

## FOREWORD

The abstracts of contributed papers, contributed posters, symposia presentations, the President-Elect's banquet address, and the plenary address for the 2000 meeting of the Botanical Society of America (BSA) are printed in this volume. The conference was held from 6–10 August 2000 at the Oregon Convention Center and Doubletree Lloyd Center in Portland, Oregon.

Abstracts are listed within the BSA disciplinary Sections chosen for presentation by the authors, and the Sections are arranged alphabetically. Within each Section, the abstracts are organized in alphabetical order by last name of the senior author within symposium, contributed paper, and contributed poster categories. In addition, each symposium includes a summary abstract. Abstracts from members of other professional societies participating in the meeting are included within affiliated BSA Sections. These include the following: American Bryological and Lichenological Society (ABLS) with the BSA Bryological and Lichenological Section; American Fern Society (AFS) with the BSA Pteridological Section; American Society of Plant Taxonomists (ASPT) and International Association for Plant Taxonomy (IAPT) with the BSA Systematics Section. The abstracts are numbered consecutively from 1 to 564, and these abstract numbers are provided for each author in the Author Index.

Assembling this abstract volume and the scientific program for the 2000 meeting 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: William Buck (Bryological and Lichenological Section–ABLS), Elizabeth Harris (Developmental and Structural Section), Massimo Pigliucci (Ecological Section), Felix Coe (Economic Botany Section), Jeri Higginbotham (Genetics Section), Vassiliki Betty Smocovitis (Historical Section), David Hibbett (Mycological Section), Steven Manchester (Paleobotanical Section), Jeffrey Johansen (Phycological Section), Denise Seliskar (Physiological Section), Emanuel Johnson (Phytochemical Section), Thomas Ranker (Pteridological Section–AFS), Sterling Keeley (Systematics Section–ASPT), Rob Reinsvold (Teaching Section), Susanne Renner (Tropical Biology Section), Tod Stuessy (IAPT), Clyde Calvin (BSA Local Representative), Keith Karoly (BSA Local Fieldtrip Coordinator), Judy Harpel (ABLS Local Representative), David Wagner (AFS Local Representative), and Carol Wilson (ASPT Local Representative). In addition, I would especially like to thank Wayne Elisens (BSA Meetings Coordinator) and Scott Russell (BSA Webmaster) for their help. These two individuals work tirelessly for the BSA and for the success of the Botany 2000 meeting.

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Cover Illustration: The deltoid balsamroot, *Balsamorhiza deltoidea*, is one of several species of balsamroot found in the Pacific Northwest. *Balsamorhiza deltoidea* is common in the central and eastern regions of the Columbia River Gorge in open meadows and oak woodlands, flowering from mid-April through May. Indigenous peoples used seed of *Balsamorhiza* species as a food source, and roots, stems and leaves as medicine.

Photo Credit: Ken Denis (1540 NE 65 Avenue, Portland, OR 97213), a local photographer whose focus is the Columbia River Gorge, particularly its great diversity of plant life.

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## I. Plenary Address

- 1** MEYEROWITZ, ELLIOT M. Division of Biology 156-29, California Institute of Technology, Pasadena, CA 91125—*Genes, genomes, and plant developmental biology.*

A central question in botany is “How do plants grow and develop?” Without a mechanistic answer, we will not be able to understand how plants interact with their environments, how they reproduce, or how they evolve. In the past decade there has been much learned from developmental genetics, starting with plants mutant in single genes, and from experiments with these plants to infer the role of individual gene products in developmental processes. Such studies have led to an outline of the mechanism of floral induction and some aspects of flower development, and of cell behavior in root and shoot apical meristems. This year we will complete the complete genomic sequence of a plant, the mustard *Arabidopsis thaliana*. From this sequence, we can roughly identify the complete list of genes necessary for all of the cellular and organismal processes of a plant. This list of parts gives us, for the first time, a view of the total complexity of a plant and its life processes. It also gives us, based on earlier work on single genes, a series of testable hypotheses for the mechanisms by which plant cells communicate with each other, and learn their positions in developing tissues. One conclusion is that plants have hundreds of receptor protein kinases of a type not found in animals, that appear to form a regulatory network for communication between plant cells that may act to control relative rates of cell division and differentiation. The *Arabidopsis* genome contains, in addition to many genes whose biochemical function can be inferred from comparison to known genes, over 10,000 genes that code for proteins that are completely unfamiliar. Thus the genomic sequence also allows us to quantitate our ignorance; the quantity is large.

## II. Address of the President-Elect at the Annual BSA Banquet

- 2** GENSEL, PATRICIA G. Department of Biology, University of North Carolina, Chapel Hill, NC 27599—*Plants, fossils, and evolution: Lessons from the fossil hunters.*

In paleobotany, and all other areas of botany, broad dissemination of the nature and significance of botanical information to lay persons, teachers, other scientists, and government officials is needed more than ever, in order to better educate them about plants and the value of understanding plant biology and diversity and the patterns and processes of evolution. The following is a template for sharing such information; merely substitute specifics from your area of inquiry in place of the underlined words. The plant fossil record, while incomplete, provides information about the history of plant life as well as contributes an historical perspective important in developing and shaping diverse investigations, including molecular approaches, of extant plants or other organisms. Major discoveries are not entirely the result of chance; in some cases specific questions were or are being pursued; examples are presented of fossil hunters who searched for, and found, evidence of 1) the pre-Silurian existence of land plants; 2) the presence of gametophytes in the Early Devonian; 3) the Devonian occurrence and radiation of seed plants; and 4) the Early Cretaceous radiation of angiosperms with great variation and innovation in floral evolution. In addition to such benchmark events, much has been learned about [insert specifics about your own field here] how and why plants have evolved; how different plants are related to one another; homology of tissues (meristems) or organs such as roots, leaves, or reproductive structures; the composition of past communities or vegetation associations and what they tell us about past climates, adaptive strategies; variations in reproduction, and importance of competition; and the distribution of various taxa throughout time. Integrating data from fossils with that derived from modern plants, at all levels from molecules to whole organisms, promises to enrich our knowledge and allow for predictions of future changes.

## III. Past-President's Symposium: New Frontiers in Botany

- 3** BASKIN, CAROL C. School of Biological Sciences, University of Kentucky, Lexington, KY 40506-0225 and Department of Agronomy, University of Kentucky, Lexington, KY 40546-0091—*New Frontiers in Botany.*

As we come to the end of the 20th century, it seems appropriate to contemplate not only the accomplishments that have been made in the plant sciences, but to wonder about the future. The papers and posters to be

presented at the Botany-2000 meeting give us a good perspective on the current state of our knowledge of a wide range of botanical topics; thus, the purpose of the symposium is to look toward the future. What can we predict (hope for!) in terms of discoveries on the origin and evolution of plants? What can we expect with regard to the impact of global change on the world and especially its impact on plants? Each of the symposium speakers has been asked to share their thoughts on how we should be training students of today, so they will be qualified to deal with the challenges of the next century.

**4** CRANE, PETER R. Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AB, U.K.—*Paleobotany: back to the future.*

Paleobotany traces its origins to the mid-nineteenth century, but at the beginning of the twenty-first century data from fossil plants have never been more relevant to understanding large scale patterns of plant evolution. Part of this renaissance has been fuelled by advances in paleobotany that have emphasised thorough integration of paleobotanical data with information from living plants. The relevance of paleobotanical data has also been greatly facilitated by renewed interest in plant phylogeny and the application of cladistic methods to both living and fossil taxa. Placed in a phylogenetic context paleobotanical data significantly expand our sample of plant diversity in time and space, and also provide a basis for beginning to understand the origins of modern plant diversity by calibrating rates of diversification. An integrated phylogenetic and paleobotanical approach to investigating plant diversification is also of great importance for understanding the origin of modern biogeographic patterns, and this is likely to be a major focus of research on plant diversity in coming decades.

**5** DONOGHUE, MICHAEL J. Harvard University Herbaria, 22 Divinity Avenue, Cambridge, MA 02138 and Department of Ecology and Evolutionary Biology, Yale University, New Haven, CN 06511—*Frontiers in phylogenetic biology.*

Although tremendous progress has been made in resolving phylogenetic relationships, phylogenetic biology is still in its infancy, and we will see major breakthroughs both in phylogenetic analysis and in the use of phylogenetic trees in solving problems. For the last decade much of the effort of the plant systematics community has been focused on a relatively few phylogenetic problems and genes. This has been productive, but extensions are needed in several directions. Much more attention is needed to the smallest phylogenetic problems, involving very closely related lineages. This will require new markers and new coalescence-oriented theory. In studies of character evolution and rates of diversification we should take better advantage of the phylogenetic knowledge that is accumulating. Methods for piecing together this information need more attention, as do methods for inferring character changes and historical correlations. I also imagine a new set of links between phylogeny and ecology, focused especially on the structure and assembly of ecological communities. These links will leverage the methods of historical biogeography and co-diversification, but require a variety of new models and tools. Finally, in view of the unprecedented rate of clade discovery, and the increasing desire to make use of phylogenetic hypotheses, we desperately need new approaches to nomenclature and to databasing phylogenetic knowledge.

**6** LEDLEY, TAMARA SHAPIRO. TERC, Cambridge, MA 02140—*Global climate change: An Earth system perspective.*

The Earth system, encompassing the atmosphere, hydrosphere, geosphere, cryosphere, and biosphere, is very complex with each component affecting and being affected by every other component on a wide range of time and space scales ranging from seconds to the age of the Earth and from microscopic to thousands of kilometers. As a result of this complexity the implications of particular climate changes for each of the components of the Earth system, the predication of future climate change, and the identification of causes of climate change are very difficult to determine. Worldwide temperature measurements indicate that there has been a warming of the global annual mean surface temperature of between 0.3°C and 0.6°C over the last 150 years. However, this warming has not been steady, with fluctuations amounting to a significant fraction of the overall warming. Such changes in the surface temperature have implications for other parts of the climate system including precipitation, evaporation, sea level, and the biosphere. In this talk the kinds of changes that have been observed over the last 150 years and predictions of changes for the next 100 years will be discussed. We will explore the impacts and potential impacts of these changes on the different components of the Earth system. Finally, the possible causes of the observed and predicted climate changes and the difficulty of identifying the causes with respect to natural variability and anthropogenic influences will be discussed.

7

SCHEMSKE, DOUGLAS W. Department of Botany, University of Washington, Seattle, WA 98195—*Ecological genetics of adaptation and speciation: Merging the old and the new.*

Most of the fundamental questions in evolutionary biology remain unanswered. For example, we still do not know how many genetic changes are required for adaptation, nor do we understand how populations acquire sufficient reproductive isolation to attain the status of biological species. The greatest progress on these issues was made 50 years ago, when Grant, Stebbins, and the Carnegie group began their classic biosystematic studies. These pioneers of plant evolutionary biology established the first links between ecology and genetics, conducting comprehensive studies of the ecology, crossing relationships, and cytogenetics of closely related species. New molecular tools provide the opportunity for a second major advance in the field. Using genetic mapping techniques, we can examine the genetic architecture of traits that contribute to adaptation and speciation in natural populations. The objective is to estimate the number of Quantitative Trait Loci (QTL) that contribute to adaptive traits, as well as the mode of action, location and magnitude of effect of each QTL. Subsequent studies use the genetic mapping information to perform marker-assisted selection, moving particular QTLs into the genomes of sister taxa. In this way we can simulate single mutations, and investigate the fitness consequences of alternative evolutionary trajectories. These methods are now being used to study the evolution of pollination systems in temperate monkeyflowers and neotropical gingers, and the evolution of serpentine adaptation in a California wildflower. Our results provide clear evidence for the role of major genes in adaptive evolution. This finding is at odds with Fisher's infinitesimal model of evolution, but is consistent with recent theory suggesting that genes of large effect are advantageous during the early stages of adaptation. This work is motivated by our desire to rebuild the links between ecology and genetics that were first established a half-century ago.

## IV. Bryological and Lichenological Section / American Bryological and Lichenological Society

### Contributed Papers

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BELL, NEIL E.\* AND ANGELA E. NEWTON. Department of Botany, Natural History Museum, London SW7 5ED, UK—*Preliminary studies of characters associated with pleurocarpy in the Rhizogoniaceae (Bryales).*

The Rhizogoniaceae is a predominantly southern hemisphere family of eubryalean mosses with a centre of diversity in Australasia and a distribution pattern suggestive of a late mesozoic Gondwanic origin. Many of the taxa are unusual with respect to characters associated with the distinction between acrocarpy and pleurocarpy, having been variously considered acrocarps or pleurocarps due to the occurrence of lateral perichaetial modules basally or distally on upright, tufted, determinate shoots. Such observations are consistent with recent cladistic analyses suggesting that at least some members of the family may be critical to the understanding of the evolution of pleurocarpy. As a prelude to a planned combined morphological and molecular phylogenetic study of the group, a preliminary examination of morphological characters was undertaken within the context of recent clarifications and redefinitions of pleurocarpy and acrocarpy. Initial observations confirm that the family contains both unambiguously acrocarpous and unambiguously pleurocarpous taxa according to currently accepted definitions and further suggest that the forms of pleurocarpy found within the Rhizogoniaceae are associated with sets of character states that are different from those associated with the "true pleurocarps".

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BENNETT, JAMES P. Institute for Environmental Studies, University of Wisconsin, 504 Walnut St., Madison, WI 53705—*Algal layer thickness in *Parmelia sulcata* as an environmental indicator.*

Samples of *Parmelia sulcata* from North American sites were sectioned and the algal layer thickness measured to test for differences from different national parks and other localities. Total thallus thickness and algal layer thickness and their ratio varied across the country, but the overall variability was low. Sites nearer urban areas tended to have lower algal layer ratios, indicating that the photobiont may be the more sensitive component to air pollution. Differences were observed even though no discoloration or other signs of stress were apparent.



- 10** BERRYMAN, SHANTI D.\* AND BRUCE MCCUNE. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97333—*Differences in epiphytic lichen communities and biomass among forest stand types in the Blue River watershed of western Oregon.*

Epiphytic macrolichen communities were compared among forest stand types in the Blue River watershed. These stand types were used to project forest management strategies as defined by the Blue River Landscape Administrative Study. Stand types were defined by stand structure, which was classified by the age of the younger cohort and the percent retention of the older cohort trees. Topographic position (upland and riparian) and vascular plant association (*Tsuga heterophylla* and *Abies*) also classified stand types. Ordination analysis revealed that the strongest differences in lichen community composition were related to an elevation gradient, which correlated to the vascular plant association. Species richness and live basal area were also important gradients in differentiating lichen communities. Sites with high species richness tended to have high basal area of live trees. Results suggested that most lichen communities with abundant cyanolichens were sampled in sites of low elevations, older age, and in riparian areas (specifically those with perennial streams). Lichen biomass was estimated for three functional groups: cyanolichens, forage lichens, and green-algal foliose lichens. Relationships between lichen community composition and biomass data were determined, and will be used to develop a model for estimating lichen biomass in different lichen communities. We acknowledge the support of the USDA National Forest Service, Willamette National Forest.

- 11** BRATT, CHARIS C.\* AND DANIEL LAHR. Santa Barbara Botanic Garden, 1212 Mission Canyon Road, Santa Barbara, CA 93105—*A comparison of the lichens on deciduous and non-deciduous oaks.*

A study was undertaken to determine if deciduous oaks had more lichen species than non-deciduous oaks. Pairs of trees close by one another and of the same size were sought in various locations. All of the lichen species were collected, identified and recorded for each site. Comparisons were made for each site and for the overall study. Bark samples were taken from each tree and measure for acidity.

- 12** BRAY JR., JAMES R. Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509—*The genus Fossombronia Raddi in North America, north of Mexico.*

Fifteen taxa have been listed for the genus *Fossombronia* Raddi in North America, north of Mexico. The difficulty in delimiting species based on gametophyte morphology has led the majority of bryologists to identify species of *Fossombronia* using characters of the distal spore wall architecture. Attempts to compare these data with other morphological and ecological data are lacking, leading to a total misunderstanding of the species within this genus. Also, many reports were based on previous literature rather than on a thorough evaluation of type material. As part of a complete revision of the genus for Europe and North America, north of Mexico, a character set generated from light and SEM analysis of type collections, supplemented with other collections and live material, was compared in a phylogenetic framework and used to generate parallel descriptions of all accepted taxa. Common garden experiments were conducted to assess morphological plasticity of the gametophyte and spore wall characters through successive generations. Based on specimen evaluation, common garden results and taxonomic reduction, a total of ten species are here recognized for North America, north of Mexico.

- 13** CARGILL, D. CHRISTINE. Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901—*A taxonomic revision of the genus Fossombronia, suborder Fossombroniinae in Africa.*

As European colonization extended across the globe, into the continents of the New World, Africa and Australia, so too the numbers of collections of plants expanded worldwide, even in inconspicuous groups such as the genus *Fossombronia*. Due to its close proximity to Europe, the continent of Africa was one of the earliest regions to yield new species within this genus. To date 37 species have been reported from the continent and surrounding islands only seven of which are cosmopolitan species common to Europe. Certainly the majority of species have been described from South Africa which exhibits a temperate to arid environment. Whether the remaining 30 taxa are truly endemic is problematic, however, since a comprehensive study of the genus in Africa has never been undertaken. In this revision, a combination of morphometric, molecular and traditional morphological methods have been used to evaluate the systematic status of all previously named species. Evaluation of the taxa described up until the early 1950's, has reduced the taxa recognized as good species to 10, many species having been moved to the genus *Austrofossombronia*. The remaining fourteen new species named by Perold from 1997-1999 are still under evaluation.

- 14** CHRISTIANSON, MICHAEL L.\* AND STEPHEN H. DUFFY. Division of Biological Sciences, University of Kansas, Lawrence KS 66045—*Salicylate-regulation of development in the moss, Funaria hygrometrica*.

While the canonical plant hormones, auxin, cytokinin, abscisic acid, gibberellic acid, and ethylene, were originally isolated and described in vascular plants, each has also been shown to be able to regulate one or more aspects of growth and development in mosses. Since mosses are the sister clade to the vascular plants, this common set of hormones is hardly surprising. There are now some additional growth regulators discovered in vascular plants, jasmonates, salicylates, brassinolides, as well as oligosaccharins and even peptide hormones, and it is not known if these molecules are also ancestral regulators or represent physiological innovations unique to the vascular plants. Using the classic bioassay system, bud-formation in the moss *Funaria*, our experiments find that exposure to salicylates produces dose-dependent inhibition of bud formation, with half-maximal inhibition at micromolar concentrations. Characterization of the time at which salicylates affect bud formation and the kinetics of the interaction with cytokinin concentration show the inhibition is not a direct antagonism of cytokinin. While these experiments do not show that mosses regularly use salicylates to regulate growth and development, they confirm the presence of a salicylate signal perception-transduction pathway in mosses and suggest its presence in the common ancestor of mosses and vascular plants. Research support, KU Undergraduate Biology Research Fund, NSF OSB-9550487.

- 15** CLEAVITT, NATALIE L. Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9—*Disentangling moss species limitations: the role of substrate specificity*.

Substrate specificity has been pinpointed as key both in explaining plant species' distributions and in differentiating types of plant rarity. The relative importance of substrate specificity to moss occurrence and rarity was evaluated for the rare moss species, *Mielichhoferia macrocarpa*, *Mnium arizonicum* and *Didymodon johansenii* and the taxonomically allied common species, *Bryum pseudotriquetrum*, *Mnium spinulosum* and *Didymodon rigidulus* var. *icmadophilus*, respectively. Substrate pH and percent organic matter were measured within five sites for each species. Sensitivity to these two substrate parameters was tested by a fragment regeneration experiment on native and non-native substrates. Evidence from field plot data and establishment experiments further resolved the role of substrate specificity in limiting *M. macrocarpa* and *D. johansenii*. There was no clear trend relating rarity to substrate specificity. The rare *M. macrocarpa* and common *D. rigidulus* var. *icmadophilus* were determined to be most specific for substrate chemistry. These two species were the only species to have a significant substrate effect in the regeneration experiment. Although *M. macrocarpa* is sensitive to substrate chemistry, quadrat data and field establishment experiments both suggest that competition may be limiting its occurrence more directly. In contrast, *Didymodon johansenii* is less sensitive to substrate chemistry than the common *D. rigidulus* var. *icmadophilus*, yet it is clearly habitat specific as it never occurs on logs without a silt layer and occurs significantly more often on larger logs of older decay stages. Significantly higher regeneration on plots with versus without silt confirm the importance of a silt layer to *D. johansenii* and further suggest that silt initially may be most important in terms of securing the fragments to log substrates. Overall, these studies highlight that 1) substrate specificity is only one factor explaining species' occurrences and 2) observed substrate limitation sometimes may result from physical rather than physiological constraints on establishment.

- 16** COX, CYMON J.\* AND TERRY A. J. HEDDERSON. Department of Botany, Duke University, Durham, NC 27708, USA and, Department of Botany, University of Cape Town, Private Bag, Rondebosch 7701, South Africa—*Molecular phylogenetic analyses of the Bryaceae (Bryales, Musci)*.

Phylogenetic relationships among the traditional taxa of the Bryaceae have been highly contentious due to uncertainty associated with homology assessment of morphological characters within the family. In particular, the reliance on sporophytic characters for the delimitation of genera has been questioned. Previous analyses based on molecular data have provided insights into the evolution of the group and established a framework for classification. Following these analyses, the Bryaceae has recently been recircumscribed to include only those members of the traditional sub-family Bryoideae (except *Leptobryum*), namely, the genera *Acidodontium*, *Anomobryum*, *Brachymenium*, *Bryum*, *Plagiobryum*, and *Rhodobryum*. Here we present analyses based on chloroplast DNA sequences (rps4 and trnL-trnF) to evaluate phylogenetic relationships within the recircumscribed family. The deepest division within the Bryaceae resolves a clade containing *Rhodobryum*, *Brachymenium* section *Leptostomopsis*, and *Bryum* section *Capillaria* subsection *Rosulata* as the sister group to the remaining sections of *Bryum*, plus *Brachymenium* sect. *Dicranobryum*, *Acidodontium*, *Anomobryum*, and *Plagiobryum*. Within the latter clade, section *Capillaria*, section *Leucodontium* subsection *Calophyllo-*



ideae, and section Caespiticia subsection Cernuiformia of *Bryum* are resolved with *Plagiobryum*. Within the sister group to this clade, section *Bryum* and Caespiticia subsection Caespiticia of *Bryum* form a clade with *Brachymenium* section Dicranobryum, *Anomobryum* is resolved as sister to *Acidodontium*, and *Bryum* sections Limbata and Apalodictyon subsection Alpiniformia form a clade. These analyses provide a preliminary basis for the interpretation of natural groups and morphological evolution in the Bryaceae.

- 17** CRANDALL-STOTLER, BARBARA. Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509—*Biology and evolution of the Fossombroniineae*.

Investigations into the biology of the four genera of the Fossombroniineae has resulted in several unexpected discoveries, a few of which will be detailed in this presentation. For example, although generally regarded as soil-dwelling, r-selective annuals of disturbed habitats, many species of *Fossombronia* are actually perennial-stayers and some may even form extensive mats over rocks and roots. Populations are often comprised of single genets which are self-fertile, spore dispersal is local and gene flow between populations is low. Cosmopolitan taxa are anthropogenic and endemics are common. *Austrofossombronia* comprises several turf-forming species, distributed not only on Antarctic Islands, but also at high elevations around the world. Within the suborder three different mechanisms of drought tolerance and/or avoidance have evolved. These include 1) forming dormant, fleshy stems, with whitened leaves which may regreen on wetting, 2) developing subterranean tubers, and 3) forming endospore-like, endogenous gemmae. Anatomical studies verify that *Petalophyllum* and *Sewardiella* form pseudoperianths and shoot calyptrae, but that *Fossombronia* and *Austrofossombronia* form a developmentally distinct, analogous structure, here termed a caulocalyx. Preliminary molecular data suggest that *Petalophyllum* is basal in the suborder and that *Fossombronia* is derived.

