

ABSTRACTS



Aquatic and Wetland Plants: Wet & Wild

THE ANNUAL MEETING OF THE FOLLOWING
PROFESSIONAL SOCIETIES

BOTANICAL SOCIETY OF AMERICA

AMERICAN SOCIETY OF PLANT TAXONOMISTS

AMERICAN BRYOLOGICAL AND LICHENOLOGICAL SOCIETY

AMERICAN FERN SOCIETY

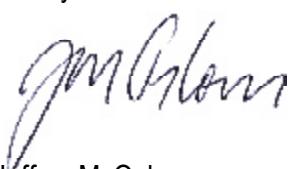
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Mobile, Alabama

The abstracts of contributed papers, contributed posters, special papers, symposia and colloquia presentations, the BSA President-Elect's banquet address, and the plenary address for the Botany 2003 conference are printed in this volume. Botany 2003 represents the annual meeting of four professional societies, including the American Bryological and Lichenological Society (ABLS), the American Fern Society (AFS), the American Society of Plant Taxonomists (ASPT), and the Botanical Society of America (BSA).

Abstracts are listed within special lecture, symposium and colloquium, and BSA disciplinary Section/affiliated society categories, with the Sections are arranged alphabetically. Abstracts for special lectures as well as symposia and colloquia are solicited on an invitational basis by the organizers. Papers and posters are submitted on a contributed basis to the disciplinary Section/affiliated society chosen for presentation by the authors. Within each symposium, colloquium, and disciplinary Section category, the abstracts are organized in alphabetical order by last name of the senior author. In addition, each symposium and colloquium includes a summary abstract, and each disciplinary Section includes contributed paper and contributed poster subcategories. The abstracts are numbered consecutively from 1 to 424, and these abstract numbers are provided for each author in the Author Index.

In addition to this volume, all abstracts are electronically archived and can be extensively browsed and searched on-line at the conference web site: <http://www.2003.botanyconference.org/>.

Assembling this abstract volume and the scientific program for Botany 2003 required the hard work and help of many people, including sectional/society program officers, local representatives, and several others. In particular, I would like to thank the following individuals: James D. Lawrey (Bryological and Lichenological Section—ABLS), Larry Hufford (Developmental and Structural Section), Joseph Colosi (Ecological Section), David M. Spooner (Economic Botany Section), Stephen J. Novak (Genetics Section), Lee B. Kass and Larry Davenport (Historical Section), Kathleen Pigg (Paleobotanical Section), Richard M. McCourt (Phycological Section), Henri R. Maurice (Physiological Section), Emanuel Johnson (Phytochemical Section), Thomas A. Ranker (Pteridological Section—AFS), Andrea D. Wolfe (Systematics Section—ASPT), J. Phil Gibson (Teaching Section), Susana Magallón (Tropical Biology Section), Brian J. Axsmith (BSA and AFS Local Representative), Al Schotz (Fieldtrip Coordinator), Lowell E. Urbatsch (ASPT Local Representative), and C. Smoot Major (ABLS Local Representative). In addition, I would especially like to thank William Dahl (BSA Executive Director) and Johanne Stogran (BSA Meetings Manager) for their help. These individuals work tirelessly for the BSA and for the success of Botany 2003.



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PLINARY ADDRESS

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The All-Species Initiative and the Future of Life

The past 250 years of systematic effort, formally dated from the introduction of binomial nomenclature by Carolus Linnaeus, has resulted in the discovery, diagnosis, and naming of probably only on the order of ten percent of living species. The unknown majority are chiefly the small invertebrates, fungi, and microorganisms; but even so, large numbers of plants and vertebrates also await discovery. With accelerating advances in information and genomics technology, systematists can in theory complete the mapping of Earth's diversity to the species level within 25 years. An all-out effort to do so, even if it falls short, has the power to transform biology. For the first time ecosystems could be fully censused and monitored at every trophic level. Biomedical research would be broadened by exact knowledge of pathogens of potential risk to humans, and by the generation of novel classes of pharmaceuticals. Agriculture can be expected to find new strength from the development of new crop species and transgenes. An encyclopedia of life, giving single-location access to the known biology of every species in turn, from its ecology to its genome, would open doors serendipitously, leading to avenues of research currently unimagined. Not least, such a comprehensive map of the biosphere at the species level, followed by monitoring, will illuminate the full status of biodiversity. Its data base will enable a maturing conservation biology to become persuasive and maximally cost-efficient in its urgent mission of protecting all of the rest of life while our own species is straightening out its own affairs.

ADDRESS OF THE BSA PRESIDENT-ELECT

2 GRAHAM, LINDA

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A tale of two liverworts: The importance of organismal biology as an essential link between molecular and systems biology

It was the best of times for early land colonizers similar to the modern liverwort *Marchantia*; plenty of light and carbon dioxide, no herbivores, and adaptations for resistance to microbial attack favored lush growth. But it was the worst of times for more delicate forms likely resembling modern evanescent *Blasia*; drying winds, damaging sun, and decay microbes prescribed a short lifetime. Yet both organisms are widespread and common today, and the fossil record suggests this was also likely true for ancient relatives. Though *Blasia* may be ephemeral, its gemmae are able to recall it to life, contributing to a super-colonizer lifestyle. Wefts of resistant *Marchantia* rhizoids have woven a persistent memory through time, in the form of enigmatic fossil nematophytes. Elucidating the molecular, biochemical, cellular, structural, reproductive, and ecological traits of such organisms yields a clearer picture of a dramatic revolution, transformation of a nearly bare land surface into a vegetation-rich landscape. Organismal data provide a crucial link between increasingly rich molecular data, such as *Marchantia* organellar genomic and EST databases (and expected BAC libraries) and biogeochemical models, such as the climate-altering carbon cycle dynamics of the earliest vegetation on Earth. Though a few model systems, including *Marchantia*, are invaluable as we seek a deeper understanding of biological phe-

nomena at the cell level and below, the grander vision becomes available only through the lens of organismal diversity, including the humble *Blasia*. As we seek to use scientific knowledge to better understand and manage natural resources, continued research commitment to the organismal connection is well advised.

ANNALS OF BOTANY LECTURE

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Wet and Wild: Conserving and Restoring Plant Diversity in Wetlands

There is a compelling need to protect existing wetlands and to restore wetlands in degraded landscapes. This must proceed guided by sound scientific principles, practical conservation tools, and clear priorities. With perhaps 1/3 of the world's flora facing extinction, scientists and conservation managers will need to work rapidly and collaboratively, recognizing each other's strengths and limitations. To guide such work, I will begin with the largest scale: the world's largest wetlands. I will also review some related global patterns in biodiversity. Then, turning to the more local scale, I will explore six empirical (that is, pragmatic) scientific models that already exist to guide managers in protecting and restoring plant diversity in wetlands, illustrating them with examples from the literature and from my own experience. (1) Area: Larger areas contain more species. (2) Infertile sites/eutrophication: Applying Grime's "humped-back" model of plant diversity to wetlands shows that infertile habitats support the most rare wetland plants. (3) Competitive hierarchies: In the absence of constraints, large species such as *Typha latifolia* tend to dominate patches of landscape, thereby excluding most of the local biological diversity; eutrophication accelerates this process; natural disturbance such as fire may counteract it. (4) Heterogeneity/Centrifugal organization: Multiple intersecting environmental gradients maintain the regional diversity in landscapes, and can be engineered into restoration projects. (5) Core and satellite patterns/the canonical distribution: In any landscape, a few species are common and most are locally rare. (6) Water levels: Water level gradients create more types of habitat. Water level fluctuations within and among years (within prescribed limits) are essential for maintaining diversity in wetland plant communities including wet meadows and wet prairies.

PLINARY SYMPOSIUM

RECENT ADVANCES IN RESTORATION OF AQUATIC AND WETLAND HABITATS

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Recent advances in restoration of aquatic and wetland habitats: Introduction

To paraphrase Charles Dickens, it is the best of times; it is the worst of times. More ambitious and more extensive wetlands restoration projects are supported by stronger science and growing numbers of talented scientists. Public appreciation of wetlands, estuaries and terrestrial landscapes continues to increase. Philanthropic organizations and private industries contribute to restoration projects in sensitive habitats and to land acquisition for long term protection. At the same time, an array of environmental laws—the Clean Water Act,

the Endangered Species Act, the Clean Air Act, the National Environmental Policy Act, the National Forest Management Act, to name a few—are at risk in the current political and economic climate. Coastal and riverine wetland erosion is reaching critical levels throughout the U.S., and municipal and industrial wastes threaten wetlands and oceans as never before. In light of all these circumstances, it is most appropriate to convene this symposium here in Mobile, Alabama. We are in close proximity to the remarkable 300-square mile Mobile-Tensaw delta, to the National Wetlands Research Center, and to a number of researchers active in conservation and restoration of aquatic and wetland habitats. This symposium is intended to highlight several of the key issues and relevant considerations which must be factored in to planning and implementing wetland conservation and restoration goals. Interdisciplinary science is more than a buzzword in efforts to understand and manipulate natural and disturbed communities, respectively, as this lineup of speakers and their topics show. Integration of such varied disciplines as hydrology, plant biology, genetics, fire ecology and modeling—with a fiddler crab or two thrown in for zoological balance—provides the basis for the sound science which can advance efforts to address the critical ecological and biological issues in aquatic and wetland habitats.

- 5 MIDDLETON, BETH A.
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Hydrologic and Disturbance Regimes in Wetlands: Restoring the Natural Balance

Without the re-incorporation of hydrologic and disturbance regimes that resemble those originally associated with the system, it is unlikely that restoration can bring about self-sustaining wetlands. Recently, the importance of reestablishing more natural hydrologic and disturbance regimes has been recognized in the restoration of types of wetlands in North America, Europe and Australia including flood pulsed riverine wetlands, tidally pulsed salt marshes and mangrove swamps, as well as northern peatlands and sedge meadows. The role of disturbance is not as widely accepted, but undoubtedly, periodic fire, herbivory or woody debris deposition can be important. The inability of the system to resume successional dynamics after disturbance is an indicator of failed restoration. Depending on regional climatic factors, water level fluctuation can be crucial in maintaining both animal and plant populations because of the constraints set by their early life history. A specific example will be described to demonstrate the importance of flood pulsing in the regeneration dynamics of *Taxodium distichum* swamps. The species of these swamps do not regenerate without winter to summer changes in water level because of the narrow environmental requirements of their early life history. Seed dispersal is tied to high pulses of water in winter, which move aquatically dispersed seeds to elevations that will dry during the summer season. Seeds germinate in moist, well aerated conditions but die if they become reflooded during the growing season following dispersal and germination. Sapling and adult stages of species are typically more tolerant of flooding than those in earlier life history stages, but have lower levels of production in flooded environments. The problems created by the worldwide alteration of waterways for development (transportation, farming, urbanization) have created hydrologic settings that are impacting not only our ability to restore wetlands, but also to maintain nature conservation reserves.

- 6 PROFFITT, ED^{*1}, TRAVIS, STEVE¹, EDWARDS, KEITH², CHIASSON, REBECCA³ and OWENS, ALAINA³

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Population and Community Ecology Analyses of Restored Salt Marshes

Population and community level studies are critical in determining functional success of ecological restorations. In saline areas, unvegetated flats created from dredged sediment are colonized by the marsh grass *Spartina alterniflora* initially via rafting and in later years by clonal growth and seed set, and by the annual pickleweed *Salicornia bigelovii*. Genetic and clonal diversity of *S. alterniflora* increases over time for a number of years and then decreases probably due to selection and genet-genet competition. *S. alterniflora* colonizes throughout a large elevation range, grows faster at lower elevations, and has some genets that are better adapted to higher elevation than others. Experiments indicate that burrowing by the fiddler crab *Uca* sp increases *S. alterniflora* growth, and crab densities are greater in grassed areas suggesting mutual benefit. *S. alterniflora* excludes *S. bigelovii* apparently by competition for light, but *S. alterniflora* also serves to facilitate recruitment by certain other plants. At higher elevations succession leads to dominance by high marsh grasses and woody plants such as *Baccharis halimifolia* and *Iva frutescens*, and high densities of the annual *Aster subulatus*. Preliminary experimental burn studies suggest that fire may not be an effective control technique for *I. frutescens* adults. There has also been limited colonization of one site by the invasive exotic saltcedar (*Tamarix gallica*) which may become a problem in the future. Soil organic matter increased from <5 to about 20 % over 20 years. These studies show that development of saline marsh communities that are similar in vegetative composition to reference marshes can occur on dredged sediment sites, but that dominance by woody species, and invasion by exotics such as saltcedar, may also occur at some elevations or under certain hydrologic conditions.

- 7 TWILLEY, ROBERT
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Conceptual Ecological Models for Planning and Evaluating the Louisiana Costal Area Ecosystem Restoration Plan

Louisiana is experiencing the most critical coastal wetland erosion and land loss problem in the United States. There are many causes for this loss but reductions in freshwater and sediment inputs have been identified as key factors. The Louisiana Coastal Area (LCA) Comprehensive Ecosystem Restoration study was established to develop a conceptual framework to focus an intense effort to rehabilitate this degrading coastal zone. The study includes four major tasks that are in various stages of research and development including: 1) develop 'Conceptual Ecological Models' that can be used to integrate ecological needs and opportunity with engineering designs that can provide the most benefit to coastal Louisiana; 2) Evaluate accurate rates of wetland loss and carry those forward to describe the most likely without project future; 3) Establish broad quantitative goals and objectives for restoring coastal wetlands and barrier islands based on the succession of geomorphic and ecological systems; 4) Develop large-scale project features and measures related to restoring the large-scale geomorphic and hydrologic processes that would lead to rehabilitation of a coastal delta. Restoration is predicated on an understanding of ecosystem succession; and ecosystem trajectories require causal linkages between disturbances, ecological effects, and

ecosystem response. A modeling program has been developed that is a hybrid of hydrodynamic and ecological simulations that project ecosystem attributes. This science support system is used to evaluate benefits of different alternatives as part of the comprehensive restoration plan. The development of this framework has the purpose of contributing to an adaptive management protocol by establishing the use of hypothesis testing as part of the implementation plan. This requires a comprehensive monitoring program that can evaluate ecosystem response and also contribute to future simulation model development.

- 8 ZEDLER, JOY
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Wetland vegetation degradation and limits to restorability

Wetland plant communities are vulnerable to hydrological alterations and other types of disturbance, with the result that species richness declines. Botanists seek understanding of the species that are increasingly rare; ecologists ask whether or not lost diversity matters to ecosystem function, and restorationists ask if the patterns are reversible. Summarizing experience with Californian salt marshes and Wisconsin sedge meadows, I conclude that patterns of degradation can be predicted, that loss of species affects ecosystem function, and that the simplification of vegetation is not easily reversed. Attempts to retain species diversity in wetlands will likely require more than setting aside reserves and planning restoration projects. In addition, we will need new approaches for reestablishing diverse vegetation, a goal that will require experimentation at multiple scales. We will also need active efforts to retain the full list of native species in reserves and novel approaches for providing a diversity of species for use in reestablishment and restoration.

SYMPOSIA AND COLLOQUIA

TRANSGENIC CROPS: SCIENCE, POLICY, POLITICS

Sponsored by BSA Economic Botany, Genetics, Tropical Biology, Ecological, Physiological, and Systematics Sections

- 9 SPOONER, DAVID M.
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Transgenic crops: science, policy, politics

The plants we use for food and fiber today have resulted from centuries of selection from wild relatives, and more recently from plant breeding programs often involving traditional sexual crosses and long periods of recurrent selection. While these breeding methods have produced wonderfully successful products to benefit modern society, recent biotechnological tools have introduced novel methods to circumvent some inefficiencies of traditional breeding, and has allowed the incorporation of novel traits not possible before. The incorporation of some of these "transgenic" crops has been dramatic. In the United States alone, the use of transgenic crops has risen dramatically, and for some crops, like cotton and soybeans, more than half of the acreage is planted in transgenic crops. Other economically important transgenic crops include potato, tobacco and maize. Common genes transferred to transgenic crops include a gene

that kills insects when they eat the plant, a gene that confers herbicide resistance, a gene increasing the shelf life of fruits and vegetables, and a variety of disease resistance genes. There is considerable debate about the economic benefits and risks of the adoption of transgenic crops. Such debate varies from scientific concerns of transgene escape into non-transgenic crops or to native plants, to the definition of what constitutes transgenes of potential concern, to food safety. Debate also concerns social issues of consolidated control of the seed industry, reduction in the number of small family farms, to broader social and economic questions. Opinions are often highly polarized, and discussion is hindered by misinformation or distrust of alternative views. This symposium explores these topics from experts in a variety of fields ranging from ecology to policy, and in a variety of backgrounds from government to industry.

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Defining Biotechnology: Increasingly Important and Increasingly Difficult

For society to develop effective means for managing biotechnology, there must be a common understanding of what it is. Early definitions of "biotechnology" were quite broad; here, "traditional" is distinguished from "modern" biotechnology. The latter is equated with "genetic engineering," an extension and evolution of crop breeding, which is problematic to define. Many current definitions focus on "foreign genes" transferred into crops across "natural barriers." But viruses and bacteria regularly transfer "foreign genes" into plants, and "traditional" plant breeding techniques may effectively breach such "natural barriers." Thus, the preceding definitions might be unsuitable for society's need to effectively managing genetic engineering. Rather, if society wishes to reduce the inferred risks of transgenic crops without impeding crop improvement, a genetically-engineered crop might be defined as "one with recombinant DNA derived in part from DNA that was extracted from sources not sexually compatible with that crop, modified *in vitro*, and asexually reinserted by human-directed processes." This definition, explicitly derived from societal value judgements, attempts to describe in clear technical terms what products might be candidates for special managerial regimens (e.g., labeling). Importantly, the preceding definition is based on the "manufacturing process," rather than on the tangible properties of the ultimate product. Regulating a product based on the process used to create it presents significant inherent operational difficulties, such as developing and implementing practical means for reliably distinguishing such products from others. Monitoring and certifying crop production, handling, and processing may be a more effective approach than focusing detection technologies on the ultimate product. Should "genetically-engineered" products be labeled, it must be understood that, as with "organic foods," such designation does not necessarily reflect the attributes of the product but, rather, society's perceived need to regulate the production process.

- 11 HORSCH, ROBERT B.
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Development and Use of Transgenic Plants

In this year of the golden anniversary of the discovery of the double helical structure of DNA, applications derived from this discovery have changed and improved many aspects of our lives. In the early 1980's, advances in three separate technologies converged to make possible deliberate modifications of genes in plants: recombinant DNA, plant tissue culture, and Agrobacterium vectors. In January of 1983 I and my colleagues and two other groups of scientists reported suc-

cessful expression of an engineered gene in transgenic plant cells. Later that same year, we reported regeneration of fertile plants whose progeny showed normal, Mendelian inheritance of the newly introduced genes. In 1987 we conducted the first field tests of transgenic tomatoes with genes conferring tolerance to virus, insect or herbicide. A decade later, in 1996, the first commercial transgenic crops were introduced after regulatory review and approvals from FDA, USDA and EPA in the US, and a variety of other regulatory agencies around the world. As a result of strong demand from farmers for these traits, last year, more than 145 million acres were planted with transgenic crops by almost six million farmers in 16 countries. In parallel with the development and use of transgenic traits in agriculture, molecular biology and transgenic technology has revolutionized the studies of plant science, genetics, biochemistry, physiology, ecology and evolution, and every major plant science research institution in the world uses molecular techniques to better understand plant biology. Transgenic plants have also served as a vehicle to open broader public debate about a host of issues ranging from food safety to the sustainability of agriculture to stewardship of the environment to global trade and governance. I will briefly review the science behind transgenic plant technologies and highlight some of their uses as a foundation for the broader discussion.

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Transgenic maize in Mexico: risks and reality

Mexico is a center of origin for several crops, and among these, maize plays an extremely important biological, economic, and cultural role in the country. More than 60 landraces of creole (locally adapted varieties) have been recognized in Mexico, and the southern part of country harbors wild relatives of maize. The environmental release of transgenic corn in Mexico could involve the occurrence of gene flow among genetically modified individuals and local varieties or wild relatives. There has been controversial evidence for the presence of transgenic constructions of maize in local populations in Oaxaca, Mexico. The National Institute of Ecology (INE) and the National Commission for the Knowledge and Use of Biodiversity (CONABIO) are involved in research to corroborate or refute claims of the presence of transgenic maize in Mexico. Ears of corn have been collected from several localities where transgenic bulked samples had been reported, and from other localities in the region. ELISA, PCR and Southern blot tests were performed on individual seedlings. To date, our results confirm the presence of transgenic sequences but further studies are being conducted for more detailed corroboration and to establish the particular events of transformation. Traditional agricultural practices, such as open exchange of seeds among farmers, are still common in regions of high maize diversity, and have contributed in the past to maintain and enhance this diversity. The same practices, however, could make it difficult to prevent or control transgenic maize from spreading into traditional landraces. The possible consequences of gene flow still have to be evaluated according to the introduced gene and the particular environment where different biological and cultural interactions occur.

- 13 PAARLBERG, ROBERT L.
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The International Policy Struggle Over GM Crops

The future development of GM crops will depend heavily on the global regulatory environment. Will the international regulation of GM crops in areas such as food safety, biosafety, trade, and intellectual property rights be permissive toward this new technology (e.g., similar to United States regulations) or highly precautionary (e.g.,

in Europe)? Increasingly, it seems that a more precautionary European regulatory approach will become the internationally norm. This precautionary approach is spreading into the nations of the developing world through at least four different channels: intergovernmental organizations (which tend to be heavily influenced by Europe), international development assistance (where Europe is the largest donor region), European-based international non-governmental organizations (NGOs), and international food markets (where Europe is the biggest customer). These more precautionary EU-style policies will be seen by exporters of GM crops in the United States as a threat to the trade and the United States Government will be tempted to challenge Europe's restrictions on GM crops (including its continuing moratorium on new crop approvals and its looming regulations concerning traceability and labeling of GM foods and feeds) using the dispute settlement mechanisms of the World Trade Organization. The United States may win such a challenge legally in the WTO, yet still lose politically and commercially. The EU has no history of altering its internal food safety or environmental protection policies in response to a WTO challenge, and a trade-led U.S. challenge in the WTO might only harden world opinion against GM crops and foods. This would be an unfortunate outcome for poor farmers in developing countries who may need GM crop applications in the future to overcome the unique crop production constraints they face, from insect pests, disease, water stress, and low soil fertility.

- 14 RODEMEYER, MICHAEL
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Policy Implications of Transgenic Crop Gene Flow

Gene flow from transgenic plants has raised a number of environmental, economic and market issues that are generating political attention. Within Mexico, possible gene flow from illegally-planted GM corn has raised concerns about impacts on the genetic diversity of native maize varieties in a center of biological origin. Within the U.S., in the wake of the StarLink episode, gene drift from transgenic crops has raised concerns from organic growers, as well as from conventional farmers and grain processors who need to separate non-GM crops for export markets where GM varieties are not accepted. More recently, food manufacturers have raised concerns about potential gene flow to food crops from field trials of transgenic crops modified to produce pharmaceuticals. All of these issues are generating questions about the adequacy of the regulatory system and the potential economic liability associated with undesirable gene flow, as well as greater interest in gene flow management. The presentation will explore these and other policy implications of transgenic gene flow management.

- 15 SNOW, ALLISON
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A plant ecologist's view of genetically modified (GM) crops

Scientists have created genetically modified crops by moving genes from bacteria, viruses, and other organisms into food plants. From a scientific perspective, this method of altering crop plants has tremendous potential for improving agriculture, but it also has possible risks. In some ways, transgenic crops are similar to their predecessors, but in others are radically different. For example, engineered maize can be used to produce human vaccines or novel industrial chemicals. Also, transgenic crops that are commercialized in the USA may not be sanctioned in other countries, leading to political disputes. I will discuss these issues, general ecological benefits and risks of

transgenic crops, and highlights from my research on gene flow from crops to their wild and weedy relatives. Recent research has shown that gene flow from crop-to-crop and from crops to other species is much more common than was previously assumed. Surprisingly little is known about the consequences of gene flow (although the threat of "superweeds" is often mentioned by the media). Transgenes that confer resistance to herbicides, plant pests, and environmental stress have the greatest likelihood of causing environmental problems. Many GM traits are likely to be innocuous, and some could lead to more sustainable agricultural practices. Members of the public are eager to see results from independent scientists who are assessing the risks of GM crops. However, the biotechnology industry has only recently made much of an effort to address these concerns, and funding from federal agencies has been meager. Thus, there is a great need for academic researchers and others to become more involved in studying the ecological risks and benefits of GM crops. Likewise, it is crucial for molecular biologists, crop breeders, and industry to gain a better understanding of ecological and evolutionary questions about the safety of new generations of GM crops.

DATING IN THE 21ST CENTURY: THEORY AND REALITY IN FINDING A DATE FOR YOUR CLADE

Sponsored by: BSA Paleobotanical and Systematics Sections, and ASPT

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Dating in the 21st Century: Theory and Reality in Finding a Date for your Clade

The use of quantitative techniques to estimate ages of clades is becoming more common in evolutionary studies. Analytical methods and software applications for calculating ages have proliferated and become more sophisticated than earlier simplistic approaches that assume a constant molecular clock. The biological and historical questions being asked today are more diverse and interesting than simply "how old is my group?" The methods and software packages are relatively easy to use, but there are numerous theoretical and practical questions that must be considered before and after such analyses are conducted - and study of recently published literature shows that many studies have failed to do so. This full-day symposium is designed to focus in detail on the important theoretical and practical issues that must be understood, followed by a selection of case studies that employ different methods and assumptions, and use the resulting dates to address a variety of biological and historical questions. The symposium concludes with a period for general discussion.

- 17 DAVIS, CHARLES^{*}, BELL, CHARLES² and

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High latitude Tertiary migrations and Afroasian biogeography: Evidence from the tropical clade Malpighiaceae

Phylogenetic investigations of the angiosperm lineage Malpighiaceae suggest that amphiatlantic disjunctions between several New and Old World sister clades occurred at times starting in the Tertiary when Africa and South America were isolated from each other. Estimates of their divergence times argue against a previous connection in western Gondwana to explain their origin. Instead, fossil and phylogenetic evidence suggests that interchanges between these New and Old World sister groups may have occurred along high latitude migrational routes during times starting in the Eocene when climates supported tropical forests. Similar investigations in the malpighi clade, Acridocarpus, provide insight into diversification of Malpighiaceae within Africa. The aridification of Africa throughout the Tertiary is thought to have been a major factor in the extinction of many African humid-tropical lineages, and in the present-day disparity in species diversity between Africa and other tropical regions. This primarily geologically based model can be tested with independent phylogenetic evidence from widespread African plant groups containing both humid- and xeric-adapted species. Divergence-time estimates within the acridocarpoid clade, suggest that the initial divergence occurred between African and Southeast Asian lineages ~50 million years ago (mya), perhaps after a southward ancestral retreat from high-latitude tropical forests in response to intermittent Eocene cooling. Dispersion of Acridocarpus from Africa to Madagascar is inferred between ~50 and ~35 mya, when lowland humid tropical forest was nearly continuous between these landmasses. A single dispersal event within Acridocarpus is inferred from western Africa to eastern Africa between ~23 and ~17 mya, coincident with the widespread replacement of humid forests by savannas in eastern Africa. Although the spread of xeric environments resulted in the extinction of many African plant groups, our data suggest that for others it provided an opportunity for further diversification.

- 18 DOYLE, JAMES A.

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Tying fossils to molecular phylogenies: examples from Cretaceous basal angiosperms

Integrating fossils into cladograms of extant taxa based on molecular data and using them to date nodes requires careful attention to the concepts of crown group, stem lineage, and stem relative, and analysis of characters of the fossils as synapomorphies with extant clades. Synapomorphies found throughout a crown group provide only a minimum age of the stem lineage of the extant clade; a synapomorphy of an extant subgroup is needed to establish a minimum age for the crown group. When fossils have a mixture of crown-group synapomorphies and more plesiomorphic states, they can be identified as stem relatives, but they do not indicate that the crown group had not yet evolved. Among Cretaceous fossils related to Chloranthaceae (based on an analysis by Eklund, Doyle, and Herendeen), Barremian-Aptian fruits with tepals and *Asteropolis* pollen provide evidence for the stem lineage of *Hedyosmum* and a minimum age for the family, but not for crown-group *Hedyosmum*, which may be much younger, as suggested by molecular dating. The same is true for Turonian and Santonian tripartite androecia, which appear to represent stem relatives of *Chloranthus*. Cenomanian *Couperites* fruits with "Clavatipollenites" pollen are more equivocal, because they may be either nested within the family or stem relatives; they only provide a minimum age for the stem lineage. Barremian-Aptian monoporate tetrad pollen (*Walkeripollis*) can be associated with Winteraceae, but its finer sculpture and elliptical pores indicate it is a stem relative, providing a minimum age for Winteraceae plus Canellaceae; definite crown-group Winteraceae are younger. Barremian tricolporate pollen may represent either crown or stem eudicots; the first definite crown-group eudicots are Albian *Nelumbites* and *Sapindopsis*, representing the near-basal subgroup Proteales.

In this case, because of its dense record, dispersed tricolpate pollen may provide a maximum age for crown-group eudicots.

19 FOOTE, MICHAEL

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Evaluating discordances between molecular and paleontological divergence times

The fossil record is sufficiently incomplete that it cannot be read literally. It is not so defective, however, that any discrepancy between molecular and fossil divergence times can be attributed categorically to paleontological incompleteness. Rather, a postulated divergence time that disagrees with the known fossil record implies specific limits to the quality of the record. If the record, appropriately measured, is substantially more complete than required by a postulated divergence time, then the divergence time must be modified. There are at least two complementary approaches for comparing molecular and paleontological divergence times when the former are substantially older than the latter. (1) The implied gap in the fossil record and the minimum richness when the clade first appears in the record are combined with an assumed diversification model to estimate the number of species, and the sum of their durations, missing from the record. This constrains the lowest sampling probability that is reasonably compatible with the postulated divergence time. If the measured sampling probability of taxa that are preservationally similar to those in question falls at or below this constraint, then the divergence time can be accepted despite its conflict with the time of first fossil appearance. (2) The observed diversity history of a group, coupled with an empirical estimate of sampling probability, can be projected back, via an assumed diversification model, from the time of first fossil appearance of the group to the likely time of origin. The relative merits of these and other approaches have yet to be explored in detail, but any one of them is preferable to accepting molecular or paleontological dates uncritically.

20 FOREST, FELIX^{*1}, RUTSCHMANN, FRANK² and CRANE, PETER R.³

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Inferring molecular age estimates in the birch family (Betulaceae) using multiple calibration points and minimum age constraints

Studies using multiple calibration points from the fossil record to infer age estimates from DNA-based phylogenies are sparse. The extensive fossil record of the birch family (Betulaceae), both from extant and extinct genera, combined with the level of phylogenetic resolution, permits multiple calibration of a phylogenetic tree of Betulaceae based on nuclear ribosomal DNA sequences (5S spacers and internal transcribed spacers, ITS). We infer molecular age estimates using the nonparametric rate smoothing (NPRS) and penalized likelihood (PL) methods of Sanderson, calibrated using six unequivocal fossils from the fossil record of Betulaceae from five of the six genera of the family. We compare the molecular estimates obtained with NPRS as implemented in the software TreeEdit (Rambaut and Charleston) with estimates obtained with the software r8s of Sanderson (both NPRS and PL). A feature of r8s, which is not available when inferring molecular estimates with TreeEdit, is the possibility of imposing an age constraint on one or more nodes other than the one used as calibration point. For each of the six fossils, we calculate molecular estimates using the five other fossils as minimum age constraints. For the crown group of genera *Alnus*, *Betula*,

and *Corylus*, molecular estimates produced using NPRS are much younger than inferred from the fossil record. This appears to reflect differences in molecular rates of evolution among lineages. The use of the fossil record to set minimum age constraints permits a better estimate of deeper nodes in the family. In general, estimates obtained with PL are younger than those infer with NPRS, but still older than fossil-based estimates.

21 HUELSENBECK, JOHN

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Bayesian estimation of divergence time

Bayesian estimation of phylogeny suggests a natural way to estimate divergence times of clades: Inferences are based on the posterior probability distribution of divergence times conditional on the observations. The Bayesian approach also allows one to relax the molecular clock assumption, account for phylogenetic uncertainty (and uncertainty in other model parameters), and to accommodate uncertainty in the calibration times.

22 LAVIN, MATT^{*1}, WOJCIECHOWSKI, MARTIN F.²,

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MICHAEL J.⁴

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Timing and patterns of diversification in papilionoid legumes

With a rate of approximately $5\text{--}10 \times 10^{-10}$ substitutions per site per year, the plastid matK locus is rich in nucleotide sequence variation so as to resolve robust relationships, as well as estimate absolute divergence times for many deep branching clades within the legume family, Fabaceae. Eight time constraints derived from fossil evidence were incorporated in the rates analyses: a minimum age of the Fabaceae crown group at 60 Ma, a minimum age of the Cercideae, Mimosoideae and Papilionoideae crown clades at 55 Ma, a Cladistic crown group at 38 Ma, a Robinia stem clade at 34 Ma, an IR-lacking crown clade at 29 Ma, and a Tipuana stem clade at 8 Ma. As such, the ages of all major papilionoid subclades, including genistoids, dalbergioids, millettiod-phaseoloids, and hologalegina, occurred well before the end of the Eocene. In contrast to the major tropical papilionoid subclades, the most significant temperate legume radiation (the IR-lacking clade) began to rapidly diversify well after 30 Ma. Although a molecular clock is rejected by likelihood ratio tests, penalized likelihood and local molecular clock approaches yield results highly similar to that of a rate-constant model, especially for Papilionoideae. The greatest discrepancy among the different rate smoothing approaches was confined to the more basally branching lineages, including many subclades representing Mimosoideae and Caesalpinoideae, as well as a few of the most basally branching subclades within the papilionoid crown group. Younger ages for these subclades, by over 10 Ma, were estimated with a rate-constant model as compared to rate-smoothed models.

23 LUPIA, RICHARD^{*2}, WAGNER, PETER J.¹ and

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Using fossil distributions to calibrate phylogenies—an example using heterosporous ferns

Fossils have been used to date minimum divergence times for clades in order to estimate divergence between other clades and/or calculate rates of molecular evolution. Depending on the number of calibration points used and the inferred relationships (stem or node) between fossil(s) and extant taxa, results have been varied from overestimates to underestimates at odds with the observed fossil record. Recently, confidence intervals (CIs), probabilistic extensions to observed fossil ranges, have been employed in a molecular analysis to estimate true first occurrence and move beyond minimum divergence times. CIs on stratigraphic ranges might have the potential to improve estimates of divergence times, but require modification to account for assumptions underlying their use in calibration. For example, species CIs are most robust within taphonomically equivalent paleoenvironments from the same biogeographic units, but many phylogenies will incorporate (fossil) species that are widely distributed and must be correlated, usually by grouping global records into discrete intervals (typically epochs or ages) based on the geologic timescale. In this study, we demonstrate how confidence intervals may be used, discuss their pitfalls and examine their sensitivity to violations of assumptions. For a “best case” data set, we discuss a method for using the occurrence of fossils within discrete intervals to improve confidence limits.

24 MAGALLÓN, SUSANA^{*1} and SANDERSON,

MICHAEL

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Estimating the age of angiosperms using constraints from the fossil record

The effects on estimates of the age of the angiosperms of different genes, codon position partitions, single gene vs. concatenated datasets, and the inclusion of fossils as age constraints are examined. A phylogeny derived from ML analysis of two slowly evolving chloroplast genes is used as a backbone topology. Penalized Likelihood, a method that allows a range of modes for among-lineage rate of substitution, from a nearly clock-like behavior to a condition in which each branch is allowed its optimal substitution rate, is used to estimate ages. For each examined case, the optimal level of rate heterogeneity was determined through a data-driven cross validation, and applied in age estimations. Eight independent point estimates of the age of angiosperms were obtained from two different codon position partitions for each of four slowly evolving genes. Estimated ages span the earliest appearance of the clade in the fossil record, but are widely divergent. Minimum ages of some clades were obtained from a critical examination of the fossil record, and used to constrain the ages of nodes in the topology. Ages obtained using the constrained topology are also widely divergent, and nearly always older than those derived from unconstrained topologies. The interval of ages obtained from independent gene/partition datasets was compared with point estimates derived from concatenated datasets. In one case, the age estimated from the concatenated data set fell outside the interval derived from its independent component data sets. These results indicate that widely divergent age estimates can result from different uses of data, particularly regarding the inclusion of temporal con-

straints to topologies, and emphasize the need for further exploration of the effects of several relevant factors in estimating timing of lineage divergence.

25 MANOS, PS^{*1}, MANCHESTER, SM³, SOLTIS, PS², STONE, DE¹, SOLTIS, DE² and DILCHER, DL³

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Integrating fossil taxa in phylogenetic analysis: examples from the angiosperm family Juglandaceae

The rich Tertiary fossil record of Juglandaceae provides an unparalleled opportunity to examine various methodologies for incorporating fossils into phylogenetic analysis with modern taxa. Several issues, including relative support, methodologies for integrating morphological and molecular data, and, especially, the effects of missing data, were explored. Using five of the most complete fossils known for Juglandaceae, we investigated the effects of fragmentary taxa on morphological and morphological + DNA analyses with specific reference to: 1) placement of fossils; 2) influence of certain taxa, characters and character sets; and 3) combined analysis vs molecular scaffolding. For the five fossils, 51% of the morphological matrix was scored as missing, the least “fossilized” data coming from vegetative structures. Although the addition of fossils increased the number of most parsimonious trees, the strict consensus was well-resolved and bootstrap levels decreased only slightly. Overall, levels of homoplasy remained constant and fossils were placed within terminal clades of largely extant taxa. While these analyses aided in interpreting the position of extinct taxa, the topology of the eight modern genera was not significantly altered by the addition of fossils. Combined analysis with fossils scored as missing for DNA yielded three trees with moderate to high support throughout. Uncertainty was restricted to the position of *Cruciferae* and its relationship to *Pterocarya* and *Cyclocarya*. Various types of data exclusion showed that combined analysis with 22 floral characters alone retrieved similar topologies, whereas analyses with complete “fossilized” data (19 characters) placed fossils as unresolved lineages closer to the base of the tree. The use of DNA scaffolds (of various bootstrap constraints) + morphological data provided less robust results than combined analysis. Estimated node dates derived from multiple fossil calibration points will be discussed in the context of morphological innovation.

26 RENNER, SUSANNE S.

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A comparison of five approaches to dating when data are not clock-like

Likelihood ratio tests commonly show that substitution rates vary significantly across lineages. Available methods to obtain age estimates in the absence of clock-like nucleotide substitution are: (1) non-parametric rate smoothing (Sanderson 1997), using one fixed calibration point as implemented in TreeEdit (Rambaut and Charleston 2001); (2) local clocks, also using one calibration point at a time and implemented in Yang's PAML package (Yoder and Yang 2000); (3) a Bayesian approach that allows for simultaneous use of multiple age constraints, implemented in Thorne's program package (Thorne, Kishino, and Painter 1998); (4) penalized likelihood, allowing multiple simultaneous age constraints or fixed calibration points, implemented in r8s (Sanderson 2002); and (5) direct use of clock-enforced likelihood branch lengths, regardless of possible rate heterogeneity. This talk will address whether these approaches have a consistent effect on age estimates, using original fossil-calibrated sequence data sets for Araceae, Chloranthaceae, Gnetales, Melastomataceae, and Monimiaceae as test cases.

- 27 SAVOLAINEN, VINCENT^{*1}, CRANE, PETER¹,
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Ages of basal angiosperm clades: molecular and paleobotanical evidence

A matrix of 108 taxa and 11 genes from all three plastid, nuclear and mitochondrial plant genomes was used to evaluate the ages of basal angiosperm lineages. Using various combination of the data and multiple fossil-based calibration points, trees were made ultrametric with four different methods: PATH, nonparametric rate smoothing, penalized likelihood and bayesian inferences. Comparison between methods and 'molecules versus fossils' in dating phylogenies are discussed and synthesis for dating angiosperm lineages is proposed.

- 28 YODER, ANNE D.
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Testing island biogeographic models with molecular data

The mechanisms by which organisms move about the planet are a central focus of evolutionary biology. For those investigators interested in island biota, these questions can be particularly perplexing. It is often the case that the comparison of geological data and organismal natural history data appear to be in conflict. This situation is acutely true for the terrestrial mammals of Madagascar. Geological data tell us that Madagascar had reached its currently isolated position long before crown placentals appear in the fossil record. This begs the questions: when and how many times did terrestrial mammals colonize Madagascar? And how did they manage these colonizations, given that an immense water barrier stood in their way? Finding an answer to these questions is confounded by the fact that Madagascar has no terrestrial fossil record for the Tertiary. Thus, the resolution of these questions requires molecular phylogenetic techniques that permit age estimation of ancestral nodes. I will discuss maximum likelihood and Bayesian methods that allow for the relaxation of the molecular clock, and for the use of multiple calibration points. The application of these methods for testing competing biogeographic models for mammalian dispersal to Madagascar will be discussed.

SEX AND INDIVIDUALITY IN LICHENS: INTRODUCTION

Sponsored by: ABLS and BSA Bryological and Lichenological Section

- 29 LAWREY, JAMES D.
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Sex and individuality in lichens: Introduction

Lichens represent more or less mutualistic symbiotic associations of fungi (mycobionts) and photosynthetic organisms (photobionts) that exist in nature almost entirely as symbioses, only rarely as dissociated mycobionts and photobionts. In such tightly coevolved obligate associations, "individuals" can be viewed as symbiotic, consist-

ing always as associates linked together by physiological constraints. Once formed, then, lichen "symbiotic individuals" succeed or fail as composites, not isolated associates. The genetics of such individuals is still unclear, however. Recent studies indicate a lichen thallus can be a genetic mosaic since different portions can have different physiological behaviors, chemistries, or isozyme banding patterns. Many investigators assume that thallus heterogeneity, especially that evidenced by enzyme banding patterns, is caused by presence of more than one mycobiont genotype, perhaps even more than one species. These have been called "mechanical hybrids," mosaic lichen thalli formed by merger of several genetically distinct propagules. If this is true, it complicates an already complex concept of individuality. If a lichen thallus is made up of several, even dozens of mycobiont and/or photobiont genotypes, how is genetic variation partitioned within and between lichen populations? How does the breeding system of lichens contribute to this variation? How does partitioning lead to formation of new species? Our symposium speakers will explore some of these ideas and report results of recent research that sheds light on breeding systems and genetic individuality in lichens.

- 30 CRITTENDEN, P.D.*¹, DYER, P.S., SEYMOUR, F. A. and MURTAGH, G.J.
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Sex and individuality in lichen-forming fungi

What constitutes an individual in lichen-forming fungi? In the majority of lichen species the thallus is a clearly delimited entity and, for all intents and purposes, an individual. However, whether individual thalli comprise a single or a consortium of fungal genotypes remains largely unknown. Intra-species contacts within crustose lichen communities can sometimes result in either imperceptible coalescence or in visible barrages along their mutual frontier. To explore this phenomenon further we have attempted to run vegetative incompatibility tests between identical and different genotypes of lichen-forming fungi in axenic culture. We have also investigated individuality in lichens by DNA-fingerprinting spores derived from different ascocarps on the same thallus. Species under study include *Graphis scripta*, *Ochrolechia parella* and several species of *Cladonia* and *Buellia*. At the same time, comparison between spores derived from the same ascocarp has provided information on the breeding system involved in the fungal species. This has some bearing on individuality. Homothallism (selfing) could potentially yield clonal populations where coalescence of thalli would not modify the genetic status of the individual. Heterothallism (outbreeding) will potentially yield genetically more diverse populations in which coalescence of neighbouring thalli might be less frequent but in which mating could be promoted by the presence of multiple genotypes in "individuals".

- 31 DEPRIEST, PAULA T.¹, LUTZ, SUE¹ and LAWREY, JAMES D.*²

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Genetic analysis of individualism in *Umbilicaria* *mammulata*

There are many levels of individuals in any lichen association. In the simplest case, the lichen association contains an individual fungal and an individual algal symbiont. However, lichens may be far more complex, with clear evidence of parasites, parasymbionts, and even multiple algal individuals. Over thirty years ago, some lichenologists even proposed that multiple fungal individuals occur within individual lichen associations, accounting for patchy differences in chemical or allozymic phenotypes. We are reexamining one of these

cases, the lichen *Umbilicaria mammulata*, to test if we can detect patches with different allozymic phenotypes and link them with distinct DNA genotypes. Because the phenotypes and genotypes of the patches represent composites of algal and fungal genotypes that may be confounded by other parasites and parasymbionts, we are asking first if the symbiotic genotype (the composite genotypes of symbionts and perhaps other inhabitants) is spatially homogeneous within a lichen association. Later we will genetically identify and quantify the organisms within sample patches. By linking these thirty-year old observations with fine scale genotypic analysis, we hope to elucidate the complexity of interactions among the genetic individuals that make up this particular lichen association.

32 FAHSELT, DIANNE

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Populational variation in physiological features of photobionts

Populational variability has previously been observed with respect to several lichen characters, for example, interthalline differences are known in secondary products, as well as in isozymes and mycobiont base sequences. By inference other polymorphisms exist in lichens as well, some of these seemingly in the photobiont, as recent studies have shown that three years of selection on copper-enriched media, drew a strain of *Trebouxia erici* with demonstrated facility for tolerating high concentrations of copper from wild type populations. Several quantifiable photobiont features associated with copper tolerance pertain to carbon assimilation, including integrity of chlorophyll a, total amount of chlorophyll a, photosynthetic efficiency and capacity for growth. Tolerant strains of *T. erici* also exhibit higher carotenoid content than wild type, as well as greater dehydrogenase activity, as measured by a formazan test. The present study characterizes and quantifies these features and others in *Trebouxia* isolated from *Umbilicaria* populations growing under typical uncontaminated field conditions. The extent of natural photobiont variation in part reflects the virtual absence of sexual reproduction and sets limits for survival in the event of future exposure to heavy metal stress.

33 STOCKER-WÖRGÖTTER, ELFIE

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Are selected species of the genus *Neuropogon* composed of two different mycobionts?

*N*eupogon (Usneaceae) is a bipolar genus, with the majority of the 15 known species confined to Antarctic and Subantarctic regions. The growth forms of the thalli are fruticose, erect or pendulous. One of the most striking features of *Neuropogon* species is the yellow or green yellowish thallus surfaces that are variegated by black or purplish black bands. The banded yellow and black surfaces have been often interpreted as an adaptation to various light conditions, perhaps functioning as a sunscreen. However, our culture experiments of selected species demonstrated that the aposymbiotically grown mycobionts were also composed of bright and dark bands. Furthermore, exposure to various light conditions did not affect the color of the isolated fungi. We were able to separate the bright and dark parts of the mycelia. When grown separately, they developed mycelia with two different growth forms. It became obvious that two different fungi are probably involved in the thallus formation of the tested *Neuropogon* species. After several months of incubation, the "bright yellow" mycobiont of *N. sulphureus* produced considerable quantities of usnic acid, whereas the "dark" fungus did not form either depsidones or usnic acid. DNA-analysis (ITS rDNA) showed that the two isolated fungi are not closely related. Therefore, the possibility

exists that the "second" mycobiont is an acid-deficient chemotype. In general, our experimental studies indicate that species of the genus *Neuropogon* have more than one fungal genotype. This conclusion certainly obscures the concept of individuality of some lichen genera.

METHOD AND MYTHS ABOUT CONDUCTING RESEARCH IN BOTANY EDUCATION

Sponsored by: BSA Teaching Section, McGraw Hill Higher Education

34 SUNDBERG, MARSHALL D.*¹ and WANDERSEE, JAMES H.²

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Botany Education Research and Botanical Research: Some Important Differences and Similarities

Botanists often harbor myths about the methods and the quality of botany education research. Perhaps this is because the nature, methods, standards, and limits of doing research on human subjects may differ markedly in some respects from those for the plant sciences. This symposium focuses on several important differences in research methodologies, and it exposes a number of prevailing myths that may otherwise impede progress, devalue, and discourage application of the botany education research base. Using the lens of *Botany for the Next Millennium* (BSA, 1995), we assume that the aim of research studies in botany education is to improve instruction—so that botanical learning is demonstrably enhanced and a whole-plant perspective is ultimately advanced. We claim that botany instruction and its effects on student learning can be studied scientifically and that science educators are scientists. Where trustworthy findings have been applied, research in botany education has already contributed, and will continue to contribute to improved learner understanding of fundamental botanical concepts and principles, while preventing or addressing potential misconceptions. Salient evidence and exemplars can be provided. Given that we know much more about *How People Learn* (2000, National Research Council) than we did just a few decades ago, it seems paradoxical to us that the contributions of botany education research are still rarely evident in texts, laboratories, presentations, discussions, or course design. We are reminded that: ?The common call for more effective teaching is one that every botanist can and must answer? (BSA, 1995).

35 MOORE, RANDY

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Standards of evidence applied to botany education research

During the past 16 years, more than 100 botany-related manuscripts have been submitted for publication in *The American Biology Teacher*. The most important features cited by reviewers for publication of these manuscripts have been 1) evidence to support conclusions, 2) quality of writing, and 3) uniqueness of manuscript. Reviewers have been consistently biased against the presentation of alleged "good ideas" that are not accompanied by supporting evidence (e.g., that a proposed activity increases learning). These data and others will be discussed relative to the best strategies for publishing botany-related education articles.

36 NOVAK, JOSEPH D.

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The evidence that botany teaching is not the same as botany learning—and its implications

A research-based perspective of botany education shows that science teaching does not necessarily yield scientific understanding. This fact helps underscore the need for instruction that focuses on improving student learning. Great progress in understanding how humans learn has been made since I last taught college botany several decades ago. There have also been important advances in our understanding of the nature of knowledge and of knowledge creation. When combined with the explosive development of the Internet and associated communication technologies, we stand poised to make a significant improvement in educational practices—an advance at least as important as the invention of the printing press in 1460. There exists a huge gap between what we now know to improve learning and use of knowledge and the practices currently in place in most schools and colleges. There are promising projects in progress that may help to achieve accelerated gains. These include projects in schools at all educational levels, including projects in Columbia, Costa Rica, Italy, Spain, and the United States, and collaborative projects with corporate organizations and distance learning projects. Results to date have been encouraging and suggest we may be moving from the lag phase of educational innovation to a phase of exponential growth. However, antiquated assessment practices continue to plague both teachers and students. It is not easy to assess how a young mind is grasping new meanings and skills, especially in the traditional classroom setting. The result is that much of educational assessment captures little more than the student's acquisition of facts, problem solving algorithms, and concept definitions, with little attention to whether or how they are building powerful knowledge structures. However, new strategies for using and "scoring" other forms of assessment are being developed and some assistance from computer-aided assessment is likely in the future.

37 SUNDBERG, MARSHALL D^{*1} and WANDERSEE, JAMES H²

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Qualitative Research in Botanical Education is Quality Research

A common misconception about educational research, especially among scientists, is that qualitative assessment techniques are "softer" than quantitative research. That is, because the data are subjective and not amenable to statistical testing, they must be less reliable and less useful than quantitative scores. In fact, good qualitative assessment provides a much richer understanding of the complexity of student learning in the classroom. While quantitative research can provide "broad brushstrokes" by surveying large numbers of students, it is less useful in pinpointing the gaps, overgeneralizations, alternative conceptions, and confusions that impede scientific understanding. Open-ended qualitative research produces detailed information to "fill in between the brushstrokes." We will describe five methodologies of qualitative research, including: observation, clinical interviews, focus groups, concept mapping, and journal writing/minute papers and provide two examples of the use of qualitative research in botanical education. One study focused on specific gaps in students' understanding of photosynthesis and the other concentrated on basic concepts of plant cells, photosynthesis, and evolution. In each case valuable insights were gained into how students were learning - - or not.

38 SUNDBERG, MARSHALL D.¹ and WANDERSEE,

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A proposed research agenda for botany education

Because there is not enough time (or resources!) to conduct all the botany education research that BSA members would like, we agree with Ahlgren that "not having priorities is tantamount to saying that [our] research doesn't really matter much." (AAAS, 2002). We therefore propose a research agenda for BSA's Teaching Section—an agenda justified by recommendations from the recent science education research literature and from BSA's own *Botany for the Next Millennium* (1995). We therefore recommend: 1. shifting our research studies' relative emphasis from describing innovative teaching to documenting learning outcomes (AAAS, 2002); 2. focusing our research on teaching "the whole plant," and on botanical knowledge integration (BSA, 1995); 3. designing and conducting research studies that identify successful ways of infusing awareness of plants throughout the curriculum and enhancing public awareness of the fundamental importance of plants to society (BSA, 1995). 3. probing, analyzing, and addressing students' prior botanical knowledge and its effects on learning outcomes (NAS, 2000); 4. studying the effects of using various metacognitive (mental self-monitoring) strategies and tools (such as concept maps) on students' understanding and retention of botanical concepts and principles (NAS, 2000); 5. conducting some longitudinal and cross-level studies to assess how students' botanical understanding advances and how their knowledge base grows as they progress through a series of related botany courses (AAAS, 2002; NAS, 2000). 6. replicating promising research findings in many different labs and contexts, to see how generally valid they are—"in contrast to everyone choosing his own favorite-and perhaps unique-topics, activities, and measures" (AAAS, 2002). The implications of this proposed research agenda for the content and direction of BSA's proposed new journal of botany education will also be explored.

39 UNO, GORDON

Exemplary Studies in Botanical Education

The number of exemplary studies in botanical education is limited; these studies represent a very small subset of the much larger field of biological education. The dearth of botanical studies reflects the current trend of many biology departments to reduce or eliminate the study of plants within their programs, and to reduce the number of or eliminate botanists who might conduct such investigations. The lack of botany in biology labs is surprising because plants can be manipulated with little cause for concern about their welfare and because they are relatively inexpensive to grow, so it might be expected that biologists would use plants more frequently as the lab organisms of choice. The limited number of interesting, and well-known, plant labs has a negative effect on the number of pre-college experiences students have in botany, and this has many ramifications for the future of botany as a discipline. Many of the educational studies that have been conducted revolve around the successful botanical lab projects such as C-ferns and Fast Plants. These highly successful plant projects, which have had a major impact on the narrow field of botanical education, will be highlighted, and a discussion will be held about the importance of botany and botanical studies at the pre-college level. In addition, NSF programs that are possible sources of funding for educational studies dealing with plants and for botanical projects will be identified.

**STRUCTURAL AND FUNCTIONAL ADAPTATIONS
OF VASCULAR PLANTS TO WETLAND
ECOSYSTEMS**

Sponsor: BSA Developmental and Structural Section

- 40 SEAGO, JAMES L. JR.¹, EWERS, FRANK W.² and FRIEDMAN, WILLIAM^{*3}

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Structural and functional adaptations of vascular plants to wetland ecosystems

In keeping with the theme of the Mobile meetings, the speakers in this symposium take various approaches to their studies of wetland plants. From extinct to extant ferns and flowering plants, roots, rhizomes, stems, leaves, or reproductive parts of plants are examined by different speakers to elucidate various structural or functional adaptations of plants to both freshwater and saline wetlands. While some speakers present results of recent experimental analyses, others integrate sets of observations into a synthesis of ecological, evolutionary, or physiological considerations of wetland plants in these important ecosystems. The symposium concludes with a summary overview and open discussion by participants and audience.

- 41 ANGELES, GUILLERMO* and ORTEGA-

ESCALONA, FERNANDO

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Ecoanatomy of the secondary xylem of four mangrove species from the Gulf of Mexico

Anatomical characteristics of the secondary xylem of stems of *Avicennia germinans*, *Conocarpus erectus*, *Laguncularia racemosa*, and *Rhizophora mangle* were studied in the mangrove of La Mancha Lagoon (Veracruz, Mexico), along a gradient of salinity and flood levels. Vessel density and diameter were measured from samples taken at dbh, from three individual of each species, from each site. These parameters were chosen for their direct influence on the hydraulic properties of the xylem. Five sites with clear differences in topography, closeness to the beach, and greater influence of fresh water were chosen for this study. *C. erectus* grows only in two of the sites (tidal and non-tidal), so this species was considered separately. In *C. erectus*, significant differences in vessel diameter, but not in vessel density, were found between sites. For the other three species, *L. racemosa* showed the largest vessel diameters at every site, particularly at the most saline site. *A. germinans* and *R. mangle* did not differ significantly in vessel diameter at any site. For vessel density, *L. racemosa* showed the lowest values at every site. *A. germinans* and *R. mangle* did not differ significantly in vessel diameter, except at the hypersaline site, where the first attained its largest density. Both species showed a clear tendency to increase vessel density with salinity. In contrast, vessel diameter did not seem to be affected by salinity, except at the hypersaline site, where *L. racemosa* attained its largest diameter. Differences between sites for a species were often greater than differences between species at a given site. We are analyzing other anatomical characteristics such as vessel distribution, vessel and fiber length, wall thickness, and

intervessel pit apertures in other woody species associated with mangroves (lianas and shrubs) to find out how do they change in relation to salt concentration and flood level.

- 42 EWERS, FRANK W.

Michigan State University, Department of Plant Biology, East Lansing, MI, 48824

Structure and function of mangrove plants

Mangroves are taxonomically diverse associations of trees and shrubs that form the dominant vegetation in tidal, saline environments of tropical and subtropical ecosystems. Mangrove species have a number of morphological and anatomical features that have independently evolved in at least 16 families. Among these are floatable seeds, vivipary, large stilt roots and pneumatophores with aerenchyma, xeromorphic leaf features including salt glands, and xeromorphic xylem features including vessels that are relatively narrow, thick-walled, and densely distributed. The presumed adaptive significance of those features was admirably reviewed by Tomlinson in 1986 (*The Botany of Mangroves*, Cambridge University Press). Although there are about 54 mangrove species worldwide, most of the structure and function studies have been on *Rhizophora mangle*, *Avicennia marina* and *A. germinans* and there have been relatively few recent studies making quantitative structure and function comparisons between different mangrove species. Recent research suggests: (1) viviparous seeds of *Rhizophora* develop gelatinous fibers in their hypocotyl to re-orient the shoot and quickly raise the pumule, snorkel-like, above immediate tidal influence; (2) pneumatophores of *Avicennia* may possibly carry on low levels of photosynthesis in addition to providing aeration; (3) although roots filter much of the salt in the soil solution, considerable salt moves through the xylem sap up to vein ends in leaves, where it enters the symplast prior to secretion by salt glands of *Avicennia*; (4) in several mangrove species mature leaves thicken over time due to salt storage in the hypodermis; (5) the water transport and photosynthetic rates are fairly high in mangroves considering the degree of water stress that mangrove plants experience and (6) many quantitative morphological, anatomical and physiological features of mangrove roots, stems and leaves are highly plastic in response to the salinity and the depth and duration of flooding events under which the plants are grown.

- 43 FISHER, JACK B.

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Plant Adaptations to Wetlands: Summation of Talks

Highlights of each talk are reviewed. The structural and functional features that seem to be particular to plants in these habitats are noted. The degree to which structures, functions and habitat limitations can be correlated will indicate where adaptations are clearly demonstrated and where further research is needed.

- 44 LOPEZ-PORTILLO, JORGE* and PAREDES,
CLAUDIA
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Xylem transport physiology of mangroves

Tolerance to salinity (physiological dryness) results in different zonation patterns corresponding to salinity and flooding gradients, both in species-rich (Asian and Australian tropics) as well as in species-poor (New World tropics) mangals. We tested the hypothesis that a higher vulnerability to vessel cavitation would be found in species that are less tolerant to salinity. We measured xylem hydraulic conductivity before and after embolisms were removed from stem segments with iso-osmotic water under pressure in three mangroves (*Laguncularia racemosa*, *Avicennia germinans* and *Conocarpus erectus*). We also used published data on *Rhizophora mangle* to compare among the four species. In this respect, *Avicennia* and *Rhizophora* were less vulnerable to embolism than *Laguncularia* and *Conocarpus*: the first two lost 50% of their hydraulic conductivity at c.a. -6.2 MPa while the other two lost the same amount at c.a. -3.8 MPa. We also compared, during the rainy season, the hydraulic specific conductivity and leaf specific conductivity of pairs of individuals of *Avicennia* and *Conocarpus* (these two species representing salinity tolerance extremes) in an ecotone where their branches touched. Paired t-tests indicated that values in specific conductivity, leaf specific conductivity and water potential of *Conocarpus* were significantly higher than those of *Avicennia*, but no significant differences were found in percent loss conductivity, which was around 40%. Extremes in tolerance of salinity, low water potentials, and resistance to embolism may make *Avicennia* competitive at the more saline sites, except when salinity is so great that only halophytic shrubs such as the leaf succulent *Batis maritima* can persist. At the fresh water sites, species like *Conocarpus* and *Laguncularia*, with higher specific conductivity but lower resistance to embolism, may be most competitive.

- 45 MARICLE, BRIAN R.* and LEE, RAYMOND W.
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99164-4236

Oxygen transport through aerenchyma in *Spartina* (Poaceae)

Estuarine cordgrasses of the genus *Spartina* have the ability to develop extensive aerenchyma systems. Aerenchyma serves as an open passage that can ventilate submerged portions of the plant with atmospheric oxygen as well as lower metabolic demands by reducing cell numbers. These physiological benefits help to make *Spartina* grasses formidable invasive species in areas where they have been introduced. Internal oxygen transport was investigated in *S. alterniflora*, *S. anglica*, *S. densiflora*, and *S. patens* maintained in greenhouse experiments under various waterlogging and salinity conditions. Oxygen transport capacities provided information about the plants' oxygen demands and the overall effectiveness of their aerenchyma systems. Plants kept under waterlogged soil conditions transported slightly more oxygen than plants maintained under drained conditions. Increasing salinity had no effect on oxygen transport in any species. *S. anglica* plants were able to transport substantial oxygen to their roots, while *S. alterniflora* plants transported much less. Little or no oxygen transport was detected in *S. patens* or *S. densiflora* plants under the same conditions. Relative rates of oxygen transport between species and treatments were correlated to enzymatic activities diagnostic of aerobic and anaerobic metabolism. Oxygen transport abilities are crucial for survival on anoxic estuarine mudflats. Different rates of oxygen transport can therefore help explain estuarine zonation patterns and are likely to be the reason introduced *Spartina* can successfully invade mudflats that are inhospitable to native species.

- 46 RICHARDS, JENNIFER H.
Dept. of Biological Sciences, Florida International University, Miami, FL
33199

Understanding population structure in large, perennial, wind-pollinated wetland species: Insights from sawgrass (*Cladium jamaicense*)

Marshes are frequently dominated by a single species that is a large, perennial, wind-pollinated monocotyledon. Examples include *Phragmites australis*, *Spartina alterniflora*, *Typha* spp., *Juncus* spp., and *Cladium jamaicense*. These species reproduce both vegetatively and sexually. The interplay between these two modes of reproduction structures populations in these wetlands; this dynamic, however, is often unknown. Thus, these vast stands may consist of a single individual or a multitude; if a multitude, individual genotypes can be dispersed evenly or as clumps in different sized patches. Answers to questions about population structure will influence management and restoration decisions, such as where to harvest plants for restoration, what type of population structure should be restored, and how plant reproduction might respond to or facilitate restoration. Current research on sawgrass, *Cladium jamaicense*, in the Everglades of south Florida answers some of these questions. Sawgrass is sympodial. A rootless rhizome grows horizontally, then turns vertically and begins to produce adventitious roots and photosynthetic leaves in a rosette. Buds in the axils of these leaves grow out as rhizomes or short lateral branches; rhizome production is the predominant mode of vegetative reproduction. Allozyme studies of 18 Everglades populations of sawgrass showed that sites had an average of 4.9 genotypes per site and 79% of the m² quadrats sampled had > 1 genotype. This suggests that seed reproduction occurs and there is some outcrossing. The upright shoot terminates in an inflorescence. In south Florida plants flower from late April to early June. Inflorescences can have thousands of 2-flowered spikelets; typically spikelets mature a male flower, then a protogynous hermaphroditic flower, so spikelets pass through male, female, and male phases. Sawgrass is wind pollinated and self-compatible. Inflorescence synchronicity reduces within-inflorescence selfing. Data on population structure from sawgrass will be compared to that for dominant species of other marsh ecosystems.

- 47 SCHNEIDER, HARALD*¹ and PRYER, KATHLEEN²
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Convergent evolution in vegetative and reproductive characters of aquatic vascular plants

Aquatic vascular plants provide numerous examples of convergent evolution of similar structures in non-closely related groups. Although these similarities are usually explained as being in response to similar functional constraints, very little is actually known about the evolutionary processes that cause these convergences. These structural similarities include body plan simplification, dwarfism, and innovations such as aerenchyma. A phylogenetic framework is applied to explore these and other morphological and physiological similarities that appear to be a consequence of terrestrial plant lineages colonizing aquatic habitats. As an example of convergent evolution in vegetative morphology, we show evidence for similar heterochronic shifts and body plan reduction events in heterosporous ferns (Salviniales) and duckweeds (Lemnaceae) – two distantly related lineages that have adapted to a floating growth form. The comparative study of convergence in reproductive biology provides “windows” for us to better understand the evolutionary history of particular structures that are obscured by the extinction of intermediate taxa in at least one of the groups under study. Here we use this approach to gain

new insight into the enigmatic evolution of seeds. Heterospory evolved independently several times in land plants, but it is thought that each occurrence likely coincided with the colonization of freshwater habitats by homosporous terrestrial vascular plants such as lycophytes, ferns, and the ancestors of seed plants. Extant heterosporous plants display different degrees of heterospory, such as simple heterospory (heterosporous lycophytes), extreme heterospory (heterosporous ferns), and seeds (seed plants). It has been proposed that extreme heterospory was an important precursor in the evolution of the seed habit. This condition is present only in living heterosporous ferns allowing us to study all aspects of the reproductive biology associated with extreme heterospory. We propose the use of heterosporous ferns as a model to explore functional and developmental constraints in which the seed habit evolved.

48 SEAGO, JAMES L., JR.

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Structural Adaptations of Roots and Rhizomes to Wetland Habitats

Roots and rhizomes of wetland plants have no unique characteristic that may be specifically used to associate them with wetlands. Indeed, while their roots have an endodermis as the inner layer of the cortex, the cortex may or may not be aerenchymatous, and a hypodermis with or without an exodermis may underlie the epidermis. In some monocotyledons, an exodermis is multiseriate and may be the outer layer of the root if the epidermis has sloughed off. There is greater variation in the root hypodermis in monocotyledons than in dicotyledons which typically have an exodermis, when present, with Caspary bands and suberin lamellae only. An interesting feature of rhizomes is that monocotyledonous plants either have no endodermis or have an endodermis surrounding a central core of vascular bundles with or without an exodermis in the outer cortex. Rhizomes, upright stems, and even petioles of dicotyledonous plants, especially certain invasive species which will be emphasized, may have an endodermis around the entire stele, but an endodermis is usually around individual vascular bundles; dicots normally do not have an exodermis. Aerenchyma may or may not be present in underwater shoots; when present, it may not resemble that of roots of a given species.

49 SORRELL, BRIAN K.

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Fresh Perspectives on the Functional Significance of Aerenchyma in Wetland Plants

Aerenchyma in wetland plants is a gas-phase pathway that allows oxygen to be delivered to submerged tissues in oxygen-depleted environments, enhancing survival and growth in a habitat that is hostile to aerobic life. This talk critically re-examines both the benefits of aerenchymatous oxygen transport for plant aerobic metabolism and rhizosphere oxidation, and the costs and disadvantages incurred by aerenchyma development. Diffusion is the sole gas transport mechanism in the vast majority of plants that develop aerenchymatous tissues for aeration. Fluxes of oxygen in aerenchyma are controlled by tissue porosities, permeabilities and respiratory oxygen demands within and outside the plant. Key under-appreciated principles of aeration are that: (a) Roots do not simply release oxygen that is surplus to their own requirements; rather, root function is enhanced by release patterns that allow some sub-lethal internal hypoxia in exchange for rhizosphere oxidation and lateral branching. (b) Internal aerenchyma does not exist "in excess" of plant oxygen requirements, because the amount of underground biomass that can be sustained is intimately

linked to the amount of oxygen transported. In some plants, diffusion is enhanced by pressurised gas flows. Two distinct pressurised flow mechanisms exist, viz. (a) a physical pressurisation driven by the vapour pressure deficit in some floating-leaved and emergent species, and (b) a metabolic pressurisation driven by internal accumulation of photosynthetically-generated oxygen in some submerged aquatic plants. In both cases, pressurised flows allow growth in deeper water and maintenance of greater underground biomass than possible using diffusion alone, by elevating internal oxygen concentrations and root oxygen release rates. The major cost of aerenchyma development is the mechanical fragility of porous tissues, which makes shoots vulnerable to buckling and collapse, and roots vulnerable to compression and crushing. Energetic costs related to reduced respiratory and storage capacity have also been suggested, but need further investigation.

50 STEVENS, KJ*, PETERSON, RL and READER, RJ

Department of Botany, University of Guelph, Guelph, Ontario, Canada, N1G 2W1

Root system characteristics and plant performance under conditions of flooding and drought: can predictive models of wetland plant response be constructed using root system characteristics?

The importance of wetland ecosystems is increasingly being realized but so too is the considerable threat to these areas posed by altered hydrological regimes resulting from Global Climate Change and increased development. Understanding how wetland ecosystems respond to changes in hydrology will be crucial to their management and conservation; yet there are few predictive models of wetland plant community response to flooding and drought and those that exist are limited. We contend that this reflects an incomplete understanding of how wetland plants respond to flooding and drought and which plant traits confer flooding and/or drought tolerance. To address this we asked three questions: 1-How do root systems respond to flooding and drought? 2-How are anatomical and morphological characteristics related to plant performance? 3-How well can plant performance be predicted using root system characteristics? Based on current understanding, several predictions were established regarding root system responses to flooding and drought and which traits would be related to performance. Morphological and anatomical responses of root systems of 17 wetland species to flooding and drought were quantified and the relationship between the responses and performance determined. Many of the predicted responses were not realized nor were the predicted relationships between root system characteristics and performance. Plant responses and the relationship between root system traits and performance varied considerably among levels of water availability, among genera and among genera at each level of water availability; few generalizations could be made regarding plant responses and plant performance. Consequently, it was not possible to establish models of plant response to flooding and drought based on root system traits that would apply to a range of wetland species. This implies that responses of root systems to flooding and drought and their relationship to plant performance may be considerably more complex than currently thought.

- 51 STOCKEY, RUTH A.
Department of Biological Sciences, University of Alberta, Edmonton AB, Canada

Structural and functional adaptations of fossil vascular plants to wetland ecosystems

Aquatic vascular plants in the fossil record show numerous structural adaptations to life in the water. Fossil sites in the Upper Cretaceous and Paleocene of Alberta and the Middle Eocene of British Columbia show excellent preservation of floating and emergent angiosperms and pteridophytes. Primary aerenchymatous tissues, reduced vascular systems, and heterophyllly are all common structural characters. Secondary tissues that form aerenchyma (spongy phellem) are similar to those present in extant aquatic Lythraceae. Seeds with an integumentary palisade of interlocking sclereids and opercula for germination are common in aquatics from the Princeton chert. Seeds that produce mucilage on contact with water like those in extant lasioid Araceae are also known from this locality. Floating rosettes of leaves are known for three different groups of angiosperms at the Cardston and Dinosaur Park localities in Alberta. Distinct apical pores on leaves, epidermal trichomes and highly branched underwater roots and leaves are present in several taxa. Sporocarps containing the sori of heterosporous aquatic ferns are present in hydropteridaleans. The excellent preservation of delicate tissues in these localities from western North America not only has helped to reconstruct the paleoenvironments but shows that similar structural adaptations to those of living plants originated at least 70 million years ago.

BIOGEOGRAPHY OF ALPINE PLANTS ON THE LARGE SCALE: CURRENT STAGE AND PROSPECTS

ASPT Colloquium

- 52 NYFFELER, RETO
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Biogeography of Alpine Plants on the Large Scale: Current Stage and Prospects

The alpine life zone is characterized by a suite of climatic factors and harbors a unique spectrum of plant growth forms. At high altitudes above the thermal treeline, this life zone is fragmented into numerous more or less isolated regions, that are nested within various regional floras. There is a wide field for studies on the historical biogeography of alpine taxa. Investigations into the composition and origin of the diverse alpine floras of the world have been conducted for more than a century. Current consensus is that they consist of a mixture of ancestral elements, immigrants from other alpine areas, and some recently evolved lineages. The objective of the present colloquium is to provide an overview of the current stage in biogeographical studies that employ rigorous phylogenetic methodology and focus on plant groups well-represented in alpine zones. Knowledge of the relationships among alpine species and their lowland relatives provides the basis for addressing questions concerning the historical structuring and diversification of alpine floras. Ultimately, we would like to be able to compare different mountain systems in terms of their similarities and differences in the composition and formation of their alpine floras. The introduction to this colloquium will focus on a few examples from the floras of the European Alps and from the South-

ern Alps of New Zealand. Possible approaches to investigate large scale biogeographical patterns and their prospects for providing insights into the formation of alpine floras will be discussed.

- 53 ARROYO, MARY T.*¹, HERNÁNDEZ, CLAUDIA¹,

PÉREZ, FERNANDA¹ and ZARUCCHI, JAMES²

¹Millennium Center for Advanced Studies in Ecology and Research on Biodiversity (CMEB), Facultad de Ciencias, Universidad de Chile, Casilla 653, Santiago.; ²Missouri Botanical Garden, P.O. Box 299, St. Louis, MO 63166-0299, USA.

The South America Andes: a fertile ground for molecular evolutionary studies

The South America Andes traverses some 65 degrees of latitude along the western side of the continent, passing from tropical to subantarctic latitudes. This mountain corridor contains perhaps the world's richest above-treeline (or its phytogeographic equivalent) vascular flora, with high phylogenetic diversity. Occurring in a habitat of recent origin, the high elevation Andean flora constitutes a fertile ground for molecular evolutionary studies. The richness of the high Andean flora results from lineage garnering from lower elevations, rapid in situ radiation and possibly long-distance dispersal. A major aridity barrier centered in the northern Chilean Andes is paralleled by latitudinal distribution gaps and the evolution of many endemic genera, while appearance of the mediterranean-type climate flora in central Chile in the Tertiary has paved the way for strong upward migration. Targeted phylogenetic studies in the Andes have the potential to solve major biogeographical and evolutionary questions, such as the rapidity with which life-forms may change, the timing of aridity in the northern Chilean Andes, the effects of altitudinal turnover in pollinator composition and abundance on floral morphology, whether the rigorous high elevation habitat selects for breeding systems determining high levels of genetic variation, and whether the latter per se has provoked rapid evolutionary radiation. Molecular phylogenies for *Chaetanthera* (Asteraceae), *Schizanthus* (Solanaceae) and *Tropaeolum* (Tropaeolaceae) are presently being undertaken in our laboratory with some of these questions in mind. Research financed by FONDECYT-Chile 10980705 and 1020956 (MKA), FONDECYT-Chile 2010023 (FP) and Chilean Millennium Scientific Initiative, P99-103-F ICM

- 54 BELL, CHARLES

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Phylogeny and biogeography of Valerianaceae (Dipsacales), with special reference to the alpine South American species

Valerianaceae is a relatively small (ca. 300+ species), but morphologically diverse, lineage of angiosperms. Although the species of Valerianaceae are primarily distributed in the Northern Hemisphere, and our data imply that Valerianaceae diversified initially within Asia (the Himalayan *Patrinia* and *Nardostachys* falling at the base of the clade), the center of species diversity for the group is in the Andes of South America with as many as 150 species restricted to that area, especially in high alpine areas. Previous hypotheses concerning the origination of the South American Valerianaceae have suggested that as many as three colonization events may have occurred and subsequently led to the diversity we see there today. However DNA sequence data from both the chloroplast and nuclear genomes suggest that the South American Valerianaceae form a clade, with its closest relatives in North and Central America. In order to estimate divergence times, fossil data from Valerianaceae and related taxa (other Dipsacales) were used to estimate divergence times using a variety of methodologies and previously published datasets.

Estimated dates for the common ancestor of the South American taxa indicate a rapid diversification of this clade.

