>2</sup>University Of Wisconsin-Milwaukee, Department Of Biological Sciences, PO BOX 413, MILWAUKEE, WI, 53201, USA

715 YOUNG, HELEN

### Landscape features affect bumblebee abundance in Vermont

Since their introduction to the United States over 250 years ago, honeybees have become important pollinators of many plant species. The recent decline in native pollinator species diversity could be due, in part, to habitat degradation and/or fragmentation, as well as competition with non-native honeybees. I studied the relationship between habitat fragmentation and bumblebee abundance in Vermont in two summers. I studied bees at the flowers they visited in meadows and old-fields of varying sizes and degrees of isolation from both other meadows and from forests. Agricultural fields (corn, alfalfa, and pasture) and urbanization adds to the fragmented landscape that these pollinators navigate. Using GIS, I examined the effects of land-use cover on bumblebee abundance. The proportion of visits to flowers by bumblebees was positively correlated with percent forest cover and negatively correlated with percent pasture cover. In addition, bumblebee abundance increased with increasing distance to honeybee colonies and with the proportion of the plant species in the fields that are native. These results suggest that bumblebee abundance is affected by many factors: density of honeybees (competition), floral composition in fields (floral morphology), and forest cover (nesting habitat).

Middlebury College, Biology Department, Bicentennial Hall, Middlebury, VT, 05753, USA

716 GOODWILLIE, CAROL\* and STEWART, EMILY

### Consequences of cleistogamy and chasmogamy in *Triodanis*

The evolutionary explanation for the maintenance of cleistogamous (CH) and chasmogamous (CL) flowers in many plant species remains elusive. Two widely distributed subspecies of *Triodanis perfoliata* have diverged in their relative allocation to CH and

CL flowers. As part of an investigation of the selective factors responsible for this divergence, we compared the fitness contribution of CH and CL flowers in the two species. Seeds were collected from each fruit type of each species in a zone of contact in Pitt County, NC, and offspring were raised in a growth room experiment to quantify and compare germination, survival, biomass and fruit production. We found no evidence in either species for a fitness advantage of CH flowers that would compensate for the greater expense of producing them. In fact, in one of the taxa, CL seeds germinated at a significantly higher rate than CH seeds. We found morphological evidence for hybridization in CH offspring, particularly of *T. perfoliata* ssp. *biflora*. We consider the implications of CH and CL strategies for the rate of hybridization between the taxa and its consequences.

East Carolina University, Biology, Mail Stop 551, Greenville, NC, 27858, USA

**717 POLICHA, TOBIAS<sup>1</sup>,  
MANOBANDA, ROCIO<sup>2</sup>, MCALPINE,  
JESSE<sup>1</sup>, DENTINGER, BRYN<sup>3</sup> and ROY, BITTY<sup>1</sup>**

### **Reproductive Biology of Mushroom Mimicking *Dracula* Orchids**

**P**ollination biology is fundamentally the study of interactions between a plant and its environment. Floral mimicry adds complexity to this interaction. *Dracula* orchids look and smell like mushrooms, and are pollinated by mushroom associated flies. One hypothesis is that the plants take advantage of this fungal phenotype to overcome the problems of density-dependent visitation. Like many orchids, neither *Dracula felix* nor *D. lafleuri* have very high fruit set rates. *D. lafleuri* set fruit on only 5.7% of its buds (n=35), while *D. felix* was somewhat more successful, producing fruit from 45.5% of its buds (n=44). One explanation for the higher rates in *D. felix* is its capacity for insect-mediated selfing. In a hand pollination experiment, manipulated 'selfed' flowers, geitonogamously pollinated, and out-crossed flowers all set fruit at similar rates, but unmanipulated flowers did not set any fruits (n=102). In support of a density-dependent visitation hypothesis, when number of flowers per plant was regressed against total number of visitors, there was a clear positive relationship ( $r^2 = 0.49$ ,  $p=0.001$ ). The next hypothesis tested was: if these flowers are mimicking fungi, then they should derive some benefit from the resemblance. When assaying visitation rates in different contexts with *D. felix*, we found not only that flowers next to other flowers received more visits than singleton flowers, but that flowers next to mushrooms received the same number of visits as the 'next to flowers' treatment (n=16 reps;  $p=0.0199$ ). In *D. lafleuri* we asked the same question, but instead of single flowers we positioned whole plants either next to mushrooms or by themselves. We again found that plants next to mushrooms had more visits than plants away from mushrooms (n=6reps;  $p=0.0218$ ). Finally,

looking at natural variation in plants that were either near to, or far away from mushrooms, we found a similar pattern (n=4 reps;  $p=0.0500$ ). Our data support the hypothesis that *Dracula* orchids derive a benefit from their resemblance to mushrooms.

<sup>1</sup>University of Oregon, Center for Ecology and Evolutionary Biology, 5289 University of Oregon, Eugene, OR, 97403, USA<sup>2</sup>Quito, Ecuador<sup>3</sup>Royal Botanic Gardens, Kew, Jodrell Laboratory, Richmond, Surrey, TW9 3DS, UK

**718 SUMMERS, HOLLY\*<sup>1</sup> and RAGUSO, ROBERT A.<sup>2</sup>**

### **Intraspecific variation in floral display and breeding system in *Oenothera flava* (Onagraceae)**

**A**ngiosperms have developed diverse strategies for sexual reproduction, but the evolutionary transitions between self-fertilization and outcrossing are still a topic of ongoing interest. The two subspecies of the North American mixed-mating Yellow Evening Primrose, *Oenothera flava* (Onagraceae), vary in floral display and degree of outcrossing. *O. flava* subspecies *flava* is a predominantly self-fertilizing annual common at low elevations in the western United States and Mexico. It produces yellow flowers about 2 cm in diameter with hypanthia up to 6 cm long. *O. flava* subspecies *taraxacoides* grows at higher elevations on discrete mountaintops in the American southwest and Mexico. This annual-to-perennial subspecies produces showy flowers (up to 20 cm long with a corolla diameter up to 8 cm) which emit high levels of nitrogenous scent compounds. These volatiles, common in hawkmoth-pollinated taxa, are not well studied. Disjunct populations of *taraxacoides* also display discrete variation in scent and morphology. Here I provide a case study of intraspecific variation in reproductive strategy by investigating 1) the mechanisms of pollinator attraction using comparative transcriptomics and volatile metabolomics, 2) inter-population variation in floral development, examined through dissection of buds grown in a common garden from field-collected seeds, 3) adaptive value via field and laboratory pollinator behavioral trials and 4) the phylogenetic history of each subspecies using next generation sequence generated markers.

<sup>1</sup>Cornell University, Plant Biology, 215 Tower Rd, W343 Mudd Hall, Ithaca, NY, 14853, USA<sup>2</sup>Cornell University, Department of Neurobiology and Behavior, Room W355, Seeley G Mudd Hall, 215 Tower Road, Ithaca, NY, 14853, USA

719 MCCARTHY, ELIZABETH W.\*<sup>1</sup>,  
KNAPP, SANDRA<sup>2</sup>, CHASE, MARK W.<sup>3</sup>,  
BALDWIN, IAN T.<sup>4</sup>, LEITCH, ANDREW R.<sup>1</sup>  
and LE COMBER, STEVEN C.<sup>1</sup>

### The Evolution of Floral Morphology in *Nicotiana* Polyploids of Different Ages

The evolution of floral morphology in *Nicotiana* (Solanaceae) allotetraploids, ranging in age from a few generations (synthetic allotetraploids) to ~4.5 million years old, was examined using geometric morphometrics of floral limb shape, corolla tube length and width metrics, and spectral reflectance measurements of floral color. Floral limb shape in *Nicotiana* is well described by two characters: the outer shape of the limb, which ranges from round to star-shaped, and the relative size of the corolla tube opening to the floral outline, which ranges from small to large. In floral limb shape, younger allotetraploids tend to be intermediate in shape between those of their diploid progenitors, while older allotetraploids have more divergent forms; however, divergence in floral limb shape can occur rapidly following allopolyploidization. In corolla tube length and width, the majority of allotetraploids have wider and shorter corolla tubes, suggesting more generalist pollination after allopolyploidization. In floral color, allotetraploids can either be intermediate between their progenitors, like one or other progenitor, or divergent. The floral color of *N. tabacum* is divergent and seems to have resulted from the inheritance of floral plastids which lack chlorophyll from its maternal progenitor and the inheritance of anthocyanin pigmentation from its paternal progenitor. Evidence for convergent evolution of floral form in green/yellow-flowered *Nicotiana* seems to be linked to hummingbird pollination. Overall, the combined study of floral shape, size, and color in *Nicotiana* sheds light on the evolution of allopolyploids in the context of pollination.

<sup>1</sup>Queen Mary, University of London, School of Biological and Chemical Sciences, Mile End Road, London, E1 4NS, UK<sup>2</sup>Natural History Museum, Department of Botany, Cromwell Road, London, SW7 5BD, UK<sup>3</sup>Royal Botanic Gardens, Kew, Jodrell Laboratory, Kew, Richmond, Surrey, TW9 3AB, UK<sup>4</sup>Max Planck Institute for Chemical Ecology, Department of Molecular Ecology, Beutenberg Campus, Hans-Knoll-Str. 8, Jena, 07745, Germany

720 FIGUEROA-CASTRO, DULCE\*<sup>1</sup>,  
VALVERDE, PEDRO<sup>2</sup> and AGUILAR-  
GARCÍA, SANDRA<sup>1</sup>

### Is reproductive success in *Pachycereus weberi* (Cactaceae) constrained by pollination success or resource availability?

Numerous studies have shown that floral traits such as size, shape, color and floral display have a significant effect on flower attractiveness towards pollinators and thus, affect reproductive success. Recently, it has been shown that flower angle and flower direction (components of flower orientation) are also important traits affecting reproductive success. It has been suggested that in columnar plants within the Cactaceae family, flower reproductive success is constrained by the amount of resources on each rib, since photosynthetic active radiation (PAR) is heterogeneous around the stem and there is not carbohydrate translocation among ribs within the stem. Therefore, reproductive success might be constrained by resource availability and floral attractiveness. In this study we attempt to determine if flower orientation has an effect on floral attractiveness and on reproductive success using *Pachycereus weberi* as the study system. We collected flowers and fruits with different orientations (Northeast vs. Southeast). We tested if flower length, corolla diameter, ovary diameter, flower volume, ovule and pollen production and pollen:ovule ratio were different among flowers with different orientations. Seed set, seed weight and percentage of germination were used as estimators of reproductive success. Among all the floral traits that we measured, only ovule production was significantly different between flowers with contrasting orientations. Flowers oriented towards the Southeast produced significantly more ovules than flowers oriented towards the northeast. Seed set was not significantly different among flowers with different orientations, but seed weight and percentage of germination were significantly greater for flowers oriented towards the southeast. Our results indicate that flower orientation does not have an effect on flower attractiveness and seed set; thus, similar rates of visitation and similar reproductive success would be expected. Contrastingly, seed quality (an estimator of reproductive success) was different, suggesting that resource availability is the main factor affecting reproductive success in *Pachycereus weberi*.

<sup>1</sup>Universidad Autónoma de Puebla, Escuela de Biología, Blvd. Valsequillo y Av. San Claudio, Edif. 112A., Ciudad Universitaria, Col. San Manuel, Puebla, Puebla, 72570, México<sup>2</sup>Universidad Autónoma Metropolitana-Iztapalapa, Biología, México, D.F., México

721 ANDERSON, GREGORY\*<sup>1</sup>,  
CRAWFORD, DANIEL<sup>2</sup>, BERNARDELLO,  
GABRIEL<sup>3</sup>, SANTOS, ARNOLDO<sup>4</sup> and  
PEREZ DE PAZ, JULIA<sup>5</sup>

### Reproductive Biology of Island Plants

Islands possess an intrinsic interest for most, an attraction that is inordinate in that they constitute less than 5% of the Earth's land surface. In the plant world, however, their high regard is deserved in that 25% of the endemics are insular. Furthermore, 5-10% of insular endemics are highly threatened; thus conservation efforts are critical. Various elements of plant reproductive biology (RB) must be taken account of for a conservation plan to be successful; without successful reproduction, only the current generation will survive. Three of the four elements of RB (i.e., not including dispersal) - pollination, breeding systems and mating systems are discussed. Respectively, they are increasingly difficult to fully understand, and there is proportionately less information for each category. Furthermore, there is comprehensive information on RB for very few archipelagos. Pollinators are often conflated with flower visitors; there is relatively little compiled for breeding systems of island floras; and too often such things as compatibility alone substitute for an understanding of gene flow. Not all colonists arrive on new islands at the same time, and the legendary diversification associated with morphology and ecology of island colonists may not apply in the same way to elements of RB. Island plants may also retain features of their continental relatives that can mislead conclusions about pollination. Examples are given of some pitfalls in data and interpretations, and of the growing comprehensive pictures for some archipelagos. More comprehensive data sets will facilitate comparisons among archipelagos and with continental source floras, allowing a better understanding of evolutionary scenarios and phylogenies.