- 18** DE LUNA, EFRAIN\*, HIROMI TSUBOTA, DOLORES GONZALEZ, SACHIKO MAEDA, HIROYUKI AKIYAMA, TOMOTSUGU ARIKAWA, RAY TANGNEY, CYMON J. COX, ANGELA E. NEWTON, KEIKO KOSUGE, MASANOBU HIGUCHI, AND HIRONORI DE-GUCHI. Departamento de Sistemática Vegetal, Instituto de Ecología AC, Xalapa, VER 91000 Mexico—*An overview of phylogenetic relationships among families of pleurocarps: implications from variation in 16S rbcL sequences*.

As a result of several coordinated projects, *rbcL* sequences from nearly all hypnobryalean families have been obtained and compiled. Our goal was to investigate what a large data matrix of *rbcL* sequences can tell us about the relationships within the pleurocarps, what groups of taxa are supported by this sequence, and how well the *rbcL* sequence resolves the relationships between the groups. Cladistic analyses of this sequence divide the pleurocarps into three primary clades: Hookeriales A, Hookeriales B, and Hypnales *sensu lato*, which includes the Leucodontales. The strict consensus shows good resolution within groups of families, but not among the groups. Robust clades of families revealed by the present analyses include the following: [Leucodontaceae, Climaciaceae, Anomodontaceae], [Neckeraceae, Leptodontaceae, Echinodiaceae, Lembo-phyllaceae], and [Hypnaceae, Thuidiaceae, Entodontaceae, Sematophyllaceae]. The general tree topology is not congruent with previous hypotheses of relationships among suborders and superfamilies in the traditional Leucodontales and Hypnales. The phylogeny of the pleurocarps is not as yet resolved, but this study shows that the current classification of three suborders in the Hypnales and four in the Leucodontales, is no longer tenable.

- 19** DUCKETT, JEFFREY G.\*, ROBERTO LIGRONE, NEIL ANDREWS, AND KAREN SUE RENZAGLIA. School of Biological Sciences, Queen Mary & Westfield College, London, E1 4NS, UK—*The enigma of pegged and smooth rhizoids in marchantialean hepatics; a functional explanation*.

Though long cited as a key feature of complex thalloid liverworts, the functional significance of their dimorphic rhizoids has never been investigated experimentally. Cryo-scanning electron microscopy of hydrated, dehydrated and rehydrated thalli now provides the likely answer. Pegged rhizoids recover their structural and functional integrity after dehydration, whereas smooth rhizoids tend to remain completely flattened. The grooves in the carpocephala of Marchantiales may be regarded as an 'internalized' external water conducting system with the pegged rhizoids therein being the functional equivalent of hydroids and tracheids. In contrast smooth rhizoids anchor thalli to their substrata and act as gateways to the inner thallus cells for endophytic fungi. Some marchantialean taxa (eg *Monoclea*, *Neohodgsonia*) have only smooth rhizoids but these fall into two size classes. The smaller are interpreted as derivatives of pegged rhizoids that have lost their wall thickenings and desiccation-resistant properties due to existence in perpetually wet habitats.

- 20** EAKIN, DAVID A. Department of Biological Sciences, Eastern Kentucky University, Moore 235, Richmond, KY 40475—*Preliminary results of a study of the unique peristome of the genus Macrohymenium [Sematophyllaceae] using conventional and scanning electron microscopy.*

The moss genus *Macrohymenium* [Sematophyllaceae] is characterized by a peristome unique among moss genera. The author will present preliminary results of an investigation of this peristome by means of conventional and scanning electron microscopy. The outward similarity of this peristome to that found in the Regmatodontaceae will be discussed. The differences among species of *Macrohymenium* sensu Eakin will be discussed.

- 21** ELLYSON, WILLIAM J. T.\* AND STEPHEN C. SILLETT. Department of Biological Sciences, Humboldt State University, Arcata, CA 95521—*Epiphytic Bryophytes and Lichens on Sitka Spruce Trees in an Old-growth Redwood Forest.*

Old-growth redwood forests represent an extreme in the realm of forest ecology. Their canopies reach extraordinary heights (over 110 m), and individual trees can live for more than two millennia. Ferns, shrubs, and even trees are abundant as epiphytes on large branches of enormous redwood trees. However, these trees do not generally support a diverse and abundant flora of lichens and bryophytes, presumably because their bark peels easily away. In contrast, Sitka spruce, the second largest tree in redwood forests, harbors such non-vascular epiphytes in staggering abundance. Until now, no one has described the assemblage of epiphytic lichens and bryophytes on Sitka spruce. Using rope techniques for canopy access, we have conducted a floristic survey of five tall Sitka spruce trees in Prairie Creek Redwood State Park, CA. We have quantified the distribution and abundance of all non-vascular epiphyte species by sampling a fixed proportion of each tree's total branch and twig surface area. Biomass estimates were extrapolated to tree totals. Results reveal a high diversity of lichens, including abundant cyanolichens (especially *Lobaria pulmonaria*) in the upper and outer portions of tree crowns. Thick mats of mosses and liverworts dominate large branches lower in the crowns.

- 22** FORD, C. HEATHER\* AND BARBARA CRANDALL-STOTLER. Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901—*A monographic study of the genus Petalophyllum Nees & Gottsche ex Lehm.*

*Petalophyllum* is a simple thalloid liverwort that has been placed in the family Fossombronaceae along with three other genera, *Austrofossombronina*, *Fossombronina* and *Sewardiella*. In 1844, Lehmann named the genus to include *P. preissii* from the Swan River in Australia. Since its naming, there have been six other species attributed to the genus. With the exception of a few well-studied localities in the British Isles, *Petalophyllum* is poorly known. It has been accepted that this is an important genus in terms of evolution within liverworts, but its actual position within the Metzgeriidae is debatable. This study was undertaken to define species limits and variation potential, determine evolutionary trends in shoot/sporophyte associations and sporophyte anatomy and describe biogeographical patterns within the genus. Loans were obtained from herbaria worldwide and lectotype specimens were designated. Morphological characters were studied using scanning electron and optical microscopes and paraffin-sectioning techniques. Consequently, previous segregation of *Petalophyllum* along with *Sewardiella* into a separate subfamily, the Petalophylloideae, has been re-evaluated. Of the seven original *Petalophyllum* species named, only *P. preissii* in New Zealand and Australia, *P. indicum* in India and Pakistan and *P. ralfsii* in Europe and Algeria are maintained. *P. bolivianum*, named from Bolivia, was determined to be *Gongylanthus*.

- 23** GIGNAC, L. DENNIS\*, LINDA A. HALSEY, AND DALE H. VITT. L. Dennis Gignac, Faculte Saint-Jean, University of Alberta, Edmonton, AB T6G 2E1, L.A. Halsey and D.H. Vitt, Biological Sciences, University of Alberta, Edmonton, AB T6G 2E1—*Evaluating GCM outputs for 0ka BP and 6ka BP using the distribution of Sphagnum-dominated peatlands in North America.*

A model was constructed that projects the presence or absence of Sphagnum-dominated peatlands in climatic space using two variables: mean annual temperature (MAT) and mean annual total precipitation (MATP). The climatic variables in the model were then coupled to those measured at weather stations in order to plot the projected distribution of Sphagnum-dominated peatlands in North America. The projected distribution was then compared to the current bog and poor fen distribution that was reconstructed from the abundance of Sphagnum spores in cores obtained from lake sediments. That comparison revealed that the Sphagnum-

dominated Peatland Distribution Model (SPDM) had an accuracy of 90%. The climatic variables in the SPDM were then coupled with the reconstruction of the current climate (0ka BP) produced by two General Circulation Models (GCMs). The resulting geographic projections were then compared to the current distribution of Sphagnum-dominated peatlands. Results indicated that the accuracy of the Canadian Climate Centers (CCC) GCM output varied between 77 and 82% while the General Fluid Dynamics Laboratory (GFDL) GCM had an accuracy of 56%. Errors for both GCMs were mostly located in areas immediately east of the Rocky Mountains and in north-eastern North America. The SPDM was then coupled with the GCM reconstructions for the climate at 6ka BP and the resulting geographic distribution was compared to the distribution of Sphagnum-dominated peatlands that was reconstructed from Sphagnum spore counts in lake sediments for the same time period. Results indicated that the CCC output had an accuracy of 70% while the GFDL output was 45% accurate. Errors produced by the changes in climate between 6ka BP and 0ka BP (anomalies) projected by both GCMs were also evaluated. The accuracy for the CCC GCM anomalies was 69% while the GFDL anomalies accuracy was equal to 40%.

- 24** GLEW, KATHERINE. Department of Botany, The Field Museum, Roosevelt Road at Lake Shore Drive, Chicago, IL 60625—*Lichen Conservation: Rare lichens found in Washington state.*

Lichens are an important component of the environment, contributing to the diversity, nutrient cycling, animal habitat, and soil amelioration in ecosystems. Vegetation surveys for Washington state are now including cryptogams, such as lichens, realizing their importance as indicators of forest health. Some significant lichen species are infrequently found in Washington state and efforts to monitor their status has become a high priority. Of special interest are lichens associated with a Mediterranean climate found in the San Juan Islands, Whidbey Island, and the northeastern portion of the Olympic Peninsula. Following a preliminary survey completed in 1997, a list was compiled for the Department of Natural Resources and the Natural Heritage Program to determine the rarity of lichens in the state. The list consists of 110 Washington lichens. Thirty-five species are listed as Priority One, indicating that they are endangered, threatened, or sensitive. A second list of lichens, Priority Two, consists of those needing to be monitored, due to questionable status. Accurate field data and identification are required to ascertain the status of these lichens. The present list may reflect under collected species rather than rarity. Particularly problematic are the crustose lichens, due to difficulty in species determination. Distributions for these lichens are just beginning to be recorded. As taxonomic treatments of crustose lichens are developed and qualified lichenologists are employed in the state, more species are likely to be added to these lists.

- 25** GOFFINET, BERNARD\* AND A. JONATHAN SHAW. Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs CT, 06269 and Department of Botany, Duke University, Durham NC, 27708—*Phylogenetic inferences in the Orthotrichoideae based on trnL-F and rps4 (cpDNA) sequence data.*

The genus *Orthotrichum* Hedw. is one of the largest genera of mosses. Together with *Ulota*, *Stoneobryum*, *Muelleriella* and *Orthomitrium* it composes the Orthotricheae. Generic concepts in the Orthotrichaceae are based primarily on gametophytic features, whereas the infrageneric classification of *Orthotrichum* has traditionally relied almost exclusively on sporophytic features, and particularly the architecture of the peristome teeth and the degree of exposure of the stomatal guard cells. The classification of the Orthotrichaceae has recently been tested against a phylogenetic concept of taxa. This study revealed among others that species of *Orthotrichum* do not compose a monophyletic genus. Paraphyly is partially due to the recognition of oligospecific genera but also to the close affinities of some species of *Orthotrichum* to *Ulota*. Analysis of sequences of two chloroplast loci (trnL-trnF and rps4) obtained for nearly 80 exemplars of Orthotrichoideae lead to following results: *Orthotrichum*, and most of all speciose subgenera are para- or polyphyletic; *Muelleriella*, a genus of saxicolous subantarctic mosses is nested within a clade that can be defined by immersed vs. superficial stoma; subg. *Orthophyllum* is sister to the latter forming a lineage characterized by n=11 vs n=6. The hypotheses that diploidization and immersion of the stoma occurred twice in the Orthotricheae can be rejected. Similarly it is likely that dioicy is not a plesiotypic conditions, but rather evolved multiple times from monoicy. The loci sequenced hold about 10% parsimony informative characters and the trnL intron comprises about 20 unambiguous indels which define lineages within the clade of aneuploid taxa. Noteworthy is also the observation that the doubling of chromosome number is accompanied by a conspicuous acceleration of the rate of molecular evolution.

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JESSUP, STEVEN LEE. Biology Department, Southern Oregon University, Ashland, OR 97520—*Phycobiont fidelity in Umbilicaria*.

Lichen phycobionts have generally been thought to have low fidelity with mycobionts at the species rank, but that assertion has been based on scant empirical evidence. Phycobionts from populations of several *Umbilicaria* species growing both sympatrically and in disjunct single-species populations were isolated from lichen thalli and cultured. DNA was extracted from cultures and characterized with RAPD fragment profiles. Distinct phycobiont haplotypes are identified. Phycobiont haplotype fidelity within and among mycobiont lineages is analyzed. Do mycobiont and phycobiont lineages mix at random, or is there some degree of fidelity of phycobionts within and among species of *Umbilicaria*, or within and among mixed and single-species populations? Does large-scale geographic structure of phycobiont haplotypes correspond with geographic distributions of species in *Umbilicaria*? Evidence from fidelity analysis of phycobiont and mycobiont lineages across a wide geographic sample in *Umbilicaria* provides an empirical foundation for generalizations about these and other questions pertaining to cospeciation, host-switching, and geographic structure of symbiont diversity in lichens.

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JOHANNES FISHER, KIRSTEN M. Department of Integrative Biology and University and Jepson Herbaria, University of California, Berkeley, CA 94720—*The heteroblastic series in leucobryoid mosses*.

An emphasis is being placed on integrating development into systematic and evolutionary research programs. Plants provide an excellent opportunity for ontogenetic studies, as they are modular organisms which record a temporally-ordered array of leaves arrested in successive stages of development, the heteroblastic series, that arises from a single initial cell (as opposed to a meristematic region of cells in seed plants). In acrocarpous mosses, a new branch module is initiated sympodially following the production of archegonia, so the heteroblastic series is reiterated along each new branch, providing an investigator with numerous replicates. Earlier studies have indicated possible parallels between the heteroblastic series and phylogenetic transformations. Within the haplolepideous mosses, a very distinct leaf architecture known as the 'leucobryoid' morphology has arisen at least five times. Leaves of mosses with this unique architecture are dominated by at least two strata of large thin-walled dead cells (hyalocysts), with one or more layers of green cells (chlorocysts) intercalated between them. Traditional interpretation of the tissue homologies for these leaves, derived from observations of *Leucobryum* and related taxa, contends that the leucobryoid morphology arose via a gradual expansion of the costa and simultaneous reduction of the lamina. Here I examine the heteroblastic leaf series for two taxa which represent independent derivations of the leucobryoid morphology, *Leucobryum sanctum* and *Arthrocormus shimperi*, and those of their respective sister taxa, *Campylopus* and *Syrrhopodon*. When placed in a phylogenetic framework, the heteroblasty of these taxa suggests that different developmental modifications have been involved in the origins of the leucobryoid leaf. In a comparative context, heteroblasty provides evidence for transformational homologies which may not be apparent at the level of the mature plants.

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KRAYESKY, DAVID M. Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509—*A Revision of the Genus Fossombronia Raddi in north and east Asia, Oceania, the Malay Archipelago, and New Zealand*.

Since 1886 twenty-six taxa of *Fossombronia* Raddi have been reported from northern and eastern Asia, Oceania, the Malay Archipelago, and New Zealand. Of these, sixteen were named as new taxa. Although several regional studies have been published, no detailed systematic study of these taxa has ever been undertaken. I have conducted a comprehensive study of the gametophyte and sporophyte characters of all the taxa reported from the region to determine the true diversity of the genus in the study area. My study of type specimens was complemented with extensive collections of *Fossombronia* from the major herbarium of the region. This study showed that gametophyte characters, such as, oil body and pseudoperianth morphology, gametangia arrangement, thallus branching habit, and thallus color are systematically important characters that were ignored by earlier workers. Examining all characters of both generations, I conclude that there are only twelve taxa represented in the study area. Of these taxa, species such as *F. cristula* Austin, *F. foveolata* Lindb., *F. pusilla* L., *F. wondraczekii* (Corda) Dumort. ex Lindb., and *F. loitesbergii* Shiffn. have a wide distribution, being reported from several continents throughout the world. In contrast, the remaining seven species, *F. microspora* Herzog, *F. reticulata* Steph., *F. kashyapii* Srivastava et Udar, *F. intestinalis* Taylor, *F. papillata* Steph., and two species new to science, have very narrow distributions, being reported from but one or two continents.



- 29** LA FARGE, CATHERINE. Department of Biological Sciences, University of Alberta, Edmonton, Alberta T6G 2E9—*The Circumscription of the Dicranaceae (Bryopsida), with special emphasis on the subfamily Dicranoideae Based on cp DNA: trnL and rps4.*

Chloroplast DNA regions (trnL(UAA) - trnF (GAA)) are used to explore the systematic relationships of families and subfamilies within the Dicranales. Special emphasis is given to subfamily Dicranoideae of the Dicranaceae, with 17 of the 23 genera represented. 77 taxa are sequenced for trnL - trnF and 69 for rps4, 1247 characters were aligned in the final matrix, of which 1000 characters were used for the analyses. The combined data set was analyzed using maximum parsimony (MP) and maximum likelihood (ML) to examine the generic and familial relationships within the order. Bootstrap values and decay indices show that our data support the following relationships within the Dicranales: 1) the Dicranaceae are polyphyletic, 2) the subfamilies Paraleucobryoideae and Dicranoideae are polyphyletic, 3) the Rhabdoweisiaceae (cf Vitt 1984) are expanded to include members of the Dicranaceae, 4) the subfamily Campyloporioideae has a firm sister relationship to the Leucobryaceae, 5) the Dicranelloideae are excluded from the Dicranaceae sensu stricto, 6) the Dicnemonaceae form a monophyletic clade, including Mesotus (subfamily Mesotoideae, cf Allen 1987) that are nested within the Dicranaceae, and 7) the Ditrichaceae are polyphyletic. The cpDNA data strongly suggest the need for a reevaluation and circumscription of the Dicranaceae. Within the Dicranaceae sensu stricto there are 4 major clades: 1) Leucoloma - Sclerodontium as the basal clade, 2) Dicranoloma - Braunerfelsia - Cryptodicranum - Holodontium, 3) Chorisodontium - Orthodicranum - Paraleucobryum - Dicranum - Eucamptodontopsis - Schliephackea - Holomitrium, and 4) Dicnemon - Eucamptodon - Mesotus clade. Excluded from the Dicranaceae sensu stricto are Arctoa, Brothera, Campylopus, Cynodontium, Dicranella, Dicranodontium, Dicranoweisia, Hydrodicranum, Kiaeria, Kingiobryum, Oncophorus, Oreas, Symblepharis, and Trichodontium.

- 30** LIGRONE, ROBERTO\*, KAREN SUE RENZAGLIA, NEIL ANDREWS, AND JEFFREY G DUCKETT. Facolta di Scienze Ambientali, Secondo Ateneo Napoletano, Via Arena 22, 81100 Caserta, Italy—*Multiple evolution of water-conducting systems in bryophytes.*

All internal water-conducting elements in land plants have three common features; they are dead at maturity, have specialized cell walls and conduct water preferentially as a consequence of transpiration. In bryophytes these elements range from short, thin-walled cells with small plasmodesma-derived holes in Calobryales and *Takakia*, elongate, thick-walled cells with large perforations in a few metzgerialean taxa (*Pallavicinia*, *Symphyogyna*) to very highly elongate imperforate cells (hydroids) in endohydric mosses. Developmental cytological studies indicate that, contrary to long established dogma, none of these are the same as tracheary elements in vascular plants but appear to have closer affinities with elements found in Devonian fossils. Cryo-scanning electron microscopy reveals that the "hydrolysed" appearance of the end walls of hydroids, as seen by transmission electron microscopy is an artefact of aldehyde fixation. The unique ability of hydroids to retain their functional integrity through periods of dehydration is related to a protein moiety in their end walls that renders the cells highly resistant to cavitation.

- 31** MCCUNE, BRUCE. Department of Botany, Oregon State University, Corvallis, OR 97331-2902—*Lichen transplant results pose a treetop paradox.*

Three groups of students designed and executed lichen transplant studies in an old-growth *Pseudotsuga-Tsuga* forest at the Wind River Canopy Crane in the southern Washington. Each team focused on a particular question or hypothesis of their own choosing. This paper does not address their specific hypotheses, but rather summarizes differences in growth with respect to height in the canopy. Four species of macrolichens grew much faster in middle to upper canopy positions than in the lower half of the canopy, based on 300 transplants. This held true for species that peak in the upper canopy (*Letharia vulpina* and *Usnea filipendula*) as well as those with peak abundance in mid canopy (*Lobaria oregana* and *Lobaria pulmonaria*). Lichens lost weight or died below the light transition zone. These results can be mimicked by a simple model of lichen net photosynthesis (Ps) as a function of cumulative leaf area (CLA) - leaf area above a certain level in the canopy. CLA influences both light and moisture regimes. We hypothesize that gross Ps, integrated over a year, increases to a plateau with canopy height, while respiration decreases linearly with canopy height. The dependence of CLA on height in the canopy will vary a lot from forest to forest and is likely to be an extremely important variable in controlling the epiphyte profile. The paradox is that some species (*Lobaria oregana* and *Lobaria pulmonaria*) grow faster at higher levels in the canopy than in their stratum of peak abundance. Possible resolutions of the paradox invoke competition, uncommon extreme environmental events (such as extreme high or low temperatures), and dispersal limitations.



- 32** MCDANIEL, STUART F.\* AND JON SHAW. Department of Botany, Duke University, Durham NC, 27708—*Morphological change is decoupled from molecular evolution in disjunct populations of *Pyrrhobryum mnioides* (Hook.) Manuel.*

Many morphologically defined bryophyte species show intercontinental disjunctions, a pattern rare among vascular plants. Morphologically similar forms in geographically disparate bryophyte populations may also be genetically similar, as a result of either limited evolutionary potential or very effective long-distance dispersal. Alternatively, disjunct populations of bryophytes may be genetically differentiated, but morphology may be a poor indicator of molecular evolution. I employed phylogenetic analyses, in conjunction with morphological studies, to evaluate these two hypotheses in the case of *Pyrrhobryum mnioides*, a moss common in moist temperate forests in Southeastern Australia, Tasmania, New Zealand, Patagonia and Andean South America. DNA sequence data from the nuclear (ITS and 26S) and chloroplast (*trnL* and *rps4*) genomes indicate that Australasian and American populations of *P. mnioides* are reciprocally monophyletic. The results show evidence of neither intercontinental gene flow nor depressed levels of molecular evolution. The morphological analyses support the assertion of Fife (1995) that populations from the two continental regions are subtly different.

- 33** MEIJER, WILLEM. School of Biological Sciences. University of Kentucky, Lexington KY 40506-0225—*Aims and prospects for the global biodiversity studies of Bryophytes, Hornworts and Lichens.*

With all our efforts for genetic research do we care for what the general public would like to learn about our non vascular embryonic cryptogams? If we stay in our ivory towers we may ultimate loose all public support and cryptogam studies might wither away as fast as the habitats we like to see preserved. Our efforts in research, teaching and public education are in need of rethinking. People walking in the rich forests of the Appalachian mountains or somewhere in the Rockies or the temperate rainforests of the Pacific Northwest and naively looking for some users friendly books on our beloved cryptogams will be disappointed. In Great Britain, the Mid European region and Japan, good non-vascular cryptogam floras, pocket editions of floras are now available, but not in the Malesian area between China and Australia. Rudi Schuster once said, for Eastern North America, “we need an integrated survey of the field of Hepaticology”. After he finished his monumental work forty years later who can afford to buy his flora? What we should do is to make the Federal agencies dealing with National parks, National Forests and Wild life areas more aware of this. Bold plans for the speedy production of concise user friendly guides are needed. Microscopes should be considered as much needed as Computers at Field research stations and at local magnet schools surrounded by Natural Areas. Young people should be introduced to the life of non vascular cryptogamic plants at their high schools if not earlier. The production of local florulas should be sponsored as much as possible. Emphasis should be put in the first place on distinction of genera, the study of living plants and their ecology. For several reasons this is much more needed for liverworts than mosses.