55 HOOT, SARA B.

Department of Biological Sciences, University of Wisconsin, Milwaukee, WI 53201

Phylogeny and biogeography of alpine Anemone species

While *Anemone* species are generally found in cooler habitats, few of them actually occur in alpine regions. Employing combined nuclear (ITS) and chloroplast (*atp-rbcL* spacer) data, the phylogeny of *Anemone* and related genera is used to explore the origins of the alpine taxa. The alpine habit appears to have arisen at least four times in evolutionary history. *Baneoudia*, a compact alpine species found in South America, is the first branching taxon. Two alpine clades reflect possible Gondwanan distributions. One of these clades consists of species from New Zealand (*A. tenuicaulis*), the Andes region of South America (*A. antucensis*), and the Northern Hemisphere (e.g., *A. richardsonii*, *A. trullifolia*, *A. obtusiloba*, *A. narcissiflora*). The other "Gondwanan" clade includes the alpine genus *Oreithales* of South America and various montane *Anemone* species from South America (e.g., *A. hepaticifolia*, *A. sellowii*, *A. helleborifolia*) and Tasmania (*A. crassifolia*). This latter clade is in turn sister to a clade consisting of anemones from South Africa and Mexico. The last remaining alpine clade (e.g., *A. drummondii*, *A. lithophila*, *A. parviflora*) is more derived and has a geographical distribution within North America and Asia. While the alpine taxa frequently appear to have evolved from montane or lowland species, the opposite is not true; the alpine habit appears to be a terminal condition in extant *Anemone*. Many species of *Anemone* with a Gondwanan distribution (from New Zealand, Tasmania, and South America) are montane or alpine, raising some interesting questions related to their dispersal and distribution.

56 MADRIÑÁN, SANTIAGO

Laboratorio de Botánica y Sistemática, Universidad de los Andes, Apartado Aéreo 4976, Bogotá, DC, Colombia

Patterns and processes of Páramo plant diversification

Páramos are the tropical, high elevation, ecosystems of the northern Andes. Their flora is the richest of all high mountain ecosystems, and the great majority of vascular plant species found in the Páramos can be found nowhere else. The highest diversity of Páramo flora is found in Colombia where more than half of the total species are represented, and one third are endemic to this country. Generic affinities of the Páramo flora suggest a complex biogeographical history resulting from the *in situ* evolution of autochthonous tropical elements, and the immigration and further diversification of allochthonous south- or north-temperate elements. Although endemism at the level of named genera has been downplayed for the páramo flora, molecular phylogenies from original studies of three widespread genera, *Hypericum*, *Berberis*, and *Oreobolus*, as well as from other recently published works reveal the existence of several endemic, highly diverse clades. In some cases, previous biogeographic hypothesis relating to the direction of the migration paths have been overturned. The possibility of inferring divergence times from molecular phylogenies, together with geological and orogenic data, is used to evaluate hypotheses of range expansion, and distinguish between vicariance and dispersal events. Furthermore, observed low levels of sequence variation coupled with high species diversity within several Páramo clades, suggest multiple radiation events, the explanations of which are beginning to be explored. As more phylogenetic studies of Páramo

plants become available, it will be possible to propose a detailed biogeographical history of the Páramos as a whole, as well as aiding in our understanding of the processes responsible for the evolution of their unique and diverse flora.

57 REE, RICHARD

University of British Columbia Botanical Garden, Vancouver, B.C. Canada

Morphological and phylogenetic analyses of sympatric species of *Pedicularis* (Orobanchaceae) in south-central China

Pedicularis is a conspicuous component of the endemic alpine flora in south-central China, where it has diversified extensively since the mid-Tertiary. In this region species of *Pedicularis* commonly occur in sympatry. Ecological theory suggests that sympatric species should occupy different niches to alleviate competition, and should therefore be more divergent phenotypically and less closely related (on account of "phylogenetic niche conservatism") than expected under a null model of community assembly. In this study I test these hypotheses using a dataset of collections from 178 localities in south-central China representing 89 species of *Pedicularis*.

58 VON HAGEN, BERNHARD

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Causes for the rapid radiation of *Halenia* in neotropical mountain ranges

The distribution of species diversity of the widespread and predominantly alpine genus *Halenia* (Gentianaceae-Swertiaeinae) is very asymmetric between continents. Few species occur in Asia and North America, some in Central America and the majority of species in S America. A well supported molecular phylogenetic analysis and the application of a molecular clock approach revealed that *Halenia* originated in Asia and that the extensive South American radiation is secondary but very fast and started in the quaternary only. We also observed a cline of species diversity from many well separated and therefore older species in Colombia and Venezuela to only one species yet in northern Argentina and attribute this to the first immigration from the North via mountains of Central America. The explosive radiation of *Halenia* and other originally northern temperate plants, e. g. *Gentianella*, may be caused by the low competition of poorly adapted native plants in the geologically very young high Andes. Another possibility was that the nectary spurs present in *Halenia* acted as a key innovation promoting rapid speciation in the new environment of the pollinator-rich tropical and subtropical mountain ranges. These issues are discussed using mainly a novel lineage through time plot method.

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Evolution of the New Zealand alpine flora: origins, diversification and dispersal

The mountains of New Zealand provide a unique system in which to study the evolution of alpine plants. The contrast between a recent uplift of mountain habitats (5-2 MYA) and the diversity of the contemporary alpine flora has polarized hypotheses on the evolution of New Zealand's alpine plants; suggestions have ranged from origins in a low-

land flora with ancient histories in New Zealand to recent arrival by long distance dispersal. Molecular phylogenetic analyses are now available for numerous plant groups represented in the New Zealand mountains and these provide a means to investigate the evolution of this unique flora. Taken together these studies strongly suggest that many alpine plant groups arrived in New Zealand during the late Tertiary or more recently (correlated with the formation of alpine habitats). In addition it appears that New Zealand has been an important source of lineages for the mountain floras of Australia and New Guinea. The molecular data also suggest that the ecological and morphological diversity of many species-rich alpine plant groups has arisen since the latest Tertiary (correlated with both geological change and climatic fluctuations). Ongoing studies are using interdisciplinary approaches to investigate both pattern and process in the evolution of the New Zealand alpine flora.

BRYOLOGICAL AND LICHENOLOGICAL SECTION /ABLS

CONTRIBUTED PAPERS

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Elemental chemistry of *Xanthoparmelia scabrosa* on roads and sidewalks in New Zealand

Xanthoparmelia scabrosa is a foliose lichen that grows abundantly on sidewalks and pavement in New Zealand, which are considered inhospitable habitats for lichens. Samples were collected at five localities ranging from urban streets to very rural roads and analyzed for 22 chemical elements in order to determine elemental chemistry and to test hypotheses about tolerance mechanisms. Anthropogenic elements (Cr, Cu, Pb and Zn) decreased significantly from high to low pollution areas, while nutritional elements (K, P and S) increased. Samples from polluted sites contained 10% calcium, probably extracted from sidewalk surfaces. Sulfur was elevated at both polluted and clean sites, possibly due to pollution in the former site and higher levels of sulfur-containing scabrosin esters at the clean site. Elevated Se at the polluted sites might be due to increased levels of phytochelatins, which contain Se.

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Sporophyte anatomy and systematic relationships of *Xenothallus vulcaniculus* R. M. Schust
Xenothallus vulcaniculus

R. M. Schust. is a rare, endemic, simple thalloid liverwort, found in a few isolated localities in New Zealand. The genus was placed by its naming author in the Pallaviciniaceae, albeit with "some misgivings," based on 1) the presence of a central strand of thick-walled cells in the midrib of the trumpet-shaped, stipitate frond, 2) dorsally positioned gynoecia that are subtended by posterior lamellae, and 3) the formation of fleshy perigynia around the embryonic sporophytes. The most striking character of *X. vulcaniculus* is the prolific develop-

ment of small, yellowish, few-celled gemmae over the entire dorsal surface of the thallus. Mature sporophytes have never been observed. To investigate developmental patterns in this taxon, specimens collected on South Island in January 2002 were placed on vermiculite in an environmental chamber with a 12 hr photoperiod and 15° C temperature. After 3 months, three mature sporophytes were harvested for study. The seta is of the general type and nonarticulate. The capsule is short cylindric, and abruptly rounded at the apex, with a terminal nipple-like apical projection; the capsule wall is two-layered, with the cells of the outer layer much larger than those of the compressed inner layer. All radial walls of the outer cells are equally thickened. Capsule dehiscence occurs along 2 longitudinal slits, with the apex remaining intact. Elaters range from 135-165 µm in length, are 3- or 4-spiraled and are occasionally branched. The spores are 30-40 µm in diameter and possess a verrucate to cristate proximal face architecture that is reminiscent of *Jensenia* spores. These features of sporophyte anatomy support the alignment of *Xenothallus* with *Symphyogyna*.

- 62 DUFF, R. JOEL*¹, CHARGILL, CHRIS² and RENZAGLIA, KAREN³

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Hornwort Phylogeny and Classification Revisited

Hornworts are a distinctive group of early land plants. Although clearly a monophyletic group, taxonomic boundaries and interrelationships among hornwort species and genera remain confused. Existing classification schemes for the group are incongruent and conflicting generic concepts recognize from five to nine, totaling 12, genera. To assess the competing taxonomic hypotheses put forward for hornworts we obtained more than 30 sequences for the *rbcL* (chloroplast DNA) gene. Phylogenetic analyses strongly support hornworts as a monophyletic group consisting of two main clades. The first contains members typically placed in the genus *Anthoceros*, including *Folioceros*, while the second contains the remaining taxa. The second, larger clade includes two main lineages: *Phaeoceros* plus *Notothylas* and *Megaceros* plus *Dendroceros*. However, none of the well-recognized hornwort genera, except perhaps *Notothylas*, are monophyletic. The *Megaceros* clade contains two assemblages of species, one of which includes *Dendroceros canaliculatus* and the other *Phaeoceros coriaceus* and *P. hirticalyx*. Our results do not support any of the four current classification schemes but show more congruence with that of Hassel de Menendez (1988).

- 63 EAKIN, DAVID A.

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Additions to SEM determinations of endostome and exostome characteristics in various species of Regmatodon (Regmatodontaceae) and Macrohymenium (Sematophyllaceae)

Although in different families, the peristomes of Regmatodon and Macrohymenium bear remarkable similarities. The endostome segments are unique among mosses. The author will present the

results of continued SEM studies of the similarities and differences between the two genera, and between different recognized species *sensu* Eakin.

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Biodiversity of North American lichens and lichenicolous fungi

A checklist of numbers of lichens and lichenicolous fungi is presented for more than 80 geographical units of North America, including Greenland and Mexico, the states of the USA and the provinces of Canada. A dendrogram of the similarity among the single floras is also shown. The completeness of the lists is estimated, and targets for future investigations are indicated.

65 FISHER, KIRSTEN M.

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Reproductive patterns in the *Syrrhopodon involutus* complex: A case of the island syndrome in mosses

In *Island Biology*, Carlquist proposed the existence of what he terms "the island syndrome". This syndrome, characterized by dioecy, polymorphism, and low rates of reproduction derives from the high incidence of these features observed in island floras, and may relate to selection for loss of dispersability after lineages have become established on remote islands. Carlquist's emphasis, however, is on angiosperms, following the general assumption that spore bearing plants (such as ferns and mosses) are profligately sexual and very dispersive, so that continuous gene flow prevents the divergence of these island plants from their continental counterparts. The *Syrrhopodon involutus* complex is a group of closely-related mosses in the family Calymperaceae which occur throughout the paleotropics. Phylogeographic evidence suggests that the complex has its origins in Indomalaya/Melanesia, and that it has dispersed to remote oceanic islands in both the Indian and Pacific Oceans. While the clade occupying the Indian Ocean has diverged very little, the Pacific Ocean taxa have diverged significantly, both molecularly and morphologically, from the more basal continental/hear continental taxa. Interestingly, initial observations of voucher material from this complex suggested that specimens collected from oceanic islands were far less likely to contain sporophytes than those collected from continents or near-continental archipelagos. Here I present data on the reproductive status of specimens representing the phylogenetic and geographic breadth of the *S. involutus* complex. Both number of gametangia and sporophyte frequency are considered, as well as the presence of asexual propagula (gemmae). Contrary to traditional expectations for bryophytes, the *S. involutus* complex displays significantly reduced sexual reproduction on islands, following Carlquist's island syndrome.

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A molecular phylogeny of the simple thalloid liverwort family Fossombroniaceae

(Marchantiophyta) as inferred from the chloroplast genes rps4, trnL and rbcL

The Fossombroniinae are characterised by spherical capsules that lack lines of dehiscence; spore discharge occurs by the irregular break-up of the capsule wall. In this, the group differs from all other Metzgeriidae (simple thalloid liverworts). The suborder is composed of *Petalophyllum* (six species; global) and *Sewardiella* (monotypic; Indian subcontinent) in the Petalophyllaceae, and *Astrofossombronia* (three to five species; Antarctic Islands and high elevations globally) and *Fossombronia* (about 70 species; predominantly areas with Mediterranean or continental climates, with most species diversity in Australia and Africa) in the Fossombroniaceae. Fossombroniaceae is separated from Petalophyllaceae on the basis of scattered (not clustered) archegonia, the presence of a caulocalyx (not a pseudoperianth), and the absence of outer capsule wall thickenings. Many species are adventives, most abundant in either disturbed or seasonally dry habitats. Endemics are common, and the group includes several rare and/or endangered species. A perceived difficulty in delimiting species based on gametophyte morphology has led to a traditional focus on characters of the distal spore wall architecture. To test whether these spore characters reflect a natural classification, we have generated DNA sequence data from the plastid genes *rps4*, *trnL* and *rbcL*, for 14 *Fossombronia*, two *Astrofossombronia* and one *Petalophyllum* species (a total of 24 accessions), plus a further five outgroups. Analyses of these data are in progress, and will be augmented by a morphological matrix. Preliminary results suggest that *Astrofossombronia* is polyphyletic, with South American *A. peruviana* and New Zealand *A. australis* resolving in two separate clades, one of which is nested within *Fossombronia* and thus renders it paraphyletic. There are two well supported clades within *Fossombronia*: the first includes reticulate-spored species, the second, species with lamellate or papillate spores. Thus it appears that spore characters, traditionally important in species delimitation and identification, may define natural units within this group.

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Habitat use by the sexes of a dioicious liverwort

Marchantia inflexa Habitat specialization by the sexes may provide fitness advantages associated with costs of reproduction but may also result in spatial segregation of the sexes and, in bryophytes, reduced sexual reproduction. *Marchantia inflexa* is a dioicious liverwort that is sexually dimorphic in traits related to growth and reproduction. For successful sexual reproduction in the field, males produce and mature sex structures before females. Results from greenhouse experiments show that both sexes grow larger, produce more asexual propagules and more sex structures in high light compared to low light. However, males either fail to produce sex structures or produce sex structures later than females under low light. We examined habitat use of female and male *M. inflexa* in two Trinidad

- populations and 10 populations in the USA to determine whether the sexes specialize on different microhabitats. We compared habitat characteristics, with emphasis on light environments, between the sexes among populations. The sexes used areas of similar substrate, soil composition and exposure within and among populations. In USA populations, males were found in areas with more open canopy than females and overall, there was a trend for males to live in areas of higher light than females. Sex ratios varied among populations and the proportion of males in a patch in Trinidad populations was positively correlated with amount of light received in the patch. Thus, *M. inflexa* inhabits a well defined range of microhabitats and the sexes overlap in distribution within populations, but very subtle differences of the light environment are related to differences in distribution of the sexes.
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- Phylogenetic affinities of North American populations of *Dendriscocaulon* based on inferences from variation in the ITS nrDNA sequences
- The genus *Dendriscocaulon* was established to accommodate fungi that are lichenized with a cyanobacterium, forming densely shrubby, sterile thalli. These associations have been shown to involve a fungal species typically known to lichenize with green algae. In North America, 'Dendriscocaulon' thalli have been assigned to three species, *Lobaria amplissima*, *Sticta wrightii* and *S. oroborealis*. However, the identity of most thalli is ambiguous. In the absence of diagnostic morphological features the specific identity of free-living thalli is uncertain. We have sampled populations of 'Dendriscocaulon' to 1) examine the haplotype diversity in North America, and 2) test their phylogenetic affinities. The pattern of variation in the ITS sequence suggests that six entities occur in North America. Most populations of 'Dendriscocaulon' belong to *L. amplissima* and *S. wrightii*. Both species occur primarily as dendriscocauloid lichens along the Pacific coast. *Sticta oroborealis* an endemic to NW British Columbia, is identical in its ITS sequence with *Pseudocyphellaria anomala* and *P. anthraspis*, which are undifferentiated based on this locus. Populations from Minnesota and Maine, that represent *Dendriscocaulon intricatum*, share identical ITS sequences with the sympatric *Lobaria quercizans*, which was previously only known in its green algal form. One sample from British Columbia is phylogenetically allied to a group of *Sticta*, including the sympatric cyanolichen *S. fuliginosa*. Finally, one population from Alaska, seems only distantly related to these taxa, and no chlorolichen has been identified to be closely related to it. Our study reveals 1) that the Dendriscocaulon-type life form occurs in all three genera of the Lobariaceae, 2) that lichen-forming fungi that have the ability to establish associations with either green alga or a cyanobacterium, can occur predominantly in one form, in part of their range. Whether this pattern reflects the availability of particular cyanobacterial strain, or selection along ecological gradients is not clear.
- 69 GOFFINET, B.*¹, BUCK, W.R.², COX, C.³, SHAW, A.J.³ and WICKETT, N.¹
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- Circumscription and affinities of the Sematophyllaceae (Bryophyta, Hypnales) based on multigenomic phylogenetic inferences
- Buck and Goffinet included 46 genera in the family Sematophyllaceae (Bryophyta, Hypnales). This circumscription followed recent phylogenetic inferences based on morphological characters. This hypothesis has recently been challenged based on variation in sequence data. We have obtained DNA for representatives of 37 genera, and sequenced four loci from three genomes: the trnL region and the rps4 gene (cpDNA), the 5' half of the 26S gene (nrDNA), and the 5' half of the nad5 gene (mtDNA). Analyses of cpDNA data (114 OTUS total) suggest that the family includes *Acanthorrhynchium*, *Acroporium*, *Aptychella*, *Aptychopsis*, *Brotherella*, *Chinostomum*, *Clastobryella*, *Clastobryophilum*, *Clastobryopsis*, *Clastobryum*, *Colobodontium*, *Donnellia*, *Heterophyllum*, *Iscadiella*, *Mastopoma*, *Meiothecium*, *Papillidiopsis*, *Paranapiacabaea*, *Potamium*, *Pterogoniidium*, *Pterogoniopsis*, *Pylaisiadelpha*, *Radulina*, *Rhaphidostichum*, *Rhaphydorrhychium*, *Schroeterella*, *Sematophyllum*, *Taxithelium*, *Trichosteleum*, *Trismegistia* and *Wijkia*. The genera *Foreauella*, *Pylaisiopsis*, and *Struckia* may belong to the Hypnaceae or Entodontaceae, whereas the hypnaceous genera *Isopterygium* and *Platygyrium* show affinities to the Sematophyllaceae. Furthermore, the genera *Sematophyllum*, *Acroporium* and *Brotherella* are resolved as polyphyletic lineages. We are testing these hypotheses based on analyses of independent and combined data sets of the three loci.
- 70 JOHNSON, ERIC*, SCHUETTE, SCOTT and RENZAGLIA, KAREN
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- Aspects of the Morphology and Ultrastructure of the Sporophyte of *Sphaerocarpos texanus* Austin
- As the putative basal-most extant liverwort, *Sphaerocarpos* is a genus of immense phylogenetic significance. In spite of its evolutionary importance, the basic biology of *Sphaerocarpos* is poorly described. In this study, the sporophyte of *Sphaerocarpos texanus* was examined in the SEM, TEM, light and fluorescent microscopes during different stages of development. Archegonia, and consequently sporophytes, are individually housed within obovoidal involucres. The first division of the zygote is transverse, forming an epibasal and hypobasal cell. Following a filamentous stage, the capsule develops from the epibasal cell, while the seta and foot originate from the hypobasal cell. The mature sporophyte is attached to the gametophyte by a small, spheroidal foot. Transfer cells with extensive wall labyrinthins develop late on both the gametophyte and sporophyte sides of the placenta. The seta is virtually nonexistent at only one to three cells long and becomes necrotic as the sporophyte matures. Capsules are large, spheroidal, nonemergent and completely enclosed by the involucrum. The capsule wall consists of a single layer of cells that lack wall thickenings. There are approximately 60-70 spore tetrads accompanied by twice as many nurse cells. The nurse cells are photosynthetic and appear mitotically active until spore maturation. This first comprehensive ultrastructural study of *Sphaerocarpos* provides informative data in evaluating the rapid morphological changes that accompanied early land diversification.

- 71 KINSER, ABEL J.* and CRANDALL-STOTLER, BARBARA J.
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The liverwort genus Moerckia

The simple thalloid liverwort *Moerckia* Gottsche has never been monographed on a world wide basis. For this reason, and the fact that distantly related taxa have been placed within it, the circumscription of the genus has been unclear. As a consequence of my monograph of the genus, I recognize *Moerckia* to comprise *M. blyttii* (Moerch) Brockm., *M. flotoviana* (Nees) Schiffn., *M. hibernica* (Hook.) Gottsche, and *M. japonica* Inoue. These plants are found on soil, sand or sometimes "floating" intermixed with other bryophytes from 5-2850m in mostly boreal habitats of Asia, Europe, and North America. Diagnostic characters of the genus include: 1) 3-10 celled ventral slime hairs; 2) a ventrally convex midrib that is 12-28 cells thick; 3) the presence or absence of paired conducting strands; 4) elliptical to ovoid capsules; 5) a 2-6 stratose capsule wall; 6) 2 to 5-valved capsule dehiscence with the valve apices never adhering; 7) large spores (30-50 µm). For vegetative material, a simple cross section of the thallus will separate this genus from the remaining simple thalloids within its range that are often mistaken for *Moerckia*. The interspecific variation seen in gametangial scale morphology and position, rhizoid color, and spore morphology are easily observed characters that distinguish the 4 species in this genus. Critical study of type specimens and herbarium collections has confirmed that *M. flotoviana* and *M. hibernica*, which have been conspecific in modern floras and checklists, are separate taxa that possess several morphological distinctions and distinct geographic distributions. Without exception, every liverwort flora of the 20th century to include *M. hibernica* has actually only described and/or illustrated *M. flotoviana*.

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The Family Rutenbergiaceae (Rutenbergia and Neorutenbergia) in Africa, Madagascar and the Mascarenes

The Rutenbergiaceae is a small, highly distinctive family of epiphytic pleurocarpous mosses, restricted to east Africa and the islands of the western Indian Ocean. They are characterised by a distinct marginal limbidium and lamina cells that are small to minute and frequently bistratose, giving the leaf surface a minutely rugulose appearance. Two of the species are moderately well known and have been found with sporophytes (*Neorutenbergia usugarae*, *Rutenbergia madagassa*), but the others have rarely been collected and are represented by very few specimens. In connection with the projected Generic Flora of African Bryophytes, revision of the family was found to be necessary. Phylogenetic analysis of molecular and morphological data was used to resolve the relationship of the monotypic *Neorutenbergia* with *Rutenbergia*, resulting in the synonymisation of these taxa. On morphological grounds *Rutenbergia borbonica* is synonymised with *R. madagassa* and *R. cirrata* is synonymised with *R. limbata*. The family Rutenbergiaceae now consists of one genus (*Rutenbergia*) with 4 species: *R. madagassa* Geh. & Hamp., *R. usugarae* Dix., *R. limbata* (Hamp.) Besch. and *R. priodon* (Besch.) Ren.

- 73 POLI, DOROTHYBELLE*¹, JACOBS, MARK² and COOKE, TODD J.¹
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Auxin Regulation of Axial Growth in Bryophyte Sporophytes: Its Potential Significance for the Evolution of Early Land Plants

In order to identify developmental mechanisms that might have been involved in the evolution of axial sporophytes in early land plants, the effects of auxin-regulatory compounds was examined in the sporophytes of the hornwort *Phaeoceros personii*, the liverwort *Pellia epiphylla* and the moss *Polytrichum ohioense* representing the three divisions of extant bryophytes. The altered growth of isolated young sporophytes exposed to applied auxin (indole-3-acetic acid) or an auxin antagonist (p-chlorophenoxyisobutyric acid) suggests that endogenous auxin acts to regulate the rates of axial growth in all bryophyte divisions. Auxin movement in young hornwort sporophytes occurred at very low fluxes, was insensitive to an auxin transport inhibitor N-(1-naphthyl)phthalamic acid), and exhibited a polarity ratio close to 1.0, which implies that auxin moves via simple diffusion in these structures. Emerging liverwort sporophytes displayed somewhat higher auxin fluxes that were sensitive to transport inhibitors but lacked any measurable polarity. Thus, auxin movement in liverwort sporophytes appears to result from a unique type of apolar facilitated diffusion. In young *Polytrichum* sporophytes, auxin movement was predominantly basipetal in its orientation and occurred at high fluxes exceeding those measured in maize coleoptiles. In older *Polytrichum* sporophytes, acropetal auxin flux had increased beyond the level measured for basipetal flux. Insofar as acropetal and basipetal fluxes exhibit different inhibitor sensitivities, these results suggested that moss sporophytes carry out bidirectional polar transport in different cellular pathways, which resembles the transport in certain angiosperm structures. Therefore, it appears that the three lineages of extant bryophytes had evolved independent innovations for the auxin regulation of axial growth, with similar mechanisms operating in moss sporophytes and vascular plants.

- 74 RICE, STEVEN K.* and SCHNEIDER, NICOLE
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Canopy size and the control of water balance in *Leucobryum glaucum*

In bryophytes, the duration of the hydrated state controls net carbon gain. Favorable water status can be maintained via several mechanisms that include a canopy organization that reduces water loss and an ability to store excess water in specialized cells, tissues or in decayed peat. These mechanisms vary in their effect as a function of cushion size. However, they are not expected to exhibit similar scaling relationships with size and neither should they be influenced equivalently by environmental variation or by fine-scale differences in cushion surface roughness. Using a combination of morphometric, boundary-layer and photosynthetic studies under controlled conditions, we explored the size dependence of water loss and water storage characteristics and developed a water balance model for cushions of *Leucobryum glaucum*. This model was evaluated during a five-day field drying experiment where water loss and chlorophyll fluorescence ('F/F_m') were evaluated at regular intervals on 18 4-34 cm diameter cushions. Under wind-tunnel conditions, conductance to water vapor was reduced by the -0.7 power of canopy diameter. This difference was not realized in the field experiment due to the formation of forest floor boundary-layers that eliminated size dependent

variation in water loss. However, the duration of positive net carbon gain, measured using 'F/Fm', varied from 1.4 to 4.4 d and was significantly longer in larger diameter cushions. Thus, under field conditions, size dependent changes in surface area:volume relationships influence hydration time and carbon balance more than factors that control boundary-layer properties.

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Comparison of lead tolerance potential in *Marchantia* and *Plagiochasma* and their application in active biomonitoring

Very little is known about the physio-chemical responses of bryophytes to metallic pollutants under field and laboratory conditions. The intensity of stress can be used in identification of tolerant species and also as a scale for qualitative mapping of pollution load. The present study correlates the metal bioaccumulation and physio-chemical responses of *Marchantia* and *Plagiochasma* to varying concentrations of lead under laboratory and field conditions. Photosynthetic pigment (chlorophyll), nitrogen, protein, carbohydrate and *in vivo* nitrate reductase activity declined, and proline content and peroxidase activity increased with the increase in external metal concentration (0.01 mM - 10 mM). The magnitude of stress varied from plant to plant and was more pronounced in *Marchantia* than in *Plagiochasma*. *Marchantia* thalli were transplanted in plastic net at different monitoring sites of Almora, Nainital, Ranikhet, and at Mukteswar for a period of 12 months from 1997 and onward. Every year, after exposure period of 12 months these transplants were harvested for metal analysis and in place, fresh transplants were exposed at same height for another 12 months. Higher lead content was observed in the plants transplanted to urban sites of Almora and concentration decreased at peripheral rural sites, while comparatively low lead content was detected in the transplants of Ranikhet. Higher lead concentration was detected in those transplants harvested from proximity of the road and its concentration gradually decreased in the transplants exposed away from road at same monitoring site. A map of air quality in terms of Pb concentration in liverworts harvested from various sites along the gradients from 1998-2002 was prepared with data obtained by AAS analysis. Hyper-accumulation potential with minimum change in physio-chemical parameters of *Plagiochasma* indicates its high tolerance capability, and therefore, it can be used for biomonitoring and phytoremediation studies.

76 STARK, LLOYD R.*¹, NICHOLS II, LORENZO¹ and MCLETCHEE, D. NICHOLAS²

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Are females at an advantage in leaf regeneration in the desert moss *Syntrichia*?

The extremely skewed female-biased sex ratio in the desert moss *Syntrichia caninervis* (*Tortula caninervis*) was investigated by an assessment of the regeneration capacity of detached leaves of various ages. Juvenile, green, yellow-green, and brown leaves equating to approximately 0, 2, 6, and 12 years of age, respectively, were detached from individuals of *S. caninervis* collected from 10 field populations, and grown in a growth chamber for 58 days at low light intensities under a 12 hr photoperiod with day/night temperatures of 20/8C, thus approximating winter/early spring conditions in the Mojave Desert. Younger leaves tended to have a greater viability, regenerate more quickly, extend their protonemal filaments farther, produce shoots

(gametophores) more quickly, produce more numerous shoots, and accumulate a greater biomass than older leaves. Among younger leaf classes (juvenile, green) regenerating female leaves were more likely to produce a shoot than male leaves, produced the first shoot in shorter time, and produced more shoots than male leaves. The sexes did not differ significantly in time to emergence, linear extension of protonemata, or total biomass produced. However, regenerating male leaves tended to emerge more quickly and produce a greater total biomass, consisting mostly of protonemata, than female leaves. The more rapid proliferation of shoots by female leaf regenerants may help to understand the rarity of males in this species.

77 WICKETT, NORMAN J.

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Molecular evolution of the achlorophyllous liverwort, *Cryptothallus mirabilis*

Among bryophytes, only *Cryptothallus* (Jungermanniopsida, Aneuraceae) is achlorophyllous. In the absence of photosynthesis, this simple thalloid liverwort obtains carbon from a relationship with an ectomycorrhizal fungus. It is expected that selection pressure is relaxed on chloroplast genes that are involved in photosynthesis, removing any structural and functional constraints on the evolution of their nucleotide sequence. In achlorophyllous angiosperms this has led to pseudogene formation or the complete deletion of some genes. Individual loci have been sequenced to determine whether they are present and whether there have been any structural changes in the coding sequence. Presently, no gene deletions have been observed and successfully sequenced loci appear structurally intact. Comparisons to taxa with the genes of interest known to be functional and translation of protein coding genes give no evidence of pseudogene formation. Statistical methods of pseudogene formation using outgroup comparisons are currently being explored. The implications of a structurally and functionally intact chloroplast genome may include recent speciation (which must be discussed in a phylogenetic framework) or the retention of functional constraints as genes continue to be expressed, possibly serving other metabolic functions. Different approaches to the characterization of the chloroplast genome of *Cryptothallus mirabilis*, and to understanding the implications of a reduced or a fully functional chloroplast genome, will be discussed.

78 YAHIR, REBECCA*¹, VILGALYS, RYTAS J.¹ and DEPRIEST, PAULA T.²

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Specificity and selectivity in lichen symbiosis: photobiont associations shift along a geographic gradient in *Cladonia* species

The taxonomic and geographic scales at which symbiotic associations are investigated may determine the patterns of specificity and selectivity among symbionts that are found. For example, observations across large taxonomic and geographic scales may result in relatively deep phylogenetic associations, i.e. at the family or genus level. In contrast, over short evolutionary time scales such as those equivalent to the species or local site level, symbiotic partnerships may be more dynamic. We sampled photobiont (*Astrochloris*) ITS from samples at two geographic scales (sites and regions) to test the null hypothesis that the composition of lichen symbioses is consistent across these scales. Across 8 *Cladonia* species sampled from 6 Florida scrub sites, we used phylogenetic and population genetic

methods to demonstrate that associations are consistent across sites and are determined by fungal species. From this sample, we chose fungi that demonstrate intermediate photobiont specificity for further study. We sampled these from several regions outside Florida scrub including coastal plain sandhill (NC), several piedmont forest sites (NC and PA), and the Ozarks (MO and AR). Across regions, associations are non-random and appear correlated with habitat and geographic range. Collectively, these results suggest stable associations and differentiation of photobionts between fungal species and at a regional scale, but dynamism and homogenization at a local scale. Lichen fungi may actively select photobiont partners according to locally-determined preferences from a set of available types.

CONTRIBUTED POSTERS

- 79 ATWOOD, JOHN J.* and CHUEY, CARL F.
Department of Biology, Youngstown State University, Youngstown, OH 44555

Additional Records and Confirmations to the moss flora of Ohio

New records as well as confirmations for Ohio are plotted on distribution maps as additions to *A Catalog and Atlas of the Mosses of Ohio* (Snider and Andreas, 1996). As noted in this checklist, the northeastern region of the state, although with many cryptogamic habitats, is underrepresented by the number of taxa published. The nomenclature used follows that of Anderson (1990) and Anderson et al. (1990). All vouchers are deposited in the Herbarium (YUO) of Youngstown State University.

- 80 RUSHING, ANN E.*¹ and FOWLER, TIFFANY B.²
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Thallus growth and branching of the lichen *Ramalina stenospora*

The fruticose lichen *Ramalina stenospora* is characterized by an erect, highly branched thallus. Scanning electron microscopy was used to examine thallus growth and branching patterns. Growth of the thallus is primarily by apical extension of spherical meristem initials, or growing regions, at the tip of each thallus branch. Branching is by a combination of dichotomous divisions of the apical growing regions and by lateral formation of new spherical initials. The first visible sign of dichotomous branching of the thallus apex is the enlargement of the spherical initial. Enlargement is followed by the formation of a centrally located indentation that divides the apex into two nearly equal units. Each new meristem gives rise, by apical extension, to a narrow branch. Lateral branching results from the outward protrusion and extension of a portion of the thallus margin at right angles to the main thallus. After the initial extension, meristems of lateral branches enlarge, become spherical, and subsequently branch by dichotomous divisions similar to those of the main thallus. The small, spherical meristems and the extensive dichotomous and lateral branching characteristic of *Ramalina stenospora* are considered to be evolutionarily derived features.

- 81 WASHBURN, STEPHEN J.* and CULLEY, THERESA M.
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Impact of Ambient Ozone Levels on Lichen Flora in the Greater Cincinnati Area: Computer Analysis of Ambient Ozone Concentrations

Despite documented air quality improvements in the urban/suburban environment, high levels of ozone remain a significant air quality challenge today. Lichens are known to be sensitive to several types of air pollution, and consequently have been used as indicators of air quality. Preliminary evidence suggests that lichen abundance differs between rural and urban habitats where ozone levels may vary, but it is unknown if lichen abundance directly correlates with ozone concentrations. A first step is to determine if an ozone gradient is present. This was examined by analyzing ambient ozone concentration data from 14 urban, suburban, and rural monitors in the greater Cincinnati area, obtained from U.S. EPA's AIRS database. The hourly ozone data was used to calculate values for several cumulative ozone indices, each of which was examined for existence of an ozone gradient across the Cincinnati area. Future research will focus on quantifying lichen abundance to determine if it is associated with the ozone indices reported here.

DEVELOPMENTAL AND STRUCTURAL SECTION

CONTRIBUTED PAPERS

- 82 BOYCE, C. KEVIN*¹, CODY, GEORGE D.², ZWIENIECKI, MACIEJ A.¹ and HOLBROOK, N. MICHELE¹
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Biochemical and physiological innovation during the proliferation of vascular cell types

Since their origin, the number of functional roles that tracheophyte vascular tissues have fulfilled has continued to increase to match rises in plant size and complexity. For example, the tracheid cell type was involved only in water conduction in the earliest vascular plants, but soon became the primary source of structural support and subsequently evolved roles in damage responses and the reversible regulation of water and nutrient supply. Specializations also evolved for the original function of water conduction, such as for efficient long distance transport versus equitable short distance distribution of water and for conduction in mature versus young, actively expanding tissues. Tracheid function is entirely dependent upon wall structure since the cells are dead at maturity. Because of this, tracheid functional characteristics have typically been evaluated in terms of cell dimensions, and the thickness and morphological details of their walls. However, cell wall chemistry may also be extremely important since

tracheid walls are composed of both lignin and polysaccharides. The distribution of these hydrophobic and hydrophilic compounds within different wall layers could greatly influence all aspects of tracheid function and the optimal lignin distributions for alternative functions can be mutually contradictory. Technical limitations have long prevented the easy, precise evaluation of lignification, but X-ray spectromicroscopy now allows determination of lignin distribution within wall layers with submicron resolution. We have found that the diversification of vascular cell types and functions has been accommodated by several revolutions in fine scale distribution of chemical constituents in different wall layers. By these means, a large increase in the morphological and functional complexity of land plants could evolve through an increase in the number of cell types, in coordination with genetic and biochemical pathways already in place in the simplest early vascular plants.

- 83 BUZGO, MATYAS^{*1}, SOLTIS, DOUGLAS E.¹, SOLTIS, PAMELA S.², KIM, SANGTAE¹, MA, HONG³, LEEBENS-MACK, JAMES³, HAUSER, BERNHARD A.¹ and DEPAMPHILIS, CLAUDE W.³

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32611-7800, USA; ³Department of Biology, the Huck Institute for Life Sciences,

The Pennsylvania State University, University Park, PA 16802, USA

Perianth development in Basal Monocots

Previous studies on the perianth development of basal monocots indicated that the differentiation of tepals and bracts, or that of sepals and petals, had not fully evolved in Acoraceae and some Alismatales (namely the lineage comprising Juncaginaceae and Potamogetonaceae). Described floral similarities between *Acorus* and *Triglochin* (Buzgo & Endress 2000) were challenged by two hypotheses: 1) What was described as a "flower" is a pseudanthium (an inflorescence that looks like a flower), and the "perianth" consists of bracts; 2) There is no outermost "tepall" reminiscent of a flower-subtending bract, but flower development commences with two lateral (or adaxial) tepals. We discuss the development of some spicate inflorescences and flowers in basal monocots with respect to "organ identity", "homology" and developmental genetics. The two hypotheses are not supported by our data: *Triglochin* does not have a pseudanthium, and the perianth consists of tepals. Flower development is unidirectional with a leading abaxial tepal. However, there are putative reductions in flowers within a single inflorescence, in both *Acorus* and *Triglochin*. In young stages of inflorescences of *Triglochin*, an ortholog of *APETALA3* was found to be transcribed in the inflorescence axis; later restricted to anthers.

- 84 CAMERON, KENNETH M.
The Lewis B. & Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458-5126

The Structure and Occurrence of Trilocular Ovaries within Orchidaceae

Orchidaceae are typically described as having unilocular ovaries with parietal placentation. There are a few genera in the family, however, that exhibit trilocular ovaries that appear to possess axial placentation. This latter condition is considered plesiomorphic in the family based on outgroup comparison, but its systematic significance has not been addressed fully. The occurrence of trilocular ovaries in

Orchidaceae was investigated and found to be the result of placental intrusion into the ovary resulting in three false locules. For this reason, placentation is interpreted as parietal in all such cases. The condition is rare in Orchidaceae, but present in at least three of the five subfamilies: Apostasioideae, Cypripedioideae, and Vanilloideae. Within the latter, trilocular ovaries have been studied in *Eriaxis*, *Clematepistephium*, and *Lecanorchis*. They may serve as a synapomorphy for these three genera. Curiously, the rate of inward growth is not equal among the three placentae in *Lecanorchis*, although the result is still a three-chambered ovary. Within a greater phylogenetic context, the "retraction" of placentae to form a unilocular ovary has occurred at least four times in the orchids. The possible adaptive significance of this phenomenon will be discussed.

- 85 CHRISTIANSON, MICHAEL L.
Plant and Microbial Biology, U. California, Berkeley

Probing the determinate nature of erect shoots of *Psilotum*

The switch from indeterminate to determinate growth is a profound developmental decision. Indeed, the innovation we know as determinate growth is one of the most ancient events in the evolution of plant morphology. Plants of the enigmatic genus *Psilotum* grow as an indeterminate, plagiotropic, dichotomizing rhizome. Some branches, however, become determinate, erect, dichotomizing, aerial shoots that bear sporangia. The observation that tips of immature shoots show multiple rounds of dichotomies led to seeing determinate growth in *Psilotum* as a simple consequence of elongation of internodes in a set of preexisting dichotomies: no additional dichotomies are generated as shoots mature. This standard view links the switch from plagiotropic to orthotropic growth with the change from indeterminate to determinate growth. Testing this classic story with experimental manipulations of growing shoots of *Psilotum* reveals that aerial shoots are NOT determinate from inception. A series of newly emerging shoots were treated in one of two ways. One set of shoots had one sister-branch sliced off as each dichotomy developed. Another set of shoots was allowed to develop without this ablation. If all dichotomies were present as the shoots emerged from the soil, manipulations after emergence could not increase the number of nodes. My experimental ablation, however, increases the mean number of dichotomies some 50%, from 6.42 to 9.11, and almost doubles the maximum number of nodes seen, from 9 to 16. These differences are statistically significant. This simple experiment shows that determinate growth of *Psilotum* shoots is the result of developmental regulation DURING the growth of the shoot. *Psilotum* shoot apices can continue to dichotomize for far longer than they usually do. My work was stimulated by papers from Erin Irish (determinate growth of *Zea*) and Carl McDaniel (with *Nicotiana*) and is facilitated by the hospitality of Lewis Feldman and his lab.

- 86 COOK, MARTHA E.
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Further studies of the enigmatic charophycean green alga *Entransia fimbriata* (Charophyceae)

Based on molecular, ultrastructural, and biochemical data, the charophycean green algae are considered to be the closest living relatives of plants. Hence, comparative studies of these algae may increase our understanding of ancestral characteristics in the streptophyte lineage (charophyceans + embryophytes). Recent molecular phylogenetic analysis suggests that *Entransia fimbriata* is a

deeply branching charophycean that is perhaps affiliated with the order Klebsormidiales (Karol and Delwiche unpublished). Electron and light microscope studies (Cook unpublished) of an *Entransia fimbriata* isolate (UTEX 2353) that had been in the UTEX culture collection for 20 years support this hypothesis. Characteristics common to both *Entransia* and at least some members of the genus *Klebsormidium* include an unbranched filamentous form, cells with a single chloroplast, pyrenoids traversed by membranes, H-shaped walls that sometimes have clusters of bacteria associated with them, and cytokinesis that does not involve microtubules or plasmodesmata. Unique to *Entransia* are highly lobed chloroplasts with multiple pyrenoids; short cells that die and collapse, functioning as necridia; and some unusual cross walls having wall protuberances or wall gaps. *Entransia* is rarely found and little studied. In order to determine whether these unusual features might be artifacts due to the long period of time the organism had been in culture, studies were conducted on a recently collected isolate. These same unusual features were found to be present, hence they appear to be typical of the species. Furthermore, the new isolate (but not the UTEX culture) was induced to produce zoospores, a characteristic of at least some species of *Klebsormidium*. These findings support the molecular evidence indicating that *Entransia* may be affiliated with Klebsormidiales.

- 87 DI STILIO, VERONICA S.*¹, BAUM, DAVID A.² and KRAMER, ELENA M.³

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Floral MADS box genes and the evolution of dioecy by homeosis in dioecious meadow rues (Thalictrum, Ranunculaceae)

Most unisexual angiosperm flowers develop initially as hermaphrodites and then abort either stamens or carpels. This indicates that sex-determination is acting late in flower development, after floral organ identity has been established. The genus *Thalictrum*, the meadow-rues, includes both hermaphroditic and dioecious species. Based on observations of mature unisexual flowers of *T. dioicum*, no aborted floral organs are present. This raises the possibility that sex determination involves differential assignment of organ primordia to either stamen or carpel identity. Moreover, the presence of a sepaloid perianth in female *T. dioicum* flowers, is reminiscent of *Arabidopsis thaliana* mutants lacking activity of the B-class MADS-box genes *PISTILLATA* (*PI*) and *APETALA3* (*AP3*). In these homeotic mutants, petals are converted into sepals and stamens into carpels. Conversely, over-expression of B class genes onto the fourth whorl results in a male phenotype. Based on this evidence, our working hypothesis is that B function is extended onto the fourth whorl in male *Thalictrum* flowers, thereby replacing carpels by stamens, whereas female flowers lack expression of one or both of the B class genes (*AP3/PI*), therefore replacing stamens by carpels in the third whorl (and having a sepaloid perianth). Developmental microscopy confirmed that *T. dioicum* flowers are unisexual from inception and do not show selective organ abortion. Using an RT-PCR approach, we cloned and characterized the expression patterns of homologs of the organ identity genes *PI*, *AP3* and *AGAMOUS* (*AG*) from *T. dioicum* and *T. thalictroides*. One of the B class genes is expressed in males only, consistent with our hypothesis. One of two C class genes isolated is female specific, suggesting sub-functionalization of carpel and stamen identity functions. We propose to develop *T. dioicum* and related species as a system for the study of the evolution of dioecy by homeosis.

- 88 DIGGLE, PAMELA K.*¹ and MILLER, JILL S.²

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Floral size dimorphism in taxa with unisexual flowers: a search for underlying causes

Size dimorphism is common among taxa with unisexual flowers and a variety of hypotheses have been proposed to explain the evolution of this floral sexual dimorphism. These range from "non-functional hypotheses" that postulate developmental constraints to "functional hypotheses" that emphasize presumptive biological roles for the perianth or the optimization of resource allocation to characters associated with male or female function. We explore the possibility that two additional and previously overlooked developmental features, architectural effects and developmental plasticity, may contribute to floral size dimorphism. Quantitative variation in flower morphology was examined in six species of andromonoecious *Solanum* section *Lasiocarpa* (Solanaceae). Both multivariate and univariate analyses show that hermaphroditic flowers are significantly larger than staminate flowers for all features measured. Thus, the flowers could be characterized as sexually dimorphic. However, when size variation due to flower position (architecture) is controlled experimentally, differences between the floral genders for the non-gynoecial characters disappear; there is no difference in corolla or androecium size for these six species of *Solanum*. In these species, staminate flowers are generally smaller than hermaphroditic flowers, not because of any difference related to primary sexual function, but because they tend to occur in the distal regions of each inflorescence. Review of the literature on taxa with unisexual flowers suggests that male and female flowers of dioecious taxa (or male and hermaphroditic flowers of andromonoecious taxa) are often located in distinctly different positions within inflorescences or within the overall architecture of individuals. It is quite possible that positional variation, unrelated to primary gender function, could explain sexual dimorphism in these taxa as well. Thus, it is critical to identify the underlying sources of variation in floral morphology, including variation due to architecture, before evolutionary hypotheses related to flower function are generated and evaluated.

- 89 FRIEDMAN, WILLIAM E.* , GALLUP, WILLIAM N.

and WILLIAMS, JOSEPH H.

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Female gametophyte development in *Kadsura*: implications for Schisandraceae, Austrobaileyales, and the early evolution of flowering plants

Recent phylogenetic analyses of angiosperms have identified a set of "basal" angiosperm lineages (*Amborella*, *Nymphaeales*, and a clade that includes *Illiciaceae*, *Schisandraceae*, *Trimeniaceae*, and *Austrobaileyaceae*) that are central to the study of the origin and early diversification of flowering plants. Remarkably little is known about the basic embryological features of members of this grade of flowering plants, particularly with respect to the nature and development of the female gametophyte, and the ploidy and genetics of the endosperm. Here, we report that *Kadsura japonica*, a member of the *Schisandraceae*, develops a four-celled female gametophyte with an egg cell, two synergids and a uninucleate central cell. The pattern of free nuclear divisions in the female gametophyte of *Kadsura* precisely

matches what has recently been reported for four-celled gametophytes in the Nymphaeales. Following the first mitosis, there is no migration of one of the two nuclei to the chalazal pole of the female gametophyte, as would occur in a Polygonum-type female gametophyte. Rather, both nuclei remain close together in the micropylar domain where they undergo one additional mitotic division to yield four free nuclei prior to cellularization. Microspectrofluorometric analysis of relative DNA content of the central cell nucleus shows that this nucleus is haploid and contains the 1C quantity of DNA prior to fertilization. Thus, the endosperm of *Kadsura* should be diploid and biparental, as is the case in *Nuphar* and other Nymphaeales. It now appears that four-celled female gametophytes (with consequent production of diploid endosperms) are common among the most ancient lineages of angiosperms (with the sole exception, to date, of *Amborella*). Finally, based on an analysis of the modular nature of the angiosperm female gametophyte, we provide developmental evidence that four-celled female gametophytes that yield diploid biparental endosperms are likely to be plesiomorphic for flowering plants.

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Training techie tools for the anatomy trade: automated anatomy characterization using artificial neural nets

The description and characterization of plant anatomy is central to many fields of botany including physiology, studies of form and function, and systematics. Nonetheless, few tools are available for the direct analysis of anatomy. Automated identification of cell types, densities, and distributions within stem sections would aid the quantification of patterns of cell types and development. Such analyses would facilitate rigorous tests of morphological evolution and physiology. Non-linear discrimination using simulations of artificial neural nets (ANN) allows for this automation. I digitized stem sections of 50 species of *Adenia* (Passifloraceae), and trained a backpropagation multilayer perceptron ANN to identify the cell type to which a sampled image pixel belongs. After extracting 25x25 pixel windows surrounding target pixels, 53 texture measures were computed for each window to describe the patterning and variation in pixel intensities. I sampled over 4000 such subwindows of 15 cell types using "point-and-click" software I developed for the job. The samples were partitioned into three sets for each species. Training and evaluation sets were used to train the net and optimize network structure. The network was tested for accuracy using the third set. By training and testing the net species by species, the training error dropped to between 0.1 and 1.5%, and the testing error ranged between 0.75 and 8% (average = 5.3%). The trained network can be used to identify the cell type to which each pixel in an image belongs. An accurate estimate of cell type, density, and distribution is thereby automated.

91 HORNER, HARRY T.¹, HEALY, ROSANNE¹, CERVANTES-MARTINEZ, TERESA¹ and PALMER, REID G.^{*2}

¹Department of Botany and Bessey Microscopy Facility, Iowa State University, Ames, IA 50011; ²Departments of Agronomy and Zoology/Genetics, USDA ARS CICGR, Iowa State University, Ames, IA 50011

The soybean floral nectary: an interesting secretory gland with unique features

The soybean floral nectary is a small, circular mound around the base of the central gynoecium. It forms just prior to flower opening and degenerates in about 24 hours, just after the flower opens. The epidermis of the nectary contains many prominent guard cells with open pores, whereas the interior of the nectary consists of special parenchyma cells and fingers of phloem, the latter made up of sieve elements and companion cells. Once formed, each special parenchyma cell vacuole enlarges and fills with unidentified substances interspersed with ribosome-like particles. The cytoplasm is enriched with ribosomes, ER, Golgi bodies, mitochondria, and undifferentiated plastids with little or no starch but containing phytoferritin. Three unusual cytoplasmic structures appear prior to break down of these cells: bundles of tubules tightly associated with the vacuole membrane; cytoplasmic bridges extending into the vacuole; and straight tubes free in the cytoplasm and sometimes traversing plasmodesmata. The tubes contain ribosome-like particles. The special parenchyma cell cytoplasm and vacuole contents eventually mix, and each cell collapses, which in turn leads to nectary collapse. Small bead-like bodies of unknown composition occur in guard cell pores and on the nectary surface at this time. This holocrine-type of secretion suggests programmed cell death, not reported in any other legume nectary. In addition, the surface of the gynoecium displays three types of trichomes, one being glandular. The latter appears active during nectary secretion and may contribute substances, in addition to the sugars and other substances in the nectar secreted by the nectary.

92 JARAMILLO, M. ALEJANDRA^{*} and KRAMER,

ELENA M.

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Perianth development in the family Aristolochiaceae (Piperales)

The family Aristolochiaceae is part of the order Piperales, a group of mainly herbaceous magnoliids closely related to the Winterales. The Aristolochiaceae have a well-developed perianth comprised by one (*Aristolochia*, *Asarum* and *Thottea*) or two (*Saruma*) whorls of organs. Many recent studies have agreed that the uniseriate perianth of *Aristolochia*, *Asarum* and *Thottea* is homologous to the calyx of *Saruma*. The perianth primordia of *Asarum*, *Aristolochia* and *Thottea* are similar to the sepal primordia of *Saruma* in position, shape and developmental kinetics. Nevertheless this uniseriate perianth has several petaloid characteristics and represents the main attractant to pollinators, especially in the genus *Aristolochia*. We cloned the homologs of petal identity genes, APETALA3 and PISTILLATA, from all genera of Aristolochiaceae. The molecular evolution of these homologues will be discussed. Expression data will be presented for the genera *Saruma* and *Aristolochia*.

- 93 KANG, JULIE, TANG, JOHN, DONNELLY, PETRA and DENGLER, NANCY*
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Primary vascular pattern and expression of ATHB-8 in shoots of Arabidopsis

Primary vascular pattern determines pathways of long distance transport for water, nutrients and signaling molecules within plant shoot systems. Expression of an *Arabidopsis thaliana* homeobox gene-8::GUS construct is restricted to procambium and provides a molecular marker for vascular pattern at early developmental stages. Primary vascular pattern and phyllotaxis are highly coordinated, with vascular sympodia corresponding to phyllotactic parastichies. During vegetative development, primary vasculature forms a reticulate pattern with each leaf trace derived from two vascular sympodia. Shoot phase change is marked by alterations of this fundamental pattern. Formation of leaf trace procambial strands is temporally coordinated with primordium initiation but *ATHB-8::GUS* expression is discontinuous in these strands at early stages. The interconnection of vascular sympodia provides alternate pathways for long distance transport in shoots of *Arabidopsis thaliana* and reflects the limited secondary growth in this species. *ATHB-8::GUS* expression identifies a prepattern that precedes anatomical definition of procambium. The longitudinal discontinuity in *ATHB-8::GUS* expression indicates that one function of this gene is to define the xylem components of vascular radial pattern.

- 94 KELLY, WANDA* and COOKE, TODD
Cell Biology and Molecular Genetics, University of Maryland, College Park, MD 20742

Geometrical Relationships Specifying the Phyllotactic Pattern of Aquatic Plants

The complete range of various phyllotaxes exemplified in aquatic plants provide an opportunity to characterize the fundamental geometrical relationships operating in leaf patterning. A new polar-coordinate model was used to characterize the correlation between the shapes of shoot meristems, and the arrangements of young leaf primordia arising on those meristems. In aquatic plants, the primary geometrical relationship specifying spiral vs. whorled phyllotaxis is primordial position: primordia arising on the apical dome (as defined by displacement angles less than 90 degrees during maximal phase) are often positioned in spiral patterns, whereas primordia arising on the subtending axis (as defined by displacement angles greater than or equal to 90 degrees during maximal phase) are arranged in whorled patterns. A secondary geometrical relationship derived from the literature, shows an inverse correlation between the primordial size to available space ratio and the magnitude of the Fibonacci numbers in spiral phyllotaxis or the number of leaves per whorl in whorled phyllotaxis. The data available for terrestrial plants suggests that their phyllotactic patterning may also be specified by these same geometric relationships. Major exceptions to these correlations are attributable to persistent embryonic patterning, leaflike structures arising from stipules, congenital splitting of young primordia, and/or non-uniform elongating of internodes. The geometrical analysis described in this presentation provide the morphological context for interpreting the phenotypes of phyllotaxis mutants and for constructing realistic models of the underlying mechanisms responsible for generating phyllotactic patterns.

- 95 KORN, ROBERT
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The marginal band, a new structural component of the developing dicot leaf

The marginal band, a newly described structure of the dicot leaf, plays an essential role in the formation of this organ. It arises along the two edges of a leaf as several files of adaxial epidermal cells during the peg stage of ontogeny. Functionally, it appears to serve as the pre-pattern for a number of secondary features including (i) the marginal growth meristem present in all leaves as examined in mountain laurel, (ii) rows of lobes and spines as in *Salvia* and *Ilex*, (iii) pigmentation as in some cultivars of *Hydrangea*, (iv) propagation as in the plantlets of *Kalanchoe pinnata*, (v) marginal ridges for support in a few varieties of *Viburnum* and *Ilex*, and (vi) marginal necrosis as in *Strelitzia* for blade partitioning.

- 96 MATTHEWS, MERRAN L.* and ENDRESS, PETER K.
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Cucurbitales: floral structure and systematic relationships

Support for the current circumscription of the order Cucurbitales (Cucurbitaceae, Anisophylleaceae, Begoniaceae, Daticaceae, Tetramelaceae, Corynocarpaceae, Coriariaceae) and its exact position in rosids based on molecular results is low to moderate (APG, 1998; Schwarzbach and Ricklefs, 2000; Wagstaff and Dawson, 2000; Soltis et al., 2000; Savolainen et al., 2000). Molecular studies have so far failed to elucidate the relationships within the order, with perhaps the exception of the possible (and surprising) sister relationship of Corynocarpaceae and Coriariaceae, and the division of Daticaceae into two families (Daticaceae and Tetramelaceae). A relationship between Cucurbitaceae, Begoniaceae and Daticaceae s.l. was suggested previously in traditional classifications, however the other families were not considered closely related: Anisophylleaceae were previously placed near Rhizophoraceae although floral structure (including fossil evidence) suggests a possible relationship with Cunoniaceae (Oxalidales), while Corynocarpaceae and Coriariaceae were essentially unplaced. We compared the floral structure (morphology, anatomy and histology) of members of Cucurbitales with the hope of shedding light on possible interfamilial relationships. Preliminary results support the sister relationship of Corynocarpaceae and Coriariaceae, and differences between their floral structure are likely to be the result of their different pollination biology (insect vs. wind). Anisophylleaceae remain elusive and isolated within Cucurbitales and still show more similarities with Oxalidales. Cucurbitaceae, Begoniaceae, Daticaceae and Tetramelaceae share a number of interesting traits in various combinations. In addition, some families share unusual and rare features as found by other authors, such as andro dioecy (Daticaceae and Cucurbitaceae) and a symbiotic relationship with the nitrogen-fixing *Frankia* (Daticaceae and Coriariaceae). Although it is too early to suggest possible synapomorphies for the entire order, synapomorphies for pairs (or groups) of families are emerging.

- 97 MCKOWN, ATHENA D* and DENGLER, NANCY G
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The specialized vein pattern in C4 *Flaveria* species is not strongly developmentally canalized

The vein pattern of C4 species *Flaveria australasica* has higher vein density, greater frequencies of vein branch points and freely ending veinlets, and lower interveinal distance in comparison to C3 *F. robusta*. Developmental studies indicate that venation differences arise early during leaf ontogeny, and that *F. australasica* has a delayed maturation of protoxylem compared to *F. robusta*. Shade experiments have shown that C4 anatomy is not strongly developmentally canalized and is plastic with respect to vein pattern and other features. In simulated shade conditions, *F. australasica* was found to have a similar vein density, and frequencies of vein branching and freely ending veinlets as the C3 species. Interveinal distance in the C4 species was lower in both full light and shaded conditions compared to the C3 species, indicating that there are limitations to the range of plasticity exhibited by the C4 species. The weak developmental canalization of venation in C4 *F. australasica* suggests this may be a contributing factor to the poor competitive ability of C4 plants in shaded conditions, as they are unable to maintain the interveinal distance required for C4 photosynthesis.

- 98 MIKESELL, JAN
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Reproductive capacity in *Alliaria petiolata*

Parameters of fruit and seed development were monitored during two separate years in garlic mustard plants which emerged in the same location. In 1997, individual seed and fruit mass decreased acropetally by 20 % and 18 %, respectively. Seed number per fruit increased acropetally by 29 %. Seed and fruit mass as well as seed number per silique differed significantly among varying plant levels; i.e. the bottom, middle and tops of plants developed seeds and fruits having different weights, and siliques at these levels contained different seed numbers. In 2002, values for the three reproductive parameters were not as variable among the different plant levels. There remained an acropetal decrease in individual seed mass (4 %) and an acropetal increase in seed number per silique (33 %). Thus, the inverse relationship between individual seed mass and seed number within fruits remained constant during the two years. The lightest and most numerous seeds developed in siliques of upper branches. However, individual fruit mass increased acropetally by 32 %. When analysing the average seed mass developing within proximal (basal) and distal siliques of all branches, significantly heavier seeds usually developed in proximal siliques. Heaviest seeds developed within proximal siliques 76 % of the time, and in distal siliques 6 % of the time. Seeds contained within basal fruits were almost half again (47 %) heavier than their lighter counterparts developing within distal siliques. In those few instances where heavier seeds developed in distal fruits, there was only a 9 % increase in individual seed mass. Individual fruit mass was 15 % heavier on main stems than axillary branches, but individual seed mass was nearly identical. Monitoring seed size at different levels in siliques and throughout plants revealed that seeds developing at the stigma end were about 13 % lighter.

- 99 MITCHELL, CAROLINE H.* and DIGGLE, PAMELA K.
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Breaking down Dioecy: A morphological and developmental characterization of unisexual flower types in dioecious taxa

In 1884, Darwin recognized two types of unisexual flowers. One type exhibits vestigial gynoecia in the male flowers and vestigial androecia in the female flowers. The other type exhibits no rudiments of the opposite sex. In 1957, Heslop-Harrison furthered this distinction and proposed that two different developmental patterns result in the two types of unisexual flower. Beyond these initial distinctions between the two types of unisexual flowers, no analyses of general evolutionary significance have been formulated. This investigation gathered morphological data on mature dioecious flowers. Male flowers with rudiments of a gynoecium and female flowers with rudiments of an androecium were deemed "type-one" flowers, whereas male and female flowers with no rudiments of the opposite sex were deemed "type-two" flowers. Overall, type one flowers are more common among dioecious taxa than type two flowers and type one flowers also appear to have more independent evolutionary origins. A character map of dioecious flower type illustrates some trends that clarify the repeated evolution of dioecy in some clades. This investigation also examined the development of type one flowers and identified a range of developmental programs that yield unisexual flowers. Both Darwin and Heslop-Harrison speculated on the association of type one flowers with predominantly hermaphroditic clades and type two flowers with predominantly unisexual clades. This hypothesis was tested.

- 100 NOYES, RICHARD D.
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Function of unreduced (diplosporous) ovules across generations in *Erigeron* (Asteraceae) - insights into the evolution of apomixis

Genes for apomixis in flowering plants redirect wildtype sexual reproduction via transitions from 1) reduced to unreduced ovules, and, 2) fertilization-dependent to autonomous endosperm and embryo development. In daisy fleabane (*Erigeron annuus*; Asteraceae), experimental crosses yield F1s exhibiting separate elements of apomixis including plants that produce unreduced, diplosporous ovules, but that fail to produce autonomous seed. Crosses were conducted to test the function of ovules in diplosporous but nonapomorphic plants over two generations. In generation one, a triploid ($2n=27$) diplosporous seed parent crossed with a sexual wildtype diploid ($2n=18$) pollen donor yielded predominantly tetraploid ($2n=36$) progeny that exhibited no diminution of diplospory. In the second generation, a tetraploid from generation one was crossed with a second sexual wildtype diploid pollen donor to yield a population consisting mostly of pentaploid ($2n=45$) individuals. Results suggest that faithful inheritance of diplospory can lead to marked increases in ploidal level over just a few generations. Further, the effective, independent function of unreduced ovules suggests that diplospory is only loosely integrated into the apomorphic developmental regime.

- 101 O'QUINN, ROBIN* and HUFFORD, LARRY
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Homology and evolution of subterranean perennation structures in Claytonia sect. Claytonia (Portulacaceae)

Vegetative diversity of Montieae is extensive and manifest primarily in shoot architecture and specializations for perennation. Various vegetative characters have been used in the taxonomy of Montieae and have provided the basis for hypotheses of evolutionary relationships. Questions remain, however, about the homology of many of these vegetative characters. Critical assessment of structural (primary) homology to evaluate morphological correspondences are essential to derive robust characters that can be applied in phylogeny reconstruction and analyses of diversity. In the monophyletic *Claytonia* sect. *Claytonia* (including *C. megarhiza*), ramets have large spherical to obconic subterranean structures of uncertain homology. These subterranean specializations, having distal rosette shoots and basal roots, have been considered to be taproots or hypocotyls by different workers. Preliminary histological and morphological data indicate that the subterranean specializations of *C. megarhiza* and probably *C. umbellata* consist primarily of distal hypocotyl subtended by a short basal region of root that is continuous with a taproot. The more spherical subterranean specializations of other members of sect. *Claytonia* appear to consist only of hypocotyl. Based on molecular phylogenetic results, these spherical specializations appear to be derived from those that have an enlarged, elongate hypocotyl that is continuous with a taproot.

- 102 OSBORN, JEFFREY M.*; SCHWARTZ, JULIE A.,
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Pollen and anther development in Cabomba (Cabombaceae, Nymphaeales)

The Nymphaeales, or water lilies, have a cosmopolitan distribution in fresh water habitats and comprise two families and eight genera: Nymphaeaceae (*Victoria*, *Euryale*, *Nymphaea*, *Ondinea*, *Barclaya*, *Nuphar*) and Cabombaceae (*Cabomba*, *Brasenia*). Water lilies are widely regarded to be among the most primitive flowering plants, as recent phylogenetic studies have consistently indicated that either *Amborella* or *Amborella* plus Nymphaeales is the sister group to the remaining angiosperms. Although studies of pollen development provide important data for assessing phylogeny, little is known about these characters in *Cabomba*. In this presentation, pollen and anther ontogeny will be described for *Cabomba caroliniana* Gray, which have been studied using scanning electron, transmission electron, and light microscopy. Anthers at the sporogenous tissue, microspore mother cell, tetrad, free microspore, and mature pollen grain stages will be documented. Events including the deposition of a microspore mother cell coat, a callose 'special' wall, a primexine, and the sporoderm layers will be discussed. The tetrad stage proceeds rapidly, and all tetrads are of the tetragonal type. Significant exine deposition, including formation of the columellae and tectum, and the subsequent development of a series of tectal/columellar microchannels, occur during the tetrad stage. The endexine lamellae, foot layer, and suprarectal sculptural rods form during the free microspore and early grain stages. The principal characters of anther ontogeny discussed will include the number and size of anther wall

layers, changes in tapetum morphology, and timing of tapetum dissolution. Significantly, an amoeboid tapetum was observed for the first time in *Cabomba*. *Cabomba caroliniana* is fly-pollinated and mature pollen grains are coated with copious amounts of tapetally derived pollenkit, which may be stored in the exinous microchannels. In addition to the possible adaptations for pollination, the new ontogenetic data will be discussed regarding systematic and phylogenetic interpretations of *Cabomba*.

- 103 RYERSON, KIRSTEN C.*¹, MILLER, JILL S.² and
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Andromonoecy in *Solanum palinacanthum*: the emergence of new variation in patterns of staminate flower production

We examined the effects of genetic variation, phenotypic plasticity, and architecture on patterns of staminate (male) and hermaphroditic (bisexual) flower production in andromonoecious *Solanum palinacanthum* (subgenus *Leptostemonum*, section *Acanthophora*). Plants were grown from seed and propagated vegetatively to form clonal replicates of multiple genotypes. In order to examine changes in staminate flower production in response to fruit set, half of the plants of each genotype were pollinated every other day while the other plants were left unpollinated. The position (relative to the branch and the inflorescence) and sex of each flower was recorded for both treatments and the proportion of staminate flowers per inflorescence was calculated and used as the response variable in an ANOVA. *Solanum palinacanthum* displays strong andromonoecy (a high proportion of staminate flowers per inflorescence) and is phenotypically plastic, that is, staminate flower production increases in response to the fruiting treatment. Staminate flowers are borne in an architecturally distinct pattern similar to that of closely related *Solanum* species. While *S. palinacanthum* is similar in architecture to other andromonoecious species of *Solanum* subgenus *Leptostemonum*, the association between plasticity and strong andromonoecy is unusual. This association may be species specific or may characterize andromonoecy for section *Acanthophora*.

- 104 STILES, JEFFREY C.*; WHEAT, BRIAN, FOONG,
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Aspects of root development in GMO cotton and maize

We examined seedling root development in GMO varieties of maize (DG5516 line-parental and RR) and cotton (DPL line-parental,RR,Bt,RR+Bt). In RR maize, stelar cells lignified slightly earlier than in parental maize, and in the hypodermis there were typically more lignified cells in RR maize roots. In parental cotton, primary growth revealed no exodermis, but there was an exodermis in many, but not all, RR, Bt, and RR+Bt roots. Cotton secondary growth was characterized by earlier phloem fiber production in all GMO roots. The endodermis in all varieties redivided with new Caspary bands in every new cell, and the exodermis, where present in GMO roots, also redivided before being sloughed off.

- 105 VON BALTHAZAR, MARIA^{*1}, ALVERSON, WILLIAM S.² and BAUM, DAVID A.¹

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Floral development and androecium structure of the Malvatheca clade (Malvaceae)

The delimitation of families in the core Malvales has traditionally been problematic, and taxa have often been moved between Bombacaceae, Malvaceae, Sterculiaceae, and Tiliaceae. Molecular phylogenetic studies have confirmed the monophyly of the core Malvales, but do not support the traditional family level classification. One of the newly recognized monophyletic groups was named Malvatheca and comprises the traditional Bombacaceae (except for Durioneae), traditional Malvaceae, and some taxa of uncertain affinities (e.g., *Fremontodendron* and *Pentaplaris*). Stamen number and arrangement, level of filament union, and anther structure are highly variable within the Malvatheca clade. Here we present results from a comparative study of floral development in Malvatheca. We use the developmental data within a phylogenetic framework to elucidate evolutionary pathways of specific androecial characters. Thereby, we test alternative transformational hypotheses that have been used to explain the origin of the modified anthers. Basal lineages of Bombacoideae and Malvoideae clade have elongated, often sessile, anthers with multiple transverse septa and are therefore polysporangiate. This suggests that bisporangiate anthers evolved independently in core Bombacoideae and core Malvoideae. Basal groups of the Malvatheca clade most often have filaments united along most of their length and it is suggested that the 'unzipping' of the filament tube led to free apical filament parts and monothecate anthers in Bombacoideae. However, Malvoideae have long staminal tubes with lateral monothecate anthers. Malvoid anther primordia develop in two rows in a centrifugal pattern on five staminal lobes, subsequently each primordium splits into two monothecate halves.

CONTRIBUTED POSTERS

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Vegetative Propagation in Australian Tuberous and Pygmy Sundews (Drosera; Droseraceae)

Australian members of the genus *Drosera* (Droseraceae) include sundews with normal mechanisms of vegetative propagation which are rare or unknown in sundews from most other geographic regions. These unusual mechanisms include the summertime production of tubers in species such as *D. peltata* and the wintertime production of gemmae in species such as *D. callistos*. Tubers form at the ends of negatively geotropic subterranean stems in response to increased heat and decreased soil moisture, while gemmae form in the center of the rosette of leaves on a pygmy sundew from the stipules of winter leaves. Preliminary data will be shown indicating a role for cytokinins in directing the development of these vegetative propagules along with the most effective concentrations of the cytokinins tested (BA, TDZ). Studies in tissue culture show that tuber formation and an intermediate phenomenon between tuber formation and formation of normal vegetative stems, which the authors refer to as "pseudotuberization," can be induced by addition of cytokinins. This

includes induction of tubers from the glandular hairs of tuberous sundews' leaves, a phenomenon observed for some species in nature. In addition, a phenomenon which resembles gemma formation in tissue culture can be similarly induced using cytokinins. In addition to preliminary data, plans for further investigation of the developmental control of vegetative propagation of Australian sundews at the molecular level will be considered.

- 107 DOTY, KAREN F.*, BETZELBERGER, AMY M. and COOK, MARTHA E.

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Microtubule dynamics in the charophycean alga *Chaetosphaeridium* (Charophyceae)

Based on molecular, ultrastructural, and biochemical data, the charophycean green algae are considered to be the closest living relatives of plants. Hence, studies of these algae may increase our understanding of ancestral characteristics in the streptophyte lineage (charophyceans + embryophytes). The complex process of cytokinesis has special significance in plants, due to the impact of cell wall placement on plant form. New cell walls synthesized between daughter cells during plant cytokinesis become part of a permanent support system that is built upon as the plant continues to grow. The morphologically diverse order Coleochaetales presents a unique opportunity for studying the evolution of cytokinesis. It has long been known that cytokinesis in the morphologically complex circular thalloid forms *Coleochaete scutata* and *Coleochaete orbicularis* is associated with a phragmoplast. Recent work has shown that *C. soluta* and *C. irregularis*, morphologically less complex members of the genus *Coleochaete*, also undergo cytokinesis by means of a phragmoplast (Doty et al. unpublished). Cytoskeletal dynamics have not previously been explored in the genus *Chaetosphaeridium*, another member of the order Coleochaetales, which is known to have a branching pattern quite different from that of *Coleochaete*. We are using fluorescence localization techniques to identify microtubular structures in *Chaetosphaeridium*. Comparison of microtubule dynamics in *Coleochaete* and *Chaetosphaeridium* will allow us to further test the hypothesis that phragmoplasts arose in a common ancestor of Coleochaetales, Charales and embryophytes.

- 108 GHOSH, NABARUN^{*1}, CAMACHO, RENE¹, SCHNIEDERJEN, ELIZABETH¹, SMITH, DON², SAADEH, C³ and GAYLOR, MICHAEL³

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The Aeroallergen Index and meteorological condition in the Texas Panhandle

We report the data on the aeroallergen count that we recorded for the year 2002-2003. This study was aimed to detect any possible correlation between the daily pollen and spore indices with the meteorological conditions of the Texas Panhandle. We also report the major types of aeroallergens that are prevalent in the Texas Panhandle area. The Burkard spore trap, containing a drum on which Melinex tape coated with paraffin wax, suctions air at a rate of 10 liters per minute capturing aeroallergens. The collection of tape was done every day at 10:00AM CDT. The tape was collected and placed on a slide containing water and an emulsion Gelvatol was then added to the cover slip. A drop of 2% Safranin was added to the emulsion to facilitate observation of aeroallergens. After mounting, the slide was observed using a BX-40 Olympus microscope. Tapes were analyzed

with a minimum of five latitudinal traverses, and daily concentration was assessed. These counts also provided the data on counts at the five different intervals of the day. The concentrations were multiplied with a predetermined correction factor of 2.899 to have the aeroallergen index. We noticed a gradual reduction of the pollen and spore counts with the advent of winter. With the freezing temperature the pollen and spore counts reached '0'. With the return of warm dry weather conditions the dry air spora increased that including *Alternaria*, *Cladosporium*, *Curvularia*, *Pithomyces* and many smut teliospores. Diurnal levels of these spores usually have peaks during the afternoon hours under conditions of low humidity and maximum wind speeds. By the end of February the mold count reached moderate level and weed pollen count reached high since the weather conditions promoted the production and dispersal of fungal spores and weed pollens with a few centimeter rain and warmer weather.

- 109 KIRCHOFF, BRUCE K.*¹ and CANELOSI, ROSS ²

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Visual data presentation techniques for the study of flower development

Science is as much about presenting data intelligently as it is about discovering truth. Though data may be compelling to those who collect it, without convincing methods of presentation its force must remain a private matter. Statistics allows the analysis and display of quantitative data, but qualitative data have not received the same amount of attention. Graphic artists are experts in the display of qualitative data. Can graphic art techniques contribute to the presentation of flower development? We explored this question using Scanning Electron Micrographs of flower development in *Musa velutina* (Musaceae) as our data source. Since publication of these data was our ultimate goal, we restricted our layouts to those that would be acceptable to major botanical journals. In addition to size constraints, this imposed constraints on the density of our layouts. Only layouts that produced dense packing of the images were acceptable. Planning for graphic presentation began during data collection. Every primordium on a young inflorescence was photographed and its position on the inflorescence recorded. The whole inflorescence was also photographed from all sides so that every primordium was visible in at least one view. This procedure had the benefit of documenting variation in floral shape at all stages of development. Instead of portraying development as a linear array of unvarying stages, we produced an array of photographs in which every developmental stage had several shape variants. Our layout presented this data by showing the position of each flower on the inflorescence. Since the flowers are younger acropetally, a layout that preserves positional information also presents the photographs in a developmental sequence. The result is a plate that can be read in many differently ways (ca. 15), instead of the one reading most plates allow.