<sup>1</sup>University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Road, Unit 43, Storrs, CT, 06269-3043, USA<sup>2</sup>University Of Kansas, Department Of Ecology And Evolutionary Biology, 1200 Sunnyside Avenue, Haworth Hall, Lawrence, KS, 66045-7534, USA<sup>3</sup>Museo Botanico, Avda. Velez Sarsfield 299, Cordoba, N/A, 5000, Argentina<sup>4</sup>Unidad de Botánica (ICIA), Puerto de la Cruz, Tenerife, Canary Islands, Spain<sup>5</sup>Jardín Botánico "Viera y Clavijo" Unidad Asociada CSIC, Las Palmas de Gran Canaria, Gran Canaria, Canary Islands, Spain

## POSTERS

722 MILLER, ANDREW PAUL

### Temporal Patterns of Pollinator Assemblage Diversity at a Neotropical Daisy (*Wulffia baccata*)

Little is known about pollinator assemblages of non-economic plants. I therefore studied membership of a pollinator assemblage of the rainforest daisy, *Wulffia baccata* in Guyana, South America. Insects were the only pollinators to visit this plant, and had the highest species richness during Time Block-II (TB-II; 0900-1159 h; 23 species), and second highest in TB-IV (1300-1459 h; 22 species). These diurnal visitors were represented by several taxa and included flies, wasps, bees, and butterflies. The majority were observed during TB-II (401 insects-mostly stingless bees), and tapered off during succeeding TBs. Richness was also mirrored by the information-theoretic Shannon diversity index ( $H'$ ) with TB-IV providing the highest  $H'$  of 2.32, and TB-V (1800-1900 h) the lowest value of  $H'$  at 1.71. It seemed as though the individual flowers of each inflorescence began filling with nectar at sunrise, which may explain why only a few small-to-medium sized pollinators frequented the plant during the first Time Block. I speculate that nectar levels were optimal 4-5 hours after sunrise, and that less effective pollinator species visited *W. baccata* during the afternoon hours. This is the first documentation of *W. baccata* pollinator assemblage diversity, and these results suggested that time-of-day was related to variation in floral visitation.

University of Missouri-St. Louis, Biology, 1 University Blvd., 63121, 13 JoAnn Place; 63126, Saint Louis, MO, 63121, USA

723 DIERINGER, GREGG\*<sup>1</sup> and  
CABRERA R., LETICIA<sup>2</sup>

### Ecological Relationship Between Floral Thermogenesis and Pollination in *Nelumbo lutea* (Nelumbonaceae)

Floral thermogenesis is a well documented floral trait. Yet there is limited understanding of how this trait influences plant reproduction. The present study was undertaken to better understand the ecology of floral thermogenesis as it pertains to pollinator attraction and consequent plant reproduction using *Nelumbo lutea*. We conducted field studies on floral thermogenesis, flower sexual development, floral visitation patterns, breeding system using experimental hand-pollinations, and floral scent production using gas chromatography-mass spectrometry. The most abundant visitors to the thermoregulatory flowers included the Phoridae (Diptera) and the Chrysomelidae (Coleoptera). Chrysomelid beetles were frequent visitors to both first day

female- and second day bisexual-phase flowers while phorid flies were most common in bisexual-phase flowers. 1,4-dimethoxybenzene was the most predominant component of the floral scent comprising 81% of all identified volatiles followed by pentadecane (4%) and  $\alpha$ -farnesene (3%). This study is the first to document thermoregulation for *Nelumbo lutea*. While the flowers received a taxonomically wide assemblage of floral visitors, the study is also the first to provide strong support that chrysomelid beetles comprise the dominant portion of floral visitors that are capable of consistently affecting cross-pollination despite the general acceptance of the flower's characteristics as adapted to beetle pollinators. We suggest that thermogenesis aids in dispersing the main floral scent component, 1,4-dimethoxybenzene, while thermoregulation causes chrysomelid beetles to actively seek out new flowers for evening residence with this search behavior likely resulting in consistent cross-pollination.

<sup>1</sup>NORTHWEST MISSOURI STATE UNIVERSITY, 800 UNIVERSITY DR., MARYVILLE, MO, 64468, USA<sup>2</sup>Iowa Western Community College, Clarinda Campus, 923 East Washington, Clarinda, IA, 51632, USA

**724 HUANG, YA-LUN\*<sup>1</sup> and KAO, WEN-YUAN<sup>2</sup>**

### Does Baker's rule also apply to the invasive plant, *Bidens pilosa* var. *radiata*, in Taiwan?

Reproduction plays an important role in colonization. According to Baker's rule, plants capable of uniparental reproduction are more likely to be successful colonists than plants being self-incompatible. In this study, breeding systems of one invasive (*Bidens pilosa* var. *radiata*) and two non-invasive varieties (*B. pilosa* var. *minor* & *B. pilosa* var. *pilosa*) of *B. pilosa* were compared to test the rule. Bagging and open pollination treatments of capitula were conducted for the three varieties. Results of the experiment revealed that capitula of *B. pilosa* var. *radiata* in bagging treatment produced almost no seed indicating of self-sterility of the variety. For the other two varieties, the bagged capitula did produce seeds, however, seed number and seed/ovule ratio from bagging treatment were less than that of open pollination treatment. To explore possible mechanisms contributing to the failure of seed production in bagged capitula of the invasive variety, we examined pollen tube growth of florets in bagging and open pollination treatments. Results suggested that self-sterility in *B. pilosa* var. *radiata* was the result of self-incompatibility. Thus, the contrast breeding systems between the invasive and non-invasive varieties seem contradicting to the rule. However, we found that *B. pilosa* var. *radiata* has better clonal growth ability than the two non-invasive varieties. The clonal growth ability might complement the disadvantage of self-sterility of the invasive variety to ensure reproductive success. By avoiding selfing, the

invasive variety might have higher genetic diversity than the other two non-invasive varieties, which would benefit the invasive variety in heterogeneous environments.

<sup>1</sup>National Taiwan University, Institute of Ecology and Evolutionary Biology, Rm. 1230 Life Science Building, NTU, No. 1, Sec. 4, Roosevelt Road, Taipei, 10617 Taiwan, Taipei, 10617, Taiwan<sup>2</sup>National Taiwan University, Institute of Ecology and Evolutionary Biology, Rm. 1230, Life science building, 1, Sec. 4, Roosevelt Rd., Taipei, N/A, 10617, Taiwan

**725 MUIR, JENNIFER\*<sup>1</sup> and VAMOSI, JANA<sup>2</sup>**

### Generalization alters the probability of plant community invasion

Species-rich communities are well known to be a double-edged sword: while often thought to be more stable as a consequence of high redundancy in mutualistic interactions, a positive association between native and exotic species richness has also been observed. In animal-pollinated plants, increased species richness may dilute pollinator visitation in the face of a limited pollinator pool. However, the presence of showy exotic plants at low densities may actually facilitate the pollination of natives by attracting generalist pollinators to the community. Here, we model the invasion of a resident plant community with particular interest in whether the allocation to floral display in an exotic plant affects the outcome of competition for pollination with native species on a disturbed landscape, and whether the diversity of species within a community can help or hinder its resistance to invasion. We find that there seems to be an optimal resource trade-off between floral and seed allocation in exotic plants, as invaders with low floral allocation do not attract enough visits for full seed set, and too much floral attraction results in seed limitation. Increased pollinator sharing in the resident community does seem to increase the probability of invasion, presumably because the invader is usurping pollinators from natives that share a common pollinator pool.

<sup>1</sup>University of Calgary, Biological Sciences, 2500 University Drive NW, Calgary, AB, T2N 1N4, Canada<sup>2</sup>University Of Calgary, 2500 University Dr. NW, Calgary, AB, T2N1Z4, Canada

726 FAGUA GONZALEZ, JOSE\* and  
ACKERMAN, JAMES

### Consequences of floral visits by ants and invasive honeybees to the hummingbird- pollinated, Caribbean cactus *Melocactus intortus*

The pink, tubular, nectariferous flowers of *Melocactus intortus* (Cactaceae) in Puerto Rico are visited by native hummingbirds (*Anthracothorax dominicus*), but also by invasive honeybees (*Apis mellifera*) and ants (*Solenopsis* sp.). We sought to determine if the bees and ants significantly alter the pollination of *M. intortus* by measuring pollinator effectiveness. Using traditional estimates of effectiveness (visitation rate and seed set), our results show that hummingbirds were the most effective pollinators as expected. Bees and ants were less effective, and their contributions were one-fourth to one-tenth of that observed for hummingbirds. We then modified this measure of effectiveness by adding two components, fitness of progeny and temporal availability of visitors, both of which refine estimates of flower visitor effectiveness. With these new estimations, we found that the effectiveness values of all three animal visitors decreased; however, the role of hummingbirds as the principal pollinator was maintained, whereas the effectiveness values of bees and ants approached zero. By these new measures of overall pollinator effectiveness, the invasive honeybees and ants have little effect on the reproductive success of *M. intortus*.

University Of Puerto Rico, Faculty Of Natural Sciences, PO Box 70377, San Juan, PR, 00936-8377, USA

727 LOFTY, CHRISTOPHER\*, STOEVA-  
POPOVA, PRAVDA and SMITH III, JULIAN

### Microscopic Examination of Epidermal Floral Organ Cell Size in Tomato Species and the Specific Effect of Cytoplasmic Male Sterility

Cytoplasmic male sterility (CMS) and the genetics underlying it have been studied in many species. The main effect of CMS is observed in staminal development: stamens are greatly reduced, with anthers void of functional pollen. Other changes correlated with the CMS phenotype are changes in the second whorl, affecting petal size and color. In tomato species, CMS does not occur naturally; however, crossing *Solanum peruvianum* (pistillate parent) with *S. pennellii* (pollen parent) successfully yielded *CMS-pennellii* (*CMS-p*), possessing a CMS phenotype. Here we have focused on the comparative analysis of the size of epidermal cells from abaxial and adaxial sides of petals and stamens of mature flowers from *CMS-p*, *S. pennellii*, *S. peruvianum*, *S. lycopersicum*

and three *S. lycopersicum* X *CMS-p* hybrids. Epidermal surface profile area (cell size) was measured by confocal laser-scanning microscopy (CLSM) in petals and stamens stained with calcofluor and additionally in anthers prepared for scanning electron microscopy (SEM). Both CLSM and SEM gave statistically identical measurements of cell size. Statistical analysis across species and organs revealed both species- and floral organ-specific differences in epidermal cell sizes. The observed significant reduction of the cell sizes on both surfaces of the anthers can largely explain the smaller anthers in *CMS-p*. On the other hand, *CMS-p* filaments are considerably longer than the filaments of *S. pennellii*, which, in view of the reduced cell sizes in *CMS-p*, implies increased cell division and probably an alteration in the proportions of cells differentiating into filament and anther tissue. The results for petals indicate that the reduction of the size of the petals in the *CMS-p* can be a consequence of reduced rate of cell division. In summary, our results suggest that CMS affects cell enlargement, cell division and the developmental pattern of cells in stamens and petals.

Winthrop University, Biology, 701 Oakland Avenue, Rock Hill, SC, 29733, USA

728 MURCH, SUSAN\*<sup>1</sup> and  
TOMLINSON, P. BARRY.<sup>2</sup>

### Chemical composition of pollination drops in *Gnetum gnemon* (Gnetales) Suggests Gender Differences.

**Introduction.** Pollination drops (Pds) are secreted by the exposed ovule in the majority of extant "gymnosperms" as the site of reception for wind-borne pollen. Pds apparently existed in many extinct groups of seed-plants. Pds are characteristic of all three genera in the Gnetales, but insects may be the usual vector. In *Gnetum gnemon* trees are dioecious but the strobili of each gender possess ovules. Only female plants produce viable seed. Both male and female ovules secrete a Pd but the function of the Pd in male trees has not been defined; it may function as an attractant or reward for pollinators. Pollinators (moths in other species of *Gnetum*) would be required to visit separate trees of the two gender types for successful pollen transfer. Pds then could be seen as a step towards animal pollination as seen in flowering plants. **Methods.** Pollen drops were collected from intact trees and cut branches from late January - March, 2009 at the Kampong Garden, Miami, Fla. Female trees set abundant viable seed, but insect visitors were not observed in either day or night studies. **Results and Discussion.** Male and female Pds of *Gnetum gnemon* were chemically distinct and separated by gender in PCA analysis. Male Pds were also chemically richer than the female drops, containing 2516 distinct putative metabolites as compared with 2139 putative metabolites in the female Pds. The majority of the metabolites characteristic of male Pds fell within the polarity and molecu-

lar weight range indicative of indoles, flavonoids and polyphenols. Additionally, male Pds contained complete profiles of common protein amino acids while female Pd did not contain detectable levels of many of the amino acids. *Conclusion.* Differences in the chemical composition of Pds may indicate different functions of the ovules in the two types of strobili such that males may extend the period over which a pollinator remains on any strobilius and females may deter lengthy visits to any one ovule.

<sup>1</sup>University of British Columbia, Chemistry, 3333 University Way, Kelowna, BC, V1V 1V7, Canada<sup>2</sup>National Tropical Botanical Garden, The Kampong, 4013 Douglas Rd, Miami, FL, 33133, USA

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## Population Genetics

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### ORAL PAPERS

729 THEISS, KATHRYN\*<sup>1</sup>, MATESANZ, SILVIA<sup>2</sup>, SULTAN, SONIA<sup>3</sup> and HOLSINGER, KENT<sup>4</sup>

#### Genetic structure in the invasive

#### *Polygonum cespitosum*

*Polygonum cespitosum* (oriental lady's thumb) is an introduced annual found throughout the eastern United States, the mid-western US and parts of Canada. It is presumed to have been introduced to North America from its native range in eastern Asia within the last century, and it has recently become invasive in New England. Although once restricted primarily to disturbed habitats along shaded roadsides and forest trails, it is now beginning to invade more open sites in New England. Here we use genetic markers to investigate the genetic structure of 20 populations of *P. cespitosum* -- 16 from New England and four from its native Asian range. We genotyped 20-30 individuals per population using 7 newly developed microsatellite loci and examined the levels of genetic diversity within populations and the degree of genetic differentiation among populations. Consistent with high rates of self-fertilization in this species, assignment analysis of individual genotypes revealed high levels of genetic structure: individuals from the same population have genotypes much more similar to one another than those from different populations. We also compare rates of contemporary gene flow among New England populations estimated from assignment analyses with estimates of long-term gene flow estimated from coalescent analyses to gain insight into the dynamics of this species' invasive spread.