- 34** MIADLIKOWSKA, JOLANTA\* AND FRANÇOIS LUTZONI. Department of Botany, The Field Museum, Chicago, IL 60605—*Coevolution of symbiotic associations within peltigerous lichens (Peltigerineae, Ascomycota).*

The common occurrence of tri-membered symbiotic associations in the Peltigerinae offers a unique opportunity for studying coevolutionary trends among all symbionts involved in lichen symbioses. Based on a phylogenetic study of SSU and LSU nrDNA from the mycobiont and the cyanobiont found in a broad selection of species belonging to the Peltigerineae, a monophyletic circumscription of the suborder is proposed here. Ancestral symbiotic states (bi- versus tri-membered symbioses) for peltigerous lichens were reconstructed using maximum likelihood as the optimization criterion. In addition, the pattern of transmission (horizontal versus vertical) of cyanobacterial lineages during the evolutionary history of the Peltigerineae was investigated.

- 35** MILLER, DONNA H.\*, HARVEY A. MILLER, SHILOH JONES, AND PAUL SPARKMAN. Department of Biology and Environmental Science, University of West Alabama, Livingston, AL 35470—*Bryophytes of the Alabama Black Belt chalklands.*

The Alabama Black Belt parallels the southern edge of the Fall Line Hills and is characterized by Cretaceous chalk exposures sometimes overlain by a shallow layer of alluvial loams. Chalk exposures vary from nearly level surfaces to perpendicular bluffs of different directional orientation. Flat to sloping chalk soil areas are characterized by Virginia red cedar and grasslands. Steep sided gullies are more mesic and support hard-

woods. Bryophytes collected from Black Belt sites have yielded many new county records reflecting mostly the lack of previous collecting. When compared to the bryophytes reported from European, especially Great Britain, chalk areas, species parallels were noted as well as many generic congruities. Although diversity is not so great as occurs in the geologically diverse mountainous areas in the northern part of the state, the flora is clearly rich as well as reflecting the uniqueness of this physiographic province.

- 36** MILLS, SUZANNE ELIZABETH\*, S. ELLEN MACDONALD, AND DALE H. VITT. Department of Renewable Resources, University of Alberta, Edmonton, Alberta, T6E 7E6—*Patterns of bryophyte species diversity at three scales in conifer dominated boreal forest stands.*

The maintenance of species diversity is becoming a key component of sustainable forest management. In the boreal mixedwood of northern Alberta, conifer dominated stands over one hundred years old are among those most threatened under present harvesting regimes. These stands are also important habitat for many bryophyte species. Wise management requires an understanding of the mechanisms controlling bryophyte species richness and evenness in order to either facilitate the identification of species rich areas or to improve the bryophyte habitat in managed stands. This study examines the relationship between microclimate and substrate availability, and bryophyte species richness and evenness at different scales. I sampled bryophyte species occurrence and abundance at three scales: the stand (10 ha), the mesosite (25 X 25 m plots to capture within stand variation), and the microsite (structural elements of the boreal forest providing unique substrates for moss colonization). Percent full sun, PPFD (Photosynthetic Photon Flux Density), soil moisture and pH, vascular plant species richness, microtopography and area of available substrate were measured to estimate inter-mesosite variability. Microsite variability was estimated using a relative measure of mean exponential temperature in combination with descriptive classes of substrate quality. Sampled microsites consisted of 74 stumps, 88 logs, 90 trees, 90 patches of undisturbed soil and 33 patches of disturbed soil. Light and temperature were more variable within stands than between stands (57% and 19 % of the variation respectively), while soil moisture and pH were more variable at the stand level (72% and 30% of the variation respectively). The stand with the greatest species richness had the greatest vascular plant species richness, as well as the highest soil moisture and pH. Bryophyte species richness and evenness is related to variability in forest structure and environment both within and between stands.

- 37** NEWTON, ANGELA E.\*, CYMON J. COX, EFRAIN DE LUNA, AND LARS HEDENAS. Department of Botany, Natural History Museum, London, SW7 5BD, UK, Duke University, Durham NC 27708, U.S.A., Instituto de Ecología, A. C., Xalapa, Veracruz, Mexico and Swedish Museum of Natural History, Stockholm—*Evolutionary radiation of the pleurocarpous mosses: phylogenetic analyses incorporating morphological characters with rbcL, rps4 and trnL-trnF sequence data.*

The three hypnobryalean orders of pleurocarpous mosses, Hookeriales, Hypnales, and Leucodontales, are difficult to define using morphological criteria, with "defining" characters of a group often appearing elsewhere and species and genera repeatedly shifting allegiances. Similarly, the circumscription and relationships of the eubryalean pleurocarps, and their relationship to the hypnobryalean pleurocarps and acrocarpous outgroup taxa, is also problematic. Results of phylogenetic analyses of pleurocarpous mosses using molecular sequence data, from the rbcL, trnL-trnF, rps4 and 18S genes, have underscored this problem. In the current analysis, using molecular characters, the hypnobryalean orders form a monophyletic group with exemplars from the Hookeriales in a clade sister to exemplars from the Hypnales and Leucodontales, but with these two orders paraphyletic and poorly resolved. This pattern, seen also in earlier studies, indicates a rapid evolutionary radiation, with very short internodes that are difficult to resolve satisfactorily with the molecular sequence data at hand. However, whereas molecular sequence characters are generally thought to evolve in a regular, "clock-like" fashion, morphological characters are thought to evolve following a different pattern, with long periods of stasis interspersed with periods of rapid change. Morphological characters may therefore be able to resolve the relationships of taxa involved in rapid radiation events. Many moss morphological features are difficult to define as characters and states for cladistic analysis, especially those "gestalt" characters that have played a large part in taxonomic concepts. Other features show extensive and complex variation that may represent several different characters. Branching architecture and rhizoid morphology are two such complex features that have been deconstructed to yield characters for inclusion in cladistic analyses, and to provide a basis for study of the evolution of these features.

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PONZETTI, JEANNE\* AND BRUCE MCCUNE. Department of Botany and Plant Pathology, Cordley 2082, Oregon State University, Corvallis, OR 97331-2902—*Biotic soil crusts of the Columbia River Basin: landscape level variation in community composition.*

We examined biotic soil crust communities in the Horse Heaven Hills of Benton County, Washington, USA. Our study area consisted of over 5,000 acres of arid shrub-steppe habitat dominated by *Pseudoroegneria spicata* and *Poa secunda*, with scattered patches of *Artemisia tridentata*. We stratified the area into six topographic positions: ridges, toe slopes and benches, cool slopes, warm slopes, cool draws, and warm draws. We collected abundance data on species and morphological groups of terricolous lichens and bryophytes in 350 plots. Dominant species and morphological groups at this site include *Tortula ruralis*, short mosses group, *Cladonia pocillum* group, *Diploschistes muscorum*, *Leptochidium albociliatum*, *Leptogium* spp., and *Trapeliopsis bisorediata* sp. nov. We found that the biotic soil crust communities varied by topographic position and previous soil disturbance. Warm draws and cool draws had the lowest crust cover and the fewest species. Crust cover and diversity were inversely related to cover of *Bromus tectorum*. In addition, community composition varied by aspect, slope, and soil chemistry. The biotic crust communities appeared resilient to historical fires known from the past 18 years. Overall, we found considerable variation in biotic soil crust communities within this study area. We recommend that land managers consider the landscape level variability in soil crusts when monitoring and assessing impacts to these organisms.

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PRICE, MICHELLE J. Missouri Botanical Garden, P.O. Box 299, St. Louis, MO 63166-0299, USA—*A preliminary cladistic analysis of the Dicranoideae (Dicranaceae, Musci) based on morphology.*

The Dicranaceae, a large and variable moss family, contains around 1000 species and 55 genera that are divided into several weakly demarcated subfamilies. The large subfamily Dicranoideae is generally characterized by: a narrow costa; well developed alar cells; differentiated perichaetial leaves; a short capsule neck; phaneroporic stomata; and variously bifid or undivided papillose peristome teeth. A preliminary cladistic analysis of 51 taxa using 35 morphological characters indicates that there are two main groups in the subfamily. One centered around *Holomitrium* (including *Eucamptodontopsis* and *Schliephackea*) and one around *Dicranum-Leucoloma*. This analysis has highlighted some of the problems associated with character evaluation in a group where characters are variable both between and within genera.

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REEB, VALERIE C.\*, CLAUDE ROUX, AND FRANCOIS M. LUTZONI. University of Illinois at Chicago, Department of Biological Sciences (M/C 006), 845W Taylor Street, Chicago IL 60607. The Field Museum, Department of Botany, 1400S Roosevelt Road, Chicago IL 60605. Faculté des Sciences et Techniques de St-Jérôme, Institut Méditerranéen d'Écologie et de Paléoécologie, case 461, Av. Escadrille Normandie Niemen, F-13397 Marseille Cedex 20, France—*A phylogenetic study of the Acarospora and Acarosporaceae (lichen-forming ascomycetes) and their position within the ascomycetes.*

The genus *Acarospora* and the family Acarosporaceae are among the most complex and poorly known lichen-forming ascomycetes. Cryptolecanorine apothecia and multiple post-meiotic mitoses resulting in polyspory are features that characterize the family. Because many characters are cryptic or are highly variable within *Acarospora*, their classification at almost all levels (species to order) is very unstable. Preliminary DNA sequence data revealed that *Acarospora* is among the basal members of the "Lecanoromycotina". This basal phylogenetic position renders it of particular importance for understanding the evolution of the majority of lichenized ascomycetes. We will report on results from phylogenetic analyses of SSU nrDNA, LSU nrDNA, and ITS sequence data and present evidence for a re-circumscription of *Acarospora*. We will test for monophyly of the yellow (subgenus *Xanthothallia*) and brown (subgenus *Phaeothallia*) *Acarospora* and suggest approaches for achieving a new and stable classification for Acarosporaceae.

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RICE, STEVEN K.\* AND DAVID COLLINS. Department of Biological Sciences, Union College, Schenectady, NY 12308—*Living within boundary layers: the functional significance of variation in bryophyte canopy structure.*

In most bryophytes, the thickness of boundary layers (i.e., unstirred layers) that surrounds plant surfaces governs rates of water loss. Since bryophytes lack short-term control of this process, architectural features of canopies that influence boundary layer thickness affect the water balance of bryophytes. Using field samples (9.5 cm diameter cushions) from 12 species (n=3 per species) of mosses and liverworts, we evaluated the relationship between canopy structure and boundary layer properties. Canopy structure was char-

acterized using a contact surface probe that measures canopy depth at spatial scales ranging from 0.08 to 3 cm at 186 points per sample. Variance in depth measurements at different spatial scales was used to estimate surface roughness (SR). Boundary layer properties were measured by evaporation of ethanol from samples in a laminar flow wind tunnel (0.8 to 3.5 m s<sup>-1</sup>) and applied to characterize mass transfer of cushions using principles of dynamic similarity (i.e., using dimensionless representations of conductance and flow). All bryophyte cushions exhibited the characteristics of turbulent as opposed to laminar boundary layers that results from the generation of turbulent flow over rough bryophyte surfaces. Bryophyte canopies with higher SR (at 0.8 cm sample scale) had greater conductances at all windspeeds. However when compared to species with high SR, species with low SR had proportionally greater increases in conductance at higher windspeeds, a pattern associated with increased turbulence. Thus, canopies with low surface roughness retain laminar boundary layers at low windspeeds, and maintain low rates of evaporation. However, at high windspeeds these species experience greater turbulence causing increased evaporation rates which approach those found in species with high SR.

- 42** RUSSELL, ANGELA J.\*, RIADH FRANCIS, ROBERTO LIGRONE, JEFFREY G. DUCKETT, AND DAVID READ. School of Biological Sciences, Queen Mary and Westfield College, Mile End Road, London., E1 4NS, UK—*Symbiotic fungal associations in liverworts.*

Three fungal phyla, which form mycorrhizas in higher plants, also form symbiotic fungal associations in liverworts. Zygomycetous fungi colonise a range of thalloid liverworts where they produce structures analogous to those seen in the vesicular-arbuscular (VA) mycorrhizas of higher plants. Experiments reveal that glomalean fungi forming typical VA mycorrhizas with a higher plant (*Plantago lanceolata*) can colonise a thalloid liverwort (*Pellia fabroniana*) producing arbuscules and vesicles in the thallus. Some members of the Jungermanniales and Metzgeriales form associations with basidiomycetous fungi, which produce intracellular hyphal coils similar to the pelotons seen in orchid mycorrhizas. The fungal associates of the autotrophic *Aneura pinguis* and its heterotrophic relative *Cryptothallus mirabilis* have been isolated. Resynthesis experiments have shown that the fungal symbiont of *Cryptothallus* is an ectomycorrhizal associate of *Betula* suggesting an explanation for the apparently obligate nature of the association between the two. Ascomycetous associations are found in the Cephaloziaceae and Lepidoziaceae. Cross-inoculation experiments have shown that a typical mycorrhizal endophyte of ericaceous plants, *Hymenoscyphus ericae* will colonise the rhizoids and underground axes of these plants. Ascomycete-containing hepatics are particularly conspicuous associates of the Ericaceae and Epacridaceae. Metzgeralean genera with VA-fungi are most diverse in the podocarp forests of New Zealand. Nutrient exchange between these hepatics and seed plants via common mycobionts is currently under investigation.

- 43** SASTRE-DE JESÚS, INÉS\*, DOLORES GONZÁLEZ, AND EFRAIN DE LUNA. Biology Department, University of Puerto Rico, Mayagüez Campus, Mayagüez, Puerto Rico. 00681—*Phylogenetic position of the Neckeraceae (Musci) based on rbcL gene sequences.*

The Neckeraceae have been placed within the Leucodontales suborder Neckerinae. Some authors have suggested a relationship of the family with *Climacium*, *Hypnodendron*, *Phyllogonium* and *Echinodium*. Our objective is to determine the phylogenetic position of the Neckeraceae within the pelurocarpous mosses using nucleotide sequences of *rbcL*. These sequences were determined for 10 genera of the Neckeraceae (for example *Neckeropsis*, *Homalia*, *Porotrichum*) and added to 30 other sequences available from exemplars of families in the Climaciineae, Leucodontineae, Pterobryineae. Cladistic analyses of 40 taxa showed that the Neckeraceae is a monophyletic group as represented by *Neckera*, *Homalia*, *Homaliiodendron*, *Porotrichum*, and *Neckeropsis*. This clade is sister to the Lembophyllaceae, Echinodiaceae, and Myuriaceae. Basal to this large clade are exemplars of the Brachytectiaceae and Plagiotheciaceae.

- 44** SILLETT, STEPHEN C.\*, BRUCE MCCUNE, JERILYNN E. PECK, AND THOMAS R. RAMBO. Department of Biological Sciences, Humboldt State University, Arcata, CA 95521—*Four years of epiphyte colonization in Douglas-fir forest canopies.*

In 1995, we installed surface-sterilized Douglas-fir branches with either rough bark or smooth bark in clear-cuts, young forests, and old growth. Half of the experimental branches were inoculated with propagules of the epiphytic cyanolichen, *Lobaria oregana*. In 1997, we concluded that *L. oregana* was associated with old-growth Douglas-fir forests because of dispersal limitation; addition of *L. oregana* propagules resulted in a marked increase in establishment rates. In 1999, we revisited the experiment to determine whether other epiphytes had colonized the tree branches. We also checked to see if the 1997 results of the experiment persisted. A total of 26 epiphyte genera (9 bryophytes and 17 lichens) had colonized the branches. Lichen



colonization was generally fastest in clearcuts. Colonization by alectorioid lichens was rapid in both clearcuts and old growth but slow in young forests. In contrast, bryophyte colonization was relatively rapid in all age classes but slowest in clearcuts. Colonization was generally more rapid on smooth bark than on rough bark, although *Cladonia* was more frequent on rough-barked branches. Bryophytes, cyanolichens, and *Sphaerophorus globosus* were more frequent on inoculated branches than on control branches, implying that the *L. oregana* propagule mixture used in 1995 was contaminated with other epiphytes. Like *L. oregana*, these species may also be dispersal-limited. The number of established *L. oregana* thalli in clearcuts and young stands decreased from 1997 to 1999, but the number of thalli remained relatively stable in old growth. After four years, established *L. oregana* thalli were larger in clearcuts than in either young stands or old growth. Overall, the fourth-year results of our experiment confirm the importance of dispersal limitation as the cause of old-growth association in *L. oregana*.

- 45** STARK, LLOYD R. Department of Biological Sciences, University of Nevada, Las Vegas, NV 89154-4004—*Widespread sporophyte abortion following summer rains in Mojave Desert populations of *Grimmia orbicularis*.*

The normal phenological sequence in *Grimmia orbicularis* restricts sporophyte elongation in Mojave Desert populations to the winter months, when low temperatures and sufficient rainfall occur. During 1997, however, heavy rainfall was restricted to the summer months. Coincident with these summer rains, over 50% of the cohort sporophytes aborted, with the time of abortion traceable to the period that followed the summer rains. Abortive sporophytes were arrested at or near the end of the embryonic phase, just prior to seta elongation. It is postulated that the unusually high frequency of abortive sporophytes was caused by the absence of winter rains in conjunction with torrential summer rains. The accelerated hydration/rehydration cycles that occur during summer rains allow insufficient time for desiccation recovery processes critical for sporophyte survival.

- 46** STOTLER, RAYMOND E.\*, JAMES R. BRAY, JR., AND D. CHRISTINE CARGILL. Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509—*Typifications in the genus *Fossombronia* (Marchantiophyta) - Problems and solutions.*

Due to the overwhelming lack of modern taxon studies in the Marchantiophyta, relatively few species have been typified. As a result, it is not uncommon to find that the current interpretation of a species is not compatible with the actual type specimen. This is the problem that we encountered with *Fossombronia angulosa*, the type of which proved to be *F. pusilla*. The only solution, in this case, that will preserve current usage of *F. angulosa* is to propose conservation. A second kind of problem was encountered with type collections that contained two or more species of *Fossombronia*. In several instances, such mixed collections were compounded by the issue of exsiccatae sets. These problems have been found associated with several European and North American species. In this scenario, careful selection among the duplicates is most critical to maintain contemporary application of each name. Type specimen designations, such as those we have effected with all taxa in the genus *Fossombronia*, are essential not only to circumscribe correctly each taxon, but also to insure stable nomenclature for the future.

- 47** VON KONRAT, MATTHEW J.\* AND JOHN E. BRAGGINS. Plant Sciences, School of Biological Sciences, The University of Auckland, Private Bag 92019, Auckland, New Zealand—*Studies on sporophytic characters in *Frullaniaceae* (Hepaticae) using novel techniques.*

The systematics of Frullaniaceae is traditionally based mainly on characters of the gametophyte, while the relevance of sporophytic characters has, with few exceptions, not yet been critically investigated. However, there are many potentially useful taxonomic and phylogenetic characters associated with the sporophyte and critical examination of these is essential for any modern systematic study of the group. Various factors have contributed towards the paucity of detailed sporophytic examination. Firstly, sporophytes for critical taxa were unknown until recently, and secondly, morphological and anatomical characters associated with the sporophyte are frequently difficult to objectively analyse and draw. The practical difficulties in examining these characters include: the three dimensional structure of the capsule wall thickenings and the surface ornamentations of the spores and elaters; the often very small size of the valves; and their heavy pigmentation. Therefore, special preparative and microtechnical procedures are required to examine characters associated with the sporophyte, especially the different layers of the capsule wall. Here we present, results of our comparative studies using new techniques that largely overcome these difficulties in interpretation and analysis. These techniques can also potentially be applied to other hepatic genera and families and to other types of tissue with appropriate modifications. Characters evaluated include: anatomy of capsule wall thickenings;



elater number and arrangement; and surface ultrastructure of the capsule walls, elaters, and spores. The taxonomic and phylogenetic value of these characters for several *Frullania* species is discussed.

- 48** WALL, DENNIS P. Dennis P. Wall, Department of Integrative Biology &, University and Jepson Herbaria, University of California, Berkeley, Berkeley, CA 94720—*Population structure and diversification patterns in the paleotropical endemic moss, Mitthyridium.*

Studies of diversification rate shifts require knowledge of both phylogeny and time. Yet, even with these components, the picture remains incomplete if the goal is to determine causal factors driving such shifts. The present study uses biogeographic, ecological and biological data within one phylogeny of a paleotropical endemic moss, *Mitthyridium* to dissect causal factors driving its relatively recent radiation. *Mitthyridium*, a monophyletic and distinct group, has a relatively narrow geographic distribution including several island endemics and may represent a model radiation. Relationships of lineages below the traditional species level in the group were discovered through phylogenetic analysis of faster evolving regions in the nucleus (Glyceraldehyde-3 phosphate dehydrogenase (GPD)), and chloroplast (3' spacer regions of *rbcL* and *rps4*) using samples from across most of the distribution of *Mitthyridium*. GPD is a single copy nuclear gene that provides appropriate variation for phylogeography. The present study introduces this glycolytic gene as new to studies of moss systematics and demonstrates its utility for phylogenetic reconstruction, with special emphasis on the population structure of *Mitthyridium*. Results show that subspecific lineages are biologically distinct and island specific. A particular biological feature distinguishing the lineages—variability in sexual expression (from fully sexual to vegetative)—was mapped to the phylogeographic structure to test the influence of reproductive mode on rate shifts. Preliminary results indicate trends towards increasing asexuality among island populations of *Mitthyridium* that are correlated with geography. The shifts in reproductive mode, when localized along the phylogeny, are significantly concentrated with changes in rates of diversification, both in anagenetic and cladogenetic contexts. These results allow for a rigorous examination of causal mechanisms driving rapid evolutionary radiation on oceanic islands.

- 49** WEAKLEY, ALAN S.\*, MELISSA M. KARANOSKY, AND LARRY E. MORSE. Association for Biodiversity Information and The Nature Conservancy, 4245 N. Fairfax Dr., Arlington, VA 22203—*Conservation priorities for North American bryophytes and lichens: A progress report.*

The need for conservation of bryophyte and lichen species and their habitats is being increasingly recognized in the United States and Canada. However, relatively few species in these groups have been formally identified as conservation priorities. Scientific staff of The Nature Conservancy (and now the Association for Biodiversity Information), working in cooperation with various bryologists and lichenologists and with state and provincial conservation botanists, began documenting bryophyte and lichen species of conservation concern in the mid-1980's. By early 2000, initial review had been completed for all North American liverworts and hornworts and most mosses, but only a few hundred lichen species. Data are being developed using the Conservancy/Heritage system of global conservation priority ranks (G1 - G5, with G1 for rarest or most vulnerable, and G5 for widespread, abundant, and secure). Our goal is to conduct initial screening of all species accepted in the pertinent ABLS checklists, determining an estimated rank for each. We can then give greater attention to those initially considered globally rare (G3 or rarer). Data sources include revisions and floras, articles in *The Bryologist* and other journals, consultation with experts, and information from interested conservation botanists, such as those at state Natural Heritage Programs, provincial Conservation Data Centers, and federal land-management agencies. Nominations of species that are rare, threatened, declining, or vulnerable from a range-wide (global) perspective, as well as confirmations that various other species (when considered range-wide) are indeed widespread, abundant, and secure, are both sought by the authors from interested specialists. Results of this work are being provided to federal conservation agencies and other partners, and will be distributed publicly through ABI's web site *NatureServe*.