- 110 PARSLEY, LARISSA C.*² and RUSHING, ANN E.¹

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The sequence of development of leaf propagules in *Bryophyllum daigremontianum*

Bryophyllum daigremontianum (Hamet & Perrier) Berger, a succulent plant, produces propagules on the leaf margins that are an effective means of vegetative reproduction. These propagules develop shoots, leaves, and roots, allowing them to grow independently from the parent plant. The sequence of propagule initiation and development was followed using scanning electron microscopy obser-

vations. The first visible changes of the parent leaf are the enlargement and extension of notches at the dentations of the leaf margin. Within the notch, an apical meristem is initiated that gives rise to a pair of leaf primordia. These primordia, on opposite sides of the apical meristem, produce leaves that are unequal in size during early development, with the outer leaf of the pair (positioned away from the leaf margin) developing more rapidly. A second pair of leaves initiates perpendicular to the first. These leaves are equal in size at initiation and throughout development. The third pair, and presumably all subsequent pairs, are equally sized and at right angles to the previously initiated pair. Root primordia typically arise at about the same time as the second pair of leaf primordia and form on the undersurface of the enlarged propagule base. The developing roots push the propagule away from the parent leaf and lead to detachment of the propagule.

- 111 RUEHLE, JON

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The Petunia Inflorescence Pattern Results from Iterating Cycles of Axillary Meristem Initiation and Identity

Dynamic processes of pattern formation in inflorescence development are difficult to analyze unless they can be resolved into discrete initiation events at the shoot apex. Results using the mold-replica technique for scanning electron microscopy demonstrate that the reproductive axes of petunia are generated by a succession of axillary renewal meristems in relay fashion. Each meristem initiates the two bracts and terminal flower of a renewal shoot in a precise sequence of events. Bracts are placed alternately at different nodes along the shoot axis, although minimal internode elongation gives them the appearance of being opposite. Each bract forms in the "next available space" on the parent apex so that the spiral phyllotaxy of successive shoots alternates handedness with each renewal cycle. Successive renewal meristems form in the axil of the distal bract primordium of the preceding shoot. Renewal meristems initiate development while both the meristem and its subtending bract primordium are still on the flanks of the parent apex. Precocious development produces a distinctive pattern where the axillary renewal meristem is contiguous with the parent apical meristem. This accelerated axillary meristem development has often been described as an undifferentiated apical mass generating separate flower and vegetative shoots like callus tissue or as a bifurcation of the apex. All shoots comprising the petunia plant body eventually initiate this sympodial renewal pattern and follow it without variation. Paired bract phyllotaxy, precocious initiation of axillary meristems and strict regulation of developmental potential indicate that petunia expresses an inflorescence identity independent from both vegetative and floral phases. Inflorescence identity passes from meristem to meristem along the reproductive axis in a rhythmic sequence of events that produces the distinctive petunia architecture. This sympodial model of the petunia inflorescence avoids singular mechanisms of branching, and demonstrates how fundamental processes can generate complex patterns.

- 112 SCHMIDT, RACHEL E.* and BROWN, GREGORY K.
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Systematic Leaf Anatomy in Bromeliaceae subfamily Bromelioideae

The subfamily Bromelioideae has not been surveyed for leaf anatomical characters. As part of a larger project investigating generic circumscriptions and phylogenetic relationships within the Bromelioideae, we have examined 215 individuals (representing 210 species in 23 genera) for leaf anatomical characters. Twenty characters were scored, including epidermal features, features of the structural fiber bundles, intracellular crystals and morphology of the hydrenchyma and aerenchyma. Of particular interest was the abundance of calcium oxalate druse crystals in nearly all samples. This type of crystal has been considered rare in monocots and has not been previously documented in Bromeliaceae. We explored the taxonomic usefulness of these characters with UPGMA cluster analysis. Overall, clustering into genera was poor, although some clusters contained a majority of some genera. For example, *Orthophytum* and *Cryptanthus*, thought to be sister taxa based on *ndhF* sequence data, were united by their absence of structural fiber bundles. However, some species in other genera also lack bundles, and leaf anatomy characters were insufficient to separate *Cryptanthus* and *Orthophytum* from the other surveyed genera or from each other. Discriminant analysis indicated that *Cryptanthus* and *Orthophytum* can be separated using a combination of characters including arrangement of the cells surrounding the vascular bundle, distinctness of the aerenchyma and binding of toluidine blue dye to the aerenchyma cells, but none of these characters was consistent. Anatomical leaf characters appear to be too homoplastic for taxonomic or phylogenetic utility, though they may prove to be useful autapomorphies for species identification.

- 113 SEVENER, HEATHER C*¹, KELLOGG, ELIZABETH A² and SCHAAL, BARBARA A.¹

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Molecular Evolution of APETALA1 Homologs in Poaceae

Flower development and the MADS family of transcription factors have been well studied in the model dicot system *Arabidopsis thaliana*. *APETALA1* is a member of the MADS family of transcription factors which determines floral meristem identity as well as organ identity in the first and second whorls of the *Arabidopsis* flower. Homologs of *AP1* have been discovered in many monocot species, including the model cereals *Oryza sativa* (*RAP1*) and *Zea mays* (*ZAP1*), where the gene appears to have been duplicated. At least one homologous copy of *ZAP1* and *RAP1* has an expression pattern in rice and maize flowers analogous to expression of *AP1* in *Arabidopsis*. This study seeks to characterize the molecular evolution of grass *AP1* homologs, as well as examine change or maintenance of the expression pattern of duplicate copies. We are creating a gene genealogy of *AP1* homologs in grasses, with a primary focus on the relationship of the duplicates within and between species, to create an evolutionary framework for further studies. We are currently using PCR to amplify the C-terminal region of *AP1* homologs in several major genera within Poaceae for cloning and sequence analysis. Preliminary data indicates a duplication event early in the evolution of the grass family, with a subsequent loss of intronic sequence in one class of duplicates.

- 114 SHERMAN, TIMOTHY D.*¹, BARGER, T. WAYNE²,

HOFFMAN, JOHN C.³ and VAUGHN, KEVIN C.³

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The unusual role of the Dodder (*Cuscuta pentagona*) seedling root

Seedlings of dodder are unique amongst dicotyledonous plants in that they emerge as a leafless, cotyledonless shoot, with only a small, swollen root-like structure. Although growth of the shoot end of the dodder seedling is dramatic, no change in "root" length is noted and the root tip withers within days after germination. Unlike most roots, the dodder root has neither recognizable root cap nor apical meristem. A strand of vascular tissue extends all the way to the root apex and is already differentiated into vascular elements upon germination. Cortical cells swell dramatically and contain large vacuoles. Nuclei in these cortical cells are extensively lobed, and are much larger than nuclei in shoot tips, indicating endopolyploidy. Microtubules are detected, although they are much less abundant than in shoot tissue of dodder or roots of other dicots, especially in roots older than one day past germination. Similarly, both \pm - and 2 -tubulin protein, as detected by immunoblots, are faint bands in root extracts, although both are easily detectable in extracts of shoot tissue. Cell walls of 1-2 day old roots have normal structure and contain well-defined cellulose microfibrils and well-developed middle lamellae. In contrast, later stages of development reveal cell wall loosening complexes and the degradation of wall structure, with a shift to a predominantly pectin wall composition. By 5-7 days post germination, all of the cortical cells have degenerated leaving the vascular strand as the last remnant of intact tissue in these roots. From these data, we conclude that the swollen appearance of the dodder root is due to the low level of microtubules, so that neither mitotic divisions nor cell elongation may occur and the loosening of the cell wall allowing for isodiametric expansion. Implication of these characteristics, with regard to the parasitic lifestyle, will be addressed.

- 115 TIAN, HUI QIAO², RUSSELL, SCOTT D.*¹ and YUAN, TONG¹

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Cell cycle synchronization in the male and female gametes of *Nicotiana tabacum*

Nuclear DNA content of male and female gametes of tobacco was determined using 4',6-diamidino-2-phenylindole (DAPI) using quantitative microfluorimetry. Pollen grains are released with generative cells in G₁ with a 2C DNA complement. Generative cell mitosis occurs in the pollen tube 8-12 h after germination, resulting in sperm cells with a 1C DNA content. This 1C DNA complement persists throughout pollen tube elongation in the style. Sperm cells deposited in the degenerated synergid have a DNA content between 1C and 2C, indicating that once in the synergid, sperm cells proceed through S-phase. Concomitant with pollen tube arrival, egg cells increase in DNA quantity from 1C (at pollination) to between 1 and 2C in egg cells at 48 h after pollination. Without pollination, S-phase in the egg cell is delayed by over a day compared to pollinated ovules. Newly-formed zygotes contain nuclear DNA concentrations between 3C and 4C at 52 h after pollination as nuclei near karyogamy. The zygote approaches 4C, at 84 h after pollination, long before zygote division. Tobacco displays cell fusion after completion of S-phase occurring at G2. Failure to achieve an optimized system for in vitro

fertilization in *Nicotiana* despite sustained long-term experimentation may reflect the challenges of achieving cell cycle synchrony in gametes isolated during protracted S-phases. Such male and female gametes may only reach cell cycle congruity moments before fusion.

116 TRUMAN, PATRICIA A. and HAYDEN, W. JOHN*

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Acalypha deamii: Distribution East of the Appalachians and Comparative Studies of Reproductive Anatomy

Acalypha deamii, once thought restricted to flood plains of the Ohio and mid-Mississippi River systems, is now documented from similar habitats in Virginia, Maryland, and West Virginia along the James, Potomac, Rappahannock, Roanoke (Staunton), and Shenandoah rivers. This species is recognized by two-carpellate gynoecia, large seeds, and the routine occurrence of allomorphic flowers and fruits, a feature sporadically found within this large genus. Stamineate, pistillate, fruiting, and allomorphic reproductive structures of *Acalypha deamii* and a closely related species, *Acalypha rhomboidea*, were studied via LM and SEM. Stamineate flowers are composed of four crystal-encrusted valvate sepals and ca eight stamens that bear divergent vermicular anthers with helically thickened endothecium, amoeboid tapetum, and tricolpate pollen. Pistillate flowers are bracteate, but otherwise naked, two-carpellate (*Acalypha deamii*) or three-carpellate (*Acalypha rhomboidea*), and have bitegmic, crassinucellate, anatropous ovules arising from an apical, axile placenta. Fruits from pistillate flowers are covered with trichomes, some gland-tipped, some simple and uniseriate. Internally, fruit walls bear a prominent inner-zone of sclerified cells involved in dehiscence and ballistic dispersal of seeds. Seeds are mottled tan to dark brown. Testa contains two prominent cell layers of the inner integument: the arcuate outer-most cells are sclerified and the inner-most cells are tracheid-like. Allomorphic reproductive structures largely match those of typical pistillate flowers and fruits. In contrast with pistillate flowers, allomorphic structures lack gland-tipped trichomes but have a markedly muricate surface, a one-carpellate ovary, and more weakly developed mechanical layers in the fruit wall. Further, allomorphic seeds of *Acalypha deamii* possess weak sclerification within the testa. Notably, materials studied clearly show presence of embryos within allomorphic seeds of both species.

ing and following breakup of the "Arcto-Tertiary" forest. The hypothesis of the late Daniel I. Axelrod is that the physiological and ecological characteristics of modern taxa have not changed from those of their Tertiary ancestors. The hypothesis of Jack A. Wolfe, on the other hand, is that taxa diverged in their physiological and ecological characteristics as they were exposed to climatic changes through geologic time. These two hypotheses were evaluated via a comparative study of seed dormancy and germination characteristics of four closely-related *Aristolochia* species in subgenus *Siphisia* that diverged from a common ancestor in the Tertiary: the California endemic *A. californica*, the Appalachian endemic *A. macrophylla*, the southeastern U.S. species *A. tomentosa*, and the east Asian *A. manshuriensis*, sister species to *A. macrophylla*. The embryo in all species is underdeveloped and physiologically dormant; thus, the seeds have morphophysiological dormancy (MPD). However, they differ in their dormancy-breaking and germination requirements. Seeds of *A. californica* require low temperatures (e.g. 10°C) to come out of dormancy and to germinate. In contrast, seeds of *A. macrophylla*, *A. tomentosa*, and *A. manshuriensis* require cold stratification (e.g., 5°C) to come out of dormancy, but they need temperatures of 15/6°C or higher to germinate. Thus, seeds of the temperate rainy-climate species *A. macrophylla*, *A. manshuriensis*, and *A. tomentosa* have nondeep simple MPD, and those of the Mediterranean-climate species *A. californica*, have nondeep complex MPD. These results support Wolfe's view on physiological and ecological changes in taxa within a lineage.

118 BASKIN, CAROL C.*³, BASKIN, JERRY M.¹ and YOSHINAGA, ALVIN Y.²

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Seed dormancy and germination of four Hawaiian montane lobelioid shrubs

From what we know about the world biogeography of the various classes of seed dormancy, it is apparent that little attention has been given to taxa in the tropical montane zone. Prior to this study, seeds of only nine tropical montane shrubs had been investigated in any detail. Thus, our purpose was to elucidate the dormancy-breaking and germination requirements of seeds of four endemic shrubs in Campanulaceae subfamily Lobelioideae (*Clermontia hawaiiensis*, *C. kakeana*, *Cyanea angustifolia*, and *Trematolobelia macrostachys*) from the montane zone in Hawaii. Seeds of all four species are water-permeable and have fully-developed embryos. After 4 wk of incubation, fresh seeds of *C. hawaiiensis*, *C. kakeana*, and *C. angustifolia* had germinated to 60% or more at 25/15 C but to 0% at 15/6 and 20/10 C, while those of *T. macrostachys* had germinated to only 0-2% at the three temperatures. However, after 6-20 wk of incubation at 15/6, 20/10, and 25/15 C, seeds of all four species had germinated to near 100% at the three temperatures. One-month-old seeds of *C. hawaiiensis*, *C. kakeana*, and *C. angustifolia* incubated at 28/20 C had germinated to 100% after 6, 3, and 10 wk, respectively, but no seeds of *T. macrostachys* had germinated after 12 wk. Following 1 mo of dry storage at room temperature, rate (speed) of germination increased for seeds of all species, especially at 15/6 and/or 20/10 C. Also, a 4-wk incubation period at 15/6 C, during which seeds were cold stratified at 6 C for 12 h each day, increased germination rates of seeds of all species subsequently incubated at 20/10 C. These results show that seeds of the four lobelioids have physiological dormancy. Of 13 shrubs in the world's tropical montane zone for which dormancy has been documented, eight have physiological dormancy, and five have physical dormancy.

ECOLOGICAL SECTION

CONTRIBUTED PAPERS

117 ADAMS, CHRISTOPHER A.*, BASKIN, JERRY M. and BASKIN, CAROL C.

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Comparative seed ecophysiology of four closely-related *Aristolochia* species: a test of two hypotheses on changes in ecological and physiological requirements and tolerances in plant lineages

This research examined two opposing views on changes in physiological and ecological requirements and tolerances of species in the same clade that evolved in response to changes in climate dur-

- 119 BASKIN, JERRY M.*¹, BASKIN, CAROL C.², DAVIS, BARBARA H.¹ and GLEASON, SEAN M.³

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Physical dormancy in seeds of *Dodonaea viscosa* (Sapindales, Sapindaceae) from Hawaii

Dormancy in seeds of *Dodonaea viscosa* is due to a water-impermeable seed coat (physical dormancy, PY) only; the embryo is not dormant. Thus, mechanically-scarified seeds imbibed water (ca. 95% increase in mass) and germinated to high percentages over a wide range of temperature regimes in both white light and darkness, whereas nonscarified seeds did not take up water. Dry heat at 80–160 °C and dipping in boiling water for 1–60 seconds also broke dormancy in a high percentages of the seeds, and continuous far-red light was not inhibitory to germination. However, dry storage in the laboratory for >1 year did not overcome dormancy. Seeds made water-permeable by boiling imbibed water, and thus germinated, at a much slower rate than those made water-permeable by mechanical scarification. We suggest that boiling opened the “water gap” in the seed coat (not yet described in Sapindaceae but present in other taxa with PY) and that water entered the seed only through this small opening, thereby accounting for the slow rate of imbibition and subsequent germination. Physical dormancy now has been shown to occur in seeds of this polymorphic, pantropical species from Australia, Brazil, Hawaii, Mexico, and New Zealand. The low amount of dormancy reported for seed lots of *D. viscosa* in China, India, and Pakistan probably is due to collecting seeds before they dried to the critical moisture content for development of water-impermeability of the seed coat. Germination of nondormant seeds over a wide range of temperatures and in white light, far-red (leaf-canopy shade) light, and darkness are part of the germination strategy of a wide range of taxa whose seeds have PY at maturity.

- 120 BELL, TIMOTHY*¹ and BOWLES, MARLIN²

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Variation in Persistence Probability Among Subpopulations for a Restored Illinois Population of the Federal Threatened Pitcher's Thistle (*Cirsium pitcheri*)

This is the first study of a restored endangered plant to evaluate the population's ability to persist. Pitcher's thistle (*Cirsium pitcheri*) is a short-lived herb endemic to western Great Lakes sand dunes where it colonizes successional habitats and requires frequent cohort replacement to maintain populations. It is federal threatened and went extinct from its Illinois habitat before 1920. As part of federal and state recovery planning, suitable restoration habitat was identified at Illinois Beach Nature Preserve and population restoration began in 1991 using Wisconsin, Indiana and Michigan seed sources. Because this species is monocarpic, annual translocation of greenhouse-propagated plants was used to build up large cohort numbers. All transplants and their descendants have been monitored since restoration began. Stage structured demographic analysis indicates that population growth rate varies among years and between subpopulations. Minimum viable population size and probability of persistence will be compared for these subpopulations.

- 121 BOYD, ROBERT

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Factors Affecting Seed Production by the Endangered Chaparral Shrub

Fremontodendron californicum ssp. *decumbens* (Sterculiaceae). Insect herbivory can greatly decrease plant reproductive success. This experiment reduced insect herbivore damage to branches of the federally endangered Pine Hill flannel bush, *Fremontodendron californicum* ssp. *decumbens*, during two flowering seasons to explore interactions among factors that can limit reproductive output (e.g., resource limitation, pollen limitation, seed predation). Experimental treatments included insecticide and control (water spray) treatments in 1983, with these and an insecticide plus enclosure treatment in 1984. Enclosures were designed to decrease herbivory of fruits by rodents. Reproductive stages (flower buds, flowers, and fruits) were counted and examined periodically for damage, and mature fruits were collected and seeds counted. In both years, insecticide treatment greatly decreased insect herbivory, increasing survival of flower buds, flowers, and fruits so that seed production increased 14- to 27-fold. Pollination success was unaffected by treatments, but fruit abortion increased significantly on insecticide-treated branches. Rodent herbivory of fruits greatly impacted fruit production on insecticide-treated branches in 1983, an El Niño-Southern Oscillation (ENSO) year, but was relatively unimportant in 1984 (a non-ENSO year). I concluded that: 1) seed output is limited by insect herbivores and can be greatly increased by insecticide treatment; 2) other limiting factors (resource limitation, rodent herbivory) increase in importance and partially compensate for increased fruit survival when insect herbivory is lessened by insecticide treatment; and 3) rodent fruit herbivory varies with climate, being greater during years characterized by an ENSO event.

- 122 BROWN, SARAH M.* and STEPHENSON, ANDREW G.

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The effect of two environments on the fitness of Campanula plants that differ in their self-compatibility phenotype

Campanula rapunculoides is a perennial herb possessing an SI (self-incompatibility) system that discourages self-fertilization; however, there is variation in the strength of SI among individuals in a population, and this variation has been shown to be heritable. If an individual is weakly SI, self-fertilization can occur by two methods: autogamous pollination, when the stigmatic lobes of aging flowers reflex to touch the pollen-coated style, or through geitonogamous pollination, when pollinators transfer self pollen within an inflorescence or from an adjacent inflorescence from the same plant. Previous studies have shown that the rate of self-fertilization in a population varies with differing access to pollinators. We tested the hypothesis that selfing rates in environments with different pollinator access will vary according to a plant's SI phenotype. Pollinator exclusion cages were used to create two treatments. Pollinator limited treatment cages remained closed for three days and were opened for 24 hours every fourth day, while control cages remained open continuously. Each cage had 14 pollen donor plants and 2 clones of each of two phenotypes, one with very weak SI and one with strong SI, that served as recipient plants. Recipient plants had an alternate allele at the GPI locus. The resulting seeds were collected and scored for paternity. We found that the two phenotypes performed differently in

different environments. In cages with full pollinator access, the two phenotypes had the same selfing rate. However, in pollinator-limited cages, the weakly SI phenotype produced a significantly higher proportion of selfed seeds. In addition, seed production was reduced by limited pollinator access, and this reduction also varied with phenotype. Because a plant's selfing rate varies according to its SI phenotype and pollinator availability, selection pressure favoring a particular phenotype can also vary, which can support the stable maintenance of a mixed mating system.

- 123 CULLEY, THERESA M.*¹, DUNBAR-WALLIS, AMY K.², SAKAI, ANN K.², WELLER, STEPHEN G.² and CAMPBELL, DIANE R.²

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The quantitative genetics of ecophysiological traits in the gynodioecious shrub, *Schiedea salicaria* (Caryophyllaceae)

The potential for ecophysiological traits to respond to selection was examined with a quantitative genetic approach in *Schiedea salicaria*, a gynodioecious species endemic to the dry shrubland of the Hawaiian Islands. We measured narrow-sense heritabilities and trait means for a number of ecophysiological and fitness-related morphological traits in females and hermaphrodites. Stomatal conductance (g) and photosynthetic rate (A) were heritable in hermaphrodites ($h^2 = 0.38$ and 0.25, respectively), indicating the potential for adaptation, but the same traits were not heritable in females. Instantaneous water-use efficiency (A/g) and intercellular CO_2 concentration (C) lacked significant heritability for either sex. Sexes did not differ significantly in mean values of A, g, A/g, or C, but hermaphrodites had greater specific leaf area than females. Females produced significantly more flowers with greater seed biomass per flower than hermaphrodites, but both sexes had similar numbers of fruits and seeds per flower. Floral traits on a per flower basis were significantly heritable in hermaphrodites (h^2 ranged from 0.24 to 0.56), but not in females. There were no genetic correlations between ecophysiological and morphological traits associated with fitness. Although the potential exists for some ecophysiological traits to respond to selection in *S. salicaria*, it may be complicated by other factors influencing differences in heritability between the sexes.

- 124 DEVALL, MARGARET S.* SCHIFF, NATHAN M. and SKOJAC, STEPHANIE A.

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Introduction of the endangered pondberry (*Lindera melissifolia* [Walt.] Blume) to new sites in Mississippi

Pondberry (*Lindera melissifolia* [Walt.] Blume, Lauraceae) is an endangered shrub that occurs in seasonally flooded wetlands and on the edges of sinks, ponds and depressions in the southeastern United States. It is a stoloniferous, clonal shrub and is dioecious, with small yellow flowers that bloom in spring. Its distribution and abundance have been affected by clearing of land and habitat destruction and alteration. We investigated establishing new pondberry populations as an aid in conserving the species. We dug young pondberry stems from a natural population, planted them in pots, and

kept them for several weeks in a greenhouse. We then translocated them to five protected locations in the field in Mississippi. Each pair of male and female plants was surrounded by a wire cage on wooden supports, and was labeled. We watered the plants during dry spells, monitored them, and applied pesticide and fertilizer as needed. After two years, survival of the plants has been good. At one site, the plants were infested with scale. Many of the plants had stems that increased in height, although the height of the tallest stems decreased. Many of the plants produced new stems, but some older stems died during the year. The Lower Mississippi Alluvial Valley, in which most of the present pondberry populations occur, is one of the most endangered ecosystems in the United States. Much of the former forest has been cleared for agriculture and other uses. Most pondberry habitat is fragmented today, thus dispersal is very limited and populations that die out usually will not be replaced. Existing pondberry populations should be protected and searches for new populations should continue, but this study indicates that introduction of pondberry to new protected sites can be helpful in assuring survival of the species.

- 125 DEVLIN, DONNA

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Effects of an Seedling Predator of Distribution of Rhizophora mangle

Predators that feed differentially, selecting only one or a few species can eliminate propagules and seedlings of certain canopy species and structure species diversity and abundance patterns of the canopy. In a manipulative experiment, I studied the affect of a specialist propagule and seedling predator, *Coccotrypes rhizophorae* on its host, *Rhizophora mangle*, in the Ten Thousand Islands National Wildlife Reserve (TTINWR) in southwest Florida. The experiment was conducted in three forest (canopy) types on each of 12 different islands. Six of the islands were located on the interior edge, near the mainland of the TTINWR and six were located on the exterior gulf edge. I found that in *C. rhizophorae* was the most important seedling predator of *R. mangle*, in the TTINWR. In one forest type this predator was responsible for the mortality in over 90% of *R. mangle* seedlings. Predation rates varied with light levels and tidal frequency and period of inundation. There were significant differences in predation rates among forest types and between interior and exterior islands.

- 126 EVANS, M. E. K.*¹, HAHN, W. J.² and HEARN, D.¹

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Testing life history theory in a phylogenetic context: the association of climate and habit in evening primroses (*Oenothera*, Onagraceae)

Evolutionary ecologists have long sought to understand the conditions under which perennial (iteroparous) vs. annual (semelparous) life histories are favored. Based on the classic models of Charnov and Schaffer (1973), we predict that a reduction in adult survival should favor the annual habit. We assume that in herbaceous plants without the capacity to store water, increasing aridity should reduce adult survival. We tested for an association between aridity and annuality in the context of phylogenetic hypotheses for a monophyletic lineage of herbaceous plants that includes annuals (7 taxa), perennials (12

taxa), and 2 taxa plastically capable of more than one habit (sections *Anogra* and *Kleinia* of the genus *Oenothera*, Onagraceae). We quantified aridity via descriptive statistics summarizing long-term records of temperature and precipitation from weather stations near herbarium localities throughout the range of each taxon. The phylogenetic hypotheses were based on DNA sequence data from one nuclear (ITS, 700 base pairs) and two chloroplast spacer regions (trnL-trnF and trnH-trnK, 425 and 1,535 base pairs, respectively). We mapped habit and climate onto all trees consistent with the maximum likelihood tree, and examined the correlation of phylogenetically independent contrasts of habit and climate. Despite phylogenetic uncertainty, we can say that habit has changed several times in this small group. Changes toward annuality have generally been associated with increased temperature, and in some cases with decreased precipitation in the season immediately following reproduction. These data are consistent with the idea that reduced adult survival, as a result of increased aridity, favors the annual habit. We further suggest that increased temperature favors the annual strategy for another reason: because the high growth rates needed to move through the life cycle rapidly are achievable in warmer environments.

127 FAIVRE, AMY E.

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Self-Incompatibility Systems and Effective Pollinators of Seven Understory *Psychotria* Species on Barro Colorado Island, Panama

Distylous plants produce flowers of two different morphologies and have a unique self-incompatibility system. Studies of distylous species have recorded quite a bit of variation in the expression of this incompatibility system. To explore this variation further, the incompatibility systems of six distylous *Psychotria* species and one homostylous species were studied on Barro Colorado Island, Panama. *Psychotria* contains the greatest number of distylous species of any angiosperm genus. Hand-pollinations were done on bagged flowers of *P. acuminata*, *P. chagrensis*, *P. deflexa*, *P. emetica*, *P. hoffmannseggiana*, *P. horizontalis*, and *P. ipecacuanha*. With the exception of *P. hoffmannseggiana*, these species are distylous. Pollen tubes from hand-pollinations were observed using fluorescence microscopy. Preliminary results suggest that in all six distylous species, the incompatibility system in the short-styled floral morph operates at the stigma surface. For long-styled flowers, the incompatibility system often leads to pollen tube growth inhibition within the style, though some individuals were found with pollen tube growth inhibited at the stigma surface. Long-styled flowers of two species, *P. acuminata* and *P. deflexa*, rarely had self or intramorph pollen tube growth inhibited, suggesting the incompatibility system within the long-styled floral morph may be absent in these species. Similar results following out-crossed and selfed pollen of homostylous species *P. hoffmannseggiana* indicated this species is self-compatible. Insect visitors to each species were observed and effective pollinators were determined. *Paratetrapedia calcarata* and *Trigona fulviventris* are thus far the most effective pollinators of *P. acuminata*, *P. hoffmannseggiana*, *P. horizontalis*, and *P. ipecacuanha*. *Osiris mourei* is also an effective pollinator of *P. ipecacuanha*. *Psychotria chagrensis* is effectively pollinated by *Trigona pallens*.

128 FUMERO-CABAN, JOSE J.*¹ and MELENDEZ-ACKERMAN, ELVIA²

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Behavior and pollination efficiency of flower visitors of *Pitcairnia Angustifolia* (Bromeliaceae).

Pitcairnia angustifolia is a large terrestrial bromeliad with nectar rich, long tubular, red flowers, a morphology that suggests a pollination syndrome by long-billed hummingbirds. To test this idea, we recorded the identity and frequency of visitation of all flower visitors in natural populations of *P. angustifolia* at the Rio Abajo Forest Reserve, Puerto Rico. In addition, we estimated the pollinator efficiency of these visitors by counting the number of pollen grains that were deposited by each of these visitors on stigmas of newly open flowers. In total there were four species of flower visitors to this plant species including a long-billed hummingbird (*Anthracothorax viridis*), honeybees (*Apis mellifera*), bananaquits (*Coereba flaveola*) and a short-billed hummingbird (*Chlorostilbon maugaeus*). While all flower visitors deposited pollen upon visitation, our observations indicate that only the first two carry out legitimate pollinations while the last two behave primarily as nectar robbers. In agreement with a long-billed hummingbird pollination syndrome, *A. viridis* was the most efficient pollinators. Nevertheless, visits by *A. viridis* ranked low in frequency while the most frequent flower visitors were bananaquits. The overall results suggest the potential for antagonistic selective forces on flower traits that may serve in pollinator attraction.

129 HAWKINS, TRACY S.¹, BASKIN, JERRY M.¹ and BASKIN, CAROL C.*²

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A comparative study of biomass allocation in seed- and ramet-derived plants of *Cryptotaenia canadensis* (Apiaceae): a monocarpic species of the North American temperate deciduous forest

Life cycle phenology and biomass allocation patterns were studied for plants of *Cryptotaenia canadensis* (Apiaceae) growing in a temperate deciduous forest in eastern Kentucky, USA. This species reproduces sexually by seeds and asexually via monocarpic ramets. Seed-derived plants reproduced both sexually and asexually in the second growing season. Ramet production was concurrent with flowering, and the parent plant died at the end of the growing season. Emergence, growth, and development of the ramet occurred in the same growing season in which it was produced, and flowering occurred the following summer. Thus, seed-derived plants behaved as biennials, and ramet-derived plants behaved as annuals. Seed-derived juveniles had a slightly higher percent survivorship to flowering than did ramet-derived juveniles. However, fewer surviving seed-derived plants flowered than did surviving ramet-derived plants. Biomass allocation for plants harvested at four growth stages over two complete life cycles were significantly different between plant derivations during vegetative growth stages (fall and spring rosettes). During reproductive growth stages (flowering and late-fruiting), biomass allocation did not differ between ramet- and seed-derived plants harvested in the same year. Sexual reproductive mass was strongly correlated with vegetative mass for both ramet-derived ($r^2 = .8081$) and seed-derived ($r^2 = .8125$) plants, with no significant difference be-

tween slopes ($P = .2254$) or intercepts ($P = .3665$). Ramet mass was less dependent on plant size (ramet-derived, $r^2 = .6143$; seed-derived, $r^2 = .6823$), and slopes ($P = .4252$) and intercepts ($P = .2904$) were not significant. Regressions of sexual vs. asexual reproductive mass varied with year and cohort, and no direct trade-offs were observed. This is one of a very few studies of biomass allocation in a plant species with the *Cryptotaenia*-type life cycle.

- 130 HUANG, MINGJUAN^{*1}, SPENCER, LAWRENCE J.¹, STRICKER, NATHANIEL J.², WU, CHANGSHAN³ and RAMIREZ, J. RAUL¹

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Vegetation Classification of Killbuck Wildlife Area, Ohio, Using Multi-Seasonal Landsat TM Imagery

Remote sensing has become an increasingly important tool for mapping and monitoring vegetation over large spatial extents. This paper presents our effort in mapping the land cover of Killbuck Wildlife Area as the pilot study of the Ohio Gap Analysis Project, undertaken in partnership with U.S. Geological Survey (USGS) and Ohio Department of Natural Resources (ODNR). Landsat Thematic Mapper (TM) data of leaf-on and leaf-off periods were processed with Tasseled Cap transformation using ERDAS IMAGINE 8.5. The transformed image was then stratified into separate units of upland, wetland, and urban areas using the National Land Cover Data set (NLCD) and Ohio Wetland Inventory (OWI). A hybrid supervised/unsupervised classification was conducted in producing the vegetation map. Other ancillary digital data including National Elevation Dataset (NED) and the aerial photographs acquired by the National Aerial Photography Program (NAPP) and ODNR were used with ground-truth data to generate signatures for classification and assess the accuracy of the final vegetation map. Our initial results indicate an improved accuracy in vegetation classification in comparison with previous Ohio GAP studies. Potential applications of the Killbuck vegetation map to animal modeling and land use planning will also be discussed.

- 131 JONES, CYNTHIA^{*1}, RYAN, NANCY¹, SCHLICHTING, CARL¹ and NICOTRA, ADRIENNE²

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Leaf shape, size and specific leaf area in the highly diverse South African genus, *Pelargonium*

Recent studies have shown that across a broad range of angiosperms, specific leaf area (SLA) is highly correlated with several functional leaf traits. However, there is little evidence of a strong relationship between SLA and leaf size. We were interested in whether a stronger relationship could be detected at a smaller scale, i.e. within a highly variable genus, and whether that relationship would show a significant phylogenetic component. The diversity of leaf shape, size and growth form in *Pelargonium* (Geraniaceae) presents an opportunity to explore these issues. *Pelargonium* is distributed largely in South Africa, and the genus is thought to represent a relatively recent radiation that occurred in response to aridification resulting from the establishment of the cold Benguela current. We grew pairs of spe-

cies with more-lobed and less-lobed leaves from six sections in a greenhouse experiment with two levels of water availability, "normal" and low water. For the overall analysis of plants in the normal water treatment, both section (i.e. the phylogenetic effect) and species (nested within section) explained significant amounts of variation in all leaf traits measured. More-lobed leaves had lower SLA values in all species pairs. The relationship between SLA and leaf area was not significant but there was a significant relationship between SLA and lamina length, presumably because longer leaves were more lobed in four of six pairs. When treatment was included in the overall analysis, the effect of treatment on SLA was significant. Interestingly, all species except one responded to water stress with higher SLA values. These results indicate strong phylogenetic effects on SLA within *Pelargonium*. SLA is correlated with leaf shape and length. Plasticity in SLA was observed in response to water stress, but the direction of the response was counter to that shown in several other studies.

- 132 KIM, G. Y.*¹, LEE, C. W., PARK, S. B. and JOO, G. J.
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Grazing by wintering waterfowl on food plant *Scirpus triquetus* in a tidal mudflat

The influence of waterfowls' grazing activity on their foodplant in an estuarine ecosystem was evaluated using enclosures. The Nakdong River estuary (S, Korea) is an important habitat for wintering birds in the international flyway. *Scirpus triquetus*, a major foodplant for wintering waterfowls (swans, ca. 3,000 ind.; geese, ca. 3,500 ind.; ducks, ca. 60,000 ind.), was dominant in the estuary (ca. 200 ha). Enclosures (12 plots, each of 1.5m x 1.5m, mesh size 3 cm) were placed to compare the impact of grazing on aboveground and underground biomass from October to February. The tubers were distributed in 10-30cm depth underground (10-20cm, 29.1%; 20-30cm, 65.4%, n=10). Ten-day to monthly interval measurements indicated that the waterfowl foraged mainly on *S. triquetus* tubers. Waterfowls extensively grazed over 60% of tubers in the first 10 days after their arrival in mid October, thereafter the feeding rate gradually decreased. Within this layer, biomass of tubers in Feb. were statistically different between grazed (1.1 ± 0.9 g×dw m⁻², n=10) and ungrazed sites (86.1 ± 19.3 g×dw m⁻², n=10) ($|t|=13.9$, $p<0.001$, $\pm=0.05$). Impacted plant bed became an almost plant free mudflat while decomposition of plant in covered area was very slow. Plant growth response in intensively grazed area during the growing season (May-October) deserves a further study.

- 133 KOPTUR, SUZANNE^{*1} and PINTO-TORRES, ELENA²

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Pollinators and their activity at flowers of *Jacquemontia reclinata*, an endangered morning glory of south Florida coastal strand

The coastal environment of southeastern Florida has been dramatically transformed by development and human habitation so that the coastal strand endemic, *Jacquemontia reclinata*, is federally listed as endangered. Though individual plants are much larger and vegetatively somewhat distinct from its sister pine rockland endemic, *Jacquemontia curtissii*, its flowers and floral biology are remarkably similar. Both of these neoendemic species have generalized, entomophilous flowers with rotate, white corollas, containing nectar, last-

ing only one day. Both species are visited by a wide array of insects (primarily Diptera, Hymenoptera, and Lepidoptera). At all sites visitors to flowers of *Jacquemontia reclinata* have been observed, though diversity was greatest at the largest sites where the majority of individual plants exist.

- 134 LAWLESS, P.J.*¹, BASKIN, J.M. and BASKIN, C.C.
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Analyses of Richness, Diversity, and Similarity in Seven Xeric Limestone Prairies in the Interior Low Plateaus Physiographic Province in Kentucky

Xeric limestone prairies (sensu J. Baskin et al. 1994. *Castanea* 59: 226-254; J. & C. Baskin 2000. *Ann. Missouri Bot. Gard.* 87: 286-294) are characterized by shallow rocky soils, dominance of C4 perennial grasses (*Schizachyrium scoparium*, *Sorghastrum nutans*, *Andropogon gerardii*, and/or *Bouteloua curtipendula*), a forb flora rich in species of Asteraceae, and susceptibility to woody plant invasion. A nested subquadrat sampling design adapted from R.K. Peet et al. (1998. *Castanea* 63: 262-274) was used to quantitatively sample seven xeric limestone prairies in the Shawnee, Highland Rim, and Bluegrass sections of the Interior Low Plateaus physiographic province in Kentucky. Frequency was determined at multiple scales, and cover was estimated in 100-m² quadrats. Relative cover and relative frequency values in 100-m² quadrats were used to calculate an I.V. for each species within a site. Coefficients of community (Sorensen's index weighted for cover) were used to determine number of associations. Statistical analyses were performed to investigate potential correlations between collective cover of annual grasses, species richness, and species diversity (relative cover used as a surrogate for proportional dominance index). More than 190 species were recorded in the 42 100-m² quadrats sampled. Families with highest species richness were Asteraceae, Poaceae, and Fabaceae. *Schizachyrium scoparium* had the highest I.V. in all seven sample sites. *Echinacea simulata* had the highest I.V. among forbs in five of seven sites. *Juniperus virginiana* and *Cercis canadensis* ranked first or second in percent relative frequency of trees in four of the seven sites. Xeric limestone prairies in Kentucky are similar to communities referred to as "glades" or "limestone glades" in the Ozarks and Midwest and "barrens" in the Southeast. These C4, perennial grass-dominated communities are distinctly different from the C4, annual grass-dominated limestone cedar glades in the Central Basin of Tennessee and other physiographic regions of the Southeast.

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Effects of water depth on growth and biomass allocation in *Eleocharis cellulosa* Torr.

Fluctuating water levels pose significant constraints on emergent macrophytes, as in the long-hydroperiod marshes of the Florida Everglades. We studied both the acclimation and rapid responses of *Eleocharis cellulosa* Torr. (Cyperaceae) to water depths of 7 cm and 54 cm in large tanks. After acclimation to water depths for 80 weeks, deep water plants produced (1) taller, thicker and fewer shoots; (2) fewer ramets; (3) less total biomass; and (4) a higher percentage of biomass allocated to shoots and relatively less to roots and rhizomes.

Despite the differences in shoot lengths between the two treatments, shoot heights above the water surface were similar. Shoots in both treatments varied in anatomy and mass/length above and below the water surface. Tissues above the surface were more robust with thick secondary walls in the outer pericinal and radial epidermal cells, and several chlorenchymatic palisade layers beneath. Those beneath the surface lacked such characters. When shallow water plants were transferred to deep water, shoots elongated rapidly, with younger shoots responding more than old ones. When deep-water plants were transferred to shallow water, emergent shoots quickly died and were replaced by new shoots. Overall, plants exposed to rapid changes in water level quickly adjusted allocation patterns towards those of control plants in their new environment, but deep-grown plants adjusted much more slowly than shallow-grown plants. The costs of transition from deep to shallow water are greater than the reverse, in large part due to rapid, high shoot mortality. These plastic shifts in morphology, shoot demography and biomass allocation allow individuals of *E. cellulosa* to produce shoots with optimal characters for biomechanical support and adequate surface exposure to allow gas exchange for the pressure flow of oxygen into the rhizomes and roots.

- 136 LIU, HONG* and KOPTUR, SUZANNE
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Breeding System and Pollination of a Narrowly Endemic Herb of the Lower Florida Keys: Impacts of the Urban Wildland Interface

We examined the breeding system and pollination of *Chamaecrista keyensis* Penell (Fabaceae: Caesalpinoideae) and the effects of urban edge and mosquito control on reproduction of this rare endemic herb of the Lower Florida Keys. Controlled hand-pollination treatments were applied to plants in the field. Although *C. keyensis* flowers are self-compatible, they are not capable of automatic selfing. Inbreeding depression was observed in both seed set and percentage seed germination. Bees of seven genera were observed visiting *C. keyensis* flowers during the peak flowering season (June to July). Only *Xylocopa micans* and *Melissodes* sp. may be effective pollinators for *C. keyensis*, as they were the only bees that "buzz-pollinate" this species, which has poricidal anther dehiscence. *Chamaecrista keyensis* received substantially more visits by *X. micans*, but fewer visits from *Melissodes* spp. in urban edge vs. forest sites. Aerial mosquito spraying may exacerbate the existing pollinator limitation suffered by *C. keyensis* by reducing the number of visits by the buzz-pollinating bees. Individuals of *C. keyensis* at urban edges produced fewer seeds per fruit than did individuals in a pristine forest mainly because of greater insect seed predation.

- 137 LUCKEYDOO, LEE
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Vegetation Occurring in Passively Revegetated Constructed Wetlands Receiving Agricultural Drainage Waters in Northwest Ohio

Constructed wetlands and sedimentation ponds are introduced into the agricultural landscape for many reasons, including wetland habitat and water quality improvement. Three such wetlands have been constructed at Wetland Reservoir Subirrigation Project (WRSIS) sites on previously converted cropland adjacent to agricultural fields in northwest Ohio. Revegetation in these constructed wetlands relies on passive recruitment from the seed bank and immigration. Surveys of constructed wetland vascular vegetation were conducted from 1998-

2001, ending six years post-construction of the basins, resulted in total species list of 77 unique species for the three combined constructed wetland sites. The greatest diversity of species occurred in the infrequently submerged and waterline (frequently submerged) zones. Wetland indicator species comprised approximately 40% of species for each location, and of the wetland indicator species, the majority, ranging 71-86% for the three studied sites, were native to the United States. Dominant species, species with high importance factor (IF) rankings, of the studied WRSIS constructed wetlands were most likely from local sources. Some of the high IF species were considered weeds in local agricultural fields and nearby drainage ditches and streams, including *Polygonum persicaria* and *Scirpus atrovirens*. Many species were supplied from erosion control efforts, for example *Medicago sativa* and *Echinochloa crus-galli* which were originally seeded into the buffer zones. Species included in IF lists and the occurrence of less than 50% wetland indicator species suggest planting or seed may expedite desired vegetation development in WRSIS or similar constructed wetland basins.

138 METTLER-CHERRY, PAIGE A.*¹ and SMITH,

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Effects of the flood of 1993 on Illinois River floodplain vegetation and its relationship to the threatened species, *Boltonia decurrens*

The 1993 flood of the Mississippi River and its tributaries is widely regarded as the largest flood event recorded in this river system in terms of depth and duration. The Illinois River flows from Chicago (IL) to the confluence of the Mississippi and Missouri Rivers immediately north of St. Louis (MO). The effects of the 1993 flood were more severe on the southern end of the Illinois River, creating a gradient of flood effects from the headwaters of the river to its terminus. As part of a larger study examining the population dynamics of the threatened, floodplain species, *Boltonia decurrens*, we studied the effects of flooding on vegetation at *Boltonia decurrens* population sites. Four sites spanning the range of *Boltonia decurrens* were studied from 1994-2000. Three belt transects (10m x .25m) were established at each site, vegetation was identified at anthesis, number of individuals recorded and cover class (Braun-Blanquet) estimated for each species. Community composition was analyzed using Detrended Correspondence Analysis (DCA). Spearman Rank Correlations were calculated to determine the relationship of the ordination axes to the four environmental variables measured (flood length, plot elevation, number of years since the 1993 flood and time of annual flood recession) and the number of *Boltonia decurrens* individuals. The first DCA axis was most strongly correlated with flood length ($r=0.415$, $p=0.0001$) and the second axis was most strongly correlated with elevation (0.369, $p=0.002$) and number of years since the 1993 flood (0.635, $p=0.00009$). The number of *Boltonia decurrens* individuals was positively correlated with axis 1 (.279, $p=0.0206$) indicating larger populations of *Boltonia decurrens* are correlated with longer flood periods, and negatively correlated to axis 2 (-0.349, $p=0.0034$), indicating a decline in individuals with greater time since the 1993 flood.

139 MOODY, MICHAEL L.* and LES, DONALD H.
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Hybrid watermilfoil (*Myriophyllum spicatum* x *M. sibiricum*; Haloragaceae) populations: an invasive threat to North American lakes

Eurasian watermilfoil (*Myriophyllum spicatum*) has been considered the most problematic submerged aquatic invasive in freshwater lakes throughout North America. It was first recognized in North America in 1942 and is now known from 45 states and 3 Canadian provinces. Hybridization has been linked to aggressiveness and invasiveness in several wetland plants. Invasiveness in hybrid plants is often attributed to hybrid vigor or novel genotypes with a selective advantage. Recently invasive populations of hybrids between the nonindigenous *M. spicatum* and the indigenous *M. sibiricum* were identified in lakes of Minnesota and Wisconsin. Further evidence now shows that in lakes where the invasive hybrid is found pure *M. spicatum* is absent. In addition, 13 lakes throughout Minnesota and Wisconsin, previously believed to have invasive *M. spicatum*, have now been found to be infested with hybrid plant populations. The extent of the geographic range of the invasive hybrid has yet to be determined, but the increasing number of hybrid populations being uncovered suggests the hybrid genotype may be common. There is correlative data that suggest environmental differences exist in lakes where either pure *M. spicatum* or the hybrid is robust. There is also some correlative evidence suggesting the hybrid genotype may influence the effectiveness of the watermilfoil weevil (*Euhrychiopsis lecontei*) as a biocontrol agent.

140 NE'EMAN, G.*; SCHWARTZ, R. and PEREVOLOTSKY, A.
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The effect of grazing on reproduction and population dynamics of the Mediterranean geophyte *Anemone coronaria*

The Mediterranean flora of Israel consists of about 1000 species, including 10% geophytes, most of which grow in open habitats. *Anemone coronaria* L., a beautiful geophyte, produces dense flowering fields that attract many visitors to open landscapes. Grazing may affect plant's reproduction, survival and consequently population dynamics. Geophytes have underground regeneration buds and are considered as a grazing resistant growth form. A few experimental studies examined the mechanism of grazing impact on plant reproduction and population dynamics. We have investigated the effect of cattle grazing on plant reproductive capacity and population density of *A. coronaria* in northern Israel. Ten pairs of experimental plots were established, and one of each pair was fenced against grazing. Monitoring took place for five years. Two weeks of continuous cow grazing reduced the herbaceous biomass by 75%, grass height by 90% and increased sun radiation at ground level by 40%. Cows avoided eating *A. coronaria* flowers, but damaged mature plants by trampling. We have found that the number of flowers and fruits per plant as well as fruit-set were not affected by grazing, but the number of dispersal units per plant decreased from 0.8 to 0.4. Five years of grazing exclusion reduced the density of flowering plants from 13 to 6 plants/m² and seedling density from 1.5 to 0.6 individuals/m². The results indicate that dense annual herbaceous vegetation interferes with *A. coronaria* mainly through limiting germination sites and competition for light. The fact that the average height of *A. coronaria* flowers was

26% higher without grazing implies that light is scarce for the geophyte when grasses are abundant. Grazing lowers competition from the herbaceous sward and enhances seed germination and seedling establishment, plant growth and reproduction. In conclusion, grazing seems to be essential for the development and maintenance of large *Anemone* populations.

- 141 O'BRIEN, ERIN* and BROWN, JOEL
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Effects of spatial heterogeneity on the Tragedy of the Commons response to competition

The Tragedy of the Commons theory has successfully been applied to belowground competition in annuals. Earlier experiments have shown that plants "over-proliferate" roots in patches shared with neighbors compared to patches they exclusively occupy. In many cases this results in reduced reproductive output. Here we introduce spatial heterogeneity into the interaction using two annual asters native to the tallgrass prairie in a split-root, multiple-pot design. Our results show that when competition is symmetrical, heterogeneity significantly alters the allocation patterns observed in homogeneous scenarios with correlated effects on the growth of other tissues. However, introducing asymmetries via resource distribution that favor or disfavor an individual in a pair of plants appears to have only a minimal impact on the other individual's root allocation strategy. These results suggest that the application of the Tragedy of the Commons model must be expanded to incorporate patch heterogeneity in order for its predictions to apply outside of an agricultural context.

- 142 PINTO-TORRES, ELENA* and KOPTUR, SUZANNE
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Investigating the breeding system of an endangered coastal dune plant, *Jacquemontia reclinata* (Convolvulaceae)

Jacquemontia reclinata, a coastal perennial vine endemic to Florida, was given endangered species status under the Endangered Species Act in 1993. Its remaining populations, threatened by habitat loss to development, persist in isolated habitat fragments along the southeastern coast of the state. The estimated total number of remaining plants is less than 900, with most in two relatively large sites. The species' breeding system was studied by conducting hand pollination and seed germination experiments using 65 plants grown from the seeds of 16 individuals in the two largest populations. To determine whether outcross pollen is necessary to produce viable seeds, six hand pollination treatments were performed on 665 flowers of the experimental plants. Seeds from successful crosses were weighed and placed in pots to germinate individually. There were significant differences among hand pollination treatments in fruit and seed set, but not mean seed weight. Percentage of seed germination differed substantially among treatments two months after planting. The results of these experiments indicate that *Jacquemontia reclinata* has a mixed mating system; it is able to set fruit with viable seeds with self pollen, but outcrossed pollen produces significantly greater fruit and seed set than self pollen.

- 143 RICE, STANLEY A.

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Anti-herbivore defense in male and female bois-d'arcs, *Maclura pomifera* (Moraceae) in southern Oklahoma

Bois-d'arcs are native to southern Oklahoma but have been planted widely through the United States. Their pollination strategy is not fully understood, and the seed dispersers may be extinct. Bois-d'arcs have two major defenses against herbivores (some of which may also be extinct): thorns and leaf toxins. There are tradeoffs between defense and growth: when thorns grow at leaf axils, fewer leaves are produced at these axils; and production of toxins reduces the production of molecules useful for growth. I hypothesized that, since females had a greater reproductive expenditure (large compound fruits) than males (catkins), females would be better defended against herbivores. Thorniness of stems was quantified on bois-d'arcs in two populations in late winter; in spring, their sex was determined. Females had slightly, but significantly, more thorn production. Leaves were removed from bois-d'arc trees in midsummer, and their toxicity determined by brine shrimp bioassays. Leaves from female trees had slightly, but significantly, greater leaf toxicity. No herbivory was observed on leaves of any of these trees. Therefore female bois-d'arc trees appear to have greater anti-herbivore defense than male trees.

- 144 ROSENTHAL, DAVID*¹, STILLER, VOLKER²,
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Patterns of plant and soil water relations along a cold desert ecotone: significant differences on a small ecological scale

In arid ecosystems, soil texture is an important determinant of plant available soil moisture. There is a rapid shift from active sandy soils to stabilized better developed soils along the ecotone between desert sand dunes and adjacent stabilized dune habitats. In general, soil clay and nutrient content increase across this boundary. Plants on fine textured soils should exhibit more negative water potentials, increased resistance to cavitation and root more shallowly than plants on coarser soils. At Little Sahara Sand Dunes, Utah, we studied plant available water for three species of differing life forms that occur along a narrow sand dune/desert ecotone. For all species measured, seasonal plant predawn (ψ_{pd}) and midday (ψ_{md}) water potentials were significantly higher on dunes than off dunes. Plants growing on active sand dunes maintained relatively high ψ_{pd} (> -1.5 MPa) throughout the summer season whereas plants growing off dunes were very water stressed from July on ($\psi_{pd} < -1.5$ MPa). Hardly any water was available for plants in shallow soils, but soil water potential increased with depth. Water was available for plants at 50 cm depth and below on dunes, but only below 75 cm depth off dunes. As predicted soil clay content was higher at off dune sites. These findings suggest plants may not root at greater depths on the dunes. We tested the prediction that on dune plants have lower cavitation resistance by measuring percent loss of xylem conductivity as a function of xylem tension in two species of wild annual sunflowers. Differences in cavitation resistance between congeners restricted to either side of the ecotone support the observed differences in plant water status for species that span the ecotone.

145 ROTH, AGATHA MARIE¹, KEDDY, PAUL^{*1},
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Does competition control the herbaceous diversity of longleaf pine savannas?

Wet longleaf pine savannas have exceptional numbers of plant species. The understory flora contains a remarkable and complex mixture of species, including groups with Madrean and Caribbean and even South American biogeographic affinities. The Poaceae, Cyperaceae and Asteraceae are particularly baffling, while families such as the Eriocaulaceae, Haemodoraceae, Melastomataceae, and Xyridaceae have biogeographic linkages to the Guyana Highlands of northern South America. The greatest diversity of carnivorous plants in North America also occurs here. Studies from Louisiana show that species-area curves have particularly high slopes, hence diversity increases strongly with area. Logging and fire suppression have reduced these savannas to three percent of their original area. Does competition control the herbaceous diversity of longleaf pine savannas in Louisiana? A removal study was performed for two years to evaluate the competitive effects of a dominant grass *Andropogon virginicus* L.) on the rest of the herbaceous flora. Mantel tests showed that the removal of the dominant species, *Andropogon virginicus*, did not change the composition of other species as compared to control plots. Nor did this removal change the relative abundance of functional groups. The lack of a competitive effect from this dominant species is unexpected. It may be the result of low competition intensity or the symmetry of interspecific competition in pine savannas. Other hypotheses for the high diversity of pine savannas include the small stature of many species (limiting competition for light), the diversity of functional types, redundancy within functional types, low soil fertility or repeated disturbance.

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The evolution of within-community land plant diversity over the Phanerozoic

Variation in the number of taxa within a community (alpha diversity) often is linked to environmental factors or biological innovations that allow some organisms to subdivide niche space more finely and thus increase the carrying capacity of a habitat. Land plants in particular show marked variation in alpha diversity in modern communities, with higher values associated with tropical communities and lower latitudes. Previous work has suggested that alpha diversity in

plant communities increased steadily through the mid-Paleozoic to a late Paleozoic – Mesozoic plateau, followed by a dramatic increase in mean alpha beginning in the Late Cretaceous and continuing through the Cenozoic. This pattern parallels estimates of global diversity through the Phanerozoic, leading to suggestions that increases in global diversity were driven by increases in alpha. However, subsequent compilations indicated that the observed alpha diversity pattern might be an artifact of temporal changes in preserved environments and spatial and stratigraphic sampling constraints. Here we analyze species lists drawn from over 3200 paleobotanical collections compiled in the Paleobiology Database (www.paleodb.org) from primary literature and personal field work and vetted by specialists. Analyses were restricted to North American and European macrofloras preserved in fluvial, deltaic, and lacustrine environments where specimens were collected from geographically well-constrained (e.g., < 10 x 10 m) and stratigraphically well-constrained (e.g., a horizon) sites. Results indicate that maximum alpha diversity increased through the Devonian – Permian, declined in the Triassic and Jurassic, and then increased steadily through the Cretaceous and Cenozoic. Sampling standardization of collections per interval does not greatly alter the pattern. We also assess the association of alpha diversity with paleolatitude, paleoenvironment, and plant organ type. These preliminary results suggest that the major intervals of increase in global plant biodiversity during the Phanerozoic were driven by increases in within- rather than among-community diversity.

147 SNYDER, JENISE M.^{*} and RICHARDS, JENNIFER H.
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Spikelet phenology and floral compatibility of sawgrass, *Cladium jamaicense* (Cyperaceae) in the south Florida Everglades

Both self-incompatibility and self-compatibility have been reported in the Cyperaceae and is unknown in sawgrass, *Cladium jamaicense*. Sawgrass is the dominant macrophyte in the Florida Everglades, thus factors that affect its population structure, such as incompatibility, are of major concern for restoration plans. Research has only recently begun to address sawgrass's population biology, and little is known about its anemophilous breeding system. To assess basic biological parameters of sexual reproduction in sawgrass, flowering phenology and compatibility reactions were studied. Studies took place in *ex situ* and *in situ* sawgrass populations in south Florida over 2 years. Flower maturation was relatively synchronous within an inflorescence. Along the entire inflorescence, functionally male flowers emerged initially (protandry), followed by stigmas, then anthers of hermaphroditic flowers (protogyny). Within a spikelet, each sex expanded over 2 days, with less than 1 day in between, resulting in 6-7 days for completion. Five treatments were used to test the compatibility response. Sawgrass was self-compatible, as self- and cross-pollination treatments did not differ significantly in fruit set. Open pollinations produced fruit set similar to self- and cross-pollinations. In autogamy and manipulation controls fruit set was low; these tested the effect of intrafloral self-fertilization and pollination manipulations, respectively. Thus, outcrossing in sawgrass depends on the timing of floral maturation of other inflorescences within a clone and of other individuals in a population. Although empirical studies within the family are limited, self-compatibility in sawgrass concurs with other Cyperaceae, including some species of *Carex*. The pollination manipulation controls, in conjunction with the other treatments used in this study, will be useful in compatibility studies of wind pollinated graminoid species *in situ*. These results provide a greater understanding of sawgrass reproduction, which is of particular importance in modeling distribution patterns and optimizing conditions for revegetation and transplantation in Everglades wetland restoration.

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The effect of competition and physiological integration on fitness-related traits: A two-year study of *Viola blanda*

Physiological integration of physically connected ramets may increase fitness-related traits, such as plant size and reproduction. In contrast, competition among plants may reduce these traits. This study examined the interactive effect of competition and physiological integration on fitness-related traits over the 2001 and 2002 growing seasons. Ramet pairs ($N=200$) from two populations of *Viola blanda* in southeastern Kentucky were exposed to a competition treatment (with vs. without competitors) and an integration treatment (intact vs. severed ramet connections) in a factorial design. Fitness measures included plant size (total leaf area), sexual reproduction (# of seedpods) and clonal reproduction (# of stolons). Predictions of treatment effects were: 1) intact ramet pairs with competitors would be reduced in size and produce equivalent values of seedpods and stolons, 2) intact ramet pairs without competitors would produce the highest values of plant size, seedpods and stolons, 3) severed ramet pairs with competitors would be reduced in size and produce more seedpods than stolons, and 4) severed ramet pairs without competitors would also be reduced in size but produce fewer seedpods than stolons. Although the data from both the 2001 and 2002 growing season mostly supported these predictions, significance was greatly dependent on site and time. The two populations were found to have significant differences in both quality and quantity of light, percent ground cover and soil moisture. The second population of *V. blanda* produced significantly less total leaf area and number of stolons and had very few significant treatment effects. However, the first population had significant competitive and integrative treatment effects in all three fitness traits. These results suggest that site quality and seasonality may play an equally or more important role in plant fitness above that of competition and/or physiological integration.

149 THOMPSON, JENNIFER N., WALCK, JEFFREY L.*
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The microhabitat of the federally endangered *Dalea foliosa*: implications for establishing new populations

The federally endangered *Dalea foliosa* is associated with limestone cedar glades in central Tennessee and northern Alabama and with dolomite prairies in northeastern Illinois. The microhabitat of *D. foliosa* was characterized by comparison to that of the sympatric *D. gattingeri* and to a site in which neither species grows but appears suitable for *D. foliosa* (control site). Ten mature plants of both species, as well as ten points in the control site, at each of five locations in Tennessee were randomly selected. Coverages of various biotic and abiotic factors, soil depth, and soil fertility were determined during the 2001 growing season. As compared to *D. gattingeri* sites, *D. foliosa* sites have significantly ($P \leq 0.05$) lower coverages of gravel and *Nostoc*, higher coverages of leaf litter and herbaceous vegetation, and deeper soils. On the other hand, both species grow on sites with relatively low coverages of moss. The control sites had significantly more moss and had shallower soil than the *D. foliosa* sites. Coverage of *D. foliosa* was negatively correlated with that of associated (neighboring) species. In terms of soil fertility, there were no appreciable differences

noted between sites. Based on the information obtained in the present study, it is recommended that new populations of *D. foliosa* be established on sites that are relatively free of competition and potential allelopathic interactions from other herbaceous and woody plants and moss, that are in full or partial sunlight, and that have soil depths >4 cm. Disturbance possibly plays a role in the population regeneration and maintenance by creating safe sites for germination and establishment and by reducing competition.

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Demographic variation between scrub and roadside populations of *Hypericum cumulicola*, an endangered herb of the Lake Wales Ridge, Florida

Hypericum cumulicola is virtually restricted to gaps in Florida scrub, but also occurs in sandy roadsides and firelanes. We used six years of census data from replicated sites to compare *H. cumulicola* population dynamics in Florida rosemary scrub, oak scrub and roadside habitats (road and berm). Seedling recruitment varied independently between populations in the scrub and those in the roadside. Seedling cohorts in the roadside started flowering earlier and had shorter lives than those in the scrub. Vegetative plants were more frequent in the scrub. Population fluctuations and population growth rates were more variable among roadside than among scrub populations. Roadsides may not necessarily function as refugia for plants that decline in long-unburned scrub because roadside populations are more extinction-prone and may select for different life history traits than periodically burned scrub. Roadside networks in scrub should not exceed minimal requirements for access and fire management.

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Genetic constraints on the evolution of dispersal are mediated by phenotypic plasticity

We investigated the quantitative genetics of seed dispersal in *Arabidopsis thaliana* and found a novel genetic constraint on the evolution of dispersal that is mediated by phenotypic plasticity. We grew several ecotypes of *A. thaliana* in high and low density, measured maternal plant characters, and then characterized seed dispersion patterns in a wind tunnel. We identified maternal plant traits that influenced seed dispersion patterns and found significant genetic variation for these maternal traits. The genetic variation for maternal traits that influence seed dispersion patterns, moreover, did not differ with density. However, these plant traits determined dispersal more strongly when plants were grown at high density than when they were grown at low density. In addition, we found significant genetic variation for both dispersal distance and for seed density after dispersal. Genetic variation for seed density after dispersal, however, was only detectable at high density. Therefore, as increased dispersal ability evolves and plants experience lower densities as a result, the expression of genetic variation for dispersal is expected to decline. Thus, a limit to the evolution of dispersal would result. In this study, we therefore detected a novel environment-dependent genetic constraint that is mediated by the evolution of the trait itself.

CONTRIBUTED POSTERS

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Changes in leaf morphology and biomass allocation reflect soil nitrogen availability in a carnivorous plant

Sarracenia rosea, a recently described Gulf Coastal species of carnivorous pitcher plant, occurs mainly in the western Florida panhandle and adjacent areas of Georgia, Alabama, and eastern Mississippi. The leaves (pitchers) serve as both photosynthetic organs and prey-capture devices, and plants procure nutrients from both soil and prey. I hypothesized that increased soil nitrogen-availability would be reflected by 1) changes in leaf morphology to maximize surface area (i.e. decreased structural allocation to carnivory) and 2) decreased biomass allocation to roots. I estimated potential N-availability in two S. rosea habitats characterized by different soils using buried-bag incubations to assess net N-mineralization rates. I then measured leaf wing width (a larger wing results in greater leaf surface area) and percent biomass allocated to roots in plants from the two sites. The mean annual rates of N-mineralization were significantly different at the two locations. Leaves of plants from the site with the higher rate of N-mineralization had significantly larger wings and allocated significantly less biomass to roots, compared to plants from the lower N-mineralization site. These results suggest that S. rosea responds to differences in available soil nitrogen by altering leaf morphology and patterns of biomass allocation to roots. These responses by the plant may be indicative of a decreased dependence on prey-derived nitrogen when growing in soils with higher levels of available nitrogen.

153 CARTER, GREGORY A.*¹, KNAPP, ALAN K.²,
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Indicators of phytodiversity in hyperspectral imagery of the Konza Prairie, Kansas

Spectral radiance reflected from 12 watersheds on the Konza Prairie Long-Term Ecological Research site was evaluated to test the hypothesis that its spatial variability would serve as a generic indicator of plant species diversity. A 224 channel hyperspectral data set gathered in June 2000 by the Airborne Visible and Infrared Imaging Spectrometer (AVIRIS) provided complete coverage of the 400–2,500 nm range at 10 nm per channel. The flight altitude of 20 km yielded a ground spatial resolution of 20 m. The data were radiometrically corrected for atmospheric absorption and georeferenced to ground coordinates of 94 long-term transects. For each transect location, a mean spectral reflected radiance was computed from values within 10–20 pixels. These mean spectra, their standard deviations and coefficients of variation corresponded with mean vegetation parameters that were determined previously for each transect and obtained through the Konza LTER 2000 data archive. Linear regression analysis at each spectral band indicated no significant relationships between within-transect spatial variability in reflected radiance and species richness or the Shannon-Weiner diversity index. Thus, the initial hypothesis was rejected. However, several band ratios of radiance per se in the 760–950 nm range correlated significantly ($p=0.01$) with species richness (maximum r-squared=0.42). Further research addressing diversity-productivity interactions and temporal variation in landscape spectra will expectedly yield greater efficacy for remote sensing in the estimation of phytodiversity.

154 CLAERBOUT, A.E.*¹ and COONS, J.M.²

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Comparison of *Physaria ludoviciana* (Silvery Bladderpod) Populations Across Their Range

Physaria ludoviciana (formerly *Lesquerella ludoviciana*) (silvery bladderpod) (Brassicaceae) is an endangered and threatened plant of Illinois, Minnesota, and Wisconsin sand prairies that occurs commonly in western states. The objective of this study is to compare populations of *P. ludoviciana* throughout their range. *P. ludoviciana* populations on the fringe of their range in IL and MN as well as those in the central part of their range in CO and ND were surveyed in June 2002. Information collected from each population included: 1) flower, fruit, and seed production per plant, 2) insects visiting flowers, 3) plant density including seedling, vegetative, and reproductive stages, 4) soil samples, 5) dominant associated species, and 6) atmospheric and locality descriptions. The Illinois population had the greatest number of flower stalks per plant (6.2 stalks). North Dakota populations had the greatest number of flowers per stalk (6.3 flowers/stalk). Plants in Illinois and Minnesota had the greatest number of fruits per stalk with means of 23.7 and 21.7, respectively. Populations were not significantly different for seed production per fruit. To date, three orders of visiting insects were identified including Coleoptera, Hemiptera, and Hymenoptera. The Illinois population had the greatest plant density with 0.5 seedlings/m², 1.5 vegetative plants/m², and 4.2 reproductive plants/m². Soils were loamy sand and sand with pH ranging from 7.9–8.1. Cation exchange capacity ranged from 8.2–23.2 Meq/100g. Percent organic matter of soils ranged from 2.1–2.3%. Dominant associated species included, *Artemisia frigida*, *Oenothera* sp., *Opuntia* sp., *Rhus aromatica*, and *Schizachyrium scoparium*. All sites had full sun exposure on southwestern facing slopes. These comparisons of populations throughout their range help to explain the statewide limitations of *P. ludoviciana* in the Midwest and will allow for better management decisions in populations near the fringe of its range.

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Herbivore Defense as an Explanation for Hyperaccumulation: Relative Heavy Metal Toxicity to Diamond Back Moth (*Plutella xylostella*)

Plants that sequester large amounts of metals in their tissues (hyperaccumulators) may do so as a defense against herbivores. Hyperaccumulation is defined as a plant tissue concentration of greater than 1,000 ppm of Ni, Co, Pb, Cd, Cr, or Cu, or greater than 10,000 ppm of Mn or Zn. We determined the relative toxicities of these eight commonly hyperaccumulated metals, using larvae of the Diamond Back Moth (*Plutella xylostella*) as representative generalist herbivores due to its short generation time and small size. Larvae were fed artificial diet amended with varying concentrations of each

individual metal added as the chloride salt. Percent survival was calculated for each concentration, and survival values were compared using analysis of variance to determine the concentration of each metal at which survival differed significantly from control (unamended) diet. Approximate relative metal toxicities (from high to low toxicity) were: Cd, Pb, Ni, Co, Cr, Cu, Zn, Mn. All of the metals tested were toxic at levels below the concentration used to define hyperaccumulation in each case. This result provides further evidence that metal hyperaccumulation may defend plants against generalist insect herbivores.

- 156 FRAZIER, CHRISTOPHER K. and LOWREY,
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Combined Natural History Collections Web-accessible Database for New Mexico

New Mexico is the fifth largest state in terms of area and it harbors impressive biodiversity. This biodiversity is poorly catalogued and understudied. The Institute of Natural Resource Analysis and Management (INRAM), funded by the National Science Foundation and the state of New Mexico as part of the New Mexico EPSCoR Infrastructure Program, has embarked on a three-year program to database and geo-reference the major biological museum collections in NM. INRAM has developed and is providing a data management system for participating museum collections. The five participating New Mexico Natural History Museum collections are capturing all accessioned specimen data (plant, animal, and fossil) into a computerized relational database, which will integrate the data into a searchable geospatial format accessible through the INRAM website. These data will be accessible via a web-based interface that supports more advanced analysis of these and other natural resource geospatial data. Over the three years of our funding period, we will greatly increase access to biodiversity and other natural resource data from NM and provide it in a context that supports more advanced scientific study.

- 157 GOODRICH, KR.*¹, ZHIIRA, MI.² and RAGUSO, RA¹
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Sex-and time-specific scent production in Pawpaw (*Asimina triloba*: Annonaceae) flowers

Annonaceae is a large, predominately tropical family of woody plants characterized by two whorls of petals, three outer that are attractive and three inner that frequently form a chamber. *Asimina*, the pawpaw, is the only temperate genus of Annonaceae. *Asimina triloba* has banana-like fruit, and is currently being considered as a tropical food crop that is native to the U.S. The flowers of *A. triloba* are strongly protogynous, with readily visible changes from immature (green) flowers to facultatively female flower (petals maroon, stamens immature) to facultatively male flowers (petals maroon, stamens mature). *A. triloba* flowers have a fermented odor and attract several families of flies and beetles. We examined floral scent production of *A. triloba*, comparing volatile emissions from flowers 1) during different developmental stages (immature, female and male), and 2) during day vs. night. Scent was collected from attached flowers in the field and the laboratory (from cut branches in 10% sucrose), and also from isolated flower parts. We used both static and dynamic headspace trapping methods, with Solid Phase Micro-extraction (SPME) fibers and SuperQ polymer traps respectively. Compounds were separated with gas chromatography-mass spectrometry (GC-MS) and identified us-

ing authentic standards. Our results show clear transitions in floral compound emissions accompanying phenological shifts, from sesquiterpene-dominated immature flowers to pollen-bearing flowers with fermentation volatiles.

- 158 JHEE, EDWARD M.*², BOYD, ROBERT S.² and EUBANKS, MICKY D.¹
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Nickel hyperaccumulation defends *Streptanthus polygaloides* (Brassicaceae) against an oligophagous herbivore

Nickel hyperaccumulating plants contain more than 1000 mg Ni kg⁻¹ dry mass when grown on Ni-amended soils. We hypothesized that Ni hyperaccumulated by *Streptanthus polygaloides* serves as an elemental defense against the Diamondback Moth, *Plutella xylostella* by deterring oviposition. An oviposition experiment used 2 X 5 arrays of *S. polygaloides* grown on Ni-amended (high-Ni) soil interspersed with plants grown on unamended soil (low-Ni). Diamondback Moths exhibited a significant oviposition preference for low-Ni plants. Moths allowed to oviposit on aluminum foil sheets dipped in extracts of hi-Ni or low-Ni plants significantly preferred low-Ni extracts. To determine if Ni was the factor influencing oviposition preference, we allowed moths to oviposit on foil sheets coated with low-Ni plant extract to which varying amounts of Ni were added. No difference in oviposition was observed, suggesting that factors other than Ni influence oviposition preference. Previous research has shown that hyperaccumulating *S. polygaloides* plants have a lesser concentration of glucosinolates. This trade-off might influence oviposition by an oligophagous herbivore since glucosinolates stimulate oviposition and feeding by Lepidopteran specialists on members of the Brassicaceae. To contrast fitness of high- and low-Ni plants, eggs were allowed to hatch and larvae feed freely among plants in the arrays. High-Ni plants had significantly greater biomass as measured by change in number of leaves and plant height. Reproductive effort (number of flowers) was also significantly greater for high-Ni plants. Ni hyperaccumulation may be an effective plant elemental defense against an oligophagous herbivore. By hyperaccumulating Ni, fitness of *S. polygaloides* is increased by toxicity to *P. xylostella* caterpillars and by decreasing oviposition by adults.

- 159 JOHNSON, SANDRA L.
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Trends in the abundance of cedar glade plants following prescribed burn

Low intensity burns were prescribed and executed in an effort to halt the ingressions of eastern red cedar trees (*Juniperus virginiana*) into limestone glades in central Tennessee. Although grasses and herbaceous vegetation dominate the shallow soils in these glades, where limestone lies near or at the surface, the tree inventory revealed more than 20 woody species present on the four sites studied. Plots ranged from one to seven tree species, with eastern red cedar represented in every plot. There were significantly more trees of all species in the smallest size class (< 0.5m, P < 0.005). A species list was compiled for each plot, but cover was calculated by plant type with little bluestem (*Schizachyrium scoparium*) making up a significantly larger proportion of the cover than leaf litter, which was significantly more of the cover than other types, including lichens,

mosses, other grasses and forbs ($P < 0.0001$). The four limestone glades studied were statistically similar before the burn treatment. Postburn data indicated that cedar abundance declined significantly more than other woody species ($P < 0.0001$) and cover analysis showed significant differences among types ($P < 0.0001$). Little bluestem was still the dominant cover species, however significantly more bare soil was exposed than previously, potentially opening the habitat to the invasion of alien species. After the burn, litter covered significantly less of the habitat than previously, indicating that the important accumulation of litter is a slow process on these glades. These results indicate that although prescribed burns may support the short-term objective of removing woody species from the cedar glades of central Tennessee, long-term preservation goals may be compromised by the use of fire.

160 KALLER, MATTHEW* and HESTER, MARK

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Effects of herbivory, nutrient addition, and disturbance in a reciprocal transplant study between an oligohaline and mesohaline marsh in southeastern Louisiana

Shifts in plant communities are often associated with wetland loss, which in Louisiana can be as high as 12,700 hectares per year. Important factors leading to plant community change and wetland loss include both natural and anthropogenic causes, such as diminished sedimentation, altered hydrology, and salt-water intrusion, along with altered nutrient regimes, disturbance, herbivory, and interactions between plant species. Throughout 2001 and 2002 a pair of concurrent reciprocal transplant studies were established and monitored within two dissimilar marsh types in southeastern Louisiana. Our objective was to elucidate the factors involved in the transition of a degraded oligohaline marsh to a mesohaline marsh. The reciprocal marsh investigated was one that remained an apparently healthy oligohaline marsh in the same basin. The first study focused on the main effect of nutrient addition, whereas the second focused on herbivore protection. Both studies were established in a factorial design with the main effects, as well as lethal and non-lethal disturbances, applied to the marsh area surrounding the transplanted sods. Results indicate that total vegetative cover of the surrounding marsh was influenced by the time of year, location, and vegetative treatment, and also showed trends of increasing cover with the exclusion of herbivores and the addition of nutrients. Total sod vegetative cover changed over time and was dependent on location and the plant species present. Sod stem counts also tended to increase with disturbance. Herbivore exclusion and fertilization tended to increase the stem counts of the sods and the species richness of the surrounding marsh. Interstitial salinity, pH, sulfide concentration, and soil Eh changed over time and differed between the two marshes. Furthermore, ammonium concentrations in both the sod and surrounding marsh were found to differ between marsh locations with greater concentrations occurring in the degraded, transitional marsh.