<sup>1</sup>University of Connecticut, Ecology & Evolutionary Biology, 75 N. Eagleville Road, U-3043, Storrs, CT, 06269-3043, USA<sup>2</sup>Wesleyan University, Biology, Middletown, CT, 06459-0170, USA<sup>3</sup>WESLEYAN UNIVERSITY, Biology Department, Hall -Atwater Labs, 237 Church St, Middletown, CT, 06459-0170, USA<sup>4</sup>University Of Connecticut, Department Of Ecology & Evolutionary Biology, 75 N. Eagleville Road, U-3043, STORRS, CT, 06269-3043, USA

730 BARRIBALL, KELLY\*, MCNUTT,  
ERIN and ROCHA, OSCAR

**Examination of the genetic structure of southwestern Ohio populations of *Lonicera maackii* to determine invasion patterns.**

*Lonicera maackii* (Rupr. (Herder), Caprifoliaceae) is an invasive honeysuckle shrub that is native to Asia, introduced to the U.S. in 1898 with multiple separate introductions since its initial introduction. *Lonicera maackii* is currently the dominant understory shrub in southwest Ohio. In order to understand how *L. maackii* is expanding its range, it is important to determine whether this species utilizes long-distance dispersal events followed by local expansion or spreads along an expanding front. It has been proposed that *L. maackii* is expanding its range through multiple independent dispersal events. To test this hypothesis, we sampled *L. maackii* from 36 woodlots within Hamilton, Franklin, Butler, Preble, Darke and Miami counties in Ohio, and Wayne County in Indiana. Darke County is the most recent site in Ohio experiencing a rapid colonization, and the majority of the populations we examined are within this center of colonization. Geographic distance between all sample populations ranges from 2.0 km to 104 km. Genetic analysis was conducted using five polymorphic microsatellite loci that were especially designed for this study. A total of 77 alleles were found across all loci, and average mean  $N_a$  was 8.37 with a lower mean  $N_e$  of 4.97. Average observed heterozygosity was 0.725 and average expected heterozygosity was higher at 0.764. The values for  $N_a$  and  $H_e$  suggest high levels of genetic diversity, with low levels of inbreeding ( $F_{IS} = 0.05$ ). An AMOVA showed that 90% of the observed variation is found within populations, indicating relatively low levels of genetic differentiation. Our data revealed a significant correlation between geographical and genetic distances among populations (Mantel correlation  $r = 0.65$ ,  $p$ -value 0.05) suggesting that established populations serve as seed sources for the colonization of nearby uncolonized woodlots. Further analysis using the program Structure revealed a significant level of admixture within individuals and within woodlots, suggesting that long-distance seed dispersal also plays a key role in the spread of this species.

Kent State University, Biological Sciences, 256 Cunningham Hall,  
Kent State University, Kent, OH, 44242, USA

731 WASELKOV, KATHERINE\*<sup>1</sup>,  
OLSEN, KENNETH<sup>2</sup> and SCHAAL, BARBARA<sup>3</sup>

**How does a weed arise? Genetic evidence for the origin of the Midwestern agricultural weed *Amaranthus tuberculatus* (Amaranthaceae)**

Many researchers are interested in the question of how pest plants adapt to agricultural practices, but few studies have investigated the origin of a recently arisen crop field weed. *Amaranthus tuberculatus*, waterhemp, is a native riverbank pioneer that was first observed invading Midwestern soybean and cornfields around 1950, and has since become a major agricultural problem in the region. We hypothesize that secondary contact and hybridization between diverging geographical varieties of the species in the Mississippi Valley region, possibly facilitated by land use changes, led to the development of a "weedy" variety of the species. Using SSR markers, we have genotyped agricultural and riverbank populations of waterhemp from across the species' range. Despite little genetic differentiation at a local scale, we find evidence of two ancestral genetic clusters within the species. A previous hypothesis, that introgression from the weedy congener *Amaranthus hybridus* was involved in waterhemp's adaptation to crop fields, is not supported. Analyses using the program IMA and Slatkin's private alleles method will allow us to evaluate population genetic models of the historical origin of weedy *A. tuberculatus*.

<sup>1</sup>Washington University in St. Louis, Biology, 1 Brookings Drive, Campus Box 1137, Saint Louis, MO, 63139, USA<sup>2</sup>Washington University, BIOLOGY DEPT, BOX 1137, 1 BROOKINGS DRIVE, St. Louis, MO, 63130-4899, USA<sup>3</sup>Washington University, Department Of Biology, CAMPUS BOX 1137, 1 Brookings Drive, St. Louis, MO, 63130-4899, USA

732 ZAVADA, TOMAS\* and KESSELI, RICK

**Deciphering the phylogeny of weedy/invasive and domesticated species in the genus *Cichorium* (Asteraceae)**

The genus *Cichorium* possesses two well-known cultivated species, *C. endivia* (endive) and *Cichorium intybus* (chicory). Endive is an annual, selfing species that is only known from cultivation. Chicory is a perennial, outcrossing species that was domesticated, but also recently categorized as an invasive plant taking over the US Midwest range. *Cichorium pumilum* is a self-compatible annual with unclear delineation within the genus. There are only a few morphological characters available for the estimation of genetic variability, thus the genetic variation within this genus is best studied with molecular markers. We have screened 41,704 ESTs derived from *C. intybus* and *C. endivia* in

the Composite Genome Project database (<http://comp-genomics.ucdavis.edu>) and identified SSRs with 10 or more repeats. Microsatellite markers were tested on 32 *C. intybus* individuals coming from a single population in Boston, MA and on 17 different *C. intybus* populations coming from the native Eurasia (6 samples per population). These markers crossamplified on *C. endivia* and *C. pumilum* populations. The number of alleles per locus ranged from 5 to 11, with marker 6865 showing the most polymorphism. Significantly lower observed heterozygosity was detected among endive populations due to inbreeding and lower number of present alleles. Fixed heterozygosity present in several *C. endivia* and *C. pumilum* loci suggests gene duplication events. We plan to obtain *C. intybus* samples from US invasive ranges of chicory in order to uncover alleles possibly responsible for invasiveness, and assess the genetic diversity among chicory herbarium samples and current New England populations that might show the changes in the species genetic make-up over the past 200 years.

University Of Massachusetts, Biology, 100 Morrissey Blvd., Boston, MA, 02125, USA, Boston, MA, 02125, USA

**733 AHRENS, COLLIN\*<sup>1</sup> and AUER, CAROL<sup>2</sup>**

### The population genetics of feral creeping bentgrass and cultivated turfgrass on a golf course

*Agrostis stolonifera* (creeping bentgrass) is a perennial turfgrass species commonly used on golf courses. However, the same species is often found as a weed in cultural landscapes and natural areas, creating questions about the potential for gene flow if transgenic creeping bentgrass were utilized in U.S. golf courses. In two previous studies, we established the distribution of creeping bentgrass in a cultural landscape surrounding a Connecticut golf course, and in 10 habitat types spanning two ecoregions. Our habitat suitability modeling study showed that 36% of the area around a golf course (8.5 km<sup>2</sup> study site) provided highly suitable habitat for *A. stolonifera* and related species. Our transect study (190 transects) showed that *A. stolonifera* had unequal distribution across habitat types, was more common in the inland ecoregion (especially in roadsides and meadows), and was frequently found in plant communities containing closely-related *Agrostis* species. The aim of this study is to use molecular markers (microsatellite SSR) to establish the relationship between feral populations and cultivated creeping bentgrass on a golf course. DNA samples have been collected from individuals in the golf course, three populations outside the golf course, and common cultivars grown in the greenhouse (e.g. A4, Crenshaw). PCR was performed using primer pairs for eight microsatellite markers (see Reichman et al., 2011) and fragment analysis was conducted. The results have been analyzed in STRUCTURE, NTSYS-pc, and GeneMarker. Preliminary results suggest that the

golf course plants belong to the same conceptual genotype observed for at least one feral individual found outside the golf course. Further analysis of all populations, outgroups, and cultivars will indicate whether gene flow (via pollen or stolons) from golf course populations has contributed to feral bentgrass populations nearby. Supported by a grant from the USDA Biotechnology Risk Assessment Grant program.

<sup>1</sup>University Of Connecticut, Department Of Plant Science, 111 W. Main St, # 2, Stafford Springs, CT, 06076, USA<sup>2</sup>University Of Connecticut, Plant Science, 1390 Storrs Road, U-4163, Storrs, CT, 06269, USA

**734 HAWKINS, ANGELA\*<sup>1</sup>, ARCHAMBEAULT, ALAN<sup>2</sup>, CANNON, BRANDI<sup>2</sup>, FAUST, AMBER<sup>2</sup>, LEVSEN, NICHOLAS<sup>3</sup>, WILLIAMS, JUSTIN<sup>2</sup> and RANDLE, CHRISTOPHER<sup>2</sup>**

### Subspecific classification within *Phoradendron serotinum* (Viscaceae): Morphological and molecular markers for assessment of population genetic structure.

*Phoradendron serotinum*, (leafy mistletoe) is a hemiparasitic plant of the family Viscaceae found in the United States and Mexico. *P. serotinum* is the only species in *Phoradendron* (234) that has been given subspecific classification. Subspecies *macrophyllum*, *serotinum*, and *tomentosum* occur in the eastern United States from southern New Jersey to southern Florida, through the Midwest south of Oklahoma and into Mexico, and on the west coast from Oregon to Baja California. Subspecies *angustifolium* grows in isolated regions of central Mexico. Subspecies are difficult to identify based on morphology alone. Identification of *P. serotinum* subspecies in eastern Texas is especially difficult as characters that are otherwise diagnostic of subspecies do not adequately separate three of the subspecies (*macrophyllum*, *serotinum*, and *tomentosum*) that overlap in this region. Molecular and morphometric analyses were utilized to resolve taxonomic confusion within *P. serotinum* and test the hypotheses that: 1) The four subspecies of *P. serotinum* represent separate cohesive genetic units and 2) The subspecies of *P. serotinum* share a single population of origin that is likely within the current distribution. It was predicted that the four subspecies of *P. serotinum* would not represent separate cohesive genetic units and that molecular data would provide justification needed to synonymize the subspecies as *P. serotinum*. It was further predicted that east Texas was the single center of origin for subspecies divergence. Morphometric measurements were recorded for nearly 200 vouchers that were analyzed from a majority of the growth range. Microsatellite loci were isolated and seven were amplified and scored for 95 individuals representing the growth range in its entirety.

Results, both morphological and molecular, support the hypothesis that the four subspecies of *P. serotinum* represent separate cohesive genetic units. Further, molecular data support a single central location for subspecies divergence; however both morphological and molecular data equivocally support east Texas as the center of divergence while simultaneously supporting a population in the west as the center of origin.

<sup>1</sup>Texas A & M University, Biological Sciences, Texas A&M University Dept. Of Biology, 3258 TAMUS, College Station, TX, 77843-3258, USA<sup>2</sup>Sam Houston State University, Department of Biological Sciences, 1900 Avenue I, Huntsville, TX, 77340, USA<sup>3</sup>Texas Tech University, Department Of Ecology & Evolutionary Biology, Department Of Biological Sciences, Lubbock, TX, 79409, USA

**735 MCGLAUGHLIN, MITCHELL\*<sup>1</sup>, BRESOWAR, GERALD<sup>2</sup>, HELENURM, KAIUS<sup>3</sup> and WALLACE, LISA<sup>4</sup>**

### **Isolation among islands as a driver of divergence in the endemic *Lotus* (Fabaceae) of the California Channel Islands**

The California Channel Islands represent a unique system to study insular plant evolution due to variability in island age, size, and separation, and the proximity of the entire island chain to the continental mainland. The evolutionary diversity created by the California Channel Islands is exemplified in the island endemic taxa of the genus *Lotus* (Fabaceae). *Lotus argophyllus* consists of five varieties, three of which are endemic to the Channel Islands, and primarily occur on the drier southern islands. *Lotus dendroideus* consists of three varieties endemic to the Channel Islands, and primarily occur on the wetter northern islands. Both species are close relatives and are members of the same subgenus, but they are not sister taxa. Based on morphology, the two species are believed to have independently colonized the islands and should independently exhibit monophyly. Population level sampling of sequence data from the low copy nuclear region *Adh-A* has been used to examine the evolutionary history of the island taxa and close relatives that occur on the mainland. Of the sampled island taxa, neither *L. argophyllus* or *L. dendroideus* are monophyletic. Despite clear morphological differences, evolutionary history appears to be determined by island of occurrence, not taxonomic designation. In general, varieties were found to be monophyletic within islands or among adjacent islands, but when two or more varieties occur on a single island, they tend to have a sister relationship. Interestingly, *L. argophyllus* var. *niveus*, which is endemic to Santa Cruz Island, was found to be very distinct from other island *Lotus* taxa, showing a strong affinity to the mainland *L. heermanii*. Overall, this research illustrates how genetic data can resolve evolutionary histories that are signifi-

cantly different than those inferred from morphology.