- 50** WHEELER, JOHN A. University Herbarium, Jepson Herbarium, and Department of Integrative Biology, University of California, Berkeley, CA 94720-2465—*A phylogenetic analysis of the genus Riccia L. (Marchantiales): volatile morphology that is not reflected in the underlying genetic history.*

Molecular phylogenies of the marchantioid liverwort genus *Riccia* were reconstructed using independent nuclear and plastid data sets in the hope of better understanding relative age, relationships and character evolution in this taxonomically puzzling and putatively ancient radiation. Cladistic analyses are based on three nucleotide sequence alignments: 1) partial nuclear-encoded Large Subunit rDNA (LSU rDNA), 2) the plastid-encoded *trnL-F* region and 3) a data set consisting of combined nuclear and plastid alignments.

Alignment ambiguous regions of each alignment were culled. Independently-derived strict consensus topologies based on 17-18 species of *Riccia* representing 5/8 of subgenera and 13/19 of sections (*sensu* Schuster 1992) are largely congruent; combining the data results in a strict consensus tree with even higher overall bootstrap and decay support. A comparison of the nuclear and plastid trees reveals that five specific clades are common to both; moreover, in the combined strict consensus topology, six clades are indicated with bootstrap support greater than 75%. All analyses (nuclear, plastid and combined) affirm the biological reality of a monophyletic *Riccia* (rooted on outgroups *Ricciocarpos* and *Oxymitra*). Striking morphological divergence within well-supported terminal clades, suggests a propensity in *Riccia* for volatile morphology that is not reflected in the underlying genetic history; characters emphasized in prior systematic treatments are apparently unstable and therefore perhaps largely unreliable for the purpose of discriminating phylogenetically meaningful higher-level intrageneric taxa.

- 51** WILL-WOLF, SUSAN. Department of Botany, University of Wisconsin, Madison, WI 53706-1381—*Lichen communities of old-growth vs managed forests in the northern Great Lakes states.*

We have compared lichen communities in three layers (canopy, trunk, ground) of 15 old growth and managed Northern Hardwood and Hemlock-Hardwood forest plots in Michigan and Wisconsin, to develop an old-growth forest indicator system and to assess the impact of forest management. Old-growth stands of both forest types have more lichen species than managed stands. Equivalent stands of the two forest types have about equal numbers of species and of nitrogen-fixing cyanolichens. Hemlock-Hardwood stands have species evenly distributed among forest layers, while Northern Hardwood stands have more species in taller layers. All managed stands of both forest types have fewer and less abundant cyanolichen species than do old-growth stands. Species loss occurs most in canopy and trunk layers of managed Northern Hardwood stands, but trunk and ground layers of managed Hemlock-Hardwood stands. Large, long-dead standing snags and large partially-decayed coarse woody debris (CWD: especially mossy logs) are particularly important substrates fostering increased species diversity of forest lichen communities. Bark-living lichen species tend to be substrate-selective both with respect to tree species and to tree age, so a wide range of tree sizes as well as a variety of tree species fosters increased lichen community diversity. Lack of snags and CWD is more critical in Hemlock-Hardwood stands because trunks and bases of living hemlocks are too shady for most lichens. Management of forest stands which leaves abundant snags and old-tree islands, and leaves or enhances large CWD should deter loss of lichen community diversity. Nitrogen-fixing lichens and ground-layer lichens are two identifiable lichen "guilds" whose diversity is negatively impacted by logging.

- 52** WILLISTON, PATRICK S. Department of Botany, University of British Columbia Herbarium, #3529-6270 University Boulevard, Vancouver, B.C., Canada, V6T 1Z4—*Successional patterns of microbiotic crusts in ponderosa pine forests of southern inland British Columbia.*

Microbiotic crusts are an important component of the ecology and species diversity of terrestrial ecosystems in semiarid regions. This study documents 72 lichen species and 48 bryophyte species occurring in the ponderosa pine forests of southern inland British Columbia. Successional patterns are described for lichens and bryophytes along a disturbance gradient reflecting past grazing activity by livestock. While species richness among vascular plants varied little with disturbance, microbiotic species richness was found to differ significantly. Maximum richness occurred in moderately disturbed sites. Indicator species for early versus late successional sites were discerned using Principal Components Analysis. Xerophytic crustose and squamulose lichens often dominated early successional sites, while late successional sites also supported foliose lichens, fruticose lichens, and bryophytes. It is hypothesized that this trend from smaller to larger species relates to increased moisture retention, and denotes a positive feedback mechanism. This study contributes to our understanding of the ecology of one of British Columbia's most restricted ecosystems.

- 53** YAHR, REBECCA. Duke University, Department of Botany, Durham, NC 27708—*Post-fire recovery of terrestrial lichens in Florida scrub, with emphasis on Cladonia perforata.*

Prescribed fire is a common tool in the maintenance of natural landscapes and high diversity in Florida scrubs, plant communities well known for supporting many fire adapted endemic plants and animals. However, the role of fire in these lichen communities has not been studied. *Cladonia perforata*, an endangered terrestrial lichen, co-occurs with several other congeners on bare sand of endemic-rich rosemary scrub. A prescribed fire at Archbold Biological Station on the southern end of the Lake Wales Ridge impacted three separate populations of *C. perforata* in July 1993, leaving only remnant unburned patches scattered among completely burned areas. I investigated the rate and mode of post-fire recovery of *C. perforata* in comparison

with co-occurring common species in order to inform management decisions consistent with maintenance of these lichen populations. Detailed GPS maps of individual patches of this lichen were made in January 1997 and compared with those made in August 1999. Abundance of all lichen species was monitored yearly during the winters of 1997-1999. Although all of the other terrestrial species in the same habitat recovered from juvenile stages, no juvenile forms of *C. perforata* were recorded. The area occupied by *C. perforata* increased by more than 200% on average, over the three sites. However, population growth (abundance measures for all species) is so far too slow to have documented and did not change markedly over this interval. Therefore, dispersal of unburned *C. perforata* into burned areas may be the primary method of short-term population recovery.

- 54** YIP, KWOK LEUNG. Herbarium (CINC), Department of Biological Sciences, University of Cincinnati, Cincinnati, OH 45221-0006—*Lectotypification of Pleuridium subulatum and P. acuminatum (Bryophyta).*

Two widespread and morphologically similar species, *P. subulatum* (Hedw.) Rabenh. and *P. acuminatum* Lindb., have caused much confusion since their inception. Correlations of key characters (sexual conditions and lamina thickness) with chromosome numbers suggest that the two species are distinct. The two species are maintained and lectotypified.

## Contributed Posters

- 55** ANTOINE, MARIE E.\* AND WILLIAM E. WINNER. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331—*Analysis of nitrogen, carbon, and water use by Lobaria oregana, a cephalodiate lichen at the Wind River Canopy Crane site.*

*Lobaria oregana* is a nitrogen-fixing cephalodiate lichen that is abundant in old-growth forests west of the Cascades. Although this lichen is believed to be an important source of nitrogen input to the old-growth ecosystem, few studies have measured in situ rates of nitrogen-fixation for *Lobaria oregana*. In this project, we are using the Wind River Canopy Crane Research Facility to sample *Lobaria oregana* thalli growing in the canopy, thereby measuring and linking instantaneous rates of nitrogen-fixation, photosynthesis, and water content. We will assess these physiological processes at regular intervals throughout the year. Additional samples are collected and brought back to the lab for analysis of thallus nitrogen content, and for rehydration experiments to determine the lichen's capacity for recovering metabolism following desiccation. We are using the Acetylene Reduction Assay as a surrogate measurement of nitrogen-fixation capacity, and net photosynthesis is measured with a Li-Cor 6400 Portable Photosynthetic Meter. Initial measurements made in December, 1999 indicated levels of nitrogen-fixation and photosynthesis for *Lobaria oregana* that were below detectable thresholds. Using the physiological data derived from this project, meteorological data from the WRCCRF, and lichen biomass data available from earlier studies, we will determine seasonal trends of metabolic activity in *Lobaria oregana*, and estimate its potential contribution of fixed nitrogen to the forest.

- 56** BONINE, MARY L.\*, LLOYD R STARK, D. NICHOLAS MCLETCHE, AND BRENT D. MISHLER. Department of Biological Sciences, University of Nevada-Las Vegas, Las Vegas, NV 89154-4004—*Spatial Distribution of Desert Bryophyte Populations.*

Populations of the desert moss *Syntrichia caninervis* Mitt. were sampled on a 1.5 hectare site in order to study spatial distributions of male, female, and mixed sex populations. Populations were also categorized in reference to their microhabitat (shaded versus exposed) and mapped on a coordinate grid system including prominent topographic trends. Exposed populations were found to be significantly clustered near trails and washes. Shaded populations, both mixed-sex and single-sex (female), were clumped in arrangement, but single-sex populations were more clumped than mixed-sex populations. This study provides a basis for exploring the potential mechanisms involved in the origins and maintenance of these patterns. We provide three potential explanations for these patterns: a leptokurtic hypothesis of spore dispersal, failure of the species to colonize new habitats via spores, and limitation of mixed-sex populations by the vegetative self-propagation of single-sex populations.

- 57** BROWN, PATRICK J.\* AND DAVID A. DALTON. Biology Department, Reed College, Portland, OR 97202—*Nitrogen fixation, photosynthesis, and growth by Lobaria oregana in an old-growth forest canopy.*

*Lobaria oregana* is a nitrogen-fixing cyanolichen that is spectacularly abundant in old-growth forests of the Pacific Northwest. This species provides a major source of nitrogen for older forests, but the ecological

factors that determine its distribution are not well understood. In this study, we used the Wind River Canopy Crane Research Facility (<http://depts.washington.edu/wrccrf/>) to study the physiological activities and growth of transplanted pendants of *L. oregana* at 3 positions in the canopy: Top (62 m above the ground), Middle (39 m), and Bottom (2 m). There was a complex pattern of seasonal and spatial variation, but in general nitrogen fixation was greatest at the Middle position and photosynthesis at the Top position. Greatest growth was found at the Middle position where there was a 16.4 % increase in dry weight over the 10-month study period. Lichens at the Bottom position died after transplanting. Activities were strongly correlated with hydration except that very high hydration (>200%) inhibited photosynthesis. Laboratory experiments showed that photosynthesis increased at PPFD's of up to 1000  $\mu\text{mol m}^{-2} \text{sec}^{-1}$ . This study represents the first attempt to describe how the physiological activities of *L. oregana* respond both spatially and temporally to the extremely variable environment within the canopy.

- 58** BUSCHBOM, JUTTA\* AND FRANÇOIS LUTZONI. Field Museum of Natural History, Botany Department, 1400 S. Lake Shore Drive, Chicago, IL 60605 and University of Chicago, Committee on Evolutionary Biology, Culver Hall 402, 1025 E. 57th Street, Chicago, IL 60637—*A molecular phylogenetic study of the genus Porpidia (Porpidiaceae, Ascomycota).*

The lichen-forming genus *Porpidia* (Porpidiaceae, Ascomycota) provides a model system for studying the evolutionary significance of sexual and asexual reproduction. The present study forms the basis for future detailed population genetic studies by analyzing the molecular phylogenetic relationships of the genus. Based on DNA-sequence variation in fragments of the nuclear large subunit ribosomal RNA gene (1.4 kb) and the  $\beta$ -tubulin gene (1 kb) the relationships within *Porpidia* and its relationships to closely related allies will be reconstructed. Included in the analysis are selected species of all described subgroups within the genus, representative species of potentially closely related genera within the Porpidiaceae and additional families, as well as relevant outgroup taxa. The results of both gene phylogenies will be discussed.

- 59** CAO, TONG\*, SHUILIANG GUO, AND CHIEN GAO. Institute of Applied Ecology, Academia Sinica, Shenyang, Liaoning, 110015, China—*Comparison of bryoflora and geographical elements between Racomitrium and Grimmia in China.*

Based on revisional study, 23 species of *Racomitrium* and 24 species of *Grimmia* have been recognized in China. Analyses of geographical elements and distribution patterns of the two genera showed: 1) There are obvious differences of geographic elements between the genera *Racomitrium* and *Grimmia* in China. High proportion of East Asian elements together with some tropical elements was found in the genus *Racomitrium*, while the genus *Grimmia* was rich in north temperate elements. 2) For Chinese *Racomitrium*, it seems that Hengduan Mountain Ranges, southwest China, were not only a center of species diversity but also one of origin areas of the genus. 3) *Grimmia* is much more widely distributed in northwest China, while *Racomitrium* is somewhat widely distributed in south China than *Grimmia*. 4) Some species of these genera are characterized by their disjunctive distribution in China.

- 60** CAO, TONG\*, SHUILIANG GUO, AND WEI SHA. Institute of Applied Ecology, Academia Sinica, Shenyang, Liaoning 110015, China—*Distribution of Ptychomitrium muelleri (Mitt.) Jaeg. with its synonyms.*

During previous taxonomic study of the genus *Ptychomitrium*, we discovered that *Ptychomitrium eurybasis* Dix. and *P. neo-caledonicum* (Broth. et Par.) Card. were synonymous with *P. microblastum* (C. Muell.) Par. (Guo & Cao 1999). The further study shows that *P. microblastum* and *P. balanse* Besch. are two new synonyms of *P. muelleri* (Mitt.) Jaeg., which was described and recorded from Australia. The discovery of the present synonyms resulted in remarkable range extensions for *P. muelleri* from Australia to New Caledonia, South Africa and South America. It seems that *Ptychomitrium muelleri* is an important species in the floral relationship among Australia, South America and South Africa in the genus *Ptychomitrium*.

- 61** GEISER, LINDA H. USDA-Forest Service, Siuslaw National Forest, PO Box 1148, Corvallis, OR 97339—*Establishing background ranges and mapping of lichen sulfur, nitrogen and metal concentrations in Pacific Northwest forests.*

Lichen data are being collected in western Oregon, Washington and southeastern Alaska to aid decision-making processes that affect air quality on national forests. Common lichens are analyzed for tissue concentrations of pollutants such as sulfur, nitrogen, lead, and metals. To identify geographic areas of concern and assess the significance of trends over time, forest managers must be able to distinguish elevated values



from values typical of background sites. To determine background ranges, tissue data from 8 national forests were compared after removing sites close to urban areas, roads and high human activity. Ranges of anthropogenic elements in southeastern Alaska were similar to OR and WA Forests. The 97.5% quantiles of the combined "clean sites" database were used as cut-offs for elevated values. All values were then mapped. Elevated values for sulfur and nitrogen were observed along the Columbia River Gorge National Scenic area (CRGNSA), the northern half of the Mt. Hood National Forest, the I-5 corridor, urban areas and near national forest boundaries. Lead was highest in urban areas, the CRGNSA and along the crest of the Cascade Range. Other metals were elevated in the CRGNSA, in urban areas, in areas with serpentine soils on the Umpqua National Forest, and in the north half of the Gifford Pinchot National Forest corresponding to areas of greatest ash deposits from Mt. St. Helens eruptions. A next step is to determine whether adverse effects on forest health, community composition or ecological function can be detected in areas where natural events or conditions cannot explain elevated values.

62

HALL, CHRISTINA C.\* AND JEFFREY C. NEKOLA. Department of Natural and Applied Sciences, University of Wisconsin- Green Bay, Wisconsin 54311—*Influence of scale-dependent environmental factors on the distribution of cliff moss species.*

Worldwide, cliffs represent stable ecosystems that have been little disturbed by human activities, and are important reservoirs for regional biodiversity. Community composition patterns at >1 m<sup>2</sup> scales in cliff habitats, across a wide range of taxa groups (including bryophytes), demonstrate abrupt changes perpendicular to cliff faces but relatively little variation parallel to them. Significant variation in community structure parallel to cliff faces, however, has been documented at smaller scales (0.01-1 m<sup>2</sup>; Larson et al. 1999). What is not clear is the level to which scale dependence in environmental variation is responsible for these differing patterns. In this study, the frequency of cliff bryophyte species and habitat variation across three different scales were analyzed to determine how environmental at various scales affects moss distribution. Four sites were investigated along a 100 km section of the Niagaran Escarpment in northeastern Wisconsin. At each site, transects were laid out at 4 m intervals in bryophyte rich areas from outcrop top to bottom (maximum height = 3 m). 1-2 areas were sampled per site, with 5-12 transects within each. Along each transect, 10x10 cm quadrats were placed sequentially along the entire length. Moss species and microhabitat (face, ledge, overhang, horizontal cracks, vertical cracks, and pits) frequency was recorded from each quadrat. These data were analyzed to determine the relative importance of micro- (microhabitats within quadrats), meso- (outcrop aspect and exposure), and macro-scale (bedrock chemistry, site isolation, and history) environmental factors in predicting the abundance of individual cliff moss species.

63

KEON, DYLAN B.\* AND PATRICIA S. MUIR. Dept. of Botany and Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331—*Factors limiting the distribution of the sensitive lichen *Usnea longissima* in the Oregon Coast Range: habitat or dispersal?*

The sensitive lichen *Usnea longissima*, formerly a common circumboreal species, has been extirpated from much of its range (e.g., most of Scandinavia). Although the U.S. Pacific Northwest remains a relative stronghold for the species, *U. longissima* faces increasing pressure in the region from several factors, including habitat loss, air pollution, and commercial harvesting. *Usnea longissima* has a patchy distribution at both stand and landscape levels, which may result from a lack of suitable habitat, dispersal limitations, or both. We used two approaches in this study. First, data were collected in the Oregon Coast Range from an equal number of sites where *U. longissima* was present and absent (n = 75 each) to determine habitat requirements for the species. In addition to identifying the variables that define suitable habitat for *U. longissima*, analysis of the data yielded a model that was used in combination with a GIS to predict suitable habitat for the species. Second, 360 transplants were divided among 12 sites in 4 habitat types within the Oregon Coast Range, and their growth (change in biomass) was measured after one year. Habitat types were based on analysis of the habitat data, and represented a range of suitability for the species, ranging from sites of unlikely suitability where it did not occur through highly suitable sites where the species was abundant. While habitat conditions in the presence and absence sites types differed significantly (p < 0.01), results of the spatial analysis indicate that suitable habitats do not appear to be limiting at the landscape level. Additionally, preliminary data from the transplant experiment indicate that dispersal may play a more important role than habitat conditions in limiting the distribution of *U. longissima* in the Oregon Coast Range, as the species grew well over a wide range of site conditions.



- 64** MILLER, DONNA H. Department of Biology and Environmental Science, University of West Alabama, Livingston, AL 35470—*A review of the synoicous species of Cyclodictyon (Musci).*

Over 100 species have been described in the Hookeriaceous genus *Cyclodictyon*. Of these, 13 have been described as being synoicous and included in the present study which represents the first part of a monograph for the whole genus. Greatest diversity occurs in tropical Latin America with a second center of speciation in tropical Africa. A single species with several varieties extends across Malesia from Tahiti westward to Ceylon and northward into the Philippines and Taiwan. The Malesian *Cyclodictyon blumeianum* is synoicous as well as several species each in continental South America and Africa. Synoicous species are so far unknown in Central America or the Antilles. Recognition of taxa depends mainly on combinations of vegetative characters including size, length-width ratios of leaves, costal morphology, leaf border morphology and areolation. As a result of examination of types and other material of synoicous species, 10 are recognized, one is placed in synonymy and 4 have been reduced to varietal status.

- 65** RUCHTY, ANDREA\* AND BRUCE MCCUNE. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331—*Influence of canopy type on the biodiversity of epiphytic lichens and bryophytes in riparian forests.*

In order to understand whether changes in tree species composition in riparian zones result in significant changes in epiphytic lichens and bryophytes, we need to know how diversity and species composition of these epiphytes vary among riparian forests with different canopy dominants. Understanding the link between riparian canopy type and epiphytic lichen and bryophyte species composition and abundance will facilitate more effective monitoring of potentially at risk species and management of epiphytic lichen and bryophyte communities. We explored the influence of canopy type on the biodiversity of epiphytic lichen and bryophytes by comparing communities between seven different riparian stand types in the Oregon coast range. Our questions of interest included, do communities differ between stand types? and what biotic and/or abiotic factors influence community composition? We found that lichen and bryophyte communities do differ between stand types. Stand basal area in hardwoods, elevation, stand age and floodplain width all appear to be important factors influencing lichen and bryophyte community composition. A transplant experiment performed using four lichen species, including *Cetrelia cetrarioides*, *Hypogymnia inactiva*, *Lobaria oregana* and *L. pulmonaria*, explored the effect of canopy type on lichen growth. Lichen transplants were placed beneath canopies of *Alnus rubra*, *Acer macrophyllum* and *Pseudotsuga menziesii* in five separate stands. After a year, transplants were collected and growth was calculated. Lichen species were not differentially affected by canopy treatment, though, as a group, lichens experienced inferior health and survival under *Acer macrophyllum* canopies. *Hypogymnia inactiva* showed lower mean and median percent growth and health than the other three lichen species. We acknowledge the support of the Cooperative Forest Ecosystem Research (CFER) program.

- 66** SELF, SHERRY L.\*, C. HEATHER FORD, AND BARBARA CRANDALL-STOTLER. Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509—*Shoot/ sporophyte associations in the Fossombroniaceae.*

The Fossombroniaceae comprise four genera of simple thalloid liverworts, namely, *Fossombronia*, *Austrofossombronia*, *Petalophyllum* and *Sewardiella*. A character presumed to unite the taxa of the suborder is the enclosure of the sporophyte in a calyptra which is in turn surrounded by a leaf-like pseudoperianth. Although many authors accept this interpretation of the shoot/sporophyte association, the developmental studies of Chalaud (1928. Rev. Gen. Bot. 41: 1-343, 8 Pl.) suggest that the structures produced in *Fossombronia* are not homologous to the pseudoperianths of the other taxa. Using serial paraffin sectioning and SEM techniques, we have investigated pseudoperianth formation and growth in several species of *Fossombronia* and *Petalophyllum*. In *Petalophyllum* a true pseudoperianth, formed from extensions of the lamellae, surrounds the cluster of unfertilized archegonia; following fertilization, the pseudoperianth expands and a shoot calyptra develops around the sporophyte. In contrast, *Fossombronia* first forms a perigynial mass beneath the fertilized egg. One or two leaf-like scales are subsequently produced at the apex of this perigynial mass at its point of juncture with the calyptra. This developmental sequence agrees with Chalaud's interpretation and verifies that the leaf-like structure that encloses the sporophyte in *Fossombronia* is not a pseudoperianth.

- 67** STUBBS, CONSTANCE S. Department of Biological Sciences, University of Maine, Orono, ME 04469—*Long-term biomonitoring (1988-1998): lichen distribution, abundance, and health on red spruce, Picea rubens Sarg.*

Lichens are useful bioindicators of environmental quality. Lichen mapping, one of the oldest biomonitoring techniques, examines the distribution and abundance of lichens. Lichen mapping provides a direct measure

of lichen health and an indirect measure of air quality within ecosystems. In environments with poor air quality, pollution intolerant species become depauperate, extinct, or replaced with pollution tolerant species. Lichen diversity, abundance, and external health (based on “normal” thallus morphology, color, and lichen prevalence) have been monitored in permanent study quadrats on the boles of red spruce, *Picea rubens*, at one inland (University of Maine Experimental Forest) and three coastal sites (Small Point, Isle au Haut, Roque Island) in Maine every two years since 1988. Baseline (1988) measurements demonstrated intra- and intersite differences in presence, abundance, and external health and suggested that lichens were less healthy at Small Point and the inland site and more healthy at Isle au Haut and Roque Island. *Hypogymnia physodes* was the most prevalent species at all sites. Overall, 27 macrolichen species have been found in study quadrats. Red spruce at Roque Island has had the greatest diversity: 23 lichen species in 1988, but only 16 species in 1998. Over the 10-year biomonitoring period, local extirpations of pollution intolerant species outnumbered new recruits except at the inland site. By 1998, Small Point, the site closest to the northeast urban-industrial corridor, had the greatest relative negative change in lichen diversity, abundance, and external health. In contrast, only the inland site showed relative positive change. The trends manifested after the initial baseline measurements demonstrate the value of long-term biomonitoring for better understanding the distribution and abundance patterns of lichens.