161 KIL, BONG-SEOP^{*1}, YOO, HYUN-GYEONG¹ and

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Allelopathic Effects of *Artemisia lavandulaefolia*

The allelopathic effects of *Artemisia lavandulaefolia*(donor plant) were studied using several test plants and microbes. Aqueous extracts and volatile compounds of the donor plant inhibited seed germination, seedling and root growth of the test species such as *Achyranthes japonica*,etc. The root growth of test species was more affected than shoot growth by allelochemicals from the donor plant. Essential oil of donor plant has antibacterial and antifungal effects. However, the antibacterial activity of the essential oil was dependent upon the microbial species and concentrations. Callus growth of test species was sensitive by the essential oil of the donor plant. Twenty three chemical compounds were identified from the donor plant oil by gas chromatography. Primary allelochemicals of them were 1,8-cineole, 1- \pm -terpineol, \pm -terpinene, camphor, 2-buten-1-ol and azulene. We concluded that aqueous extract and essential oil of the donor plant were responsible for allelopathic effect.

162 LEY, COURTNEY¹, ZJHIRA, MICHELLE² and

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How do red, yeasty Pawpaw flowers attract their pollinators?

Pawpaw (*Asimina triloba*) represents the northern most extension of the otherwise tropical family Annonaceae. Their blood-red flowers and yeasty odors represent unusual floral traits in the North American flora. Pawpaw fruits resemble small bananas and are being investigated for their potential as a native tropical fruit crop of the United States. One difficulty of growing pawpaws commercially is the low fruit set per tree. We studied flower visitors and aspects of floral attraction to better understand the pollination biology and potential pollinator limitation of the pawpaw. Many flies and mosquitos visited flowers and perched on tepals for up to several minutes. Three spider species were resident on 5% of all male or female stage flowers, but not on immature green flowers. Predation by spiders may exacerbate pollinator limitation in this system. We marked pollen with fluorescent dyes to track insect movement within a woodland Pawpaw population. Dye placement suggested bi-directional visitor movement throughout the population and considerable movement within individual flowers. We used sticky "Delta traps" to test whether odors alone can attract insect visitors. Delta traps baited with hidden male Pawpaw flowers trapped 3-4 fold more flies and mosquitos than control traps or those baited with baker's yeast. In addition, we constructed artificial flowers by covering small plastic cups with dyed cheesecloth. We de-coupled odor from red color by placing Pawpaw flowers or baker's yeast into some of these cups and leaving others empty. Mosquitos were attracted to odors from Pawpaw flowers and baker's yeast when coupled with red color, but not to unscented red or white traps. Pawpaw odor appears to be highly attractive to dipteran floral visitors, and may synergize with red color to increase visitation or landing by these insects.

163 MARTINE, CHRISTOPHER T.*¹, LUBERTAZZI,DAVID¹ and DUBRUL, ANDREW²¹Ecology and Evolutionary Biology, University of Connecticut, U-3043, Storrs, CT 06269; ²Florence Memorial High School, Florence, NJ

A long-term study on the reproductive biology of the endangered dioecious shrub *Corema conradii* (Empetraceae): Preliminary notes on post-fire seedling recruitment

Corema conradii (broom-crowberry) is a rare, dioecious, low-growing shrub with a disjunct distribution from Newfoundland to New Jersey. In New Jersey, the plant is a characteristic component of an uncommon xeric habitat type known as the pine plains. A hot fire burned through one of the most extensive populations of this state-endangered species during the summer of 2001 (near Warren Grove, NJ) and resulted in nearly complete mortality of *Corema* in the burned areas. In the fall of 2002, new seedlings were observed in abundance. Research plots are now established as part of a long-term monitoring project with a focus on reproductive biology, including the significance of sexual dimorphism in the ecology of this species and the role played by ants in seed dispersal and seedling establishment.

164 MIDDLETON, BETH* and MCKEE, KAREN

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Latitudinal variation in primary production and carbon stores in baldcypress swamps of the Mississippi River Alluvial Plain: a surrogate for global climate change prediction

Baldcypress swamps form an extensive network of wetlands along rivers and depressional features in the southeastern United States and potentially can form a sink for carbon from atmospheric sources. Our preliminary study of litter production in baldcypress swamps across latitudes will be used to examine potential shifts in carbon sequestration and species' distributions in response to changes in climate. Five replicate sites have been established to study leaf litter production at each of five latitudes spanning the distribution of baldcypress (*Taxodium distichum*) in the Mississippi Alluvial Valley (from Louisiana to southern Illinois). Based on an analysis of metadata from other studies, we predicted that primary production patterns will follow a curvilinear pattern across latitudes. We also plotted metadata from impounded sites that show that impoundment reduces the amount of leaf litter production by about 50% from that of sites with normal hydrology at any given latitude. At an impounded long term research site (Buttonland Swamp, Illinois) near the northern extreme of the region, the values of leaf litter production appear to be near a minimum level. Production needs to be considered on a species by species basis, since the impact of depth of impoundment and time of impoundment differs between species. For example, *Taxodium distichum* is somewhat more productive in shallow flooding than other species, but nevertheless decreases in leaf litter production over time of impoundment.

165 MOFFETT, JR., J. MINCY*, BOYD, ROBERT S. and

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Effects of post-hurricane sand-fencing and fertilizing restoration techniques on vegetation recovery along the Ft. Morgan Peninsula, Alabama

Coastal beach and dune systems of the U.S. Gulf Coast are frequently impacted by tropical storms and hurricanes. We studied the effects of sand fencing and annual fertilization on beach/dune vegetation at Bon Secour National Wildlife Refuge, a barrier peninsula system near Gulf Shores, AL, for five years (1998-2002). Pairs of sampling grids were established at three locations in the Refuge: two in an area of mature relatively stable tertiary dunes (Perdue Unit) and one in a more dynamic and exposed area of secondary dunes and swales (Ft. Morgan Unit). One member of each pair was sand fenced, with each sand-fenced grid subdivided into three fertilized and three unfertilized areas. Fertilized areas were treated with 13-13-13 fertilizer (rates ranging from 140-260 Kg/Ha/yr) applied in early April of each year. Sand fence "broken-chevrons" were installed at the seaward edge of the primary dune. Total plant cover, species richness, diversity (Shannon-Wiener Index), and dominance (Simpson's Index) were determined each year and analyzed for treatment effects. Fertilizing significantly increased total plant cover, species richness, and species diversity, but not dominance, over time in the Perdue Unit. Fertilizing had no significant effect on any variable in the Ft. Morgan Unit. Sand fencing in the Perdue Unit significantly increased plant cover and diversity, but species richness was unaffected. These effects were localized in a narrow zone bordering the sand fence. In the Ft. Morgan Unit, sand-fencing did not significantly affect any variable. Our results show these restoration treatments can significantly accelerate post-disturbance vegetation recovery, but that site-specific factors can influence the overall success of these treatments.

166 SMITH, BRENT* and CALIE, PAT

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High resolution GIS mapping of *Solidago shortii* (Asteraceae), a Kentucky endemic species

Short's goldenrod, *Solidago shortii*, is an endemic goldenrod with a restricted distribution found in and around the Blue Licks locality in north central Kentucky. The species is found as a set of distinct "populations", or demes. Previous maps made in 1987 demarcated the general boundaries of each population and have been republished several times, but no update of the original map had been attempted. We obtained latitudinal and longitudinal data for each population cluster of *S. shortii* with a GPS device. These data coordinates were entered into an Excel spreadsheet, exported to a comma separated text file, and then exported into ArcView GIS 3.0 as a table. An event theme was created from this table. A georeferencing file was compiled with a topographic map projection and our field data. An aerial photographic image was then superimposed over the topographic image for the final map image. The population densities for each discontinuous section were determined by combining the area total with current population counts, obtained in 2001 through a field census. The mapping efforts indicate a dramatic decrease in population area when compared with the original map of 1987, and a dra-

matic decrease in stem count when compared with previous estimates of population size made in 1986 - 88. Over the previous 7 years (1995-2002) three of the original populations have been observed to be extirpated, three are in serious decline, 5 are stable (though with significantly less stems than described in 1986 - 88), and one has increased in stem count. We have determined two distinct distributional patterns (polygonal vs. linear) and several different temporal patterns of persistence for 11 different populations.

- 167 SMITH-HUERTA, NANCY L.
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Nectar Production in *Clarkia unguiculata* (Onagraceae) as affected by nutrient supply

The pollen and nectar produced by flowers provide rewards to insect pollinators. Flowers with plentiful rewards are usually more attractive to pollinators and may be visited more frequently than those with fewer rewards. Hence, any factor that influences nectar production could have significant effects on reproduction. This research tested the effects of supplemental nutrient supply on nectar production in an herbaceous California wildflower, *Clarkia unguiculata*. Plants were grown in a growth chamber and watered as needed with either a full-strength nutrient solution (NPK 20-20-20) or with distilled water only. Flowers of *C. unguiculata* are protandrous, shedding pollen for approximately 3 days before the stigma is receptive. Nectar was sampled in flowers 2 days post-anthesis (male phase) or at 5 days post-anthesis (female phase) by absorbing nectar on to filter paper wicks. Nectar concentration for each flower was determined spectrophotometrically with an anthrone method. Male phase flowers watered with distilled water produced significantly more nectar than those watered with nutrient solution. Female phase flowers showed no significant difference in nectar production between nutrient treatments.

- 168 STANFORD, ALICE M.* and DELSOL, TIMOTHY
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Genetic diversity of *Bastardioptis eggersii* (Malvaceae), a rare Virgin Islands endemic

The Virgin Islands were almost completely deforested for cultivation during the seventeenth century. The islands' ecosystems, adapted to frequent disturbance in the form of hurricanes, recovered considerably following the abolition of slavery and the subsequent collapse of the sugar cane economy in the nineteenth century. Currently, development, habitat loss, invasive plant species (such as genip), and exotic animal species (such as goats) continue to threaten the forests of the Virgin Islands. Many plants collected during the nineteenth and early twentieth centuries are now extinct, extremely rare, or confined to just a few islands. Rare Virgin Islands endemic *Bastardioptis eggersii* (E.G.Baker) Fuertes & Fryxell (Malvaceae) has a known total population of fewer than 1500 individuals. Although once found in Puerto Rico and Culebra (and probably throughout the Virgin Islands), *B. eggersii* has recently been found only on Jost Van Dyke, Guana Island, and Ginger Island in the British Virgin Islands. In order to assess the genetic diversity of this species, we tested 15 randomly selected 10-mer primers to perform RAPD (randomly amplified polymorphic DNA) fingerprinting analysis. Allele frequencies (p), heterozygosity (H), polymorphism (P), and similarity matrices, were calculated for each population, including a haphazardly planted population on Guana.

- 169 STRIBLING, JUDITH*¹, CORNWELL, JEFFREY² and GLAHN, OLIVIA¹

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Microscale spatial variability in brackish marsh vegetation and associated patchiness of sediment biogeochemistry

In some Mid-Atlantic marshes, there is marked fine-scale spatial variability in the form of clumping of vegetation interspersed with bare sediment. This variability is especially evident in estuarine marshes, where salinity fluctuations and flood duration produce stressful conditions, and it is reminiscent of the "islands of fertility" microtopography of desert systems. In two Chesapeake Bay marshes, we have investigated the distribution of this hummock/hollow topography, its interannual stability, its relationship to salinity and to sediment biogeochemistry, and its persistence over longer temporal scales. We examined two tidal marshes, an oligohaline/fresh marsh and a brackish marsh, both of which exhibited strongly clumped distribution of vegetation. The former marsh lost this spatial heterogeneity in the second year of the study, when salinity shifted from unusually high to normal levels. The topography of the brackish marsh was stable over at least a decade, but it also contained a creakbank region of stable, homogeneous plant distribution. Sediment porewater nutrient and sulfide levels, and solid phase chemistry, reflected the presence or absence of spatial heterogeneity in the marsh vegetation at both sites. Using ²¹⁰Pb dating, we have also investigated the relative age of the creakbank (homogeneous) and interior (heterogeneous) regions of the brackish marsh, in order to determine whether the hummock/hollow topography reflects an aging, sediment-starved system or a newer, developing marsh.

- 170 SUSTACHE JOSE¹, CORTES, CARLA*², OLVERO, SOFIA⁴, MELENDEZ, ELVIA³, ARAGON, SUSAN², MORALES, MARIELY², FERNANDEZ, DENNY⁴ and GARCIA, MIGUEL⁴

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Characterization of the plant diet of introduced pigs and goats in Mona Island Reserve, Puerto Rico

The introduction of feral ungulates (i.e. goats and pigs) is one of the most common and impending threats to the biodiversity of island biotas around the world. Introduction of these animals to Mona Island, a dry forest Reserve located between the islands of Puerto Rico and Hispaniola occurred 500 years ago by Spanish settlers. While some data suggests that these animals may regulate some plant communities in the island, a detailed characterization of the diet of these animals is lacking. Current management of populations of these animals include a three month hunting season coordinated by the Department of Natural Resources and the Environment (DNRE) of the Commonwealth of Puerto Rico. We used this management strategy as an opportunity to directly characterize the plant species that make up the diet of these animals. This information could be valuable in

identifying those species that might be most susceptible to herbivory by these animals. Preliminary results indicate that many plant species appear in the stomach of these animals including species highly toxic secondary compounds (e.g. *Euphorbia petiolaris*) and an endangered cactus endemic to the island (i.e. *Harrisia portoricensis*).

- 71 WELLS, TAMI^{*1}, CARTER, GREGORY²,
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Assessing Aboveground Primary Productivity in Mississippi Gulf Coast Tidal Marshes by Remote Sensing

Estimation of primary production in salt marshes using traditional techniques is labor intensive and extremely destructive to the habitats under investigation. Even non-destructive monitoring methods require physical access to marsh plants which results in the trampling of vegetation and compression of substrate. This damage may persist for years after a sampling event. Remote sensing technology provides a suite of alternative, innovative techniques to measure aboveground primary productivity effectively with limited destruction to the environment. Furthermore, it can enhance the accuracy and precision of productivity estimates through its capacity to sample a much greater geographical area with extremely high replication. The present study utilizes aircraft and ground-based multispectral camera systems to estimate aboveground net primary production in *Juncus roemerianus* and *Spartina alterniflora* marshes. In a scaled approach, images with a nadir view angle were acquired using a ground-based camera system for leaves clipped at the soil surface and spread evenly on a black platform, and for intact areas of marsh located within meter-square quadrats. Images of the same monospecific areas were acquired also from an aircraft platform. In each case, image data, including single-band reflectance and derived multiband indices, were regressed with above-ground fresh and dry biomass. Results indicated a high correlation (maximum r-squared of 0.7) between several image parameters and annual aboveground biomass production. The vast improvement in sampling enabled by remote sensing of monospecific marshes eliminates the bias encountered in previous studies that arises from limited replication and constraints imposed by protection of endangered and critical habitats.

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Results of Louisiana Quillwort (*Isoetes louisianensis*) Monitoring on Camp Shelby Training Site, MS

Louisiana quillwort, an aquatic species growing in or near intermittent and perennial streams in south Louisiana, Alabama and Mississippi, is federally listed as endangered. Monitoring of 7 colonies of Louisiana quillworts in the Poplar Creek watershed on Camp Shelby Training Site, Mississippi over a 3 year period documented response of the quillworts to varying environmental conditions. In November 1999, 2 permanent .46 m² plots containing between 2 and 22 quillworts were established for 6 colony sites. Because of restricted distribution of quillworts, only one plot was established at the 7th site. Individual plants were mapped and monitored monthly. Plants appeared to be able to withstand temporary burial (< 2 months) by leaf packs, but

plant numbers in 4 plots declined in the presence of persistent leaf packs (3 months or greater). Quillwort persisted for several months in 2000 in 2 plots despite increased water depths resulting from a newly formed beaver dam; however, continued monitoring has been hindered by high water levels. Plant numbers and sizes were unaffected by 5 rainfall events of greater than 10 cm in a 24 hr period. Plants in the driest 6 plots became dormant during the summer and fall drought conditions of 2000, but recurred in December 2000/January 2001 as conditions became wetter. Spearman's correlation coefficient for quillwort numbers and mean temperature of previous 2 months was -0.663, (p <0.000). Leaves disappeared as plants became dormant and were often chewed or broken off; but under favorable conditions leaf growth of individual plants occurred during any month of the year. Maximum leaf length recorded was 64 cm.

- 173 ZHANG, SULI^{*2}, TU, HUIBIN² and LI, JIANHUA¹
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Characteristics of floristics and vegetation of Yellow River Old Course Avian Nature Reserve in northern Henan, China

Since 602 BC the Yellow River of China has changed courses several times southward, leaving behind alluvial planes in the north that contain lakes, swamps, meadows, and highlands. These diverse ecosystems provide habitats for many rare and endangered birds and other organisms. The Yellow River Old Course Avian Nature Reserve is located in northern Henan between E114°07'-114°29' and N34°54'-35°24' with a size of 61,231 acres. A descriptive study of characteristics of floristics and vegetation was conducted to provide benchmark data for avian conservation and wetland management. The zonal vegetation is the warm temperate forest. Natural forest has long disappeared due to extensive farming and has been replaced with plantations. There are, nonetheless, parcels of natural vegetation on sand dunes and in lakes, swamps, and lowlands. There are 256 species of vascular plants belonging to 55 families with 38 species being woody and others herbaceous. The dominant families include Potamogetonaceae, Ceratophyllaceae, Nymphaeaceae, Hydrocharitaceae, and Lemnaceae in open waters, and Typhaceae, Poaceae, and Cyperaceae in swamps. Among the 41 species in wetland, 11 are cosmopolitan, 6 temperate, 12 subtropical-temperate, 12 tropical temperate, and none tropical-subtropical. Dominant species include *Phragmites communis*, *Typha angustifolia*, *Myriophyllum spicatum*, *Ceratophyllum demersum*, *Potamogeton crispus*, and *Lemna minor*. Terrestrial floristics is composed of 215 species and 42 families, and the dominant families include Poaceae, Asteraceae, Fabaceae, Cyperaceae, Chenopodiaceae, and Rosaceae. There are three major vegetation types in the reserve: 1) the aquatic type with 11 communities, 2) the psammophyte type with 5 communities, and 3) the saline type with 4 communities. The plant communities represent different stages of succession and are essential to the wellbeing of birds and other organisms in the reserve.

ECONOMIC BOTANY SECTION

CONTRIBUTED PAPERS

- 174 AMPORNPAN, LAAW^{*1}, DHILLION, S.S² and WERUKAMKUN, P¹

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Aquatic Plant Diversity and Use by Two Village Communities in Na Haeo, Northeast Thailand

Aquatic plants diversity and use by local communities of two mountain villages (480 – 650 m.a.s.l.) were studied in Na Haeo district, Northeast Thailand. Nutritional data on the species used was also gathered. The plants were studied in eight different sites, using ten quadrats (1x1 m²) per site placed 10 m apart along a transect. Forty-three aquatic plant species were recorded from 3 different seasons, summer, rain and cold. Number of species fluctuated due to the seasonal changes. None was found in all sites. They were distributed within 28 plant families and 1 green algae. Four aquatic plant functional groups were identified (submerged, floating leaves, floating and emerged). The emerged plants were the highest number, 33 species. Twenty-three species are used for food and medicine. Five of these are used as vegetables nation-wide. The study shows that the local communities depend upon the plant resources for their subsistence.

- 175 BURKS, K. C.

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Snowflakes in Florida:*Nymphaoides cristata* (Roxb.) Kuntze and other new invasive non-native aquatics introduced via the water garden and aquarium trade

Often marketed as "snowflake," the Asian floating-leaf aquatic *Nymphaoides cristata* has continued to turn up as naturalized in more Florida waterbodies since its first report as a New World introduction in 2000. These stands expand quickly into shingled canopies at the water surface that shade out native submersed plants; the infestations are also proving difficult to remove with standard control methodologies. Other invasive exotics introduced recently in Florida include *Salvinia molesta* Mitchell, a federal Noxious Weed and Florida Prohibited Plant documented as arriving originally through an order of misidentified plants from a commercial water garden website, and *Rotala rotundifolia* (Roxb.) Koehne, a traditional aquarium plant originating from India. It is likely to have escaped through dumping of excess aquarium material. While the giant salvinia is under eradication watch in Florida, the others appear established. Distinguishing features of these species will be presented, along with recommendations for the trade.

- 176 HINKLE, ANYA E.

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Distribution of a male sterile form of *Cordyline fruticosa* (Lomandraceae) in the eastern Pacific

Cordyline fruticosa (L.)

Chev. is an aboriginal introduction to the Pacific and is ubiquitous throughout the region. It is a cultivated and naturalized plant prized by Polynesian settlers for its numerous material and cultural uses. At the eastern extreme of its prehistorically introduced range, the plants appear to be male sterile and are propagated by humans. The present study confirms the sterility of pollen in the aboriginally introduced form of *C. fruticosa* in eastern Polynesia. Additionally, the geographic pattern of this form is investigated from the central Pacific to the isolated archipelagos of eastern Polynesia. Cytological evidence for factors underlying sterility is considered and the significance of sterile plants in the Pacific is discussed.

- 177 YOUNG, COLIN A

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A Comprehensive and Quantitative Assessment of Belizean Creole Ethnobotany: Implications for Forest Conservation

With the current rates of deforestation and acculturation of local and indigenous cultures throughout the world, there is a real sense of urgency for ethnobotanical research. Ethnobotany as a discipline has been criticized as "vague and imprecise" and lacking in methodological rigor. This perception of ethnobotany has led to the development of "quantitative" ethnobotany to introduce "scientific" robustness into the discipline. Quantitative techniques have been used to assess various aspects of ethnobotanical research including assessing the importance of different habitat types to people and assessing the number of useful species per hectare. Nonetheless, many ethnobotanical studies still suffer shortcomings that cast doubts on the generality and applicability of conclusions. The current research systematically documents Belizean Creole ethnobotany and assesses the ethnobotanical importance of different forest types using a modified version of the "informant-indexing" and "walk in the woods" approaches. The number of useful species within each forest type will be assessed using twenty-seven 0.25 hectare sites in three geographical areas along a rainfall gradient with three plots each occurring in young secondary, old secondary, and old growth forests in Belize. Nested, contiguous quadrats are used to sample trees, shrubs, herbs, vines, and lianas. Forest importance Value will be calculated by summing species importance values for each category of use within a forest type. Selected collaborators will be re-interviewed two months after the first "walk in the woods" episode to ensure reliability of ethnobotanical information. The proposed methodology will hopefully improve current methods by (i) minimizing researcher bias in assigning species importance values, (ii) identify collaborator-indexed use categories, (iii) allowing differentiation of uses within each category, and (iv) allowing greater reliability and applicability to research findings.

CONTRIBUTED POSTERS

- 178 CHIKARMANE, SONA , REHSE, TANIA* and
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Tracing the cultural and botanical origins of turmeric (*Curcuma longa* L.)

Curcuma longa, or turmeric, is a perennial herb in the Zingiberaceae. Turmeric is among the most important commercial spices of the world. Used since antiquity as a dye and a condiment, it is said to have originated in South Asia and subsequently moved to other parts of the world. This study focuses on the historical migration patterns of people within South Asia and between South Asia and Southeast Asia, especially in relation to the origin, spread, and cultivation of turmeric. Inherent in the migration of people is the concomitant transportation of certain plant products, modification in the practices surrounding their cultivation, and changes in the uses of these plants. It has been hypothesized that the historical migration patterns of people in South Asia may have directly impacted the evolution and distribution patterns of turmeric. By searching ancient literature and analyzing historical patterns of movement of South Asian and Southeast Asian people known to have used turmeric, we have assembled cultural data and evidence of migratory patterns that suggest turmeric was introduced into Southeast Asia via Indian colonization in the early Christian centuries AD. An increase in colonization events from South India during this time period was apparently because of discoveries in navigational science and desires to expand civilizations, rather than military conquests. The cultural expansion from South India supports the introduction of turmeric cultivation to Southeast Asia via human means, just as many other advances to the Neolithic culture were passed on from the colonization. These human migratory patterns are compared to a phylogenetic analysis of DNA sequence data within *Curcuma*, and suggest that key locations such as the Isthmus of Kra were important not only to human movement but to species evolution in *Curcuma*.

- 179 MORNINGSTAR, DAWN*¹, PERKINS-VEAZIE,
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Lycopene extraction from freeze-dried tomatoes

Lycopene, a carotenoid pigment with powerful antioxidant properties, imparts the red color to tomatoes, watermelon, and red grapefruit. Tomatoes provide much of the dietary lycopene to the Western world, primarily in processed forms as ketchup, tomato sauce, and juice. Lycopene for dietary supplements is extracted from cannery waste (mostly tomato skins, the primary location of lycopene in tomato fruit). Solar or freeze drying is done to reduce water and facilitate extraction by non organic solvents, such as liquid CO₂. Watermelons, which contain lycopene in the internal red flesh, lose 50% of total lycopene after freeze drying. Lycopene in watermelons may be protected by the high soluble solids content (12% fresh weight), or alternatively, the increased hygroscopicity may promote lycopene oxidation. This study was done to determine the stability of lycopene in tomato after freeze drying. Tomatoes from a standard variety (Homestead), and a high pigment type (T5020) were harvested at breaker

(about 10% red) and fully ripe stages. Equatorial slices were removed from fruit and held at -20 C. One quarter of each slice was lyophilized and one quarter of the same slice homogenized. The total soluble solids content of the tomatoes ranged from 4 to 7%. Lycopene was determined by hexane extraction and spectrophotometric absorption at 503 nm. Lycopene loss in freeze dried tomatoes ranged from 20 to 40%. Therefore, selection of high lycopene content tomatoes for extraction is important for economic recovery of lycopene.

GENETICS SECTIONCONTRIBUTED PAPERS

- 180 BAUM, DAVID A.*, OLDHAM, REBECCA L. and
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Moving genes between species to test the role of LEAFY (LFY) in the evolution of plant architecture in Brassicaceae

We have utilized a transgenic strategy to see if the floral meristem identity gene *LFY* contributed to the evolution of rosette flowering in three lineages of Brassicaceae. *Arabidopsis* manifests the ancestral condition, inflorescence flowering; flowers lack subtending leaves and are borne on elongated stems. Some lineages of Brassicaceae have lost the inflorescence and produce flowers from the axils of subtending rosette leaves. *LFY* was cloned, with 3 Kb of 5' DNA and 1 Kb of 3' DNA, from *Arabidopsis thaliana* (*At*) and three rosette-flowering species: *Ionopsidium acaule* (*Ia*), *Leavenworthia crassa* (*Lc*), and *Idahoa scapigera* (*Is*). These were then introduced into *lfy* mutant *Arabidopsis* to see if the exogenous *LFY* genes could rescue the *Arabidopsis lfy* mutation and if the exogenous genes would induce some aspects of rosette flowering. Whereas the *AtLFY* and *IaLFY* genes rescued transgenic plants to wildtype, *LcLFY* and *IsLFY* induced novel architectural phenotypes. In addition to affecting the primary shoot, *LcLFY* caused the conversion of paraclades in the rosette from indeterminate shoots (e.g., paraclades) into short, determinate shoots with terminal flowers. Since rosette flowering can be caused by conversion of axillary shoots to flowers, this suggests a role of *LcLFY* in this evolutionary event. *IsLFY* did not cause any homeotic conversions but tended to prevent internode elongation and to derepress bracts. Thus, *IsLFY* could also have contributed to the evolution of rosette flowering but via a distinct mechanism to that implicated for *LcLFY*. Nonetheless in all cases *LFY* was not the sole locus of morphological evolution but appears to have coevolved with other developmental genes.

- 181 BURKE, JOHN M.*¹ and RIESEBERG, LOREN H.²
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The fitness effects of transgenic disease resistance in wild sunflowers

The transfer of genes from crop plants to their wild relatives has emerged as one of the primary risks associated with the commercialization of genetically-engineered crops. Previous studies have re-

vealed relatively high levels of hybridization when crop plants come into contact with their wild relatives. However, little is known about the frequency of such contact across the range of cultivation of any given crop taxon, and even less is known about the fitness effects of transgenes following their introduction into wild populations. We have performed a multi-year, range-wide survey of the potential for reproductive contact between cultivated and common sunflower (*Helianthus annuus*). We have also investigated the fitness effects of a transgene conferring resistance to *Sclerotinia sclerotiorum* (white mold) in a predominantly wild sunflower genetic background. The results of this work indicate that the opportunity for crop-wild hybridization exists throughout the range of sunflower cultivation, making transgene escape a virtual certainty. Somewhat surprisingly, however, the white mold resistance transgene had no detectable effect on fitness when transferred into wild sunflowers, even following a severe pathogen challenge. When viewed in the context of natural infection rates in the wild, which we found to be negligible, our results suggest that the transgene will do little more than diffuse neutrally following its escape into wild sunflower populations. Taken together, these results illustrate the importance of assessing the risks and benefits of genetic modification on a case-by-case basis rather than dismissing transgenic approaches entirely, or introducing transgenic crops in the absence of appropriate scientific scrutiny.

182 EUBANKS, MARY W.*², REYNOLDS, JAMES F.¹ and RIEDELL, WALTER E.³

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A Bridging Cross to Enhance Genetic Diversity and Sustainability in Maize

Eastern gamagrass (*Tripsacum dactyloides* L.) is a relative of maize that has valuable genes for crop improvement and sustainability. This genetic resource has had limited usefulness in maize breeding programs due to sterility in maize-gamagrass hybrids. Crosses between gamagrass and teosinte, the closest wild relative of maize, have yielded fully fertile recombinants that are cross-fertile with maize and provide a genetic bridge to move *Tripsacum* genes into maize. This paper describes the gamagrass-teosinte genetic bridge, and reports on progress in a molecular-marker assisted recurrent selection breeding program focused on conferring protection against insect damage and drought tolerance in maize. Corn rootworm (*Diabrotica virgifera* LeConte), which is the worst insect pest of maize, is estimated to cost growers over \$1.2 billion a year in crop loss and insecticide costs. The insecticides used to control this pest are among the most toxic to humans and the environment. Eastern gamagrass, which co-evolved with *Diabrotica*, has internal mechanisms that protect the plant from herbivory damage. Rootworm tolerant plants have been selected from insect bioassays that screened over 140 gamagrass-introgressed lines in a maize backcross breeding program. Artificially-infested field tests in South Dakota have confirmed natural rootworm tolerance is expressed in some of these Sun Dance Genetics lines. Gamagrass also has strong ability to withstand drought. Sun Dance Genetics hybrid families grown in summer nurseries have not required irrigation when typical maize crops in the same growing area have been lost to drought. This reduction in water requirement is being investigated and characterized in controlled environment growth chamber drought tests. Under experimental water deficit conditions the Sun Dance hybrids performed better and had significantly higher yields than the corn controls

183 GITZENDANNER, M.A.*², WEEKLEY, C.W.¹,

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Genetic diversity and mating type identification in *Ziziphus celata* (Rhamnaceae), a critically endangered Florida shrub species

Endemic to the Lake Wales Ridge of central Florida, *Ziziphus celata* Judd and Hall (Rhamnaceae) is known from only seven populations, only one of which occurs on publicly protected land. Previous research using isozymes and RAPDs identified 11 multilocus genotypes and confirmed that most populations of this self-incompatible species consist of a single clone. An extensive cross-pollination program has yielded very few fruits and suggests that there may be as few as three mating-type alleles in the samples tested to date. We have used AFLPs to reassess patterns of diversity and survey a larger number of individuals. Most AFLP genotypes are consistent with the other markers; however, new genotypes, possibly corresponding to new mating types, have been identified. Using data from seedlings obtained from a known maternal parent, we have conducted paternity analysis to identify likely sires. In order to more directly characterize the mating type of the individuals, we have also examined DNA sequence variation at the S-locus (an S-RNase encoding locus mediating gametophytic self-incompatibility). These data together with the AFLP genotypes will allow a more efficient and effective breeding program with the goal of generating material to use to establish new populations of the species on suitable protected habitats within the historical range of the species.

184 GOU, XIAOPING, YUAN, TONG and RUSSELL, SCOTT D.*

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Selection of differentially expressed gene products in the sperm cells of *Plumbago zeylanica*

Pollen of *Plumbago zeylanica* contains two sperm cells with differing morphology and organelle content. The larger of these two cells contains abundant mitochondria, lacks plastids, and is physically associated with the tube nucleus, whereas the other sperm cell contains numerous plastids and relatively few mitochondria. The latter preferentially fuses with the egg cell to form the zygote and embryo, whereas the former sperm cell preferentially fuses with the central cell and forms the endosperm. To discriminate between genes active in each cell, we separated the two sperm cell populations at anthesis using a microinjector, reverse transcribed cDNA from mRNA, and constructed a PCR-amplified library of ESTs representing genes expressed in the sperm cells. Libraries to each of the sperm cells were screened against GenBank using BLASTX and BLASTP, and functional categories were assigned for the putative gene products. Microarray screening was conducted using PCR amplified products cloned into pCR2.1-TOPO vector. The inserts were PCR amplified and spotted onto glass slides for screening. A total of 4608 spots, representing 2304 clones of each suppression subtractive hybridization (SSH) cDNA library, were examined using SSH and non-SSH screened cDNA probes. Suppression subtractive hybridization appeared to facilitate the selection of genes expressed differentially in the two sperm cells. Several hundred clones with gene expression

strongly amplified in a specific sperm cell type have been identified. These clones will be used to isolate upstream controlling elements, with particular emphasis on promoters in clones corresponding to membrane-binding polypeptides. Virtual northern hybridization and RT-PCR have verified the expression pattern of seven clones. One of them, clone A7, is homologous with an arabinogalactan protein of *Arabidopsis*. This gene expresses a signal peptide sequence and transmembrane domain - features that would be characteristic of a cell recognition molecule.

185 JENNINGS, LINDA* and WHITTON, JEANETTE
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Genetic, morphological and ecological variation within and between two Southern Utah endemics, *Townsendia aprica* and *T. jonesii* var. *lutea* (Asteraceae)

Utah has the 3rd highest percentage of rare plants in the United States, and more than 10% of its species are endemic. Fifty percent of Utah's endemic flora occurs along the Colorado Plateau, a region of tremendous ecological diversity that runs through the middle of the state. Last Chance Townsendia, *Townsendia aprica* Welsh & Reveal (Asteraceae) is an herbaceous perennial, narrow endemic within this region, listed as a Federally Threatened Species in 1985 under the Endangered Species Act. Management agencies have speculated that populations of *T. aprica* form morphologically and ecologically distinct northern and southern groups. Isozyme data from 12 loci will be used to detect levels of genetic variation among 12 populations sampled throughout the range, to test for this north-south differentiation. Comparisons between close congeners have become increasingly important in conservation genetic studies, but few studies compare patterns in closely related narrow endemics. *Townsendia jonesii* var. *lutea*, another narrow endemic to the Colorado Plateau region, is closely related to *T. aprica*, and preliminary surveys by the Bureau of Land Management suggest that the two taxa are ecologically distinct. The ranges of the two taxa are described as adjacent and non-overlapping. By analyzing patterns and levels of genetic diversity within and between these two taxa and attempting to correlate these with morphological measurements, elevation, geographic distance and soil features, we will provide an important comparison of the characteristics of these two related narrow endemics.

186 KONG, H.* NI, W., LEEBENS-MACK, J.,
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Highly Heterogeneous Rates of Evolution in the SKP1 Gene Family in Plants and Animals: Functional and Evolutionary Implications

Skp1 is a core component of SCF ubiquitin ligases and mediates protein degradation, thereby regulates eukaryotic fundamental processes such as cell cycle progression, transcriptional regulation, and signal transduction. Among the four components of the SCF complexes, Rbx1 and Cullin form a core catalytic complex, F-box protein acts as a receptor for target proteins, and Skp1 serves as an adaptor that links one of the variable F-box proteins to Cullin. Whereas protists, fungi and some vertebrates have a single *SKP1* gene, many animal and plant species possess multiple *SKP1* homologs. It has been shown that the same Skp1 homolog can interact with more than one F-box proteins, and different Skp1 homologs from the same species sometimes can interact with the same F-box protein. In this study,

based on structural, phylogenetic and expression studies, we demonstrate that multiple Skp1 homologs from the same species have evolved at highly heterogeneous rates. The slowly evolving members are relatively conserved in structure and expressed widely and/or at high levels, suggesting that they serve the most fundamental function(s). The rapidly evolving members, however, are structurally more diverse and usually expressed at low levels, in specific tissues, or possibly under specific conditions, suggesting that they may have lost their original function(s) and/or acquired new function(s). In addition, unlike previous studies, our analyses indicate that multiple Skp1 homologs from the same species do not necessarily form a single clade; the phylogeny of the most slowly evolving members from each species tend to follow the phylogeny of species, suggesting that these sequences have evolved under functional constraint. The other members of these species, however, show very complex evolutionary patterns that are the outcome of gene birth-and-death processes. Some rapidly evolving members may have originated by recent gene duplication, as suggested by their chromosome locations, sequence similarity and phylogenetic affinity.

187 LEXER, CHRISTIAN* and RIESEBERG, LOREN H.
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Natural selection for salt tolerance QTLs in wild sunflower hybrids: Implications for the origin of *Helianthus paradoxus*, a diploid hybrid species

For a new diploid or homoploid hybrid species to become established, it must diverge ecologically from parental genotypes. Otherwise the hybrid neospecies will be overcome by gene flow or competition. We have initiated a series of experiments designed to understand how the homoploid hybrid species, *H. paradoxus*, was able to colonize salt marsh habitats, when both of its parental species (*H. annuus* X *H. petiolaris*) are salt sensitive. In this contribution we will report on the results of a quantitative trait locus (QTL) analysis of mineral ion uptake traits and survivorship in 172 BC2 hybrids between *H. annuus* and *H. petiolaris* that were planted in *H. paradoxus* salt marsh habitat in New Mexico. A total of 14 QTLs were detected for mineral ion uptake traits and three for survivorship. Several mineral ion QTLs mapped to the same position as the survivorship QTLs, confirming previous studies, which indicated that salt tolerance in *Helianthus* is achieved through increased Ca uptake, coupled with greater exclusion of Na and related mineral ions. Of greater general significance was the observation that QTLs with effects in opposing directions were found for survivorship and for all mineral ion uptake traits with more than one detected QTL. This genetic architecture provides an ideal substrate for rapid ecological divergence in hybrid neospecies and offers a simple explanation for the colonization of salt marsh habitats by *H. paradoxus*. Finally, selection coefficients of + 0.126, - 0.084, and - 0.094 for the three survivorship QTLs, respectively, are sufficiently large to account for establishment of new, homoploid hybrid species. Genetic mapping of Ca-dependent salt tolerance ESTs (expressed sequence tags) in interspecific BC2 hybrids is underway, and first results of this work will be presented.

188 LORING, HEATHER A.*¹, COX, ANNE C.³, GITZENDANNER, MATTHEW A.¹, SOLTIS, DOUGLAS E.¹ and SOLTIS, PAMELA S.²

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Conservation and population genetics of the federally endangered species

Asimina tetramera (Annonaceae) *Asimina*, the sole temperate genus in the tropical family Annonaceae, comprises eight species, five of which are narrowly distributed. The four-petal pawpaw (*Asimina tetramera*) is unique in *Asimina* in that the calyx and sometimes a whorl of petals are tetramerous. All other *Asimina* have the trimerous perianth characteristic of Annonaceae. *Asimina tetramera* inhabits sand pine scrub and open scrub of Pleistocene sand dunes in southern Florida. This habitat is highly threatened due to commercial and residential construction. *Asimina tetramera* is federally endangered, as less than a handful of populations remain in Martin and Palm Beach Counties. Levels and patterns of genetic diversity are unknown. This information is crucial for successful conservation efforts given that the few remaining populations are small and fragmented. Molecular evidence from ISSRs (inter-simple sequence repeat markers) is used to evaluate within- and among-population genetic variation in *Asimina tetramera*, compared to the widespread *Asimina reticulata*. The use of these genetic data for conservation of *Asimina tetramera* will be discussed.

189 MYLICRAINE, KRISTIN A.*², KUSER, JOHN E.², SMOUSE, PETER E.² and ZIMMERMANN, GEORGE L.¹

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Rangewide allozyme variation in Atlantic white-cedar: Geographic patterns and implications for historical biogeography

Historical processes can have a significant impact on the amount and distribution of genetic variation within and among populations, and genetic data can be used to infer those historical processes. We examine the extent and pattern of allozyme variation in Atlantic white-cedar (*Chamaecyparis thyoides*), an important wetland tree species found along the Atlantic and Gulf coasts of the United States. We discuss the implications of these patterns for determining the Quaternary history of the species. We sampled 43 populations from Maine to Mississippi, and found significant regional variation, particularly in

the southern portion of the species range. Among Atlantic Coastal populations, there is no clear separation into subregions, and only a weak relationship between genetic and geographic distances, but we do see a significant negative relationship between latitude and the mean number of alleles per locus and the percentage of polymorphic loci. This suggests a glacial refugium along the southern Atlantic coastal plain, followed by a northward post-glacial migration, resulting in the progressive loss of rare alleles, as colonization moved northward. Among the peninsular Florida and Gulf Coast populations, significant genetic structure is apparent, with four subregions identified, and a strong relationship between genetic and geographic distances. These patterns suggest (1) historical separation of Atlantic coastal populations from peninsular Florida and Gulf Coast populations, and (2) historical isolation among subregions along the Gulf Coast and peninsular Florida. We discuss the Pleistocene history of peninsular Florida and the Gulf coast, and how this may explain the observed genetic divergence among populations.

190 NOVAK, STEPHEN*, MARSH, DEAN, DEINES,

LYNELL and RAUSCH, JOSEPH

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Genetic variation in *Taeniatherum caput-medusae* (Poaceae): amount and distribution of variability

The amount and distribution of genetic variation for any species is influenced by a large array of factors. For an invasive plant species two of the most important of these factors are its mating system and its pattern of introduction. *Taeniatherum caput-medusae* (Poaceae) is a primarily self-pollinating annual that has invaded large areas of the western United States. Given that this species experienced multiple introductions into its new range, we assessed allozyme diversity of *T. caput-medusae* using enzyme electrophoresis. Forty-five populations from California, Idaho, Nevada, Oregon, Utah, and Washington, were analyzed for their genotypes by staining for 15 enzymes that were coded for by 29 putative loci. Only 16 of 45 populations analyzed in this study exhibited any genetic polymorphisms. On average, populations of *T. caput-medusae* possessed 1.02 alleles per locus, 1.8% of loci were polymorphic, and the mean observed heterozygosity was 0.0001. The among-population component of the total gene diversity is very high ($G_{ST} = 0.929$), indicating substantial genetic differentiation among populations. The amount and distribution of allozyme diversity within and among these populations suggests that gene flow levels are low. Compared to other diploid seed plants allozyme diversity in this species is low. However, values for the parameters described above are consistent with previous reports for other highly selfing introduced plant species. Multiple introductions into geographically distinct localities and the mating system of *T. caput-medusae* appear to have played a large role in influencing the genetic structure of this species in its new range.

191 RAMP, JENNIFER M^{*1}, RANKER, TOM A¹ and
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A comparative study of population genetic variability in eight populations of the endangered vernal pool annual *Lasthenia conjugens* (Asteraceae)

Knowledge of population level genetic variation can be informative in determining conservation strategies for endangered plant species. California vernal pools are endangered due to habitat destruction. Vernal pools are ephemeral wetlands having both aquatic and terrestrial traits. Conservation of remaining vernal pool habitat is essential for persistence of several endangered species. The vernal pool annual *Lasthenia conjugens* (Asteraceae) is federally endangered. Historically it was found in seven counties ranging from the Central Valley to Santa Barbara. Upon listing in 1997, only 13 populations were known from 4 counties. Samples have been collected from 8 populations representing 5 counties. Four populations were sampled in Solano County, and one each from Contra Costa, Napa, Alameda, and Monterey counties. The population from Monterey County has been discovered since the 1997 listing. Between 14 and 40 individuals per population have been analyzed using Inter Simple Sequence Repeat (ISSR) markers. Levels of hierarchical genetic structure both within and between populations are being examined. Preliminary analyses indicate that all populations show moderate levels of genetic variability. The populations located in Solano County show fairly high levels of variability and low levels of genetic divergence from one another. The population in Monterey County has the lowest levels of genetic diversity. The populations located in Alameda and Monterey counties are the most divergent from the other 6 localities. This may be the result of a long geographical separation of the two groups. The populations in Alameda and Monterey counties are located on the west side of the Coast Range, whereas the other 6 populations are located within the Central Valley. These data will be used along with various kinds of ecological data to address conservation management issues.

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Genetic Variation in the Invasive Grass
Taeniatherum caput-medusae (Poaceae): Randomly Amplified Polymorphic DNA (RAPD) Analysis

Studies about the level and structure of genetic variation for invasive species provide information on ecological and evolutionary processes like founder effects and bottlenecks. Results from such work benefit when combined with information on the history of introduction and range expansion of the species. *Taeniatherum caput-medusae* is an annual, self-pollinating grass that has invaded millions of acres of the semi-arid western United States. Genetic variability of 12 populations from California, Idaho, Nevada, Oregon, Utah, and Washington was assessed using random amplified polymorphic DNA (RAPD) analysis. Special emphasis was given to select populations that represent early collection localities or reputed introduction

sites. Twenty individuals were sampled from each population ($n = 240$), and variability was assessed with 6 RAPD primers (48 primers were originally screened). We detected 121 putative loci or bands, of which 38 (31.4%) were polymorphic. A total of sixteen multilocus genotypes were observed across all 12 populations of *T. caput-medusae*. Eight populations did not exhibit any variation. Most of the genetic variation can be attributed to differences among populations ($G_{ST} = 0.89$). Genetic diversity in *T. caput-medusae* is generally consistent with that reported for other highly selfing, introduced plant species. Seven multilocus genotypes were often associated with early collection sites, and an analysis of molecular variance (AMOVA) indicates that 59% of the genetic variation is partitioned among geographic regions representing these early collections. This suggests separate introductions into these localities and subsequent local range expansion within the regions. Results and conclusions were similar to those obtained by allozymes.

193 RICHARDSON-AHEDOR, ADJOA^{*1}, WILLIAMS,
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Evidence of introgression in the Broad Hybrid Zone of the Buckeye Genus *Aesculus* L. (Hippocastanaceae)

Determining the genetic architecture of a hybrid zone plays a critical role in understanding the dynamics and evolutionary outcomes of hybridization. The buckeye genus *Aesculus* represents one of the best examples of natural hybridization in woody plants. Extensive hybridization among species of the monophyletic group, section *Pavia*, in the southeastern United States has resulted in hybrid zones of over 200 km wide. Morphological and allozyme studies have suggested that hybrids between *A. pavia* and *A. sylvatica* occur in an asymmetric distribution, with most hybrids that express *A. pavia* morphologically diagnostic characters occurring within the distributional range of *A. sylvatica* but outside the range of *A. pavia*. Genetic markers from seven microsatellite loci were employed to determine the genetic structure of the hybrid zone and to test previous hypotheses from morphological and allozyme studies regarding the asymmetric distribution of hybrids. A detailed analysis of individuals from four hybrid populations and three populations of each parental species indicated that two hybrid populations, located in close proximity to two *A. sylvatica* populations, were genetically most closely related to *A. sylvatica* due to appreciable rates of introgression, detected by the presence of *A. sylvatica* diagnostic alleles in these hybrids. The other two hybrid populations, located in the northern section of the zone were found to be genetically most closely related to two parental populations of *A. pavia*, located on the southwestern border of the hybrid zone. The presence of *A. pavia* diagnostic alleles in individuals from these two hybrid populations and the lack of isolation by distance between *A. pavia* and hybrid populations suggests current introgression of *A. pavia* into hybrid populations, potentially through long-distance pollen dispersal.

194 ROALSON, ERIC H.*¹, MCCUBBIN, ANDREW G.¹

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Evolutionary dynamics of genome structure in *Carex* section *Lupulinae* (Cyperaceae): assessing hypotheses of chromosome evolution in a phylogenetic framework

The precise role chromosomal changes play in evolutionary diversification remains debated, even though they are a prominent feature of diversification in diploid taxa. In the Cyperales an extremely large aneuploid series coexists with holocentric chromosomes (chromosomes that contain diffuse or non-localized centromeres). A commonly accepted mechanism for the origin of the aneuploid series is the persistence of chromosomal fragments after breakage due to presence of centromeric elements on all or nearly all possible fragments. This process, coupled with potential fission events, is referred to as the agmatoploid model of chromosome evolution. Here we explore the gross pattern of genome structure evolution in *Carex* section *Lupulinae* in a phylogenetic context. Examining chromosome number and genome size distribution allows us to (1) hypothesize individual steps in the evolution of genome structure in this group, and (2) evaluate whether agmatoploidy is the sole mechanism of genome change, or if other factors such as true aneuploidy or polyploidy have played a role.

195 SYMONDS, V. V.* and LLOYD, A. M.

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An analysis of microsatellite locus diversity in *Arabidopsis thaliana*: mutational dynamics and application

Microsatellite loci are among the most commonly used molecular markers. These loci typically exhibit variation for allele frequency distribution within a species; however, the factors contributing to this variation are not well-understood. To expand on the current knowledge of microsatellite evolution, 20 microsatellite loci were examined for 126 accessions of the model flowering plant, *Arabidopsis thaliana* (Brassicaceae). Substantial variability in mutation pattern among loci was found, much of which cannot be explained by the assumptions of the traditional Stepwise Mutation Model or Infinite Alleles Model. Here it is shown that degree of locus diversity is strongly correlated with the number of contiguous repeats possessed by the mean allele class for a locus, more so than the total number of repeats. These findings support a strong role for repeat disruptions in stabilizing microsatellite loci, demonstrating that marker selection can have a profound impact on estimates of genetic diversity. Results of cluster analyses are also presented, demonstrating the potential of microsatellite markers for resolving intraspecific relationships within *A. thaliana*.

196 WINDER, CHARLES

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Conservation genetics of the endangered Cumberland stitchwort, *Minuartia cumberlandensis* (Caryophyllaceae)

Minuartia cumberlandensis (Caryophyllaceae) is entirely restricted to five contiguous counties on the Cumberland Plateau of Tennessee and Kentucky, where unusual geological formations known as "rockhouses" provide the shady, cool, moist environments that define the narrow ecological niche of the species. Populations of *M. cumberlandensis* generally contain dozens to hundreds of individuals, and occur as discrete "islands," often isolated from one another by significant distances. This distributional pattern has important implications for the conservation of genetic resources in the species, impacting the processes of genetic drift within populations and gene flow among populations. Sequences of a low-copy nuclear gene, *G3pdh*, have been used to quantify genetic variation within populations and among populations, and to examine phylogeographic structure, offering insight into the contemporary and historical population genetic processes affecting the species, and thus informing conservation management decisions.

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Microsatellite Polymorphism and Genetic Structure of a broad hybrid zone of *Aesculus* (Hippocastanaceae)

Eight microsatellite loci were analyzed for a broad *Aesculus* hybrid zone involving three species, *A. flava*, *A. pavia*, and *A. sylvatica*, in northern and central Georgia. The objectives were to characterize the genetic structure of the zone and to test previous hypotheses on patterns of gene flow. We analyzed 29 populations within parental ranges and across the hybrid zone with sampling ranging from 15 to 47 individuals for most populations. Results revealed a high level of polymorphism for all loci; the number of alleles per locus ranged from 15 to 35. Among all loci, 187 alleles were detected with 43 unique to parental species and ten unique to hybrid populations. Genetic diversity, measured by numbers of alleles and genotypes, were similar among parental species and hybrid populations, suggesting no evident increase in the hybrid zone. Observed heterozygosity was significantly lower than expected for both parental species and hybrids. F-statistics suggest overall restricted gene flow among species and hybrids and some degree of inbreeding and population subdivisions. However, obvious gene flow was detected among *A. pavia*, *A. sylvatica*, and *A. flava*, via the hybrid zone, evidenced by distribution of unique alleles and Fst values. The *A. pavia* X *A. sylvatica* populations carry more alleles unique to *A. pavia*. Our microsatellite evidence agrees with the previous hypothesis that there is long distance gene flow of *A. pavia* from the coastal area into the zone up to northern Georgia Mountains and the genetic structure of the zone is asymmetrical, but also suggests there may be extensive gene flow between *A. sylvatica* and *A. pavia* across the zone horizontally.

CONTRIBUTED POSTERS

198 CALIE, PATRICK J* and SHACKLEFORD,
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Variability of seed germination within and
between populations of the Kentucky endemic,
Short's goldenrod (*Solidago shortii*-Asteraceae)

Solidago shortii is an endemic species located in the Blue Licks area of Kentucky. The species is represented by 12 distinct "populations", or demes. To determine the amount of variation among and within populations with respect to seed germination, seeds were sampled from six populations, each population being represented by 10 randomly chosen individual stems. 24 seeds were randomly chosen from each individual sampled stem's inflorescence (240 seeds per population). To follow the fate of specific seeds, each sampled seed was placed in Murashige and Skoog minimal salts solid medium in an individual well of an enclosed 96 well microtiter plate, up to 96 seeds (4 individual stem samples) per plate. Successful germination was defined by the emergence of the radicle from the imbedded seed. Among the six populations, the collective germination rate ranged from 10% to 40%, with a mean of 25%. The highest germination rate for a single plant was 82%, the lowest was 0%. The random samples of seeds tested in five of the six sampled populations contained a mixture of normal, aborted and mechanically damaged seeds. Aborted seeds were characterized by physical distortion (twisting) of the seed and a dark color to the seed coat. Mechanically damaged seeds exhibited broken ends distal to the pappus. In these five populations the range of normal seed composition was 10% - 38%, with a mean of 23%. Both aborted and damaged seeds exhibited 0% germination. We posit the effector of seed abortion is likely inbreeding depression (due to the small population sizes of Short's goldenrod) and the physical damage due to the parasitism of bruchid beetles. The ecological agents responsible for the seed herbivory and seed necrosis could represent significant threats to the long-term survival of those affected populations.

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Phylogenetic relationships of *Citrullus*
(Cucurbitaceae) using DNA sequences from
several coding and noncoding chloroplast DNA
regions: implications for evolution of watermelon

The genus *Citrullus* comprises four species, one of which, the cultivated watermelon, *C. lanatus* var. *lanatus* (Thunb.) Matsum & Nakai, is grown worldwide. Wild citron type watermelons are classified as *C. lanatus* var. *citroides*. The other species are *C. ecirrhosus*, *C. colocynthis*, and *C. rehmii*. PCR-RFLP analysis of cpDNA from more than 75 *Citrullus* Plant Introduction accessions collected from many different geographical areas, revealed phylogenetically informative nucleotide diversity at *ndhA*, *ndhF*, *trnC-trnD*, *trnS-trnM*, and *trnR-atpA*. A diagnostic haplotype for the cultivated watermelon was detected at the 3' flanking region of *ndhF*. A diagnostic haplotype for citron at the *ycf6-psbM* region. Three haplotypes were detected within *C. colocynthis*, associated with distinct geographic areas of origin. Sequencing of variable coding and non-coding sections of *ndhF*, *trnC-trnD* and *trnS-trnM* were carried out using *Praecitrullus fistulosus* as

an outgroup. No haplotype variability was detected between cultivated watermelon or between citron types. One insertion in *C. colocynthis* shed light on possible migration routes and provided phylogeographic information. Patterns and rates of nucleotide substitutions were studied. Parsimony analysis support the placement of *C. ecirrhosus* as ancestral to the cultivated watermelon

200 DEPAMPHILIS, C.¹, MA, H.¹, SOLTIS, D.², SOLTIS, P.²,
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The Floral Genome Project: Comparative analysis of sequence and expression of florally expressed genes

Much of the knowledge about genes controlling flower development is derived from studies of a few model plants from the eudicot and monocot groups. However, a great deal of floral morphological diversity is found among the basal angiosperm and basal eudicot lineages. How the floral developmental program originated and diversified, and how much of what we already know from models is generally applicable to floral development in other species, remain central questions. The Floral Genome Project (FGP) aims to identify florally expressed genes from 13 angiosperm species that occupy important phylogenetic positions, and reproductive genes of two gymnosperm species. Thousands of ESTs will be generated per species from early (premeiotic) floral (or reproductive) libraries, and a subset of complete cDNA sequences will be determined from selected species. Phylogenetic analysis will be performed with many gene families to identify homologs of known floral regulatory genes and to uncover new floral genes and gene families. An extensive set of sequence data and clones, as well as high quality floral cDNA libraries, are now available as public resources. Microarray and *in situ* hybridization will be used to determine their expression patterns. The FGP sequences and expression data will be compared with data from other species to derive a consensus set of floral regulators. At the same time, genes that might be specific to a lineage or responsible for distinctive structural properties can be identified and characterized. Progress during the first 1.5 years will be presented and their implications for the conservation and divergence of floral regulators will be discussed. This work was supported by N.S.F.'s Plant Genome Research Program. Additional authors for this work include: L. Cui, L. Landherr, P. K. Wall, Y. Hu, D. Ilut, V. Albert, J. Doyle, J. S. Farris, D. Oppenheimer, and G. Theissen.

201 DUAN, FAPING¹, FAN, SHUGUO*², LI, YUANQING²
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Effects of Liberty and bar-transgenic Rice Residue on Microorganisms and Activity of Soil Enzyme

Effects of Liberty on numbers of soil microorganisms (bacteria, actinomycetes, and fungi) and activity of catalase, polyphenol oxi-

dase, coverzyme, urease were not obvious. The numbers of microorganism and activity of catalase, coverzyme, urease of soil by plant residue treatment is higher than that of soil, which were not treated by plant residue. There were no significant difference in microorganisms and activity of soil enzyme of the soil treated by plant residue between the transgenic rice and the original parents.

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Poisonous Mechanism of Gufosinate and Resistant Mechanism of bar-transgenic Rice

Glutamine synthetase (GS) activity in leaves of non-resistant rice Cypress was inhibited after 4 hours by spraying Liberty. Accumulation of free ammonia increased. Chlorophyll content, chlorophyll a/b ratio, intrinsic efficiency of PSII photo-chemistry (Fv/Fm), quantum yield of photosystem a-electron transport/EPSP_a and coefficient for photochemical quenching (qp) of leaf chlorophyll fluorescence were decreased significantly. Photosynthetic rate was defined. Finally the seedlings of Cypress were dead. Glutamine synthetase (GS) activity in leaves of bar-transgenic rice Cypress PB-6 was also inhibited after 4 hours by spraying Liberty, but GS activity recovered after 36 hours by spraying Liberty, then the level of free ammonia decreased. The effects of Liberty on chlorophyll content, chlorophyll a/b ratio/intrinsic efficiency of PSII photo-chemistry (Fv/Fm)/EPSP_a of PSII photo-chemistry (qp) of leaf chlorophyll fluorescence were relieved. Photosynthetic rate was recovered. The seedlings of Cypress PB-6 grow normally.

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Studies on Resistant Inheritance of bar-transgenic Rice and Expression of bar Gene

The resistance to Liberty of herbicide resistant bar-transgenic rice (GulfmontBengal HU-100Bengal HC-110Cypress PB-6 and Cypress PB-13) was controlled by a single dominant nuclear gene. The inserted loci of bar gene were different among the five herbicide resistant parents. There was a Liberty-sensitive plant of Zhenshan 97A/Cypress PB-6; the results of PCR indicated that there is bar gene in it. There were no evidently different in chlorophyll content, chlorophyll a/b ratio, photosynthetic rate/parameters of chlorophyll fluorescence (Fv/Fm/qp/PSI/EPSP_a)/glutamine synthetase (GS) activity and accumulation of free ammonia in leaves of bar-transgenic rice comparing with the corresponding original parents. Physiological characters changed significantly in leaves of various parents after two days by spraying 1.0% Liberty. There were bad effects of bar gene on yield characters of transgenic rice comparing with the original corresponding parents. According to the resistant level, photosynthetic rate and yield characters, Gulfmont, Bengal Hu-10 and Cypress PB-6 were the better among five resistant parents which can be used as donors of bar gene in breeding.

204 ELLER, MICHELE^{*} and KNAP, HALINA
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Genomics of Polyamine Biosynthesis Genes in Soybean

Polyamines are organic cations with diverse contributions to plant growth and development and stress response. Information regarding putrescine biosynthesis is relatively well established; however, limited information exists concerning the enzymes catalyzing spermidine and spermine biosynthesis in plants. A small number of genes constitute the spermine biosynthesis pathway (cystathione gamma synthase (CGS), cystathione beta lyase (CBL), 5-methyltetrahydropteroylglutamate-homocysteine methyltransferase (MSY), S-adenosylmethionine synthetase (SAM), S-adenosylmethionine decarboxylase (SAMDC), spermidine synthase (SPDS), and spermine synthase (SPMS)). Based on expressed sequence tags (ESTs) in the soybean libraries constructed from different organs, cDNA probes were designed and used in Southern analysis. Genomic analysis and sequence assembly of ESTs indicated that the spermine biosynthesis genes are present in small to medium gene families in the soybean genome, similar to *Arabidopsis*, suggesting evolutionary pressure for the number of polyamine genes in higher plants. Expression analysis indicated that soybean fasciation mutant had overall elevated levels of transcripts compared with the wild-type. In both genotypes, higher transcript abundance in leaves than roots for the first five genes in the pathway were detected. Similar to *Arabidopsis*, expression of the two final genes in the pathway, SPDS and SPMS, was higher in roots than in leaves. Elevated expression levels of SPMS in the mutant apical meristem at transition to floral stage compared with wild-type immature flowers suggest importance of spermine to cell division and differentiation.

205 LIU, XIANAN¹, SWIRE-CLARK, GINGER² and BAIRD, WM. VANCE^{*2}

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Differential Expression of Genes Regulated in Response to Abiotic-stress in Sunflower

Drught and high salinity limit plant growth and crop production worldwide. Knowledge of the molecular mechanisms underlying the response to these abiotic stresses is important for an understanding of stress tolerance and for germplasm improvement. Using differential mRNA display and quantitative RT-PCR, at least thirteen genes regulated by drought- and/or salinity-stress were identified in sunflower (*Helianthus annuus* L.). Results showed that certain genes respond to both stresses, while others are uniquely regulated either in terms of the stress stimulus or the plant tissue. Overall, their individual expression patterns defined three regulation categories, and suggest cross-talk between signal transduction pathways during stress response. Sequence analysis of the clones identified only five with homology to known genes. The possible functions of these genes in plant stress-response are discussed.

206 LIU, XIANAN² and BAIRD, WM. VANCE^{*1}¹Horticulture Department, Clemson University, Clemson, SC 29634-0375;²Department of Plant Biology, 190 ERML, University of Illinois, Urbana, IL 61801

Identification of a novel gene, HaABRC5, up-regulated in response to drought, salinity and exogenous abscisic acid from *Helianthus annuus* (Asteraceae)

Using the differential display technique, we obtained a partial cDNA clone, RSC5-U, that is up-regulated by exposure to high salinity. A cDNA of 812 nucleotides, designated *HaABRC5*, was then cloned by rapid amplification of cDNA ends. The full-length cDNA contains an open reading frame of 423 nucleotides encoding 141 amino acids with a 'bipartite nuclear targeting sequence'. The deduced amino acid sequence showed no similarity to known functioning genes in the database. The expression of *HaABRC5* was investigated in more detail using quantitative RT-PCR. *HaABRC5* is up-regulated by drought, high salinity and exogenous application of abscisic acid (ABA). The promoter sequence of 229 nucleotides, up-stream of *HaABRC5*, was cloned using rapid amplification of genomic ends. Three ABA-responsive elements were found within the *HaABRC5* promoter region. Therefore, *HaABRC5* is probably an ABA-responsive nuclear protein playing a role in plant stress response.

207 MEEROW, ALAN W.*¹, GIDEON, MICHAEL² and CLAYTON, JASON R.¹¹USDA-ARS-SHRS, National Germplasm Repository, 13601 Old Cutler Rd. Miami FL 33158 USA; ²15455 SW 233rd St., Goulds, FL 33170 USA

Microsatellite DNA variation in *Iris hexagona*

Walter Iris *hexagona* is reportedly the only native iris species in Florida. It is a member of the section *Hexagonae*, a small complex of 4-5 species and numerous hybrid populations known popularly as Louisiana iris. *I. hexagona* occurs mostly in open, freshwater swamps in Texas, Louisiana, Mississippi, Alabama, Georgia, South Carolina and Florida, although this broad range assumes synonymy of *I. giganti-caerulea* with *I. hexagona*. *I. hexagona* achieves its broadest geographic range in Florida, occurring throughout the peninsula. One of us (M.G.) has observed populations of this species throughout Florida, and has documented much broader variation in morphology and habitat than has been previously associated with this species. He has identified unusual populations in Highlands County, Florida that occurs in much drier habitats than usually associated with the species. We have developed a microsatellite DNA library from *I. hexagona*. Currently, we have completed a survey of 30 populations of the species, 27 from Florida and 3 from Louisiana, across 10 SSR loci. An additional 4-6 loci are in process. The primer pairs have also been used successfully on *I. fulva*. Our hypothesis is that populations of *I. hexagona* within any major Florida drainage system represent unique genetic assemblages then radiated from refugia during inter-glacial periods of inundation when Florida was reduced to a series of islands. It is also possible that the northernmost populations within the state represent unique and perhaps more recent entries from contiguous states, while southern Florida populations may have radiated from relict populations that survived on highland islands during the last period of inundation. Moreover, we hypothesize that *I. hexagona* has also been influenced by pre-Columbian human migration patterns in the state. We will present the results of analysis of our data across these 30 populations.

208 MYLÉCRAINE, KRISTIN A.*², KUSER, JOHN E.²,¹ZIMMERMANN, GEORGE L.¹, SMOUSE, PETER E.² and STRUWE, LENA²¹Division of Natural Sciences and Mathematics, Richard Stockton College of New Jersey, PO Box 195, Pomona, NJ 08240; ²Department of Ecology, Evolution and Natural Resources, Rutgers, the State University of New Jersey, 14 College Farm Road, New Brunswick, NJ 08901

Varietal status of *Chamaecyparis thyoides* var. *henryae* supported by allozyme and morphological data

Atlantic white-cedar, *Chamaecyparis thyoides* (Cupressaceae) is a wetland tree species found along the Atlantic and Gulf Coasts of the United States. White-cedar populations along the Gulf Coast and surrounding areas have been considered by many to belong to a different taxon. These populations were first described as a separate species, *Chamaecyparis henryae* Li, and included the western Florida panhandle, southern Alabama, and southeastern Mississippi. This taxon was later reduced to varietal status, *C. thyoides* var. *henryae* (Li) Little, but some authors have not accepted its recognition as a unique taxon. There has been debate concerning the taxonomic relevance of this taxon and its appropriate geographical delineation. We use both allozyme and morphological data to address this issue. Both allozyme data and preliminary morphological examination support the varietal distinction, although there is additional allozyme variation, particularly in the southern portion of the species range, that is not accounted for by the varietal designation. These data suggest that *Chamaecyparis thyoides* var. *henryae* should be delineated to include populations of the western Florida panhandle and Alabama. This subspecific taxon is morphologically distinct, because the facial glands are eglandular, while those of *C. thyoides* var. *thyoides* are glandular. Preliminary data also suggest that the two varieties differ in the number of cone scales.

209 TERCEK, MICHAEL*, HAUBER, DONALD and DARWIN, STEVEN

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Ecology and evolution of geothermally adapted *Agrostis* of North American and the Kamchatka Peninsula

Agrostis species have been known to rapidly evolve ecotypes in response to geographically localized variations in soil chemistry. Two *Agrostis* taxa occur in the geothermal habitats of Yellowstone National Park: *Agrostis rossiae* is endemic to Yellowstone, and *Agrostis scabra* occurs both in thermal areas and in non-thermal habitats. Every thermal *Agrostis* population is surrounded by a non-thermal population of *A. scabra* that is reproductively isolated from the thermal area by its later flowering time. This suggested that ecotype evolution had happened twice, producing thermal *A. scabra* and *A. rossiae* in separate events. Randomly amplified polymorphic DNA (RAPD) markers were used to resolve the historical relationships among the Yellowstone thermal populations, non-thermal *A. scabra* populations, seven other non-thermal *Agrostis* species that occur in Wyoming, and thermal *Agrostis* populations in California and Kamchatka. Contrary to the original hypothesis, none of the thermal taxa are ecotypes of non-thermal *Agrostis scabra*, but instead constitute a previously unrecognized endemic taxon that currently has four names. A UPGMA phenogram showed that while the thermal populations form geographically distinct subclusters, populations of the morphologically distinct

A. rossiae and thermal *A. scabra* do not cluster independently. Field and laboratory experiments, as well as extensive field monitoring, showed that there are no important ecological differences between *A. rossiae* and thermal *A. scabra*. The ecological factor primarily responsible for the geographic separation of the thermal and non-thermal populations is the seasonal fluctuation of soil temperature relative to the life cycle of the plants. Lethal summer soil temperatures in the thermal areas are selecting for precocious flowering, which excludes the more slowly maturing nonthermal plants. The thermal plants do not grow in the non-thermal matrix in prevailing cool field temperatures, but do grow in these habitats under artificially elevated temperatures. The thermal taxa may have reduced competitive ability at cooler temperatures.

HISTORICAL SECTION

CONTRIBUTED PAPERS

210 DAVENPORT, L. J.

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Charles Mohr and the Medicinal Plants of Alabama

Charles Mohr (1824-1901), German-born Mobile pharmacist and botanist, is best known for the monumental *Plant Life of Alabama*, published shortly after his death. Praised as a "model" for similar works being published at that time, *Plant Life* remains as the only complete flora for the state. Mohr was a prolific writer, especially during the last twenty years of his life, producing over 80 works. (Many were published both in English and German.) His main topics included bryology, medicinal chemistry, ballast plants and other "waifs," forestry and forest products, descriptions of new species, mineralogy, and general natural history. In 1890, Mohr combined his interests in botany, chemistry and medicine in a 17-page paper, "The Medicinal Plants of Alabama," in the *Proceedings of the Alabama Pharmaceutical Association*. In this paper, he treated 167 native and naturalized species, providing for each its scientific name and major synonyms, common name, plant part used in medicine, flowering season, best collecting season, preferred habitat, and distribution within Alabama. In contrast to *Plant Life*, "Medicinal Plants" is a disappointing paper, lacking the details and personal descriptions that characterize the author's other works. Simply an expanded checklist, it records little of Mohr's vast experience in both botany and pharmaceuticals.

211 HALBROOKS, MARY C

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History of the Restored English Garden at Stan Hywet: An Ellen Biddle Shipman Designed Landscape

Stan Hywet Hall and Gardens in Akron, Ohio is a nationally significant historical estate and cultural landscape. Originally home to the Seiberling family in the early 1900s, it was designed by renowned Boston architect Warren Manning between 1911 and 1917. Of the thousands of properties Manning had surveyed, very few offered, in his opinion, "such varied incidents that will give a home estate distinction and interest". Manning collaborated with architect Charles Schneider to create garden rooms as extensions of the Tudor-style

manor home. One of these, the English Garden, was a walled garden — a favorite retreat for Mrs. Seiberling. In 1928, Ellen Biddle Shipman, the foremost among women landscape architects of that time, was commissioned to redesign the garden. Her design was implemented and maintained until the early 1950s. After the deaths of Mr. and Mrs. Seiberling, the estate was turned over to a private foundation in 1955 and opened to the public. During the 1960s and 70s, the Akron Garden Club maintained and replanted the English Garden eventually transforming it into a shady retreat under a perimeter of towering evergreens. Little of the original garden plantings, or its architectural integrity, remained by 1985. The decision to restore the English Garden to Shipman's design, and not Manning's, was made in accordance with Stan Hywet's Landscape Policy that the period of greatest historical significance for the restoration of its garden landscape is 1912 - 1930 and because Shipman's planting plans had been preserved. In 1991, the English Garden was restored architecturally and horticulturally and re-opened to the public. Archival records and period photographs document the history of the garden since 1912 and the complex restoration process that re-established the elegance of the garden as envisioned by Ellen Biddle Shipman.

212 MUSSELMAN, LYTTON JOHN

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The Botanical Activities and herbarium of George Edward Post (1838-1909)

After earning degrees in medicine, theology, and dentistry, Post accepted a position in 1863 in Tripoli, Syria (modern day Lebanon) as a missionary. He immediately began collecting plants throughout the region. In 1868 he joined the medical faculty of the Syrian Protestant College (now the American University of Beirut-AUB) and established the herbarium. Fluent in Arabic, Post edited a medical journal in Arabic, produced the first concordance of the Arabic Bible, and wrote extensively on archeology and natural history of Bible lands. His Flora of Syria, Palestine, and Egypt is one of the early works on Middle Eastern plants. From 1877-1900 he corresponded extensively with the Boissier Herbarium in Geneva and published a series of papers, *Plantae Postianae*, reporting floristic research and describing new species. I have catalogued the types of Post in the herbaria in Geneva (G) and Beirut (BEI). In addition to Post's specimens and those of his students, the Post Herbarium (BEI) includes exsiccatae from prominent European botanists (Autran, Barbey, Bornmüller, Haussknecht, Schweinfurth) and specimens obtained through a little-known exchange program by a student of Asa Gray, Horace Mann, Jr (1844-1868, son of the famous educator). Despite years of neglect and war, the Post Herbarium is intact and an underutilized resource for the Middle East flora. It also contains bryophytes of the Hawaiian Islands (possibly through Mann) and Sri Lanka, a fern collection from New Zealand (distributed by Craig?), and a number of specimens by such American luminaries as W. M. Canby, A. H. Curtis, D. C. Eaton, C. Mohr, and E. S. Palmer. Fortunately, there are plans to maintain and properly curate the Post Herbarium.

PALAEOBOTANICAL SECTION

CONTRIBUTED PAPERS

213 AXSMITH, BRIAN

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A reevaluation of the Late Triassic conifer *Pseudohirmerella* based on cones, associated leafy shoots and anatomically preserved wood from North America

The conifer genus *Pseudohirmerella* Arndt was recently established for ovulate cone scales from the German Keuper originally described as *Glyptolepis platysperma* Maegdefrau. These scales bear five distal lobes and paired bulging structures recently interpreted as *Taxus*-like arils. A conifer with similar cone scales was described from the Passaic Formation of New Jersey as *G. delawarensis* Bock. A re-evaluation of *Pseudohirmerella* is presented based on rediscovered components of Bock's collection, and newly collected specimens from the type locality. The New Jersey collections include articulated ovulate cones proving that the putative bulges on the scales are not arils but casts of concavities in the original scale surface as originally suggested by Bock. The supposed openings at the "aril" apices are ovule attachment scars. The aril interpretation is also unlikely based on functional considerations. Although no *Classopollis* pollen has been found directly associated with these fossils, cheirolepidiaceous affinities are suspected based on cone scale morphology and associated organs including robust pollen cones and *Pagiophyllum-Brachyphyllum* leafy shoots. This study also includes the first description of associated wood, which shows features consistent with cheirolepidiaceous affinities including semi-araucaroid (mixed) tracheid pitting, cupressoid crossfield pitting, resinous tracheids, and an absence of resin canals.

214 BOUCHER, LISA

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Paleobiogeography of Cretaceous Macrofloras in Southern North America

Macrofloral assemblages from Santonian to early Maastrichtian sites in southern North America were compared relative to paleogeographic positions along the epicontinental seaway. First-hand data and information from publications were used in a preliminary assessment of macrofloral composition at sites south of 50°N paleolatitude. Most plant remains consist of leaf impressions, compressions and reproductive structures and these types of assemblages were the focus of the analysis. Floras from the Blackhawk Formation in east-central Utah, Fruitland and Kirtland Formations in New Mexico, the Olmos Formation in northern Mexico, and the Eutaw, Ripley, and Black Creek Formations of the Eastern coastal plains were considered. The macrofloras contain well over one hundred genera, of which most are angiosperms, within similar paleoenvironmental settings along the coast. Comparisons are limited by temporal resolution, taxonomic identification, taphonomic differences, and other sampling bi-

ases. However, an initial assessment indicates that some taxa are shared between the eastern and western regions, considering age, paleoclimate and depositional environment. Taxa in common include some unique angiosperms such as Manihotites. Some of those shared taxa do not appear to be present before the Santonian and are not widespread, implying they were able to disperse across the epicontinental seaway. However, additional collections and temporal resolution are essential for completing more robust analyses. These preliminary results provide a framework for conducting future studies and comparing other available specimens, such as mesofossils, wood, and microfossils

.215 BOYCE, C. KEVIN*, ZWIENIECKI, MACIEJ A. and HOLBROOK, N. MICHELE
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How to make a leaf? 400 million years of repeated developmental, physiological, and biochemical answers to the same evolutionary question

Basic leaf morphologies include linear and dichotomizing structures with a single vein per segment, laminate leaves with one or two orders of marginally ending veins (commonly associated with ferns), and laminate leaves with several vein orders that include internally directed veins and vein endings (commonly associated with the angiosperms). Each of these morphologies has evolved independently numerous times among the fossil and extant lineages of vascular plants. Our recent work has shown that this morphological convergence has required the convergent evolution of developmental processes as well. Here, we now demonstrate that these morphological and developmental alternatives also appear to represent physiological alternatives. These different leaf types employ opposing strategies to ensure an even supply of water to the entire photosynthetic surface. Exploitation of these physiological alternatives has involved the correlated evolution of changes in anatomy, hydraulic resistance properties, transport regulation capabilities, and vascular cell wall chemistry. Therefore the basic leaf types that can be recognized in the fossil record represent highly integrated developmental, biochemical, and physiological syndromes that have evolved repeatedly.