<sup>1</sup>University of Northern Colorado, Biology, 501 20th St, Greeley, CO, 80639, USA<sup>2</sup>University Of Northern Colorado, 501 20th Street, Greeley, CO, 80639, USA<sup>3</sup>University Of South Dakota, Department Of Biology, Vermillion, SD, 57069, USA<sup>4</sup>Mississippi State University, Biological Sciences, 295 Lee Blvd., Mississippi State, MS, 39762, USA

**736 WEINGARTNER, LAURA<sup>1</sup>, HARKESS, ALEX<sup>2</sup>, BROWN, JENNIFER<sup>2</sup> and MOORE, RICHARD\*<sup>2</sup>**

### **Contrasting patterns of polymorphism and divergent on the *Carica papaya* X and Y chromosomes**

The sex chromosomes of the tropical crop papaya (*Carica papaya*) are young and consequently allow for the examination of evolutionary forces that affect early sex chromosome formation. We sequenced six X/Y gene pairs and 12 autosomal gene pairs from 42 papaya accessions from natural populations and analyzed the data for molecular signatures of selection. In most sex chromosome systems, the Y chromosome displays significantly reduced polymorphism levels while the X chromosome maintains a level of polymorphism comparable to autosomal loci. However, the four papaya sex-linked loci that we examined display diversity patterns that oppose this trend. The X alleles exhibit significantly reduced polymorphism levels while the Y alleles maintain expected or greater than expected levels of diversity. Molecular population genetic analyses suggest that genes on the X associated with male function have undergone selective sweeps. Conversely, we find evidence of divergent haplotypes on the Y that extend across the bulk of the non-recombining region of the Y. We hypothesize that the X chromosome has recently undergone a selective sweep while elevated Y polymorphism is due to population structure.

<sup>1</sup>Indiana University, Jordan Hall, 1001 E Third St., Bloomington, IN, 47405, USA<sup>2</sup>Miami University, Botany, 316 Pearson Hall, Oxford, OH, 45056, USA

**737 BROWN, JENNIFER\*<sup>1</sup>, LAWRIE, JOSEPH<sup>1</sup>, ROCHA, OSCAR<sup>2</sup> and MOORE, RICHARD<sup>1</sup>**

### **Impacts of demographic history, population subdivision, and non-random mating on the genetic structure of natural populations of *Carica papaya***

In Costa Rica, dioecious, small-fruited papaya, *Carica papaya*, have been observed growing within secondary lowland forests. Within the Costa Rican landscape, agricultural abandonment has promoted the resurgence of secondary forest growth, with papaya serving as a pioneer species. The goal of this research is to address

the impacts of demographic history, population subdivision, and non-random mating on the genetic diversity within these natural populations of papaya from Costa Rica. Diversity was assessed in using two datasets from five natural populations: 1) twenty microsatellites were genotyped for 184 accessions and 2) twelve loci were sequenced for single nucleotide polymorphisms (SNP) within 42 accessions. Analyses of microsatellite diversity indicate natural populations exhibit a deficiency of heterozygotes ( $H_o=0.3-0.4$ ,  $F_{IS}=0.312$ ). Low levels of silent site nucleotide diversity ( $\pi_{sil}=0.00104$ ,  $\theta_{sil}=0.00085$ ) were observed within the SNP loci, supporting previous reports of reduced levels of diversity within papaya. Microsatellite data indicate low to moderate pairwise  $F_{ST}$  values, reflecting little genetic variation among natural populations. STRUCTURE analyses support the presence of cryptic genetic population structure. Two microsatellite-based indices were used to assess the demographic history of the natural populations. A significant value of the Garza-Williamson index ( $M=0.52$ ) indicated the occurrence of a population bottleneck within the natural populations. Our estimates of the Imbalance index support a recent reduction in population size followed by population expansion for these natural papaya populations ( $\ln\beta_1=2.11-2.37$ ,  $\ln\beta_2=2.58-2.78$ ). The observed population bottleneck and expansion were possibly promoted by the abandonment of agricultural fields and the spread of secondary forests. These insights will provide useful information for the conservation and maintenance of genetic diversity for the cultivated plants.

<sup>1</sup>Miami University, Botany, 316 Pearson Hall, Oxford, OH, 45056, USA<sup>2</sup>KENT STATE UNIVERSITY, Department Of Biological Sciences, 256 CUNNINGHAM HALL, KENT, OH, 44242, USA

### 738 OLEAS, NORA\*<sup>1</sup>, MEEROW, ALAN<sup>2</sup> and FRANCISCO-ORTEGA, JAVIER<sup>3</sup>

#### Population genetics in a geographic context, the *Phaedranassa* (Amaryllidaceae) case study

Speciation can be understood as a continuum occurring at different levels, from populations to species. The recent molecular revolution in population genetics has opened a pathway towards understanding species evolution. At the same time, these patterns can be better explained by incorporating a geographic context, which can now be accomplished with the use of geographic information systems (GIS). *Phaedranassa* (Amaryllidaceae) is a genus restricted to one of the most biodiversity hotspots, the Northern Andes. We studied seven *Phaedranassa* species (Amaryllidaceae) from Ecuador. Six of these species are endemic to the country. The topographic complexity of the Andes, which creates local microhabitats ranging from moist slopes to dry valleys, might explain the patterns of species differentiation. With a Bayesian approach, we assessed the genetic structure of the genus throughout Ecuador using twelve

microsatellite loci. We also used bioclimatic variables and species coordinates under a Maximum Entropy approach to generate distribution models of the species (niche models). Our results show that *Phaedranassa* species are genetically well differentiated. Furthermore, with the exception of two species, all *Phaedranassa* species showed non-overlapping distributions, which suggests that allopatric divergence could be the driver of genetic differentiation. *P. viridiflora* and *P. glauciflora* were the only species that had a broad species distribution based on niche models, but this pattern seems to be related to species delimitation issues in both.

<sup>1</sup>FTU, 11200 Sw 8th St. OE167, Miami, FL, 33199, USA<sup>2</sup>USDA-ARS-SHRS, UNITED STATES DEPARTMENT OF AGRICULTURE, 13601 Old Cutler Road, Miami, FL, 33158, USA<sup>3</sup>Fairchild Tropical Botanic Garden, 11935 Old Cutler Road, Coral Gables, Miami, FL, 33156, USA

### 739 KOELLING, VANESSA\*, MONNAHAN, PATRICK and KELLY, JOHN

#### Estimating outcrossing rate and inbreeding depression from marker data when family sizes are small

Accurate measures of population outcrossing rates and inbreeding depression are required to fully understand the evolution of plant mating systems because different population outcomes are predicted under different conditions. One approach to estimate outcrossing rates and inbreeding depression is to estimate the outcrossing rate ( $t$ ) and inbreeding coefficient ( $F$ ) from the same genetic marker data. Since inbreeding depression reduces the homozygosity of adult plants relative to predictions based on the outcrossing rate, under various assumptions, the magnitude of the discrepancy between the observed and predicted  $F$  can be used to estimate the relative fitness of inbred and outbred plants. This method is ideal because it allows for estimates under natural conditions.  $t$  and  $F$  are typically estimated from progeny arrays. The ideal experimental design for estimating the joint distribution of  $t$  and  $F$  is to sample more parents and fewer offspring per family. However, the software most widely used to estimate these values, MLTR, does not perform well below family sizes of eight. To address this problem, we developed a Bayesian estimation program for  $t$  and  $F$  that gives accurate estimates with family sizes as small as four. We believe this program will significantly advance the accuracy and cost-effectiveness of studies in the evolution of plant mating systems.

University of Kansas, Ecology and Evolutionary Biology, 1200 Sunnyside Ave., Lawrence, KS, 66045, USA

740 THOMPSON, KIM\*<sup>1</sup>, CULLEY,  
THERESA<sup>2</sup> and LENTZ, DAVID<sup>3</sup>

### Genetic Diversity and Structure of a Tropical Fruit, Timber and Latex Tree, *Manilkara zapota* (Sapotaceae)

*Manilkara zapota* (L.) P. Royen is a tropical fruit, timber and latex tree in the Sapotaceae family. *M. zapota* trees have long been protected by the Maya in its native region of Mexico and Central America and continue to be valued as an ecological, economic and scientific resource. The goals of this project were to (1) quantify levels of genetic variation in *M. zapota* from the Peten region of Guatemala, and (2) describe how that genetic variation is structured among populations from diverse habitat types and histories. Levels of genetic diversity were analyzed within and among populations from ancient Maya sites and indigenous Maya home gardens using microsatellites. We expected that deforestation by the Maya would have led to (1) reduced levels of variation in microsatellites, compared to neotropical trees from non-Maya areas, and (2) genetic structuring, (theta greater than 0) due to reduced gene flow between populations. Our results suggest instead that *M. zapota* populations in Maya developed forests contain high levels of polymorphism with low levels of genetic structuring. Together, nuclear and chloroplast microsatellite analysis will enable us to distinguish the contributions of natural patterns of gene flow from anthropogenic events. Reduced polymorphism and increased population genetic structure in home gardens indicate that management or fragmentation is influencing the genetic composition of *M. zapota*. Characterizing the variation and structure of *M. zapota* will elucidate patterns of gene flow in neotropical forests, benefit studies of ancient Maya agroforestry practices, and support tropical forest conservation efforts.

<sup>1</sup>University Of Cincinnati, Biological Sciences, Rieveschl Hall, Cincinnati, OH, 45221-0006, USA<sup>2</sup>University Of Cincinnati, Department Of Biological Sciences, 614 Rieveschl Hall, Cincinnati, OH, 45221-0006, USA<sup>3</sup>University Of Cincinnati, Biological Sciences, PO Box 210006, Cincinnati, OH, 45221, USA

741 BRADBURY, ELIZABETH JANE\*<sup>1</sup>,  
DUPUTIÉ, ANNE<sup>2</sup>, DELÈTRE, MARC<sup>3</sup>,  
ROULLIER, CAROLINE<sup>3</sup>, EMSHWILLER,  
EVE<sup>4</sup> and MCKEY, DOYLE<sup>5</sup>

### Genetic Differentiation of Bitter and Sweet Cassava (*Manihot esculenta* Crantz) at the Global and Continental Levels: new analyses distinguish between competing hypotheses of genetic drift and migration

Cassava (*Manihotesculenta* Crantz), one of the most important tropical food crops, is commonly divided into two main use-categories: those varieties that are processed prior to consumption ("bitter") and those that are cooked without processing ("sweet"). These use-categories are biochemically differentiated as those roots that contain less than 50 mg/kg fresh weight of HCN ("sweet") and those whose roots contain more than this amount ("bitter"). However, very little research has been conducted investigating patterns in genetic structure among "sweet" and "bitter" cassava populations at scales greater than a village or national level. The objective of this study is to provide initial insight into patterns of genetic differentiation among bitter and sweet cassava on the continental and global scales. Using eight microsatellite loci, we genotyped 363 cassava accessions from South America, Africa, and the South Pacific. Sampling included 139 bitter accessions and 214 sweet accessions. Results show a pattern of genetic division between bitter and sweet accessions in South America. However, this pattern is not observed in Africa. Results are inconclusive regarding potential founder effect in Africa. The loss of genetic differentiation in Africa is likely the result of either genetic drift in the African bitter populations over time or the introduction of "sweet" alleles into the African bitter populations through migration. Recently conducted analyses help distinguish between these competing hypotheses.

<sup>1</sup>University of Wisconsin-Madison, Botany, 430 Lincoln Drive, Birge Hall, Madison, WI, 53706, USA<sup>2</sup>Centre National de la Recherche Scientifique, Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier, France<sup>3</sup>Muséum Nationale d'Histoire Naturelle, Paris, France<sup>4</sup>University Of Wisconsin-Madison, Botany Dept, 321 Birge Hall, 430 Lincoln Drive, Madison, WI, 53706-1313, USA<sup>5</sup>CEFE CNRS, 1919 ROUTE DE MENDE, MONTPELLIER, F-34293, France

742 ESTEP, MATT C<sup>\*1</sup>, VAN MOURIK, THOMAS A<sup>2</sup>, MUTH, PETER<sup>3</sup>, GUINDO, DIARAH<sup>4</sup>, PARZIES, HEIKO K<sup>3</sup>, KOITA, OUSMANE<sup>5</sup>, WELTZIEN, EVA<sup>2</sup> and BENNETZEN, JEFFREY<sup>1</sup>

### Genetic diversity of a parasitic weed, *Striga hermonthica*, on sorghum and pearl millet in Mali

Eleven populations of witchweed, *Striga hermonthica*, were collected in four regions of Mali and investigated with twelve microsatellite markers. Extensive genetic diversity was observed, with most plants heterozygous for most markers. Allelic diversity was broadly distributed across populations with little genetic differentiation and large amounts of gene flow. Nearby fields of pearl millet and sorghum were found to have indistinguishable witchweed populations. Some population structure was apparent, but did not correlate with the local environment or host genotype, suggesting that seed transportation or other human-driven variables act to differentiate central Malian *S. hermonthica* populations from southern Malian populations.