- 68** YU, JING\*, TONG CAO, AND QUANXI WANG. Institute of Applied Ecology, Academia Sinica, Shenyang, Liaoning 110015, China—*Studies on spore morphology of the genera Trematodon and Microcampylopus (Dicranaceae) from China by SEM.*

Spore morphology of two species of Trematodon and two of Microcampylopus were observed and studied by Scanning Electronic Microscope (SEM) for the first time in China. All spores of both genera are spheroid and characterized by obvious differentiation of distal and proximal surface and distinct ornamentation with large bacula, spinose process or tumors. In a genus, differences of size and ornamentation between two species are distinct and can be used as taxonomic characters on species level. The spores of *T. ambiguus* and *T. longicollis* are 19.1-18.8 µm and 20.5-20.2 µm, respectively. Distal surface of *T. ambiguus* are covered with coarse spinate process up to 2.5-4 µm. The proximal surface has obvious tetrad surrounded by a convex circle with fine verrucae on it. The distal surface of *T. longicollis* are covered with large bacula, while proximal surface with no distinct tetrad surrounded by a circle formed by regular bacula and covered with relatively small bacula on it. The spores of *Microcampylopus laevigatus* and *M. kasianus* are 21.9-20.5 µm and 19.2-18.6 µm, respectively. The distal surface of spores of both two species are covered with large tumors, but the tumors of *M. laevigatus* are much larger and more irregular in size than those of *M. kasianus*. In addition, the proximal surface of *M. laevigatus* is distinct and surrounded by a few large verrucae and covered with dense and small granules, while that of *M. kasianus* is not distinct and covered with small verrucae.

## V. Developmental and Structural Section

### Symposium: Open space

- 69** KIRCHOFF, BRUCE. Department of Biology, University of North Carolina at Greensboro, P.O. Box 26174, Greensboro, NC 27402-1674—*Open Space Symposium.*

Open Space is a symposium format that allows participants to determine the content and organize the sessions on the day of the event. Open Space will allow us to incorporate more discussion into our meetings, to deal with subjects that are new, and to include topics that cannot be easily accommodated in traditional lecture formats. The impulse for Open Space comes from the observation that the most valuable parts of a conference are the informal meetings that take place during coffee and meal breaks. During these times we meet old friends, discuss our research, and make plans for the coming year. Open Space is designed around the idea of a structured coffee break. An Open Space symposium begins with a brief introduction of the concept of Open Space and a preview of the activities to follow. Participants are then asked to come forward to suggest topics for discussion or presentation. Each topic becomes one of the sessions of the symposium. The person who suggests a topic becomes that session's convener. The convener is responsible for the session. She may lead a discussion, present a lecture, or simply open the floor to contributions from the people in attendance. After presenting their idea for a session, the conveners post their topics to a time/room grid, thus scheduling it for later in the symposium. Participants continue to come forward until the grid is filled, or there are no more suggestions from the floor. The main duties of the session conveners are to start the session and to assure that a record is kept of any discussions. Because this is the first year of Open Space, we have

prepared two sessions in advance. These will focus on characters states (Peter Stevens) and a mentoring session for graduate students (Nancy Dengler).

**70** DENGLER, NANCY G. Department of Botany, University of Toronto, Toronto, ON M5S 1A1—*Mentoring graduate students.*

One of the best ways to encourage students to enter a field and to assure their advancement is by providing them with role models and mentors. A supportive environment is one of the best things we can offer our younger colleagues, and mentoring is one of the best ways to create that environment. This session of Open Space will provide a time when graduate students and established scientists can meet and exchange information on the many aspects of becoming a scientist. Although we welcome discussion of technical research questions, we also hope to use this opportunity to deal with questions of gender, social aspects of teaching and research, faculty expectations at research and teaching institutions, obtaining funding, departmental politics, and other aspects of scientific work that are seldom discussed.

**71** STEVENS, PETER F. Department of Biology, University of Missouri St Louis, St Louis, MO 63121-4499, and Missouri Botanical Garden, P.O. Box 299, St Louis, MO 63166-0299—*Organisms, form and characters.*

In the development of phylogenetic systematics over the last decade our approach to morphological characters has remained at a preDarwinian level, even as we use ever more sophisticated tools for looking at plants. A largely neglected area is that of the relationship between characters, their states, and organisms. One especially problematic set of issues concerns the documentation of morphological observations and their general availability, whether as measurements, s.e.m.s, etc. (cf. gene sequences in GenBank, and associated voucher specimens). Another concerns the relationships between the observer, observations, characters, and their states. Are there alternative ways an organism can be atomised into characters that would aid our understanding (perhaps think of the monocot flower here)? Are there alternative ways a character can be atomised into states? How can we justify one atomisation over another in any particular situation? Do we have to? Does terminology constrain our vision of the world and, if so, how? Is seeing forgetting the name a thing is called? What is the relationship between the purely morphological and systematic approaches to studying plants? We will discuss these and related issues as they arise during the session.

## Contributed Papers

**72** BANASIAK, ALICJA, S.\* AND BEATA ZAGÓRSKA-MAREK. Institute of Botany, University of Wrocław, Kanonia 6/8, 50-328 Wrocław, Poland—*Torreya case indicates autonomy of shoot apical meristem generating phyllotaxy.*

In shoots with spiral phyllotaxy axial homodromy occurs when ontogenetic helix continues its course in successive flushes of the axis. The opposite case is axial antidromy when the helix course alters every year. Initially, we thought that in conifers axial homodromy occurs without exception, suggesting that the apical meristem is not autonomous in a process of primordia formation but is influenced by the older, well-developed parts of the shoot. Recently, however, we have discovered that in *Torreya nucifera* characterized by bijugate phyllotaxis the direction of ontogenetic helix is every year either the same or the opposite to that of the previous year. Discontinuity of organogenetic process in the region of bud scales, resulting perhaps from changing primordia identity, was considered to be one of the causes. The comparative studies showed that in genera with axial homodromy, such as *Abies*, *Picea*, *Cephalotaxus* and *Taxus*, phyllotaxy in a region of bud scales is as regular as in the area of normal leaves. In *Torreya*, however, the divergence angle between successive pairs of scales increases gradually leading to the decussate arrangement. Its symmetry guarantees the random selection of a new configuration of ontogenetic helix in a subsequent growing season. Another possible reason for the special behavior of *Torreya* is system of internal signaling. If the initiation of leaves is governed by the vascular system, then the axial homodromy should result from the system mature and close enough to this area where primordia are initiated. *Torreya* case might result from isolation of the meristem from the signals sent by vascular system. It appeared that indeed in *Torreya*, the topology of vascular strands and collenchymatous plate is such, that neither differentiated, nor the procambial, vascular strands penetrate the plate. In other conifers they clearly pass the plate reaching out for the level of lowest primordia.

- 73** CAMPBELL, LISA M.\*, DENNIS WM. STEVENSON, AND GUSTAVO A. ROMERO-GONZÁLEZ. New York Botanical Garden, Bronx, NY 10458 and Harvard University Herbaria, 22 Divinity Ave., Cambridge, MA 02138—*Anatomical features of Aratitiopea (Xyridaceae)*.

*Aratitiopea* (Xyridaceae) comprises one species with two subspecies that occurs at mid to high elevation on sheer rock faces and waterfalls. It is known from a few populations on sandstone mountains (tepui) on the Guayana Shield of northern South America. Unlike most Xyridaceae, *Aratitiopea* is caulescent. The leaf blades have a marked zone of articulation, and the persistent leaf sheaths function as tanks accumulating water and debris. The escapose inflorescence, unique in Xyridaceae, combined with the habit give the plant a bromeliaceous appearance, and the species was originally described as a *Navia* (Bromeliaceae). *Aratitiopea* is poorly known anatomically due to the paucity of preserved material. An anatomical survey is being conducted on vegetative collections made in January 2000 and compared to the other Xyridaceae. Preliminary results show that leaf anatomy of *Aratitiopea* is most similar to *Orectanthe*, one of the other four genera in the family.

- 74** CARLQUIST, S. AND EDWARD L. SCHNEIDER.\* Santa Barbara Botanic Garden, 1212 Mission Canyon Road, Santa Barbara, CA 93105—*Anatomical studies of Amborella*.

As reported by Bailey and Swamy, *Amborella* has tracheids that tend to have scalariformly pitted end walls but smaller oval to circular pits on lateral walls. SEM studies of tracheids from both sections and macerations reveal that there are small pores in the end wall pit membranes, but pore size is smaller than in dicots with vessels that contain porose pit membrane remnants in perforations (e.g., *Illicium*). The size difference is not sharply different, showing that tracheids and vessels, although identifiable, are close to being an intercontinuous system. *Amborella* is alleged to lack mucilage/oil cells, but thin-walled sclereids containing sphaeroidal non-staining contents are present in leaves. Anatomy of *Amborella* is compatible with the concept of a relationship to Illiciales (s. l.)

- 75** CLEVINGER, JENNIFER A. AND ELIZABETH M. HARRIS.\* Department of Biology, James Madison University, Harrisonburg, VA 22807, Department of Evolution, Ecology and Organismal Biology, Ohio State University Herbarium, Columbus, OH 43212—*Floral primordia complexes in the Engelmanniinae (Asteraceae: Heliantheae)*.

Asteraceae inflorescence meristems are physically constrained as to the position of the individual floral meristems so that the floral primordia are tightly packed. New floral meristems are generally initiated in regular phyllotactic spirals at an angle of 137.5 degrees that converge at the apex of the inflorescence as shown by several recent studies that have plotted and quantified the positioning of floral primordia on simpler Asteraceae models. The models are not absolute for all taxa in the Asteraceae, however. Certain basal taxa in the tribe Heliantheae display a marked deviation from the expected pattern of packing. Most of the taxa of the subtribe Engelmanniinae (*sensu* Clevinger and Panero), including *Engelmannia*, *Berlandiera*, *Chrysogonum*, and *Lindheimera* produce peripheral multi-meristem complexes that consist of one ray flower primordium, two or more disk flower primordia as well as the associated involucre and receptacular bract primordia. These primordia complexes act as coordinated units as far as timing of initiation and development is concerned and also display distinct heterochronic development when compared to their closest neighbor floral and bract primordia. They remain evident at anthesis and beyond as cypsela complexes that presumably aid in dispersal. Some (but not all) species of the terminal taxon of the Engelmanniinae, *Silphium*, possess similar primordia complexes but do not go on to develop cypsela complexes. The trait is completely lacking in some of the more basal members of the subtribe: *Dugesia*, *Wyethia*, and *Borrichia*.

- 76** COOPER, RANESSA L.\* AND DAVID D. CASS. Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9—*Leaf structure of Salix species (Salicaceae) endemic to the Lake Athabasca sand dunes of northern Saskatchewan, Canada*.

The Athabasca sand dunes, located on the south shore of Lake Athabasca in northern Alberta and Saskatchewan, Canada, are the largest northern dunes. They were formed (after deglaciation) about 10,000 years ago and were vegetated soon thereafter. Over 200 plant taxa occupy this region, but only 40 occur on open sands. Ten plant species are dune endemics, including four representatives of the genus *Salix* (Salicaceae). These endemic willows (*Salix brachycarpa* Nutt. var. *psammophila* Raup, *S. planifolia* Pursh ssp. *tyrrellii* (Raup) Argus, *S. silicicola* Raup, and *S. turnorii* Raup) share several morphological features with their putative widespread progenitors. However, certain leaf characters (e.g. amphistomatic leaves, thick cuticles, and high pubescence) of these endemic willows have been described as being 'adaptive' to the open sand habitat.



Leaf anatomy and morphology were evaluated for endemic *Salix* taxa and their progenitors using light and scanning electron microscopy. *Salix planifolia* ssp. *tyrrellii* and *S. turnorii* have amphistomatous leaves, while *S. brachycarpa* var. *psammophila* and *S. silicicola* have the greatest trichome densities. Endemic willows have thicker cuticles than their widespread progenitors. Compact leaf mesophyll in endemic *Salix* species suggests adaptation to this high light intensity environment.

- 77** DOUST, ANDREW, N.L. Department of Botany, University of Missouri-St Louis, St Louis, MO 63121—*Floral morphology and development in Winteraceae*.

The flowers of Winteraceae show great diversity in number and arrangement of organs. In most genera of Winteraceae a continuity of initiation from sepals through petals, stamens, and carpels results in relatively few floral arrangements, these being variations on decussate and whorled patterns. However, a diversity of phyllotactic patterns is found in the flowers of *Drimys winteri*, resulting from the unconstrained placement of petal primordia following a delay between sepal and petal initiation. In all taxa there is within-pattern variation in divergence angle and plastochrone ratio correlated with the eccentricity of the floral meristem. Differences in floral form define the genera of the Winteraceae and these differences are controlled by the timing and duration of primordial initiation, the position of initiation of the primordia, the shape of the floral meristem, and the relationship between size of meristem and size of primordium. An understanding of these ontogenetic processes is important in understanding diversity and evolution of floral form in Winteraceae.

- 78** DOUST, ANDREW, N.L.\* AND ELIZABETH, A. KELLOGG. Department of Biology, University of Missouri-St Louis, St Louis MO 63121—*Patterns of inflorescence development in Setaria (Panicoideae, Poaceae)*.

The development of the inflorescence in *Setaria italica* (foxtail millet), *S. verticillata*, *S. viridis*, and *S. grisebachii* was examined. The inflorescences of the different species differed in numbers of orders of branching, with *S. italica* having 2 or more orders as compared to one order in the other three species. All species initiate spikelets paired with bristles, but many of the spikelets are suppressed during development. In *S. grisebachii* pairs of spikelets and bristles appear together on the branches, in *S. verticillata* and *S. viridis* a single spikelet at maturity is surrounded by a series of bristles, and in *S. italica* three or four spikelets and at least twice as many bristles appear on the primary branches. Differences between the species appear early in development and have the potential, along with density of branches in the spike, to be major determinants of yield. The different mature morphologies of the inflorescences are similar to various mutant phenotypes of maize, such as *ids1*, *ts6*, and *ral* & 2, which raises the prospect of using genes identified from maize to identify differences in inflorescence morphology in a comparative manner across species groups. The present study is a step towards relating advances in model plant genetics to an understanding of natural morphological differentiation in plants.

- 79** FISHBEIN, MARK\*, LARRY HUFFORD, AND DOUGLAS E. SOLTIS. School of Biological Sciences, Washington State University, Pullman, WA 99164-4236—*Reversals to hypogyny in Saxifragales: comparative ontogenies and evolutionary correlates*.

Saxifragales is a small, but morphologically diverse, clade containing Saxifragaceae, Crassulaceae, Hamamelidaceae, Haloragaceae, Paeoniaceae, and related taxa. Of many diverse vegetative and reproductive characteristics, the range of ovary positions is notable. This variation, which is manifest at levels ranging from closely related species to families, appears to violate hypotheses of Stebbins and Grant that ovary position is an evolutionarily conservative feature. Apparent reversals from inferior ovaries (epigyny) to superior ovaries (hypogyny) also contradict widely-held beliefs in an evolutionary trend towards epigyny; the derivation of hypogyny from epigyny is considered to be exceedingly rare. We use ontogenetic criteria established by Kaplan to assess the homology of ovary position across Saxifragales. SEM and histological study of early floral buds were used to characterize the conformation of the floral apical meristem throughout organogenesis. We find that nearly all clades of Saxifragales are characterized by epigynous development, regardless of apparent ovary position in mature flowers, affirming the conservative nature of the developmental basis underlying ovary position. Apparent variation in ovary position in the clade is due largely to allometric shifts in the relative rate of growth in the upper and lower portions of the ovary late in development, rather than shifts in the conformation of the meristem during the earliest stages of floral development. However, at least one reversal to hypogynous development is documented unequivocally; this represents the first well-documented case of a reversal to hypogyny. We explore evolutionary changes in other floral characters that are correlated with changes in ovary position. Reversal to hypogyny in Saxifragales may be associated with



the derivation of apocarp in the clade, although the limited number of reversals precludes quantitative assessment of the association.

- 80** FLOYD, SANDRA K.\* AND WILLIAM E. FRIEDMAN. Department of Environmental, Population, and Organismic Biology, Campus Box 334, University of Colorado, Boulder, CO 80309—*Endosperm development in Amborella trichopoda: implications for the origin and early evolution of angiosperm reproductive biology.*

The recent unprecedented concurrence of several independent phylogenetic analyses of basal angiosperm taxa has led to the identification of the three earliest diverging lineages of extant flowering plants: *Amborella trichopoda*, Nymphaeales, and Illiciales. With a more confident identification of the earliest angiosperm lineages, we are now in a better position to resolve character polarity and identify character state transitions during the earliest radiation of extant flowering plants. Because of its phylogenetic position as sister to all other angiosperms, *Amborella* is critical to assessing angiosperm character polarity and evolution. However, little is known about the basic biology of *Amborella*, which is endemic to New Caledonia, not widely cultivated, and thus insufficiently studied. In particular, embryological data are completely lacking. Endosperm is the sexually-derived embryo-nourishing structure that is unique to the life cycle of angiosperms. We provide the first report of endosperm development in *Amborella*. The endosperm exhibits a bipolar, cellular developmental pattern that is quite similar to other basal angiosperm taxa we have investigated, most notably *Illicium*, another representative of the three earliest-diverging lineages of flowering plants. In contrast, endosperm in *Amborella* is quite unlike endosperm in *Cabomba* and other Nymphaeales. The implications of these findings for understanding the origin and evolution of this distinctive aspect of the reproductive biology of flowering plants are discussed.

- 81** GERRATH, JEAN M. Department of Biology, University of Northern Iowa, Cedar Falls, IA 50614-0421—*Tendrill development in Antigonon leptopus Hook. & Arn. (Polygonaceae).*

Tendrils are cylindrical coiling organs used as a climbing and support mechanism by a number of vines. The morphological origin of tendrils varies, and may be the leaf, shoot, or inflorescence rachis, depending on the species. Thus tendrils are a good example of convergent evolution. Coral vine (*Antigonon leptopus*), a native of Mexico and Central America, possesses tendrils on the axillary inflorescences. Typically, bract-subtended flowers develop on the basal portion of the inflorescence. A transition zone consisting of one or two nodes with tendril-subtended flowers occurs in the middle portion of the inflorescence, and the inflorescence is terminated by three "empty" tendrils. Tendrils are initiated in the same manner as a leaf or a bract, but they remain cylindrical except for what appears to be a rudimentary blade at the tip. Developmental and histological evidence indicates that the tendril in this species is a leaf homologue. The initial thigmotropic response and coiling take place in the tendrils, but subsequently, coiling also occurs in the inflorescence rachis which becomes sclerified and forms the permanent support structure for the vine. Thus, this species uses both stem and leaf homologues for support.

- 82** GIBSON, J. PHIL. Department of Biology, Agnes Scott College, Decatur, GA 30030—*Developmental differences between ray and disc achenes in heteromorphic species of Prionopsis and Heterotheca.*

In most species, all fruits produced by a plant have uniform morphological and ecological characteristics that reflect a balance among conflicting fruit characteristics, such as seed number vs. seed size, and optimization of complementary characteristics such as seed size and seedling survival. Numerous species in the Asteraceae have evolved achene heteromorphism in which different ray and disc florets within the same capitulum produce morphologically and ecologically dissimilar achenes. One achene class is typically larger, have a thicker pericarp, lack dispersal structures, and require specific conditions to germinate. The alternative achene class tends to be lighter, have dispersal structures such as a pappus, and do not require specific stimulus to break dormancy. Ecological and population genetic studies have shown that achene heteromorphism is a bet-hedging strategy whereby plants offset the contrasting spatial and temporal risks of seed dispersal by partitioning reproductive output between two ecologically and genetically different seed pools. What is not known about achene heteromorphism is how development differs between floral meristems to produce morphologically distinct achenes. Furthermore, it is not known whether plants can adjust the proportions of distantly and locally dispersed achenes that are produced in response to different environmental conditions. Anatomical and developmental studies indicate that allometric differences produce dissimilar achene types, and that some species are able to alter the proportions of achene types produced.

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GOLA, EDYTA M. Institute of Botany, Wrocław University, Kanonia 6/8, 50-328 Wrocław, Poland—*Lycopod vasculature - unique system in plants.*

Lycopod specific features including appearance of microphylls, wide spectrum of phyllotaxis, high frequency of phyllotactic transformations, shoot dichotomy significantly affect their vasculature and make it exceptional in plants. Partitioning of the stele into vertically oriented protoxylary ribs (PXR)s affects the pattern of the vascular connections with microphylls. The number of PXR)s in the stele is not correlated to the type of phyllotactic pattern or its expression. In shoots with whorled phyllotaxis microphylls from one to three phyllotactic ortostichies connect to one PXR. In shoots with helical phyllotaxis the vertical course of PXR)s and the regular microphyll pattern cause the characteristic “zig-zag” course of stelar parastichies: each PXR supplies microphylls from different foliar parastichies - traced on the surface of the stem. As each trace connects to the nearest vertical PXR, the microphyll traces must vary in length, unlike as in seed plants where megaphyll traces are of rather equal length. The regulating role of the apex is expressed by efficient packing of primordia and its control of the stelar diameter. During dichotomy of the shoot, circumferential discontinuity of the microphyllous phyllotaxis is paralleled by the reconstruction of the stelar system: the change of a stele symmetry and architecture. Changing number of PXR)s is associated with appearance of endarchic protoxylem elements inside of the stele. Parallelism of the stem and stele surfaces, with regularly distributed elements, results in spatial adjustment of microphyll and PXR patterns. In this light lycopod vasculature seems to be the first, maybe imperfect yet, supplying system for superficial elements.

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HARDY, CHRISTOPHER R.\* AND DENNIS WM. STEVENSON. L.H. Bailey Hortorium, Cornell University, Ithaca, NY 14853-4301 and New York Botanical Garden, Bronx, NY 10458-5126—*The unusual androecium and pollination system in Cochliostema (Commelinaceae).*

Flowers of the neotropical genus *Cochliostema* are the largest and among the most complex and fragrant in Commelinaceae. *Cochliostema* is further characterized by its peculiar androecium consisting of three fertile stamens and three antherless staminodes. The fertile stamens are on one side of the flower and united by their filaments, forming a compound structure that curves to the flower's right as the flower opens. The anthers are longitudinally dehiscent, spirally coiled, and enveloped by petaloid extensions of the filaments of the two lateral stamens contributing to the three-staminate structure. The coiled form of the mature anthers is achieved through the prolonged and spiral growth of the apical portions of the developing thecae. The coiling of the thecae in this manner results in a significant increase in volume devoted to pollen production in a relatively compact space. The two petaloid envelopes (or “cuculli”) emerge as papillate processes on either side of the filaments of the two antepetalous stamens. Laminar growth of the cuculli proceeds such that both contribute equally in the formation of a common chamber surrounding all three anthers. Field and laboratory studies indicate that pollen is expelled from the chamber primarily through the apical terminus of a hose-like, slightly supervolute, extension of each cucullus through vibration of the entire staminal structure by certain pollen-collecting bees. Euglossine and xylocopine bees found “buzzing” the flowers of *Cochliostema* in the field were captured and observations using an SEM revealed an abundance of *Cochliostema* pollen deposited on the bees' hind legs. These data indicate that the cuculli of *Cochliostema* are, in many respects, functionally analogous to the poricidal thecae of many buzz-pollinated flowers, thereby confirming the predictions made by previous authors. These data also identify certain euglossine and xylocopine bees as probable vectors in pollen transfer between flowers of *Cochliostema*.