216 CHEN, JUDY¹, MANCHESTER, STEVE¹ and CHEN, ZHIDUAN²

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Permineralized seeds of Nymphaeaceae from the early Eocene of eastern China

Well preserved, permineralized, seeds conforming morphologically to the Nymphaeaceae have been recovered along with early Eocene mammals from the coal mines of Wutu, Shandong, China. The seed morphology and anatomy are very similar to extant genus *Nuphar*. The fossil seeds are obovate, subpyriform, 4.5 mm long with a clearly visible raphe ridge, and a truncate apex capped by a circular operculum ca1 mm in diameter bearing a central micropylar protrusion. These features, along with the thick cuticle, and testa composed of a uniseriate outer layer of equiaxial pentagonal to hexagonal surface cells, a middle layer 3 to 4 cells thick composed of thick-walled, periclinally elongate sclereids correspond to the morphology and anatomy of extant *Nuphar*, and distinguish them from all other extant and extinct genera of Nymphaeales. These early Eocene

seeds provide the oldest record for the *Nuphar* lineage in Asia and are supplemented by a similar well preserved specimen from the late Paleocene of North Dakota, USA. These data, together with the prior recognition of *Brasenia* (Cabombaceae) in the middle Eocene, indicate that the families Nymphaeaceae and Cabombaceae were distinct by the early Tertiary.

217 CORBETT, SARAH L.

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Implications of the Miocene flora of Alum Bluff, Liberty County, Florida

The Miocene flora of Alum Bluff, Liberty County, Florida is significant because of the relative rarity of Tertiary fossil plant localities in the southeastern U.S. coastal plain. By conducting a floristic study of the fossil plant assemblage at the site, implications for understanding Miocene climate, biogeography, and paleoecology of the region are inferred. The first study of the flora of the Alum Bluff site was conducted by E.W. Berry in the early twentieth century. Berry identified 12 leaf species, however recent collections and further examination of specimens reveals that more than 12 leaf and pollen morphotypes are present in the flora and that some of Berry's identifications may be incorrect. Berry described the flora as being essentially similar to the modern flora of the Florida panhandle, however recent finds such as *Paliurus*, which is extinct in North America but present in East Asia today, suggests different floral affinities. The composition of the flora is compared with modern floras to determine climatological conditions and biogeographical implications of the Florida panhandle region during the Miocene. The associations of plant fossils and sedimentary environment at the Alum Bluff site are used to infer paleoecology of the plant community. The nature of this study synthesizes many fields of botany, and in doing so contributes significantly to paleobotanical understanding of the southeastern coastal plain region.

218 DUNN, MICHAEL T.

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The Fayetteville Flora of Arkansas, USA: An Upper Mississippian (middle Chesterian/ lower Namurian A) Plant Fossil Assemblage with Permineralized and Compression Remains

Fossil plants have been known from the Fayetteville Formation of Northwestern Arkansas since at least 1937, and since that time numerous individual taxa have been described, but no synopsis of the assemblage has been compiled. The Fayetteville flora contains a unique Upper Mississippian fossil assemblage with allochthonous permineralized plant remains recovered from offshore marine black shales, and two coalified compression assemblages: one compression assemblage represents an autochthonous terrestrial/deltaic assemblage, and the other was recovered from near-shore strata. This report summarizes previous reports and adds new data to produce a comprehensive floristic survey of this important fossil assemblage. The flora consists of 40 morphospecies: 18 permineralized species and 22 compression species that represent at least 13 whole plants. Lycopid remains are the most numerous and pteridosperms are the most diverse. Sphenopsids are common, but mono-generic and ferns are rare. *Lyginopteris royalii*, *Trivena arkansanus*, *Megaloxylon wheeleriae*, *Quaestora amplecta*, *Rhynchosperma quinnii*,

Chlamidostachys chesterianus, and *Telangiopsis arkansanum* are known only from these strata. The occurrence of *Rhetinangium* and *Megaloxylon* records the first report of these genera in North America, and the occurrence of *Medullosa* is the oldest unequivocal evidence for this genus anywhere in the world. The co-occurrence of compression and permineralized species of the same genera facilitates the formation of hypotheses concerning the reconstruction of whole plants. Perhaps most importantly, the identification of two plant community level ecosystems, nested within the landscape level ecosystem preserves a snapshot of the distribution of diversity in the clastic swamp biome at Upper Mississippian time. The occurrence of spacial sub-units of the ecosystem, nested within a larger ecological unit has not been recognized in known Mississippian terrestrial fossil assemblages, and sheds new light on the evolution of terrestrial ecosystem structure.

219 GARCIA-MASSINI, JUAN L.* and TAYLOR, THOMAS N.

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Fungi with affinities to the Glomales in the Permian of Antarctica

Two compact clusters of terminal and intercalary chlamydospores occur in decaying remnants of silicified tissue from the Permian of Antarctica. Chlamydospores are pyriform to subglobose, and sometimes broadly triangular. Most possess two pores, each located at the opposite end of the spore. In some spores three or four pores are present and these are also symmetrically arranged. Pores vary in size (2.5-18 μ m), and maybe circular to slightly elliptical. Some possess a slightly thickened rim along the edge of pore. A few spores appear to have been terminal and are attached to nonseptate, subtending hyphae. In approximately half of the chlamydospores the spore wall consists of three layers; the outer is thick and laminated, the middle is non-laminated and tightly appressed to the outer wall, and the inner is of membranous appearance and sometimes detached and wrinkled in the center of the spore. The outer wall of the chlamydospore as well as the subtending hyphae appears to be ornamented with small protuberances sometimes resulting in a slightly reticulate pattern; however, since specimens with psilate walls are also present, the ornamentation observed could be the result of diagenetic processes. Morphologically these fungi resemble extant and fossil members of the Glomales. The presence of ornamented terminal and intercalary clusters of chlamydospores with an elaborated spore wall structure are characteristics seen in the genus *Glomus* within the family Glomaceae. This report constitutes the first *Glomus*-like fungi known from the Permian, and points to the importance these fungi have had since their first appearance in Ordovician times in shaping terrestrial ecosystems.

220 HERNANDEZ-CASTILLO, G. R.*¹, STOCKEY, R. A.¹ and ROTHWELL, G. W.²

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Architecture, stature, and life cycle of primitive conifers from Euramerica

Conifers constitute one of the most important components of temperate and boreal floras world wide. Traditionally, conifers are represented by large tree-sized individuals that conform to Rauh's and Massart's architectural models where a main stem bears series

of pseudowhors of lateral branches. Lateral branches may be irregular or plagiotropic and bear simple, linear, needle-like or S-shaped leaves. Internal anatomy is characterized by eustelic stems, pycnoxylic wood and tracheids with uni- or biseriate circular bordered pits. In addition, conifers are also characterized by terminal compound ovulate cones and simple pollen cones. However, recent findings demonstrate that not all conifers were large trees with simple pollen cones and compound seed cones. Specimens from Pennsylvanian and equivalent deposits in North America and Europe document small conifer trees with a variety of ovulate and pollen cone organizations and positions, position-dependent heterophyly, and internal anatomy that is similar to other Paleozoic coniferophytes. Species from the USA, France and Germany serve as examples of the variability expressed by primitive conifers and conifer-like coniferophytes. These data reveal that the architecture of primitive conifers resembles juvenile araucarian individuals, and suggest that more recent large conifer trees evolved from small trees by a combination of an extended vegetative growth phase and canalization of cone structure and position. Within the Araucariaceae, these also include hypermorphoses in leaf development.

221 KELLOGG, DEREK^{*} ¹, TAYLOR, THOMAS¹ and KRINGS, MICHAEL²

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The ultrastructure and function of glandular trichomes in *Sicana odorifera* (Cucurbitaceae)

Touch-sensitive glandular trichomes are epidermal outgrowths that rapidly release a sticky or quickly solidifying secretion when ruptured by contact and occur in several angiosperm families (e.g., Cucurbitaceae, Solanaceae). The substances secreted provide highly effective chemical and physical deterrents against herbivores. While the mechanisms by which the secretions physically obstruct the performance of small herbivorous arthropods are generally well-understood, one aspect that has rarely been addressed concerns the susceptibility of different types of arthropods to physical obstruction. For example, we found that, in *Sicana odorifera* (Cucurbitaceae), the physical component of the defense (i.e., a quickly solidifying secretion) only functions on those animals that (1) possess a certain minimum size, (2) are characterized by a certain mouthpart morphology, and (3) do not display particular behavioral features. Preliminary studies suggest that the mechanism that causes the trichomes to rupture by contact and rapidly exude secretion involves one or two small cells that are positioned on top of the secretory cell. We utilized SEM and TEM to investigate whether particular cell wall features of the secretory cell (e.g., texture, thickness) may facilitate the opening process. This study uses extant trichomes as a proxy record to examine plant/animal interactions in the fossil record, and to document structurally similar trichomes in selected fossil plants.

222 KLAVINS, SHARON D.*[,] TAYLOR, EDITH L. and TAYLOR, THOMAS N.

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A cycad pollen cone from the Middle Triassic of Antarctica

Cycads are believed to have originated during the late Paleozoic, possibly during the Carboniferous, although fossil evidence for this hypothesis is equivocal. While there are numerous Late Carbon-

iferous - Early Permian leaf compressions that have been assigned to the cycads, there are few reports of cycad reproductive structures. The fossil record of cycads in the Mesozoic is more complete but complicated by similarities in vegetative structure of cycads and Bennettitales; reproductive structures remain rare and those that are known are preserved as compressions. Here we present a permineralized cycad pollen cone from the lower Middle Triassic of Antarctica that represents the first record of an anatomically preserved male cycad reproductive structure. The cone is small, ovoid, with helically arranged, wedge-shaped, imbricating microsporophylls. At least five spine-like projections extend from the distal sporophyll face. The vascular cylinder is dissected and produces paired traces to the microsporophylls. Three vascular bundles enter the base of each microsporophyll and divide to produce five or more vascular strands in the sporophyll lamina. Pollen sacs are arranged in two radial clusters, which are positioned near the lateral margins on the abaxial surface of the microsporophyll. Each cluster is comprised of up to eight elongate, sessile pollen sacs that are fused for approximately half their length and display longitudinal dehiscence. Pollen sacs are attached to a vascularized receptacle that is elevated from the surface of the microsporophyll. Pollen is ovoid, monosulcate, and psilate. Although the combination of characters in this cone clearly affiliates it with the cycads, it also possesses unique features that are not found in extant representatives.

223 KNAUS, M. JANE

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Plant biostratigraphy, an artifactual taxonomy, and comparative floristics based on diversity estimates

The Early Mississippian period is among the most interesting in plant and geologic evolution: the time of diversification of fully leafed seed plants and the onset of global continental accretion. The plant fossil record, however, seems to supply little detailed information about these events. Problems lie in the plants themselves. Early leaf morphology was highly variable and somewhat indeterminate. Several different leaf shapes (and previously named species) have since been shown to occur on the same plant. I propose that unrelated lineages passed through this same developmental bottleneck of incompletely laminated irregularly lobed leaflets. As a consequence, many unrelated plants had similar foliage. This has resulted in artifactual taxonomic practices in which broadly defined form genera, often heterogeneous in cladistic composition, under-estimate diversity, while species splitting based on highly variable leaflet shapes tends to over-estimate diversity. Early workers imposed additional artifacts through generic assignments based on preconceived age determinations such as *Triphylopteris*, the single zone indicator for the Visean. Diverse foliage was assigned to this form genus to establish a Visean age, while trilobed foliar elements found assumably in the Tournaisian or Upper Mississippian were assigned to other broadly circumscribed genera such as *Adiantites*, *Sphenopteris*, or *Eremopteris*. New insights concerning this period of profound geologic and climate change may rest on the ability to track compositional changes over time and geographic area that are independent of historic taxonomic assignment. Proposed approaches include quantitative comparison based on raw counts of architectural types supplemented by diversity counts of co-occurring seeds. Seed compressions are often overlooked because of the inability to associate them with foliar taxa. The seeds of this time show considerably less intergradation of taxonomic characters and appear to fall into discrete size classes, thus possibly serving as a proxy for overall diversity of the seed plant component of these floras.

224 KRINGS, MICHAEL^{*}, GREWING, ANKE², TAYLOR,

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Lageniastrum macrosporae, the oldest fossil endophytic alga

Sublagenicula nuda megasporae from the Lower Carboniferous of France sometimes contain a colonial alga, *Lageniastrum macrosporae*, as an endophyte. This biosis represents the oldest unequivocal fossil evidence for endophytic algae and the only example to date of an alga residing in the interior of spores and pollen grains of vascular plants. *Lageniastrum macrosporae* colonies consist of up to 500 unicellular, pyriform to lens-shaped algae, arranged in a single layer and held together by a thin membrane; adjacent algal cells are usually interconnected by protoplasmic strands. *Lageniastrum macrosporae* displays a striking suite of morphological characters found in extant *Volvox*, which suggests that the fossil may be related to these chlorophytes. The nature of the *Lageniastrum macrosporae*-*Sublagenicula nuda* association remains unclear since it is impossible to establish with certainty whether the alga was a saprophyte, asymptomatic "space-parasite", endoparasite, or symbiont. Regardless the nature of the association, occupying the interior of megasporae may have provided several adaptive advantages for the alga, including protection against periods of desiccation and plankton-feeding animals, and use of the spores as vectors for dispersal from one habitat to another.

225 LITTLE, STEFAN A.* and STOCKEY, RUTH A.

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Permineralized fruits of Lauraceae from the Middle Eocene Princeton chert, British Columbia

Over 25 fossil fruits assignable to Lauraceae are preserved as permineralizations from the Middle Eocene Princeton chert. Cellulose acetate peels document a developmental series showing a single superior ovary, with one pendulous ovule, attached to the receptacle with some attached perianth. Later developmental stages including mature, enlarged fruits with developed seeds are also present. The fruits, ca 6 mm in diam, are globose when mature, and some are still attached to the enlarged cupule-like receptacle. Preservation is excellent allowing observation of all fruit tissues. The exocarp is a thin epidermis surrounding the fleshy mesocarp that is composed of thin walled cells with clusters of stone cells and idioblasts. When viewed under a green light excitation filter (535 nm - 550 nm), idioblast contents autofluoresce red (at or above 580 nm), indicating that aromatic compounds such as those found in idioblasts of extant Lauraceae may still be present in some form. The endocarp, 110-180 μm , is a single palisade layer of lignified cells with stellate outlines. This combination of characters is typical for Lauraceae; however, diagnostic anatomical characters below the family level are not firmly established. These are some of the best preserved lauraceous fruits known and further developmental anatomical studies of associated lauraceous inflorescences, twigs, leaves and wood will provide characters for whole plant reconstruction.

226 MANCHESTER, STEVEN R.

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Contemplating Platanaceae

The Platanaceae has a rich fossil record in the Northern Hemisphere documenting past evolution, geographic dispersals, and extinction that could not be deduced by morphological and molecular analyses of the remaining living species of *Platanus*. Evidence from co-occurrence at hundreds of fossil localities throughout the Northern Hemisphere offers improved understanding of both reproductive and foliar morphology for several extinct representatives of this unique Eudicot clade. Mid-Cretaceous representatives include various palmately lobed leaves similar to those of extant *Platanus* associated with elongate reproductive axes bearing sessile unisexual inflorescences and lacking dispersal hairs on the achenes. By the Tertiary, five distinct groups are recognizable: 1) digitately lobed simple leaves (*Macginitia* Wolfe et Wehr) similar to extant *Platanus racemosa*, but associated with elongate reproductive axes of 15 or more pedicellate inflorescences with 5 carpels or stamens per floret, and glabrous achenes (Paleocene and Eocene of western North America); 2) ovate, prominently serrate, but unlobed simple leaves (*Platimeliphyllum* Maslova) associated with elongate reproductive axes of 11 or more sessile inflorescences, and glabrous achenes (Paleocene of Europe and Asia, Eocene of Asia and North America); 3) broadly trilobate simple leaves similar to extant *Platanus occidentalis* associated with isolated globose infructescences and hairy achenes (Eocene and younger in western North America); 4) compound leaves with a tri-lobed terminal leaflet and a pair of asymmetrical lateral leaflets (*Platanites* Forbes; reproductive structures uncertain), and 5) compound leaves with 5, 3, or reduced to one elliptical to obovate leaflet(s) (*Platanus bella* P. neptuni complex sensu Kvacek et Manchester) associated with solitary stalked unisexual inflorescences, 3-8 stamens or carpels per floret, and hairy achenes (Paleocene to Miocene of Europe, Paleocene of Asia, Paleocene to Oligocene of North America). Pollen from the associated stamens is consistently tricolporate, microreticulate. The petiole bases are expanded and hollow as in extant *Platanus* subgenus *Platanus*.

227 MANCHESTER, STEVEN R.

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Phytogeographic implications of the fossil flora of the Green River Formation

Fossil plants of the Green River Formation in Colorado, Utah and Wyoming provide a glimpse of the vegetation characterizing inland western North America during the early to Middle Eocene. Floristic diversity of the Green River Formation (including Fossil Butte, Laney, Wilkins Peak and Parachute Creek Members) includes more than 150 genera. Comparison of the Green River plants with those from lake deposits of similar age in western North America (Clarno, Oregon; Republic, Washington), central Europe (Eckfeld and Messel, Germany) and eastern Asia (Fushun and Huadian, China) provides insight into the distribution of forest types and climate across the Northern Hemisphere about 45-50 ma. The Clarno and Republic floras share several genera in common with the Green River flora, indicating that floristic exchange was possible despite the intervening topographic relief and the drier inland climate. The Green River flora includes also elements that were widespread in Eocene floras of the Northern Hemisphere, such as *Lygodium*, *Sabal*, and *Allanthus*, but many other constituents were more confined geographically. *Macginitia*, *Populus*, *Salix*, and a newly recognized extinct

salicaceous genus appear to have been endemic to western North America at that time. Some of the Green River plants are known from the Eocene of western North America and Europe but not Asia, eg. *Cedrelospermum*, *Engelhardia*, *Hooleya*, *Palaeophytocrene*, and *Vitis*. These examples may indicate intercontinental migration via the North Atlantic land bridge. The Green River genera *Chaneya*, *Craigia*, *Eucommia*, and *Koelreuteria* are shared with the Eocene of Northeastern China, but are not known from the Eocene of Europe. These genera might have passed between North America and Asia via the Beringia land bridge. However, at least 30 percent of the genera of leaves and fruits currently known from the Green River flora are unique—not known from other Eocene floras.

228 MAPES, GENE*¹, ROTHWELL, GAR¹ and HILTON, JASON²

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Anatomy of the cheirolepidiaceous pollen cone *Classostrobus*; a new species from the Jurassic of England

An anatomically preserved pollen cone bearing pollen assignable to *Classopollis* has been discovered in a calcareous nodule recovered from marine sediments of the Lower Callovian calloviense biozone, Middle Jurassic, Kellaways Beds at the Freeth Wood Gravel Pit, Ashton Keynes, near Cirencester. The cone was originally round, but is somewhat flattened laterally, measuring 1.8 cm long and 1.8 cm in greatest width. It consists of a cone axis c.a. 1.5 mm in diameter from which sporophylls diverge in a helical arrangement. Sporophylls consist of a narrow stalk up to 6 mm long, with a distal lamina approx. 1.2 cm long and 4.5 mm wide. Individual laminae are approx. 1.2 mm long, tapering apically to a pointed tip, and forming a basal keel that bends toward the cone axis. A single vascular bundle diverges from the axis, and extends distally at the contact of two distinctly different histological zones. Abaxially, the sporophyll stalks are composed of thin-walled cells with black contents, while the adaxial side consists of cells with thicker amber walls. This distinct histological zonation could be inferred to represent the fused bract and dwarf shoot of a compound cone, as has been interpreted for some Mesozoic conifer pollen cones. However, vascularization by a single bundle demonstrates that this pollen cone is a simple shoot. Several pollen sacs are located adjacent to the inner surface of each keel on the abaxial side of the sporophyll stalk. Sporangial walls are uniseriate, and show no obvious dehiscence mechanism. Pollen is roughly spheroidal, 26-34 µm in diam, with two unequal polar caps separated by a striated belt with a subequatorial furrow. This specimen provides the first evidence of internal anatomy for cheirolepidiaceous fertile organs, and helps clarify the range of variation in the morphology of Mesozoic conifer pollen cones.

229 MOIIR, DR. BARBARA*¹, RYDIN, C.² and FRIIS, E. M.²

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Gnetalean diversity during the Early Cretaceous of Brazil

The Plattenkalk limestones of the late Aptian to early Albian Crato Formation of NE-Brazil contain a rich flora of unusual complete-

ness and preservation of cellular structures. The flora is composed of lycophytes, ferns and various seed plants including conifers and a variety of angiosperms. Plants of putative gnetalean affinity make up a large proportion of the fossils and are of an exceptional diversity. Among these gnetalean fossils are several forms that closely resemble living *Ephedra* in general habitus (decussate phyllotaxis, narrow or strongly reduced leaves) and in reproductive features (male and female strobili). In one of the male strobili belonging to this group of fossils, *Ephedra*-like pollen grains occur in situ. Other gnetalean taxa also show similarity in gross morphology to *Ephedra* but contain pollen grains similar to *Welwitschia*. The flora even includes well preserved seedlings, of which one exhibits venation pattern that is comparable to that of the cotyledons of extant *Welwitschia* and to that of the normal leaves of the Cretaceous *Drewria potomacensis* from North America. In addition to the fossils with distinct gnetalean characters the flora also comprises a number of enigmatic, often broadleaved forms with phyllotaxis and overall morphology resembling taxa of Gnetales, but where critical gnetalean features have not yet been documented.

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New Plant Assemblages from the Late Oligocene Chilga Deposits of the Ethiopian Western Plateau

Little is known about the floristic and vegetational history of sub-Saharan Africa during the Paleogene isolation. The recently discovered Late Oligocene Chilga macrofloral assemblages (~27-28 Ma) from northwestern Ethiopia are significant in providing new information about floristics, vegetation, and biogeography from an inland sub-Saharan region during this poorly known period of time. The Chilga plant fossil sites include assemblages of fruits and seeds (associated with vertebrates), leaves and flowers, and *in situ* silicified forests. Among these are *Annonaspermum* seeds, large monocot leaves and stems with zingiberalean affinities, a forest grass, *Dioscorea*, *Ziziphus*, leaves with possible apocynaceous affinities, palm wood and leaves with possible flowers and fruits, and several legume leaf and fruit morphotypes. Some of the localities most likely represent a mesic tropical forest environment preserved in overbank deposits. The majority of the leaves present possess entire margins and many species have acuminate tips. The presence of palms is of interest because they are not diverse in Africa today compared to the Neotropics and Southeast Asia. The frequent presence of palms at Chilga may help to explain these differences by documenting diversity and relationships in continental Africa during the early Tertiary.

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Paleocene fruits with affinities to Actinidiaceae from the Almont and Beicegel Creek floras of North Dakota

Pedicellate capsules bearing seeds with a distinctive papillate epidermal pattern are described from the Late Paleocene Almont and Beicegel Creek floras of central and western North Dakota. Fruits are spherical to ovoid capsules, up to 10 mm long and 6 mm across with a slightly obtuse to rounded base and a pointed apex. They are borne on narrow pedicels up to 8 mm long within a cymose branching infructescence. Fruits are radially symmetric and five-loculate with around 2 seeds per locule. Seeds are elliptical, about 3 mm long and 1.5-2.0 mm wide. Each is borne on a prominent funiculus and has distinctive papillate epidermal cells. These fossil fruits are similar to members of the family Actinidiaceae, including *Actinidia* ("kiwifruit") and *Saurauia*. The North Dakota specimens document the occurrence of actinidiaceous fruits in western North American Paleocene, and provide new information about fruit anatomical structure for a group currently known in the Tertiary primarily from seeds. The fossil record of Actinidiaceae is of particular interest when placed in a biogeographical context. The family consists of *Actinidia* (Asia), *Clematoclethra* (monotypic, China) and *Saurauia* (Central and South America). The Almont/Beicegel Creek occurrences provide a valuable record useful to understanding the origin of the disjunct distribution of the family.

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Anatomically preserved vascular and nonvascular cryptogams from the Lower Cretaceous of western North America

Calcareous marine nodules from lower Cretaceous (Barremian) sediments of Apple Bay on Vancouver Island, British Columbia, Canada contain a rich terrestrial biota with exceptional preservation of small and delicate structures. Included are seed plant remains assignable to probable gnetophytes, pinaceous and cypressaceous conifers, and cycadophytes, as well as numerous vascular and nonvascular cryptogams. There is a basidiomycete porate hymenophore (polypore), at least one moss, homosporous and heterosporous lycophytes, and numerous types of filicalean ferns. The latter include exarch solenostelic rhizomes with C-shaped stipe traces, mesarch soleno/dictyostelic rhizomes with C-shaped stipe traces, osmundaceous sporangia, indusiate tree fern sori of both the dicksoniaceous grade and the cyatheaceous clade. Preliminary investigations of these fossils reveal the presence of several filicalean families including Osmundaceae, Dennstaedtiaceae, Cyatheaceae s.l. (including Dicksoniaceae), and probable Schizaeaceae or possible Loxsomaceae. This remarkable locality provides an unusually complete picture of a mid-latitude North American flora prior to the radiation of flowering plants.

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A new fossil seedling from the Early Cretaceous of South America; unique, well-preserved and closely related to *Welwitschia*

The fossil history of most extant seed plant groups is relatively well documented. Cycads, conifers and *Ginkgo* have long been known from the Mesozoic, and the understanding of early angiosperm diversity is on the increase. Gnetales are an exception. Few macrofossils have been described and character evolution within the group is poorly understood. Recently, new fossils with gnetalean affinities have been found in several localities in Brazil, China and Portugal and the knowledge of historic diversity within the Gnetales will probably expand rapidly in the nearest future. The Crato Formation of the Araripe Basin, North-eastern Brazil consists of limestone of Aptian-Albian age. The flora is diverse and includes impressions-compressions of nearly complete plants. Original tissue is sometimes preserved and several plants contain detailed information on vegetative and reproductive structures, and in situ pollen grains. Among the Crato fossils is a well-preserved seedling consisting of two cotyledons, a feeder and a root. Small areas with organic preservation show paracytic stomata, longitudinally arranged in a scattered pattern. The cotyledons have a very specific venation pattern with parallel primary veins and secondary veins fusing to form inverted "Y's between the main veins — a pattern that it uniquely shares with *Welwitschia*. Based on the "Y"-venation and the presence of a feeder, we assign this seedling to the *Gnetum-Welwitschia* clade. The plant is spectacular in several respects. Fossil seedlings are unusual and this is the first evidence of a South American plant with welwitschioid characters. Further, the fossil supports the previously suggested hypothesis that paracytic stomata is a shared derived character within the Gnetales, and it indicates that the split between *Gnetum* and *Welwitschia* had occurred in the Early Cretaceous.

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Anatomically preserved tree fern sori from the lower Cretaceous of Vancouver Island

Permineralized sori of both cyatheaceous and dicksoniaceous tree ferns occur among remains of conifers, fungi and other plants in newly discovered calcareous concretions from Lower Cretaceous (Barremian) marine sediments of Vancouver Island, British Columbia, Canada. Cyatheaceous sori are superficially attached in two rows to narrow pinnules and display a globose sphaeropteroid indusium. Annulate sporangia with multicellular stalks diverge from a basal, vascularized receptacle. The nearly vertical uniseriate annulus is not interrupted by the stalk, and the sporangia bear 64 trilete spores, 40 - 70 µm diameter with concave interradial sides and irregular granulate/echinate sculpturing of the perispore. A second type of tree fern sorus from this locality is marginal and bilateral. These sori are surrounded by two inrolled laminae, one of which represents the pinnule surface, and the other the indusium. Multicellular sporangial stalks diverge from a somewhat raised receptacle that is elongated parallel to the pinnule surface. The uniseriate annulus extends past the stalk

and is slightly oblique. There are typically 64 spores per sporangium. Spores are radial and trilete, approximately 40 - 60 µm in diameter with slightly convex interradial sides and a relatively smooth surface. These two types of fructifications are the first anatomically preserved tree fern sori from the fossil record. This material includes the most ancient evidence for fertile structures of the Cyatheaceae and demonstrates that essentially modern species of cyatheaceous tree ferns had evolved by the Early Cretaceous.

235 STEVANOVIC-WALLS, IVANA M.*¹, PFEFFERKORN, HERMANN W.¹ and ALLEMAN, VERA²

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Late Early Carboniferous lycopsids of a warm temperate climate in Gondwana (Peru)

Five lycopsids species are present in the Late Viséan rocks from Paracas on the southern coast of Peru. Four of these are trees and one a small herb. The most prominent one, *Tomiodendron peruvianum*, can be reconstructed as a whole plant while for the others only stems have been found. Several sites with standing *Tomiodendron* stumps have been observed allowing a reconstruction of monospecific forests. *Tomiodendron* is characterized by well developed leaf cushions but has no leaf scars indicating that it did not shed its leaves. It is a ligulate lycopsids that also exhibits an infrrafoliar bladder. *Tomiodendron* has a cormose base, rare dichotomies, and terminal cones. There is another tree lycopsid that is ligulate and highly variable in the presence or absence of leaf cushions. The other two are apparently undescribed forms quite distinct from established genera. The herbaceous lycopsid is fragmentary but appears to be similar to a genus known from Argentina. All these forms are different from those occurring in tropical areas of the same time interval (Amerosinian floral realm) but show some similarity with the Angaran realm in the occurrence of the genus *Tomiodendron*. This Late Viséan flora represents a warm interval in Earth climate just before the onset of the Late Carboniferous cold period (ice age s. l.). Therefore, these floras are distinctly different from older Mississippian and the younger Pennsylvanian floras in Gondwana.

236 STEVANOVIC-WALLS, IVANA M.*¹, GASTALDO, ROBERT A.² and WARE, WILLIAM N.³

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Vegetational Heterogeneity in the Blue Creek mire of Early Pennsylvanian (Langsettian) age, NW Alabama

The stratigraphy of the Black Warrior basin consists of alternating marine and terrestrial cycles that are controlled by fourth-order eustatic oscillations. The Mary Lee Coal zone, the most productive in the basin, was mined extensively both in the surface and subsurface. In both of these mining operations, coal geologists noted the presence of standing trees above all of the coal seams. One of these coal seams, the Blue Creek preserves an extensive standing forest consisting of erect canopy and understory taxa along with the ultimate forest floor litter. The forest composition was studied using seventeen 10-meter square quadrats over approximately 0.5 square kilometers in 2000 as mining operations continued in the Cedrum Brothers mine, Walker County. Forty-six form taxa have been identified in the forest litter which is composed of lycopsids (club mosses), sphagnumids (horsetails), pteridophytes (ferns), and pteridosperms (gym-

nospermous "seed ferns"), all preserved within the 10-15cm of the peat-clastic interface (a roof shale flora). The burial of the roof shale flora occurred in less than one year while the burial of erect trees has been estimated to be on the order of a decade or more. These conditions provided a unique opportunity for the examination of biomass contribution to the forest. Fossil plant material was recorded as present/absent taxa, which was the base for the raw data set. The form taxa representing reproductive and photosynthetic part of the lycopsids and calamitelean were grouped proportionally with parental stem taxa, whereas the stem material of pteridophytes and pteridosperms taxa was distributed proportionately with the leaf taxa. This resulted in the derivation of a biological data set. Data analyzed using ANOVA and Nonmetric Multidimensional Scaling reveal a forest mosaic in which a series of complex relationships between canopy, understory, and groundcover/liana taxa have been identified.

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Cretaceous tree fern radiations: new permineralized Dicksoniaceae

A distinctive new permineralized stem from marine deposits of west North America provides additional evidence for the diversity of Upper Cretaceous tree ferns. The stem occurs in a calcareous concretion from the Late Campanian Spray Formation at Shelter Point, Vancouver Island, British Columbia, Canada. It measures 20 cm long and 7 cm in maximum diameter, with adventitious roots diverging between persistent, helically arranged fronds. Frond traces are derived from an amphiphloic dictyostele, and no medullary or cortical bundles are produced. The pith has a sclerenchymatous center, and parenchymatous outer zone. Sclerenchyma sheaths accompany both caulin and foliar vasculature. Frond traces diverge as six to ten bundles, most often eight. At the stem periphery the cortex produces a homogeneous sclerenchymatous hypodermis, and is clothed by a dense ramentum of both uniseriate and large multiseriate trichomes. This novel combination of characters reveals that the specimen represents a new genus and species of tree ferns. Cladistic analysis of stem characters infers that this species conforms to the dicksoniaceous grade of Cyatheaceae s.l.. Together with other newly discovered Cretaceous tree fern material from western North America, this stem further clarifies our understanding of evolutionary diversification among Mesozoic Cyatheaceae s.l.

238 TOMESCU, ALEXANDRU MIHAIL FLORIAN* and ROTHWELL, GAR W.

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The Early Silurian Massanutten Sandstone of Virginia: an updated perspective on early terrestrial biotas

A abundant fossils in the Llandoveryan (Early Silurian) Massanutten Sandstone at Passage Creek (Virginia) provide evidence for the morphology and internal construction of the oldest terrestrial organisms. Sedimentology supports interpretation of the fossil-bearing sequence as deposits of a sheet-braided river. Within these, the fine-grained fossiliferous layers correspond to vertical accretion in the floodplain. Preserved as carbonaceous compressions, these earliest terrestrial macrofossils predate the oldest embryophyte mesofossils (*Cooksonia*, late Wenlockian) by 10 million years. Fossils exhibit principally thalloid morphologies sometimes over 4cm across, but strap-

shaped forms up to 8 cm long are also present. Some represent discrete individuals, more-or-less evenly distributed, while others form continuous organic crusts. Light and electron microscopy reveal several types of internal organization: networks of filaments, three-layered or massive structures, the latter sometimes corresponding to filaments embedded in a matrix. While the systematic affinities of the fossils are presently unclear, employing a methodology we recently developed, we can relate anatomical and ultrastructural characters to individual fossils. This will allow us to bring together morphology and anatomy in organismal reconstructions and to understand the systematic affinities of the fossils. Morphological and structural diversity of the fossils suggest a complex biota dominated by a guild of thalloid organisms/associations of organisms similar to present-day microbiotic crusts. Rather than representing an isolated case in the fossil record, thalloid forms very likely made up the bulk of the biomass in the earliest terrestrial communities. Such forms, assigned to the enigmatic nematophyte genus *Nematothallus*, were the earliest fossils previously known from terrestrial deposits (Wenlockian/Ludlovian, Bloomsburg Formation). Recently, based on morphological similarities, Graham et al. suggested that nematophyte material might represent dispersed remains of liverwort-grade plants. Generally overlooked, thalloid fossils are present in the fossil record as late as the Upper Silurian (Pridolian) where they constitute part of the classical *Cooksonia* assemblages.

239 UPCHURCH, G.R.^{*1}, MACK, G.H.² and WHEELER,
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Late Cretaceous Fossil Forests From South-Central New Mexico

L ate Cretaceous vegetation of the mid-latitudes is commonly reconstructed as evergreen forest/woodland with an open canopy. Evidence comes largely from the physiognomy of leaf megafossils, which indicate subhumid conditions and the absence of deep shade. *In situ* fossil trees from Late Cretaceous strata of south-central New Mexico reinforce leaf megafossil evidence for open-canopy vegetation and provide important information on tree size and spacing. The stumps are preserved in the Bt horizon of well-developed paleosols that are most comparable to modern Alfisols. The older site comes from the Ash Canyon Member of the Crevasse Canyon Formation (Campanian) and consists of six stumps belonging to *Metcalfeoxylon* (Malvales). The trunks measure 0.3–0.8 m in diameter above the buttresses and form two distinct clusters separated by a distance of over 30 m. The younger site comes from the Jose Creek Member of the McRae Formation (Maastrichtian) and consists of eight stumps that form two distinct clusters separated by a distance of over 40 m. The McRae stumps measure 0.1–0.5 m in diameter and consist of at least one species of conifer and at least one species of angiosperm. Estimates of crown diameter using proposed allometric relationships with stem diameter indicate that both assemblages represent vegetation where trees in a cluster may have had overlapping canopies but the areas between clusters had an open canopy. Estimates of tree height using proposed allometric relationships with stem diameter indicate that average tree height at each site was probably 10 m or greater. The pattern seen in the New Mexico sites is similar to that seen in an *in situ* fossil forest site from the Agua Formation (Campanian) of Big Bend, Texas, where two types of medium to large angiosperms (*Metcalfeoxylon* and *Agujoxylon*) formed the dominant element in vegetation with distinct tree islands.

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100 Million-Year-Old Cytoplasmic Membranes

C ytoplasmic membranes are of vital importance for cells, because they are the interface between cellular internal environment and surrounding world. Structurally preserved cytoplasmic membranes have never been reported from the fossil record. This study examines organically and structurally well-preserved cytoplasmic membranes in a shoot tip. The fossil cytoplasmic membranes shrank into angular globose form but maintained connections to plasmodesmata in cell walls. The fossil cytoplasmic membranes have a double layered structure and is compatible with the fluid mosaic model advocated by neobiologists. The absence of most cytoplasmic contents implies that the cellular content were more vulnerable to degradation than cytoplasmic membranes. This charcoalified fossil implies the involvement of fire for the fossilization. This excellent preservation implies that further search for organelles or macromolecules in fossil plants may be promising. This fossil has not only significance to paleobotany but also implications to fire ecology, taphonomy, even cell biology and physiology.

CONTRIBUTED POSTERS

241 JOHNSON, TIMOTHY* and TAYLOR, WILSON
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Ultrastructure of the patinate miospore *Cymbosporites echinatus* from the Lower Devonian of Herefordshire, England

S pores and tetrads identified as *Cymbosporites echinatus* were extracted from Lower Devonian sediments from the Woodbury Quarry, Herefordshire, England. The spores are patinate (possessing a much thicker distal than proximal wall) but their plant affinities are not known. No *in situ* patinate spores have been reported. As the term suggests, patinate spores are presumed to have a thicker distal wall due to the addition of an outer layer (a "patina") to an inner. Ultrastructural studies support this interpretation, with the structure of the thin inner layer being homogeneous to faintly lamellate, and the "patina" consisting of homogeneous and spongy regions. The patina covers the entire distal surface and the outer edge of the contact face. This pattern of deposition is reminiscent of that seen in older cryptospore dyads. Suture morphology is unusual and variable. Serial sectioning and single grain SEM/TEM preparatory techniques help unravel the complexities of suture morphology, but have yet to shed much light on the affinities of the parent plants.

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Conifer cones from the Late Cretaceous Tar Heel Formation of the Atlantic Coastal Plain of North Carolina, USA

A bundant conifer cones were recovered from the Late Cretaceous Tar Heel Formation at the Willis Creek locality in North Carolina, USA (34°51.527' N, 78°51.038' W). Cones are preserved as coalified compressions macerated from thin clay lenses interbedded in

sands. Cones are approximately 6-8 m in diameter, borne on slender (1 mm) axes, and bear helically-arranged cone scales. Scales have an acute apex, are up to 4 mm long and 3 mm wide, and bear a single seed. Bracts are not outwardly visible. Seeds are preserved as seed cuticles similar to Spermatites but appear to have multiple cuticular layers. The cones show their closest similarities to Himerellaceae, and vegetative remains of Himerellaceae are well known to occur in Tar Heel Fm. sediments.

PHYSIOLOGICAL SECTION

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Carbonic anhydrase in Charophyceae and Bryophytes

Modern algae and plants that occupy aquatic habitats encounter selection pressure in the form of dissolved CO₂ levels that are often limiting to photosynthesis. Aquatic photoautotrophs have adaptations that cope with that selection pressure in a variety of ways. These include increasing Rubisco's affinity for CO₂, acquiring the ability to use other forms of inorganic carbon, moving to land where CO₂ diffusion is faster than in water, or development of other ways to accumulate inorganic carbon (for example, expression of the enzyme carbonic anhydrase (CA) which catalyzes turnover of bicarbonate into CO₂). At least three different CA types have been reported to occur in animals, plants, and bacteria. We have immunolocalized the alpha-type CA in the periplasmic space, inner cell wall, and peripheral cytoplasm of the charophytean *Mougeotia*, and the beta type CA in the stromal space of plastids but not charosomes of Chara. This is the first evidence of beta type CA in green algal plastids. We hypothesize that other members of the charophycean line such as *Coleochaete* and *Chlorokybus* may also have beta CA in their plastids. A search for CA in hornworts with pyrenoids (*Notothylas*) and without pyrenoids (*Megaceros*) and the moss *Sphagnum*, is an approach for testing the hypothesis that the evolutionary loss of pyrenoids may be coupled with increased expression of beta-type stromal CA.

244 GRAVATT, DENNIS A.

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Crassulacean acid metabolism and survival of asexual propagules in the Texas desert rock outcrop succulent, *Sedum wrightii* (Crassulaceae)

In a desert rock outcrop, features of the environment limit reproduction and growth of plant species. *Sedum wrightii* is a succulent plant species adapted to survive in the hot, dry environment of a desert rock outcrop. However, sexual reproductive success may be limited to certain years when favorable conditions for seed germination exist. The formation of vegetative propagules, derived from existing detached leaves, may be a more efficient and successful way of reproduction given the hostile environment in which this plant species

is found. The purpose of this study was to gain an understanding of how, and to what extent, greenhouse grown *S. wrightii* reproduces using vegetative propagules. Greenhouse grown plants were the source of detached leaves used to measure vegetative propagule survival. After 120 days following detachment, leaf survival was 80%, with 98% of those leaves developing propagules. By day 120 of the experiment, detached leaves maintained malate accumulations, 36% of those on day 0, indicating that the detached leaves remained physiologically active during the study. Further discussion of the "parent" leaf, as a source of water and carbohydrate reserves, is presented.

245 THORHAUG, ANITRA*, BERLYN, GRAEME and RICHARDSON, ANDREW
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Spectral Reflectance Measurements of Low Salinity on Three Seagrasses: *Syringodium filiforme*, *Halodule wrightii*, and *Zostera marina*

The spectral reflectance of three species of seagrass was measured versus decreasing salinity (within normal storm-induced modification limits of an estuary) 32 to 16 ppt. The results of the comparison showed that *Halodule wrightii* and *Syringodium filiforme* were sensitive to changes from 32 to 16 ppt. The PRI (photochemical reflectance index) and the D750 were statistically significant (at the P less than or equal to 0.01 level) for these 2 species but were not significant for the third test species *Zostera marina* at this level. Thus, *Zostera* spectral properties were not sensitive to changes to 16 ppt sustained over 24hr. Comparing our previous ,similar low salinity incubations of *Thalassia testudinum* seedlings also measured by spectral reflectance (carried out in the same manner) to these above results, *Thalassia* was also sensitive to decreases to 16 ppt. In *Thalassia* this was measured by several spectral reflectance indices, including PRI, D750. The PRI change seen in *Syringodium*, *Halodule* and *Thalassia* suggests a lower photochemical efficiency or reduced photosynthetic potential at lower salinities.

CONTRIBUTED POSTERS

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Light Limitation and Seasonal Carbon Phenology of Mayapple (*Podophyllum peltatum*)

The rhizomatous perennial Mayapple (*Podophyllum peltatum*) commonly occurs in the understory of beech-maple forests of the Eastern United States where cool, bright conditions predominate early in the spring followed by warmer, dimly lit conditions in late spring and summer. This study assessed if, and to what degree, changes in physiology occurred to maximize carbon gain during the seasonal shift from a high light to a low light environment by examining growth, chlorophyll concentration, gas exchange and carbohydrate content in non-flowering Mayapple shoots from emergence (April 19) to senescence (June 19) in 2002. Over this period, light availability decreased from ~800 to ~25 $\mu\text{mol m}^{-2} \text{s}^{-1}$ as canopy leaf area index (LAI) increased from <1 to >4. *Podophyllum peltatum* grew rapidly, and had a plant height of ~30 cm, and a leaf area of ~400 cm^2/shoot by the time LAI was ~2. As LAI increased further Mayapple underwent several significant responses ($p < 0.01$ for all the below) typical

of shade adaptation including reductions in (i) chlorophyll a:b ratio (4.0 to 2.5), (ii) leaf dark respiration rate (~3.2 to 0.5 $\mu\text{mol m}^{-2} \text{s}^{-1}$), (iii) photosynthetic light compensation point (50 to 10 $\mu\text{mol m}^{-2} \text{s}^{-1}$), and (iv) maximum photosynthetic rate (~10 to 5 $\mu\text{mol m}^{-2} \text{s}^{-1}$), suggesting more efficient production as light levels decreased. Despite these adaptive changes for a low light environment, there was a decrease in photosynthetic quantum efficiency (~0.055 to <0.040 $\mu\text{mol CO}_2 \mu\text{mol photons}^{-1}$, $p < 0.01$) as the canopy closed. As LAI increased, the proportion of soluble sugars and starch in foliage or rhizomes was significantly affected by date ($p < 0.01$). The results suggest rapid leaf expansion, derived from stored carbon, results in a period of ~4 weeks of high carbon gain (high photosynthetic rate and large leaf area) before canopy closure occurs, after which carbon partitioning is shifted towards storage in the rhizomes.

247 TARPLEY, LEE* and KEBROM, TESFA MICHAEL H.
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Rice ratoon tiller initiation and early establishment: Responses to exogenous hormone applications

One limitation to good combined yield of the first (main) and second (ratoon) rice (*Oryza sativa* L.) crops of the Southern U.S. is inconsistent yield of the ratoon crop. Under some circumstances, this inconsistency is related to poor ratoon tiller initiation and early growth. In this study, plant growth regulator (hormonal) treatments were used in an effort to promote ratoon tiller initiation and earliness. This would increase consistency in ratoon stand establishment, ratoon yield, and thereby combined yield. The responses to particular hormonal treatments also help direct additional physiological study. In the two years of the study at Beaumont, Texas and Eagle Lake, Texas, small replicated field plots were sprayed with plant growth regulators at roughly three days post-anthesis of the main crop. Gibberellic acid and cytokinin treatments significantly increased ratoon tiller numbers more than 50% at one location. In addition, gibberellic acid and cytokinin were among treatments that promoted early ratoon tiller establishment (e.g., with a ranking equivalent to about one-third more of the tillers being moderately vigorous [greater than 15 mm at two weeks before harvest] rather than small). The main crop gibberellic acid treatment resulted in a significantly increased ratoon crop yield of 11% (about 450 kg per ha [400 lb per acre]), while main crop yield was not affected. The average combined crop yield among the treatments at this location was about 11,750 kg per ha (10,500 lb per acre). A post-flowering main crop treatment with gibberellic acid has the potential to modestly increase the combined rice main and ratoon crop yield in some circumstances, apparently acting through an encouragement of ratoon tiller initiation and establishment. We appreciate the support of this project by the Texas rice farmers through their voluntary contributions to the Texas Rice Research Foundation.

PHYTOCHEMICAL SECTION

CONTRIBUTED PAPERS

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20705-2350

Identification of Erythroxylum Taxon by AFLP DNA Analysis

Erythroxylum coca, indigenous to the Andean region of South America, is grown historically as a source of homeopathic medicine. However, in the last century, cultivation of *E. coca* and several closely-related species for the production of illicit cocaine has become a major global problem. Two subspecies, *E. coca* var. *coca* and *E. coca* var. *ipadu*, are almost indistinguishable phenotypically; a related cocaine-bearing species also has two subspecies *E. novogranatense* var. *novogranatense* and *E. novogranatense* var. *truxillense*) that are phenotypically similar, but morphologically distinguishable. The purpose of this research was to discover unique AFLP DNA patterns ("genetic fingerprinting") that characterize the four taxa and then, if successful, to evaluate this approach for positive identification of the various kinds of coca. Of 11 AFLP primers tested, a combination of five proved optimal in differentiating the four taxa as well as a non-cocaine-bearing species, *E. aerolatum*. This method of DNA fragment separation was more selective, and faster, for coca identification, as compared with analyses based on flavonoid biochemical profiles. Using the 5-primer AFLP approach, 138 known and unknown coca leaf accessions were evaluated. Of these, 38 were collected in 1997-2001 from illicit coca fields in Colombia, and all were genetically differentiated from coca originating in Peru and Bolivia. Based on the DNA profiling as well as flavonoid chemotaxonomy, we believe that the Colombian coca now represents a hybridization of *E. coca* var. *ipadu*.

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Achene Oil Concentration and Fatty Acid Composition of *Helianthus exilis*, An Endemic Serpentine Sunflower of California

Achenes are the primary storage tissue for accumulating oil in plants. The composition of the oil determines its suitability for either an edible or industrial use. The genus *Helianthus* consists of 37 perennial and 14 annual species. It has served as the genetic stock from which the cultivated sunflower has evolved and offers the potential to improve the oil quality of cultivated sunflower. The objective of this study was to determine the oil concentration and fatty acid composition of 25 populations of serpentine sunflower, *Helianthus exilis*, from serpentine areas of central and northern California. The highest oil concentration was observed in a population from northern CA with 324 g/kg. Four major fatty acids were observed, saturated palmitic and stearic acids, monounsaturated oleic acid, and polyunsaturated linoleic acid. Palmitic acid concentrations ranged from 66 to 83 g/kg, while stearic acid concentrations varied from 37 to 69 g/

kg. Linoleic acid concentrations varied from 660 to 761 g/kg and oleic acid concentrations varied from 95 to 165 g/kg. The fatty acid profile of *H. exilis* had a high linoleic concentration (averaging 720 g/kg) for a high temperature environment and southerly latitude. Sufficient variability appears to be present in serpentine sunflower for selection and improvement of the fatty acid composition in the oil of cultivated sunflower.

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The Antimicrobial Properties of *Baptisia leucophaea* Leaf Extracts

The antimicrobial activities of three crude extracts of the *Baptisia leucophaea* leaves were investigated using the disc diffusion method against four bacteria (two gram-positive and two gram-negative). All three extracts (chloroform:methanol, methanol, and ethanol) showed antimicrobial activity against four tested bacteria, *Staphylococcus epidermidis*, *Micrococcus luteus*, *Pseudomonas fluorescens*, and *Escherichia coli*. Bacterial zones of inhibition showed ranges from 8-22 mm in diameter. Chemical properties inhibiting microbial growth were evaluated by utilizing nuclear magnetic resonance, high power liquid chromatography, thin-layer chromatography, and ultraviolet spectra.

CONTRIBUTED POSTERS

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Serine, Threonine, Tyrosine and Histidine having opened functional reactive groups are Sophisticated Receptors

Protein amino acids serine, threonine and tyrosine have functional reactive HO-groups that can be easily oxidized (a hydrogen abstraction reaction) by metabolic free radicals into the living cells. Histidine having two unsaturated double bonds can react with metabolic free radicals (R.) giving a free radical of this amino acid residue (a free radical addition reaction). These groups present sophisticated receptors. All growth regulating substances before its conjugation to these amino acid residues should be activated, i.e. transformed into free radicals by endogenous metabolic free radicals or enzymes in the reaction of hydrogen atom abstraction from descriptors (a fragment of a molecule that has an active hydrogen atom) or by free radical addition reaction of metabolic free radicals to unsaturated function (double or triple bonds) of growth regulating substances. By accidental reactions of free radicals of these amino acid residues with active growth regulating chemicals (i.e. with free radicals of growth regulating chemicals that are very active agents) can be formed so called growth regulator/receptor complexes (putative biologically active structures). Also conjugated structures do not possess in chemical activity (or it is very low) and they present consequences of interactions of growth regulating chemicals with cellular substances, i.e. these events take place independently of physiological effects of growth substances. Thus, activation of growth regulators (hormones, cyclic peptides, pesticides, diverse toxins, etc.) precedes their bio-

logical action. This is the fundamental principle of biology of the living systems. The first consequences of such activation of growth regulators can be disruption of the membrane function (the free radical oxidation of lipids and fatty acids of membranes, proteins, etc.), while the transcription can take place or not. Thus, a theory of receptors is chemical nonsense, and hence, do not invent any virtual receptors, i.e. "Plurality should not be posited without necessity (William Ockham)".

PTERIDOLOGICAL SECTION /AFS

CONTRIBUTED PAPERS

252 BARBARA', THELMA* and GASTONY, GERALD J. Indiana University, Department of Biology, Jordan Hall, 1001 East Third Street, Bloomington, IN 47405-3700

Molecular phylogenetics and systematics of *Pellaea* section *Ormopteris* (Pteridaceae subfamily Chelanthoideae)

Previous molecular phylogenetic work shows that *Pellaea* sensu Tryon, Tryon, and Kramer is polyphyletic, with *Pellaea pinnata* of section *Ormopteris* more closely related to *Doryopteris* than to the other three sections of *Pellaea*: *Pellaea*, *Platyloma*, and *Holcochlaena*. We used maximum parsimony and maximum likelihood approaches to provide a molecular phylogenetic analysis of all available species of *Pellaea* section *Ormopteris* using relatively rapidly evolving expansion segments of the nuclear gene 26S, chloroplast genes *rbcL*, *atpB*, *rps4*, and *trnL*, and AFLPs. Based primarily on specimens from Minas Gerais, Brazil, the DNA sequences of the species of section *Ormopteris* show a very low level of genetic variation among themselves and indicate that these taxa all belong to the same clade. In addition to the molecular data, we present a traditional morphological analysis of the species of section *Ormopteris*, integrating this with the results of the sequencing analysis.

253 BARKER, MICHAEL S.* and HICKEY, R. JAMES Botany Department, Miami University, Oxford, OH 45056

Reiterative lamina morphologies in *Adiantopsis*

Adiantopsis Fée, a Neotropical cheilanthesoid genus, contains a wide range of lamina morphologies including pinnate, pedate, and radiate forms. *Adiantopsis radiata*, the sole species with radiate leaves, occurs throughout tropical America. Pedate lamina morphologies are found in members of the *A. pedata* species complex of the Caribbean and disjunctly in the tri-border region of Argentina, Paraguay, and Brazil. The remaining pinnate taxa are found throughout the range of the genus. We employed a combination of morphological, anatomical, and scanning electron microscopy techniques to identify taxa and elucidate the relationships of those possessing the three lamina types. Our results suggest that the pedate South American taxon is a sterile diploid hybrid derived from *A. radiata* and a member of the pinnate *A. chlorophylla* species complex, possibly *A. perfasciculata*. The pedate Caribbean *Adiantopsis* are hypothesized to be allotetraploid derivatives resulting from hybridizations between *A. radiata* and various other pinnate parents. Thus, it appears that the pedate lamina morphologies of *Adiantopsis* are convergent, having originated multiple times via hybridization. A revision of Caribbean *Adiantopsis* shows the genus to be more speciose than previously thought. Our study provides testable hypotheses of morphological and reticulate evolution in the genus and presents a novel view of Caribbean *Adiantopsis*.

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Microlepidopteran soral mimics in the Caribbean

Microlepidopteran larvae and pupae were discovered on ferns collected during a recent trip to Puerto Rico. The cocoons of these microlepidoptera are covered with harvested sporangia, and the resulting cocoons mimic fern sori. The larvae harvest sporangia by biting through the sporangial stalk base. These harvested sporangia are attached to a thin silk layer covering the outside layer of the cocoon, and thus the sporangia are not integrated structurally into the body of the cocoon. An examination of larval frass suggests that the microlepidoptera are consuming leaf tissue, but not sporangia; the latter appear to be utilized only superficially on the outside layer of the cocoon. These microlepidopteran soral mimics are restricted to ferns that are either exindusiate or have evanescent indusia and highly visible sporangia. On these ferns, the microlepidoptera construct their "soral cocoons" such that they are of a similar shape, size, and orientation as the sori on the leaf they are utilizing. These "soral cocoons" represent an adaptive strategy for evading parasitic wasps. Only a single cocoon contained a parasitoid wasp. A second cocoon was open and contained the partial, chewed remains of a microlepidopteran pupa. The microlepidoptera are avoiding wasp parasitism by mimicking sori during their immobile pupal stage. Microlepidopteran soral mimics appear to be restricted to the Caribbean, based upon herbarium specimen searches at MU and MO. This discovery is significant as it is the first report of insects mimicking a unique leptosporangiate fern structure, the sorus, to putatively avoid wasp parasitism.

255 BUDKE, JESSICA M.*, HICKEY, R. JAMES and HEAFNER, KERRY D.
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Morphological characterization of North America's first octoploid Isoetes

Diagnostic characters for *Isoetes* species have historically focused on megasporophyll ornamentation and chromosome counts. Studies in our laboratory suggest that a variety of other characters can be used in circumscribing species. Toward this end morphological and anatomical analyses were conducted on three populations from the Hiwassee River of the recently discovered octoploid *Isoetes tennesseensis*. In this species some characters exhibited dimorphism between megasporophylls and microsporophylls. These include velum coverage and the shape of the sporangial wall cells. Other characters did not have this dimorphism, but showed high levels of variation within individuals. The labium, which is very pronounced in this species, is such an example. Anatomical characters were also examined; those of interest include size differences among the lacunar canals and a distinctive pattern of hairs on the septal cells of the lacunae. After examining a variety of both morphological and anatomical characters, we are of the opinion that a number of these traditionally ignored characters can be used taxonomically. This study presents a model for the examination of characters that we propose should be standard in circumscribing *Isoetes* species.

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Water balance in the gametophyte of *Cheilanthes lanosa*

C*heilanthes lanosa* is a common xerophytic North American fern that inhabits sandstone bluffs and outcrops. The physiological basis for its survival is unclear. *Cheilanthes lanosa* gametophytes purportedly lack morphological features that prevent desiccation, yet these gametophytes are able to withstand substrate desiccation without adverse effects. Previous research demonstrated that the protonemal stage is inhibited in high water concentrations. Therefore, we hypothesized that *C. lanosa* gametophytes possess and regulate the function of aquaporins, channel proteins which facilitate the intake of water along a diffusion gradient. *Cheilanthes lanosa* gametophytes were grown on dry sand or in agar culture and then exposed to 50 mM increments of CaCl₂, NaCl and sucrose every 5 min until 500 mM of the particular solute was reached. Immediate immersion exposures to CaCl₂, NaCl and sucrose, in which gametophytes began in 100 mM solution and were immediately brought to 500 mM solution, were also conducted and the permeability coefficients in each treatment were compared. Results of permeability calculations showed a difference in the permeability coefficients between protonemal cells that experienced immediate immersion in high solute concentrations and those that experienced graded solute concentrations. In addition, permeability coefficients were higher for agar-grown gametophytes and negligible for sand-grown gametophytes. Sand-grown gametophytes also produced wax glands on trichomes, which are features not previously described in this species. These data suggest the presence and control of aquaporins and/or variations in cell wall thickness and composition. Additional *C. lanosa* gametophytes were incubated in the aquaporin inhibitor, HgCl₂, and then exposed to treatments of CaCl₂, NaCl and sucrose. Water flow was greatly impeded as compared with distilled H₂O controls, suggesting that aquaporins and a strong internal gradient, in addition to environmentally plastic morphological features, may be responsible for *C. lanosa*'s ability to balance water in arid environments.

257 HEAFNER, KERRY D.*, HICKEY, R. JAMES and WATSON, LINDA E.
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Taxonomic and Systematic Studies of the *Isoetes melanopoda* Gay & Durieu Assemblage in Eastern North America

I*soetes melanopoda* is a binomial that was first applied to quillworts collected in central Illinois from agricultural fields in the late 1800s, and characterized by the formation and retention of blackened leaf bases (phyllodia) toward the end of their phenological cycle. Subsequent to Durieu's 1864 description of *I. melanopoda*, other populations inhabiting a variety of generally acidic habitats and ranging throughout most of the eastern third of the U.S. have been subsumed under *I. melanopoda*. These habitats include upland depression swamp forests and intermittent low woodland streams in the southeastern U.S. Piedmont region, low wet edges of agricultural fields, water-filled depressions and wet edges of rock outcrops, and other seasonally wet areas. We have analyzed data sets derived from cytological, morphological, anatomical, and allozyme studies to delineate and characterize cryptic species in *I. melanopoda*, and performed phylogenetic analyses using both nuclear and plastid-encoded DNA

sequences in an attempt to arrive at a phylogenetic hypothesis regarding this group. The diploid ($2n=22$) *I. melanopoda* exhibits distinct genetic differences between those populations east of the Appalachian Mountains and those west of the Appalachians, especially at TPI-2. Morphological analyses substantiate this pattern, and we propose that *I. melanopoda* actually consists of at least two species: an eastern, woodland diploid and a western diploid of various habitats. A similar genetic pattern is observed for entities subsumed under *I. piedmontana*. This taxon may consist of as many as four distinct entities. Phylogenetic analyses weakly support this geographic pattern and further suggest that these species are relatively recently derived.

258 HICKEY, R. JAMES* and BUDKE, JESSICA M.
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The sella and its derivatives in Isoetes

The sporangium and ligule of *Isoetes* develop from distinct but separate superficial initials. At first, the ligule and sporangium grow faster than the supporting leaf tissue and as a result both structures appear as adaxial appendages. After this initial growth period the lamina growth rate surpasses that of both the ligule and sporangium. Peripheral leaf tissue enlarges and surrounds the glossopodium, or ligule base. As a result the ligule appears to be growing out of a pit, the foveola, in the leaf. The sporangium becomes enveloped by the peripheral leaf tissue in a similar manner, but the development of this tissue is most dramatically expressed along the distal edge of the sporangium where it often extends proximally to cover part or all of the sporangium. This tissue is the velum and the apparent leaf cavity in which the sporangium is located the fovea. Between the fovea and foveola a bridge of laminar tissue, the sella, extends laterally separating the ligule and sporangium. In radial longitudinal sections the sella appears to give rise to the velum as a basally projecting flap of tissue and to the labium, an apically projecting tissue. The labium is strongly expressed in tropical species of *Isoetes*, but is generally rare in temperate taxa. *Isoetes tennesseensis* is distinctive among North American species in possessing a pronounced labium and appears to be unique in having the labium develop on the surface of a downward growing sella. In this species the velum is a complex structure composed of sella and velum proper. Variation in the sella, labium and velum of several New World species are compared and discussed.

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Phylogeny of Selaginellaceae based on molecular and morphological data

The phylogeny of the heterosporous lycopod family Selaginellaceae was investigated using molecular (plastid gene *rbcL* and nuclear region 26S rDNA) and morphological data. Analyses were performed using both parsimony and Bayesian inference. An SEM survey of megaspore surface and wall structures was carried out for living species, and these data were evaluated in a phylogenetic context. The phylogenetic analyses identify many new clades, few of which correspond to groupings recognised in previous classifications. A basal dichotomy in the family splits a clade of two species *Selaginella*

selaginoides and *S. deflexa*) from a clade comprising all others (rhizophoric clade). The rhizophoric clade has two distinct morphological markers: (1) the presence of rhizophores, which are highly characteristic root-like organs, and (2) decussately arranged sporophylls. Within the rhizophoric clade a basal dichotomy is most often found, resulting in two more or less equally sized sister groups. Some of the new groups seem to have corresponding morphological synapomorphies, such as aspects of rhizophore development and megaspore characteristics. For many groups, however, no morphological markers are known. Lycopods have a lengthy fossil record and fossils with Selaginellalean affinity are found from the Lower Carboniferous onwards. The inclusion of fossil megaspores in the analyses allowed for tentative ages to be assigned to certain clades.

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The relationship between the sperm cell architecture and the female sex organ of two leptosporangiate ferns

This study was undertaken to understand more fully sperm architecture as it relates to movement within the female sex organ (archegonium). The dimensions of the archegonial neck canal were correlated with male gamete shape and size for two representatives of leptosporangiate ferns: *Lygodium japonicum*, a basal fern and *Ceratopteris richardii*, an advanced fern. Mature swimming male gametes and the neck canals of the archegonium were examined in the light microscope and scanning electron microscope. These images were correlated with transmission electron microscope observations. Each sperm cell type is highly streamlined and coils approximately 3 revolutions in *Lygodium* and 4.5 in *Ceratopteris*. The neck cells arch away from the growing notch meristem as the structures mature. In the presence of water, the male and female sex organs open. As sperm cells are released the archegonia will open exuding viscous mucilage that contains a chemical attractant. The neck canals of *Lygodium* and *Ceratopteris* are approximately the same diameter as the coils of the sperm cells. As the sperm swim into the mucilage they become greatly elongated. When the sperm cells enter the venter, which houses the egg, they reassume their original coiled architecture. Our investigations indicate that these architectural modifications to fern sperm cells may serve the following functions: 1) to enable sperm cells to swim more quickly down the neck 2) to provide room for more than one cell to enter the receptive female at the same time and 3) to remove any remaining cytoplasm contained within the sperm cells, thus reducing the potential for paternal inheritance of organelles.

261 NAKAZATO, TAKUYA*, GASTONY, GERALD and
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Genetic map-based analysis of paleopolyploidy in homosporous ferns

A genetic linkage map of the homosporous fern *Ceratopteris richardii* is under construction using RFLPs (Restriction Fragment Length Polymorphisms), AFLPs (Amplified Fragment Length Polymorphisms), and isozyme markers. To date, only preliminary maps based on AFLPs and isozymes are completed. We detected 42 linkage groups that partly correspond to the 39 chromosomes in this species. Markers with significant segregation ratio distortion tended to cluster on some

linkage groups or their segments, which may indicate the presence of factors causing inviability of gametes and zygotes due purely to genetic causes (e.g., Bateson, Dobzhansky, and Muller incompatibility and chromosomal rearrangements). The maps presented will be greatly improved with ongoing RFLP marker information, and these ultimate maps can be used to test the controversial hypothesis of a polyploid ancestry of homosporous ferns. Furthermore, the ultimate maps can provide evidence for the model of hybrid breakdown via DDC (duplication, degeneration, and complementation), which is caused by divergent resolution of common duplicated genes in sister taxa.

262 RANKER, TOM A.* and GEIGER, JENNIFER M. O.
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Molecular evidence for the phylogenetic placement of Asiatic *Hemionitis arifolia* (*Pteridaceae*) *Hemionitis* L. minimally comprises a Neotropical, monophyletic group of four diploid species (*H. palmata*, *H. levyi*, *H. rufa*, and *H. tomentosa*) and one allopolyploid (*H. pinnatifida*). Numerous synapomorphies support this group, including morphological, chemical, and molecular characters. *Hemionitis arifolia* (N. L. Burm) T. Moore is broadly distributed across southern Asia, into Malaysia and the Philippines. Aside from its striking geographical disjunction from other members of the genus, *H. arifolia* has several distinctive morphological features, including basal laminar leaf buds, cordate to hastate laminae, and unusual hairs with "ball-and-socket" joints. The distinctive morphology of *H. arifolia* led one author to describe it as the sole member of a new genus, *Parahemionitis* Panigrahi. However, the phylogenetic placement of this species with respect to *Hemionitis* s.s. and other genera of *Pteridaceae* has remained unresolved. We provide evidence from phylogenetic analysis of *rbcL* sequences that *H. arifolia* is, in fact, sister to the Neotropical *Hemionitis* s.s. clade. We recommend that this distinctive, widespread species be treated in the genus *Hemionitis*.

263 RANKER, TOM A.* and GEIGER, JENNIFER M. O.
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Phylofloristics of the Hawaiian fern flora: preliminary studies on the origins of Hawaiian ferns and testing climate-based models of dispersal

The Hawaiian Islands have always been well separated from continents and from other archipelagoes because of the mid-oceanic location of the tectonic hotspot from which they arose. Thus, all species migrating to the Hawaiian Islands must have arrived via long-distance dispersal either through the air or through or on the water. Ferns undoubtedly reached Hawaii via the wind-blown dispersal of spores. The ultimate goal of our research is to investigate the biogeographical and evolutionary origins of the majority of the pteridophyte flora of the Hawaiian Islands. Thus, we are taking a phylogenetic approach to the origin of the Hawaiian pteridophyte flora, hence the term, "phylofloristics". We are conducting molecular phylogenetic studies of multiple groups (in collaboration with multiple colleagues), beginning with groups that we believe to be the most tractable. Comparative molecular phylogenetic and biogeographical analyses of the groups studied are allowing us to test climate-based hypotheses of wind dispersal of spores to the Hawaiian Islands. Such comparisons will allow us to assess if long-distance wind dispersal to the archipelago has been essentially random across groups or if there are common patterns across groups due to the influence of shared historical processes. We will present analyses of Aspleniaceae, *Dryopteris* (*Dryopteridaceae*), and Grammitidaceae.

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Fern vegetative body is entirely developed from shoot apical meristem

It is impossible to over-emphasize the role of the shoot apical meristem (SAM) for understanding both morphogenesis and the evolutionary origin of plant form in any taxa but for six fern species *Pteridium aquilinum* L. Kuhn., *Phegopteris connectilis* (Michx.) Watt, *Gymnocarpium dryopteris* (L.) Newm., *Athyrium filix-femina* (L.) Roth, *Dryopteris carthusiana* (Vill.) H.P. Fuchs and *Matteuccia struthiopteris* (L.) Tod. SAM was shown to be directly involved in production of all sporophyte organs (leaves, roots, branches). As oppose to Angiosperms leaf initiation in fern SAM is indicated not by subsurface layers cells proliferation but by single leaf apical cell (LAC) emerging among the surface initials due to division delay and consequential enlargement. Simultaneously the root apical cell (RAC) emerges in the SAM cup-zone peripheral part on the same orthostichy. This pattern is established at the early stages of sporophyte ontogeny: the first root AC is initiated in SAM simultaneously with first leaf AC. Thus even the first stages of fern sporophyte ontogeny differ from that in angiosperms: while in angiosperm embryo ontogeny two growth poles – shoot and root apices are initiated, single fern SAM originates both first leaf and first root of the unipolar sporophyte. Dichotomous branching in *Pt. aquilinum*, *Ph. connectilis*, *G. dryopteris* and *A. filix-femina* is preceded by phyllotaxy change, which reflects apex volume increase and is followed by SAM structure disturbance: proliferation of AC and neighbouring surface and subsurface cells leads to SAM parenchimatisation and consecutive development in small median mound. New apical cells simultaneously emerge from prismatic initials on SAM flanks, thus two new SAMs of branches are originated. Adventitious buds in *Dryopteris carthusiana* and *Matteuccia struthiopteris* originate endogenously at the lower border of leaf gap at the place of RAC initiation.

265 SHAW, SHANE* and HICKEY, R. JAMES
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Comparative Morphology: Three Dimensional Rendering of the Glossopodiums of North American Isoetes Ligules One of the most distinctive features of the heterosporous lycopods is the presence of a ligule. This enigmatic structure is found only in the extant genera *Isoetes* and *Selaginella*. It is composed of a basal embedded glossopodium and a free distal region of cushion and margin. Our investigation of the morphology of this little-studied organ, emphasized the glossopodium. Previous studies have demonstrated small variations in glossopodium shape in Indian species, leading to the possibility that this structure could be taxonomically useful. We examined serial transverse cross, tangential longitudinal, and radial longitudinal sections of glossopodia from three different North American species, representing different ploidy levels: eastern, woodland *I. melanopoda* (2n), *I. virginica* (4n), and *I. tennesseensis* (8n). 3-D digital rendering of this complex organ provided comparative data for the three North American species and allowed comparisons with previous published descriptions.

266 TAYLOR W. CARL^{*}, LEKSCHAS, ANGEL R.¹,
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Phylogeny of Chinese Isoetes Species as Indicated by Chromosome Numbers and Nucleotide Sequences of the Nuclear Ribosomal ITS Region and Second Intron of a LEAFY Homolog

Four species of *Isoetes* are known from China. All are rare and endangered. *Isoetes hypsophila* ($2n=22$) is unique to high elevation lakes in the Hengduan Mountains of northwestern Yunnan Province and southwestern Sichuan Province. *Isoetes taiwanensis* ($2n=22$) occurs in Dream Lake on Seven Star Mountain in northern Taiwan. *Isoetes yunguiensis* ($2n=22$) is known from four small populations in wetlands on the Yunnan-Guizhou Plateau of southwest China. *Isoetes sinensis* ($2n=44$) is recorded from at least ten populations mostly from rivers and lakes of the Qiantangjiang River drainage system in eastern China, but only three populations are known to remain. ITS trees place Chinese *Isoetes* species in an Australasian clade that includes *I. brevicula* from Western Australia and *I. kirkii* from New Zealand. *Isoetes hypsophila* is basal in this clade. A clade consisting of *I. sinensis*, *I. taiwanensis*, and *I. yunguiensis* is sister to a clade containing *I. brevicula* and *I. kirkii*. Based on the ITS data, chromosome counts, and morphology, it was hypothesized that *I. sinensis* is an allotetraploid formed by hybridization and chromosome doubling events involving the basic diploids *I. taiwanensis* and *I. yunguiensis*. This hypothesis was tested using cloned sequences of the second intron of a *LEAFY* homolog from individuals at two of the three *I. sinensis* populations and sequences from individuals at two of the four *I. yunguiensis* populations and the sole *I. taiwanensis* population. Cladistic analysis of the intron sequences shows that the *I. sinensis* clones form a clade with either *I. taiwanensis* or *I. yunguiensis*. The results support the allopolyploid origin hypothesis for *I. sinensis*. Although these two clades are supported with bootstrap values of over 85%, autapomorphies in *I. taiwanensis* and *I. yunguiensis* indicate that these basic diploids may not be conspecific with the progenitors of *I. sinensis*.

267 WHITTIER, DEAN P.
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Induced apogamy in the Psilotaceae

Gametophytes of *Psilotum* and *Tmesipteris* grow in axenic culture on a nutrient medium containing minerals and 0.5% glucose. Gametophytes grown in the dark are cylindrical with antheridia and archegonia. If these gametophytes are grown in light, apogamous aerial stems will form in some of the cultures. The apogamous stems have the expected morphology for the aerial stems of the two genera. The green apogamous stems of *Psilotum* have vascular tissue, stomata, and enations and those of *Tmesipteris* differ only in having microphylls instead of enations. If the apogamous stems of *Psilotum* are moved to the dark, their development will shift to that of rhizomes. *Psilotum* gametophytes will form apogamous rhizomes in the dark if 6-benzylaminopurine is added to the nutrient medium. The apoga-

mous response in light is improved for *Psilotum* if the nutrient medium includes a cytokinin. Only 4% of the gametophyte apices formed apogamous stems on a medium without cytokinin, while 51% of the apices did with cytokinin present. Transferring the young apogamous stems to new cultures allowed the development of mature stems. A few stems formed sporangia under these conditions and the sporangia contained abortive spores.

CONTRIBUTED POSTERS

268 GOLA, EDYTA^{*} and JERNSTEDT, JUDY
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Detachment of *Huperzia* propagules: Letting go and leaving home

Formation of vegetative propagules—gemmae—appears early in the phylogeny of land plants. Since the likely earliest gemmae in liverwort gametophytes, the structure of the propagules as well as the mechanism(s) of their detachment and dispersal have evolved from relatively simple clusters of cells to dormant embryonic sporophyte buds with distinct layered abscission zones. Relatively little is known about the separation of gemmae, or bulbils, in lycophtyes, a basal group of vascular plants. *Huperzia lucidula* (Mich.) Trev. (Lycopodiaceae) produces gemmae seasonally and the precision of detachment suggests the existence of specialized structural and physiological adaptations for gemma separation. To investigate the process of *Huperzia* propagule detachment, immunofluorescence coupled with standard staining procedures was used. The analysis of anatomical sections and immunolocalization patterns of the anti-pectin monoclonal antibodies JIM 5 and JIM 7 revealed an anatomically distinctive region of the *Huperzia* propagule which may be considered to be an unspecialized abscission zone (AZ). It consists of small, thin-walled, mainly isodiametric cells at the periphery of the lens-shaped zone, and internal axially elongated cells surrounding the central vascular bundle. In contrast to neighboring parenchyma, cells in the AZ do not accumulate starch grains. The separation layer is not structurally distinct, but detachment occurs at a relatively consistent location due to the degradation of middle lamellae. This suggests a precise physiological specification of cells at a particular location. The rapid suberization and/or lignification of cells at the surface and sub-surface of the remnant stalk indicates the development of the protective zone. The additional deposition of callose can enhance impermeability of this layer. It is proposed that, in the ancestors of modern lycophtyes, recruitment of processes of middle lamella dissolution that previously were exclusively involved in sporangial dehiscence resulted in the abscission of the propagules.