<sup>1</sup>University of Georgia, Department of Genetics, Athens, GA, 30602, USA<sup>2</sup>International Crops Research Institute for the Semi-Arid Tropics, Bamako, Mali<sup>3</sup>University of Hohenheim, Institute of Plant Breeding, Seed Science and Population Genetics, Stuttgart, Germany<sup>4</sup>Institut d' Economie Rurale (IER), Bamako, Mali<sup>5</sup>University of Bamako, Laboratory of Applied Molecular Biology, Faculty of Science and Techniques, Bamako, Mali

743 KING, URSULA<sup>1</sup>, LOPEZ PEREDO, ELENA<sup>\*2</sup> and LES, DONALD<sup>2</sup>

### Isolation and characterization of microsatellite loci in *Najas flexilis* (Hydrocharitaceae) using 454 genome sequencing

*Najas flexilis* (water nymph) is a monoecious, hydrophilous annual. Unlike many submerged aquatic plants it cannot reproduce vegetatively. Although circumboreal in distribution, *N. flexilis* is rare in the European portion of its range and is protected under European Union law. To date little genetic information has been available for this aquatic species. The objective of this work is to develop and characterize microsatellite markers for *N. flexilis*. Using 454 GS-FLX Titanium sequencing technology 110,358 sequence reads were obtained for *N. flexilis*, with microsatellite loci detected in 5563 of these reads. Primer pairs were designed to amplify 39 of these regions and 35 of these primers have successfully amplified in *N. flexilis*. To estimate genetic diversity, these markers have been tested on 21 accessions across the entire range of the species. In addition other *Najas* species have been assessed for cross-tran-

ferability of these markers, including *N. guadalupensis* subsp. *olivacea*, the recently reported *N. flexilis* x *N. guadalupensis* hybrid, *N. muenscheri*, and *N. marina*. The majority of these markers were transferable and amplified successfully in the *Najas* species tested, with the exception of *N. marina* (the only dioecious species in this genus) where only two loci amplified. As a monoecious species, it has been assumed in the past that *N. flexilis* is outcrossing and therefore possesses high genetic diversity. However, our study has found extremely low genetic diversity in the microsatellite regions tested, even between transatlantic populations. Outcrossing is not guaranteed in monoecious species and low genetic diversity may result if much pollination occurs geitonogamously. Indeed there have been several conflicting reports on the spatial and temporal separation of flowering in *N. flexilis*. Another explanation for low diversity would be possible if *N. flexilis* were facultatively apomictic. Alternatively population genetic diversity could be intrinsically low due to vicinism or population bottlenecks. Studies currently are ongoing into the reproductive biology of this species to determine more accurately the breeding system involved.

<sup>1</sup>Trinity College Dublin, Biology, Dublin, Ireland<sup>2</sup>University Of Connecticut, Ecology & Evolutionary Biology, 75 N. Eagleville Road, Unit 3043, Storrs, CT, 06269-3043, USA

## POSTERS

744 ARCIBAL, ERICA<sup>\*</sup> and MCGLAUGHLIN, MITCHELL E

### Species Diversification in *Eriogonum umbellatum* vars. *aureum*, *majus*, and *umbellatum* (Polygonaceae) in the Colorado Rocky Mountains

*Eriogonum umbellatum* (sulfur-flower buckwheat; Polygonaceae) is a diverse plant species with over 40 identified varieties found in the western United States and parts of Canada. In this project, three varieties of *Eriogonum umbellatum* (vars. *aureum*, *majus*, *umbellatum*) with overlapping distributions are being genetically evaluated. To do so, the amplifications of highly polymorphic regions within the nuclear and chloroplast genomes are aligned, respectively, to determine if hybridization is occurring. This phenomenon occurs when genetically distinct individuals crossbreed and produce offspring expressing genetic qualities of both parents. Over time, these hybrids may be separated from the population and start to diversify, which can lead to the generation of a new variety within the species or even speciation itself. By studying hybridization patterns between the three selected varieties, we can start to understand the mechanisms by which species diversification may occur. Further understanding will also lead to new management strategies of uncommon species, since individuals within newly diversified species and varieties

are considered uncommon or rare.

University of Northern Colorado, Biology, 501 20th St, Greeley, CO, 80639, USA

**745 PAASCH, AMBER ELIZABETH\*<sup>1</sup> and FISHER, KIRSTEN<sup>2</sup>**

**Development of microsatellite markers to enable population assessment of skewed sex ratios and genetic diversity in Mojave Desert *Syntrichia caninervis***

*Syntrichia caninervis* is a dioecious desert bryophyte that reduces production of sexual organs under extreme conditions. When sex is expressed, the ratio between males and females is skewed, with males being extremely rare. In the Mojave Desert, these sex ratios differ between elevations, with the highest elevation having a ratio of 14 females to 1 male. No males were identified at the lower elevation. These ratios may be due to inhibition of male gametangial development caused by sensitivity to environmental conditions. Populations may be sustained by clonal growth. We have identified a population of *S. caninervis* growing at 1800 m elevation that contains individuals with sporophytes, indicating sexual reproduction. Sporophytes have not been observed in nearby populations at the lower elevation limit for *S. caninervis*. The development of microsatellite markers will allow us to assess genetic diversity for individual mosses and between populations at different elevations. Currently, no microsatellite markers have been identified for *S. caninervis*. Here we report our results on the variability and reproducibility of 12 microsatellite regions in three *S. caninervis* individuals. These microsatellite markers will provide a valuable tool for assessing genetic diversity in a species widely used as a model for moss reproductive biology.

<sup>1</sup>California State University, Los Angeles, Department of Biological Sciences, 5151 State University Dr., La Kretz 350, Los Angeles, CA, 90032, USA <sup>2</sup>California State University Los Angeles, Department of Biological Sciences, 5151 State University Drive, 350 La Kretz Building, Los Angeles, CA, 90032, USA

**746 HEYDUK, KAROLINA\*<sup>1</sup>, GRADY, BEN R.<sup>2</sup>, JUENGER, THOMAS E.<sup>3</sup> and SYTSMA, KENNETH<sup>4</sup>**

**Species boundaries and population genetics of *Eriogonum pelinophilum*: implications for conservation.**

*Eriogonum* (Polygonaceae), a genus limited to North America, includes a number of rare species. The conservation status of members of *Eriogonum* range from special concern to endangered, both at the state and federal level. Delineation of some species within the genus has been contentious due to different interpreta-

tions of morphological characters and the proposed recent speciation of the group. In some cases, conservation measures have been hindered by confounding taxonomic treatments. *Eriogonum pelinophilum* is a federally endangered species limited to isolated areas within two counties in western Colorado. It is morphologically similar to *E. clavellatum*, but consistent morphological characters differentiate these two species. *E. clavellatum* is restricted to the Four Corners area, a range distinct from that of *E. pelinophilum*. *Eriogonum contortum*, another morphologically and geographically distinct species, has often been considered similar to *E. pelinophilum* and *E. clavellatum*. Phylogenetic analysis of nuclear and chloroplast DNA sequence data reveals that *E. contortum* is not as closely related to the other two species as previously thought. The relationship between *E. pelinophilum* and *E. clavellatum*, however, is not as clear; the various gene trees are incongruent. Using Next Gen sequencing technology, microsatellite primers are being developed for *E. pelinophilum*. By implementing microsatellite data, we gain insight into the genetic distance between these two species. Microsatellites are used to assess genetic diversity among and between element occurrences of *E. pelinophilum*. These results will help guide conservation efforts.

<sup>1</sup>University of Wisconsin, Department of Botany, 430 Lincoln Dr., Madison, WI, 53706, USA <sup>2</sup>University Of Wisconsin-Madison, Botany, 430 Lincoln Dr., Madison, WI, 53706, USA <sup>3</sup>University of Texas at Austin, Integrative Biology, 1 University Station Stop, Austin, TX, 78712, USA <sup>4</sup>University of Wisconsin-Madison, Department of Botany, 430 Lincoln Dr., Madison, WI, 53706, USA

**747 FOTINOS, TONYA\*<sup>1</sup>, NAMOFF, SANDRA<sup>2</sup>, LEWIS, CARL<sup>3</sup>, GRIFFITH, M. PATRICK<sup>4</sup>, FRANCISCO-ORTEGA, JAVIER<sup>5</sup>, MASCHINSKI, JOYCE<sup>6</sup> and VON WETTBERG, ERIC J BISHOP<sup>7</sup>**

**Conservation genetics of the endangered Sargent's Cherry Palm, *Pseudophoenix sargentii***

*Pseudophoenix sargentii*, once a critically endangered palm inhabiting coastal areas of Florida and the Caribbean, has shown a marked increase since reintroductions have augmented the wild populations in the Florida Keys. The habitat of the Sargent's cherry palm has been degraded by agricultural encroachment, grazing, over-harvesting and hurricane effects. To assess the genetic contribution of these reintroductions and to understand the current genetic structure of the species, ten microsatellites were analyzed from 124 individuals. The individuals sampled came from wild populations on Elliott Key, Long Key, and the Bahamas, as well as the Fairchild *ex situ* collection. The individuals on Elliott Key, where reintroductions had occurred, had age classes and wild vs. reintroduced individuals analyzed separately. Several populations displayed evidence of genetic drift, inbreeding and decreased gene flow with

all populations displaying significant deviations from Hardy-Weinberg equilibrium. All populations displayed positive  $F_{is}$  values except the *ex situ* collection and the reintroduced individuals on Elliott Key. All pairwise  $F_{st}$  values were significant except comparisons between certain age classes on Elliott Key. AMOVA analysis partitioned 82.3% of the genetic variation within populations. Principal coordinate analysis based on genetic distance and Bayesian clustering analysis supported three distinct populations. The reintroductions on Elliott Key have contributed to an increase in the overall genetic diversity of the focal stand by increasing heterozygosity and lowering the inbreeding coefficient.

<sup>1</sup>Florida International University, Biology, 11000 SW 8th St, Miami, FL, 33199, USA<sup>2</sup>Rancho Santa Ana Botanic Garden, Research, 1500 North College Avenue, Claremont, CA, 91711, USA<sup>3</sup>Fairchild Tropical Botanic Garden, 10901 Old Cutler Road, Miami, FL, 33155, USA<sup>4</sup>Montgomery Botanical Center, 11901 Old Cutler Road, Miami, FL, 33156, USA<sup>5</sup>Fairchild Tropical Botanic Garden, 11935 Old Cutler Road, Coral Gables, Miami, FL, 33156, USA<sup>6</sup>Fairchild Tropical Botanic Garden, CTPC, 11935 Old Cutler Road, Miami, FL, 33156, USA<sup>7</sup>Fairchild Tropical Botanic Garden, 11935 Old Cutler Road, Coral Gables, FL, 33156, USA

#### 748 HUBBARD, ASHLEY\* and MCGLAUGHLIN, MITCHELL

### Determining evolutionary diversification and the phylogenetic placement of *Lotus* subgenus *Syrmatium*

Species taxonomic placement is essential to understanding how individuals and populations are related. Taxonomic analyses are important to understanding diversity, management practices, as well as evolutionary diversification. In this project we are examining the evolutionary relationship within *Lotus* subgenus *Syrmatium*, a group that contains 11 species with distinct morphological, ecological, and geographic characteristics. I am surveying nuclear ribosomal DNA (nrDNA) and the chloroplast genome using DNA sequencing to gain insight into variation within populations, species, and geographic regions. Data from the internal transcribed spacer (ITS) region of ribosomal DNA allows for phylogenetic examination of relationships in the nuclear genome. In contrast, chloroplast DNA is inherited from the seed producing parent as a single copy, meaning that it undergoes very slow evolution. By comparing the chloroplast genome with the nuclear genome we are able to examine the patterns of change and variation within each. Examining the patterns of diversity will aid our understanding of the phylogenetic placement and evolutionary change within taxa. *Lotus* taxa can be used to provide insight to speciation events and how the evolutionary units contained within this group need to be managed to maintain diversity.

University of Northern Colorado, 501 20th St, Greeley, CO, 80639, USA

#### 749 HARKESS, ALEX\*<sup>1</sup>, WEINGARTNER, LAURA<sup>2</sup> and MOORE, RICHARD<sup>1</sup>

### Divergent haplotype structure on the *Carica papaya* Y chromosome

The male specific region of the Y (MSY) chromosome in *Carica papaya* is estimated to have diverged from the corresponding X region approximately 2 mya. Consistent with this relatively recent divergence, suppression of recombination between the X and the MSY is confined to an approximately 8 Mbp region that spans the centromere of chromosome 1, comprising about 10% of the chromosome length. We analyzed patterns of polymorphism and divergence for six gene pairs that span the MSY region and found evidence of elevated polymorphism on the Y chromosome. This is an unexpected pattern of diversity, as examples of young sex chromosomes from other plant and animal species exhibit reduced patterns of polymorphism. We developed haplotype networks for the MSY genes and compared them to those for homologous X regions and autosomal loci. We found evidence of three distinct haplotypes associated with MSY loci, but not found in X and autosomal loci. We characterized the distribution of haplotypes across regions of Costa Rica and among cultivars and found significant heterogeneity in this pattern. These haplotypes extend across the MSY as evidenced by significant levels of linkage disequilibrium. We hypothesize that these haplotypes are the result of MSY-specific population structure due perhaps to limited pollen flow among geographic regions.