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HILL, JEFFREY P. Department of Biological Sciences, Idaho State University, Pocatello, ID 83209-8007—*Sporophyll pinna meristem development in Ceratopteris richardii.*

Sporophyll crosiers in *Ceratopteris richardii* have naked pinna meristems that can be observed non-destructively over time by sequential scanning electron microscopy (SSEM). In addition, clonal analyses of the meristematic region of the pinna surface can be straightforward because developmental relationships among cells in the primordium are often easy to infer. Anatomical study of paradermal sections of the abaxial side of sporophyll pinna tips was combined with SSEM of developing organs to characterize cellular and morphological aspects of organ growth. There were common themes in the spatial arrangement of clonal cell patches at the abaxial pinna surface, although exact patterns varied within and between pinnae. The initiation of sporangia from single superficial cells provided discrete phenotypic markers to analyze patterns of cell fate determination in the epidermis. Sporangial initial cell lineages could be traced to two sub-apical positions at the flanks of each pinna apex. During ontogeny, the principal direction of growth at the pinna tip occasionally changed its location. These changes in growth direction occurred independent of previously existing cell tile patterns. Consequently, cells near the pinna apex (including putative sporangial initials) shifted their

fates to correspond with the new local growth zone. This result suggests that the fates of epidermal cells including sporangial initials are determined in a non-cell-autonomous fashion in *C. richardii*. A model for pinna development that is consistent with these observations is proposed, stressing the existence of morphological parameters controlling fern leaf ontogeny above the cellular level.

- 86** HORNER, HARRY T.\*, ALBERT P. KAUSCH, AND BRUCE L. WAGNER. Department of Botany & Bessey Microscopy Facility, Iowa State University, Ames, IA 50011-1020, Agri-BioTech, Inc., 530 Liberty Lane, West Kingston, RI 02892, and W.L. Gore & Associates, 3250 W. Kiltie Lane, PO Box 300, Flagstaff, AZ 86002-0300—*Ascorbic acid serves as precursor for oxalate synthesis in calcium oxalate idioblasts of Yucca torreyi in liquid root culture.*

Liquid-cultured primary roots of *Yucca torreyi* L. (Agavaceae), similar to its intact roots, develop uninterrupted files of calcium oxalate crystal idioblasts in their cortex, beginning just back of the terminal meristem. Each single file of idioblasts displays an 'ontogenetic' sequence acropetally. <sup>14</sup>C-labeled glycolic acid, glyoxylic acid and ascorbic acid, potential precursors of oxalate were each added to different flasks, containing a sterile liquid root-growth medium and the isolated roots, and allowed to interact with the roots for 45 min. After thorough washing, the roots continued to grow for periods from 1.6-h to 24-h post incorporation. Autoradiography of root sections with the labeled ascorbic acid at the earlier incorporation times showed concentrations of silver grains over the idioblasts, and primarily over the vacuole crystal bundles and cytoplasmic plastids. The glyoxylic acid- and glycolic acid-labeled root sections showed a lesser amount of silver grains distributed over the entire sections, but not concentrated over the crystal idioblasts. These results strongly suggest that ascorbic acid is the primary precursor of oxalate in the crystal idioblasts of *Yucca torreyi* primary roots, and supports other recent biochemical data regarding oxalate synthesis in higher plants. The use of roots in liquid culture containing uninterrupted files of developing crystal idioblasts could serve as a model system for additional biochemical, physiological and molecular studies dealing with understanding the formation and functional significance of crystal idioblasts in higher plant organs.

- 87** KANTZ, KATHERINE E.\* AND SHIRLEY C. TUCKER. Biology Dept., Grand Valley State University, Allendale, MI 49401 and Dept. of Biology (Ecology, Evolution and Marine Biology), University of California, Santa Barbara, CA 93110—*Floral development of Chrysobalanus icaco L. and Licania michauxii Prance (Chrysobalanaceae): stamen number and formation of the gynobasic style.*

Members of the Chrysobalanaceae are distinguished by a single pistil with a gynobasic style. The purpose of this study was to examine the floral development of representatives of this family in order to determine how the gynobasic style is formed. The flowers of the two representatives examined, *Chrysobalanus icaco* and *Licania michauxii*, also differ in the number of stamens they typically have (12-26 in *C. icaco* and approximately 15 for *L. michauxii*). The pattern of stamen development was therefore also examined to determine how this difference in number is achieved. The difference in the number of stamens between the two species was found to be due to two processes: a larger number of stamens being initiated in the inner whorl of *C. icaco* flowers (typically four opposite each petal as opposed to two opposite each petal) and subsequent suppression of stamens on one side of the *C. icaco* flowers. Carpel initiation in *L. michauxii* begins when three carpel primordia become visible during initiation of the antepetalous stamen whorl. The originally distinct carpel primordia become laterally confluent in the portions below the free tips. Later in development the ovaries of two of the carpels are suppressed leaving a single developing ovary. The developing ovary expands outward and upward causing the style, which is apparently composed of tissue from all three carpels, to become gynobasic. Only two carpel primordia are initiated in flowers of *C. icaco*. Further development of the gynoecium is similar to that found in *L. michauxii* in that one of the two ovaries is suppressed leaving a single developing ovary with a gynobasic style apparently composed of tissue from both carpels. In conclusion the gynobasic style is produced by a suppression of ovaries in both species, although different numbers of carpels are initiated and suppressed in the two species.

- 88** KORN, ROBERT W. Department of Biology, Bellarmine College, Louisville, KY 40205—*Developmental leaf spots.*

Patterning of leaf spots was analyzed in the pond lily (*Nymphaea odorata* Ait.) and the spotted dracaena (*Dracaena godseffiana* Sander) and compared to that in the maize (*Zea mays*) aleurone from reverse transposition. Aleurone sectors are clearly cell lineages because (a) the number of cells follows expected geometric distribution when sizes, as log 2 number of cells, of lineages are plotted against frequency and (b) the shapes are somewhat quadrilateral. Red spots on the pond lily leaf also follow a pattern expected of cell lineages

by the shape of the areas, however, their frequencies of sizes of spots unexpectedly follow a normal distribution. These red-celled clones come from a daughter cell with an oriented specialized cell plate. By contrast, the yellow regions of the spotted laurel are circular instead of quadrilateral suggesting they do not come from a cell lineage process but by diffusion of a chloroplast inhibitor from a central source cell.

- 89** KRISTIANSEN, KIM A. Botanical Institute, University of Copenhagen, Gothersgade 140, DK-1123 CPH K, Denmark—*Typical orchid mycorrhiza and protocorm seedling biology found in *Neuwiedia*.*

Orchidaceae subf. Apostasioideae comprises the genera *Apostasia* (7 spp.) and *Neuwiedia* (8 spp.). They are not always included in Orchidaceae *s.str.*, but are traditionally regarded as “the most primitive orchids”. Recent phylogenetic analyses of morphological and molecular data place them as sister group to the remainder of Orchidaceae. Orchids are easily recognized on distinct floral characters, but several authors have pointed out that characteristics like the gynostemium, pollinia etc. make sense only in connection with the unique seedling biology with an obligate mycotrophic protocorm stage. Protocorms of spontaneous *Neuwiedia veratrifolia* seedlings have been found at three locations, and the mycobiont was subcultivated from live pelotons. The typical orchid mycorrhizal infection pattern with newly infected cells in the outer cortex and older degrading pelotons in the inner cortical cells was observed. The preliminary examination of the fungal endophyte categorizes it as typical orchid mycorrhiza belonging to the group of *Rhizoctonia*-like endophytes.

- 90** KUZOFF, ROBERT K.\*, JOHN L. BOWMAN, AND CHARLES S. GASSER. Sections of Molecular and Cellular Biology and Plant Biology, University of California, Davis, CA 95616—*Structural and functional diversification of the YABBY gene family across angiosperms.*

Members of the YABBY gene family, recently discovered in *Arabidopsis thaliana*, are crucial for the establishment of abaxial identity in diverse organs including leaves, floral appendages and ovules. YABBY genes encode putative transcription factors with a zinc finger domain near the N-terminus, a central variable region, and a YABBY domain near the C-terminus. To explore the patterns and rates of diversification among members of the YABBY gene family across angiosperms, we isolated several homologs from two Asterids, *Lycopersicon esculentum* and *Antirrhinum majus*, and a monocot, *Zea mays*. Amino acid sequences of both the zinc finger and YABBY regions from all isolated genes were easily aligned. The central variable regions among these genes exhibited some similarities but could not be unambiguously aligned. Phylogenetic analysis of these genes, using the PAM-250 amino acid transition matrix, identified five distinct molecular lineages, with high bootstrap support, that correspond to functional categories identified in *A. thaliana*. Within these lineages, the zinc finger regions, having an average sequence dissimilarity of 18.6%, are evolving more rapidly than the YABBY regions, which have an average sequence dissimilarity of 6.7%. Orthologs of *INNER NO OUTER*, a gene required for outer integument development in *A. thaliana*, have been identified in both the Asterid and monocot lineages. Orthologs of *CRABS CLAW*, a gene involved in abaxial differentiation of the carpel, have also been identified in these lineages. *In situ* hybridization of orthologs of *INNER NO OUTER* and *CRABS CLAW* in *L. esculentum* indicates that they are expressed in the same tissues as their counterparts in *A. thaliana*, but also exhibit expanded expression patterns relative to *A. thaliana*. The pattern of *INNER NO OUTER* expression in ovules of *L. esculentum* may provide insights into the origin of unitegmy in the Asterids, in particular, and the relationship between molecular and morphological evolution, more generally.

- 91** LEE, DAVID W.\*, GEORGE T. TAYLOR, AND ANTHONY K. IRVINE. Department of Biological Sciences, Florida International University, and Fairchild Tropical Garden, Miami, FL 33199—*Structural Fruit Color in *Delarbrea michieana* (Araliaceae).*

The brilliant blue fruit color of *Delarbrea michieana* (F. Muell.) F. Muell. (Araliaceae), a Queensland understory rainforest tree, is caused by a structure (an iridisome) in the epidermal cells. The iridisome is produced beneath the cell wall and above the cytoplasm, although its relationship to the plasmalemma is uncertain. Layers within the iridisomes are of the thickness to interfere constructively with light at 420-440 nm and produce the blue color. This structural coloration is unique to this single and uniquely Australian species, among six taxa in the genus. The iridisome may be of relatively recent origin. Iridescent blue color production in this fruit may aid in dispersal by mammals and frugivorous birds and may allow ripe fruits to continue photosynthetic carbon assimilation.



- 92** LUCKOW, MELISSA. L. H. Bailey Hortorium, 462 Mann Library, Cornell University, Ithaca, NY 14853—*Leaf anatomy of three genera of Malagasy mimosoid legumes: adaptations to xeric habitats.*

Leaf anatomy of the three closely related legume genera *Dichrostachys*, *Alantsilodendron*, and *Gagnebina* was studied using clearings, thin sections, and scanning electron microscopy. Although many gross anatomical features parallel those reported in other mimosoid legumes, variation was found in the distribution of stomata, types of venation, and degree and distribution of sclerification. Stomata are densest on the abaxial surface in species of *Gagnebina*, while the opposite is true in *Alantsilodendron*. The distribution of stomata is closely correlated with nyctinastic leaf movements and the position of leaflets at night or under wilting conditions. *Alantsilodendron* is characterized by having mostly brochidodromous venation, with the exception of the anomalous *A. villosum*, which was the only species studied to have acrodromous venation. In contrast, species of *Gagnebina* display eucamptodromous venation and species of *Dichrostachys* s.s. vary from nearly eucamptodromous to brochidodromous. The cells terminating the veinlets are also highly variable. Some species have only enlarged tracheids, while others may have sclereids, reticulate or pitted tracheids, and tracheoidal elements. There is a correlation between degree of sclerification and aridity of the habitat in which a species is found. There are two major mechanisms by which leaves become sclerified in this group: 1. modification of conducting cells or 2. modification of bundle sheath cells. Perhaps the most striking result of this study is the variety of ways in which leaflets become sclerified, even among closely related taxa.

- 93** MELOCHE, CHRISTOPHER G.\* AND PAMELA K. DIGGLE. Department of Environmental Population and Organismic Biology, University of Colorado, Boulder, CO 80309—*Patterns of carbon allocation in Acomastylis rossii (Rosaceae) an alpine plant exhibiting extreme preformation.*

Extreme preformation, the initiation of leaves or inflorescences more than one year before maturation and function, is common in arctic and alpine habitats. This extended pattern of development provides a potential means to alleviate an apparent asynchrony between carbon supplied by photosynthesis in the summer and carbon demanded by growth in the spring. The cost of storing carbohydrates for the next year's spring growth may be reduced by allocating carbohydrate directly from photosynthesizing leaves to the growth of preforming organs which will mature in subsequent years. Allocation of resources to preforming organs has, however, previously been unstudied in plants with multi-year patterns of preformation. Populations of *A. rossii* in the southern Rockies have been observed to initiate leaves and inflorescences two years before the year of maturation and function. Allocation to preforming organs in *A. rossii* was studied by means of a labeled carbon pulse chase experiment. Plants were labeled by exposure to a  $^{13}\text{CO}_2$  enriched atmosphere for one photoperiod during the 1998 summer growing season. Plants were then harvested and analyzed by mass spectrometry over the course of the subsequent thirteen months to determine the distribution of the  $^{13}\text{C}$  label. During the summer growing season carbon is allocated directly to preforming organs and rhizomes from the mature leaves. Additional allocation of carbohydrate into preforming organs occurs in autumn after these leaves have stopped photosynthesizing. Existing preformed organ primordia do not subsequently receive additional inputs of labeled carbon from rhizomes in the second year of development. Newly initiated organ primordia initiated in the second year do not receive any of the labeled carbon initially allocated to storage in the rhizome the previous year.

- 94** MIKESELL, JAN E. Department of Biology, Gettysburg College, Gettysburg, PA 17325—*Correlation of overcompensation and the breaking of apical dominance in Phaseolus aureus.*

Growth promotion induced by herbivory has been frequently reported and termed overcompensation. Overcompensation in browsed plants ultimately results in enhanced development as compared to intact plants. This promotion of growth can suspiciously resemble the breaking of apical dominance. A complicating factor in the activation of axillary shoots following decapitation is nutrition. To investigate influences of decapitation, terminal stem apices were excised from plants in one of three ways: 1) at the middle of the first or basal internode, 2) at the middle of the second internode, and 3) immediately subjacent to the apex itself. Nutritional influences were examined by removing one of the two basal unifoliate leaves from one-half of the plants. Stem apex and leaf removal occurred when *Phaseolus aureus* plants were thirty days old. Plants were monitored for vegetative and reproductive development for the next two months. Axillary shoot formation was negligible in intact plants. Most axillary shoot elongation took place early in treated plants during the sixty day monitoring period. Treatment plants exhibited differences in: 1) axillary shoot number, 2) individual length of axillary shoots, 3) combined axillary shoot length per plant, and 4) the length of fruit-bearing axillaries. Intact and experimental plants revealed differences in above-ground height as well as pod

length. However, pod mass was similar in control and treatment plant groups. Stem apex removal was considered more influential than leaf excision in the promotion of axillary shoot development.

- 95** RUSSELL, SCOTT D.<sup>1\*</sup>, ZHAOJIE ZHANG<sup>1</sup>, HUILING XU<sup>2</sup>, PREM BHALLA<sup>2</sup>, AND MOHAN B. SINGH<sup>2</sup>. <sup>1</sup>Department of Botany and Microbiology, University of Oklahoma, Norman, OK 73019; <sup>2</sup>Institute of Land and Food Resources, The University of Melbourne, Parkville, VIC., 3052, Australia—*Plumbago zeylanica* sperm isolation, collection and cDNA library characterization.

Sperm cells of *Plumbago zeylanica* express structural dimorphism in which the sperm cell associated with the vegetative nucleus ( $S_{vn}$ ) usually fuses with the central cell. The sperm cell unassociated with the vegetative nucleus ( $S_{ua}$ ) fuses with the egg cell. In order to investigate potential differences in gene expression between these two cells, paired sperm cells were released from pollen in a 10 mM MOPS buffer containing 0.8 M mannitol (pH 4.6). Sperm cell types were identified in paired cells based on size differences and sperm cells were collected individually with a microinjector. Viability, tested using FCR, indicates that sperm cells isolated under these conditions remain viable for at least 2 h. Two PCR based cDNA libraries were constructed using mRNAs isolated from separated  $S_{ua}$  and  $S_{vn}$  sperm cell populations. Preliminary screening of libraries establishes the feasibility of the technique and suggests differences in gene expression profiles between the two sperm cell types.

- 96** SALTER, JOSHUA\* AND JOHN E. BRAGGINS. School of Biological Sciences, University of Auckland, Auckland, New Zealand—*Comparative embryology of two New Zealand forest giants, Prumnopitys taxifolia and P.ferruginea (Podocarpaceae).*

An embryological study is being done on two New Zealand podocarp species, *Prumnopitys taxifolia* (matai) and *P. ferruginea* (miro), firstly, to fill gaps in our knowledge of their embryogeny, and secondly, to ascertain whether any differences may have taxonomic significance. During 3-4 annual cycles specimens of male and female cones have been collected and fixed at successive stages of development. Most specimens were embedded in paraffin wax, sectioned and stained for light microscopy, while some were embedded in resin for both LM and TEM. Later stages of embryo development were obtained from seeds collected, planted and exhumed at regular intervals leading up to germination. Several developmental stages not illustrated in the literature have been observed so far, and comprehensive life cycles have been constructed for both species. Two stages of taxonomic potential will be discussed: 1. the fertilization mechanism, and 2. the structure and development of the proembryo shortly after fertilization. The tiered proembryo in these podocarps conforms to the basal plan more typical for conifers than the derived embryogeny of the Pinaceae. The unusual fertilization mechanism observed in these two species has only been observed in one other conifer, *Prumnopitys andina*, their closest Chilean relative.

- 97** SCHNEIDER, HARALD\* AND KATHLEEN M. PRYER. University Herbarium, University of California, Berkeley, CA 94720; Department of Botany, Field Museum of Natural History, Chicago, IL 60605—*Spore morphology of heterosporous ferns and its possible implications for understanding the evolution of the seed habit.*

Heterospory has originated independently several times in vascular plant evolution, but seeds are known only from one living lineage. Although fossilized remains of seed plants from the Late Devonian and Early Carboniferous (ca. 340 mya) have provided exceptional insights into understanding the seed habit, events leading to its origin are still unclear. Monomegasporangy (single megaspore/megasporangium) is assumed to be one of the key innovations in the evolution of seed plants. This character state is found in only one other living group of vascular plants, the heterosporous ferns, which include two families with a fossil record dating back to the Early Cretaceous, Marsileaceae and Salviniaceae. Recent phylogenetic studies have demonstrated convincingly that heterosporous ferns are a monophyletic group nested within leptosporangiate ferns. Heterospory and monomegasporangy, therefore, evolved independently and at different times in the geological record in ferns and seed plants. Heterosporous ferns have an aquatic lifestyle, similar to that of Paleozoic seed plants. Comparative spore studies reveal remarkable similarities among the spores of heterosporous ferns, in particular, the presence of a gula, a modified perine structure above the aperture. The gula comprises inner and outer portions, which together enclose a chamber (= sperm lake). Each of the five extant genera (*Azolla*, *Marsilea*, *Pilularia*, *Regnellidium*, *Salvinia*) have their own characteristic gula, reflecting differences in ecology (e.g., amphibious versus floating growth forms). Additional differences are also found in the perine ultrastructure. Structures similar to a gula - lagenostomes - are also found in the megaspores of Paleozoic seed plants. This leads to the hypothesis that heterosporous ferns have evolved analogous

megaspore structures to seed plants and these can be used as a model to better understand the biological constraints in which the seed habit evolved.

- 98** SEAGO, JAMES L., JR. Department of Biology, SUNY, College at Oswego, Oswego, NY 13126—*The root cortex of the water lilies and lotuses.*

The roots of selected members of the Nymphaeaceae, Cabombaceae, and Nelumbonaceae were examined to determine root cortex characteristics in order to distinguish among the families. Each family has a characteristic root cortex structure. Members of the Nymphaeaceae typically have an endodermis with Casparian bands only, an extensive, hexagonally patterned aerenchyma with branched sclereids spreading from semi-regular hexagon cells and with transverse diaphragms, and a multiseriate hypodermis composed of a uniseriate exodermis with Casparian bands and suberin lamellae and with cellulose-thickened cell walls in some species. The Cabombaceae have small roots with an endodermis with Casparian bands and suberin lamellae, a simple aerenchyma without sclereids or transverse diaphragms, and a uniseriate exodermis with Casparian bands and distinctive suberin lamellae. The Nelumbonaceae have an endodermis with Casparian bands, suberin lamellae, and secondarily lignified cell walls, a hexagonally patterned aerenchyma without sclereids or transverse diaphragms, and a multiseriate hypodermis with a uniseriate exodermis of Casparian bands and suberin lamellae and an inner hypodermis with distinct patterns of lignified cell walls.

- 99** SOLTIS, DOUGLAS E.\*, LARRY HUFFORD, AND ROBERT K. KUZOFF. School of Biological Sciences, Washington State University, Pullman WA 99164. , Section of Molecular and Cellular Biology, University of California, Davis CA 95616—*Gynoecial diversification in Saxifragaceae: clarifying the evolution of epigyny.*

Variation in the gynoecia of Saxifragaceae provides an excellent system to explore the implications of developmental change in the generation of floral diversity within a phylogenetic framework. The traditional view has been that ovary position evolves from superior to inferior. Saxifragaceae are of interest because the complete range of ovary positions, from superior to inferior, has been reported not only across the family, but within individual genera. Most angiosperms with superior ovaries have an hypogynous floral ground plan and, hence, have ovaries that are “truly superior.” In contrast, most inferior ovaries arise from an appendicular epigynous ground plan. Using a phylogenetic hypothesis based on 6-genes, we found that the evolution of ovary position in the family is complex, with evolution to greater inferiority occurring in some taxa, whereas in other instances there is evolution toward increasing superiority. Significantly, we found that members of Saxifragaceae reported to have superior ovaries actually possess an appendicular epigynous ground plan. Hence, these taxa do not have truly superior ovaries; rather, they represent “superior mimics.” Furthermore, all gynoecia in Saxifragaceae are technically inferior. Our data also indicate that differences in ovary position at anthesis are a result of allometric shifts in the growth proportions of the superior vs. inferior regions of the ovary. These results have broad implications, potentially providing insights into gynoecial diversification throughout the angiosperms.

- 100** STEINMANN, VICTOR W. Rancho Santa Ana Botanic Garden, 1500 North College Avenue, Claremont, CA 91711—*Comparative anatomy of the New World succulent Euphorbia (Euphorbiaceae).*

The genus *Euphorbia* (Euphorbiaceae) contains nearly 2000 species, of which as many as a third are succulent. The majority of the succulent *Euphorbia* occurs in Africa and lower Asia. Within the New World there only about 15 succulent species. Based on a broad molecular phylogenetic analysis of *Euphorbia* and related genera, it appears that these comparatively few species represent at least five independent derivations of this habit, none of which are closely related to the Old World taxa. Succulence in the New World species is achieved by the proliferation of water-storing parenchyma in the pith and/or cortex. Periderm development is delayed, the epidermis remains intact, and the stem stays green and photosynthetic for many seasons. In addition, there is a trend towards microphyllly, and most species possess minute, caducous leaves, and the stem is the chief photosynthetic organ. Despite this convergence to reduced-leafed, green-stemmed succulents, there are many differences at the cellular level. Chlorenchyma organization varies from neatly layered rows of narrow palisade cells to unlayered zones of wide spheroidal cells. Tanniniferous cells are present or lacking. The vasculature also differs, and leaf traces that descend many centimeters through the cortex occur in one species. The vascular cambium is round in most taxa but is variously angled in others. In addition, there is diversity in secondary xylem. Some species possess highly lignified wood lacking axial parenchyma, while the wood of other species is less lignified with well-developed axial parenchyma, this sometimes

occurring in bands. Although both the molecular phylogenetics and the many anatomical differences suggest the repeated evolution of stem succulence within *Euphorbia*, it is still uncertain what promotes this trend.