269 HAUK, WARREN D.*, KENNEDY, LARKIN F. and
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Phylogenetic relationships among species of *Botrychium* s.s. (Ophioglossaceae) based on three plastid DNA sequence data sets

Botrychium s.s., commonly called the moonworts, has a nearly worldwide distribution with a center of diversity in North America. Distinguishing moonwort species can be difficult because of their small size and subtle morphological differences. Thus, there are few useful morphological characters available for constructing classifications and

assessing evolutionary relationships. A plastid DNA (*rbcL* + *trnL-F*) phylogeny of 24 moonwort species revealed three main species clades: lanceolatum (nine species), lunaria (two species), and simplex-campestre (13 species). Using the grapeferns *Sceptridium multifidum* and *S. lunarioides* as outgroups, the lunaria and simplex-campestre clades were sister, with the lanceolatum clade sister to lunaria + simplex-campestre. Within the simplex-campestre clade, four subclades were identified: campestre (four species), pallidum (two species), simplex (four species), and minganense (three species). Low levels of sequence divergence within the simplex-campestre clade limited internal support and resolution of sister group relationships among the subclades. Preliminary alignments of a third plastid DNA data set from the *rpl16* region provide additional support for the *rbcL* + *trnL-F* phylogeny. Sister group relationships among the lunaria, simplex-campestre, and lanceolatum clades as determined by *rbcL* + *trnL-F* analyses were upheld by the *rpl16* data. Autapomorphic substitutions in the *rpl16* sequences for species of the lanceolatum and lunaria clades were consistent with current species delimitations. Within the simplex-campestre clade, *rpl16* data indicated that the pallidum and simplex subclades are sister, while shared substitutions supported progenitor-descendent relationships between *B. campestre* and *B. spathulatum*, and between *B. pallidum* and *B. gallicomontanum*. Two *rpl16* substitutions and a four base pair deletion may be autapomorphies for *B. paradoxum* or, once sequences of *B. minganense* and *B. Xwatertonense* are complete, synapomorphies for the minganense subclade.

270 TOWILL, LESLIE

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Effect of Fungi on Rhizoid and Root Growth of the fern *Ceratopteris richardii*

I observed unusual growth of rhizoids and roots of *Ceratopteris richardii* growing on fungal contaminated Parker-Thompson (PT) plates. Rhizoids grew long in a spiral growth pattern. The rhizoid growth pattern was observed on two plates that were contaminated with different fungi. One plate contained spreading fungal mycelium initially without conidia whereas the fungus in the second plate had few apparent hyphae but very noticeable black reproductive structures. Growth on yeast extract sucrose (YES) plate revealed conidial characteristic of *Pithomyces* on the first plate and colony and conidiophores characteristics suggested *Penicillium polonicum* on the second plate. To confirm the gametophyte observations, spores of *C. richardii* were sown on PT agar medium and then two small agar squares from each contaminated plate transferred to opposite sides of the spore plates. Controls were not contaminated. The *Pithomyces* and the *P. polonicum* contaminated media increased the average growth of the longest rhizoid by approximately 55% and 334%, respectively. Young sporophytes grown on *P. polonicum* contaminated plates showed longer roots compared with roots grown on uncontaminated plates. Measurements revealed an average increase of 80% in total root length and a 53% increase in total leaf area compared to those on the uncontaminated plates. The average longest root was 98 to 131% longer than those from uncontaminated plates. As in the case of rhizoids, root numbers were not affected by the fungi. These results suggest *P. polonicum* and *Pithomyces* stimulate growth in length of the rhizoids and that *P. polonicum* stimulates growth of the roots of *Ceratopteris richardii*. Experiments are underway to determine if these fungi secrete substances into media that cause rhizoid and root elongation. Our goal is to have the nature of the promoting substance tentatively identified for Botany 2003.

271 WOLF, PAUL G.*¹, ROWE, CAROL A.¹, SINCLAIR, ROBERT B.² and HASEBE, MITSUYASU³¹Utah State University, Logan, UT 84322, USA; ²The Jackson Laboratory, 600 Main St., Bar Harbor, Maine 04609, USA; ³National Institute for Basic Biology, 38 Nishigounaka, Myo-daiji-cho, Okazaki 444-8585, Japan

Complete nucleotide sequence of the chloroplast genome from a leptosporangiate fern, *Adiantum capillus-veneris* L.

We determined the complete nucleotide sequence of the chloroplast genome of the leptosporangiate fern, *Adiantum capillus-veneris* L. (Pteridaceae). The circular genome is 150,568 bp, with a large single-copy region (LSC) of 82,282 bp, a small single copy region (SSC) of 21,392 bp and inverted repeats (IR) of 23,447 bp each. We annotated 118 genes, of which 85 encode proteins, 29 encode tRNAs and 4 encode rRNAs. Four protein-coding genes, all four rRNA genes and six tRNA genes occur in the IR. Most (57) putative protein-coding genes appear start with an ATG codon, but we also detected five other possible start codons, some of which suggest tRNA editing. We also found 26 apparent internal stop codons in 18 putative genes, also suggestive of RNA editing. We found all but one of the tRNA genes necessary to encode the complete repertoire required for translation. The missing *trnK* appears to have been disrupted by a large inversion, relative to other published chloroplast genomes. We detected several structural rearrangements that are potentially informative for phylogenetic studies.

SYSTEMATICS SECTION / ASPT

CONTRIBUTED PAPERS

272 ALFORD, MAC H.

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When in doubt, put it in the ... Salicaceae? Systematics of the Flacourtiaceae revisited

A recent study recommended that Flacourtiaceae and Scyphostegiaceae be included Salicaceae based on an analysis of chloroplast *rbcL* sequences. The work presented here will examine the relationships of Flacourtiaceae, Salicaceae, and Scyphostegiaceae via a phylogenetic analysis of morphological, anatomical, chemical, and chloroplast DNA sequence (*tml*, *trnL-F*, *ndhF*) data and denser taxon sampling. My results show that the tribe Samydeae is monophyletic and sister to Scyphostegiaceae, Salicaceae, and the other tribes of Flacourtiaceae. The monotypic Scyphostegiaceae is then sister to Salicaceae and the remaining Flacourtiaceae. Five east Asian genera and one Central American genus of Flacourtiaceae are sister to Salicaceae and share several morphological characters. Within the Flacourtiaceae *sensu stricto*, no multi-generic tribes are monophyletic. Some traditionally important characters, such as absence of petals, are highly homoplasious, but other often-ignored characters correlate well with the phylogeny, such as presence of arillate seeds and presence of staminodes. The distribution of morphological characters suggests an alternative classification to the recently proposed Salicaceae *sensu lato*. The results also provide insights into the evolution of complex characters like placentation, anther architecture, and sexuality.

273 ALFORD, MAC H.
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Systematics of the tribe Prockieae (Flacourtiaceae)

The relationships of genera and species of Prockieae (Flacourtiaceae) were inferred from a phylogenetic analysis of morphological, anatomical, chemical, and chloroplast DNA sequence (*trnL*, *trnL-F*, *ndhF*) data. The tribe is not monophyletic. The Central American genus *Macrohasseltia*, which lacks petals and has a capsular fruit with cottony seed, belongs to a clade sister to Salicaceae. *Pleuranthodendron* and *Hasseltia*, genera with paired glands at the base of a three-veined lamina and with glands in the flower, are sister, but their relationship to the other genera is still unresolved. The other genera (*Banara*, *Hasseltiopsis*, *Neosprucea*, *Pineda*, *Prockia*) plus *Azara* and *Abatia* form a well-supported clade, although the genera *Banara* and *Prockia* may not be monophyletic. Merosity, leaf venation, and presence of staminodes are important morphological characters. Several new species are to be described, and buzz pollination and a symbiotic relationship with ants are recorded for the first time.

274 ALLPHIN, LOREEN^{*1} and WINDHAM, MICHAEL D²
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Patterns associated with rarity and endemism in the genus *Draba* from the Intermountain region of western North America, USA

With a growing number of plant species in danger of extinction due to human induced threats, species-by-species approaches to management are becoming unrealistic. In order to protect these species, we need to determine whether there are patterns associated with rarity and endemism that would facilitate the development of management strategies applicable to a wide range of rare taxa. For this study, we surveyed species in the genus *Draba* from the Intermountain West, the region with the highest concentration of endemics. We collected data on geographic distribution, degree of endemism, chromosome number, ploidy level, breeding system and reproductive success for most of the rare, endemic *Draba* species occurring in Utah, Idaho, and Nevada. The study revealed some interesting evolutionary and biogeographic patterns. For example, endemic *Draba* species from the Wasatch and Rocky Mountain regions were primarily diploid, outcrossing, paleoendemic species with relatively low fecundity. Conversely, endemic *Draba* species from the Great Basin region of western Utah and Nevada were primarily polyploid, autogamous, neoendemics with relatively high fecundity. These patterns appear to reflect both the type of speciation that occurred and the geologic/biogeographic history of the region.

275 APPLEQUIST, WENDY L.
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Field observations and systematics of *Talinella* and *Dendroportulaca* (Portulacaceae)

Two genera of endemic Malagasy Portulacaceae are recognized: *Talinella*, comprising five species of sometimes lianoid shrubs or small trees, and the monotypic *Dendroportulaca*, previously known from only two older collections and thought to be a shrub. Field and herbarium observations of the ecology, habit and morphology of both are provided to supplement the existing revision by Eggli. The segregation of *T. microphylla* from *T. grevei* is called into question, and two collections perhaps representing an undescribed southern species are identified. *Dendroportulaca mirabilis* is a large liana, fairly common in patches of moist forest on quartzite sand in the western portion of the Horombe Plateau. Preliminary *ndhF* sequence data suggested that it was not closely related to the core lineages of Portulacaceae, a paraphyletic family whose descendants include Cactaceae, and might be removed therefrom in future efforts to achieve a more nearly phylogenetic classification.

276 BALDWIN, BRUCE G.
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Cryptic diversity, peripatric speciation, and unequal rates of phenotypic evolution in an annual tarweed clade (*Layia*, Madiinae, Compositae)

Phylogenetic studies of the tarweed genus *Layia* corroborate and extend Gottlieb et al.'s genetic evidence for rapid peripatric divergence in a clade of annual "tidy-tips" with eight pairs of chromosomes. A rate-constant tree ("chronogram") based on nuclear rDNA ITS sequences illustrates that *Layia discoidea*, a morphologically unusual, serpentine endemic of highly limited distribution in the South Inner Coast Ranges of California, diverged recently from a sublineage of the widespread (paraphyletic) *L. glandulosa*. Based on the molecular data, *L. discoidea* and interior populations of *L. glandulosa* are more closely related to one another than to outer-coastal populations of *L. glandulosa*. Morphological and ecological disparity between *L. discoidea* and *L. glandulosa* in general is striking by comparison with relatively minor phenotypic differences between the most divergent populations of *L. glandulosa*. Another $n = 8$ *Layia* lineage, including *L. gailliardioides*, provides a previously undetected, parallel example of rapid divergence and unequal rates of phenotypic evolution. Based on rDNA and cpDNA data from dozens of populations, three morphologically and ecologically disparate taxa (*L. carnosa*, *L. hieracioides*, and *L. septentrionalis*) are phylogenetically nested among four cryptic, allopatric lineages of the widespread (non-monophyletic) *L. gailliardioides*. Phenotypic evolution in the lineages represented by *Layia carnosa*, *L. hieracioides*, and *L. septentrionalis* evidently has been much more rapid than in the evolutionarily distinct lineages subsumed within *L. gailliardioides*. Irregular rates of phenotypic evolution in the above $n = 8$ *Layia* clade contrast sharply with gradual divergence in its sister group, i.e., the $n = 7$ *Layia* clade; phylogenetic data corroborate Clausen, Keck, and Hiesey's classic model of geographic speciation for the $n = 7$ taxa. The ITS "chronogram" allows for an instructive comparison of the relative timeframes for different modes of evolutionary change in plants.

277 BELL, RACHEL A* and FORD-WERTNZ, DONNA I
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A taxonomic analysis of *Allium tricoccum* s.l.

This research investigates conflicting taxonomic treatments of *Allium tricoccum* s.l. Previous studies have supported splitting the species based on morphological and phenological patterns of variation. However, overlapping circumscriptions of the split taxa complicate plant identification. Statistical multivariate analyses are being performed on morphological characters and label data from herbarium collections throughout the distribution range to test for significant clustering. Pollination studies have been conducted to determine the breeding system and compatibility relationships. Fruit set in *Allium tricoccum* s.l. was found to be highest in active autogamy treatments and lowest in crosses between color variants. A common garden plot is being studied to examine environmental influences on phenotype. The goal is to assess classification alternatives, revealing further evidence for either a single species (with or without subtaxa) or separate species.

278 BENNETT, JONATHAN* and MATHEWS, SARAH
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Phytochrome evolution in parasitic
Orobanchaceae

The change from autotrophy to partial or complete heterotrophy in parasitic plants involves the evolution of new morphological features such as haustoria. Additionally, selective pressures for the maintenance of physiological pathways such as photosynthesis may be reduced, and DNA for these functions may be lost. Phytochrome photoreceptors mediate processes that are altered in parasitic plants. These include de-etiolation, which involves the expansion of cotyledons, leaf and chloroplast development, and the expression of photosynthetic genes. Holoparasitic species of Orobanchaceae remain non-photosynthetic throughout their life cycle, and leaf development is suppressed. Hemiparasitic species produce leaves and photosynthesize for some or all of their life cycle. Parasites may also have a reduced need for shade avoidance, mediated primarily by phytochrome B, which allows plants to detect and grow away from neighbours. We are investigating the molecular evolution and phylogeny of phytochromes in Orobanchaceae. Results so far indicate that three of the four phytochromes that are widely distributed in angiosperms, *PHYA*, *PHYB* and *PHYC*, are present in at least some members of the family, while evidence for *PHYE*, which has a minor role in shade avoidance is lacking. Partial sequences of *PHYA* and *PHYB* have been used to construct a phylogeny of the family, which is broadly congruent with those obtained from analyses of chloroplast sequences in the placement of both the holoparasitic and hemiparasitic species. We have used this phylogeny to conduct tree-based tests to determine if there is an elevation in substitution rates within the family. Preliminary results suggest that *PHYA* and *PHYB* are under different selective pressures in parasites and hemiparasites.

279 BERRY, PAUL E.¹, HAHN, WILLIAM J.², SYTSMA,
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Phylogenetic relationships and biogeography of *Fuchsia* (Onagraceae) based on nuclear ITS and chloroplast *trnL-trnF* and *rpl16* data

To examine relationships within *Fuchsia*, we conducted parsimony and maximum likelihood analyses with nuclear ITS and chloroplast *trnL-F* and *rpl16* sequence data for 36 taxa representing all *Fuchsia* sections and four outgroup taxa. Results confirm the monophyly of *Fuchsia* and support previous sectional delimitations, except for *F. verrucosa*, which is nested within the small-flowered Central American sections. The basal relationships within *Fuchsia* are poorly resolved, suggesting an initial rapid diversification of the genus. Among living members of *Fuchsia*, there is strong support for a single Old World lineage, an austral South American/southern Brazilian lineage, a tropical Andean lineage, and one or two Central American and Mexican lineages. There is no clear support for an austral origin of the genus, as previously proposed, which is more consistent with *Fuchsia*'s sister group relationship with the boreal genus *Circaeæ*. A molecular clock analysis using nonparametric rate smoothing places the split between *Fuchsia* and *Circaeæ* close to 42 mya. The initial diversification of the modern-day lineages of *Fuchsia* occurred about 33 mya. The Old World *Fuchsia* lineage branches off at just over 30 mya, which is consistent with known fossil records of *Fuchsia* from Australia and New Zealand, dating back at least 25 mya. The split between the Caribbean clade represented by *F. triphylla* and the much more speciose Andean sect. *Fuchsia* is placed close to 25 mya. At least an initial diversification of the large Andean sect. *Fuchsia* occurred close to 21 mya. Two other significant dates suggested by the molecular clock analysis include the split between the southern Andean species *F. lycioides* and *F. magellanica* and the Brazilian members of sect. *Quelusia* at about 12 mya, and the split between the New Zealand species of sect. *Skinnera* and the ancestor of the Tahitian *F. cyrtandroides* at just over 10 mya.

280 CAMERON, KENNETH M.*¹ and FU, CHENGXIN²

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A Combined Nuclear and Plastid Gene Phylogeny of Smilacaceae (Smilacaceae, Liliales)

Smilacaceae are a taxonomically confused, cosmopolitan family of Liliales characterized by climbing habit, reticulate leaf venation, paired petiolar tendrils, unisexual flowers, and superior ovaries. Deviations from this generalized morphology have led to the division of Smilacaceae into at least seven different genera and five sections within the large genus *Smilax*. In particular, taxa with either fused perianth, more than six stamens, or herbaceous habit have been variously classified. Using DNA sequences of more than 140 taxa from a combination of plastid (*trnL-F*, *rps16*, *rpl16*) and nuclear (ITS) gene regions, we find support for the recognition of only *Rhipogonum* and *Smilax* s.l. in the family. *Philesia* and *Lapageria* may also be better classified within Smilacaceae rather than Philesiaceae. Within *Smilax* three major lineages are evident. The first is a monophyletic, pri-

marily Old World clade that contains species of *Heterosmilax*, the erect, woody species of *Smilax* from Asia, and the herbaceous *Smilax* species, of which some have dispersed into North America. A primarily New World clade (or paraphyletic grade in some trees) is also present. The Hawaiian species, *S. melastomifolia*, and *S. sieboldii* from East Asia, are members of this clade, indicating at least two dispersals from North America. There is also a strong geographic pattern among these New World species. The third lineage contains *S. aspera* from southern Eurasia and North Africa, which is sister to the entire genus. Its position in the cladogram is intriguing and may help to shed light on the family's biogeographic history and inflorescence evolution.

281 CARLSWARD, BARBARA

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Anatomy and molecular systematics of leafless Vandaeae (Orchidaceae)

Leafless orchids of tribe Vandaeae have undergone extreme reduction in habit and represent a unique adaptation to the canopy environment. Vandaeae form a large, pantropical group traditionally divided into three subtribes: Aeridinae, Aerangidinae, and Angraecinae. Leafless taxa occur throughout Vandaeae and are geographically distributed in Asia, Africa, and tropical America. Using ITS sequence data from representatives of all subtribes and using species of *Polystachya* as outgroups, Vandaeae form a monophyletic group. Within Vandaeae, two main clades were supported (>60% bootstrap support): Aeridinae and the combined Aerangidinae + Angraecinae. Within the Aerangidinae + Angraecinae group, New World Angraecinae genera form a derived clade of mainly leafless species. Leaflessness appears to have arisen at least six times within these two large subclades of Vandaeae: three times in Asia (Aeridinae), twice in the New World (Aerangidinae + Angraecinae), and once in Africa/Madagascar (Aerangidinae + Angraecinae). This general pattern was also supported by combined nuclear (ITS) and chloroplast (*matK* and *trnLF*) sequence data analyses using a subset of taxa from the larger ITS analysis. For the Aerangidinae + Angraecinae group, vegetative anatomy and morphology were also examined. The leafless, almost shootless, habit of Vandaeae has evolved several times in the New and Old World tropics. Monopodial growth and the presence of aeration complexes (that allow gas exchange) within roots seem to be precursors to the leafless condition. Cladistic analyses using combined molecular and structural data sets resulted in the same topology as using molecular data alone, while structural data alone gave almost no resolution among genera. Anatomical data were therefore mapped onto a molecular scaffold to answer questions about the structural evolution of leaflessness.

282 CHANDLER, GREGORY^{*1} and PLUNKETT, GREGORY²

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The phylogenetic placement and evolutionary significance of the polyphyletic subfamily Hydrocotyloideae (Apiaceae)

Recent molecular data suggests that Apiales comprises five main lineages, rather than the traditional two, and includes core Apiaceae, core Araliaceae, Pittosporaceae, the *Mackinlaya* group and

the *Myodocarpus* group, along with the inclusion of five enigmatic genera (*Aralidium*, *Griseolina*, *Melanophylla*, *Pennantia*, and *Torticellia*) within an expanded Apiales. Moreover, these data unveiled the nature and extent of the polyphyly characterizing subfamily Hydrocotyloideae (Apiaceae), often considered a "bridging group" between Apiaceae and Araliaceae, with members of this taxon found among four distinct clades within Apiales. One of these lineages is sister to core Araliaceae, containing two genera, *Hydrocotyle* and *Trachymene*, which share several morphological features with core Araliaceae, including sclerified endocarps, broadly inserted petals that lack inflexed apices, and laterally compressed fruits (shared with the araliad genera *Astroticha* and *Osmoxylon*), while lacking typical apiaiceous features such as compound umbels and vittae. The *Mackinlaya* group contains elements from Araliaceae (*Mackinlaya* + *Apiopetalum*) and several hydrocotyloid genera (the *Centella* group), which share clasping petiole bases, clawed and inflexed petals, bicarpellate gynoecia, and fruits with strong lateral compression, features more common to Apiaceae than Araliaceae, prompting suggestions that this lineage represents a fourth subfamily of Apiaceae. The *Azorella* group contains the largest number of hydrocotyloid genera, and is sister to Apioideae + Saniculoideae. A variety of morphological characters tie this group together, particularly embryological characters such as a relatively large nucellus with four (occasionally two) megasporocytes. Finally, several molecular and morphological studies support the placement of *Arctopus* in Saniculoideae rather than Hydrocotyloideae. The polyphyly of Hydrocotyloideae requires a reassessment of the evolutionary interpretation of morphological features in the order, since many assumptions were built around the hydrocotyloids being intermediate between Apiaceae and Araliaceae.

283 CLEVINGER, JENNIFER A.* and CLEVINGER, CURTIS C.

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The Systematics of *Silphium* (Asteraceae: *Heliantheae*): A Revision based upon Morphological and Molecular Data In preparation for writing the treatment of *Silphium* for the Flora of North America project, a revision was undertaken using morphological and molecular evidence. The revision includes 12 species and 13 varieties in two sections. Five of these varieties are new combinations. Newly discovered species, *Silphium glutinosum* J. Allison (Castanea 66: 183. 2001), is placed in section *Asteriscus*. Preliminary molecular data from the internal transcribed spacer (ITS) and external transcribed spacer (ETS) regions of nrDNA suggest that *S. glutinosum* is most closely related to *S. asteriscus* as well as purported hybrid *S. perplexum*.

284 COSTELLO, ANNEMARIE^{*1} and MOTLEY, TIMOTHY²

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Phylogenetic relationships within the Tetraplasandra Group (Araliaceae) revealed by Amplified Fragment Length Polymorphisms (AFLP) markers

The Tetraplasandra group encompasses four genera, *Tetraplasandra* A. Gray, *Munroidendron* (C. Forbes) Sheriff, *Reynoldsdia* A. Gray, and *Gastonie* Comm. ex Lam., that are distributed from Madagascar, through the islands of the Indian Ocean and Malesia, to the Solomon Islands, Samoa, Tahiti, the Marquesas, and the Hawaiian archipelago. Historically, systematic relationships within the *Tetraplasandra* group

have been unclear and generic delimitations were problematic. Our previous phylogenetic analyses derived from independent and combined ITS, 5S-NTS, and morphological data revealed that the Hawaiian taxa of the *Tetraplasandra* group (*Tetraplasandra*, *Munroidendron*, and *Reynoldsia sandwicensis*) form a monophyletic group and *Reynoldsia* is polyphyletic. We examined the use of Amplified Fragment Length Polymorphisms (AFLP) to potentially resolve species relationships among the Hawaiian members of the *Tetraplasandra* Group that were not resolved by cladistic analyses of DNA sequence and morphological data. The results of this study suggest that AFLP analysis is congruent with the previous data and provides reliable markers for resolving evolutionary relationships in closely related species resulting from rapid radiations.

285 COTA-SANCHEZ, HUGO

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Phylogeny of the subfamily Cactoideae: A look at the epiphytic cacti based on sequence data from cpDNA

Among all angiosperm families, few are as morphologically diverse and taxonomically complex as the Cactaceae. The family is among the top ten epiphytic-rich families of vascular plants. Approximately 10% of the species have been able to radiate successfully in the epiphytic habit due to a complex suite of adaptations. In general, epiphytic species make up about 10% of vascular plants and represent a significant proportion of tropical diversity, yet this lifestyle remains one of the least studied growth habits in plants. In the Cactaceae, epiphytic and semi-epiphytic lineages have evolved independently several times in the Cactoideae and are primarily represented in two tribes, the Hylocereeae (in North and Central America) and the Rhipsalideae (South America). Epiphytism, however, has also evolved in tribes Pachycereeae and Trichocereeae. The phylogenetic relationships among the different epiphytic lines in the family are poorly understood due in part to convergent evolution of vegetative and reproductive characters. Here I discuss preliminary results based on independent and combined data sets from the *rbcL* gene and the intergenic spacer of the *trnL-F* genes to understand the phylogenetic intertribal relationships of the Cactoideae and, in particular, to investigate the multiple origin of epiphytism in the family. Additionally, morphological seed characters have been optimized onto the phylogeny to elucidate major changes involved in the transition from ground to canopy. There is an apparent trend in decreasing seed size from the terrestrial to the epiphytic habit, with the maximum reduction in the Rhipsalideae. Maximum parsimony analyses support the monophyly of the Rhipsalideae and the Hylocereeae, but the relationships among the other tribes remain unresolved. Some intergeneric relationships are also discussed.

286 CRONK, QUENTIN^{*1}, REE, RICHARD¹ and CITERNE, HELENE²

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Natural selection on florally expressed developmental genes associated with transition between floral types in *Lupinus* (Fabaceae)

Species of *Lupinus* have two florally expressed TCP genes (developmental genes of the class known to be involved in floral symmetry in *Antirrhinum*). We have characterised these genes (LEGCYC1A and LEGCYC1B) in several lupin species. They have some potential for providing information on the evolutionary relationships of the north American lupin "species flock", which are difficult to resolve by other means. One of the included species, *Lupinus densiflorus*, has a distinctive floral form with a small standard and relatively large wings. We examined the molecular dataset for evidence of positive selection associated with this change in morphology. Likelihood modelling of the non-synonymous and synonymous substitution rates provides evidence for relatively strong positive selection on some codons along the branch leading to this species. Generally the genes show only weak purifying selection, allowing for the fast evolution of these genes. These patterns of selection will be discussed relative to the possible role of these genes in producing floral differences between *Lupinus* species.

287 DATWYLER, SHANNON*, CLEMENT, WENDY, SWENSON, STEPHANIE and WEIBLEN, GEORGE

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Where did the figs come from? Phylogenetic relationships in Moraceae based on *ndhF* and 26S sequences

The Moraceae include 37 genera and approximately 1100 species with a broad range of breeding systems, inflorescence morphologies, and pollination syndromes. The majority of species are figs (*Ficus*). We sequenced nearly 2000 bp from the chloroplast gene, *ndhF* and approximately 1000 bp of 26S nuclear ribosomal DNA to examine relationships among Moraceae genera to elucidate shifts in breeding systems and pollination syndromes, and to identify the closest living relatives of the figs. *ndhF* sequences provided over 600 phylogenetically-informative characters (31%). These data strongly support the monophyly of Dorstenieae and Ficeae, whereas the Moreae appear as a basal grade with respect to Artocarpeae and Dorstenieae. Furthermore, these data provide strong support for the sister group relationship of a revised Castilleae and Ficeae. In contrast, 26S sequences provide 131 phylogenetically-informative characters (13%). Although Dorstenieae, Castilleae and Ficeae are recovered as monophyletic, these groups have weak bootstrap support. However, 26S provides some resolution at the generic level not seen with *ndhF*. A combined analysis provides greater resolution within tribes and supports the major lineages recovered with the *ndhF* data set. Our results suggest that dioecy is the ancestral breeding system of Moraceae, with several independent origins of monoecy. Furthermore, wind pollination appears to be the ancestral condition, with at least two independent transitions to insect pollination. The ancestral inflorescence appears to have been a raceme or spike, with several independent origins of discoid inflorescences and a single origin of urn-shaped inflorescences in the Castilleae+Ficeae clade. The sister

group relationship of these two tribes, both with urceolate inflorescences and insect pollinators breeding among the flowers, suggests that entomophily preceded the evolution of the obligate pollination mutualism in *Ficus*. These data further support the hypothesis that the complete enclosure of the fig inflorescence may have served a protective function against flower parasites.

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Species diversity and phylogeography of the Atlantic-east-Pacific mangrove genus *Avicennia*

The pan-tropical mangrove genus *Avicennia* is composed of Indo-west-Pacific and Atlantic-east-Pacific species. The former are more diverse and this, with other evidence has led to the hypothesis that the genus entered the proto-Atlantic before the closure of the western Tethys and differentiation of the two groups may have occurred following closure of the Mediterranean Sea in the late Eocene. Today, three species occur in the Atlantic-east-Pacific, of which one, *Avicennia germinans* is found throughout the region and the other two are more locally endemic; *A. schaueriana* to the Atlantic coast of South America and to some Caribbean islands and *A. bicolor* to the Pacific coast of Central and South America. Our AFLP and chloroplast molecular data show low levels of differentiation among these three species, suggesting relatively recent divergence. Within the species *A. germinans*, both genomic DNA (AFLP) and chloroplast DNA show a much greater differentiation across the Central American Isthmus (CAI) than across the Atlantic Ocean, suggesting that long distant dispersal events across the Atlantic have maintained population cohesion. Chloroplast haplotypes that we have detected from West African populations are identical to those of the South American coastline. The greatest haplotype diversity occurs along the Pacific coast and none of the haplotypes that we detected from these populations were shared with Atlantic populations. The lack of haplotype sharing across the Central American Isthmus suggests that populations may have been very much reduced, perhaps as a result of successive shoaling during the period prior to final uplift of the isthmus. The distribution of chloroplast haplotypes in the Atlantic and Caribbean region are correlated with surface ocean currents that can potentially transport propagules over great distances in short periods of time.

289 DOUGLAS, NORMAN A* and MANOS, PAUL S

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Phylogenetics and selfing in *Boerhavia* (Nyctaginaceae)

The family Nyctaginaceae has presented serious taxonomic difficulty, both in the identification of major lineages, and in the delimitation of species. Molecular phylogenetic study of the family Nyctaginaceae has indicated that the non-arborescent genera form a clade centered in the deserts of North America. Sequence data from ITS and the chloroplast spacers *rpl16* and *rps16* support the monophly of most currently recognized genera, though relationships among some clades remain uncertain. Some surprising clades have emerged, notably the close relationship of the genus *Boerhavia* and the morphologically divergent strand species *Okenia hypogaea*. The genus *Boerhavia* is among the most taxonomically intractable in the Nyctaginaceae. Sequence-based phylogenetic work indicates that

Boerhavia is comprised of four major lineages, two widely distributed, and two centered in the Chihuahuan and Sonoran deserts. One clade is comprised of the two widespread perennial weeds, *B. coccinea* and *B. diffusa*, another includes Australian, African and Pacific perennials, including *B. repens*. Both widespread clades possess sticky-glandular fruits. The Chihuahuan clade includes 3 glabrous-fruited perennial species. The Sonoran clade is most diverse in terms of described species (26), and is characterized by an annual habit. Two annual clades are distinguished by inflorescence structure. Flower size and stamen number varies greatly among the species of *Boerhavia*. AFLP data have revealed that *Boerhavia* have a mixed mating system, and this technique is being employed to investigate the relationship between flower size and natural outcrossing rate. Additionally, AFLPs are being used to describe the genetic structure among populations, which should be related to the outcrossing rate. The potential for simple changes in flower size to affect inter-population divergence will be discussed in the context of the recent radiation of this genus.

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Floral development and molecular phylogeny support the generic status of *Tasmannia* (Winteraceae)

The taxonomic status of and evolutionary relationship between *Tasmannia* and *Drimys* have been the subject of controversy for many years. However, a molecular phylogenetic analysis of the family with sequences of previously unpublished *Tasmannia* and *Drimys* species confirms earlier conclusions that *Tasmannia* and *Drimys* do not form a monophyletic group, despite the fact that they appear to share distinctive inflorescence and floral morphological attributes. A detailed analysis of floral development in *Tasmannia lanceolata* and *T. xerophila* indicates that sepal initiation differs in *Tasmannia* and *Drimys*, but that there is a similar prolonged period of calyx tube growth leading to the formation of a calyptra. Optimization of developmental characters onto the phylogeny indicates that the persistent calyptra is not a synapomorphy for the two lineages. *Tasmannia lanceolata* has an intermediate pattern of sepal initiation between the other species of *Tasmannia* and the pattern of initiation in the rest of the family (including *Drimys*). The first three whorls of floral organs in both species of *Tasmannia* are positioned as two decussate whorls followed by a whorl of four organs, although the identity of organs in these whorls differ. Further organs initiated may be less precisely placed, as a consequence of asymmetry in floral meristem shape and degree of tilt away from the floral axis. Current work is focused on understanding the genetic control of perianth differentiation within the family.

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Maximum information and minimum sequencing: resolving phylogenetic relationships among closely related species of *Columnea* (Gesneriaceae) using multiple genes

Resolving phylogenetic relationships among closely related species using sequence data has been a challenge for many taxonomic groups. Regions that are often used because they are easily amplified and sequenced such as chloroplast genes and ITS often do not provide sufficient variability to resolve relationships, let alone

provide strong support for relationships. In recent years many low copy nuclear genes have been examined, providing variability for many different groups. *Columnea* comprises an estimated 300 Neotropical species. Examination of several genes that have provided utility for phylogenetic analyses at the species level in other taxa have not provided a strongly supported phylogenetic hypothesis for a sampling of *Columnea* species when used individually. A combination of genes is essential, and this study examines several regions from the chloroplast and nuclear genomes as a means of assessing the best combination of data to resolve among relationships in this group.

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The phylogeny of subtribe Scorzonerinae (Asteraceae) as inferred from ITS sequence data

Scorzonerinae are a well-defined subtribe of the Lactuceae (Asteraceae: Cichorioideae) with its center of geographic distribution in the Mediterranean and Middle East. Scorzonerinae appear to be well supported as monophyletic; however, generic circumscription and relationships within the group have been problematic. For example, Bremer (1994) recognized seven genera in the subtribe, whereas others have recognized as many as twelve. One of the more problematic genera is *Scorzonerina*, a large and morphologically diverse genus, whose monophyly is questionable. Several smaller genera, such as *Podospermum* and *Takhtajaniantha*, have been segregated from *Scorzonerina*. To investigate the monophyly of the recognized genera and intergeneric relationships, we conducted a phylogenetic analysis of subtribe Scorzonerinae using ITS sequence data. Sixty accessions from 52 species from all recognized genera were included in the analysis, and *Sonchus*, *Cichorium*, and *Lactuca* (all members of subfamily Cichorioideae) were used as outgroups. Our results reveal that most genera including *Tragopogon*, *Epilasio*, *Podospermum*, *Pterachaenia*, *Tourneuxia*, *Koelpinia*, and *Lasiospora* are monophyletic. However, *Lasiospora* is nested within a clade that contains several *Scorzonerina* spp. *Scorzonerina* is clearly not monophyletic and forms multiple clades with other genera. *Geropogon*, which has often been grouped with *Tragopogon*, is phylogenetically removed from the highly supported *Tragopogon* clade. These results support the current delimitation of most genera in this clade. However, *Scorzonerina* is not monophyletic, and we recommend that it be split into several genera.

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Testing concordance of [phylogenetic signal from crossing data and nuclear ITS sequence variation among climbing snapdragons

The 20 North American species making up subtribe Maurandyinae have been treated in two to seven genera and are noted for exhibiting diverse floral morphological features and wide interspecific compatibilities in artificial crosses. To test taxonomic hypotheses and to evaluate inferences about genetic relatedness based on crossing and interfertility data, 15 species representing all supraspecific taxa

and four outgroup species were analyzed for nucleotide variation among nrDNA ITS sequences. Parsimony analyses resulted in a high level of support for monophyly of the group and sister group status for the SW European and Mediterranean genera *Asarina* and *Cymbalaria*. Within the Maurandyinae, the monotypic *Epixiphium* is indicated as sister to a trichotomy encompassing *Holmgrenanthe* + *Maurandy*/*Maurandella* + *Lophospermum*/*Mabrya*/*Rhodochiton*. Neighbor-Joining trees of cross-compatibility and hybrid fertility data from 14 reciprocally crossed species recognize two primary groups, *Epixiphium*/*Maurandy*/*Maurandella* + *Lophospermum*/*Mabrya*/*Rhodochiton*, although species relationships differ among analyses of data partitions. The highest indices of crossability and interfertility are found among closely-related species of *Maurandy* and *Lophospermum* that have similar but not identical topological placement on ITS and NJ trees. The often segregated monotypic genera *Epixiphium* and *Homgrenanthe* are characterized by long branch lengths and the lowest indices of crossability. Species previously segregated in *Mabrya* appear paraphyletic, which supports their merger in an expanded *Lophospermum* and is consistent with crossing data.

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Characterization of anthocyanin regulatory gene in *Cornus* – utility in evolutionary studies of the genus

The dwarf dogwood species complex (*Cornus* subgen. *Arctocrania*) exhibits various patterns in petal coloration. We characterized the structure and examined the sequence variation of anthocyanin regulatory gene in the complex. The goal is to determine relationship between molecular evolution and phenotypic diversity in petal coloration, while assessing the utility of the gene in polyploid and hybridization studies in the complex. Genbank sequences, TA cloning, thermal asymmetric interlaced PCR, and automated sequencing were used in the study. Two copies of the gene were detected from analyses of the 5' end among ten samples representing all three species and two hybrid categories in the complex. The entire genomic sequence of the "A" copy was characterized and spans approximately 4000 bp. This copy consists of eight exons and seven introns arranged in an order corresponding to the intron-exon structure of *jaf13* of *Petunia* and *lc* gene of *Zea mays*. The sizes of exons are similar to those from other dicots (e.g., *Petunia*, *Antirrhinum*, and *Arabidopsis*). However, the sizes of introns in the dwarf dogwoods are different from these plants. At DNA sequence level, the gene in dogwoods is highly divergent from those in *Petunia*, *Antirrhinum*, *Arabidopsis*, and *Zea mays*, alignable among these taxa only in the core conserved region of exons. Sequence analysis of intron 1 for 43 populations detected both indels and site mutations among species and populations and revealed low diversity at sequence level, but high diversity in haplotypes within the complex. Comparisons of entire sequences of the gene for a limited number of samples indicate that the 3' end is less conserved than the 5' end; a fragment of 12 bp coded for LDAA in the 6th exon was absent in white-flowered plants, but present in purple-flowered plants and coexisting in plants with a mosaic of purple and white petals.

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Phytogeographic survey of Trilliaceae

Trilliaceae are plants of North Temperate forests with a holarctic distribution, and the family has been proposed to be Arcto-Tertiary in origin. Even though it has a pan-north temperate distribution, there is a high degree of endemism within the family; only one species has a widespread distribution. Of the six genera, three are monotypic endemics. There are many interesting distributional patterns in the family relating to morphology, merosity, and ploidy levels. The center of diversity of tribe Trilliaceae is in the southeastern United States; the center of diversity for tribe Parideae is in China. Molecular phylogenetic analyses show that the basal most lineage is restricted to the Siskiyou Range of the Pacific Northwest; in addition, the basal lineages in the major clades appear to be restricted to Asia or the western U.S. This suggests that the origin of the family is in this region with subsequent radiations to Asia and eastern North America.

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Phylogeny and infrageneric classification of *Symplocos* (Symplocaceae) inferred from DNA sequence data

The woody angiosperm genus *Symplocos* (Symplocaceae) consists of about 230 species distributed in the American and east Asian montane tropics, with a few lowland and temperate outliers. The most recent comprehensive taxonomic revision of *Symplocos* delimited four subgenera: *Symplocos*, *Epigenia*, *Hopea*, and *Microsymplocos*. Subsequent authors conducting regional taxonomic revisions of the genus have accepted only two or three of these. To help clarify the infrageneric classification of *Symplocos*, we conducted phylogenetic analysis of the genus based on DNA sequence data from four genes: ITS, *rpl16*, *matK*, and *trnL*. In the combined analysis of all data, three of the four subgenera are demonstrably nonmonophyletic, and the samples of *Epigenia* form an unresolved clade with several members of *Hopea*. Section *Cordyloblaste* of subgenus *Symplocos* and the sole deciduous species of the genus, *S. paniculata* of *Hopea*, form the first- and second-diverging clades, respectively. This suggests that at least subgeneric status for these groups is warranted. Section *Neosymplocos* of subgenus *Microsymplocos* is nested within a clade comprising the remaining members of subgenus *Symplocos* (i.e., the tropical American section *Symplocos*). Section *Urbaniocharis* of *Microsymplocos* is placed as sister to the clade comprising section *Symplocos* + *Neosymplocos* with weak support. Most Asian species of *Hopea* form a clade; *S. Wikstroemiifolia* of eastern Asia, *S. tinctoria* of the eastern United States, and *S. longipes* of southern Mexico group in the same clade as the samples of *Epigenia*. Preliminary biogeographical analysis based on the phylogenetic estimate suggest an eastern Asian origin for *Symplocos*, whereas fossil data suggests a North American origin.

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Phylogenetic relationships of tribe Coronanthereae (Gesneriaceae): evidence from multiple genes

Tribe Coronanthereae of Gesneriaceae is a group of seven to nine genera, each with only one or two species each with the exception of *Coronanthera*. Coronanthereae have long been recognized as distinct from other Gesneriaceae with the unique feature of the nectary fused to the ovary wall. Additionally species in this tribe are characterized by high chromosome counts, implying ancestral polyploidy. Most previous analyses that have included Coronanthereae have shown the tribe to be sister to the remainder of subfamily Gesneroideae, although a few analyses have shown ambiguity among the relationships of Coronanthereae, Napeantheae, Beslerieae and subfamily Cyrtandroideae. In this study we investigate the generic level relationships of Coronanthereae as well as try to place the tribe with representatives of other Gesneroideae and Cyrtandroideae. Two low copy nuclear genes provide resolution for relationships among these genera, one of which (GCYC) has two clear paralogs that provide identical topologies. Other genes have resulted in numerous paralogs that prevents unambiguous phylogenetic analysis. In general the tribe is split into two clades that correspond to the South American and South Pacific genera. The combined data analysis places the tribe as sister to Gesneroideae, although some genes analyzed independently show a closer relationship to tribes Napeantheae and Beslerieae.

298 GARCIA, VICENTE

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Phylogenetic and ethnobotanical studies of *Piper* (Piperaceae) taxa from the South Pacific

There are over 1000 species in the genus *Piper* L. (Piperaceae) making it one of the larger genera among angiosperms. The group has a pantropical distribution with a center of diversity in the Neotropics. Several species are of great economic and cultural importance including *Piper nigrum* and *P. methysticum*. Current understanding of the phylogenetic relationships within *Piper* distinguish Neotropical from Paleotropical taxa. The Paleotropical group has been divided further into an Asian and a South Pacific clade. *Piper* from the South Pacific provides an ideal system to investigate ethnobotanical questions in a phylogenetic context. Here I present preliminary results of a phylogenetic study using ITS sequence data to test the monophyly of the South Pacific clade and elucidate relationships within the group. This study will also determine the utility of the mitochondrial *nad1* intron 2 region and the chloroplast *atpB-rbcL* spacer region for resolving intraspecific relationships within *Piper* taxa. The relationships within *Piper methysticum* cultivars are of particular interest in testing patterns of plant movement across Pacific islands by the ancient Polynesians.

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Phylogeny and classification of *Pinus* (Pinaceae) based on cpDNA sequences

We will present a combined *rbcL* and *matK* phylogeny for over 80 of the approximately 110 recognized species representing all major lineages of the genus *Pinus*. Based on the phylogeny, *Pinus* is biphytic, composed of subgenus *Pinus* (the diploxylon, or hard pines), and subgenus *Strobus* (the haploxylon, or soft pines). Subgenus *Strobus* can be divided into two monophyletic sections: sect. *Parrya* composed of western North American subsects. *Cembroides*, *Nelsoniae*, and *Balfourianae*; and sect. *Quinquefolius* composed of Asian subsects. *Gerardiana*, *Krempfiana*, and Eurasian-North American subsect. *Strobi*. Subgenus *Pinus* can also be divided into two monophyletic sections: sect. *Pinaster* composed of Eurasian subsect. *Pinaster* and primarily Eurasian subsect. *Pinus*; and North American sect. *Trifolius* composed of subsects. *Contortae*, *Ponderosae*, and *Leiophyllae*. Within the latter subsection, three weakly supported clades are found, corresponding to the California closed cone pines, the southeastern US yellow pines (excluding *P. echinata* and *P. palustris*), and a heterogeneous group of primarily Caribbean and Mexican species. Overall cpDNA and nDNA phylogenies are congruent, except for the placement of subsect. *Contortae*. The comprehensive species sampling allows us to examine trends of morphological evolution and provide divergence time estimates for *Pinus* lineages.

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Patterns of evolution in Neotropical Bignoniaceae: relationships within Crescentieae

Three major groups of Bignoniaceae are represented in the Neotropics: Bignonieae, the lianas, Tecomeae, the trees with dehiscent fruits, and Crescentieae, the trees with indehiscent fruits. Historically, Crescentieae, have been aligned with the Coleeae on the basis of their cauliflory, and dehiscent fruits. This presented a conundrum in the form of a bizarre, disjunct distribution since the Crescentieae are endemic to Central America, and the Coleeae are endemic to Madagascar. However, Gentry showed, using morphological data, that these two groups were more closely related to arborescent Bignoniaceae from their respective continents than to each other; the Coleeae were more closely allied with Bignoniaceae from Africa, while the Crescentieae were related to those from South America. These findings were later corroborated by molecular evidence. Crescentieae are nested within the large genus *Tabebuia*, and sister to a clade of species distributed throughout Central America. The purpose of this study is to further explore the relationships within the Crescentieae. This is done using chloroplast DNA sequences for *ndhF* and the intron and spacer from *tRNA/F* and an intron sequence from the *pep C* gene found in the nuclear genome. Current results indicate that the three genera of Crescentieae are monophyletic, with *Crescentia* sister to *Amphitecna* and these two sister to *Parmentiera*.

On morphological grounds, this is not altogether surprising, as *Parmentiera* shares more plesiomorphic traits with *Tabebuia* than do the other two genera. It often is a canopy tree, and has fruit morphology very similar to a juvenile *Tabebuia* fruit: completely bilocular ovary and winged seeds. This is quite distinct from *Crescentia* and *Amphitecna*, which have varying degrees of unilocularity, and vestigial wings, if any at all, on the seeds.

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The phylogeny of Cocoeae (Arecaceae) with emphasis on *Cocos nucifera*

Cocoeae (20 genera/206 species); a tribe in the subfamily Arecoideae (Arecaceae) contains several economically important palms including *Cocos nucifera*, *Elaeis guineensis*, *Attalea cohune* and *Bactris gasipaes*. This generic level phylogeny based on the nuclear gene, phosphoribulokinase (*prk*) addresses the monophony of the five subtribes of Cocoeae; evolution of the endocarps; the closest relatives of *Cocos nucifera* and biogeographical implications of its distribution. Cocoeae was found to fall into two major clades: the spiny and non-spiny species respectively. The spiny group contains all the Bactridinae and *Elaeis guineensis* and *E. oleifera*. The non-spiny Cocoeae includes Beccariophoenix, Voanioala, Jubaeopsis, Attalea, Lytocaryum, Syagrus, Allagoptera, Parajubaea, Polyandrococos, Cocos, Butia and Jubaea. Subtribes Attaleinae and Bactridinae are monophyletic; Butinae is paraphyletic and Elaeidinae is apparently polyphyletic. The evolution of hardened endocarps with three germination pores is confirmed as synapomorphic for Cocoeae. Endocarp pores may be apical, equatorial or basal - equatorial position being plesiomorphic under ACCTRAN optimization. *Cocos nucifera* falls within the non-spiny group but its closest relative is unresolved; however, it is allied with (Butia + Jubaea), (Allagoptera + Polyandrococos), (Syagrus amara+ S. smithii) and Parajubaea; all of which are from the neotropics. Molecular data alone suggests that *Cocos nucifera* did not originate in the western Pacific. Cocoeae fossils from Africa, Australia, Easter Island, Germany, India, New Zealand and South America indicate a more widely distributed Cocoeae in the past. Several of the fossil fruits were used as calibration points on the maximum likelihood topology to estimate times of divergence of the clades. A possible hypothesis for the biogeographical distribution of *Cocos nucifera* based on the phylogeny is tested using divergence times, fossil evidence and corroboration with tectonic events.

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Molecular Phylogenetics of Palmae and Gondwanaland breakup.

The large number of Angiosperms currently distributed across the southern continents strongly suggests that vicariance due to Gondwanaland breakup was a major factor in early flowering plant evolution. However, the fossil evidence to support this scenario is scant and several molecular clock-based studies have failed to demonstrate dates of divergence early enough to be consistent with tectonic events. Emerging estimates of phylogenetic relationships for the Palmae indicate several sister-taxon relationships that offer tests of the Gondwanaland break-up vicariance hypothesis. I examined five clades in which two or more taxa are distributed across the southern continents and evaluated whether the patterns of cladogenesis correspond to patterns of continental breakup reconstructed from geo-

physical data. Additionally, I used three different molecular clock approaches to determine if the dates of divergence are consistent with estimated dates of tectonic events. Approximately 10 kb of DNA sequence data from the nucleus and chloroplast were analyzed to derive estimates of phylogenetic relationship and estimate dates of divergence. Molecular clocks were calibrated with recently described fossil evidence. In all cases studied, the patterns of cladogenesis were consistent with geophysical models for the pattern of Gondwanaland breakup and estimated dates of divergence were well within the range of estimates for dates of continental separation.

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Phylogeny, molecular dating, and biogeographic patterns of Core Brassicales

Core Brassicales (Brassicaceae, Capparaceae, Cleomaceae, Emblingiaceae, *Forchhammeria*, Gyrostemonaceae, Pentadiplandraceae, Resedaceae, *Tirania*, and Tovariaceae) exhibit remarkable variation in habit, floral structure, breeding systems, species diversification, and areas of endemism. The Capparaceae, Cleomaceae, plus Brassicaceae subclade (Brassicaceae s.l.) is the most diverse with over 4,000 species whereas the remaining lineages are small or monotypic. In addition, members of this subclade have a cosmopolitan distribution whereas other lineages in the order are more isolated and restricted. In order to examine diversification rates and biogeographic patterns, ages of clades are needed. We used various dating techniques (nonparametric rate smoothing and penalized likelihood) on chloroplast sequences data (*tbcL*, *matK*, and *ndhF*). The maximum likelihood trees were calibrated by (1) use of the fossil *Dressiantha bicarpellata* which was incorporated into the phylogenetic framework using morphological data and a constrained molecular tree and (2) independently derived molecular dates. The divergence dates of Core Brassicales vary based on calibration, but all analyses indicate younger dates than have been previously published, especially for the Brassicaceae and *Arabidopsis*. The phylogenetic results, lineage dates, and biogeographic distributions are discussed using known geological information.

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California as a Phylogenetic Sink for Portulacaceae Diversity

Among North American geopolitical regions, California has the greatest diversity of "western American Portulacaceae." Of 97 taxa recognized by Flora North America, 67 occur in California, 46 in Oregon/Washington combined, and <25 in any other state or province. California has 26 endemic taxa versus a total of seven in all other states/provinces. This pattern is artifactual of the geopolitical distribution of North American biomes. However, biome distribution explains the disproportionate incidence of Portulacaceae in California and not historical biogeographic relationships among or between either geographic regions or habitats. Analysis of ca. 200 rDNA-ITS and cpDNA *ycf3-trnS* spacer sequences suggests multiple immigrations into California from peripheral regions, with perhaps one instance of subsequent emigration. Key to this interpretation are data for *Cistanthe* s.l. Contrary to morphology, the sequences refute a unique shared ancestry for sect. *Cistanthe* with "*Calyptidium* s.l." (sects. *Amarantoideae*, *Calyptidium*, and *Philippiamra*). The data indicate

that sect. *Calyptidium* and *C. ambigua* descend from 1-2 South American immigrations to the Sonoran desert. As with morphology, both rDNA and cpDNA sequences from the north Cascade endemic *Cistanthe tweedyi* are "relictual," showing symplesiomorphic similarity with those of *Cistanthe* sect. *Cistanthe*. Nevertheless, the data reveal a largely montane-alpine clade comprising this species, *Lewisia*, and *Montiae*, suggesting that California members of the last two descend from immigrants from the north and/or east. The two California species of *Calandrinia* s.str. may represent independent immigrations from the northern Andes, and *Cistanthe maritima* is probably a recent immigrant from the South American coastal desert. The Portulacaceae lineages also exhibit evolutionary inertia with respect to habitat: most species in the various lineages occur in the likely ancestral habitat of that lineage. Supported by FONDECYT (Chile) and the Mellon Foundation.

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The origin and biogeography of the Hawaiian and South Pacific Ocean island endemic species of *Plantago* section *Plantago*

Plantago section *Plantago* (Plantaginaceae) comprises 36 species including the worldwide weed *P. major*. Most of the species occur in the Northern Hemisphere with three endemic species (*P. pachyphylla*, *P. princeps*, and *P. hawaiiensis*) currently recognized in the Hawaiian Islands. Nine endemic species in section *Plantago* are found in the Southern Hemisphere and, while this section is conspicuously absent in New Guinea, Australia, New Zealand, and South America, five species occur on four South Pacific Ocean islands or island groups, Rapa Island (*P. rapensis* and *P. rupicola*), Lord Howe Island (*P. hedleyi*), Juan Fernandez Island (*P. fernandezia*), and the Auckland Islands (*P. aucklandica*). The remoteness of the Hawaiian Islands and the great distance between the widely disjunct South Pacific island taxa and other taxa in section *Plantago* pose interesting questions as to the origin, biogeography, and evolution of these island species. Morphological variation between species in section *Plantago* is low and indicate little as to how the species are grouped/related. In this study, we use a phylogeny based on nuclear internal transcribed spacers (ITS) sequence data and morphological data to examine some of these questions. Section *Plantago* is monophyletic in our analyses and our phylogeny supports a hypothesis that *P. macrocarpa* was dispersed from Asia to North America giving rise to at least four of the North American species in section *Plantago* (*P. eriopoda*, *P. rugelii*, *P. sparsiflora* and *P. tweedyi*), one of which gave rise to the three Hawaiian Islands taxa followed by long-distance dispersal and subsequent speciation on South Pacific Ocean islands.

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Evolution of floral pattern formation and mature floral structure in *Hibbertia* (Dilleniaceae)

The largely Australian genus *Hibbertia*, here taken in a broad sense to include the segregate genera *Adrastaea* and *Pachynema*, shows more bauplan-level variation in floral structure than perhaps any other angiosperm genus. While the perianth of *Hibbertia* is almost always 5-merous, the androecium may have from 1 to over 200 members (which may be partly staminodal), and the gynoecium may have 1 to 10 carpels. Also impressive is the variation in symmetry of the androecium, which may be polysymmetric to conspicuously monosymmetric, with stamens occurring on only the (as is typically presented) abaxial side of the flower. The floral morphological evolution of *Hibbertia* was investigated by the analysis of pattern formation data, mature structure, and anatomy in the context of a nearly completely sampled species-level phylogeny of the genus derived from nucleotide sequence data from the plastid *rpl16* intron and the ITS region. Results indicate the evolution of androecial symmetry is complex, with as many as 4 independent gains of monosymmetry, and 2 independent, unambiguous reversions back to polysymmetry. Pattern formation data, taken in the context of the phylogeny, suggest that androecial monosymmetry has arisen due to a heterochronic shift in the timing of the initiation of the stamen and carpel primordia. In species with polysymmetric androecia, the carpel primordia initiate at a point distinctly after the initiation of the stamen primordia, whereas in species with monosymmetric androecia, the (2) carpels are initiated at the same time as the stamen primordia. Evidently, the increasingly precocious initiation of the carpel primordia relative to the initiation of the stamen primordia has diminished the amount of meristematic tissue available for stamen formation in one plane of the flower to the extent that, in extreme cases, only 1-5 fertile stamens are formed in (only) a single plane of the flower.

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Phylogeny and systematics of Loasaceae subfamily Loasoideae

The monophyletic Loasaceae subfamily Loasoideae is characterized by great androecial diversity and complexity. It consists of ~200 species distributed primarily in Central and South America and the Caribbean (disjuncts are found in Africa, the Arabian peninsula, and Marquesas Islands). Generic circumscriptions, especially for the larger genera *Cajophora* and *Loasa*, have been controversial and several segregates have been suggested. Tribal boundaries have also been questioned recently. We apply phylogenetic systematics using DNA sequence data from the plastid regions *matK* and *tml-F* to infer monophyletic groups and resolve taxonomic problems. Basal nodes of Loasoideae receive little support, although *Huidobria* appears to form a basal grade. Thus, Loaseae as circumscribed by Urban and Gilg are not monophyletic. We find limited support for the placement of *H. chilensis* as the sister of *Klaprothiaeae* + *Kissenieae*. A group of Loaseae, consisting of *Aosa*, *Chichicaste*, *Nasa*, *Presliophytum*, *Blumenbachia*, *Cajophora*, *Scyphanthus*, and *Loasa*, is monophyletic. Despite suggestions that *Cajophora* s. l. is not monophyletic, our sampling has so far found strong support for its monophyly, including sections *Bialatae* and *Bicallosae*. *Cajophora*, *Blumenbachia*, and *Scyphanthus* form a monophyletic group with elements of *Loasa* section *Loasa*. Although not strongly supported,

Cajophora is placed as the sister of a Chilean-Argentinean clade that consists of *Loasa* series *Pinnatae* + *Scyphanthus*. Similarly, limited support is found for the placement of *Blumenbachia* as the sister of *Loasa* series *Macrospermae*. The *Blumenbachia* + *Cajophora* + *Scyphanthus* + *Loasa* section *Loasa* clade is placed as the sister of the segregate *Presliophytum* + *Loasa malesherbioides*. *Aosa*, a recent *Loasa* segregate, forms a strongly supported monophyletic group that also includes *Chichicaste*, another recent *Loasa* segregate. The segregate *Nasa*, which consists of *Loasa* section *Loasa* series *Grandiflorae*, *Alatae*, *Saccatae*, *Carunculatae*, and the *L. venezuelensis* group, is strongly supported as monophyletic.

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Leaves, acorns, and character variability in *Quercus* (Fagaceae)

Vegetative characters are often viewed as having less taxonomic utility than reproductive characters. One reason for this is the observation that vegetative characters, e.g., leaf characters, are more variable than reproductive characters, e.g., flower and fruit characters. In our work with two species of oaks, *Quercus ellipsoidalis* E. J. Hill and *Q. rubra* L., we have collected samples from 10 "pure" populations of each species as well as from populations in an area in which the two species are sympatric and appear to be hybridizing. Here we report the results of analyses of separate sets of leaf (vegetative) and acorn (reproductive) characters from these populations. Character variability within populations was examined using sample coefficients of variation. In general, leaf characters illustrated greater variability than acorn characters: for the eight characters in each data set, leaves had an average CV almost 50% greater than for acorns. Over all populations, the least variable character was nut length and the most variable character was number of bristle tips per leaf (the only discrete character in either data set). The least variable leaf character was a measure of leaf dissection while the most variable acorn character was cup depth. Despite the much greater variability of leaf characters, when the data sets were used for multivariate analyses, the separate leaf and acorn analyses yielded essentially the same pattern of among-population relationships: a Mantel test comparing the two among-population distance matrices revealed a highly significant ($p < 0.001$) association between elements of the two matrices. These results indicate that patterns of phenetic relationship based on vegetative characters are just as robust as those based on reproductive characters.

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Status of *Boltonia asteroides* complex (Asteraceae: Astereae)

Boltonia asteroides as generally treated consists of three varieties, var. *asteroides*, var. *latisquama* and var. *recognita*, restricted to the wet habitats of the eastern United States. Variety *latisquama* was initially described as a species consisting of the typical variety plus var. *recognita*. However, characters used to differentiate them from *B. asteroides*, long cypselae awns and cuspidate phyllaries, were considered not sufficient to treat them as a distinct species. Our phylogenetic analysis of ITS and ETS showed that var. *latisquama* and var. *recognita* are more closely related to *B. decurrens* and *B. apalachicolensis* than to *B. asteroides* var. *asteroides*. Floral characters for the three varieties of *B. asteroides* were subjected to princi-

pal component analysis. Phyllary size and cypselae awn length had the highest loadings; when plotted produced two slightly overlapping clusters: one with var. *asteroides* and the other one with var. *latisquama* and var. *recognita*. Additional multivariate analyses will be performed in order to address the question of species recognition within *B. asteroides* complex.

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Subgeneric Division of *Sisyrinchium* (Iridaceae), a Western Hemisphere Genus

Sisyrinchium is a large Western Hemisphere genus of approximately 150 species, with the greatest diversity in Argentina. Analysis of the *matK* gene and flanking 3' *trnK* intron (2000 bp), and 1000 bp of the *ndhF* gene for 20 *Sisyrinchium* species and seven outgroups (*Pattersonia*, *Iris*, *Gladiolus*, *Crocus*, *Orthosanthus*, *Libertia* and *Olsynium*) indicates that current subgeneric divisions are not monophyletic. Parsimony and maximum likelihood analyses resulted in trees with high bootstrap values. Three clades are resolved by the current data set. Clade 1 consists of yellow-flowered species with unmarked tepals, partially free filaments, long anthers, and spreading style branches. Clade 2 consists of yellow-flowered species with marked, cupped tepals, intermediate levels of filament fusion, short anthers and short style branches. Clade 3 consists of variously colored flowers, fused filament column, short or no style branching. This analysis resolves clades 2 & 3 as sister with intermediate levels of support, but analyses by other workers using ITS sequence data resolved clades 1 & 2 as sister. The resolution of three clades that are consistent with flower morphology suggests that flowers will provide synapomorphies that define each clade. Results also suggest that both the Gulf Coast and western Mexico have been sites of dispersal of *Sisyrinchium* into North America.

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Mixed-model analysis for phylogeny estimation from multiple data sets

A new feature in the bayesian inference program Mr. Bayes highlights the importance of recognizing and accommodating heterogeneous mutation patterns in DNA sequences. Most phylogenetic analyses rely on limited data (usually much less than 10,000 characters). In such cases, the accuracy of phylogeny estimations can be compromised by random and systematic error, particularly when data partitions are evolving under different evolutionary constraints. One solution is to create a 'mixed-model' system in which character partitions that demonstrate dissimilar mutation patterns can be assigned unique and appropriate evolutionary models within a single phylogenetic analysis. An example of 'mixed-model' analysis is presented for phylogeny estimation in Myoporaceae based on three data sets: the *rpl16* intron, the *trnT-trnL* spacer, and a morphological cladistic character set. The complexities of this analysis will be used to illustrate the need for standardizing mixed-model analyses for phylogeny estimations based on multiple combined data sets.

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Are Aristolochiaceae monophyletic?

Different cladistic analyses have yielded conflicting results as to whether or not Aristolochiaceae are monophyletic. While these analyses are based on diverse sources of morphological and molecular data, few studies have directly focused on the naturalness of the family. To address this question, and examine the monophyly and relationships of the four broadly defined genera of Aristolochiaceae, seventy-two morphological characters were coded from representatives of these genera. The analysis also incorporated data from a broad selection of potential outgroups, including other families of dicotyledonous "paleoherbs", as well as selected monocots and woody magnoliids. The data support monophyly of the Aristolochiaceae, and do not suggest that *Lactoris*, or any other outgroup taxon, is nested within the family. *Aristolochia*, *Thottea*, and *Asarum* are also supported as monophyletic and genera of Aristolochiaceae are grouped into two clades: *Thottea* + *Aristolochia* and *Asarum* + *Saruma*. These results are well supported and stable, despite lack of a well-resolved hypothesis as to the relationships of the family.

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Phylogeny and diversification of B-class genes in angiosperms: reconstructing a 250 million-year-old duplication

We obtained 24 new *AP3* and *PI* sequences representing critical lineages, including the basal angiosperms *Amborella*, *Nymphaeaceae*, and *Illicium* (Austrobaileyales). Structural analyses revealed that the ancestral size of exon 5 in *PI* of angiosperms was 42 bp (typical of the size of exon 5 in other MADS genes). This 42 bp length is found in the *PI*-homologues from *Amborella* and *Nymphaeaceae*. Following these basalmost branches, a deletion occurred in exon 5 yielding a length of 30 bp — this condition unites all other angiosperms. Several shared amino acid strings, including a prominent *Amborella* motif, are present in the *AP3*- and *PI*-homologues of *Amborella*. These are ancestral motifs that were present before the duplication that yielded the *AP3* and *PI* lineages. These conserved amino acid strings were modified after the node basal to *Amborella*, reinforcing the placement of *Amborella* alone as sister to all other angiosperms. Other new structural motifs were found — one motif in the *AP3* lineage unites the previously described *TM6* clade; a deletion in *AP3* unites all Magnoliidae. Phylogenetic analyses of *AP3*- and *PI*-homologues (using parsimony and Bayesian inference and multiple alignments) generally provided low resolution and support of relationships regardless of whether amino acids or nucleotides sequences were used. In general, however, the gene trees track organismal phylogeny. With both *AP3* and *PI* amino acid sequences, we found that *Amborella* and *Nymphaeaceae* are the sisters to all other angiosperms. Using the *AP3* and *PI* data sets, we employed nonparametric rate smoothing (NPRS) and estimated that the duplication that produced the *AP3* and *PI* gene lineages is approximately 250 mya, placing it after the split between extant gymnosperms and angiosperms.

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Phylogenetic relationships of *Menziesia*
(Rhodoreae, Ericoideae, Ericaceae) based on
nrITS and matK sequence data.

Menziesia is a small genus of five to eight species that occurs in Japan and North America. Sometimes referred to as "false azalea", *Menziesia* comprises shrubs with deciduous leaves, flowers that are tubular or nearly so, and capsular fruits. Without flowers, individuals of *Menziesia* appear very similar to some of the deciduous azaleas and the group has traditionally been considered closely related to *Rhododendron*. Some previous studies have indicated that *Menziesia* may be a derivative from within *Rhododendron*, namely section *Tsutsusi*, with which it shares the presence of flattened hairs on the leaves. However, the hairs of *Tsutsusi* are ferruginous and occur on the surfaces of the stems, leaves, and floral bracts, whereas the flattened hairs of *Menziesia* are colorless and restricted to the abaxial midvein of the leaves. Sequences of five taxa from the *matK* and *nrITS* regions were analyzed using parsimony in the context of 42 other species from within the clade Ericoideae. *Cassiope mertensiana* was used to root the tree (sister to Ericoideae based on previous large scale studies). The results indicate that *Menziesia* is monophyletic and likely sister to *Rhododendron* (excluding *Therorhodion*). Within the *Menziesia* clade the two North American species form a clade that is sister to the remaining (Japanese) species. Sequence variation among the Japanese species is very low, and it is interesting to note that species limits within *Menziesia* are not well defined within the Japanese taxa.

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The first genetically confirmed intersubgeneric F₁ hybrid in *Nymphaea* L. (Nymphaeaceae Salisb.)

Hybridization has been difficult to document conclusively in aquatic plants because of their extensive phenotypic plasticity, alternative causes of sterility and the inadequate demonstration of hybridization criteria. These issues are particularly germane to cultivated *Nymphaea* (water lilies), because hybridizers often are secretive about their methods, inadequately control their crosses, and/or fail to provide definitive evidence of hybridization in cultivars. Water lily breeders often rely solely on morphological intermediacy in progeny as the criterion for demonstrating a successful hybrid cross, despite the fact that hybrid phenotypes frequently exhibit more complex patterns. Genetic markers have provided more definitive evidence of hybrids in natural water lily populations (e.g., *Nuphar*), but have not been used extensively in studies of cultivated taxa. Despite numerous reports of hybrid *Nymphaea* cultivars in the literature, none has yet involved a cross between *Nymphaea* subgenera as defined by H. S. Conard. Crosses between *Nymphaea* subgenera are generally regarded as impossible to attain, although there has been the suggestion that natural hybridization may have occurred between subgenera *Lotos* and *Hydrocallis*. However, that possibility remains unsubstantiated. Recently, an intersubgeneric cross was attempted using *Nymphaea colorata* (subgenus *Brachyceras*) and *N. gigantea* (subgenus *Anecphya*). The offspring exhibited morphological intermediacy

in several traits, as well as some novel characteristics. We used DNA sequence data to evaluate the cross genetically. For biparentally inherited DNA (nrITS), the assumed F₁ hybrid was polymorphic at each nucleotide that differed between the parents. Sequencing of subcloned PCR fragments demonstrated that hybrid plants possessed a mixture of alleles matching one or the other parental type, thus providing evidence of genetic contributions from both parents. Maternal markers (from cpDNA) matched the hybrid to *N. gigantea*, the maternal parent of the cross. DNA sequence data provide the first conclusive evidence that artificial hybridization between different *Nymphaea* subgenera indeed has been achieved.

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Evolutionary Relationships in the Evening Primrose Family (Onagraceae): Tribes Onagreae and Epilobieae

Onagraceae are a well studied family, with much known about important traits such as cytology, pollination, and anatomy. However, there is not yet a robust phylogenetic hypothesis with sufficient taxon sampling to examine the evolution of these characteristics within an evolutionary framework. In this study, we used DNA sequence data from one nuclear region (ITS) and two chloroplast regions (*tRNA*-*tRNA*F and *rps16*) to infer phylogenetic relationships among 93 taxa, with concentrated sampling in the large tribe Onagreae. Results strongly suggest that tribe Gonylocarpeae is sister to tribes Epilobieae + Onagreae, both of which are monophyletic. Within Onagreae, *Camissonia* seems to be broadly paraphyletic, and *Oenothera* is also paraphyletic. In *Oenothera* there appear to be two lineages, one of which has *Gaura* + *Stenosiphon* nested within it. At the base of the Onagraceae phylogeny, we have clarified previous confusion regarding conflicting placements of *Hauya* and *Lopezia* based on nuclear versus chloroplast data. These results will facilitate studies of character evolution and biogeography, which we are now examining.

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Phylogenetics of Calycanthaceae based on molecular and morphological data, with an emphasis on sequence heterogeneity of nrDNA ITS region

Calycanthaceae is a small family of four genera and 10 species. It is monophyletic and phylogenetically positioned in Laurales. Putative synapomorphies of Calycanthaceae include opposite phyllotaxy, numerous, undifferentiated tepals, cup-like receptacle, and 1-many achenes. *Sinocalycanthus* and *Chimonanthus* are endemic to

eastern Asia, *Calycanthus* is distributed in eastern and western North America, and *Idiospermum* occurs in tropical forests in Queensland, Australia. Previous phylogenetic analyses based on RFLP and DNA sequence data (Wen et al., 1995; Zhou and Wen, unpublished) suggest that *Chimonanthus* is basal and sister to the clade of *Sinocalycanthus* and *Calycanthus*. In this study six species representing all four genera of Calycanthaceae were sampled, each of which was represented by two or more accessions except for *Idiospermum* (one accession available). We conducted parsimony analyses of morphological and chloroplast *matK* sequence data and our results were consistent with previous analyses. Nevertheless, sequence heterogeneity was found in the nrDNA ITS region in all species. Different alleles of the ITS region were thus cloned. The alignment of sequences from *Idiospermum* and other genera are ambiguous in the spacer regions, but unambiguous in the 5.8S region. Recombined sequences were detected in the 5.8S region using both phylogenetic approach and Maximum chi-square method. Based on sequence divergence in the 5.8S region and secondary structure stability of the spacer regions as estimated using mFOLD computer program, two sequence types were discerned, one of which had little variation in the region across species and genera. Base composition differed significantly between the two sequence types across all taxa. Phylogenetic analyses of the first sequence type generated trees that were congruent with those from other data, but with weak bootstrap support. Sequences of the second type differ greatly from the first type as well as among themselves. Several sequences had long indels, indicative of potential pseudogenes.

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Preliminary documentation of hybridization between species of New World

Cupressus (Cupressaceae) New World species of *Cupressus* are almost exclusively restricted to isolated monospecific stands. Although each population may contain hundreds or even thousands of individuals, most species have only a handful of highly restricted populations. Relative to other New World species, *C. sargentii* and *C. macnabiana* are widely distributed in northern California along the Sierra Nevada and Coastal ranges. In Lake and surrounding counties there are several populations of *C. sargentii* and *C. macnabiana* that occur in very close proximity—in some cases the edges of the populations are in contact producing limited sympatry. Morphologically these two species are easily distinguished: the primary and secondary branches of *Cupressus sargentii* occur in multiple planes while those of *C. macnabiana* occur in only one plane; the leaf glands of *C. sargentii* are obscure and active only occasionally on some older leaves, in contrast *C. macnabiana* has conspicuous, highly active leaf glands on younger and older leaves. Individuals displaying a mixture of character states have been observed where these species occur in sympatry. Although several investigators have examined these specimens and provided an intuitive analysis, only one explicit analysis of these putative hybrids has been conducted. Unfortunately these investigators found little correlation between the morphology and the leaf monoterpenoid content. I will present an explicit morphological analysis coupled with an analysis of chloroplast and nuclear DNA markers. Some specimens identified on the basis of morphology as being possible hybrids have sequence markers consistent with a hypothesis of hybrid origin. While other specimens could be explained (equally as well) in the context of extreme morphological variation present in either of the presumed parental species—although the possibility of a hybrid origin cannot unambiguously be refuted.

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A new generic classification for Bignonieae (Bignoniaceae)

The neotropical tribe Bignonieae, with approximately 360 species, is the most speciose tribe in the Bignoniaceae. It includes all the neotropical lianas with a loculicidal capsule in the family, and is the most diverse and abundant group of lianas in the neotropics. Bignonieae are, however, problematic systematically. As currently circumscribed the genera do not reflect phylogenetic affinities, and lack diagnostic features. Except for Bentham and Hooker, Sandwith, and Gentry who all decreased significantly the number of genera in the tribe, the classification of Bignonieae has been dominated mainly by those who described new genera, but in the absence of phylogenetic information. Here, chloroplast and nuclear sequences, and morphological data are used to estimate the phylogeny of the tribe. The whole gene *ndhF* was sequenced for a total of 121 species (47 genera), the fourth intron of the nuclear gene *PepC-Large* was sequenced for 104 species (43 genera), and 100 morphological characters were studied for 121 species (47 genera). The hypothesis of phylogeny produced suggests that several traditionally circumscribed genera are polyphyletic, paraphyletic, or are nested within larger genera. The phylogeny forms the framework on which a new generic classification for Bignonieae is based. *Perianthomega* is transferred from Tecomeae into Bignonieae and the 47 previously recognized polymorphic genera of Bignonieae are reduced to 21. The changes proposed involve mainly the breaking up of the polymorphic *Arrabidaea*, and lumping several smaller genera into larger monophyletic units. The “new” genera are characterizable by morphological synapomorphies. Wood anatomy, branchlet section, tendril type, number of ovules per placenta, and pollen type are among the morphological characters that are most consistent with the phylogeny of Bignonieae. (Financial support: CAPES/Brazilian Government, NSF, ASPT, BSA, Garden Clubs of Missouri, ICTE, Compton, Des Lee, UMSL, and MOBOT).