<sup>1</sup>Miami University, Botany, 316 Pearson Hall, Oxford, OH, 45056, USA<sup>2</sup>Indiana University, Jordan Hall, 1001 E Third St, Bloomington, IN, 47405, USA

#### 750 MADSON, HANNAH\*<sup>1</sup>, CARUSO, CHRISTINA<sup>2</sup> and CASE, ANDREA<sup>1</sup>

### Effects of non-selective mechanisms on structured population sex-ratio variation in gynodioecious *Lobelia siphilitica* (Lobeliaceae)

Gynodioecy - the coexistence of females and hermaphrodites in a population - is a common genetic polymorphism in plants. Such polymorphic systems are useful for examining variation across a species' geographic range when the two sexes are unevenly distributed. Variation in sex ratio may reflect both selective mechanisms, if the relative fitness of the sexes varies among populations, and non-selective mechanisms, if drift, founder effects, and gene flow affect the distribution of sex-determining alleles. Here, we used chloroplast sequence variation to evaluate hypotheses about how non-selective mechanisms affect population sex-

ratio variation in *Lobelia siphilitica*. Females are more common in the southern-central portion of the range, where mean annual temperatures are higher, but populations are also smaller ( $N < 100$ ). Central populations may experience higher gene flow than peripheral populations, while smaller populations may exhibit stronger effects of genetic drift. We found substantial among-population variation ( $F_{st} = 0.67$ ) that was not explained by either population size or sex ratio. Although evidence for isolation by distance was weak, four out of five rare chloroplast haplotypes were geographically restricted, and distance from central populations explained a significant portion of the among-population variation. Thus, population dynamics may differ in the peripheral compared to the central portion of the species range. If metapopulation dynamics differ at the range edge, this may explain why females are rare in peripheral populations of *L. siphilitica*.

<sup>1</sup>Kent State University, Department of Biological Sciences, Box 5190, 256 Cunningham Hall, Kent, OH, 44242-0001, USA<sup>2</sup>University Of Guelph, Department Of Integrative Biology, New Science Complex, 50 Stone Road East, GUELPH, ON, N1G 2W1, Canada

751 MATHEWS, KATHERINE\*<sup>1</sup>, PATE, SARAH<sup>2</sup>, CLEMENT, JASON<sup>3</sup>, LOONEY, PATRICK<sup>3</sup> and MCCOY, JOE-ANN<sup>4</sup>

### Use of Genetic Markers and Chemical Quantification to Identify Populations of *Actaea racemosa* (Black Cohosh) With Desirable Properties for Breeding a Regional Cultivar

The first year of a collaborative project to characterize genetic, chemical and growth characteristics of the medicinal herb, black cohosh (*Actaea racemosa*), has yielded promising results. Over 60 individual plants from 20 populations collected throughout the species' native range are being propagated in control-pollination regeneration field cages to provide research materials for both genetic and analytical testing. Growth data collected include morphological descriptors, emergence dates, flowering dates, and seed production rates. HPLC quantification of triterpenoid glycosides and other biologically active compounds are being performed to observe both intra- and interpopulation variation throughout the native range of the species. DNA samples were collected from leaves of all individuals and used to develop microsatellite markers for the species. Multiple microsatellite primers are being screened for variability within and among accessions, as well as among *Actaea* species. Ultimately, we hope to correlate genetic markers with superior phytochemical production and desirable growth traits for the creation of a regional cultivar that can be unambiguously identified. Given the increasing demand for high-quality herbal products, the creation and production of a cultivar with demonstrably higher levels of triterpenoid glycosides

could prove advantageous to western North Carolina growers.

<sup>1</sup>Western Carolina University, 132 NATURAL SCIENCE BUILDING, CULLOWHEE, NC, 28723, USA<sup>2</sup>Western Carolina University, Department of Biology, 132 Natural Science Building, Cullowhee, NC, 28723, USA<sup>3</sup>Western Carolina University, Department of Chemistry and Physics, Cullowhee, NC, 28723, USA<sup>4</sup>The North Carolina Arboretum, Bent Creek Germplasm Repository, 100 Fredrick Law Olmsted Way, Asheville, NC, 28806, USA

POSTERS

752 KOZIOL, ELIZABETH  
KATHERINE\* and BEVER, JAMES

**Weedy and domesticated populations of *Helianthus annuus* are less drought tolerant and dependant on arbuscular mycorrhizal fungi**

Weedy and invasive plants generally have increased reproductive potential, size, shoot allocation, and growth rate. The increased allocation to growth and fecundity in weedy plants may result from reduced allocation of resources to herbivore defense, drought tolerance, and allocation to fungal symbionts. To investigate whether changes in allocation patterns occur during plant domestication and the evolution of weedy plant populations, we compared the mycorrhizal responsiveness, drought tolerance, and above and below ground growth patterns of 32 populations of *Helianthus annuus* consisting of 9 native ruderals, 4 US agricultural weeds, 5 Australian invasive and 14 domesticated populations. We found that the domestication of sunflowers constrained by a trade-off between allocation to growth and drought tolerance. While well watered domesticated plants allocated more resources to above ground structures than native plants, domesticated plants were also significantly less drought tolerant than native plants in terms of leaf wilting, maintaining pot soil moisture, and ability to remain fecund with water stress. This trade-off between growth rate and drought tolerance was also evident in the variation between populations within categories. We also found evidence that drought tolerance is correlated with finer root systems. Comparisons of root characters revealed that the drought tolerant native ruderals had the thinnest diameter and most branched roots, followed by US weedy, Australian invasive and then domesticated lines. Weedy *Helianthus annuus* plants benefited most from mycorrhizal inoculation by having fewer wilted leaves. Inoculation increased pot soil moisture for US weedy and native populations, but not Australian invasive or domesticated populations. The mycorrhizal response of weedy plants, combined with drought tolerance in between those of native ruderals and domesticates, indicates that weedy plants have adapted to the margins of agricultural lands, which may still harbor undisturbed soil communities but may also have increased access to water.

Indiana University, Biology, 1001 East Third Street, Bloomington, IN, 47405, USA

753 HALL, MITCHELL D.\*, BROSI,  
SUNSHINE and PUTHOFF, DAVID

**The effectiveness of tomato plants (*Solanum lycopersicum*) modified with a Hessian fly-responsive(Hfr) gene against phloem-feeding and chewing insects**

Many of the world's crops are lost every year due to insect pests feeding on them. Insecticides constitute the largest form of control for these pests with resistant biotypes of insect increasing each year. In wheat, *Triticum aestivum* L., Hessian fly-responsive gene 1 (*Hfr-1*) was found to keep avirulent larvae from establishing a feeding site on the leaf surface (Williams et al., 2002). In addition, *Hfr-2* and *Hfr-3* have similar potential (Puthoff et al, 2005; Giovanini et al.,2007). These genes have been engineered into tomato plants (*Solanum lycopersicum* L.) via T-DNA transfer using *Agrobacterium tumefaciens*. While there are almost limitless numbers of pests that commonly host on tomato plants, some of the most devastating include: silver whitefly (*Bemisia tabaci* biotype B), fall army worm (*Spodoptera frugiperda*) and mealy bugs (*Phenacoccus* spp.). These insects will be introduced separately to each type of modified tomato plant (containing *Hfr-1*, -2 or -3) and control plants. The plants and insects will be monitored for 4 weeks. Success of the insects will be measured by total weight, weight gain, time to pupation, time between molts, time to enclosure, and fatality. The resulting number of insects will provide insight into the effectiveness of the Hfr gene to confer resistance. By developing new strategies to combat ever-evolving insect pests, the need for increased food production worldwide will become more of a reality.

Frostburg State University, Biology, 101 Braddock Road, Frostburg, MD, 21532, USA

754 ZWENGER, SAM R.\*1,  
HOFFMANN, ERICH<sup>2</sup> and BASU,  
CHHANDAK<sup>2</sup>

**Transformation of *Arabidopsis thaliana* with heat stress-related genes from a *Copaifera officinalis* using a novel "binary library" approach.**

Plant transformation studies often require gene characterization, cloning and ligation into a binary vector, which can be tedious and sometimes unsuccessful. Novel ways of generating thousands of genes of interest and ligating them into a binary vector might therefore be extremely useful in plant biotechnology. To address this issue, a small cDNA library of *C. officinalis* was generated using a plant binary vector. After sequencing reactions the 96-well plates were obtained and stored at

-80°C. Individual wells from the sequencing plates contained *E. coli* harboring unique vector-insert constructs and were later selected (according to BLASTx results) and grown overnight for subsequent plasmid miniprep. Individual *Agrobacterium tumefaciens* (EHA105) lines harboring individual constructs were then generated and used to transform *Arabidopsis thaliana* using the floral dip method. Many of the sequences identified from the library were heat stress-related, therefore a second component of this research was assessing the degree to which *C. officinalis* heat-stress associated genes provided thermotolerance in transgenic *A. thaliana*. Various stress assays, which included both *in vitro* and *in vivo* assays, were performed to help determine the degree of thermotolerance. While all *A. thaliana* lines expressed the transgenes, only some lines were thermotolerant. The findings have important plant biotechnological applications. Additionally, since global climate change is predicted to result in elevated temperatures over the next century, there are possible agricultural implications. Taken together, the results suggest that binary libraries facilitate high-throughput transformation of plants using choice-selected genes of interest and can provide thousands of vector-insert constructs to investigate. Future studies should consider the transcriptional state of an organism prior to binary library construction in order to obtain choice vector-insert constructs.

<sup>1</sup>University of Northern Colorado, Biological Sciences, Ross Hall, Room 2480, Campus Box 92, Greeley, CO, 80631, USA<sup>2</sup>

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## Symbioses: Plant, Animal, and Microbe Interactions

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### ORAL PAPERS

755 ORTIZ, IRMA <sup>\*1</sup>, SCHWARTZ, ALLISON<sup>1</sup>, SANDERS, ERIN R. <sup>2</sup>, DIENER, ANDREW C.<sup>3</sup> and HIRSCH, ANN M.<sup>3</sup>

**A *Bacillus* strain isolated by undergraduate students at UCLA promotes plant growth by procuring soil nutrients and may also serve as a biological control agent.**

The plant microbiome in the rhizosphere consists of both bacteria and fungi that exhibit many beneficial effects on plant growth. The Plant-Growth Promoting Bacteria (PGPB) offer an important solution to the negative consequences of adding chemical fertilizers and pesticides by enhancing plant yield, producing phytohormones such as auxin or interfering with ethylene synthesis, controlling plant pathogens, and obtaining critical nutrients including iron, nitrogen, and phosphorus. In this study, we analyzed the mechanisms whereby a *Bacillus* strain, isolated from the Mildred E. Mathias Botanical Garden and investigated by two UCLA undergraduate courses, could mediate a positive growth response on legumes such as *Medicago truncatula*, *Lotus japonicus*, and *Pisum sativum*. From various assays, we determined that the improvements in plant growth are likely to be the result of a combination of bacterial factors including IAA synthesis, siderophore production, and phosphate solubilization. Because PGPB are also known to protect plants from pathogenic fungi and bacteria, a co-culture assay was established on potato dextrose agar (PDA) plates. The plates were either left uninoculated or spotted with a number of different fungal pathogens, and then co-inoculated with the new *Bacillus* strain or *B. subtilis*, a well-known biocontrol agent. Our results so far suggest that the newly isolated *Bacillus* strain is a weaker biological control agent than *B. subtilis*.

We acknowledge the financial support of the Shambrom Family Foundation and the UCLA Office of Instructional Development for courses MIMG 121A and MCDDB150L. Irma Ortiz was supported by NIH grant GM55052 to Dr. Richard L. Weiss (UCLA). Other undergraduates who participated in this research are Rudy Benitez, Nigar Yusufova, Christine Kim, Ethan Mathews, Mary Motamedinia, Archie McCoy, Han Soul Kim, Kayoko Hanamoto, Walter Kim, Judy Wong, Brittany Yee, and Faith Oh.

<sup>1</sup>University of California-Los Angeles, Molecular, Cell & Developmental Biology, 621 Charles Young Dr., South, Los Angeles, CA, 90095-1606, USA<sup>2</sup>University of California-Los Angeles, Microbiol, Immunol, and Mol Genetics, Los Angeles, CA, 90095, USA<sup>3</sup>University of California-Los Angeles, MCD Biol and Mol Biol Inst, 621 Charles Young Dr., South, Los Angeles, CA, 90095-1606, USA

756 OBERLE, BRAD\*<sup>1</sup> and ZANNE, AMY<sup>2</sup>**Seeing the forest for the fungi: plant traits and decomposition rates under changing climate**

A large fraction of terrestrial carbon (C) is locked up in woody stems, both living and coarse woody debris. The rate of carbon release from these pools depends on two factors: plant senescence and wood decomposition. These factors, in turn, are modulated by wood traits. Vascular anatomy and chemical composition may influence mortality during drought. They also may affect saprotroph community structure and function. These wood traits vary among species, with important consequences for the carbon balance of forests under climate change. As part of a larger project that integrates experiments and field observations with plant traits and fungal metagenomics, we established long-term experimental decomposition plots in the Ozark Highlands Ecoregion. Plots were situated at upland and lowland sites in different watersheds. Each included stem sections from 16 locally occurring species with contrasting traits. After the first year of decomposition, we analyzed variation in mass loss across sites and species. Overall, stems lost 12-50% of their mass. Mass loss varied between sites, with moister lowland sites decaying more quickly than drier upland sites. Mass loss also varied strongly among species. Species differences alone explained 56% of the variation in initial decay rates. These species differed in a suite of functional traits, including leaf size, specific leaf area, leaf area to sapwood area ratio, wood density, C and N content, and C:N ratio. Although each trait independently explained relatively little variation in decay rates, together they explained almost as much variation in decay rates as species identity. In addition to these measured trait differences, unmeasured differences between angiosperms and conifers (i.e. clade membership) contributed to variation in decay rates. On the whole, these results reinforce the well-known effect of environment on decomposition. Furthermore, they strongly suggest that plant species' functional traits and evolutionary histories play an extremely important role in wood decomposition. Exactly how species' differences influence saprophyte community structure and function will be the subject of future studies.