- 101** SUD, RUCHIRA M.\* AND NANCY G. DENGLER. Department of Botany, University of Toronto, Toronto, ON M5S 1A1—*Cell lineage of vein formation in variegated leaves of the C4 grass Stenotaphrum secundatum.*

Clonal analysis of variegated leaves of the C4 grass, *Stenotaphrum secundatum*, indicates that invasions among meristematic layers occur during the organogenetic stage of leaf development, resulting in long, broad white and green stripes. These layer invasions cease prior to the second phase of leaf development when delimitation of leaf regions occurs. Vein precursors also arise during this second phase, so that procambial strand formation is superimposed on the lineage makeup of earlier-formed tissue. Anatomical evidence indicates that procambium arises through formative divisions within ground tissue of leaf primordia and that each strand is derived from a variable number (1-4) of ground meristem precursors. If a developing vein straddles the boundary between previously-formed green and white sectors, then the mature vein is half green and half white, reflecting its mixed cell lineage. In *Stenotaphrum*, 24.8% of the sectors observed were bounded by such "half veins". However, analysis of planes of cell division in developing veins indicates, that once, formed, procambial strands are discrete lineage units that extend longitudinally by proliferative division. Thus, lineage restriction may play an important role in the third stage of leaf development, differentiation of tissues and cells, which also includes the maintenance of cell identity.

- 102** TARBAEVA, VERONICA. Department of Botany, Syktyvkar State University, Syktyvkar, Russia 167001—*Structural evolution of seeds in gymnosperms.*

Evaluation and information of seed structure for systematics and phylogenetic considerations of angiosperm plants are reflected in a number of compiling monographs (Netolitzky, 1926; Corner, 1976; "Comparative anatomy of seeds", 1985-1999). However, publications devoted comparative seed anatomy of gymnosperms are a few (Chamberlain, 1935; Schnarf, 1937). Morphology and anatomy of developing and mature seeds and ultrastructure of seed coats of gymnosperms (124 species from 51 genera from 16 families) were studied during 1984-1998. During these long-term investigations it is established: 1) main evolutionary structural types of gymnosperm seeds; 2) peculiarities of histogenesis of seed coats in relation to their origin in different gymnosperm taxa; 3) classification of systematic evaluating characters of seed structure on species, genus, family, class levels, using complex analysis; 4) revision different systems of gymnosperms and 5) new phylogenetic scheme of gymnosperms. Obtained data are published in two monographs in Russia (Tarbaeva, 1995; 1997), but the phylogenetic scheme isn't yet published.

- 103** TURNER, GLENN W.\* AND RODNEY B. CROTEAU. Institute of Biological Chemistry, Washington State University, Pullman, WA 99164-6340—*Development of peltate glandular trichomes of peppermint.*

We describe the ultrastructure of the essential oil producing peltate glandular trichomes of *Mentha x piperita* L. During oil secretion, the cuticle covering the glandular cells separates from the cells to form an oil storage cavity. Filling of the cavity is correlated with the enlargement of gland cell plastids, and the development of an extensive smooth endoplasmic reticulum. Immunocytochemical localizations, and the occurrence of plastidial targeting sequences indicate that the enzymes responsible for the early steps of menthol biosynthesis (to limonene) occur in gland cell leucoplasts, while subsequent hydroxylation and reductions occur elsewhere.

## Contributed Posters

- 104** ARRIAGA, MIRTA O.\* AND MARY E. BARKWORTH. 1) Lab. Anatomía Vegetal, Museo Argentino de Ciencias Naturales, Av. A. Gallardo 470, 1405, Buenos Aires, Argentina., 2) Intermountain Herbarium, Utah State University, Logan, Utah 84322-5305, U.S.A.—*Leaf anatomy in Nassella and other South American Stipoid Grasses.*

The Stipeae is a widely distributed tribe of grasses of 400-500 species. *Nassella* is one of the largest genera in the Stipeae, comprising 112 species, of which 104 are native to South America. This study is part of a larger project being undertaken by the *Stipeae Working Group* to explore the diversity within the Stipeae with the ultimate goal of developing a strongly supported taxonomic revision of the tribe. We compared the



cross-sectional leaf anatomy of 28 species of *Nassella* with species from *Aciachne*, *Jarava*, *Piptochaetium* and *Stipa subg. Pappostipa*. The species of *Nassella* were chosen to reflect the ecological and geographic distribution of the genus and include all 6 species native to North America. Anatomically, the species of *Nassella* fall into two major groups, those with valvate leaves and those with flat leaves. The species with valvate leaves have a cross-sectional leaf anatomy similar to that found in the 15 species *Stipa subg. Pappostipa* examined and approach that of *Aciachne*. The leaf anatomy of the species with flat leaves was more similar to that of species of *Jarava* [= *Stipa subg. Jarava*]. The anatomy of *Nassella lepida* is intermediate between that of the two groups. The cross-section of *Nassella planaltima* is similar in some respects to that of *Piptochaetium* but differs in having upper and lower girders associated with its vascular bundles and in having no sclerenchyma in its phloem.

**105** BAINBRIDGE, TROY\*, KEVIN CURRAN, SARAH SHAW, AND DARLENE SOUTHWORTH. Department of Biology, Southern Oregon University—*Antibodies to Brassica sperm recognize diverse cell types and gametes.*

Little is known about the mechanism of fusion of plant gametes during reproduction. Studies on reproduction in animals suggest that fusion of sperm and egg includes protein recognition. We raised monoclonal antibodies against purified *Brassica rapa* sperm cells to visualize membrane proteins. Three antibodies (BRSP1, 2, 3) bound to *B. rapa* protoplasts isolated from stem, root, and leaf tissues indicating that the epitopes to these monoclonals were not specific to sperm cells. The molecular weight of the epitope to BRSP1 was 54 kDa, and it was not glycosylated. Antibodies also recognized gametes of other angiosperm species (*Arabidopsis*, *Eruca*, *Lilium*, *Plumbago*, *Nicotiana*) and a fern (*Ceratopteris*), and gametes of a green alga (*Acetabularia*). However, the molecular weight of these epitopes varied. None of the antibodies to *B. rapa* sperm prevented fertilization in assays with *Ceratopteris richardii* or with *Acetabularia acetabulum* indicating that these particular protein epitopes may not be associated with gamete fusion. Funded by NSF-RUI grant IBN-9816945.

**106** COOK, MARTHA E.\* AND COLLEEN A. LAVIN. Department of Biological Sciences, Illinois State University, Normal IL, 61790-4120 and University of Wisconsin Microscopy Resource, Biological Imaging Center, Madison, WI 53706—*Plasmodesmal ultrastructure in the green alga Coleochaete orbicularis (Charophyceae): implications for the evolution of plant plasmodesmata.*

Based on molecular, morphological, and biochemical data, the charophycean green algae are considered to be the closest living relatives of plants. Hence study of these algae may reveal how or when various features of plants evolved. Transmission electron microscopy was used to examine plasmodesmal ultrastructure in the advanced charophycean alga *Coleochaete orbicularis*. Three methods of preservation were employed: standard chemical fixation, microwave-enhanced chemical fixation, and high pressure freezing followed by freeze substitution. With all three methods, similar features were observed in plasmodesmata of *Coleochaete*. A central structure is seen in cross-sectional views of some plasmodesmata, and appears to be connected to the plasma membrane via spoke-like structures. In longitudinal section, connections between the endoplasmic reticulum and the plasmodesmata were sometimes observed. Spoke-like structures radiate away from the plasma membrane and in some cases connect with ring-like wall specializations. Wall specializations are found in some plant plasmodesmata, but were not observed in a previous study of plasmodesmata in another advanced charophycean alga, *Chara zeylanica*. Generally however, the plasmodesmata of *Coleochaete* and *Chara* are similar to each other and to the plasmodesmata of plants. Given that the central structure of charophycean plasmodesmata appears to be less commonly observed than is the desmotubule of plant plasmodesmata, it is possible that the plasmodesmata of charophyceans are less specialized than those of plants, or that they have been modified after charophyceans diverged from a common ancestor with plants.

**107** DULBERGER, RIVKA. Department of Plant Sciences, Tel Aviv University, Tel Aviv, 69978 Israel—*Variation of stigma characters in relation to their function.*

Receptive surfaces of angiosperm stigmas have been classified by cyto-physiological and histological criteria. The main categories distinguished are wet or dry, with the receptive surface papillate or smooth in each category. In most families or even orders examined, the characteristics of each category were found to be uniform. The criteria used in this classification are mainly significant for processes initiated once the pollen grains have landed on the stigma. Morphological stigma characters, on the other hand, such as shape, size, positioning, orientation, and distribution of the receptive area are likely to be relevant for capturing of pollen grains. In the last four decades most studies on stigmas were related to their interactions with pollen grains

and to incompatibility, while studies of pollination paid little attention to stigma morphology. The present work attempts to assess the variation of morphological stigma traits at various levels of taxonomic hierarchy. Is variation in these traits similar to the variation in characters significant for pollen-stigma interactions? A preliminary survey of the literature revealed dissimilar patterns of diversity for characters involved in the two functions of the stigma. Numerous examples were encountered in which details of stigma morphology relevant for pollination were among diagnostic criteria used for distinguishing between sub-families, tribes, genera, sections, and species. Diversity of stigma morphology among taxa of the same rank is mostly associated with uniformly wet or dry and papillate or non-papillate receptive areas. Properties of the receptive area functioning in pollen-stigma interactions appear to be more constant than properties involved in stigma moulding in accordance to requirements of pollen acquisition. Diversification of morphological properties frequently occurs in taxa with specialized pollination mechanisms, e.g., secondary pollen presentation or buzz-pollination. It may also serve as an isolation mechanism between sympatric species.

- 108** GOLLA, EDYTA M. Institute of Botany, Wrocław University, Kanonia 6/8, 50-328 Wrocław, Poland—*Formation of phyllotactic patterns in cactus seedlings.*

In phyllotaxis of the majority of cactus genera, especially *Mammillaria*, *Notocactus*, *Gymnocalycium*, the main Fibonacci pattern predominates. In some genera, to which *Rebutia* and *Aylostera* belong, a broad phyllotactic spectrum with the accessory patterns prevailing, was discovered. The analysis of the sequential initiation of areoles in seedlings of both groups shows that in *Rebutia*, *Aylostera*, *Pseudobolivia*, *Gymnocalycium* areoles are initiated in pairs. The first pair is circumferentially positioned exactly as cotyledons, slightly above them. The subsequent pair arises at the right angle to the first pair. Later either the decussate arrangement of areoles develops or, after a small torsion of successively initiated pairs - the main bijugy. In some cases, due to the initial tricotyly, areoles similarly form either tricussate pattern or initiate the main trijugy. In *Rebutia* occasionally areoles of one pair differ in timing of their appearance or deviate from expected circumferential position indicating the change of the pattern into simple spiral. In contrast to these situations, areoles in *Mammillaria* are initiated not in whorls but separately, the first one between cotyledons. Successive areoles appear in a spiral sequence, quickly establishing low expressions of the main Fibonacci pattern. Despite the different modes of areole initiation, the reasons for the phyllotaxis diversity in such genera as in *Rebutia* are not completely elucidated since in seedlings only the most common patterns have been found. It is suggested that the diversity of patterns in cacti is due to subsequent ontogenetic transformations of phyllotaxis. These may involve qualitative change of patterns as commonly in *Rebutia* and ontogenetic increase of contact parastichy numbers of the main Fibonacci pattern as in *Mammillaria*.

- 109** HOU, GUI-CHUAN\* AND JEFFREY P. HILL. Department of Biological Sciences, Idaho State University, Pocatello, ID83209—*Root development in sporelings of Ceratopteris richardii.*

Root morphology in *Ceratopteris richardii* sporelings exhibits heteroblastic variation. Growth analysis of the first six roots borne along the shoot shows that root 5 has a predictable pattern of development that is well suited for detailed study. The developmental anatomy of this fifth root, which is located near the base of sporeling leaf 5, is described using histological and statistical techniques. Three proximal division faces of the tetrahedral root apical cell divide in a strict sequence to produce three merophyte orthostichies in the body of the root. Formative divisions in merophytes behind the apical cell produce initials that give rise to a characteristic number of cell files in each merophyte. These formative divisions occur in a relatively regular order during merophyte ontogeny, and there are no significant differences among plants. However, the formative division pattern among merophytes within a root is not strictly the same. Predictable inter-merophyte differences arise because a two-fold anatomical symmetry that is characteristic of mature roots is superimposed on a three-fold radial symmetry that originates behind the apical cell. As formative divisions are completed, extensive proliferative divisions subsequently increase cell numbers within each cell file of a merophyte. The cellular parameters of fifth root development observed here are reminiscent of patterns previously described for the heterosporous fern *Azolla*. However, *C. richardii* should prove to be a more tractable model to further investigate the genetic regulation of root development in a non-seed plant.

- 110** KIRCHOFF, BRUCE\*, SONJA CAUBLE, ELIZABETH SHELTON, AND ALLYSON PREVETTE. Department of Biology, P.O. Box 26174, University of North Carolina at Greensboro, Greensboro, NC 27402-6174—*The Structure of the Banana Inflorescence.*

The morphology of the banana inflorescence has been described as a long terminal raceme, a terminal panicle, and a serial flower assemblage. Mclean Thompson proposed that the banana inflorescence was an aerial stem with spirally arranged leaves in the axils of which grow cones of flowers. The observations of Abraham

Fahn contest this hypothesis and favor another hypothesis also proposed by Thompson in which the flower-groups are cincinni. Our research has examined inflorescence development in *Musa velutina*. *Musa* is monocious, containing unisexual flowers arranged in hands. The number of flowers per hand varies. Each hand develops in the axil of a primary bract and consists of two rows of flowers. The entire inflorescence is made up of a definite number of female hands, a small number of transitional hands, and an indefinite number of male hands. Based on his observations of *Musa acuminata* and *Musa balbisiana*, Fahn suggests that the sequence of flower initiation begins with the primordium farthest right in the adaxial row. This is followed by the development of the primordium directly adjacent to the first. The third is the right most primordium in the abaxial row. He suggests the sequence continues to alternate, adaxial to abaxial, throughout the hand. Our research does not wholly agree with these findings. Many of the hands we studied demonstrate the sequence of flower initiation beginning from the center of the hand and progressing outward. In many instances the right-most flower appears to be younger than the flower adjacent to it. While we have observed the adaxial-abaxial arrangement of flowers we have not observed development of flower primordia following an alternating sequence between the rows.

- 111** LANDRUM, JAMES VICTOR. Biology Department, Washburn University, Topeka, KS 66621—*Effects of hormones on wide-band tracheid expression in stems of Anacampseros (Portulacaceae)*.

Wide-band tracheids (WBTs) are found in leaves and stems of species in the South African genus *Anacampseros* (Portulacaceae). Wide-band tracheids are parenchyma cells that are converted into modified tracheids with wide secondary walls intruding into the lumen. In stems, WBTs occupy rays and pith, and are thought to function as an alternative water-conduction system or water-storage system in severe water-stress conditions common to their location. Experiments were conducted to determine the effects of auxin, cytokinin, and gibberellic acid (GA) on WBT formation. Seedlings were grown on sterile sand medium inundated with hormone solution, and were harvested at 30 and 65 days. There was little difference between auxin-treated plants, kinetin-treated plants, and control plants; however, a significant difference was noted in seedlings exposed to gibberellic acid. In the GA seedlings, three of four measured traits remained similar with the exception of the cell area occupied by the wide-band, which increased from a mean of 72% in the control seedlings to a mean of 81% in the GA seedlings. The inability of auxins and cytokinins to change WBT characteristics implies that WBTs are not initiated by the same signalling pathways that usually activate tracheid production.

- 112** LANDRUM, JAMES VICTOR. Biology Department, Washburn University, Topeka, KS 66621—*Light intensity as the primary factor for wide-band tracheid initiation and development in stems of Anacampseros (Portulacaceae)*.

Wide-band tracheids (WBTs) are novel variations of more common tracheids, and are characterized by a wide, intrusive secondary wall. Limited in systematic occurrence, WBTs are found only in three angiosperm families: Aizoaceae, Cactaceae, and Portulacaceae. These cells were hypothesized as evolutionary adaptations to water-stress events; during water-stress events, common tracheids would collapse whereas WBTs would retain functionality. Experiments using WBTs found in stems of species in the genus *Anacampseros* (Portulacaceae) show that light, not water-stress, is the primary controlling factor for WBT initiation and development. Plants exposed to low, moderate, and high light levels show correlative differences in WBT traits and numbers. Light intensity is thus proposed as a pre-adaptive factor that initiates WBT formation in preparation, not in response, to water-stress.

- 113** LUCAS, JESSICA R.\* AND KAREN S. RENZAGLIA. Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901—*Anatomy, ultrastructure and physiology of hornwort stomata: an evaluation of homology*.

Stomata are integral to water transport in plants because evaporation of water through the stomatal pore draws water through the water conducting tissue. This pore also enables gas exchange, especially carbon dioxide entrance. Among bryophytes, stomata are restricted to sporophytes of mosses and three hornwort genera. This study of the anatomy and ultrastructure of the stomata in *Phaeoceros* and *Folioceros* was undertaken to evaluate homology of stomata among basal embryophytes. Light microscope studies indicate that the reniform guard cells of hornworts contain a large vacuole, one to two starch-filled plastids and a peripheral nucleus. Compared to other epidermal cells, the guard cells walls are thickened, especially adjacent to the pore. Transmission electron microscopy revealed that the pronounced cell wall is of three layers, each containing parallel microfibrils oriented in different directions. Intercellular spaces are found internal to the

stomata in the assimilative cells. Such evidence, combined with the fact that other epidermal cells lack chloroplasts, implies that hornwort stomata function in gas exchange. To evaluate whether or not these stomata open and close as a result of osmotic changes, we have performed histochemical studies on potassium and organic ion sequestration in guard cells. The role of stomata in transpiration will be evaluated in regards to water transport through the sporophyte. Comparisons will be made with stomata of lycophytes and mosses.

- 114** NIELD, BECKY A.\* AND JEFFREY P. HILL. Department of Biological Sciences, Idaho State University, Pocatello, ID 83209-8007—*Molecular genetic studies of gender expression in angiosperms: early ovule development in Nicotiana tabacum.*

Within the non-seed plants, sex determination either occurs just before meiosis (e.g., *Selaginella*) or some time after meiosis in the developing gametophyte (e.g., homosporous ferns). In angiosperms, sex determination is generally considered a feature of the sporophyte's life history, because gender-specific organs (i.e., male stamens and female carpels) are initiated well before meiosis. This study presents a different hypothesis about patterns of sex determination in flowering plants, one that is broadly based on the phylogenetic history of this trait. Due to alternation of generations, flowering plants may have elements of two independent sex determination events per sexual cycle. The first widely recognized event dictates gender expression in the sporophyte. The second event, which is an evolutionary vestige of a sex determination mechanism that predates the evolution of the seed habit, reflects the primitive state for controlling gender expression in the gametophyte phase. This research seeks to identify and characterize genes involved in early gender specialization during this second (i.e., haploid) event in *Nicotiana tabacum*. Genes expressed in early stages of ovule development, including the nascent placenta and pre-meiotic ovule primordia, are being characterized. These structures are, in a developmental morphological sense, close to the phases that appear to evoke differences in haploid gender expression in more primitive heterosporous plants like *Selaginella*. Differential Display-Polymerase Chain Reaction (DD-PCR) has been employed to initially characterize gene expression patterns among target tissues compared to leaf and stamen primordia. To date, seven putative placental-specific genes and two putative early ovule-specific genes have been found using DD-PCR, and further characterization is in progress. The results should advance the current understanding of genetic mechanisms regulating gene expression in early ovules of an agriculturally significant plant family (Solanaceae), and provide insights into the evolution of gender expression in plants at the same time.

- 115** PETERSON, CURT M., LIWEI CHEN, ROLAND R DUTE, AND MANDY N. ROGERS.\* Department of Biological Sciences, University of Northern Colorado, Greeley, CO 80639; Department of Biological Sciences, Auburn University, AL 36849—*Petiole Abscission in Cotton (Gossypium hirsutum L.): Anatomical and Ultrastructural Observations.*

Abscission limits yield and indirectly affects fiber quality in cotton. The purpose of this study was to determine the structural changes contributing to petiole abscission. Ethephon (2-chloroethyl-phosphonic acid) hastened cotyledonary leaf abscission of cotton, *Gossypium hirsutum* L. Abscission of petioles was induced in explants prepared from 14-day-old seedlings by removal of the leaf blade, and then applying either lanolin or lanolin containing 0.1% ethephon to the petiole stumps. Prominent swelling of collenchyma cells on the adaxial side of the petiole within the abscission zone provided the first morphological indication that abscission had begun. Cell separation occurred distal to this region of swollen cells and was initiated first on the adaxial side of the petiole. Swelling of ground tissue cells also was observed on the abaxial side of the petiole. Tyloses were observed within vessel members proximal to the region where cell separation was observed. Ultrastructural changes in abscission zone cells of the explants treated with ethephon occurred earlier than those of the lanolin treatment. Vesicles appeared within the mid-cell wall regions as cell separation progressed. Free cell wall microfibrils also accumulated at this time. Middle lamella dissolution and partial degradation of the primary cell wall was observed prior to abscission. The plasma membrane of most separation layers cells remained intact following cell wall degradation, and these intact cells contained degraded chloroplasts and mitochondria. Some separation layer cells broke down completely, and organelles within them became embedded in the degraded cell wall matrix. Although ethephon treatment hastens the abscission process, no other differences in structural events leading up to abscission were observed when tissues of ethephon-treated explants were compared to lanolin-treated (control) explants. These anatomical and ultrastructural changes suggest that abscission specific, cell wall hydrolyzing enzymes are being secreted following stimulation of abscission by leaf blade removal.



- 116** SUN, XIAOYONG AND ROGER D. MEICENHEIMER.\* Department of Botany, Miami University, Oxford, OH 45056—*Auxin Distribution in Pisum sativum Shoot Apical Meristems.*

*Pisum sativum* cv. Telephone were grown in a 8:16/27:22 L:D controlled environment to prolong vegetative shoot development. Shoot apices were sampled at various times during the plastochron using a stipule length plastochron index. Stems were prefixed with 1-ethyl-3-(dimethyl-aminopropyl)-carbodiimide hydrochloride to stabilize the location of free endogenous indole-3-acetic acid (IAA) in the shoot apical meristem and leaf primordia. Serial transverse sections were immunolabeled with a commercially available primary monoclonal antibody against IAA. IAA location was visualized using Western Blue stabilized substrate for alkaline phosphatase secondary antibody. Quantitative comparisons between the amount of label on the halves of the shoot apical meristem adjacent to and opposite the youngest leaf primordium were performed to test the hypothesis that just prior to leaf primordium initiation a population of shoot apical meristem cells is transformed from auxin sink cells to auxin source cells.