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Phylogenetic utility and molecular evolution of chloroplast petD intron sequences in basal angiosperms

Most studies aiming at resolving phylogenies at deeper levels such as basal angiosperms employ slowly evolving genes. Fast evolving genomic regions have been regarded unsuitable because of presumed high levels of homoplasy and frequency of length mutations resulting in their non-alignability. However, a recent study using the *tRNA-F* region (including two spacers and the group I *tRNA* intron) revealed a well resolved tree of basal angiosperms, which was largely congruent with trees obtained from combined multi-gene, multi-genome datasets. Therefore, the question arose if other fast evolving non-coding regions of the chloroplast large single copy region are similar in sequence variability. We sequenced the group II intron of the *petD* gene (and the upstream intergenic spacer) for a representative selection of 47 angiosperms and 3 gymnosperms. For the most part the sequences could be aligned easily by recognizing length mutations, most of which were simple sequence repeats. Ambiguity in alignment was confined to 4 hotspots (comprising 13-18 % of actual sequence length) which turned out to correspond to stem-loop sections of domains I and IV in the predicted RNA secondary struc-

ture. These findings are similar to *trnL* where high length mutational variability was confined to stem-loop regions in the P8 and P6 loops of the predicted RNA secondary structure. The results underscore that mutational hotspots in introns seem to be linked to certain structural elements (e.g., stem-loops), indicating a more general phylogenetic utility of such regions at deeper taxonomic levels. Phylogenetic analysis of the *petD* dataset (1821 characters, average sequence length 896 bp) using maximum parsimony and maximum likelihood approaches yielded trees with *Amborella* and Nymphaeales first branching. Eumagnoliids as comprising a Magnoliales-Laurales and a Winterales-Piperales-clade were also recovered.

- 321 MAHER, SHELLY D.* and HEMPEL, ALICE L.
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Andromonoecy and self compatibility in the rare endemic *Echeandia texensis* (Liliaceae)

Echeandia texensis Cruden, a rare South Texas endemic, was described in 1999 from only four pre-1950's collections near Brownsville, TX and was believed to be extirpated. Rediscovered in 2001, it is presently known from three populations. A preliminary self-compatibility study in 2001 showed that the plant was self compatible and in absence of pollinators no fruit was set. This study revealed the species to be andromonoecious, but it did not fit typical spatial, temporal, or resource allocation patterns. In 2002, a full greenhouse study was done with plants on loan from the U.S.F.W.S. Complete floral maps were made of fifty-seven inflorescences, and fifty-three showed an unusual andromonoecious pattern again. Over 1700 perfect flowers were hand pollinated (self and cross). In the greenhouse, male and perfect flowers not hand pollinated, did not set fruit. Cross pollinations produced a statistically significant greater percentage of fruits than self pollinations. To test for the effect of pollination frequency, in one subset, all perfect flowers were pollinated daily and remaining plants were pollinated every fourth day. Plants pollinated every fourth day set a statistically significant higher percentage of fruits. However, no significant difference was seen in the total number of fruit produced between these groups. Also effected by pollination treatment was the percent male flowers produced per inflorescence. Plants pollinated daily were male skewed compared to fourth day pollinated plants. The distinctive patterns of male and hermaphrodite flower production in *E. texensis* will be compared to other spatial, temporal, and resource allocation patterns previously described for andromonoecious plants.

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Expression patterns of the SEPALLATA gene *Oryza sativa* MADS1 (OSMADS1) across the Poaceae

MADS box genes play an integral role in determining floral organ identity and shaping morphological evolution. SEPALLATA genes have been shown to interact with other MADS box genes and mediate their expression. Previous studies suggest that expression of the OSMADS1 gene in rice is restricted to the palea, lemma and ovary. In maize, Zmm14 and Zmm8, the OSMADS1 homologs, are expressed in all organs of the upper floret. We studied the molecular evolution and expression of OSMADS1 across diverse species within the Poaceae. The molecular evolution studies recovered no evidence of positive selection within the gene. In situ hybridization expression

studies in *Pennisetum* suggest that OSMADS1 homologs are restricted to the palea, lemma and ovary of the upper floret. In situ hybridization studies in *Avena* suggest that the gene is expressed in the palea, lemma and ovary throughout the developing inflorescence. Phylogenetic reconstruction of the expression patterns suggest that OSMADS1 expression became restricted to the upper floret of the spikelet at the base of the Panicoideae clade, and the less restricted expression pattern reported in maize evolved either within maize or somewhere within the Andropogoneae clade. These studies demonstrate the utility of integrated developmental genetic-phylogenetic approaches to identify the mechanisms of morphological diversification in diverse clades.

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The phylogenetic placement of polyploid *Elymus* species within the Triticeae (Poaceae), based on sequences from a nuclear beta-amylase gene

The phylogenetic placements of tetraploid and hexaploid species of *Elymus* within the Triticeae have been previously analyzed using DNA sequence data from the chloroplast genome and from portions of two nuclear genes. Data from the chloroplast genome, and from genes for granule-bound starch synthase (GBSS1) and phosphoenolpyruvate carboxylase (pepC), indicated that North American allotetraploid species of *Elymus* were derived from *Hordeum* and *Pseudoroegneria*, in agreement with their presumed allotetraploid origin. Chloroplast DNA and GBSS1 data showed that allohexaploid *Elymus repens*, on the other hand, is far more genetically complex than can be explained by its allohexaploid origin alone; it includes as many as five phylogenetically distinct GBSS1 gene copies. In the present study, *Elymus* polyploids are further examined using data from a 1600 bp portion of a nuclear gene encoding beta-amylase (E.C. 3.2.1.2). One copy of this small gene family (corresponding to the "tissue-ubiquitous" form of the enzyme in the Triticeae) has been targeted with copy-specific primers. The phylogeny of tetraploid and hexaploid *Elymus* are examined within the framework of the diploid Triticeae, and the results are interpreted in light of previous studies based on cpDNA, GBSS1, and pepC sequence data.

- 324 MCDADE, L. A.*¹, DANIEL, T. F.², KIEL, C. A.¹ and VOLLESEN, K.³
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Acantheae (Acanthaceae) with an emphasis on relationships among Old World plants with remarkable one-lipped corollas

Acantheae are Acanthaceae s.s. (i.e., plants with seeds borne on retinacula) that share the apomorphy of monothecous anthers while lacking the morphological synapomorphies that mark the remaining plants belonging to Acanthaceae s.s. (e.g., cystoliths, porate pollen). The lineage includes 21 genera with a total of ca. 500 species, and is distributed primarily in the American and African tropics. In our earlier work, we showed this group to be monophyletic and to include two strongly supported lineages: (1) an entirely Old World group of plants marked by the synapomorphy of a one-lipped corolla and (2) a lineage comprising both Old and New World plants that

retain the plesiomorphic two-lipped corolla. Based on now complete sampling at the generic level, we have examined relationships among Old World plants using DNA sequence data from three loci (nr-ITS, cp tmL-F and rps16 intron) and morphological characters. The Malagasy genus *Achyrocalyx*, with two-lipped corollas, is placed with Old World *Stenandriopsis* as the basal members of an otherwise New World clade. Excepting these two genera, all other Old World Acantheae form a lineage marked by one-lipped corollas (i.e., all corolla lobes are oriented ventrally). *Crossandra*, *Crossandrella* and *Streptosiphon* are basal members of this one-lipped clade. The remaining members of this clade share short corolla tubes and exserted stamens with woody filaments as synapomorphies. Above *Sclerochiton*, *Acanthus*, *Acanthopsis*, *Cynarospermum* and *Blepharis* have a unique calyx with fused ventral lobes, sheathing dorsal+ventral lobes and reduced lateral lobes. We further show that *Cynarospermum* is indeed distinct from *Blepharis* and that the mangrove thistle, *Acanthus ilicifolius* is apparently distinct from other *Acanthus* species.

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Phylogeography of a Mesoamerican fruit tree (*Spondias purpurea* L., Anacardiaceae), based on chloroplast sequence data

The origins of cultivated plants have fascinated botanists since the time of Darwin. The vast majority of our cultivated plants originated in one of seven geographically distinct "centers of domestication". Although cultivated species from some centers (e.g., the Fertile Crescent) have been investigated, comparatively little is known about the evolutionary history of many Neotropical crops. This study uses molecular data to explore the origin of a Mesoamerican cultivated species, *Spondias purpurea* L. (known locally as jocote or ciruela). Jocotes are native to the tropical dry forests of Mexico and Central America. They are cultivated throughout Mesoamerica and portions of the Caribbean and South America for their fruits, which are eaten fresh, stewed, boiled and dried. Jocote trees are propagated vegetatively and are found primarily in backyards, in living fences, and in orchards. Wild populations are distinguished from cultivated varieties by their smaller, more acidic, bright red fruits. To investigate the origins of jocotes, we addressed the following questions: 1) Which native species is the closest relative of the jocote? 2) Which wild jocote populations are most closely related to cultivated jocote populations? 3) Where did cultivated jocotes originate, and how many times were they domesticated? Sequences of the chloroplast spacer region *trn G - trn S* were used to reconstruct phylogenetic relationships among jocotes and two sympatric congeners, *S. mombin* and *S. radlkoferi*. To examine jocote origins, over one hundred cultivated and wild individuals were sequenced at this locus. Haplotypes were organized in a minimum spanning tree, which reflects relationships among alleles. A phylogeographic approach was applied to infer the geographic origins of the cultivated jocotes and to approximate the number of domestication events.

326 MISHLER, BRENT D.*¹, ASKAY, SEAN¹, WEBB,
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Phylogenetically structured databases: the future of bioinformatics

Of all types of biological relationships, phylogeny provides the best general purpose classification. The single most important thing you can know about an organism is what it is related to. The centerpiece of future biological databases will be phylogenetic classification, a deeply nested hierarchy of nodes linked to all available structural and functional data at each level. Different data reside at different levels in a tree (e.g., specimen collection data, species range, synapomorphies of a genus), relating hierarchically to other data. Only by organizing databases phylogenetically can these data be related properly, thus allowing efficient retrieval of known data, prediction of unknown traits, and greater understanding of biological processes. We will demonstrate a prototype phylogenetic database for a Californian plant genus (*Lessingia*), that incorporates collection, geographical, morphological, ecological, and molecular data. Examples of queries to this unified database include searching for: the clades that occur in a specified geographic region, the morphological or ecological variation in specimens distal to a chosen node, and the subset of species with a particular combination of character states. This database can be used for such seemingly disparate tasks as herbarium management, geographic inventories, systematic studies, comparative ecology, and identification of unknown plants. We predict that data models explicitly centered on phylogenies will dominate biological databases of the future.

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Phylogenetic relationships of *Brassaiopsis* (Araliaceae) and morphological evolution based on DNA sequence data from two nuclear and two chloroplast regions

Brassaiopsis species are morphologically diverse with wide variation in growth form, including leaf architecture, inflorescence structure, and number of locules in the ovary. However, these species are inferred to be very closely related based on previous analyses of nuclear 5S and ITS data. In an attempt to increase the number of phylogenetically informative characters available for analysis and to detect possible reticulate evolution we sequenced ~ 2000 bp from each of *ndhF* and *trnC-D* chloroplast regions. The four datasets were analyzed both separately and combined using parsimony, maximum likelihood and Bayesian methods. Results of these analyses were largely congruent, supporting several main monophyletic groups, including 1) *B. glomerulata*, *B. hainla*, and *B. aculeata*, 2) *B. variabilis*, *B. grushvitzkyi*, *B. stellata*, *B. phanrangensis*, 3) *B. ciliata* and *B. hispida*, 4) *B. dumicola* and *B. palmipes*. Morphological character states hypothesized to have arisen independently more than once in the genus included palmately compound leaves, palmately lobed leaves, and the 5 locular ovary. Species with high overall morphological similarity, including *B. palmipes*, *B. dumicola*, *B. fatsioides*, *B. mitis*, and *B. ciliata*, were not supported as monophyletic.

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Phylogeny and Pollen Evolution of *Cantua*
(Polemoniaceae subfamily Cobaeoideae): Evi-
dence from Chloroplast and Nuclear DNA

Sequence Data *Cantua*, a small genus in the Polemoniaceae subfamily Cobaeoideae, is morphologically diverse and has several narrow endemics. The genus is distributed at mid-elevations in the Andes Mountains of Peru and Ecuador and is characterized by a shrubby habit, dimorphic leaves, and pantoporate pollen. Our study investigates the relationship among species in the genus *Cantua* using DNA sequences from three regions of the chloroplast genome (*trnT* - *trnL* 5' and *trnL* 3' - *trnF* spacer regions, and partial *ndhF* coding region) and the internal transcribed spacer region of nuclear ribosomal DNA. A phylogeny from our combined analysis suggests that *Cantua* is paraphyletic to *Huthia*, and that *C. coerulea* is sister to *C. querifolia*. There are two strongly supported clades within *Cantua*, a clade of *C. coerulea* and *C. querifolia*, and a second larger clade including the remaining *Cantua* species: *C. bicolor*, *C. buxifolia*, *C. candellilla*, *C. cuzcoensis*, *C. flexuosa*, *C. pyrifolia* and *C. nov. sp.* In addition, support exists for a sister relationship between *C. buxifolia* and a clade containing *C. pyrifolia* and *C. nov. sp.* The sister to *C. buxifolia* / *C. pyrifolia* / *C. nov. sp.* is a clade of *C. bicolor*, *C. candellilla*, *C. cuzcoensis*, and *C. flexuosa*, with support for an internal monophyletic clade containing *C. bicolor*, *C. cuzcoensis*, and *C. flexuosa*. This phylogenetic hypothesis is used to investigate the evolution of pollen morphology within *Cantua* and further examine a potential correlation between style length and pollen size using comparative methodology. A close correlation between these two traits has been hypothesized in the Polemoniaceae but never evaluated within a phylogenetic framework.

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Revisiting phylogenetic relationships in *Illicium*:
biogeographic implications for the position of
New World taxa

Illicium is largely Asian in distribution, but is represented in the New World by six species (*I. floridanum*, *I. mexicanum*, *I. parviflorum*, *I. ekmanii*, *I. hottensis* [undescribed], and *I. cubense*), all of which are very geographically restricted. The genus has traditionally been separated into two sections (Badiana and Cymbostemon) largely on the basis of perianth segment morphology. By this circumscription, *I. floridanum* and *I. mexicanum* were placed in section Badiana with 12 Asian species, while all other New World species were grouped with the remaining Old World species in section Cymbostemon. A recent molecular phylogeny of a limited number of *Illicium* species found very little sequence divergence in the entire internal transcribed spacer (ITS). Although bootstrap support was low within clades, support for separate North American and Asian clades was high (99%), rendering the two sections of *Illicium* paraphyletic. As the Mexican and Antillean species were not included in this study, no conclusions can be drawn regarding the relationships among these species, nor the biogeographic histories that led to their current distributions. Vicariance has long been assumed to be the driving force in this group;

self-incompatibility, clonal reproduction, and ballistic seed dispersal with seeds released near the plant makes long-distance dispersal unlikely. Our objective was to build on the previously published ITS phylogeny by increasing the taxon sampling with particular emphasis on the New World taxa. We have also sequenced additional nuclear and chloroplast regions in attempt to increase both support and resolution for the clades recovered. Preliminary results of this work provide strong support for monophyletic Old and New World clades. The biogeographic implications of relationships within the New World clade will be discussed.

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Phylogeny of Hawaiian and Pacific *Hedyotis*
(Rubiaceae): Fruit Evolution and the Implications
for Conservation and Genomics

Hedyotis is a large, polyphyletic, tropical to subtropical genus of more than 250 species. The genus is represented by 22 species in Hawai'i, twenty of which are endemic to the archipelago and two which are naturalized weeds. Sequence analyses of the ITS and 5S gene regions were used to examine the phylogenetic and biogeographic relationships of Pacific species of *Hedyotis* (Rubiaceae). Results indicate that (1) Hawaiian *Hedyotis* forms a paraphyletic group resulting from a single introduction, (2) there has been a dispersal from Hawai'i to French Polynesia, and (3) the present classification needs modification. Furthermore, the Hawaiian species form two clades, one clade having fleshy fruits and the other producing dry capsules. It is this novel, diverse morphology that is not accompanied by corresponding high levels of genetic diversity which led us to use Hawaiian *Hedyotis* as an organism for investigating fruit evolution. By examining the differences in these closely related species we hope to determine the genes regulating changes in fruit morphology (senescence of exocarp, dehiscence, and abscission layer formation). The genes in island lineages (natural mutants) have value for future plant studies, and this may advance their conservation rather than the more commonly promoted notion that they may conceal hidden cures.

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The use of optimality criteria in DNA sequence
alignment and its application in a new computer
program

The alignment of DNA sequences prior to phylogenetic analysis is of critical importance to the final result, but is often given very little attention. Different sequence alignments can, and often do, result in different phylogenetic trees. Artifacts produced by available alignment algorithms frequently require workers to manually adjust the alignment "by eye" prior to phylogenetic analysis. Unfortunately this makes it difficult, if not impossible, to exactly reconstruct published analyses and makes adding new sequence data difficult. Commonly used alignment algorithms begin by calculating a guide tree based upon pairwise distance estimates. Each sequence is then aligned to every other sequence in a pairwise manner following an input order determined by the guide tree. This approach is not guaranteed to find the optimal pairwise alignment, nor are multiple optimal solutions considered. Arbitrary choices among equally optimal paths are made independently for each clade of the guide tree, and

once made each pairwise alignment is fixed. These arbitrary decisions coupled with other errors and superfluous gaps are propagated throughout the alignment. We will present a new method for calculating an overall alignment cost (and therefore global optimality) that does not require the use of arbitrarily assigned change parameters (e.g. gap costs). This allows alternative alignments (and alignment methods) to be compared unambiguously. In addition we will demonstrate a new global multiple alignment procedure that does not use a guide tree, considers multiple optimal solutions, and is computationally much faster than existing alignment algorithms.

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Phylogenetic analysis of Kielmeyeroideae (Clusiaceae) based on ITS sequences

Clusiaceae are a family of approximately 1000 species with a pan-tropical distribution. Based on a morphological cladistic analysis, the family has been divided into three subfamilies: Hypericoideae, Clusioideae, and Kielmeyeroideae. Kielmeyeroideae are divided into two tribes: Calophylleae, a large, pan-tropical tribe (ca. 450 spp), and Endodesmieae, a small, tropical African group (comprising the two monotypic genera *Endodesmia* and *Lebrunia*) whose placement within the subfamily has been uncertain. Based on fruit characters, Endodesmieae are similar to Calophylleae; however, vegetatively, they are similar to Clusioideae. A previous family-level study based on *rbcL* sequences confirmed the monophyly of the three traditional subfamilies except that *Clusiella*, traditionally placed in Clusioideae, appeared in Kielmeyeroideae. Internal support for relationships within Kielmeyeroideae was weak, leaving it unclear as to which genera *Clusiella* is most closely related. Species of Endodesmieae were not included in the *rbcL* study. The goal of the present study is to determine the generic relationships within Kielmeyeroideae based on the phylogenetic analysis of ITS sequence data and morphological characters. We have included several species of most genera of Calophylleae, as well as *Clusiella* and the enigmatic *Endodesmia* in our analysis. *Hypericum*, *Clusia*, and *Garcinia* were included as outgroup taxa. The resulting relationships were correlated with biogeography and we also inferred the evolution of key morphological characters such as the presence of latex glands or canals, resin production in the flowers, and fruit type.

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Hybrid origin of Stephanandra (Neillieae: Rosaceae) inferred from DNA sequences

The genus *Stephanandra*, a relatively small group in Rosaceae, consists of only three species distributed in eastern Asia. Species of *Stephanandra* can be distinguished from other Rosaceae by their paniculate inflorescence of small flowers with cupulate hypanthia and by having copious endosperm. Recent molecular phylogenetic analyses of the Rosaceae have suggested that *Stephanandra* and *Neillia* together form a strongly supported monophyletic group and that *Physocarpus* is the sister to the *Stephanandra/Neillia* clade. In order to reconstruct phylogenetic relationships among the species of the two genera, we determined nucleotide sequences of the ITS and ETS

regions of nuclear ribosomal DNA, the second intron of a floral homeotic gene, *LEAFY*, and several regions of chloroplast DNA from all three species of *Stephanandra* as well as seven of nine species of *Neillia*. While relationships among species of *Stephanandra* and *Neillia* are poorly resolved by the rDNA data, *Stephanandra* is supported as monophyletic and is nested within *Neillia* in both *LEAFY* and cpDNA trees. *LEAFY* and cpDNA data, however, strongly conflicted with each other with respect to the position of *Stephanandra*: *LEAFY* trees placed *Stephanandra* as sister to the *N. affinis/N. thrysiflora* clade whereas cpDNA data suggested that *Stephanandra* is sister to *N. uekii*. Both gene trees, however, are nearly identical to each other when *Stephanandra* is excluded. Although gene duplication/extinction and lineage sorting events cannot be ruled out as possible causes of the strong conflict between the two data, the most plausible explanation for the potential source of gene tree conflict between our nuclear gene (*LEAFY*) trees and maternally inherited (cpDNA) gene trees is reticulate evolution of *Stephanandra*; i.e., *Stephanandra* might be derived via hybridization between *N. uekii* and the stem lineage of the *N. affinis/N. thrysiflora* clade.

334 PADGETT, JAMES* and MURRELL, ZACK

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Phylogeographical, ecological, micro-morphological, and molecular analysis of the species in the *Asarum heterophyllum* complex

Blomquist and Gaddy both recognized a group of eight *Asarum* (*Hexastylis*; wild gingers) that they referred to as the Virginica Group. This group was further subdivided into the three Subgroups: Virginica, Shuttleworthii, and Heterophylla. Considerable morphological overlap occurs in the Heterophylla subgroup. Kelly has recognized *Hexastylis* as a subgenus within *Asarum*, along with *Heterotropa*, an Asian species of wild ginger. *Asarum naniflorum* is a Federally Threatened species in the Heterophylla subgroup. The plant is known from a ten county area in the western piedmont of North and South Carolina. The range of *A. naniflorum* is restricted by soil type, biogeography, and ecology. We have analyzed the morphology, micro-morphology, soils, pollen, and molecular aspects of the Heterophylla complex. Using Scanning Electron Microscopy (SEM), we have found pollen characters that distinguish *A. naniflorum* from other members within the subgroup. We have also used Inter Simple Sequence Repeat regions (ISSR) to examine the genetic structure within and between species in this complex. Our results indicate that *A. naniflorum* is a well-defined species, however, *A. minus* and *A. heterophyllum* exhibit considerable overlap that make species circumscription difficult. Our intraspecific analysis of *A. naniflorum* was based on soils, ecology, and ISSR, where we compared populations in the Broad-Paolet, Catawba, and Yadkin River drainages in the Piedmont of North and South Carolina. This analysis provides information that can be used in future conservation and management efforts for *A. naniflorum*.

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Classification and biogeography of New World grasses (Poaceae)

After 13 years of collaborative research between North and South American agrostologists, the first comprehensive survey of the New World grasses is available on-line at <http://mobot.mobot.org/W3T/Search/nwgc.html>. The New World grasses include 4302 species

(3840 native and 462 introduced) in 377 genera (291 native, 86 introduced). As currently circumscribed, the grasses are represented by 10 subfamilies: Anomochlooideae (4 native spp.), Aristidoideae (126 native spp.), Arundinoideae (3 spp., 2 native), Bambusoideae (530 spp., 458 native), Chloridoideae (676 spp., 606 native), Danthonioideae (54 spp., 53 native), Ehrhartoideae (34 spp., 28 native), Panicoideae (1357 spp., 1246 native), Pharoideae (7 native spp.), and Pooideae (1511 spp., 1310 native). South America consists of 2807 species, North America (including Mexico) consists of 2003 species, and Central America consists of 1042 species. The 12 largest genera, in descending order, include: *Paspalum* (284 native spp.), *Festuca* (205 native spp.), *Panicum* (174 native spp.), *Poa* (173 native spp.), *Muhlenbergia* (147 native spp.), *Chusquea* (133 native spp.), *Calamagrostis* (132 native spp.), *Aristida* (126 native spp.), *Nassella* (116 native spp.), *Eragrostis* (86 native spp.), *Digitaria* (85 native spp.), and *Axonopus* (83 native spp.). The Bambusoideae are most diverse in Brazil (212 native spp.); the Pooideae are most diverse in Argentina (474 native spp.) and USA (411 native spp.); the Chloridoideae are most diverse in Mexico (318 native spp.) and USA (257 native spp.); and the Panicoideae are most diverse in Brazil (688 native spp.), Mexico (423 native spp.), and Venezuela (373 native spp.).

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Species limits and phylogenetic relationships in *Satyria* sensu stricto (Vaccinieae, Ericaceae)

Satyria sensu stricto, a strongly supported monophyletic group of Neotropical blueberries is a member of the Andean clade of tribe Vaccinieae (Ericaceae). Species from *Satyria* s.s. are found from southern Mexico south to Peru and east to French Guiana and the center of diversity is Colombia. Molecular data show that *Satyria* s.s. is sister to *Thibaudia costaricensis* from Panama and Costa Rica and is closely related to *Cavendishia*. Molecular phylogenetic analyses also show that species of *Satyria* from Central America form a clade but resolution and support for relationships within *Satyria* are low. The goal of the current study is to evaluate a suite of morphological and anatomical characters across the geographic and morphological range of *Satyria*, in order to identify characters that will help define species boundaries in the clade and provide morphological characters to help increase resolution and support within *Satyria* s.s. Results show that *Satyria* s.s. includes species that have equal connate filaments and alternately unequal anthers, the longer anthers with divergent, rigid and often ornamented tubules. Results also suggest that characters traditionally used to define species limits in *Satyria*, like corolla length and leaf size, vary continuously and are not useful for delimiting taxa and are uninformative for cladistic analyses. A morphological and combined molecular and morphological cladistic analysis of the clade clarifies the phylogenetic utility of traditional characters such as stamen morphology and corolla shape in *Satyria*.

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Documenting the Decline in Plant Collecting in the United States: Implications for Systematic and Floristic Research

Collections of plant specimens are the basic infrastructure for all studies of plant diversity, but there is concern that plant collecting is in decline. We acquired collection data from a diverse sample of 71 herbaria to test whether there is a decrease in rates of local collecting in the United States. The recorded data were the decade of collection for all specimens of nine exemplar genera from the local region of the herbarium. The results of all analyses suggested that local collecting is in decline. We found that the temporal pattern of collecting varied considerably from herbarium to herbarium, but that more herbaria showed a decreasing trend than an increasing trend. The total accumulation of specimens is in decline and only 21% of the sampled herbaria reached their peaks in local collecting activity in the last 20 yr. More than two thirds of the herbaria acquired fewer locally-collected specimens in the last two decades than in the prior two. These trends were consistent over all size classes of herbaria and over herbaria from all regions, though they were less severe in the Mountain region herbaria. Tests for bias indicated that our sample of herbaria was more active than typical, thus our conclusions should be considered a conservative estimate. Continued collecting is important because there are important deficiencies in our knowledge of the U.S. flora and it is constantly changing. To be certain that support for local collecting can be found, systematists need to demonstrate the importance of collecting and exploit existing and new funding sources.

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Phylogeny of early-diverging leptosporangiate ferns based on morphology and multiple genes: rbcL, atpB, rps4, and 18S

Despite considerable progress in our understanding of leptosporangiate fern relationships, a rigorous and comprehensive analysis of the early-diverging lineages is lacking. The general view of these basal lineages has been that they are very old and isolated remnants from Paleozoic and Mesozoic diversification events. To discover a best estimate of phylogenetic relationships for basal leptosporangiate ferns we sequenced more than 5000 bp from the chloroplast (*rbcL*, *atpB*, *rps4*) and the nuclear (18S rDNA) genomes for 75 taxa. In addition, morphological characters were completely revised from earlier studies for a congruent data set. Maximum parsimony, maximum likelihood, and Bayesian approaches were applied to infer the phylogeny. Our results include: 1) the confirmation that Osmundaceae is the most basal leptosporangiate family, 2) filmy ferns (Hymenophyllaceae), a large and diverse basal group of mostly epiphytic ferns, form the subsequent most deeply-branching lineage, 3)

gleichenioid and dipteroid ferns together with *Matonia* are a monophyletic basal group and not, as was once thought, a paraphyletic grade of basal ferns, and 4) we confirm a sister relationship between tree ferns and the more derived "polypodiaceous" ferns, and place heterosporous ferns (Marsileaceae and Salviniaceae) as sister to this clade; relationships among these three groups were equivocal in earlier studies. Our increased taxon sampling has resulted in a robust overall framework for leptosporangiate ferns that provides strong support for the relationships of early-diverging lineages. This enables us to work towards understanding patterns of character evolution that gave rise to the Cretaceous radiation and diversification of "polypodiaceous ferns".

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The evolution and expression of *rbcL* in
holoparasitic sister genera *Harveya* Hook. and
Hyobanche L. (Orobanchaceae): expression of
the large subunit of Rubisco despite the pres-
ence of pseudogenes

Holoparasitic plants obtain water, nutrients, and all photosynthates from host plants, resulting in the anatomical and physiological reduction of photosynthetic structures and processes. In many holoparasitic plants, reduction of the plastid genome is well documented. Once released from the functional constraint of photosynthesis, photosynthesis-related genes undergo rapid mutation resulting in amino acid substitution, pseudogene formation and gene deletion. In the holoparasitic sister genera, *Harveya* and *Hyobanche*, the gene encoding the large subunit of Rubisco, *rbcL*, has followed alternate paths of evolution. *Harveya* maintains an *rbcL* open reading frame and comparison of synonymous and non-synonymous rates of substitution reveal that *rbcL* is evolving under purifying selection in this lineage. *Hyobanche* demonstrates pseudogene formation at the *rbcL* locus; rate analysis indicates evolution free from functional constraint. However, the large subunit of Rubisco occurs in tissues of both genera. This indicates that *rbcL* may exist in multiple copies in *Hyobanche*, at least one of which codes for a functional gene. Other copies may have been translocated to other cellular compartments, after which function was restored, or multiple copies may exist within the plastid, within a single plastid genome or as heteroplasmic copies.

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Morphology, diversity, and phylogeny of *Paloue*,
Elizabetha, and related caesalpinioid legumes
from northeastern South America

Most phylogenetic analyses of species level relationships in the Leguminosae have focused on the subfamilies Mimosoideae and Papilionoideae and only recently have efforts been directed at groups within the subfamily Caesalpinoideae. Most phylogenetic work within the subfamily concentrates on higher level relationships among the tribes, subtribes, and genus groups. Over half of the genera of Caesalpinoideae are grouped in the large Detarieae s.l. clade. Within this clade, *Dicymbe* (20 spp.), *Heterostemon* (7 spp.), *Elizabetha* (10 spp.), *Paloue* (4 spp.), and *Paloveopsis* (1 sp.) are endemic to north-

eastern South America and the latter four genera are thought to be closely related. This study uses morphological and anatomical characters from vegetative and reproductive structures to explore generic limits and relationships in *Dicymbe*, *Heterostemon*, *Elizabetha*, *Paloue*, and *Paloveopsis*. The morphological data set includes 48 species, of which six are outgroup taxa, and over 110 morphological characters. Preliminary results support the monophyly of *Dicymbe*, *Heterostemon*, *Elizabetha*, and *Paloue*, and also support the recognition of *Paloveopsis* as a distinct monospecific genus. Like many other Caesalpinoideae, these members of Detarieae s.l. are characterized by morphological reduction series, especially in number of floral parts. Patterns of floral evolution implied in these results will be discussed in a phylogenetic context.

341 ROALSON, ERIC H.*¹, SKOG, LAURENCE E.²,

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Generic boundaries in the Gloxinieae
(Gesneriaceae): tracking diversification and
convergence in floral form with nuclear, chloro-
plast, and morphological cladistic data sets

The Gloxinieae (Gesneriaceae) tribe includes 22 genera and approximately 290 species, as currently circumscribed. Recent molecular phylogenetic studies have suggested that some members of the tribe (the genera *Sinningia*, *Palavana*, and *Vanhouwteia*) are not closely related to the rest of the tribe. Additionally, other species (i.e., *Gloxinia sarmentiana*) appear to not belong to the Gloxinieae. The Gloxinieae have traditionally been troublesome, both in circumscription of generic boundaries and membership in tribal classifications. This is in part due to extreme variation in floral form in this group. In order to address questions of generic boundaries, tribal classification, the evolution of floral form, and biogeographic distribution patterns, we have analyzed morphological cladistic, nuclear ribosomal ITS sequence, and chloroplast DNA *trnL-F* spacer sequence data sets with maximum parsimony and maximum likelihood. These data sets support a number of findings. These include recognition of the genus *Gloxinia*, as currently circumscribed, as polyphyletic, that the genus *Capanea* is derived from within *Kohleria*, and that the tribe may have originated in Central America and the Caribbean, with later dispersal to South America.

342 ROALSON, ERIC H.* and KU, MAURICE S. B.

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Phylogenetic relationships in *Eleocharis*
(Cyperaceae): Evolutionary origins of the C4
photosynthetic pathway and patterns of morpho-
logical innovation associated with adaptation to
specialized habitats

Eleocharis (Cyperaceae) is a well demarcated genus and includes approximately 200 species with a world-wide distribution. Central to the understanding of the diversification of organisms is understanding the evolution of critical physiological processes, the interaction of physiological processes and the environment, and the evolution of

structure and form. *Eleocharis* is of particular interest for studying the evolution of photosynthetic pathway and morphological form for several reasons. In terms of photosynthetic pathway evolution, the Cyperaceae represents the second largest diversification of the C4 pathway. Additionally, at least one species of *Eleocharis*, *E. vivipara*, is known to be capable of changing its photosynthetic pathway and anatomical type under different growing conditions. Here we explore the phylogenetic pattern of photosynthetic pathway in *Eleocharis* using a large nrDNA internal transcribed spacer region (ITS) data set and preliminary results from other nuclear gene families. Additionally we will explore the phylogenetic patterns of morphological innovation associated with adaptation to specialized habitats. There appear to be at least two separate origins of C4 photosynthesis in the genus.

343 SANCHEZ-DEL PINO, IVONNE^{*1}, FLORES OLVERA,HILDA² and MOTLEY, TIMOTHY J.¹¹Lewis B. & Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx NY 10458 USA; ²Instituto de Biología, Herbario Nacional, UNAM, A.P. 04510, Mexico D.F MEXICO

Preliminary Cladistic Analysis of the Subtribe Froelichiinae (Amaranthaceae) based on Molecular and Morphological data

Subtribe Froelichiinae (Subfamily Gomphrenoideae) in Amaranthaceae has not been investigated phylogenetically based on both molecular and morphological data. This study is to test the monophyly and resolve generic delimitation in the subtribe Froelichiinae employing data from the chloroplast *trnL-trnF* intron and spacer, the nuclear ribosomal ITS region, gross morphology and microscopic characters (gynoecium, androecium, trichomes, and pollen). Seven genera and approximately 106 species have been included in the subtribe Froelichiinae. *Tidestromia* is the only genus that all species facultatively occur in both saline and gypsum environments and many are endemic in Chihuahuan Desert. Our goal is to determine the phylogenetic relationships of the genus *Tidestromia* in the subtribe Froelichiinae and the evolutionary significance of some characters for adaptation to saline and gypsum soils. Preliminary phylogenetic analyses of morphological characters in *Tidestromia* genus have revealed an unresolved phylogenetic clade among the perennial species. DNA sequences of the *Tidestromia* ITS region have been studied to provide more resolution at the species level and to verify the monophyly of *Tidestromia*. An extensive sampling of the subtribe Froelichiinae is planned for future studies to better understand the role that gypsum and saline soils are playing in the evolution of the Amaranthaceae.

344 SCHARASCHKIN, TANYA

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Biogeographic history and character evolution of *Anaxagorea* (Annonaceae) based on phylogenetic analyses of morphological characters and non-coding chloroplast regions

The Annonaceae are a pantropical family in which *Anaxagorea* is the sister group to the rest of the family based on phylogenetic studies of both morphological characters and molecular evidence. Morphological characters suggesting a basal position for the genus include laminar stamens, inner staminodes, and an adaxial plate of vascular tissue in the midrib and petioles. Within the Annonaceae, *Anaxagorea* is the only genus with a disjunct distribution in South

and Central America and Southeast Asia. Earlier arguments on the biogeographic history Annonaceae had led to a hypothesis for a Laurasian origin for this genus based on comparisons with similar biogeographical distributions in other groups. A detailed phylogenetic study was conducted based on morphology and molecular sequences from the *atpB-rbcL* spacer, *psbA-trnH* spacer, *trnL-trnF* spacer and the *trnL* intron. Outgroups selected represent major clades in Annonaceae and other Magnoliales. Molecular analyses alone do not support the monophyly of the Asian species, but the morphological and combined molecular and morphological analyses do. All analyses place most of the Central American species in a clade, but none of them support an Asian-Central American clade. South American species form a basal grade in all analyses, thereby refuting the hypothesis of a Laurasian origin for the genus and indicating a Gondwanan origin instead, with separate dispersals from South America to Central America and to Asia. The distribution of several characters confirm that the states seen in *Anaxagorea* and shared with the outgroups to Annonaceae are primitively retained, e.g. the presence of an adaxial plate in the midrib.

345 SCHENK, JOHN J.* and LISTON, AARON

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Progenitor-derivative speciation and hybridization in the serpentine endemic

Synthyris cordata (Scrophulariaceae s.l.) Morphological and molecular analyses were conducted with *Synthyris cordata* (A. Gray) A. Heller and *S. reniformis* (Dougl.) Benth. to investigate the relationship of the two taxa. The presence of unicellular hairs in the corolla tube, and lower leaf length/width ratios consistently distinguishes *S. cordata* from *S. reniformis*. *Synthyris reniformis* is a common widespread species from southern Washington to northern California in both the Coast Range Mountains and the Cascade Mountains. *Synthyris cordata* has a smaller range, restricted to serpentine soil in southern Oregon and northern California. We examined chloroplast haplotypes (*trnT-trnL* spacer, *trnL-trnF* spacer, *trnK* intron) and nrDNA internal transcribed spacer (ITS) sequence variations in seven populations of *S. cordata* and seventeen populations of *S. reniformis* throughout their respective ranges. The two taxa have divergent ITS sequences and considerable cpDNA variation. A cpDNA haplotype tree infers *S. reniformis* as the progenitor of *S. cordata*. This is supported by the greater amount of cpDNA diversity found in *S. reniformis*. Furthermore, a population was found that has an intermediate cpDNA haplotype. This population may represent a direct ancestor of *S. cordata*. In addition, another population in northern California contained both nrDNA ITS sequences, apparently a result of secondary contact and hybridization between *S. cordata* and *S. reniformis*.

346 SCHNEIDER, HARALD^{*1}, CRANFILL, RAY², SCHUETTPELZ, ERIC⁴, MAGALLON, SUSANA³ and PRYER, KATHLEEN⁴

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Derived ferns diversified in the shadow of angiosperms: evidence from the fossil record, phylogenetic patterns, and divergence time estimates

The rise of angiosperms during the Cretaceous was part of a major biotic turnover event that witnessed a remarkable drop in the diversity and abundance of many lineages of free-sporing plants. This observation has led to the generalized hypothesis that free-sporing vascular plants were replaced by angiosperms during the Cretaceous. However, a rigorous examination of fossil evidence indicates there was in fact a diversification of derived (polypodiaceous) ferns in the Tertiary. This supports a scenario whereby angiosperms and polypodiaceous ferns diversified in parallel, rather than the replacement of one group by the other. Here we investigate the diversification patterns of polypodiaceous ferns and angiosperms using the fossil record, phylogenetic patterns, and divergence time estimates based on DNA sequence data. Our results indicate an origin of polypodiaceous ferns in the Upper Jurassic to Lower Cretaceous, two major diversification events in the Upper Cretaceous, and subsequent diversifications in the Paleocene and Eocene. Strikingly parallel diversification events are also observed within angiosperms during these same time periods. These shared patterns suggest that the polypodiaceous fern radiations were either caused by the diversification of angiosperms or that both these vascular plant lineages were responding to similar periodic abiotic stresses, such as global warming and cooling. Heterosporous ferns are a third lineage to have undergone diversification during the Cretaceous, coinciding with a decline in heterosporous lycophyte lineages that dominated fresh-water habitats in the Triassic and Jurassic.

347 SCHUETTPELZ, ERIC^{*} and PRYER, KAHLEEN M.
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Characterizing molecular rate heterogeneity between two major lineages of filmy ferns (Hymenophyllaceae)

The Hymenophyllaceae, with over 600 described species, is the largest family of basal leptosporangiate ferns. Recent phylogenetic analyses of *rbcL* data support the division of the family into two major lineages, *Trichomanes* and *Hymenophyllum*, and reveal striking differences in the rate of molecular evolution between these two groups. Molecular rate heterogeneity has been observed in many green plant taxa, and several explanations have been invoked, including generation time, speciation rate, and ultraviolet exposure. These explanations, however, are not readily applicable to the Hymenophyllaceae. To discover the reasons underlying the observed molecular rate heterogeneity in filmy ferns, it is first necessary to fully characterize the rate differences. Through relative-rate comparisons and reconstructions of ancestral rates of molecular evolution, it is possible to determine which of the two lineages experienced the change in rate, and where on the phylogeny this rate change occurred. The results suggest that a deceleration of molecular evolution occurred along the internode leading to *Hymenophyllum*, and

that the rates *within* the two major groups of filmy ferns are similar. Therefore, the short branches observed in *Hymenophyllum* are likely the result of a more recent radiation.

348 SHAW, JOEY^{*}, LICKEY, EDGAR, BECK, JOHN, FARMER, SUSAN, LIU, WUSHENG, MILLER, JEREMY, SIRIPUN, KUNSIRI CHAW, WINDER, CHARLES, SCHILLING, EDWARD and SMALL, RANDALL
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Phylogenetic utility of fifteen noncoding cpDNA regions among major lineages of seed plants

Chloroplast DNA sequences are a primary source of data for plant molecular systematic studies. A few key papers have provided the molecular systematics community with universal noncoding cpDNA primer pairs that have dominated the field. Regions like the *trnL* intron, *trnL-trnF* spacer, and *trnK* intron/*matK* gene have provided adequate information to resolve species relationships in some taxa, but may provide incomplete resolution in other taxa. To obtain additional data to provide better phylogenetic resolution, sequences from these widely used regions are often coupled with other sequence data, cpDNA or otherwise. The lack of resolution often observed may be due, at least in part, to the use of an inappropriate marker. Choosing the appropriate cpDNA region for phylogenetic investigation, however, is often difficult because of the relative paucity of information about the tempo of evolutionary rates among different noncoding cpDNA regions in different taxa. The goal of this investigation is to determine if there is any predictable rate heterogeneity among fifteen non-coding cpDNA regions identified as phylogenetically useful at interspecific and even intraspecific levels. These include both intergenic spacers and introns within the following regions: *trnH - psbA, psbA - trnK, trnK* intron inclusive of *matK, rps16* intron, *trnS - trnG, rpoB - trnC, trnC - trnD, trnD - trnT, trnS - trnM, psaA - trnS, trnT - trnL, trnL - trnF, rpl20 - 5rpS12, psbB - psbH, and rpl16* intron. To test for rate heterogeneity, three species from each of eight groups representing different phylogenetic lineages of phanerogams are included in our survey: *Taxodium* (Cupressaceae; Gnynnosperm), *Magnolia* (Magnoliaceae; Magnoliid), *Minuartia* (Caryophyllaceae; Caryophyllid), *Gratiola* (Scrophulariaceae; Euasterid I), *Eupatorium* (Asteraceae; Euasterid II), *Prunus* (Rosaceae; Eurosids I), *Hibiscus* (Malvaceae; Eurosids II), and *Trillium* (Trilliaceae; Monocot).

349 SIMMONS, MARK P.^{*1} and MIYA, MASAKI²

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Efficiently Resolving the Basal Clades of a Phylogenetic Tree Using Bayesian and Parsimony Approaches

Many phylogenetic analyses that include numerous terminals but few genes show high resolution and branch support for relatively recently diverged clades, but lack of resolution and/or support for "basal" clades of the tree. The various benefits of increased taxon and character sampling have been widely discussed in the literature, albeit primarily based on simulations rather than empirical data. In this study, we used a well-sampled gene-tree analysis (based on 100 mitochondrial genomes of higher teleost fishes) to test empirically the efficiency of different methods of data sampling and phylogenetic inference to "correctly" resolve the basal clades of a tree. By itself,

increased character sampling was an inefficient method by which to decrease the likelihood of "incorrect" resolution for parsimony analyses. Although increased taxon sampling was a powerful approach to alleviate incorrect resolution for parsimony analyses, it had the general effect of increasing the number of, and support for, incorrectly resolved clades in the Bayesian analyses. For both the parsimony and Bayesian analyses, increased taxon sampling, by itself, was insufficient to help resolve the basal clades, making this sampling strategy ineffective for that purpose. Our results suggest that the most efficient of the seven approaches considered to resolve basal clades when adding nucleotides to a dataset that consists of a single gene sampled for a small, but representative, number of taxa, is to increase character sampling and analyze the characters using the Bayesian method.

350 SIMMONS, MARK P.*¹, CARR, TIMOTHY G.² and O'NEILL, KEVIN³

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Relative character-state space, amount of potential phylogenetic information, and heterogeneity of nucleotide and amino acid characters

We quantified three of the six factors that determine whether nucleotide or amino acid characters should be preferred for phylogenetic inference based on a broad selection of matrices of protein-coding loci from a diverse array of clades and genomes. First, we quantified the difference in character-state space between nucleotide and amino acid characters. Second, we quantified the loss of potential phylogenetic signal from silent substitutions when amino acid characters are used. Third, we quantified the relative heterogeneity of nucleotide and amino acid characters, and determined how common convergent (rather than unique) shifts in nucleotide and amino acid composition are by measuring heterogeneity, as determined using the disparity index, in a phylogenetic context. The advantage of greater potential phylogenetic signal for nucleotide characters, and the greater character-state space and lower heterogeneity of amino acid characters, was confirmed. Although the greater potential phylogenetic signal for nucleotide characters was found to be enormous (average increase of 4.4 times), the greater character-state space for amino acid characters was considerably less impressive (average increase of 50.4%). The disparity in amount of possible synapomorphy is more pronounced at lower average genetic distances between terminals, particularly below average genetic distances of 0.4. Our results indicate that this advantage of amino acid characters becomes more apparent with increasing average genetic distance among terminals, only becoming pronounced with an average genetic distance between terminals of 0.3 or above. Given the ability of increased terminal sampling to better-utilize the greater potential phylogenetic signal of nucleotide characters and decrease the potential for artifacts to occur caused by heterogeneous nucleotide composition among terminals, we suggest that increased taxon sampling be performed whenever possible rather than only analyzing the amino acid characters.

351 SIMPSON, BERYL*¹, TATE, JENNIFER² and WEEKS, ANDREA¹

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Phylogeny and biogeography of *Hoffmannseggia* (Leguminosae: Caesalpinoideae): A tale of many travels

Described and later dismissed, adopted and then abandoned, *Hoffmannseggia* can now take its place as a natural clade within the *Caesalpinia* generic group (Caesalpinoideae). The genus, consisting of 21 species, has an amphitropical distribution with almost half of the species in the southwestern United States and Mexico and the remaining species in west-central South America. We have shown that two unusual monotypic South American genera are its closest relatives, not *Caesalpinia* as has been assumed in the past. Our data also show that the South African species formerly assigned to *Hoffmannseggia* belong to *Pomaria*, an unrelated genus of the *Caesalpinia* group. Phylogenetic study of all *Hoffmannseggia* species using sequence data from nuclear ITS, chloroplast *trnL*-*trnF* intron and spacer regions, and *rbcL* has revealed previously unsuspected patterns of evolution and biogeography within the genus. The genus consists of two major clades, one containing all the suffrutescent species and the other consisting of herbaceous perennials. Within the suffrutescent clade the data show that there were two exchanges between North and South America. In the herbaceous clade, based on parsimony analysis, a high Andean species is sister to the remaining 14 species. The species-rich part of this clade also contains subclades that display North America-South America disjunctions. Consequently in the genus as a whole, there was not a single colonization from South America to North America followed by a radiation in North America but rather a series of long distance dispersals between the two continents. An analysis of morphological characters shows that they are congruent with the molecular results and that previous confusion about the circumscription of the genus and its composition was caused by undue emphasis on a few homoplastic characters.

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Variation of GBSSI and rpL16 in the Malacothamnus Alliance (Malvaceae)

The granule bound starch synthase (GBSSI) gene of the nuclear genome and the rpl 16 region of the chloroplast genome are explored for phylogenetic utility in the Malacothamnus Alliance. The Malacothamnus Alliance consists of three genera, *Iliamna*, *Malacothamnus*, and *Phymosia*. Previous experiments with the internal transcribed spacer (ITS) region and the chloroplast *trnL*-F region yielded inconclusive and conflicting results. The ITS region resulted in a weakly supported tree with *Iliamna* being polyphyletic and *I. latibracteata* and *I. bakeri* in a separate clade. The *trnL*-F tree had fewer statistically supported clades than the ITS tree and had *I. corei* and *I. remota* in a clade with *Phymosia*. The combined analysis reflected the ITS-based phylogeny with an increase in bootstrap support for all clades. Currently, the GBSSI region is being explored and has been detected as three separate loci in members of the Malacothamnus Alliance. There is sufficient variation to provide statistical support of both basal and terminal branches. The genus *Iliamna* remains polyphyletic in a monophyletic Malacothamnus Alliance. The rpL16 region will be explored to show an alternative phylogeny. With

the addition of these two regions, it is hoped that the resulting phylogenies will illustrate the evolutionary and biogeographic histories of the alliance.

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Phylogeny of Hibiscus sect. Furcaria (Malvaceae) based on nuclear-encoded alcohol dehydrogenase sequences Hibiscus sect.

Furcaria (Malvaceae) is a circumtropical taxon with 200+ species. While the section is species-rich, only ten diploid species are known, nine from Africa, and one from Central and South America. The remaining species belong to one of several allopolyploid lineages including at least five tetraploid lineages, one hexaploid lineage, four octaploid lineages, and one decaploid lineage. In contrast to the relatively narrow distribution of the diploid species, the polyploid lineages are widely geographically distributed with centers of diversity in Africa, Australia, India, Central/South America and the Pacific Islands. To unravel the phylogenetic relationships among the species of *Hibiscus* sect. *Furcaria* and to identify the origins of the allopolyploid species we generated DNA sequences from two nuclear-encoded alcohol dehydrogenase (*Adh*) genes. The phylogenetic relationships among the diploid species inferred from the two *Adh* data sets are generally congruent, and provide complete and robust resolution of species relationships. In addition, by cloning and sequencing homoeologous *Adh* loci from representative allopolyploid species we were able to phylogenetically identify the diploid progenitors. The biogeographic implications of the data and the distribution of morphological characters on the phylogeny will be discussed.

354 SPOONER, DAVID*¹, PERALTA, IRIS² and KNAPP, SANDRA³

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AFLP phylogeny of wild tomatoes (*Solanum* L. section *Lycopersicon* [Mill.] Wetst. subsection *Lycopersicon*)

Wild tomatoes (*Solanum* section *Lycopersicon* subsection *Lycopersicon*) are native to western South America. Different classifications have been based on morphological or biological species concepts. Molecular data from mitochondrial, nuclear, and chloroplast DNA restriction fragment length polymorphisms (RFLP), nuclear microsatellites, isozymes, and gene sequences of internal transcribed spacers of nuclear ribosomal DNA (ITS: multiple-copy), the single-copy nuclear encoded Granule-bound Starch Synthase gene (GBSSI or waxy); and morphology, have been used to examine hypotheses of species relationships. This study is a companion study to the previous waxy gene sequence study and to the morphological study of relationships of all ten wild tomato species (including the recently described *S. galapagense*), with a concentration on the most widespread and variable species *S. peruvianum*. These new AFLP data are largely concordant with the waxy and morphological data and support the species outlined in the latest treatment by C. Rick, but demonstrate the distinct nature of the northern and southern Pe-

ruvian populations of *S. peruvianum*, and suggest that they may be distinct at the species level. *Solanum ochranthum* is supported as sister to wild tomatoes, and *S. habrochaites* and *S. pennellii* as basal in the tomato clade.

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Molecular systematics of tribe Myodocarpeae (Araliaceae s.l.)

Three of every four plants in New Caledonia are endemic. New Caledonia ranks third in the world in species density and is home to some of the most ancient lineages of flowering plants. This study focuses on the systematics of Myodocarpeae (Araliaceae s. l.), a tribe that contains 19 taxa, 17 of which are endemic to New Caledonia. The goals of this study were (1) to resolve further the phylogenetic relationships in Myodocarpeae, (2) to suggest possible progenitors of putative hybrids, and (3) to explore the biogeography of the tribe. Sequence data were obtained from the external transcribed spacer (ETS), the internal transcribed spacer (ITS), and the 5S non-transcribed spacer (5S-NTS) regions of nuclear ribosomal DNA, and the intron and intergenic spacer from the *trnL-trnF* genes of the chloroplast genome. Parsimony analyses support the monophyly of Myodocarpeae. *Pseudosciadium* is derived from within *Delarbrea*, rendering the latter paraphyletic. The tribe can be divided into two well-supported clades, *Delarbrea* + *Pseudosciadium* and *Myodocarpus*, supporting hypotheses from previous studies based on morphological and molecular data. All Myodocarpeae have pinnately-compound leaves except for one nested subclade of *Myodocarpus* that has simple leaves. Because simple leaves are reconstructed as ancestral in order Apiales, we suggest that this simple leaved subclade represents a reversal. Parents of putative hybrids involving crosses between *M. fraxinifolius*, *M. lanceolatus*, and *M. involucratus* were also resolved. *Delarbrea paradoxa* subsp. *paradoxa* appears to have dispersed from New Caledonia after its separation from Australia. The distribution of *Delarbrea michieana* may be the result of ancient vicariance, but further testing is required.

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The copperleaf conundrum: molecular and morphological data appear irreconcilable in *Acalypha* (Euphorbiaceae)

With about 450 species, *Acalypha* is the fourth largest genus in the Euphorbiaceae. It is characterized by pollen features, pendulous vermicular anthers, and the absence of a disk in the staminate flowers. In addition, most species possess laciniate styles and pistillate bracts that are accrescent in fruit. The genus is pantropical, with a few temperate species. The most-recent, comprehensive treatment was published by Pax and Hoffmann in 1924. They recognized 390 species in three subgenera: *Acalypha* (371 spp.), *Androcephala* (1 sp.), and *Linostachys* (18 spp.). Subgenus *Acalypha* was further divided into eight "series" and 36 "sections" distinguished primarily by features of inflorescence position and arrangement of the staminate and pistillate flowers. In conjunction with monographic studies and investigations on the evolution of inflorescence structure, we employed ITS and *ndhF* sequence data to reconstruct phylogenetic relation-

ships within *Acalypha*. Over 100 species have been sampled from throughout the genus. Although this work is still in progress, a number of conclusions can be reached. The genus *Acalypha* is monophyletic, as too are its subgenera *Acalypha* and *Linostachys*. Pax and Hoffmann's "series" and most of their "sections" are not monophyletic, however. Habit, inflorescence position, and the arrangement of the different sexes of flowers are labile and not good indicators of relationship. At this time we are unable to distinguish reliable morphological characters delimitate most of the clades suggested by the molecular data.

- 357 STEVENS, ANGELA C.*¹, FUNKE, MINDIE¹, DRAPER, SCOTTIE B.¹, ZADOROZHNY, TATIANA¹, DAVIDSON, CHRISTOPHER², BORNSTEIN, ALLAN J.³ and SMITH, JAMES F.¹

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A preliminary phylogenetic analysis of Piperaceae using chloroplast and nuclear genes: utility of the low copy nuclear PEPC intron within sections *Enckea* and *Arctottonia* of *Piper*

The Piperaceae are a species rich family occurring throughout the tropics. Interpreting relationships and taxonomic boundaries has been challenging in this family, in part due to small flowers that lack a perianth. Molecular data may provide information not available from morphology alone. In this study we investigate the relationships of Piperaceae by sampling taxa from putative new and old world clades and from several of the previously delimited genera in the family with a current emphasis on the Neotropical species. The results based on chloroplast genes *trnL-trnF* spacer and the *trnL* intron are congruent with a previous analysis using ITS data in that *Macropiper*, and *Pothomorphe* are imbedded within an otherwise paraphyletic *Piper*. These results provide support for several larger clades, indicating that the Neotropical species sampled to date are monophyletic and distinct from old world species. Relationships within these larger clades are either unresolved or poorly supported using the chloroplast genes. As a result additional data from the PEPC intron are investigated to determine the utility of this gene within two closely related clades of *Piper*, sections *Enckea* and *Arctottonia*.

- 358 STONE, R. DOUGLAS* and BALDWIN, BRUCE G. University and Jepson Herbaria and Department of Integrative Biology, University of California, Berkeley, CA 94720

Phylogenetic utility of two low-copy nuclear genes – G3pdh and the third intron of nitrate reductase – in a widespread and diverse group of tropical trees (Melastomataceae, subfamily Memecyoideae)

This study investigates phylogenetic relationships in a pan-tropical group that includes *Memecylon* and the closely related genera *Mouriri*, *Votomita*, *Spathandra*, *Ljindenia*, and *Warneckea*. Phylogenetic hypotheses are tested at the intergeneric level using partial sequences from the nuclear glyceraldehyde 3-phosphate dehydrogenase (G3pdh) gene, and at the intrageneric level using sequences from the third intron of the nuclear nitrate reductase gene (NIA-i3). In

each case the observed pattern of divergence among cloned isolates is consistent with intraspecific coalescence of alleles in a single-copy gene. Alignment of the G3pdh sequences was unambiguous, and a parsimony analysis rooted with sequences from *Pternandra* produced a single tree with the Afro-Malagasy genus *Warneckea* resolved as sister to the remaining taxa. The position of *Warneckea* at the base of the crown group agrees with a separate analysis based on morphological, anatomical, and cytological data. Also resolved in the G3pdh analysis is a subclade comprising *Memecylon* and *Spathandra* plus the two neotropical genera, *Mouriri* and *Votomita*. An apparent synapomorphy for this subclade is a chromosome base number of $x = 7$. *Memecylon* and *Spathandra* also share an unambiguous, 24-base deletion in the G3pdh sequence (specifically near the 5' end of the intron separating *Arabidopsis* exons 8 and 9). The NIA-i3 sequences in *Memecylon* range from 700 to 709 bases long, indicating very little length variation and no difficulty with alignment. Based on pairwise distance data and branch lengths in parsimony analyses, the variation observed in NIA-i3 is similar to that provided by two spacer regions (ITS and ETS) of nuclear ribosomal DNA. However, NIA-i3 is evidently far less homoplasious than either of the ribosomal DNA spacers in this case. From these results we conclude that NIA-i3 has good potential as a source of phylogenetically informative characters in the large paleotropical genus *Memecylon*.

- 359 TATE, JENNIFER A.*¹, SCHEEN, ANNE-CATHRINE³, CHEN, Z. JEFFREY², SOLTIS, DOUGLAS E.¹ and SOLTIS, PAMELA S.¹

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Patterns of gene expression in a recent allopolyploid of recurrent origin: revisiting the *Tragopogon* system

Although multiple origins of polyploid species have been frequently documented, little is known about the genetic and genomic consequences following recurrent allopolyploidization. Using AFLP-cDNA display, we examined gene expression differences in *Tragopogon miscellus*, an allopolyploid that has formed recurrently and reciprocally from the diploids *T. dubius* and *T. pratensis* in the last 80 years. Significantly, our data reveal differences in gene expression between *T. miscellus* and its parents, as well as between polyploid populations of separate origin. We identified several types of expression differences between the polyploids and their parents, including silencing, novel expression (potential reactivation), and maternal/paternal effects. Reverse transcription polymerase chain reaction (RT-PCR) and transcript sequencing were used to verify the AFLP-cDNA patterns. According to BLAST sequence similarity searches, the differentially expressed genes are involved in a variety of cellular processes, such as carbohydrate metabolism, signal transduction, protein transport and degradation, and cell division. Our results indicate that multiple origins contribute to genic diversity in the natural allotetraploids and that maternal and paternal genomic contributions can be detected and identified.

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Multiple origins of asexual autoploids in *Townsendia hookeri* (Asteraceae)

Townsendia hookeri is a diminutive perennial member of the Asteraceae that comprises sexual diploid and apomictic tetraploid populations. Diploid populations are restricted to Niobrara shale on the front range of the Rocky Mountains in Colorado. Polyploids, which are morphologically indistinguishable from diploids and presumed autotetraploids, extend northward to southern Alberta and British Columbia, with additional disjunct populations in the Yukon and Alaska. Our focus is to document the origins of polyploid populations. We have surveyed DNA sequence variation in two chloroplast DNA regions (portions of the *ndhF* gene and the *matK-trnK* region) in 12 diploid and 13 polyploid populations from throughout the species' range. The data set, which includes 1339 aligned nucleotides reveals levels of pairwise sequence divergence ranging from 0-4.3 percent. Phylogenetic analysis of haplotypes indicates that nearly all haplotype diversity found in polyploid populations can be accounted for by diversity observed in diploids, and that nearly all haplotypes of diploids have associated polyploid derivatives. Our analysis documents a minimum of four separate origins of polyploids in *T. hookeri*. For three of these lineages, polyploid populations share haplotypes with diploids. The fourth polyploid haplotype occurs in a single population from Kluane National Park in the Yukon Territory and represents the most divergent lineage within the species. Other Yukon populations share haplotypes with disjunct southern Alberta populations more than 1000 km away. While it is well-documented that most polyploid taxa have originated multiple times, the implications of this phenomenon remain largely unexplored. Because polyploid populations of *T. hookeri* are apomictic, the documentation of multiple origins of polyploids within this species provides a unique opportunity to study the impact of separate origins on patterns of genetic and phenotypic variation, in the absence of confounding effects of recombination. Such studies are the focus of ongoing work in *T. hookeri*.

361 TRUSTY, JENNIFER L.*³, OLMSTEAD, RICHARD G.¹, BOGLER, DAVID J.⁴, SANTOS-GUERRA, ARNOLDO² and FRANCISCO-ORTEGA, JAVIER³

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Molecular Phylogenies from Nuclear and Chloroplast Genes Support the Connection of the Macaronesian Genus *Bystropogon* (Lamiaceae) to the Radiation of the New World Mentheae

The genus *Bystropogon* (Lamiaceae) is endemic to the Macaronesian Islands and represents the best-known example of a putative phytogeographic connection between these islands and the New World. Previous morphological taxonomic studies suggested that this genus is closely related to the western South American genus *Mintostachys*. A combined maximum parsimony analyses of nucleotide sequences of the internal transcribed spacers and the 5.8S subunit of nuclear ribosomal DNA and the *trnL* gene and *trnL-trnF*

spacer of the chloroplast resulted in 21 most parsimonious trees. The molecular phylogenies show that *Bystropogon* is sister to a large clade of New World Mentheae genera including *Mintostachys*. In addition, 27 of the 28 Mentheae genera sampled in this study form a monophyletic group and give new insight into the generic relationships within the tribe.

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Phylogenetic relationships among the actinorhizal members of Rosaceae based on DNA sequences of three plastid and two nuclear regions

Past molecular phylogenies of the Rosaceae have supported a clade consisting of the four actinorhizal genera: *Cercocarpus* HBK, restricted to southwestern North America; *Purshia* DC., restricted to southwestern North America and including the taxa previously described as *Cowania* D.Don; *Chamaebatia* Benth., found in California, and *Dryas* L., with a circumpolar distribution in alpine and arctic habitats. Members of these genera form symbiotic relationships with nitrogen-fixing actinomycetes of the genus *Frankia*. We examined the phylogenetic relationships among members of this actinorhizal lineage using DNA sequences of three plastid markers (the *trnL-F* region, the *trnS-trnG* intergenic spacer, and the *rpl20-rps12* intergenic spacer) and two nuclear markers (the ITS region including the 5.8S gene and two introns contained within the *pgiC* gene). The five datasets were analyzed using both maximum parsimony and Bayesian analyses, separately and combined. Results of these analyses were largely in agreement, and resolved four monophyletic groups corresponding to the four genera. We found good support for the previous transfer of *Cowania* to *Purshia*, as well as for the sister relationship between *Purshia* and *Cercocarpus*. *Dryas* is the first branch in the clade, sister to the rest of the actinorhizal genera, followed by *Chamaebatia*, which is sister to *Purshia* and *Cercocarpus*. The data also support two well-supported clades within *Purshia*, one including taxa found in the western United States and another consisting of taxa from Mexico. We also found four clades within *Cercocarpus* which correspond to the four species complexes identified in earlier morphological studies.

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Genetic Variability of an Extended Metapopulation of *Solidago riddellii* *Solidago riddellii* is a clonal, herbaceous perennial with a localized, but widespread distribution across north central North America. The largest known population of *S. riddellii* is an interrupted streamside population on Rock Creek (RC) in north central Arkansas. Starch gel electrophoresis was used to characterize genetic structure of this metapopulation. Inferences regarding the significance of biogeography and local distribution patterns on population genetic structure were derived from allozyme data. The RC metapopulation is characterized by a patchy linear distribution adjacent to the stream. In this study it was subdivided into 7 subpopulations corresponding to high-density stands. Organization of the metapopulation and stream dynamics provides an opportunity to investigate patterns of gene flow and recruitment within a clonal, herbaceous perennial species. Potential recruitment patterns include seed distribution and ramet displacement downstream during annual floods while gene flow via pol-

len distribution is predicted to be bi-directional. Individuals at the RC subpopulations share a higher proportion of their alleles among subpopulations than within subpopulations ($FIS = 0.193$; $FST = 0.076$). Greater differentiation within the subpopulations is explained by the clonal nature of *S. riddellii*. Sampling of multiple multilocus genotypes, (clones/genets) within a subpopulation, indicated high levels of differentiation, or a lower proportion of shared alleles, within the subpopulations. Subpopulations at RC are comprised of multiple clones, outcrossing primarily among the subpopulations. The genetic structure is explained by significant levels of gene flow up and down the creek via pollen, seed, and ramet dispersal.

364 WEN, JUN*, LEE, CHUNGHEE and ZHOU,

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Geographic disjunctions, rapid radiations and species delimitations: insights from the ginseng genus (Panax L., Araliaceae)

Panax L. (the ginseng genus, Araliaceae) is medicinally important in Asia and has been taxonomically controversial. Various molecular markers have been employed to help delimit taxa, elucidate evolutionary relationships, and construct the biogeographic history of the genus. Biogeographically Panax shows a classical disjunct distribution between eastern Asia and eastern North America. In this study, we have used sequences of the internal transcribed spacer (ITS) regions of nuclear ribosomal DNA and the chloroplast *ndhF* gene and the *trnC-trnD* intergenic region, as well as AFLP data. Our analyses suggest two independent intercontinental disjunctions between Asia and North America in the ginseng genus. The first is ancient, involving the eastern North American *P. trifolius* and the Sino-Himalayan *P. pseudoginseng* – *P. stipuleanatus*. The second disjunction is suggested to have occurred in the late Tertiary, involving the eastern North American *P. quinquefolius* and the eastern Asian *P. ginseng* and *P. japonicus*. Our data also suggest that the Asian species of Panax have experienced a rapid radiation in the Sino-Himalayan region. Eighteen species are currently recognized within Panax based on morphological and molecular evidence.

365 WHITTEMORE, ALAN T.

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Interspecific hybridization in Texas Celtis

Species in the genus *Celtis* (sugarberries, hackberries) are fast growing, drought resistant trees and shrubs. The genus has not been monographed since 1848, and its taxonomy is poorly understood. The North American species have been believed on anecdotal grounds to hybridize commonly in nature, but preliminary results from crossing experiments yielded few seeds. An understanding of the nature and frequency of natural hybridization among species of *Celtis* is necessary for designing phylogenetic analyses for the genus. A pilot project was undertaken to test the extent and genetic consequences of natural hybridization between two species, *Celtis laevigata* and *C. reticulata*. Extensive natural introgression between these two species has been strongly suspected, but this has never been tested rigorously. Surprisingly, statistical study of morphological and AFLP data indicates that there is little or no natural hybridization between these species, contradicting past conclusions. The variability and apparent intergradation between the species that led to the hypothesis of introgression is apparently due to recent divergence of the

lineages (thus high levels of shared ancestral polymorphism at many loci), plus exceptionally high levels of position-associated leaf polymorphism within individual trees.

366 WILLIAMS, JOSEPH H.* and FRIEDMAN, WILLIAM E.

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Female gametophyte development in *Illicium* (Austrobaileyales) and the evolution of endosperm ploidy and genetic constitution in early angiosperms.

Endosperm, the sexually-derived embryo-nourishing tissue unique to flowering plants, has long been seen as a key innovation associated with the dramatic diversification of angiosperms. There are several hypotheses concerning the developmental and evolutionary origin of endosperm. The most widespread is that double fertilization of a monosporic, seven-celled/eight-nucleate female gametophyte to produce a triploid endosperm (with a genetic constitution identical to that of the diploid zygote) evolved in the common ancestor of extant angiosperms. A second hypothesis, suggested by recent theoretical and comparative studies, indicates that the common ancestor of angiosperms possessed a four-celled/four-nucleate female gametophyte and a process of double fertilization, which yielded a diploid endosperm (genetically identical to the zygote). Here we report that *Illicium mexicanum* (Illiciaceae), a member of one of the earliest angiosperm lineages, the Austrobaileyales ("ITA" clade), develops a monosporic 4-celled/4-nucleate female gametophyte that yields a diploid endosperm upon fertilization. Several other early angiosperms have recently been shown to possess this same pattern of monosporic female gametophyte development and diploid endosperm (other Austrobaileyales, Nymphaeales). An analysis of over 200 embryological reports on other early lineages of angiosperms reveals that a monosporic, seven-celled/eight-nucleate female gametophyte and triploid endosperm originated a single time in the common ancestor of monocots, eumagnoliids, and eudicots. A comparison of reconstructed ancestral female gametophyte ontogenies from the Nymphaeales/Austrobaileyales and the monocots/eumagnoliids/eudicots suggests that the four-celled/four-nucleate female gametophyte gave rise to the seven-celled/eight-nucleate female gametophyte by modular duplication. From that point, triploid endosperm was maintained in over 99% of extant species in the three major angiosperm clades (monocots, eumagnoliids and eudicots).

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Appendages do matter: The phylogeny, evolution, and classification of the genus *Globba* and tribe Globbeae (Zingibraceae)

The genus *Globba* (100 spp.), one of the largest genera in the Zingiberaceae, is distributed throughout Southeast Asia, with the highest concentration of species occurring in Thailand and Myanmar. *Globba* along with the small genera *Mantisia*, *Gagnepainia* and *Hemiorchis* comprise the Globbeae, one of the two tribes of subfamily Zingiberoideae. Traditional infrageneric classifications of *Globba* have always focused on the number of anther appendages: zero, two

or four. Parsimony and Bayesian phylogenetic analyses were conducted on nuclear internal transcribed spacer (*ITS*) and plastid *trnK-matK* data from a broad sampling of *Globba* and related genera. Results show *Mantisia* to be monophyletic but derived out of *Globba*, while *Hemiorchis* and *Gagnepainia* are monophyletic genera that are sister to each other. The four species of *Mantisia* are formally transferred into *Globba*. A hypothesis of four independent gains and one loss of anther appendages is supported by this phylogeny. Anther appendage number alone does not demarcate monophyletic groupings, but anther appendage characters, including number, are the most important indicator of phylogenetic relationships in *Globba*. Other characters of importance for classification purposes include fruit morphology, bract shape and persistence, and inflorescence morphology. A new infrageneric classification system is proposed for *Globba* recognizing three subgenera, seven sections, and two subsections.

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Viburnum phylogeny, biogeography and character evolution – evidence from multiple genes

Viburnum (Adoxaceae, Dipsacales) contains some 180 species of woody plants widely distributed in the Northern Hemisphere and extending into the mountains of South America and Malesia. Phylogenetic analyses of chloroplast (*trnK* intron) and nuclear (ribosomal *ITS* and GBSSI) DNA sequences have significantly improved our understanding of relationships. These analyses indicate that most of the ten traditionally recognized sections are monophyletic; a striking exception is *Odontotinus*, which is divided into a purple-fruited New World and an Old World red-fruited clade. Our molecular results also suggest three supra-section clades. One of these, containing sections *Solentinus* and *Pseudopulus*, is strictly Asian in distribution. The other two span both the Old and New Worlds. A "Lentoid" clade contains the New World section *Lentago*, the Old World section *Viburnum* and *Pseudotinus* with species in Asia and Eastern North America. A "Tinoid" clade contains the Old World sections *Tinus* and *Megalotinus*, the circumboreal *Opulus* and the two major *Odontotinus* clades. Further, section *Oreinotinus*, which contains the Latin American species is nested within the New World *Odontotinus*. We discuss these phylogenetic results in terms of several outstanding problems in the character evolution and biogeography of *Viburnum*. The structure of the vegetative buds and inflorescences are of special interest, as are disjunctions between eastern North America and eastern Asia.

369 WOJCIECHOWSKI, MARTIN F.², LAVIN, MATT¹ and SANDERSON, MICHAEL J.*³

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A phylogeny of legumes (Fabaceae) based on sequences of the plastid matK gene

Elucidating the phylogenetic relationships of the legumes (Fabaceae) is essential for understanding the origin and diversification of this large family of flowering plants. We assembled a dataset of nearly 300 complete sequences of the plastid *matK* gene, representing 200 genera of Fabaceae from 37 of 39 tribes, and five outgroup taxa from eurosids I (110 are new to this study). Results from maxi-

mum parsimony and likelihood analyses produce trees that are generally consistent with results of published studies based on other plastid sequence data *rbcL* and *trnL*). However, results from *matK* analyses show greater resolution overall and greater statistical support for many clades compared to those based on other loci, especially for the monophyly of subfamily Papilionoideae and relationships among and within its four major subclades (core genistoids, dalbergioids, millettoids-phaseoloids, and Hologlegina). Our analyses also identified several previously poorly supported relationships suggested by other studies. Among these is strong support for an expanded genistoids clade, tribe Amorpheae as the sister group to the dalbergioids clade, and a sister group relationship between South African tribe Hypocalypteae and the Australian endemic tribes Bossiaeae plus Mirbelieae. In addition, the *matK* data provides support for a clade comprising papilionoid taxa that accumulate non-protein amino acids in seed, which suggests this trait arose once in the evolutionary history of legumes.

370 WOLFE, ANDREA D.* , RANDLE, CHRISTOPHER P. and ARGUEDAS, NIDIA

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Patterns of evolution in *Hyobanche* L. (Orobanchaceae)

Hyobanche L. (Orobanchaceae) is a holoparasitic genus endemic to southern Africa from the Cape Floristic Province northward to Namibia and eastward to Swaziland. Two species complexes consisting of species having similar morphological characters makes identification of taxa problematic. *Hyobanche glabrata*, *H. rubra*, and *H. barkleyi* have glabrous, straight corolla tubes and occur in desert regions ranging from the Karoo to Namaqualand and Namibia. *Hyobanche sanguinea* has a hirsute and galeate corolla. This species exhibits regional differences in floral and inflorescence characters, and occurs in a range of habitats from sand dunes to mountain rock outcrops throughout southern Africa. Phylogeny reconstructions based on *ITS* and *rbcL* sequence data reveal sufficient differentiation among taxa to identify new species that can be segregated from the *H. sanguinea* complex, and also show distinct molecular character differences to separate *H. barkleyi* from *H. glabrata* and *H. rubra*. The biogeographic patterns emerging from these phylogenetic analyses place taxa from the west and southern coast in a basal position relative to those in the Karoo and east coast.

371 WURDACK, KENNETH J.* and ZIMMER, ELIZABETH A.

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CoxI intron evolution in Euphorbias.l. (Euphorbiaceae s.s.)

A group I intron in mitochondrial *cox1* has been gained multiple times in angiosperms by lateral transfer. It is present in at least 17 families of Malpighiales, including all surveyed members of Euphorbiaceae s.s. This study focuses on *Euphorbia* s.l. (all cyathial taxa), the largest genus of Euphorbiaceae s.s., using PCR assays and sequencing to look at the fine structure of the *cox1* intron gain. *Euphorbia* s.l. *cox1* introns are especially indel rich and appear to derive from a single gain followed by vertical transmission, based on phylogenetic and identical exonic coconversion tract evidence. An intron phylogeny resolves four major *Euphorbia* clades and is congruent with independent phylogenies (*ITS* and *ndhF*, after Steinmann

2002). All sequenced introns have degeneration of resident homing endonuclease genes. Large clades are defined by synapomorphic intron structural changes: clade "A" (Africa and Madagascar succulents) contains a mitochondrial insertion of 3.1 kb and clade "D" (including *Chamaesyce* and subgenera *Poinsettia* and *Agaloma*) contains a 2.1 kb chloroplast insertion. The latter is from the chloroplast inverted-repeat and contains partial 16S and *tRNA*-UGC bordering an intact *tRNA*-GAU gene. The results of phylogenetic analysis of chloroplast and mitochondrial intron-insertion paralogous sequences are consistent with one inter-organelle transposition. This insertion is remarkably stable, contains a footprint (flanking direct repeat and a short deletion of adjacent intron sequence) and is quite conserved in sequence across high speciation (>500 species). The chloroplast insertion is precisely lost (leaving the deletion footprint) in the deeply nested clade "D" subclade containing *E. guatemalensis* and *E. oaxacana*. A clade "D" subclade of subgenera *Cystidiospermum* and part of *Eremophyton* lacks any evidence of this insertion and may be misplaced in an unsupported position in clade "D" rather than subject to intron turnover following the cyclical model of intron gain and loss.