<sup>1</sup>University of Missouri-St. Louis, Biology, One University Boulevard, St. Louis, MO, 63121, USA <sup>2</sup>University Of Missouri - St. Louis, R223 Research Building, One University Blvd., St. Louis, MO, 63121, USA

757 CANNON, BRANDI\*, GARRISON, JESSICA, SOPAS, JAMES, VERASTEGUI, TIMOTHY and RANDLE, CHRISTOPHER

**Presentation, aroma, and flavor: Investigation of host cues in the orientation and establishment of *Phoradendron serotinum* (Viscaceae)**

Obligate parasitic plants cannot survive without the influx of water and/or nutrients from host plants. Therefore, successful establishment of haustoria (vascular organs of penetration and transport) is necessary for the survival of an emerging seedling. Extensive studies have been performed on the effect of host cues on germination, orientation, and development of haustoria in root parasites. For root parasites, host cues must be transmitted through the rhizosphere and are largely chemical. Plants that are parasitic on the aboveground stems of host plants must be able to detect hosts in a much different milieu. *Phoradendron serotinum* (leafy mistletoe) is a water parasite of broadleaf trees. While *P. serotinum* parasitizes many different hosts across its range, populations are most often locally host specific, preferring a single host even when other hosts are available. The underlying cause of this pattern of host preference is unknown, and will remain so until host cues responsible for successful establishment of haustoria have been identified. In this study, we examined the effects of light cues, physiochemical cues associated with the host surface, and gaseous chemical cues on the viability, orientation, and successful establishment of emerging haustoria on host plants. Light and physiochemical cues associated with the host substrate had a significant effect on haustorial establishment. Gaseous cues had a significant positive effect on viability and orientation. This latter result was foreshadowed by a similar finding in the stem parasite *Cuscuta*, which responds to gaseous cues emitted by host plants.

Sam Houston State University, Department of Biological Sciences, 1900 Avenue I, Huntsville, TX, 77340, USA

758 WOODARD, ANASTASIA\*<sup>1</sup>, ERVIN, GARY<sup>2</sup> and MARSICO, TRAVIS<sup>3</sup>**Defense Priming as a Mechanism to Combat Newly-Associated Insect Herbivores**

To combat insect herbivory and still achieve optimal allocation of resources, plants have evolved inducible defenses. Defense priming enhances the induced defense responses of plants by activating defense pathways prior to attack due to airborne signals released from neighboring plants undergoing herbivory. This phenomenon allows plants to mount quicker, more

intense responses specifically tailored to the threatening herbivore. Despite the number of newly-associated invasive insect species globally, the effects of defense priming in a system with a novel threat have not been considered. Here we report that plants can be induced to defend against an otherwise unrecognized, newly-associated insect herbivore when signaled by plants actively defending against a co-evolved insect herbivore. *Opuntia humifusa* and *O. stricta*, two North American pricklypear species, have not been observed to defend against the recently-introduced invasive cactus borer *Cactoblastis cactorum* in nature, although defenses such as mucilage production and tissue necrosis are commonly observed when plants are fed on by the native North American cactus borer *Melitara prodenialis*. In a recent laboratory experiment, we found that 47% of plants fed on by *C. cactorum* grown in the presence of plants fed on by *M. prodenialis* defended with mucilage and necrosis responses, whereas 17% of plants grown only with *C. cactorum* showed defenses within the first month of larval feeding. Induced defense via priming of the *Opuntia* spp. increased the larval period of *C. cactorum* by 38% (from a mean of 69 days to 95). In nature where larvae are exposed to predators, parasitoids, and pathogens, an increase in larval period is expected to decrease fitness. Our results indicate that defense priming initiated by native, co-evolved herbivores can cue naïve plants to defend against invasive herbivores. These findings have important implications for our understanding of defense priming in the context of species invasions and the influence of evolutionary history on plant-herbivore interactions.

<sup>1</sup>Arkansas State University, Department of Biological Sciences, PO Box 599, State University, AR<sup>2</sup>Mississippi State University, Department of Biological Sciences, 130 Harned Hall, Lee Blvd, Mississippi State, MS, 39762, USA<sup>3</sup>Arkansas State University, Department of Biological Sciences, PO Box 599, State University, AR, 72467, USA

**759 SOUTHWORTH, DARLENE\*<sup>1</sup> and FRANK, JONATHAN<sup>2</sup>**

### **Listening to roots: a new mycorrhizal fungus on *Cercocarpus* (Rosaceae)**

Mycorrhizal assemblages characterized by molecular data frequently differ from collections of mycorrhizal sporocarps at the same site. *Geopora* (earth pore) species are frequent mycobionts of ectomycorrhizal roots, but except for *G. cooperi*, they rarely match species by molecular methods. Among the mycobionts of ectomycorrhizas with curl-leaf mountain mahogany, *Cercocarpus ledifolius* (Rosaceae), was a fungal species with a 91% BLAST match to *G. arenicola*. To determine the species of *Geopora*, we surveyed for hypogeous sporocarps under *C. ledifolius* at sites in southern Oregon where the *Geopora* mycorrhizas had been collected and identified by DNA sequences of the ITS region. We found sporocarps of a *Geopora* species with 100% BLAST match to the mycorrhizas. Morphological char-

acters of a white hymenium, inrolled entire margin, and large spores, along with a hypogeous habit and a mycorrhizal host of *C. ledifolius* distinguished these specimens from described species. We describe a new species, *Geopora cercocarpi*.

<sup>1</sup>Department Of Biology, 866 Blaine St, Ashland, OR, 97520, USA<sup>2</sup>Southern Oregon University, Biology, Ashland, OR, 97520, USA

**760 BECKLIN, KATIE M.\*<sup>1</sup>, HERTWECK, KATE<sup>1</sup> and JUMPPONEN, ARI<sup>2</sup>**

### **Host identity has a greater impact on rhizosphere fungal communities than habitat in an alpine ecosystem**

Below ground interactions can significantly affect communities and ecosystems, yet the diversity and composition of soil biota are still relatively unknown. We evaluated the effects of habitat and host identity on the richness, diversity, and composition of rhizosphere fungi colonizing three alpine plant species, *Taraxacum ceratophorum*, *Taraxacum officinale*, and *Polemonium viscosum*. Roots were collected from open meadow and willow understory habitats above timberline on Pennsylvania Mountain (Park County, CO, USA). Fungal SSU rDNA was sequenced using 454 pyrosequencing, sample-specific DNA tags, and fungal-specific primers. We categorized operational taxonomic units (OTUs) as arbuscular mycorrhizal (AMF) or non-arbuscular mycorrhizal (NON-AMF) fungi, then tested whether habitat or host identity influenced these fungal communities. Total AMF and NON-AMF richness was similar between habitats, but varied among host species. Within individual root samples AMF richness was higher in the open meadow than in the willow understory, and both AMF richness and diversity were highest in *T. ceratophorum* compared to the other host species. Within individual root samples NON-AMF richness and diversity was similar among host species except in the willow understory where diversity was reduced in *T. officinale*. Fungal community composition was influenced by host identity, but not habitat. Specifically, *T. ceratophorum* and *P. viscosum* hosted similar AMF communities, while *T. ceratophorum* and *T. officinale* hosted similar NON-AMF communities. Our results suggest that host identity has a stronger effect on rhizosphere fungi than habitat. Furthermore, although host identity influenced both AMF and NON-AMF this effect was stronger for the mutualistic AMF community.

<sup>1</sup>University Of Missouri Columbia, 1201 East Rollins Rd, Life Science Center 311, Columbia, MO, 65211, USA<sup>2</sup>Kansas State University, Division of Biology, 433 Ackert Hall, Manhattan, KS, 66506, USA

## POSTERS

761 BOWLER, REBECCA, FREDEEN, ARTHUR and MASSICOTTE, HUGUES\*

**Investigation of carbon gain of autotrophic, mixotrophic and myco-heterotrophic species at three sites in north-central British Columbia**

Most terrestrial vascular plants rely to some degree on mycorrhizal fungi for obtaining mineral nutrition. A subset of these plants also rely on their mycorrhizal partner(s) for some (mixotrophy) or all/most (myco-heterotrophy) of their carbon. Many pyroloids (*Pyroleae* tribe of the *Ericaceae* family) and some green orchids (*Orchidaceae*) are mixotrophs. By contrast, leafless orchids of the genus *Corallorhiza* are thought to be exclusively myco-heterotrophic. We conducted a pilot project where we assessed the photosynthetic competence of autotrophic, mixotrophic and myco-heterotrophic species growing in sub-boreal forests of north-central British Columbia. Gas exchange properties of each species were non-destructively measured *in situ* at least once a month during the growing season (May to September) of 2011 using a portable gas exchange system (model LI-6400, LiCor Inc.). Individuals of these species were also replanted in the Enhanced Forestry Lab at UNBC for further analysis. After approximately one month of acclimation to non-forest light levels, light response curves of each sample were measured using the same methods as *in situ* measurements with the exception of an artificial light source. We will highlight the current implications of our results and our future plans for this study.

University Of Northern British Columbia, Ecosystem Science And Management Program, 3333 University Way, Prince George, BC, V2N 4Z9, Canada

762 YERABALLI, SAGAR\*, HICKS, SARAH<sup>2</sup>, GOSSAGE, ZACHARY<sup>1</sup>, SINSABAUGH, ROBERT<sup>2</sup>, SUDING, KATHERINE<sup>3</sup> and PORRAS-ALFARO, ANDREA<sup>1</sup>

**Response of plant-associated fungal communities to N deposition in an alpine tundra ecosystem**

Human activities have played a major role in increasing nitrogen (N) availability in terrestrial ecosystems. N enrichment facilitates plant productivity, but in certain conditions can negatively affect plant diversity and survival. The effects of N fertilization on plant-fungal interactions in alpine tundra ecosystems are poorly known. The main goal of this study was to evaluate the effect of N fertilization on fungal symbionts

associated with two co-dominant plants: *Geum rossii* and *Deschampsia cespitosa*. Seven samples were collected for each plant species from four different treatments: control, N fertilized, N fertilized/*Deschampsia* removal, *Deschampsia* removal/no N added. The study site is located at the Niwot Ridge Long Term Ecological Research (LTER) site in Colorado. Roots were harvested from each treatment and stained to quantify fungal colonization. Ninety two pure cultures of endophytic fungi were isolated on potato dextrose agar. Fungal symbionts were identified using the Internal Transcribed Spacer rDNA. Potential functions of these symbionts were evaluated in germination and greenhouse experiments. Microscopy data from 2008 and 2010 showed an increase in percentage of colonization in N fertilized plots when compared with control plots. *Geum* showed the highest colonization with arbuscular mycorrhizal fungi and dark septate fungi as the dominant colonizers. Preliminary identification of cultures showed that *Geum* is mainly colonized by fungi in the order Heliales including the dark septate fungus *Phialocephala fortinii*. Of five different fungal endophytes tested in the greenhouse, two had pathogenic activity. Direct sequencing from roots using 454 technology, showed that fungal communities are highly complex. Analysis of potential roles of these fungal symbionts needs further exploration.

<sup>1</sup>Western Illinois University, Biology, Waggoner Hall, 1 University Circle, Macomb, IL, 61455, USA<sup>2</sup>University of New Mexico, Biology, 167 Castetter Hall, Albuquerque, NM, 87131, USA<sup>3</sup>University of California Berkeley, Department of Environmental Science, Policy & Management, 137 Mulford Hall #3144, Berkeley, CA, 94720, USA

763 VIJAYARAGHAVAN, SRIVATHSAN\*, GARCIA, MARGARET<sup>2</sup>, LOWREY, TIMOTHY<sup>2</sup> and PORRAS-ALFARO, ANDREA<sup>1</sup>

**Plant-associated fungi: diversity and function in gypsophilic soils**

All plants form symbiotic associations with fungi but little is known about fungal communities associated with gypsophilic plants. Gypsophilic soils are mainly composed of calcium sulfate and are prevalent in parched areas of Earth covering more than 100 million hectares. The main objectives of this research project were to: 1. Evaluate fungal colonization patterns in roots of gypsophilic plants from New Mexico; 2. Evaluate the effect of fungal isolates on plant germination and growth; 3. Identify fungal isolates associated with gypsophilic plants and evaluate their potential cellulolytic activity. Roots were examined for nine species of gypsophilic plants from New Mexico. Microscopic analyses indicate that plants are mainly colonized by arbuscular mycorrhizal and dark septate fungi. Grasses such as *Sporobolus nealleyi* and *Bouteloua gracilis* had the highest fungal colonization. Germination experiments showed pathogenic to mutualistic activities for different fungal

isolates. Identification of fungal isolates using BLAST showed that *Alternaria sp.* was the dominant fungus found in the leaves, and *Monosporascus canoballus* was the dominant fungus found in the roots. A least 10% of these fungi showed the ability to degrade cellulose with potential applications in the biofuel industry. Based on colonization rates and diversity, fungal communities found in gypsophilic plants are complex and additional studies are necessary to evaluate the effect of fungal consortia on plant survival and establishment.

<sup>1</sup>Western Illinois University, Biology, Waggoner Hall. 1 University Circle, Macomb, IL, 61455, USA<sup>2</sup>University Of New Mexico, Department Of Biology, Albuquerque, NM, 87131, USA

**764 BEAULIEU, WESLEY<sup>T\*1</sup>, PANACCIONE, DANIEL G<sup>2</sup>, MILLER, RICHARD E<sup>3</sup> and CLAY, KEITH<sup>1</sup>**

### **New Reports of Ergot Alkaloids and Chemotypic Diversity in Convolvulaceae-Clavicipitaceae Symbiosis**

**E**rgot alkaloids are fungal secondary metabolites well known for their role in plant defense against herbivores. In plants, ergot alkaloids are produced by symbiotic fungi in the family Clavicipitaceae (Ascomycota) first discovered from associations with the Poaceae but now known to be distributed across several mono- and dicotyledonous plant families including the Cyperaceae and more recently the Convolvulaceae. Here we report on a survey of the Convolvulaceae for (1) the presence of fungal ergot alkaloids in seeds and (2) the intra- and interspecific chemical diversity therein. Our results show a worldwide distribution of ergot-positive species including representatives from North, Central & South America, Africa, Australia, Asia and Oceania. Concentrations of ergot alkaloids in the Convolvulaceae ranged from 0.1 to 4700 µg/g seed, which is up to 1000 fold greater than in Clavicipitaceae-Poaceae symbioses. Interestingly, ergot-positive species are restricted to the tribe Ipomoeae, a group of 900 tropical and sub-tropical species, primarily twining vines. While the previous literature suggested a phylogenetic signal of ergot alkaloid distribution, our expanded survey shows the picture to be more complicated. Our survey of 64 species revealed 19 ergot-positive species, seven of which were previously unreported. 12 ergot alkaloids occurred among these species in 17 different combinations (unique chemotypes). Different chemotypes were detected among accessions in several species, indicating genetic variation of symbionts. There were over 40 instances when a specific ergot alkaloid was detected for the first time in a particular species. Extensive population sampling of two species (*Ipomoea parasitica* and *I. pes-caprae*) revealed within species variation in alkaloid presence and concentration, including a significant difference in alkaloid concentrations between geographically separated populations of *I. pes-caprae* from the Gulf and Atlantic coasts of Florida. Given that there are 900 species in the

tribe, our results suggest that we have yet to realize the diversity and distribution of the symbiotic relationship between Clavicipitaceae and Convolvulaceae.

<sup>1</sup>Indiana University, Department of Biology, 1001 E 3rd St, Bloomington, IN, 47405, USA<sup>2</sup>West Virginia University, Division of Plant & Soil Sciences, 1090 Agricultural Sciences Building, Morgantown, WV, 26506, USA<sup>3</sup>Southeastern Louisiana University, Department of Biological Sciences, 808 N Pine St, Hammond, LA, 70402, USA

**765 HALLE, ERNESTINE MEFOR<sup>\*1</sup>, SSALI, FREDRICK<sup>2</sup> and GIKONYO, NANCY<sup>3</sup>**

### **Leaf production in relation to damage of seedlings in Amani Nature Reserve, (ANR), Tanzania**

**T**his study was carried out in Amani Nature Reserve (ANR), Tanzania and focused on leaf production and its response to simulated leaf damage of seedlings on four fast growing species: *Leptonychia usambarensis*, *Chostas spiras*, *Piper capense* and *Macaranga kilimandscharica*. A total of six study sites were selected in the forest gaps. Overall, the effect of damage on leaf production was strongest in *Macaranga kilimandscharica* where the rate of leaf growth decreased with increase in extent of damage. This implies that *Macaranga kilimandscharica* is more sensitive to damage compared to the other study species since its growth rate slows down when damaged. The results from this study suggest that the different species had different rates of shoot growth, leaf growth and leaf production. *Macaranga kilimandscharica* had the highest rate of leaf growth, second highest rate of shoot growth and the highest rate of leaf production. There was also no significant difference in the level of herbivory between leaves of different ages. Similar studies on leaf production in relation to damage of seedlings can be carried out on fastgrowing canopy species, such as *Macaranga kilimandscharica* in generating up to-date information so as to enhance further understanding of plant-animal interactions.

<sup>1</sup>University of Buea, Plant and Animal science, PO Box 63, Buea, SW, 237, Cameroon<sup>2</sup>Mbarara University of Science and Technology, Uganda<sup>3</sup>University of Bremen, Tropical Aquatic Ecology (ISATEC), Bremen, 49, Germany

**WS01 - Plants, People & Pictures**

*Organized by: Kim Bridges, Retired Professor  
Univ. of Hawai'i at Manoa, Bill Dahl, Botanical  
Society of America*

**W**e are going to explore digital photography in the context of both Point-and-Shoot and Digital SLR cameras. The focus is on typical botanical and ethnobotanical themes. The overall aim is to help everyone, from beginner to competent photographer, better understand the capabilities and features of this emerging digital medium. Special attention will be given to macro-photography. The workshop includes discussions, demonstrations and hands-on opportunities. All participants are asked to bring their camera gear as there will be an outdoor photo shoot. Two sessions: 1:00-5:00 PM and 7:00-8:30 PM.

**WS02 - iPlant Discovery Environment and API: Integration of Biological Data-sets, Computational Tools, and Analytical Workflows**

*Organized by: Ann Stapleton, University of  
North Carolina*

*Uwe Hilgert, iPlant Collaborative, Dolan DNA  
Learning Center, Cold Spring Harbor Laboratory*

*Eric Lyons, University of Arizona*

**W**ith current high-throughput data collection methodologies, plant biologists often find themselves overwhelmed by the amount of data to process. Similarly, there are many analytical tools from which to choose when processing these data, many of which require knowledge of using the command-line interface and high performance computers. iPlant's web-based Discovery Environment allows biologists to easily manage and share biological data, computational tools, and analytical workflows. Furthermore, iPlant provides two APIs (Application Programming Interfaces) to allow researchers to integrate additional tools and to access tools and data through the web.

This workshop will focus on using iPlant's web-based Discovery Environment to create and share workflows to process data and on using iPlant's APIs to integrate new tools.

**WS03 - DNA Subway Places Students On Fast Track To Plant Genome Analysis and DNA BarCoding**

*Organized by: Uwe Hilgert, iPlant Collaborative,  
Dolan DNA Learning Center, Cold Spring  
Harbor Laboratory*

**G**enome analysis provides opportunities for students to discover basic principles of molecular biology while embarking on research projects. DNA Subway is an educational platform for gene annotation and comparison. It bundles research-grade bioinformatics tools and databases into intuitive workflows and presents them in an appealing interface using the metaphor of a subway map. Riding on any of four different DNA Subway lines, users can predict and annotate genes in up to 150 kb of DNA (Red Line), identify homologs in sequenced genomes (Yellow Line), analyze DNA barcodes and construct phylogenetic trees (Blue Line), and analyze RNAseq data (Green Line). Work can be saved for later use and/or shared with other users. Workshop participants will use DNA Subway to upload and analyze DNA and protein data and learn how to integrate genome analysis into their own teaching.

**WS03A- Applications of Next Generation Sequencing in Plants**

*Organized and Sponsored by Roche Diagnostics*

**WS04 - Sustainable Teaching: Getting started and keeping going**

*Organized by: Clare Hasenkampf, University of  
Toronto*

**I**n this workshop I will consider some ideas about Student Learning Principles of a well-aligned course and a common sense checklist for sustainability I hope that the ideas presented will help you find your way to teach courses that regularly provide a rich learning experience for students and a satisfying intellectual endeavor for yourself. Workshop is primarily for graduate students, post docs and faculty early in teaching careers, but all are welcome.

## **WS05 - Best Practices for Image use in Keys and Guides**

*Organized by: Bruce K. Kirchoff, University of North Carolina at Greensboro*

**A**lthough illustrations have played an important role in identification keys and guides since the 18th century, their use has varied widely. Some keys lack all illustrations, while others are heavily illustrated. Even within illustrated keys and guides the way in which images are used varies considerably.

During this workshop we will review image use in selected keys and guides, and present a set of suggested best practices for image use. The best keys and guides use multiple standardized images, displayed at sizes that are easy to see, and arranged in a standardized manner so that similar images can be compared across species. It is not possible to form an adequate taxonomic concept from a single photograph. The failure to use multiple images for each species is the most common shortcoming of illustrated keys and guides. Illustrated keys and glossaries should contain multiple images for each character state so that the user can judge variation in the state. When used in glossaries, a single drawing is best used to illustrate several terms, and each term is best illustrated with several drawings. Scale bars should be used with discretion. They are not needed on every illustration and, when used indiscriminately, can distract the user's attention from the salient features. Iconic symbols and colored marginal bands can make the key easier to use, and should be used where appropriate.

## **WS06 - Preparing Digital Images for Publication**

*Organized by: Mike Vanderberg, Sheridan Press*

**T**his workshop covers general Digital Art Submission Guidelines for publishing figures in both print and online journals. It will include live demonstrations in Adobe Photoshop and Illustrator on the following topics: Imaging Foundations, RGB Image Submission and Color Management, Preparation Tips, plus a brief discussion on Image Integrity.

## **WS07 - Teaching Philosophy, Teaching Statements and teaching Dossiers-How to and Why**

*Organized by: Clare Hasenkampf, University of Toronto*

**I**n this workshop we will look at the Teaching Philosophy and Teaching Dossier as a tool for a reflective teaching practice. We will also look at the Teaching Statement and Dossier as parts of job applications, promotion files and for Teaching awards.

## **WS08 - Workshop and Roundtable Discussion: Successful Manuscript Preparation and Publication**

*Organized by: Amy McPherson, Managing Editor, American Journal of Botany*

*Richard Hund, Production Editor, American Journal of Botany*

**T**his workshop, designed for graduate students, early-career scientists, and those new to publishing, is intended to give a brief yet detailed description of what happens from manuscript submission to final publication in a scientific journal. This round-table discussion, with members of various editorial teams (including the American Journal of Botany) and your peers, will serve as a forum for questions and answers regarding successful or not so successful article publication in a scientific journal. Questions may be submitted before the workshop. The session is designed to give the new-to-publishing researcher a chance to discuss the publishing process from the author's and editor's perspectives.

## **WS09 - US Virtual Herbarium Project; Progress made, goals to achieve**

*Organized by: Mary Barkworth, Intermountain Herbarium*

**T**he workshop, which is also the official annual meeting of the US Virtual Herbarium Project, will focus on sharing of new developments and approaches to the digitization of herbaria and examples of how such information is being used or can be expected to be used in the very near future. There will also be a summary presented of some of the intermediate steps that have been taken towards attainment of the overall goal of digitizing all specimens and developing resources that enable diverse publics to benefit from access to the digitized information.

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**WS10 - Floristic projects: who does what,  
with Flora of North America as a case study.**

*Organized by: Nancy R. Morin, Flora of North America*

This workshop will be useful to anyone involved in any of the floristic projects currently underway and will provide an opportunity for participants in various projects to compare notes. Flora of North America (FNA) provides a case study. It is a massive collaborative project to produce a Flora of North America north of Mexico in print and electronic forms. Sixteen out of the projected 30 volumes have been published. The project involves more than 900 botanists in North America and elsewhere.

Missouri Botanical Garden is an FNA editorial center and also the center for botanical illustration and composition. This workshop will focus on a behind-the-scenes look at how treatments are processed and what authors, regional and taxonomic reviewers, editors, and artists do. Break out sessions will provide time for different groups (e.g. authors, regional reviewers, editors) to discuss problems and solutions. The workshop will include a tour of the composition and illustration facilities and the Missouri Botanical Garden library. It will finish with a reception for everyone interested in the project.

**WS11 - Professional Development: Applying  
to Graduate Programs**

*Organized by Ann Sakai*

This workshop is primarily for undergraduates interested in applying to graduate programs, master's degree students applying to doctoral programs, and faculty who work with these students, but all are welcome. The workshop will consist of a brief presentation of the "ins and outs" of applying to graduate school before and during the application process. This presentation will be followed by a question and answer session between the participants and several panelists. The latter will include current graduate students, as well as faculty experienced in graduate admissions procedures, from several different institutions.

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olmstead@u.washington.edu

Program Director - Patrick Herendeen  
Chicago Botanic Garden  
Glencoe, IL 60022  
(847) 835-6956  
pherendeen@chicagobotanic.org

Local Representative - Peter C. Hoch  
Missouri Botanical Garden  
St. Louis, MO 63166  
(314) 577-5175  
peter.hoch@mobot.org

### Botanical Society of America

President - Judy Skog  
George Mason University  
Manassas, VA 20110  
(703) 993-1026  
jskog@gmu.edu

Program Director - David Spooner  
University of Wisconsin  
Madison, WI 53706  
(608) 890-0309  
david.spooner@ars.usda.gov

Local Representative - Allison J. Miller  
St. Louis University  
St. Louis, MO 63103  
(314) 977-7653  
amille75@slu.edu

### Conference Director

Johanne Stogran  
125 Connemara Drive  
Granville, OH 43023  
(740) 927-8501  
johanne@botany.org

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