372 XIANG, QIU YUN^{*1}, THORNE, JEFFREY², SEO, TAE-KUN², THOMAS, DAVID¹, FAN, CHUANZHU¹ and ZHANG, WENHENG¹

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Phylogeny and Disjunct Biogeography of *Cornus* – Divergence Times and Rates of Molecular Evolution

The dogwood genus *Cornus* contains ~65 species that are mainly distributed in the northern Hemisphere, with a single species isolated in Africa and one in South America. The genus figures several historical biogeographic patterns. Several DNA sequence data sets including ITS, 26S rDNA, *rbcL* and *matK*, with nearly 7000 bp, were used to reconstruct a species level phylogeny of the genus. A Bayesian method integrating fossils and molecular data, but without requiring a molecular clock, was used to estimate divergence times and examine rates of evolution of the three coding genes. The resulting phylogeny revealed four disjunct patterns, an eastern Asian-eastern North American disjunction exhibited by the two alternate-leaved species, *C. controversa* and *C. alternifolia*, an eastern Asian-eastern and western North American disjunction by the big-bracted dogwoods, an eastern Asian-western North American-European-African disjunction by the cornelian cherries, and finally an eastern Asian-South American disjunction by two unusual species, *C. oblonga* and *C. peruviana*. Analyses of divergence times suggested that the genus evolved in the late Cretaceous and diverged into four major lineages in the early Tertiary; the disjunctions involving different areas occurred at different geological times. However, disjunctions involving the same areas (e.g., the eastern Asian-North American disjunction in the big-bracted and alternate-leaved lineages) occurred at similar times, suggesting possible common causes for the disjunction. Divergence times estimated from different genes varied, but with overlapping confidence intervals. Different patterns of rates of evolution between nuclear and chloroplast genes were observed. Rates of *rbcL* and *matK* genes showed a similar pattern of variation overtime, but synonymous and nonsynonymous substitution rates in *matK* were higher than those in *rbcL*. Relatively high selection force for *matK* was detected in the big-bracted and blue-fruited groups where high species diversity and morphological complexity occur. The results suggested likely positive selection for *matK* in these groups.

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Phylogeny and Divergence Times of the Cornelian Cherries (*Cornus* subg. *Cornus*, Cornaceae) - Congruence Among Parsimony, Maximum Likelihood, and Bayesian Analyses, and Implications for Evolution and Biogeography

Cornelian cherries (*Cornus*) comprise a monophyletic group of six living species endemic to four geographic areas in eastern Asia, western North America, Europe, and tropical Africa. We performed phylogenetic analyses of 6872 bp sequences from 26S rDNA, ITS, *rbcL*, and *matK*, and estimated species divergence times using Sanderson's NPPRS method. Parsimony, maximum likelihood (ML), and Bayesian methods were used to explore alternative phylogenetic hypotheses. We also used constrained topologies to test alternative evolutionary hypotheses under parsimony and ML methods and reconstructed biogeographical history using divergence times, fossil data, and Dispersal-Vicariance analysis. The results indicate significant discordance between 26S rDNA-ITS and *rbcL-matK* data, shown by different placements of *C. eydeana* in the two data sets suggesting that the nuclear and chloroplast genome of *C. eydeana* may have different evolutionary histories. When all four data sets were combined, the resulting tree was identical to that of 26S rDNA-ITS data. These results suggest that *C. sessilis* from western North America, rather than *C. volkensii* from Africa, is the first branching lineage within Cornelian cherries. These results suggest that the evergreen habit might have evolved independently in tropical mountains of eastern Asia and Africa; alternatively, the deciduous, early blooming trait may have evolved three times in different north temperate regions. Species divergence times based on 26S rDNA-ITS were 2-2.5 times greater than estimates based on *rbcL-matK* data, suggesting heterochrony in nuclear and chloroplast DNA divergence. According to fossil evidence, Cornelian cherries evolved by the late Paleocene and established a transatlantic connection by the early Eocene. They spread to Africa early in the Oligocene based on 26S rDNA-ITS data or in the early Miocene based on the *rbcL-matK* data. DIVA analysis indicated that the extant European species represent a lineage derived from an eastern Asian ancestor during the Miocene.

374 ZANDER, RICHARD H.
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The Reliability of Apparent Overall Convergence in Phylogenograms

D_{ancestry} is a method of establishing reliability of implied shared ancestry between lineages distant on a cladogram that applies to both morphological and molecular data sets. The method develops confidence limits based on exact binomial calculation against a hypothesis of random and equal support for all three branch arrangements for any one internode. Across two or more contiguous internodes of a most parsimonious cladogram, reliability is evaluated by comparing summed support for the optimal branches and summed support for the optimal branches and the two alternative branch arrangements for each internode through analysis after constraint and nearest neighbor interchange, looking for significant increase above

an expected level of 1/3 for the null. An example is given for a morphological data set to evaluate dependability of apparent overall convergence shown by superimposing a phenetic ordination (PCA) over a cladogram. Four of 6 apparent cases of overall convergence were reliable at a 95% confidence limit.

CONTRIBUTED POSTERS

- 375 ARAKAKI, MONICA^{*1}, PANERO, JOSE L.² and CROZIER, BONNIE²

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Systematics of the genus *Weberbauerocereus* Backeb. (Cactaceae)

Cactaceae comprise approximately 1800 species, found mostly in the tropical deserts of North and South America. The family has been the object of intensive study but it is not until recently that molecular tools have been used to elucidate phylogenetic relationships within the family. Most of the Cactaceae found along the western slopes of Peru belong to tribe Trichocereeae. Phylogenetic relationships within the tribe have been historically controversial, therefore a molecular study using chloroplast and nuclear markers was designed to elucidate phylogenetic relationships among species of *Weberbauerocereus* and the relationship of this genus to the other members of Trichocereeae. This study has been carried out in parallel with those of B. Crozier's molecular studies of Cactaceae, therefore the same markers have been used to facilitate the sharing of molecular data. We sequenced cpDNA (matK, rpoB, rpl16, trnT-L, trnL-F and petB) and nrDNA (ITS1 and ITS2) of thirty-five ingroup taxa comprising Trichocereeae and three outgroup taxa from different tribes. The analyses strongly support a monophyletic *Weberbauerocereus* with *Cleistocactus* as sister. The taxonomy of the Trichocereeae does not reflect its phylogeny based on molecular data; hence the tribe is in need of revision.

- 376 ARSENAULT, M.¹, PRESBY-GERMANO, J.², KLEIN, A.², WRIGHT, W.¹ and CAMPBELL, C.^{*1}

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Incongruence between three genomes in phylogenetic relationships within *Picea* (Pinaceae). Sequences from the nuclear gene 4CL were used to investigate incongruence in phylogenetic inferences in *Picea* based on our previous results from chloroplast and mitochondrial genomes. Our cpDNA data were the *trnK* and *trnTLF* regions for 29 of the approximately 35 species in the genus, and mtDNA data were *nad1* B/C and *nad7* 1/2 introns for 16 of the same species sampled for cpDNA. Our cpDNA and mtDNA trees are similar in several clades and placement of *P. sitchensis* of northwestern North America near the base of the tree. Trees based on these two genomes differ, however, in the composition and relationships of two important clades. *Picea glauca*, *P. engelmannii*, and *P. mexicana* form a clade in cpDNA trees, and this clade is sister to a clade of 10 mostly eastern Asian species plus *P. abies*. MtDNA does not recover a *glauca-engelmannii-mexicana* clade and instead aligns *P. mexicana* with another Mexican species, *P. chihuahuana*, and has *P. glauca* plus *P. engelmannii* as sister to *P. sitchensis* near the base of the *Picea* tree. *Picea mariana* and *P. rubens*, which are closely related according to both genomes, belong to a clade with the Serbian spruce, *P. omorika*, in cpDNA trees, whereas mtDNA places *P. omorika* within the clade containing *P. abies*. The 4CL gene, for which we have about 2600 bp of sequence from

three introns and parts or all of four exons, unites *P. glauca* (our only representative of the *abies-glauca-engelmannii* clade so far) with *P. sitchensis* and supports the *marianna-omorika-rubens* clade. Hybridization is widespread in *Picea* and has been hypothesized to contribute to conifer evolution during glacial and interglacial cycles of the Quaternary period (the last 2 million years). Conflicts between genomes presented here suggest complex reticulate evolution in the history of spruces.

- 377 BENNETT, JONATHAN^{*1} and SCOTLAND, ROBERT²

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Pollen Morphology of the Strobilanthineae

The Strobilanthineae (Acanthaceae) is characterized by an extreme level of palynological diversity among its c.350 species. Previous classifications of the subtribe have relied heavily on pollen morphology, either exclusively or in combination with gross morphology. Early investigations of pollen morphology were restricted to light microscopy. More recently, scanning electron microscopy has been used, although these studies have suffered from limited geographical sampling. In both cases this has led to an underestimation of the variation. We present the results of the most thorough investigation of pollen morphology in the Strobilanthineae to date. SEM studies have revealed a much greater range of palynological variation than has been documented previously. Much of the variation is quantitative. Many of the pollen types recognized by earlier workers, such as echinulate and ribbed pollen, are shown not to be discrete types, but are bridged by a range of intermediate morphologies. We explore the consequences of under-sampling a species-rich group, such as the Strobilanthineae, in the context of the ability to conceptualize and code morphological characters for phylogeny reconstruction. It is shown that the perception of characters and character states is dramatically affected by levels of sampling. When the density of sampling is increased, greater levels of morphological variation are discovered. However, our ability to unambiguously code this variation in to characters is reduced, and therefore the number of morphological characters available for phylogenetic analysis decreases. This contrasts with the view that an advantage of using morphological characters in phylogeny reconstruction is the ability to achieve greater levels of taxonomic sampling than in molecular studies.

- 378 CHUNG, KUO-FANG^{*1} and SCHAAL, BARBARA A.²

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Phylogenetic Biogeography of *Oreomyrrhis*: a Trans-Pacific Distributed Apiaceae

Genus *Oreomyrrhis* (Apiaceae) exhibits a remarkable distribution in alpine and subalpine habitats around the southern Pacific Rim (Central America, South American Andes, the Falkland Islands, Tierra del Fuego, New Zealand, SE Australia, Tasmania, New Guinea, Mt. Kinabalu, and Taiwan). This "exemplar" of South Pacific Gondwanan disjunctions has been a frequent subject of dispersal/vicariance debates over the origins of Pacific disjunctions. Parts of these controversies can be attributed to the dubious taxonomical placement of *Oreomyrrhis* within Apiaceae. To elucidate its phylogenetic relationship at both inter- and intrageneric levels and to test the competing biogeographical hypotheses concerning the origin of the disjunction, we have gathered sequence data of nuclear ITS from eighteen of the

twenty-five recognized *Oreomyrrhis* species, including representatives all across its geographic distribution. Combing with published ITS data matrix of Apiaceae, phylogenetic analyses designate a placement of *Oreomyrrhis* into subtribe Scandicinae, tribe Scandiceae. Within Scandicinae, *Oreomyrrhis* is nested within genus *Chaerophyllum* and, together with two North American *Chaerophyllum* (*C. procumbens* and *C. tainturieri*), forms a monophyletic clade; however, the monophyly of *Oreomyrrhis* cannot be rejected based on the poorly resolved relationship between *Oreomyrrhis* and the North American *Chaerophyllum*. This molecular-based phylogenetic relationship is concordant with several morphological features such as microstructures of mericarps and reproductive syndrome. Although interspecific relationship with *Oreomyrrhis* remains unresolved, low interspecific sequence divergence (0-1.8%) suggests a recent origin of the genus and supports a long-distance dispersal scenario to account for its trans-Pacific disjunction. Future research is directed to employ multiple sequence data from both nuclear and chloroplast genomes to increasing the resolution of the interspecific relationship and depicting a detailed pattern of long-distance dispersal.

379 CONTI, ELENA*, ARROYO, KARINA and

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Phylogenetic relationships and molecular dating of the rare *Saxifraga florulenta* Moretti: Implications for biogeography and the evolution of monocarpary

The rare *Saxifraga florulenta* Moretti is restricted to a small area (less than 100 Km²) of the Southwestern Alps, where it grows exclusively on siliceous rocks. It is a long-lived monocarpic species, therefore each individual plant remains in the vegetative stage for several years, then it blooms and dies. The distinctive life history of *Saxifraga florulenta*, coupled with habitat loss and its occurrence at very high elevations, raise concerns about the long-term prospects of this species. Global warming trends further threaten the survival of *Saxifraga florulenta*, which already occurs on mountains summits, between 2500 and 3500 m. Because knowledge of the evolutionary history of rare plants is essential for the establishment of long-term conservation plans, we reconstructed the phylogenetic relationships *Saxifraga florulenta* based on nuclear ITS and chloroplast *mat K* sequences. Both maximum parsimony and likelihood analyses revealed that *Saxifraga florulenta* belongs to sect. *Porphyron*, rather than sect. *Ligulatae*, as proposed by previous taxonomic studies. Furthermore, our analyses suggested that monocarp evolved independently three times (also in *S. mutata* and *S. longifolia*) among the European saxifrages, possibly in response to drier climatic conditions associated with glacial peaks of the Pleistocene glaciations. To test the proposed ancient (arco-Tertiary) origin of *Saxifraga florulenta*, we will also perform molecular dating analyses, both clock-dependent and clock-independent, aimed at estimating the age of this rare species.

380 DREHER, STEPHEN E.

Systematics, Ecology and Hybridization Patterns of the genus Sphaeralcea (Malvaceae)

The genus Sphaeralcea (Malvaceae), known commonly as "globe mallow", is an amphi-tropical disjunct occurring in southern South America (primarily Argentina) and western North America (primarily northwestern Mexico and southwestern United States). Mericarp mor-

phology, a primary character for species identification, shows a surprisingly similar range of forms within each disjunct group. This may be the result of multiple dispersal events or a case of developmental homoplasy. As well, species are thought to hybridize freely and polyploidy is common. The goals of this study are to 1) create a molecular phylogeny of the group using two nuclear (ITS, Adh) and one chloroplast (TRN L-F) genes; 2) incorporate that phylogeny into previously conceived patterns of evolution and classification; 3) determine hybridization patterns through controlled greenhouse experiments; and 4) use the data to make inferences regarding the biogeography and ecological behavior of species of Sphaeralcea.

381 EDWARDS, ERIKA J.*², DIAZ, MIRIAM¹ and
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What can Pereskia really tell us about early cactus evolution?

Pereskia (Cactaceae) comprises 18 species of leafy shrubs, trees, and vines that have long been viewed as representing the "ancestral cactus." Their basal position within the Cactaceae has been confirmed by several molecular phylogenetic analyses, which have also weakly suggested that *Pereskia* is paraphyletic. Resolving relationships at the base of the cacti is crucial for interpreting early morphological and physiological evolution within the group, and toward this end we present DNA sequence data for two additional chloroplast gene regions (*fbcL* and the *psbA-trnH* IGS region) for *Pereskia* and related plants (including *Maihuenia* and several other cacti and Portulacaceae species). Sequence divergence patterns are similar to prior reports, providing strong evidence for several clades of *Pereskia* species, but little support for relationships among major lineages. We also present some field data from northwestern Venezuela on seasonal water relations, photosynthesis and growth in *Pereskia guamacho*, which may represent the sister group of all other cacti.

382 FARMER, S.B.

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Phylogenetic relationships of Trilliaceae

Molecular phylogenetic analyses have been coupled with assessment of morphological data to examine questions related both to the overall placement of Trilliaceae and to its generic-level classification. Trilliaceae have been placed in Melanthiaceae based on molecular analysis, a placement that has poor morphological support. A broader analysis of ITS data confirmed a close relationship but suggested that the two are monophyletic sister groups. Other comprehensive analyses of systematic relationships within Trilliaceae were performed using both molecular and morphological data to assess problems of generic delimitations. *Pseudotrillium* (*Trillium*) *rivale* was shown to be the basal sister group to all other Trilliaceae and was elevated to genus rank. Trilliideae and Parideae were monophyletic sister groups based on molecular as well as morphological evidence. *Trillidium* (*Trillium*) *govianum* provides an unresolved problem; morphologically it is included within Tribe Parideae, but molecular data place it within *Trillium* as sister to *T. undulatum*; it is provisionally retained as a monotypic genus pending further analyses. Cladistic analyses strongly support the separation of *Paris* s.l. into *Daiswa*, *Kinugasa*, and *Paris*. The infrageneric classification of *Trillium* remains problematic; the sessile-flowered species form a monophyletic clade but pedicellate species are not monophyletic and are the subject of ongoing studies.

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The West Virginia Vascular Flora Atlas

The "West Virginia Vascular Flora Atlas" contains distribution maps (by county) for every native and naturalized plant species in the state. Its purpose is to update and complement the state flora by Strausbaugh and Core (1977), as well as to support and stimulate additional botanical investigations. This work is the result of a project begun in 1995 to enter label information from West Virginia University Herbarium (WVA) specimens into a computerized database. The system uses Foxpro software, with the specific program application (CDS) designed by Harmon. Maps are produced using WordPerfect graphic images to place dots in the respective counties indicating species presence. The Atlas is based on over 79,200 specimens, primarily from six herbaria. It maps 2,474 vascular plant taxa, about three-fourths of which are considered native to the state. The vouchers that contributed to this document are from the 1870s through 2002, with most collecting taking place in the 1930s and 1990s. Only one vascular plant species has been documented from all 55 counties of West Virginia. The number of taxa per county ranges from 299 to 1,451. Botanists are encouraged to submit new county records by reporting collections to the project.

384 GAO, LIZHI

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48109, USAComparisons of Microsatellite Variability and Population Genetic Structure of Two Endangered Wild Rice Species, *Oryza rufipogon* and *O. officinalis*, and Their Conservation Implications

We applied six and seven microsatellite loci to studying population genetic structure of six populations throughout the range of Chinese *O. rufipogon* and *O. officinalis*, respectively. The results showed that *O. rufipogon* possesses higher levels of genetic diversity but lower genetic differentiation ($RS = 2.545$, $P = 90.0\%$, $HO = 0.1401$, $HS = 0.5800$, $FST = 0.0.271$) than *O. officinalis* ($RS = 2.0545$, $P = 57.14\%$, $HO = 0.0470$, $HS = 0.2830$, $FST = 0.554$). Mean population FIS was slightly larger for *O. officinalis* ($FIS = 0.844$) than that for *O. rufipogon* ($FIS = 0.755$), indicating that *O. officinalis* has slightly higher departures from Hardy-Weinberg expectations and heterozygosity deficits than *O. rufipogon*. Phenograms suggested a positive relationship between geographic and genetic distances in *O. officinalis*, while the pattern of population differentiation generally does not correspond to geographic distance in *O. rufipogon*. In addition to different origins and evolutionary histories, *O. officinalis* has restricted gene flow, high inbreeding, isolated small populations and fewer opportunities of hybridization with other taxa, which may determine major differences in population genetic structure from *O. rufipogon*. Therefore, our results suggest the adoption of a plan of involving fewer populations but more individuals within populations for *O. rufipogon*, while both the number of populations and the individuals for a sampled population should be almost equally considered for *O. officinalis*. The observation of high degree of inbreeding in the populations of both species implies that conservation and restoration genetics should particularly focus on the maintenance of historically significant processes such as high levels of outbreeding, gene flow and large effective population sizes. We finally proposed to further estimate the role of rice gene flow in the conservation of *O. rufipogon*, and to perform detailed analysis of mating systems in both species for better conservation perspectives of their ecological and evolutionary processes.

385 GAO, LIZHI

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48109, USAPopulation genetic structure and conservation genetics of wild rice *Oryza rufipogon* (Poaceae) as detected by polymorphic microsatellite loci

Oryza rufipogon Griff. is the most agriculturally important but seriously endangered wild rice species. To better estimate how genetic structure is shaped for bringing an conservation perspective of the species, genetic variability at six polymorphic microsatellite DNA loci was examined. High levels of genetic variability were detected at six loci in 1,245 individuals of 47 natural populations covering most of the species range in China (overall $RS = 3.0740$, $HO = 0.2290$, $HS = 0.6700$). The amount of genetic variation harbored within these fragmented populations was not only similar to each other, but also was as high as those populations that have not experienced the reduction in population size. Most marginal populations possessed lower levels of genetic diversity but higher degree of within-population inbreeding and significantly higher degree of among-population microsatellite differentiation ($FIS = 0.7470$, $FST = 0.2410$) than central ones ($FIS = 0.7050$, $FST = 0.2290$). Partitioning of genetic variability showed 75.4% of microsatellite variation was distributed within the *O. rufipogon* populations. A mean value of $Nm = 0.7662$ suggested a limited extent of gene flow among the assayed populations. Heterozygote deficits for most locus-population combinations and high positive FIS values for all studied populations indicated drastic departures from Hardy-Weinberg expectations and strong linkage disequilibrium. Therefore, conservation and restoration genetics should particularly focus on the maintenance of historically significant processes such as high levels of outbreeding and gene flow and large effective population size in the species. A conservation plan of involving fewer populations but more individuals within populations should be adopted for the species.

386 GELLI DE FARIA, ANA PAULA¹, WENDT, TÂNIA^{*1}and BROWN, GREGORY²¹Departamento de Botânica, Universidade Federal do Rio de Janeiro, IB, CCS, Ilha do Fundão, 21941-590, Rio de Janeiro-RJ, Brazil; ²Department of Botany, University of Wyoming, Laramie, Wyoming, 82071 and Marie Selby Botanical Garden, Sarasota, FL, U.S.A.Morphological data and phylogenetic analysis of *Aechmea* (Bromeliaceae subfamily Bromelioideae) - a first approximation

Aechmea is the largest (ca. 225 spp.), morphologically most diverse, and geographically the widest ranging genus within Bromeliaceae subfamily Bromelioideae. The circumscription of *Aechmea* has long been problematic, and the notion that *Aechmea* s.l. (Smith & Downs 1979) is not monophyletic has recently gained support amongst students of the Bromelioideae. Data, however, have not yet been used to explore the hypothesis that *Aechmea* s.l. is artificial. We present results from a phylogenetic analysis that included 60 morphological characters for 52 species from *Aechmea* (7 of the 8 subgenera recognized by Smith & Downs, 1979). Also included were species from *Acanthostachys* (2 spp.), *Billbergia* (6 spp.), *Fernseea* (1 sp.), *Hohenbergia* (5 spp.), *Lymania* (1 sp.), *Portea* (4 spp.), *Quesnelia* (10 spp.), *Ronnbergia* (2 spp.), *Streptocalyx* (3 spp.), and *Cryptanthus* (2 spp.). Molecular data places *Cryptanthus* in the sister-taxon position to core-Bromelioideae, thus it was designated as the outgroup. Parsimony analyses resulted in 158 trees of 777 steps. The strict consensus tree suggests that *Acanthostachys*, *Billbergia*,

and *Portea* are monophyletic. Conversely, *Aechmea*, *Hohenbergia*, *Streptocalyx*, *Quesnelia* and *Rombergia* are either para or polyphyletic. Only two *Aechmea*, subgenera *Chevaliera* and *Macrochordion*, are potentially monophyletic. The morphological characters traditionally emphasized for circumscription and classification of Bromelioideae genera displayed high levels of homoplasy. Our results, while preliminary, do not support continued recognition of *Aechmea* s.l.

387 GOTTSCHLING, MARC^{*1}, PLÖTNER, JÖRG², WILLEMS, HELMUT³ and KEUPP, HELMUT¹

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Molecular phylogeny of Calcidinelloideae (Peridiniales, Dinoflagellata) inferred from ITS1, 5.8S, and ITS2 sequence data

Calcidinelloideae (Peridiniales, Dinoflagellata) comprise about 30 recognized extant species and are distributed in temperate to tropical seas of the world. These dinoflagellates have the potential to produce calcareous cysts (i.e., mostly resting stages), which is a unique feature among alveolates and argues for the monophyly of the corresponding group. Based on the fossil record, Calcidinelloideae originated in the Upper Triassic and are very diverse in the Cretaceous and throughout the Tertiary, thus many extinct species (namely their cysts) have been described. By contrast, the modern species are primarily described based on their vegetative stages (namely on their theca, which are less diverse) leading to two distinct systematics, neontological and palaeontological. In order to obtain an integrative phylogenetic system, we present a preliminary molecular tree inferred from ITS1, 5.8S, and ITS2 sequence data. Calcidinelloideae segregate into two clades, *Scrippsiella* s.l. (including, e.g., *Calcidinium*, *Calcigonium*, *Pernambugia*) and *Ensiculifera* s.l. (including "Pentapharsodinium"), and have close affinities to the Thoracosphaerales. High diversity in the primary sequences of the Internal Transcribed Spacers (ITS1 and ITS2) indicates more (cryptic) extant species than supposed so far in Calcidinelloideae. Additionally, morphological SEM studies enlighten the cyst-theca-relationship of selected species and may render phylogenetically informative characters.

388 GUGGISBERG, ALESSIA^{*1}, MAST, AUSTIN¹, KELSO, SYLVIA² and CONTI, ELENA¹

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Polyplody, biogeography and evolution of breeding systems in *Primula* sect. *Aleuritia* with special emphasis on an allotetraploid complex: an integrated phylogenetic, population genetic, and molecular cytogenetic approach

The plant genus *Primula* L. (Primulaceae), with its diversity of ploidy levels, biogeographic distributions and breeding systems, represents an ideal genus for bridging the gap between phylogenetics and evolutionary ecology. Approximately 90% of the over 400 species of *Primula* are heterostylous (distylous) and mostly diploid, whereas 10% are homostylous, generally polyploid, and predominantly grow at high latitudes or altitudes. *Primula* section *Aleuritia* Duby includes both

diploid heterostyles and polyploid homostyles, which concurrently occur in North America and Eurasia. This section therefore represents an ideal system to investigate proposed evolutionary links between polyploidy, homostyly, and extreme arctic and alpine conditions. Phylogenetic reconstruction based on several chloroplast and nuclear sequences will additionally permit to verify the hypothesis of parallel evolution in North America and Eurasia. Based on evidence from cytology, morphology, and distribution, *Primula egalisensis* Wormskjold (sect. *Armerina* Lindley) has been proposed as an inter-sectional allotetraploid homostyle between two diploid heterostyles, namely *Primula mistassinica* Michaux (sect. *Aleuritia*) and *Primula nutans* Georgi (sect. *Armerina*). Phylogenetic analyses of four chloroplast DNA regions (*matK*, *trnL* spacer, *trnL* intron and *rpl16* intron) supported the inclusion of *P. egalisensis* in a clade otherwise formed by species ascribed to sect. *Aleuritia*. Specifically, these preliminary results allowed us to identify *P. mistassinica* as the likely maternal parent of *P. egalisensis*. To confirm this assumption, genomic *in situ* hybridization techniques will be performed on the three members of the complex. Moreover, population genetic analyses based on AFLP fingerprinting will enable us to assess whether this allopolyploid has originated recurrently.

389 HEANEY, J MICHAEL

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Anatomy of *Polystachya* (Epidendreae-Orchidaceae)

Polystachya (Epidendreae-Orchidaceae) comprises approximately 150 species in fourteen sections, and is pantropical, centered in Africa. Section *Cultiformes* Kränzlin has been the only section scrutinized taxonomically in a revision. Vegetative anatomy was briefly described around the turn of the century in *Polystachya pubescens* Reichenb. f. and *P. concreta* (Jacq.) Garay & Sweet. Recent anatomical research incorporating observations on *Polystachya* have focused on wider relationships among Orchidaceae. Other endeavors have focused on particular organs, roots for example, but have found no taxonomic pattern, possibly due to uneven sampling of taxa within the genus. I present an examination of the complete vegetative anatomy of representatives from each section, including a definitive anatomical description of the genus and outgroup taxa (*Neobenthamia gracilis*, members of *Earina* and *Agrostophyllum*). Interpreted in a phylogenetic context this can provide information leading to a revision of infrageneric concepts. A cladistic analysis using vegetative anatomical characters will be presented, followed by a discussion of relationships within the genus, and the systematic significance of anatomical characters to affinities with other genera in tribe Epidendreae, and with tribe Vandaeae.

390 JARRELL, DAVID and HAMED, HOSSEIN^{*}

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Molecular Systematics of *Phalaenopsis* (Orchidaceae): a preliminary study

Phalaenopsis (Orchidaceae, tribe Vandae, subtribe Aeridinae) is a genus of approximately 63 species divided among four subgenera. The subgenera Polychilos and Phalaenopsis are further divided into four sections each. Several hypotheses exist for the circumscription of the genus and subgenera based on a small number of characters such as pollinia number, overall shape of the labellum and as well as the structure of specific regions of the labellum (Christenson, 2001; Shim, 1982; Sweet, 1980). In particular, two sections of subge-

nus *Phalaenopsis*, *Delicosae* and *Esmeralda*, were recently formed from the genera *Kingidium* and *Doritis* (Christenson, 2001). Previous studies using *matK* sequences and limited taxon sampling support the synonymy of *Kingidium* and *Doritis* with *Phalaenopsis* (Jarrell, 1996). The current study expands the sampling and phylogenetic analysis of *matK* to more than 35 species representing all subgenera and sections. The results of this study and future plans will be discussed. Our long term goal involves phylogeny construction using several chloroplast regions and at least one low-copy nuclear gene (individually and in total) from all or nearly all species of *Phalaenopsis* and numerous outgroups. The resulting phylogenies may provide insight into patterns of genomic evolution within the genus, enable comparisons of the various generic and subgeneric hypotheses, identify sister genera from representatives of the subtribe Aeridinae and provide a framework for evaluating the evolution of taxonomically prominent morphological characters.

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Towards a Revision of Goodyera Section

Otosepalum The phylogeny of Goodyera section Otosepalum was investigated using cladistic analysis of molecular and morphological data. The data set contained 32 species, including 28 Goodyera species representing two sections. Four outgroups were used for the morphological and five for the molecular data. Parsimony was used to seek the trees from the morphological data. Successive weighting of characters and reverse successive weighting were applied. Phylogenetic trees were obtained from the molecular data using parsimony and maximum likelihood. Both models support the same recognition modified concepts of sect. Otosepalum, the genus Goodyera and the subtribe Goodyerinae. Bootstrap and T-PTP tests were used to test support for groups in the tree obtained by parsimony. Morphological characters show homoplasy on most branches of the phylogenetic tree. The tree obtained from the successive weighting does not support monophyly of sect. Otosepalum, the genus Goodyera or the subtribe Goodyerinae. Similarly, the result from the molecular data show that section Otosepalum and the genus Goodyera are not monophyletic groups. However, subtribe Goodyerinae is monophyletic based on molecular data. Based on the statistics used, molecular data show better resolution of the phylogeny of the study group. Phylogenetic trees from morphology and molecular data show incongruence from placement of most of the terminal taxa, although in general the conflicts are between weakly supported groups. However there is some congruence especially in the placement of Lepidogyne sceptrum is proposed to be transferred to Goodyera, and Goodyera polygonoides should be retained in Goodyera, despite published opinion to the contrary.

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Preliminary results on the phylogeny of the Hinterhubera and Novenia groups (Hinterhuberinae: Asteraceae) based on ETS and ITS sequence data

Two separate informal groups centered about *Hinterhubera* and *Novenia* are native to the paramos in Central and South America. The *Hinterhubera* group consists of 7 genera with approximately 30 species while *Novenia* is monotypic with only one species native to

the Andes in Peru. Based on morphological data the *Hinterhubera* group was considered monophyletic, while the position of *Novenia* remained unresolved. Recent phylogenetic analysis of the ITS region by Noyes and Reisenberg revealed that certain genera of the tribe Hinterhuberinae needed further examination and repositioning within the tribe Astereae. Our preliminary results of the analyses of ETS and ITS sequence data from representatives of the *Hinterhubera* group (*Hinterhubera* spp., *Azefaster* spp., *Parastephia* spp., *Laestedia* spp., *Westoniella* etc.) indicate that the group is possibly polyphyletic, and related to various other South American taxa. *Novenia acaulis* is probably most closely related to taxa placed in the *Chilitrichum* group.

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Phylogeny and evolution of Polygonum sect. Persicaria (Polygonaceae) in eastern North America Polygonum section

Persicaria (Mill.) Meisn. consists of about 70 species of weedy herbs found in moist or disturbed areas. Preliminary sequence analyses of nuclear (ribosomal ITS) and chloroplast (*matK* including *trnK* intron) DNA from eastern North American species have provided important clues to understanding interspecific relationships and diversification in these plants. Our analyses suggest that the endemic species, *P. puritanorum* Fern., recently treated as a synonym of *P. persicaria* L., is a distinct lineage; this is also supported by our chromosome count of 2n=60. Additionally, our results indicate that *P. punctatum* Ell. is a probable hybrid species, which originated from hybridization between *P. hydropiper* L. and *P. puritanorum*. Our results also suggest the possibility of cytoplasmic introgression involving two American species (*P. careyi* Olney and *P. pensylvanicum* L.) and an introduced species (*P. lapathifolium* L.).

394 KROSNICK, SHAWN E.* and FREUDENSTEIN, JOHN V.

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Morphological and Molecular Patterns in the Old World species of Passiflora (Subgenus Decaloba Supersection Disemma)

Passiflora provides one of the most remarkable examples of floral complexity and diversity among plants. The genus is currently divided into four subgenera: *Passiflora*, *Decaloba*, *Astrophea*, and *Deidamioidea*. Of particular interest is subgenus *Decaloba*: all Old World species belong to this group, making it the only clade in Passifloraceae to span both the New and Old World in its distribution. *Decaloba* consists of six New World supersections, and one Old World supersection, *Disemma*. Within *Disemma*, four species are found in Northeastern Australia and New Zealand, one species is endemic to Papua New Guinea, and 19 species occur in China, India, and other Southeast Asian countries. While initial molecular analyses of *Disemma* using nuclear ribosomal ITS, cytosolic-expressed glutamine synthetase, and *trnL-F* spacer and intron support the monophyly of the supersection within subgenus *Decaloba*, morphological characters do not clearly indicate the same relationships. *Disemma* is particularly diverse in its morphology: species differ in the number of flowers per inflorescence, fusion of coronal filaments, inflorescence

branching pattern, and number of stamens and carpels. Historically, these differences have raised questions about the monophyly of supersection *Disemma* as a whole; it has been hypothesized that the Australian-Pacific species do not belong in *Disemma* but rather are more closely related to the New World members of *Decaloba*. Additionally, it has been suggested that *Disemma* may be linked to other genera within Passifloraceae (*Adenia*) due to the presence of branched inflorescences in several species. The differences between morphology and molecular data emphasize the importance of using a total evidence approach for the elucidation of phylogenetic relationships within *Disemma*.

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Phylogeny of *Castanea* (Fagaceae) Based on Chloroplast Noncoding Sequence Data

Castanea (Fagaceae) is one of many plant genera with a disjunct distribution pattern between eastern Asia and eastern North America. The genus comprises three sections and seven species, which are widely distributed in the Northern Hemisphere. To highlight the formation of the present disjunct distribution and the origin of the genus, phylogenetic analyses of the seven *Castanea* species were conducted using sequences of the chloroplast noncoding *trnT-F*, *ndhF1955F-607R* and *ycf6-psbM*. Research suggested a complicated history of the genus. The three Chinese species of *Castanea* were strongly supported as a single, monophyletic clade, and Japanese species (*C. crenata*) has the farthest relationship from the other species. Relationships within the North America species and between the European species (*C. sativa*) were not well resolved and merit further attention.

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Molecular systematics of the Caribbean sun-flower genera *Rhodogeran*

Griseb. and *Sachsia* *Griseb.* *Rhodogeran* *Griseb.* and *Sachsia* *Griseb.* (*Asteraceae*) are two genera endemic to Bahamas, Cuba, Southern Florida and Hispaniola. *Rhodogeran* is monotypic and endemic to Cuba. *Sachsia* has three species, one of them (*S. polyccephala* *Griseb.*) is restricted to Southern Florida, Bahamas, and Hispaniola. The remaining two species of *Sachsia* (*S. divaricata* *Griseb.* and *S. tricephala* *Griseb.*) are endemic to Cuba. Based on morphological grounds it is not certain whether *Rhodogeran* and *Sachsia* belong to the tribe Inuleae or the tribe Plucheeae. It is also uncertain whether these two genera should be merged into a single genus. We are using nucleotide sequences of nuclear and chloroplast genes to answer four specific systematic and biogeographical questions: (1) To which tribe do *Rhodogeran* and *Sachsia* belong?; (2) Do *Rhodogeran* and *Sachsia* form a monophyletic group?; (3) What are the phylogenetic relationships among the species of *Sachsia* and *Rhodogeran*?; and (4) Is there any correlation between the phylogeny of these genera and the biogeographical history of Southern Florida – Bahamas – Greater Antilles? A phylogenetic study of *ndhF* sequences suggests that *Sachsia* and *Rhodogeran* are part of the tribe Plucheeae and form a monophyletic assemblage. The ITS phy-

logeny supports that speciation in *Sachsia/Rhodogeran* has involved a recent dispersal event from serpentine soils of Cuba toward limestone soils of Cuba, the Bahamas and Southern Florida.

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Geographic patterns within the North American *Trillium erectum* complex: evidence from DNA sequence and morphometric analyses

The *Trillium erectum* complex is comprised of seven species confined to Eastern North America. Delineation of these species is complicated by unclear taxonomic boundaries, unusual floral color forms, geographic variation within species, and putative hybrids. These issues are most prevalent in the Southern Appalachians, where six species co-occur. We are working to understand the group's taxonomy, phylogenetic relationships of species and populations, phylogeography and post-glacial migration. This monophyletic group of closely related taxa, including both narrow endemics and wide ranging species, is ideally suited to such detailed analysis. Here we present preliminary results from 1) molecular phylogenetic analysis and 2) morphometric analysis of this complex. We have collected DNA samples from more than 250 populations across 23 states and 2 provinces. To date we have found virtually no useful sequence variation, even among species, using rapidly evolving regions from the chloroplast and mitochondrial genomes and the ITS region of the nuclear genome. Morphological variation within this species-complex appears not to be reflected in sequence evolution of organelle genomes, thus additional nuclear DNA markers and morphometric analyses are needed to resolve relationships among taxa. The nature of the DNA in *Trillium*'s large chromosomes poses many technical problems for the use of standard nuclear phylogenetic markers, but our preliminary data indicate that AFLPs can provide resolution of relationships within this group. Our morphometric analysis of the species complex includes data collected from herbarium specimens representing the entire geographic range of each taxon. This analysis reveals geographic patterns of morphological variation and identifies characters most closely associated with areas of species range-overlap. It also indicates geographic regions containing the most taxonomically confusing populations where we need to focus future sampling.

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Preliminary phylogenetic analysis of the parasitic plant genus *Alectra* (Orobanchaceae)

The parasitic habit in plants ranges from species which are still photosynthetic, obtaining only mineral nutrients and water from their hosts (hemiparasites), to those which have fully lost photosynthetic ability, relying completely on their hosts for all nutrient requirements (holoparasites). Within the primarily hemiparasitic genus *Alectra*, *A. orobanchoides* and *A. alba* have completely lost photosynthetic capacity. These two species provide the unique opportunity to investigate the shift in habit from hemiparasitism to holoparasitism within a single genus, allowing the exploration of the evolutionary loss of photosynthesis within the genus in a comparative phylogenetic framework. *Alectra* Thunb. consists of 30 species of root-parasites distributed along the east coast of Africa including Madagascar,

and extending into India; two species also occur in South America. Species diversity is greatest in South Africa with eight endemic species. Five species also occur in Madagascar, four of these being endemic as well. *Alectra vogelii* is the most economically important agricultural pest within the genus, parasitizing cowpea, groundnut, and other cultivated legumes, from Senegal to the Sudan, and south to South Africa. This parasitism is severely detrimental to crop production, and may result in complete yield loss. Evolutionary relationships among the species of *Alectra* are not well understood despite the economic importance of the genus. Molecular data show *Alectra* and the hemiparasitic *Melasma* to be monophyletic. More recent molecular data have suggested these two genera are sister to a holoparasitic genus, *Aeginetia*. Further sampling of taxa will help clarify evolutionary relationships among these genera, and will provide a more thorough test of monophyly.

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Comparative phytochemical analysis of *Ipomoea triloba* L. complex (Convolvulaceae) in Nigeria

Phytochemical investigation of populations of *I. triloba* showed significant variations. Quantitatively, tannins exhibited three significant variations A - 0.29, B - 0.42 and C - 0.56 mg ml⁻¹. The latter reading consisted of two slightly morphologically varied populations (C & D) whose tannin content differences {0.556 (C) and 0.546 (D) mg ml⁻¹} were insignificant. Qualitatively, phenols were present in only three variants (B, C, D). Similarly, the differences in the phenolic contents of the two closely related variants (C & D) were insignificant {2937.5 (C) and 2937.4 (D)} but slightly varied from the third 2925.1 (B). The fourth variant (A) showed no peaks for phenol. Cut pieces of intestine (5cm long) of freshly sacrificed rabbit contracted in chloroform-extracted-filtrate of the two similar variants (C & D) at 30 and 60 minutes but swelled in the other two variants (A & B). Variant A generated the greatest swelling at 30 and 90 minutes (2g) compared to variant B (0.1g). The taxonomic implication and potential medicinal application of the results are discussed.

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Fruit and seed morphology, germination and seedling behaviour of some taxa of *Ipomoea* L. (Convolvulaceae)

Fruit and seed morphology, germination and seedling behaviour of 16 taxa of *Ipomoea* were investigated. Seed and fruit morphology was used to construct identification key to the taxa of *Ipomoea* studied. Mechanical scarification increased seed germination from 35% to 100%. Seeds of *I. pileata* subsp. *uniflora*, *I. cairica* var. *cairica* and *I. carnea* subsp. *fistulosa* observed a period of dormancy ranging from three to over six months in soil. The first foliage leaf appeared between the Fourth and Twelfth Day of cotyledon emergence from the soil. Growth rate (measured by the rate of leaf production over time) was fastest in *I. quamoclit* and least in *I. asarifolia*. The time and leaf stage at which cotyledon became yellow and dried, stem became decumbent and shoot produced branches varied among the taxa. The truncate leaf bases of first and second leaves of *I. ugboea* and *I. obscura* were more primitive than the common subsequent and adult cordate leaves of most *Ipomoea* taxa which suggest common ancestry of the two species.

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Testing the out-of-India dispersal of Crypteroniaceae by molecular dating

Biogeographical and paleontological studies suggested that some ancient Gondwanan taxa have been carried by the drafting Indian plate from Gondwana to Asia. During this journey, the Indian island experienced dramatic latitudinal and climatic changes that caused massive extinctions in its biota. However, some taxa survived these circumstances and dispersed "out-of-India" into South and Southeast Asia, after India collided with the Asian continent in the Early Tertiary. To test this hypothesis, independent estimates for lineage ages are needed. A published rbcL tree supported the sister group relationship between the S and SE Asian Crypteroniaceae (comprising Crypteronia, Axinandra and Dactylocladus) and a clade formed by the S African Oliniaceae, Penaeaceae, and Rhynchocalicaceae and the S American Alzateaceae. Additionally, molecular dating estimates suggested that Crypteroniaceae split from their W Gondwanan sister clade in the Early to Middle Cretaceous, and reached Asia rafting on the Indian plate. Here we present molecular evidence from additional chloroplast DNA regions and more taxa to test the validity of the out-of-India hypothesis for Crypteroniaceae. Both clock-based (Langley-Fitch) and clock-independent age estimates (NPRS and Penalized Likelihood), based on maximum likelihood analyses of three chloroplast DNA regions (rbcL, ndhF, and rpl16 intron), were used to infer the age of Crypteroniaceae. Comparisons among the three dating methods revealed significant lineage effects in all three chloroplast DNA data sets. Our dating results confirm the ancient Gondwanan origin of Crypteroniaceae in the Early to Middle Cretaceous, followed by diversification on the rafting Indian plate in the Early Tertiary and subsequent dispersal to SE Asia. These findings are congruent with recent molecular dating estimates in vertebrates that also imply a central role for India in importing Gondwanan elements into Asia.

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Phylogeography of Rare California Bush Mallows (Malacothamnus: Malvaceae)

Species in *Malacothamnus* are endemic to California, Baja California, and Sonora, Mexico. The genus has been considered to contain from 11 up to 26 species. There is a great deal of morphological overlap between the species and the taxa are believed to undergo hybridization/introgression. *Malacothamnus* was chosen for study because many species are rare and several are on the brink of extinction or are reported extirpated. The internal transcribed spacer region (ITS) was used to perform preliminary phylogenetic analyses in examining interspecific relationships. The ITS region has proven useful in examining interspecific relationships in a number of groups. The results seem to agree that hybridization has occurred and continues to occur within the genus. The phylogeny produced is inconclusive about species relationships, however. Nested clade and TCS analysis will be explored to resolve relationships. Several samples for each species are included and imply hybridization patterns based on the phylogeny. The lack of genetic variation with the ITS region may not reflect the amount of morphological and chemical variation in the genus. Preliminary examination of morphological features has revealed several synapomorphies, which may prove useful in taxonomic classification of the genus.

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Rare Plants of the Ione Formation in California

Ione chaparral is a rare plant community endemic to western and northern Amador County, California. It occurs on the Ione formation, an ecologically unique substrate that has been called "one of California's Galapagos Islands" by Hartwell. This substrate consists of a sand/clay mix with little or no soil development. The Ione formation is a harsh growing environment for most plants due to its acidic nature and because it is high in aluminum and sulfur, and low in nutrients. Thus, due to its restricted nature and unique ecological characteristics, Ione chaparral supports a high number of adapted rare plants. Five taxa in particular have been targeted for further study and treatment in the U.S. Fish and Wildlife Service Ione Plants Recovery Plan: *Arctostaphylos myrtifolia* (Ericaceae), *Eriogonum apicum* var. *apicum* (Polygonaceae), *Eriogonum apicum* var. *prostratum*, *Helianthemum suffrutescens* (Cistaceae) and *Horkelia parryi* (Rosaceae). During botanical surveys conducted for a highly controversial landfill expansion project in the Buena Vista area, extensive stands of *Arctostaphylos myrtifolia*, *Helianthemum suffrutescens* and *Horkelia parryi* were documented. The natural history, biology, threats and distribution of Ione rare plant species are discussed. In addition, regulatory challenges and conservation opportunities presented by the project are summarized.

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Molecular Phylogenetics and Generic Concepts in the Maxillarieae (Orchidaceae)

Tribe Maxillarieae account for approximately 10% (>2800 species) of Orchidaceae and are a major component of the Neotropical epiphytic flora. Pollination systems include 1) male euglossine-bee fragrance rewards in four subtribes, 2) oil reward systems and mimicry in some groups, 3) nectar rewards in a wide range of taxa, and 4) pseudocopulation in some Maxillariinae and some Oncidiinae. Generic and subtribal limits have been chaotic. Current, ongoing taxonomic treatments offer little hope of stability unless the revisions are based upon well-sampled molecular and morphological cladograms. Several classically defined genera are widely recognized as being polyphyletic. Our delimitations of subtribes and genera in these advanced Neotropical groups are based on well supported cladograms from combined analyses of nuclear (ITS) and plastid (matK, trnL-F intron-spacer, and the atpB-rbcL intergenic spacer) sequences. We recognize subtribes Coeliopsidinae, Maxillariinae, Oncidiinae, Stanhopeinae, Zygopetalinae, and a monotypic Eriopsisidinae sister to these other subtribes. Subtribes Coeliopsidinae and Stanhopeinae are pollinated exclusively by male euglossine bees utilizing many different sites for pollinarium placement; the molecular phylogeny agrees closely with traditional generic limits based on morphology. Maxillariinae, Oncidiinae, and Zygopetalinae have a variety of pollination systems and classifications based on floral morphology disagree with molecular phylogenies, probably because of convergence to pollination-related floral characters. Oncidiinae are one of the most diverse groups in the Orchidaceae in terms of floral diversity and pollination biology, chromosomal numbers, and vegetative morphology. The subtribe has more than 1,000 species (possibly as many as 1,800 species) distributed in over 75 currently recognized genera.

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Horizontal gene transfer from flowering plants to *Gnetum*

While constructing a phylogeny of *Gnetum* based on one mitochondrial, two nuclear, and three chloroplast loci, we discovered a case of horizontal gene transfer of the mitochondrial (mt) *nad1* intron 2 and adjacent exons b/c from an asterid to *Gnetum*. We found that *Gnetum* has two copies of intron 2, a group II intron, that differ in their exons, nucleotide composition, domain lengths, and structural characteristics. One of them, which we have termed the gymnosperm-type copy, is present in all *Gnetum* except *G. africanum* and is most similar to the homologous region in Pinaceae. The other copy, which we refer to as the angiosperm-type, is almost identical to the homologous locus in angiosperms, and partial sequences of its exons b and c show characteristic substitutions unique to angiosperms. In an analysis of 60 seed plant *nad1* b/c and intron 2 sequences, including the major angiosperm clades, this copy groups with Petunia, the sole asterid fully sequenced for this locus. Optimizing the distribution of the two copies onto a four-gene tree of *Gnetum* showed that the angiosperm-type copy is limited to one Asian clade, suggesting that it was horizontally transferred from a flowering plant, perhaps an asterid, to that clade's ancestor. Preliminary molecular clock dating, using a calibration provided by 125-million-year old *Gurvanella*, with morphological characters on the *Welwitschia-Ephedra* lineage, suggests an age of 2 to 5 million years for the Asian clade that received the horizontal transfer. This finding provides the first evidence for natural horizontal gene transfer in higher plants.

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Lower Core-Eudicot Phylogeny Based on Combined Analysis of PISTILLATA, APETALA3, 18S rDNA, LEAFY, rbcL, and atpB Sequences

Lower eudicots and lower core eudicots are angiosperm lineages with erratic perianth numbers and floral morphologies. These plants are critical to understanding the evolution of the floral developmental program in the core eudicots. Previous phylogenies of lower and lower core eudicots based on 18S rDNA, *rbcL*, and *atpB* sequences demonstrated low support among these lineages. In this study, we performed a combined analysis of class B floral homeotic genes *PISTILLATA* (*PI*), *APETALA3* (*AP3*), 18S rDNA, *LEAFY*, and chloroplast genes *rbcL* and *atpB*, from major lineages in lower and lower core eudicots. The dataset includes taxa from Ranunculales, Proteales, Santalales, Trochodendrales, Dilleniales, Caryophyllales, Rosids, Asterids, and selected outgroups. Comparison between tree construction methods and evolutionary rates from these analyses were investigated. In addition, since several *AP3/PI* duplication events likely occurred along lower and lower core eudicot lineages, evolutionary trends of perianth development involving *PI* and *AP3* in these transitional lineages between basal angiosperms and core eudicots are discussed. This research may provide higher resolution of lower and lower core-eudicot phylogeny and further insight on perianth evolution.

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Chromosomal evolution in Araliaceae

Chromosome numbers of 20 species belonging to ten genera have been counted, of which 14 species are reported for the first time. This is also the first time to do chromosome study on genera of *Merrithiopanax* and *Metapanax*. The chromosome numbers of Araliaceae are quite uniform with $2n = 48$ or 24 except *Hedera*, in which they vary from 48 to 192. The basic number of the family is inferred to be $x = 12$. The Asian core Araliaceae clade includes approximately 18 genera, such as *Brassaiopsis*, *Chengiopanax*, *Eleutherococcus*, *Fatsia*, *Gamblea*, *Hedera*, *Kalopanax*, *Macropanax*, *Merrilliopanax*, *Metapanax*, *Olopananax*, *Schefflera*, *Tetrapanax*, *Trvesia*, and *Tupidanthus*. Genera of this clade have sometimes been regarded as evolutionarily primitive. The chromosomal data, however, suggest that this is a polyploid clade. *Aralia*, *Panax*, and *Polyscias* (outside the Asian core Araliaceae clade), on the other hand, contain species of both diploids and tetraploids. The newly counted diploid ($2n=24$) taxa are: *Aralia elata*, *A. franchetii*, *A. parasitica*, *Panax shangianus*, and *P. stipuleanatus*. The following taxa are herein reported to be tetraploids ($2n = 48$): *Brassaiopsis fatsioides*, *B. hainla*, *B. shweliensis*, *Eleutherococcus lasiogyne*, *E. trifoliatus*, *E. yui*, *Kalopanax septemlobus*, *Macropanax dispermus*, *Merrilliopanax listeri*, *Metapanax davidii*, *M. delavayi*, *Schefflera delavayi*, *S. shweliensis*, and *Tetrapanax papyrifer*.

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Challenges to Producing a Continental Flora

The flora of North America north of Mexico comprises approximately 20,600 species of flowering plants, gymnosperms, ferns and allies, and bryophytes growing in the United States, Canada, and Greenland, with new species continually being described. Attempts to produce a flora for this continental-size area over the last two centuries have all failed before they could be finished, although numerous state, provincial, and regional floras have been completed. The Flora of North America Association is coordinating the production of this continental flora. Currently seven volumes of this community effort have been published. At least two volumes per year are scheduled until the entire 30-volume work is completed by 2013. Production of accounts has become streamlined and decentralized, with separate editorial centers working in parallel, and with the project having taxon editors, regional editors and reviewers, and bibliographic and nomenclatural editors. The flora treatments are essential to efforts involving conservation, land management, agriculture, and recreation. Particular challenges are presented by the revolution in data management and availability of data, and by major changes in our understanding of relationships among plant groups. Providing electronic access to these data is an integral part of the project and will allow updating of taxonomic and other information.

409 ZHANG, LI-BING* and RENNER, SUSANNE S.
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Phylogeny of Cucurbitales inferred from seven chloroplast and mitochondrial loci

Based on *rbcL* (Setoguchi et al. 1999; Schwarzbach and Ricklefs 2000), Cucurbitales comprise Anisophylleaceae, Begoniaceae, Coriariaceae, Corynocarpaceae, Cucurbitaceae, Daticaceae, and Tetramelaceae. To further investigate the position of Anisophylleaceae and to appropriately root a large molecular phylogeny of Cucurbitaceae, we are investigating family relationships in Cucurbitales. Previous molecular data have identified Fagales as the sister clade to Cucurbitales, but prior to our project, Anisophylleaceae had only been sequenced for *rbcL*, which provided limited support for the monophyly of Cucurbitales. We have combined the chloroplast genes *atpB*, *ndhF*, *andrbcl*, the *trnL* intron, the *rlp20-rps12* and *trnL-trnF* spacers, and the mitochondrial *nad1* b/c intron (together 6422 bp) for 21 representatives of the ingroup families and two fagalean outgroups. Cucurbitales are strongly monophyletic, and Anisophylleaceae are sister to the remaining families, which form a trichotomy of (1) Cucurbitaceae, (2) Coriariaceae and Corynocarpaceae, and (3) Begoniaceae (Daticaceae, Tetramelaceae). The relationship between the last three families is similar to that found with restriction site and ITS data (Rieseberg et al. 1992; Swensen et al. 1998), and is further supported by the similar flowers of Daticaceae and Tetramelaceae. We are currently adding *matK* and 18S data sets, and our poster will explore the implications of the resolved family relationships for biogeography and sexual system evolution. With the exception of a few Coriariaceae and Corynocarpaceae, Cucurbitales have unisexual flowers, and plants are usually monoecious, with repeated shifts to dioecy in *Begonia*, Cucurbitaceae, *Datisca cannabina*, and Tetramelaceae, and to androdioecy in *Schizopepon bryoniaefolius* and *Datisca glomerata*.

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Eastern Asian-Eastern North American Floristic Disjunction-Rates of Molecular Evolution after Isolation

The EAS-ENA biogeographic pattern is documented in approximately 65 genera of flowering plants. Despite recent increased interest in this pattern, few studies compared the rates and pattern of evolution of these plants. We examined the rates of ITS evolution in 11 disjunct sister pairs from genera with ITS phylogenies available. We first conducted phylogenetic analyses for each genus using maximum likelihood method with the best-fit model of sequence evolution. We then calculated average branch lengths for the identified sister lineages using the Mean Path Lengths method and estimated molecular rates using Sanderson's NPRS method by dividing branch lengths by node heights. Among the 11 genera examined, eight pairs of EAS-ENA sisters, one in each of the following eight genera, *Styrax*, *Stewartia*, *Illicium*, *Hamamelis*, *Panax*, *Comus*, *Asarum* and *Buckleya*, and two pairs of EAS-NA (including both eastern and western North America) sisters, one in *Boyninia* and one in *Trautvetteria*, were recovered. Analyses of molecular rates indicated that for all EAS-ENA sister pairs, except *Buckleya*, the EAS counterparts exhibited higher rates than their ENA counterparts. In *Buckleya*, the rate in ENA was slightly higher than in EAS. Statistical test indicates that the rate difference between the two areas is significant. However, in the two

EAS-NA sister pairs, the rates in NA lineages are significantly higher, suggesting that rates in WNA may exceed EAS. A positive relationship between rates of ITS evolution and species richness was detected among the disjunct lineages, in agreement with the analysis of molecular rates in flowering plants, which similarly revealed a positive relationship between species number and rate of neutral molecular evolution in sister families. Our results appear to support the hypothesis that species diversity and speciation rate are biased toward eastern Asia compared to eastern North America.

TEACHING SECTION

CONTRIBUTED PAPERS

- 411 EAKIN, DAVE¹, HARRIS, KELLI*¹ and BEATTIE, RUTH²

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An assessment of the role of multimedia in enhancing student learning in freshman level biology courses

The number of multimedia products commercially produced in biology has increased exponentially. If students have different learning styles then different instructional approaches must be used to accommodate these styles. Although some research suggests that students benefit from using computer-based instructional materials - few studies have been conducted on the role of multimedia in enhancing student learning. This research covered a 4-week period using human subjects from a University of Kentucky summer course: Introduction to Biological Principles. We predicted that students who used multimedia to aid them in their learning would perform better on course examinations. The results, however, did not reflect higher or lower scores. There is a saying, "What is perceived - Is!" i.e., what people perceive as true - not necessarily what is true - becomes their reality. Perhaps the driving force behind the proliferation of multimedia tools is not that they help student performance - but simply that students perceive them to help.

- 412 KARPOFF, ARNOLD*¹ and KEMP, ANDREW²

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Teaching Teachers Experimental Botany

Most teachers are only exposed to botany in a freshman biology course means that when they enter the classroom they do not feel comfortable with botanical subject material. Thus, they fail to utilize plants as subjects to explain the biological concepts that are part on their curricula. Experimental Botany for Teachers is a course intended to reinforce student/teachers minimal levels of botanical knowledge and simultaneously develop teachers' understanding of the nature of science as inquiry by guiding them in conducting their own experiments with Wisconsin Fast Plants and C-Ferns. We also wished to teach them how to teach their own students through inquiry-oriented experiences. The Experimental Botany for Teachers course was co-developed and co-taught by a biology professor and a science educator. The course was designed to have pre-service as

well as certified classroom teachers experience "real" science, i.e., they posed questions, gathered and statistically analyzed their own data, etc. We attempted to convince the participants that understanding the science of botany as a process (inquiry), as well as a content area, would be eminently practical and valuable in their present and future roles as science teachers. Part of every class session involved collection of data and discussing the participants' ongoing experiments, as well as discussions of how to teach a particular concept or activity in a "real" school to "real" students. Having actual classroom teachers as class members as well as course adjuncts allowed the participants to visualize the problems teachers face translating what should work in the classroom to what actually happens in the classroom. We believe the joint planning and instruction by a scientist and science educator helped participants improve both their content knowledge of botany and their pedagogical skills. In addition, the participants' dispositions toward inquiry-oriented teaching were enhanced

- 413 KLEIER, CATHERINE

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Active Learning in the Plant Sciences Classroom

Active learning is a current buzzword in education. Traditional teaching models place the instructor in a position of manager or all-knowing sage. Active learning instructors view themselves as facilitators that enable students to learn. Active learning also incorporates real-world problem solving and student interaction on many levels. I have experimented with several active learning techniques in Plant Systematics, Plant Anatomy, Plant Physiology, and Plant Ecology. I will share techniques that have worked especially well for me such as talk to your neighbor, expert in the field, journal article review, and chest surveys. Active learning does not have to be integrated into every lesson, but it can facilitate student interest in challenging topics.

- 414 MACKLIN, MONICA

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Student Active Science in a Field Botany Course

Traditional field courses in the biological sciences have a strong taxonomic component and often includes a long list of species to be identified. Students must be able to identify specific organisms, understand the ecological role of that organism and learn the skills necessary to identify unknown organisms. The traditional field courses generally do not address many of the components of student-active-science. The Sparrowhawk Primitive Area (Cherokee County) was surveyed in 1963 when the land was given to the state of Oklahoma. A preliminary survey of the vegetation was made at that time. In this project students in a field biology course will develop a hypothesis, collect data, and evaluate changes in the arborescent vegetation that may have occurred in the 38 years since the original survey. This project will engage students in a class research project that requires collaborative learning, data collection, and analysis of that data. As a part of the research the students may collect data related to tree size, density, frequency and species composition. In addition to vegetation data the students will work with geographic data through handheld GPS units and GIS software.

415 RICE, STANLEY A.

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Use of Fast-Plants ® in laboratory studies of plasticity

Seeds of Wisconsin Fast-Plants ® are available in genetic varieties such as wild type, high anthocyanin, anthocyaninless, and rosette. While most often used for studies of inheritance patterns in biology laboratories, Fast-Plants ® are also useful for studying plasticity to light intensity. For all varieties, one would expect shade-grown individuals to have more chlorophyll and be relatively taller than individuals grown in higher light intensity. Anthocyanin has been implicated in shade tolerance, therefore the high-anthocyanin variety should grow relatively better in low light intensity than the other varieties, and the anthocyaninless variety have a less effective shade response. Finally, the rosette growth form is usually associated with high light intensity in open field conditions. I grew Fast-Plants ® of these four varieties in high and low light intensity in two experiments. My students weighed the plants, extracted chlorophyll with DMF, and measured chlorophyll spectrophotometrically. In one experiment, the high light intensity depressed the growth of all varieties, suggesting that Fast-Plants ® are useful for studying only a narrow range of plasticity. Contrary to expectation, shaded individuals did not have more chlorophyll. The high anthocyanin genotype exhibited less shade depression of growth. Fast-Plants ® plants may be very useful for quick, convenient laboratory investigations of plasticity, particularly since the genetic differences for shade tolerance characteristics are well known.

416 RICE, STEVEN K.* and WILLING, R. PAUL

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Students investigate forest succession by combining field data collection and simulation modeling using STELLA software

During the investigative process, biologists often employ simulation modeling to explore the implications of their empirically derived results. This allows them to apply their findings to broader or longer domains. However, this is rarely achieved in teaching laboratories. To create a laboratory experience where students approximate this process, we developed a laboratory exercise where students combined field data collection and simulation modeling using STELLA software to predict forest successional change. Students sampled forest composition within two early successional, temperate deciduous forest stands. They randomly chose canopy trees, identified them and counted the number of individuals of each sub-canopy tree species beneath it. These data were used to construct a transition matrix for each stand that described the probability that each canopy species would be replaced by each sub-canopy one. These parameters were derived from the average relative frequency of sub-canopy stems beneath each canopy species. Students constructed a simulation model of forest succession using STELLA software and parameterized it with their transition matrix. The modeling approach was based on a standard method that approximates forest compositional change using stationary Markov chains. With their models, students generated long-term projections of forest succession, related their predictions to compositional data, compared their quantitative projections for the two field sites, and evaluated published results from other forest communities in the region. More information and other exercises that combine simulation modeling with experiments are available at <http://www1.union.edu/~rices/STELLA/>.

CONTRIBUTED POSTERS417 KARPOFF, ARNOLD J.*¹ and KEMP, ANDREW C.²

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A Collaboration in Teacher Education: Experimental Botany for Teachers

This poster represents a continuation of our paper presented in the Teaching Section: Teaching Teachers Experimental Botany. The Experimental Botany for Teachers course was co-developed and co-taught by a biology professor and a science educator. The course was designed to have pre-service as well as certified classroom teachers experience "real" science, i.e., they posed questions, gathered and statistically analyzed their own data, etc. We attempted to convince the participants that understanding the science of botany as a process (inquiry), as well as a content area, would be eminently practical and valuable in their present and future roles as science teachers. Part of every class session involved collection of data and discussing the participants' ongoing experiments, as well as discussions of how to teach a particular concept or activity in a "real" school to "real" students. This course was intended to reinforce student/teachers minimal levels of botany knowledge and simultaneously develop teachers' understanding of the nature of science as inquiry by guiding them in conducting their own experiments with Wisconsin Fast Plants and C-Ferns. Having actual classroom teachers as class members as well as course adjuncts allowed the participants to visualize the problems teachers face translating what should work in the classroom to what actually happens in the classroom. We believe the joint planning and instruction by a scientist and science educator helped participants improve both their content knowledge of botany and their pedagogical skills. In addition, the participants' dispositions toward inquiry-oriented teaching were enhanced. Handouts will be available to detail the course as well as to present some of our initial findings on the ability of these students to gain an understanding into the nature of science as a process.

TROPICAL BIOLOGY SECTIONCONTRIBUTED PAPERS418 BREWER, S.W.*¹, REJMANEK, M.², WEBB, M.A.H.³

and FINE, P.V.A⁴

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Relationships between phytogeography of tree species and limestone topography in southern Belize

The phytogeography and diversity of tree species on limestone valley floors, lower and upper slopes, and ridges were compared in southern Belize. The proportions of species that had widespread distributions decreased significantly with increasing elevation above the valley floors. The proportions of species having northern Mesoamerican distributions increased significantly with elevation

above the valleys. The strongest phytogeographic affinities of the forests were for the Petén (Guatemala) and Mexico, and greater affinities for the Yucatán were observed with increasing elevation above the valley floors. Species with distributions including the Greater Antilles made up an increasingly significant element, in terms of species and numbers of stems, with increasing elevation above the floors of valleys. Valley floors and ridges had the highest percentages of species unique to their topographic positions and were very similar in diversity. Slope forests had the highest diversity of trees and were transitional in composition among the topographic positions. Stem density increased significantly with elevation above the valleys. Despite relatively small changes in elevation, the composition, diversity, and physical structure of the limestone forests changed significantly with topography. Such changes were presumably due to the enhanced edaphic drought experienced by these forests with increasing elevation above the floors of valleys.

419 FINE, PAUL^{*} ¹, DALY, DOUGLAS² and VILLA M., F. GORKY³

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The evolution of white sand specialization in *Protium* (Burseraceae) in Amazonian forests

Why are there so many species of trees in the Amazon basin? Current explanations of the extraordinarily high diversity of Amazonian trees often invoke the low overlap in species composition (high beta-diversity) between habitats such as flooded forests and terra firme, and between different soil types within terra firme forests. White sand forests represent an ideal system in which to study the evolution of beta-diversity patterns. Patchily distributed throughout Amazonia, white sand forests comprise a distinct habitat that harbors an almost completely unique composition of tree species. Although there are many genera that have representatives in white sand forests, *Protium* (Burseraceae) is one of the most speciose that has diverse assemblages of specialist species in all terra firme soil types. We conducted extensive surveys at nine sites in Peru, Ecuador, and Western Brazil and found five species of *Protium* white sand specialists. To study the evolution of beta-diversity patterns in *Protium*, we generated a phylogeny of 36 *Protium* species using ITS and ETS nuclear genes and mapped each species' soil type onto the phylogeny. The results from our phylogenetic analysis indicate that white-sand specialization has evolved independently five times in the group, with no reversions to other habitat types. Bayesian and Maximum Likelihood trees compared to a constraint tree enforcing white sand monophyly produced significantly lower likelihood values. These results suggest that white sand specialization did not arise early in the radiation of *Protium* and that either (1) there were repeated extinctions and subsequent recolonizations of white sand forests by *Protium* species and/or (2) parapatric speciation across edaphic gradients has been important in the radiation of *Protium* in Amazonia. Both of these possibilities highlight the role that edaphic heterogeneity has played in the evolutionary history of *Protium* and provide a working hypothesis to test in other plant groups.

420 GOTTSCHLING, MARC^{*}, WEIGEND, MAXIMILIAN²,

MILLER, JAMES S.³ and HILGER, HARTMUT H.²

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Phylogeny of Cordiaceae (Boraginales) inferred from ITS1 sequence data

Cordiaceae (Boraginales) are distributed pantropically and are an important element in the tropical deciduous forests and shrub communities. Traditionally, Cordiaceae comprise *Auxemma* (2 species), *Cordia* s.l. (300 species), and *Patagonula* (2 species). Furthermore, *Saccellium* and *Coldenia* (both formerly placed in Ehretiaceae) are included in Cordiaceae. Based on ITS1 sequence data, the phylogeny of Cordiaceae is largely resolved. *Coldenia procumbens* is probably the sister species of *Cordia* (200 species, pantropical) and *Varronia* (100 species, New World, usually included in *Cordia*), which in turn are sister groups. The large *Cordia* clade falls again into three monophyletic assemblages, the subclades *Collococcus* (100 species, New World), *Myxa* (50 species, mostly Old World), and *Sebestena* (50 species, mostly New World). This clear resolution is an advantage in face of numerous systematic concepts published for *Cordia*, which elevated well-recognizable species groups with distinct apomorphies to some taxonomic level, while completely disregarding the highly paraphyletic remainder. The progress is best illustrated by *Auxemma*, *Patagonula*, and *Saccellium*, which are morphologically distinctive and have been considered as distinct from *Cordia* since their first description. They can be clearly shown to be nested in the *Sebestena* subclade of *Cordia* based on both molecular data (ITS1) and morphological characters (wood anatomy, pollen surface). We prefer the recognition only of the two large clades in Cordiaceae at generic level, i.e., *Varronia* and *Cordia*, and the reduction of *Auxemma*, *Patagonula*, and *Saccellium* to synonymy under *Cordia* rather than the splitting into more than 10 genera as proposed by other authors (e.g., Friesen 1933). *Coldenia procumbens* is probably best placed as a third high-level taxon in Cordiaceae.

421 LOBOVA, TATYANA A.* and MORI, SCOTT A.

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Species of Piperaceae dispersed by bats in French Guiana

Piperaceae are common in the Neotropics and represented by herbs, subshrubs, shrubs, or rarely lianas. The fruits are small drupes displayed in terminal, axillary, or leaf-opposed spikes. Bats consume the fruits, digest the fleshy, thin, greenish or whitish pericarp, and disperse the seeds intact. Fruits and seeds were collected from feces of captured bats on four expeditions to French Guiana during different seasons. A total of 942 fecal samples with fruits/seeds were gathered and 147 of them contained seeds of 12 species of Piperaceae. The seeds of *Piper bartlingianum* were the most common, occurring 74 times in feces of *Carollia brevicauda*, *C. perspicillata*, *Rhinophylla pumilio*, *Sturnira lilium*, *S. tildae*, and *Uroderma bilobatum*. The seeds of *P. aduncum* and *P. hostmannianum* were found 41 and 29 times, respectively, in the feces of *Carollia brevicauda*, *C. perspicillata*, *Sturnira tildae*, and *Uroderma bilobatum* (only *P. hostmannianum*). *Pothomorphe peltata* and *Piper adenandrum* are less common in the fecal samples and were only consumed by

Carollia brevicauda and *C. perspicillata*. The seeds of *Piper aequale*, *P. alatabaccum*, *P. brownsbergense*, and *P. dilatatum* were found a few times in the feces of *Carollia brevicauda* and *Lonchophylla thomasi* (only *P. aequale*). *Piper anonifolium*, *P. nigrispicum*, and *P. reticulatum* are occasionally dispersed by *Carollia perspicillata*. Based on our collection, species of *Carollia* are the most common consumers of Piperaceae fruits. The seed sizes for the Piperaceae studied range from 0.5 mm (*Pothomorphe peltata*) to 2.5 mm (*P. brownsbergense*), and the shapes are globose, obovoid, square-globose, wedge-like, trigonous, or tetragonal. Two or three species of *Piper* can be mixed in one fecal sample, and the sample may also include seeds of *Banana*, *Cecropia*, *Philodendron*, *Pothomorphe*, *Rollinia*, *Solanum*, and *Vismia*. *Piper adenandrum*, *P. bartlingianum*, *P. brownsbergense*, and *P. dilatatum* have not been reported as bat dispersed.

422 MELENDEZ-ACKERMAN, ELVIA^{*1}, KRESS, W. JOHN², ROHENA, LEYDA¹, TOLEDO, ESTHER¹, GITZENDANNER, MATTHEW⁴, SOLTIS, PAM⁴ and SOLTIS, DOUGLAS ³

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Patterns of genetic and morphological variation in *Heliconia bihai*(Heliconiaceae) in the Lesser Antilles The understory herb *Heliconia bihai* has long been known to be a highly polymorphic species in which close to 24 varieties are believed to exist both in the wild and in cultivation. Natural populations of the species are distributed throughout the Lesser Antilles and northern South America with the most obvious sign of polymorphism manifested through differences in bract color. We performed a quantitative examination of the distribution of morphological and genetic variation within and between populations of *H. bihai* in the Caribbean islands of St. Vincent and St. Lucia. Morphological characterization was limited to flower and inflorescence characteristics including bract color, which was quantified using their reflectance spectra. AFLPs were used to investigate levels of genetic diversity within and between populations using four primer pairs. We discuss the relationship between patterns of morphological and genetic variation and the significance of our results in terms of the potential evolutionary forces responsible for the patterns of variation in this species.

423 SEZEN, UZAY U.* and CHAZDON, ROBIN L.
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Extreme reproductive dominance of the canopy palm *Iriartea deltoidea* in a tropical second-growth forest

Tropical second-growth forests are becoming increasingly important landscape elements. Re-colonization of young forests depends upon successful gene flow through seed dispersal. *Iriartea deltoidea* is an abundant, out-crossing, animal-dispersed canopy palm with a wide Neotropical distribution. Using Amplified Fragment Length Polymorphism (AFLP) technique, we genotyped all of the 192 reproductively mature trees (126 in 20ha of second growth and 66 in 10ha of old-growth) in a 30-ha study area at La Selva Biological Field Station, Costa Rica. Using 141 polymorphic AFLP loci we resolved parentage for 88 of the 126 trees in secondary forest. Out of 88 trees, 3

have no parents; 3 individuals have single parent and 82 have both parents within the old growth forest study area. Reproductive dominance was prevalent among second-growth founders. Among 66 potential parents in old-growth forest only 22 were represented as at least one of the parents of founding trees in second growth forest. Among 22 reproductive parents, two individuals were represented as one of the parents of 60 % of the founding individuals. Analysis among reproductive adult trees in old-growth forest resolved parentage for 37 of the 44 mature trees. Among these, 33 trees had no parents among genotyped individuals in old-growth forest, 3 individuals had a single parent represented, and only one individual had both parents within the old-growth forest study area. Seed dispersal distances exceeded pollen flow distances. Distances between parent pairs revealed that 36% of the pollination took place between 100-110m (mostly between the same two dominant individuals). Maximum pollen movement was up to 220m. Over 40% of founding adults were dispersed more than 500m from the parent, with a maximum dispersal distance of 875m. Gene flow into second-growth areas is a critically important, but poorly studied aspect of tropical forest regeneration.

CONTRIBUTED POSTERS

424 TRUSTY, JENNIFER L.*¹, KESLER, HERBERT C.² and FRANCISCO-ORTEGA, JAVIER¹

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A Floristic Inventory of Isla del Coco, Costa Rica

Isla del Coco (Cocos Island) is a small volcanic island located 500 km off the Pacific coast of Costa Rica. The island is legendary for its incredible marine life but nearly forgotten in terms of its floristic diversity. The island has an incredible rainfall of up to 7 m/yr that supports both humid tropical and cloud forest habitats. During three plant-collecting trips to the island in 2001 and 2002, over 500 plant collections were made. These collections represent 225 species. The total known floristic diversity of the island is approximately 300 species of which 29 are endemic. Identification of these plant collections has led to many new reports for the island and future work may lead to the description of as many as 5 species that are new to science.

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