- 117** ZAGÓRSKA-MAREK, BEATA AND ALICJA, S. BANASIAK.\* Institute of Botany, University of Wrocław, Kanonia 6/8, 50-328 Wrocław, Poland—*Vascular homodromy in branching shoots of conifers.*

In monopodial, regularly branching system of coniferous shoot, exemplified in our studies by *Picea* and *Abies*, the chirality of spiral phyllotaxis in the supporting axis is correlated either positively (homodromy) or negatively (antidromy) with that of the laterals. As neither of these two tendencies prevailed in the investigated material, it seemed that the supporting axis has no effect upon the phyllotaxis of laterals. This conclusion appeared justified especially in light of the fact that phyllotactic system of each lateral branch is generated from the initial opposite arrangement of prophylls. Thorough anatomical analysis of primary vascular system structure in branching shoots of *Picea* and *Abies* unexpectedly showed that the above conclusion should be falsified. In vascular pattern where inclination of vascular sympodia is dependent upon phyllotaxis and anatomic diameter of the shoot we found 100% vascular homodromous correlation between the inclinations of vascular sympodia in axes of all orders. This homodromy was particularly spectacular in the cases when, in the main axis, the orientation of sympodia was changing ontogenetically bringing up immediately the new orientation of vascular sympodia in laterals. In the unknown way the vascular system of the supporting axis signals the axillary meristem, recognizing its size, what the chirality of its phyllotaxis should be, to accommodate the same inclination of its future vascular sympodia. These findings point out to the leading role of the vascular system in establishing phyllotactic pattern of the shoot.

## VI. Ecological Section

### Contributed Papers

- 118** ADAMS, CHRISTOPHER A., JERRY M. BASKIN, AND CAROL C. BASKIN.\* School of Biological Sciences, University of Kentucky, Lexington, KY 40506; School of Biological Sciences, University of Kentucky, Lexington, KY 40506; School of Biological Sciences and Department of Agronomy, University of Kentucky, Lexington, KY 40506—*Seed dormancy in the Appalachian endemic Aristolochia macrophylla Lam. (Aristolochiaceae).*

The purpose of the first author's dissertation research is to compare seed dormancy-breaking and germination requirements of the three closely related species *Aristolochia macrophylla*, *A. tomentosa* (eastern U.S.), and *A. californica* (California). However, only results for *A. macrophylla* will be presented in this talk. *Aristolochia macrophylla* is a deciduous, woody vine found in mesic forests of the Appalachian Highlands Physiographic Division from southwestern Pennsylvania south to northern Georgia. Seeds of *A. macrophylla* have linear, underdeveloped embryos [ $1.99\text{mm} \pm .08$  (mean  $\pm$  SE) in length] that more than double in size before they germinate. Embryos in fresh seeds incubated at 35/20, 30/15, 25/15, 20/10, and 15/6°C in light and in dark for 90 days grew in all regimes, but the fastest growth rate was at 25/15°C. Highest germination percentages occurred at 25/15°C, where 47 and 39% of the seeds germinated in light and dark, respectively, after 30 days and 70 and 45%, respectively, after 90 days. Twenty-three percent of the seeds that did not germinate in darkness at 25/15°C did so after they were transferred to light at this temperature regime. Further, 59% of the seeds that failed to germinate in light at 25/15°C did so after 12 wk of cold stratification, resulting in 85% total germination. Thus, some freshly-matured seeds in the population had morphological dormancy (MD) and others a combination of MD and physiological dormancy (PD), i.e., morphophysiological dormancy (MPD).

ical dormancy. PD was broken by cold stratification at 5°C, but embryos did not grow at this temperature. Fresh seeds cold stratified for 12 wk in light germinated to 96 and 95% in light and dark, respectively, after 60 days at 25/15°C, and those cold stratified in dark germinated to 95 and 74%, respectively. Preliminary data suggest that the seed dormancy-breaking requirements of *A. macrophylla* differ considerably from those of *A. californica*.

- 119** BASKIN, CAROL C.\* , PER MILBERG, LARS ANDERSSON, AND JERRY M. BASKIN. School of Biological Sciences and Department of Agronomy, University of Kentucky, Lexington, KY 40506; Department of Biology-IFM, Linköping University, 581 83 Linköping, Sweden; Department of Ecology and Crop Production Science, Swedish University of Agricultural Sciences, S-750 07 Uppsala, Sweden; and School of Biological Sciences, University of Kentucky, Lexington, KY 40506—*Germination studies on three dwarf shrubs (Vaccinium, Ericaceae) of Northern Hemisphere coniferous forests.*

Freshly-matured seeds of *Vaccinium myrtillus*, *V. vitis-idaea* and *V. uliginosum* from coniferous forests in Sweden were tested for germination in light and darkness at 12/12 h daily temperature regimes at 15/5 (or 15/6), 20/10 and 25/15 C. Seeds also were tested at the same conditions after they were cold stratified. In initial tests, seeds of *V. myrtillus* and *V. vitis-idaea* germinated to 62-100% in light at 20/10 and/or 25/15 C with few (1-12%), or no seeds germinating at 15/5(6) C; however, after 12 or 20 wk of stratification germination percentages increased significantly in light at 15/5(6) C. Thus, seeds of these species are conditionally dormant at maturity. One to 20% of *V. myrtillus* and 0-2% of *V. vitis-idaea* seeds sown outdoors in southern Sweden on various dates in summer germinated before winter. Seeds of neither species germinated during late May, when minimum temperatures were about 7-10 C, but they germinated after minimum temperatures increased to  $\leq 10$  C. Stratified seeds of *V. myrtillus* and *V. vitis-idaea* required more than 2 wk of incubation at 15/5(6) C for initiation of germination. Therefore, even after habitat temperatures have reached the minimum range for germination of nondormant seeds, a slow rate of germination at low temperatures may prevent them from germinating in early spring. Nonstratified seeds of *V. uliginosum* germinated to a maximum of 5% in light and of 7% in darkness, but after 12 wk of stratification seeds germinated to 49-95% in light and to 1-60% in darkness at 15/5, 20/10 and 25/15 C. Most seeds of *V. uliginosum* were dormant at maturity, and they came out of dormancy during stratification in winter. Seeds of *V. uliginosum* germinated over the same range of temperatures as those of *V. myrtillus* and *V. vitis-idaea* by spring, but they germinated faster at 15/5(6) C than those of the other two species.

- 120** BASKIN, JERRY M.\* AND CAROL C. BASKIN. School of Biological Sciences, University of Kentucky, Lexington, KY 40506-0225 and School of Biological Sciences, University of Kentucky, Lexington, KY 40506-0225 and Department of Agronomy, University of Kentucky, Lexington, KY 40546-0091—*Seed dormancy in relation to endocarp anatomy in Anacardiaceae.*

Information in the literature was used to determine seed (true seed + endocarp) dormancy types in Anacardiaceae, and the results were examined in relation to published accounts of endocarp anatomy in this family. Reports on both seed germination and endocarp anatomy were found for seven genera in tribe Spondideae, five in tribe Anacardiaceae, 14 in tribe Rhoeae, and none in the two smallest tribes in the family, Dobineae and Semecarpeae. In Spondideae (*Spondias*-type endocarp), seeds were either nondormant (ND) or had physiological dormancy (PD), and in Anacardiaceae (*Anacardium*-type endocarp) they were mostly ND. In Rhoeae (*Anacardium*-type Rhoeae groups A, B, C, and D endocarps), on the other hand, seeds were ND or had physical dormancy (PY), PD, or both (PY + PD). PY in this tribe seems to be restricted to genera (e.g., *Cotinus*, *Rhus*) with an *Anacardium*-type Rhoeae Group A endocarp (*sensu* Wannan, B. S. and C. J. Quinn. 1990. *Botanical Journal of the Linnean Society* 102: 225-252). However, seeds of other genera (e.g., *As-tronium*, *Schinus*) with this type of endocarp and those with Rhoeae Group B (e.g., *Pistacia*), Group C (e.g., *Pentaspadon*), and Group D (e.g., *Heeria*) endocarps (*sensu* Wannan and Quinn, 1990; von Teichman and van Wyk. 1996. *Botanical Journal of the Linnean Society* 122: 335-352) are either ND or have PD. The fossil fruit record strongly suggests that seeds of Anacardiaceae with PY (*Rhus*: Rhoeae) and PD (the extinct genus *Pentoperculum*: Spondideae) extend back to at least the middle Eocene.

- 121** BIDARTONDO, MARTIN I.\* AND THOMAS D. BRUNS. Department of Environmental Science, Policy & Management, University of California, Berkeley, CA 94720-3102—*Patterns of extreme specificity in the monotropoid mycorrhizal symbiosis.*

The monotropes (Monotropoideae, Ericaceae) are non-photosynthetic plants that obtain fixed carbon from fungi with which they form monotropoid mycorrhizal associations. These fungi in turn form ectomycorrhizae

with neighboring photosynthetic plants that likely serve as the original carbon source for the monotropes. We wanted to determine if different lineages of the Monotropoideae are specifically associated with different lineages of fungi. To answer this, we sampled a total of 164 plants from 9 of the 11 recognized species in the Monotropoideae. We have obtained fungal mtLSU and nrITS sequence data from their mycorrhizal associates. To identify the fungi, sequence data were obtained from 97 basidiocarps. In addition, we obtained plant nrLSU and nrITS sequence data for the monotropes. All monotropes were highly specialized, but host-jumps to distantly related fungi have occurred several times. The snow plant (*Sarcodes*) associates exclusively with a *Rhizopogon* species complex (Rhizopogonaceae); pine drops (*Pterospora*) with two *Rhizopogon* species complexes; Sierra sap (*Pleuricospora*) with *Gautieria* spp. (Gautieriaceae); the gnome plant (*Hemitomes*) with Thelephoraceae spp.; pine foot (*Pityopus*), pine sap (*Monotropa hypopithys*) and candy cane (*Allotropia*) with *Tricholoma* spp. (Tricholomataceae); and *Monotropastrum* and Indian pipe (*Monotropa uniflora*) with Russulaceae spp. We found evidence of phylogenetic tracking in at least three clades of monotrope sister species which specialize on closely related fungal species.

**122** BISHOP, JOHN, G. AND WILLIAM F. FAGAN.\* School of Biological Sciences, Washington State University-Vancouver, Vancouver, WA 98686—*Severe insect herbivory concentrated in low density regions of lupines colonizing Mount St. Helens.*

*Lupinus lepidus* began colonizing the Pumice Plains of Mount St. Helens in 1981, one year post-eruption, beginning with a single plant. Population growth in this primary successional site was initially extremely rapid, yet extensive colonization of available habitat has been surprisingly slow. Our previous work demonstrated a major impact of lepidopteran and anthomyid herbivores on the demography and spread rate of colonizing lupines. Here we document strong spatial patterning of insect herbivory. We measured demographic parameters and herbivory in the initial colonizing patches ("core patches"), and newly-founded patches distant from the core ("edge patches"), for ~12000 plants in ~60 patches, from 1990-95. Stem-boring, leaf-mining, and seed-eating insects increased through time and severely decreased seed production and survivorship in low-density edge portions of the expanding population, and had less effect in the core. For example, in 1994-95 stem-boring tortricid moth incidence was 77% in edge patches vs. 24% in core patches; in 1993-95 noctuid leaf-miners infested 68% of plants in the youngest edge patches, vs. 8% at the core. Together, these moths increased edge mortality to ~90% in 1995, over a baseline of ~30% (1991-93). Damage data collected in 1996, 1998, and 1999 along transects running from core areas to edge areas show that the pattern of inverse density dependent herbivory has persisted and is also present at smaller spatial scales, i.e. from the center to the margin of core patches. We are investigating whether predators, parasites, or plant quality may explain the absence of herbivores in the high density core.

**123** BRUNET, JOHANNE\* AND AARON LISTON. Department of Botany and Plant Pathology, Oregon State University, Cordley Hall 2082, Corvallis, OR 97331-2902—*Breeding system evolution in the genus Thalictrum (meadow rue) Ranunculaceae.*

The phylogeny of 20 *Thalictrum* species and four outgroups was reconstructed using two molecular loci, the nrDNA ITS region (internal transcribed spacers of nuclear ribosomal DNA) and the chloroplast DNA *rpl16* intron, and 37 morphological characters. The 20 species represent 10 of 14 sections in this genus of 190 species. The nuclear data provided better-resolved trees than the morphological data. The combined analysis consensus tree had bootstrap support above 70% for the majority of clades. *Thalictrum* species vary in their breeding system and pollination mechanisms within a breeding system. Species can be hermaphroditic (all flowers have both male and female organs), dioecious (male and female individuals), or andromonoecious (male and hermaphroditic flowers on an individual) and are pollinated by wind, insect, or both. While wind-pollination is common in dioecious and andromonoecious species, and insect-pollination in hermaphroditic species, both insect- and wind-pollination occur in some dioecious and some hermaphroditic species. The evolution of the breeding system and the pollination mechanism were examined using the methods of character optimization. Two separate origins of dioecy were detected in North America, and no reversal back to hermaphroditism was observed. There was one origin of andromonoecy, and it was separated from the origins of the dioecious clades. Of the known ecological correlates of dioecy (woodiness, fleshy fruits, islands, tropical habitats, and wind-pollination), only wind-pollination is correlated with dioecy in this genus. Preliminary results suggest that wind-pollination preceded the evolution of dioecy and andromonoecy in this genus.

- 124** CHEPLICK, GREGORY P.\* AND HARRY DEMETRI. Department of Biology, College of Staten Island, City University of New York, Staten Island, NY 10314—*Population ecology of the annual grass Triplasis purpurea along the south shore of Staten Island, New York.*

To determine its potential to colonize disturbed habitats mostly devoid of other vegetation, four seedling populations of *Triplasis purpurea*, a North American native, summer annual grass, were surveyed on coastal beaches along the south shore of Staten Island, New York in early summer. For two populations, survivorship, growth, and reproduction were monitored at different distances from shore to determine the ability of this species to maintain viable populations. At three sites, *T. purpurea* occurred in >75% of all quadrats used for sampling and densities reached a maximum of 1,195 seedlings per square meter at one highly disturbed site. From 40-90 m from shore, density generally increased. Plants showed the greatest growth and reproduction at distances close to shore (30-40 m); some of this effect was due to density in one population, but when density effects were removed statistically, there still remained a decline in growth and reproduction with increasing distance from shore. Survivorship showed a Type III pattern, with low mortality throughout the summer growing season. Experimental evidence suggests that improved vigour nearest to shore may be due to continual sand deposition. By colonizing newly-deposited and continually shifting sands, *T. purpurea* can contribute to the earliest stages of dune formation and ecological succession along disturbed coastal beaches in eastern North America.

- 125** CHEPLICK, GREGORY PAUL. Department of Biology, College of Staten Island-City University of New York, Staten Island, NY 10314—*Plasticity of size and architectural traits in relation to fitness in an annual weed.*

The quantitative genetics and plasticity of size and architectural traits in relation to nutrient availability were investigated in families of *Amaranthus albus*. This summer annual continually produces flowers and seeds clustered in leaf axils along growing stems. The importance of size and architectural traits (number of branches and total branch length) to reproductive fitness (seed output) was determined. Seeds from seven maternal genotypes collected from a field in southern Wisconsin were used to raise the first generation of plants in a greenhouse under constant conditions. Seed families from four first-generation plants per genotype were used to raise a second generation in the greenhouse over a 10 week period. For each family, nine of the plants were unfertilized and nine others were regularly fertilized. In both unfertilized and fertilized groups, stepwise regression revealed that size, estimated as volume of space occupied at 5 and 8 weeks, and total branch length were all significant determinants of fitness. Genotype by treatment interactions were apparent for size and architectural traits, indicating plasticity in relation to soil nutrients. Significant effects of genotype on size and architectural traits and fitness were detected, but only for the unfertilized group. Continuous lengthening of multiple branches increases seed output throughout the growing season; plasticity in size and branching in response to improved soil resources allows opportunistic increases in fitness in a heterogeneous habitat. However, selection is most likely to differentiate among genotypes in stressful, nutrient-poor environments.

- 126** COONS, JANICE M.\*, HENRY R. OWEN, JENNIFER L. FRANKLIN, AND JOHN E. EBINGER. Biological Sciences Department, Eastern Illinois University, Charleston, IL 61920—*Reproductive potential of Silvery Bladderpod (Lesquerella ludoviciana).*

Silvery bladderpod (*Lesquerella ludoviciana*) is an endangered plant in Illinois where plants are at the eastern edge of their geographic range, occurring in blowout areas of recovering sand prairies at the Henry Allan Gleason Nature Preserve. Little is known about its reproductive potential in these areas. The objective of this study was to characterize population size, production of reproductive structures, and viability of seeds. In June 1999, three populations were identified within the Preserve. For each population, plants with and without fruits (no flowers present) were counted, and population areas were determined. Seedstalks/plant, fruits/seedstalk, and seeds/fruit were counted. Seeds were germinated on filter paper in Petri dishes at 25°C. The three populations varied in size from 275 to 2050 m<sup>2</sup> with a total area of nearly 3000 m<sup>2</sup>. Plant numbers were 900, 225, and 10,300 in the smallest, intermediate, and largest areas, respectively. The percentage of reproductive plants was lowest (28%) in the largest area and highest (88%) in the smallest area. Reproductive plants produced 6.5 seedstalks/plant (from 1 to 20). An average of 17.3 fruits/seedstalk (from 0 to 43) and 2.4 seeds/fruit (from 0 to 7) were produced. On seedstalks, seeds matured first on the lower part and last on the upper part. Total seed production for all three populations was estimated at nearly 1,200,000 seeds. Seeds germinated without any treatments to break dormancy. In summary, reproductive potential does not appear to be limited by seed production or by seed viability. Rather, reproductive potential in silvery bladderpod must be limited by other factors.



- 127** DOBSON, HEIDI E. M.\* AND MANFRED AYASSE. Department of Biology, Whitman College, Walla Walla, WA 99362; Department of Evolutionary Biology, Institute of Zoology, University of Vienna, Vienna 1090, Austria—*Does larval pollen diet influence host-flower selection in solitary bees?*

A fundamental question in bee-flower associations is whether flower selection and specialization in bees is determined by genetically based preferences or by the chemical imprinting of bees to odors of their larval pollen provisions. To evaluate the role of imprinting to pollen chemicals, females of two solitary bee species were forced to provision their nests with pollen of *Brassica napus* (Brassicaceae) and females of the next generation were tested for their preferences to flowers. In these multiple-choice behavioral experiments, bees were offered flowers from eight species and their responses to each were compared in terms of number of visits, duration of visits, and sequence of visits. In the pollen-generalist (polylectic) bee *Osmia rufa* (Megachilidae), no imprinting effect was observed. These findings will be compared to experiments conducted on a pollen-specialist (oligolectic) bee, *Chelostoma florissomne* (Megachilidae), and the implications on the development and evolution of flower/pollen specialization in bees will be discussed.

- 128** EGAN, TODD P.\* AND IRWIN A. UNGAR. Department of Biological Sciences, University of Wisconsin, Milwaukee, WI, 53201—*Similarity between seed banks and aboveground vegetation along a salinity gradient.*

Zonation of aboveground vegetation often occurs in salt marshes along salinity and moisture gradients. The aboveground vegetation and seed bank in four physiognomically different vegetation zones in a salt marsh were compared to determine their level of similarity using percent similarity as a distance measure. Ten meter transects were established along a salinity gradient through four different zones, a *Salicornia* zone, a *Salicornia-Atriplex* zone, an *Atriplex* zone, and an *Atriplex-Hordeum* zone. A UPGMA cluster analysis demonstrated that the aboveground vegetation usually was not highly correlated with the seed bank composition of zonal communities. Since seeds of these annual salt marsh species occurred in all zones, the levels of salt stress may be the main factor determining which species were found in the aboveground vegetation.

- 129** ERHART, TEMAN\*, MARK V. WILSON, AND AARON LISTON. Department of Botany & Plant Pathology, Oregon State University, Corvallis, Oregon 97330—*Population dynamics and conservation biology of *Lupinus sulphureus* ssp. *kincaidii* (Fabaceae).*

Kincaid's lupine (*Lupinus sulphureus* ssp. *kincaidii* (Smith) Phillips) is a rare endemic plant of the Willamette Valley. This member of the Fabaceae is a long-lived perennial plant of native upland prairie remnants. It was listed as a Threatened species under the Endangered Species Act in January of 2000. It is also a nearly obligate larval foodplant of a rare butterfly, Fender's blue butterfly, which was concurrently listed as an Endangered species. Low seed production and progeny fitness has been observed in many populations. This is suspected to be a result of possible self-incompatibility and inbreeding depression in small isolated populations. As part of a study of Kincaid's lupine biology, the effects of gamete source on seed production and progeny fitness were tested, with hand pollination treatments, in two natural populations. Pollination treatments were used as an indirect method to assess the effects of selfing versus crossing across various genetic distances. Inter-simple sequence repeat (ISSR) markers are also being used as a PCR-based method to genotype sampled plants in the gamete source experiment. These data will be used to calculate the genetic distance between individuals used in the crossing treatments, and these values will be correlated with seed set and progeny performance. These molecular markers will also allow estimation of genetic diversity, and may indicate population viability concerns. The extent of clonal growth and spread in the two study populations will also be documented.

- 130** FERGUSON, CAROL S.\*, KATHLEEN DONHAM, AND JENNIFER BROWN. Department of Biology, Southern Oregon University, Ashland, OR 97520—*Pollination of Clustered lady's slipper orchid, *Cypripedium fasciculatum* (Orchidaceae).*

*Cypripedium fasciculatum*, the Clustered lady's slipper orchid is one of three endemic *Cypripedium* species in the Western United States whose pollination mechanisms, until now have been unknown. The Northwest Forest Plan designated *C. fasciculatum* a 'Survey and Manage' species. Therefore, information on the pollinators of *C. fasciculatum* could aid land managers involved in the preservation and/or management of *Cypripedium* habitat. This research sought to determine the pollinator(s) of *C. fasciculatum*, and to understand the floral phenology of *C. fasciculatum* as it relates to pollination. In 1999, insect activity, floral phenology and pollen removal were monitored at two southwestern Oregon *Cypripedium* sites. This study is the first

to document a pollinator of *C. fasciculatum* and represents the first record of parasitic diapriid wasps as pollinators. Diapriids parasitize dipteran hosts including fungus gnats (Sciaridae) which were the most prevalent insects collected in the study sites. The relationships between diapriids, their insect host(s) and *C. fasciculatum* will be addressed in future research.

- 131** FESSEL, KEITH E.\* AND BETH A. MIDDLETON. Biology Department, Grand Valley State University, Allendale, MI 49401 and Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901—*Survivorship of woody plant seeds in bald cypress swamps in southern Illinois.*

Woody plant species in bald cypress swamps are recruitment limited. Seeds of most wetland plants will not germinate under water and so must survive until draw down. Therefore, seed survivorship is a crucial component for natural regeneration of these forests. A field study was conducted to examine seed survivorship of four woody plant species common in bald cypress swamps in southern Illinois. Seeds of bald cypress (*Taxodium distichum*), water tupelo (*Nyssa aquatica*), water locust (*Gleditsia aquatica*) and buttonbush (*Cephalanthus occidentalis*) were placed under flooded conditions in situ over 18 months. Considerable variation was observed in initial seed viability among the four species. There were significant declines in seed viability of all four species. Rates and patterns of seed survivorship differed among the four species. Bald cypress had the fastest decline in seed survivorship with only one half of seeds surviving 1.4 months, followed by water locust (14 months). One half of water tupelo and buttonbush seeds were predicted to survive 20 and 39 months, respectively. Bald cypress seeds had an exponential decline in viability over time, where as water tupelo and water locust seeds declined according to a second order regression line and seeds of buttonbush declined linearly over the duration of the study. Estimated maximum age of seeds was similar between water tupelo (30 months), bald cypress (25 months) and water locust (23 months). Buttonbush had the longest estimated seed longevity (150 months). These differences in seed survivorship may have significant effects on community structure by all but eliminating bald cypress seedling establishment following drawdown while favoring the establishment of buttonbush. Infrequent drawdown events are also likely to greatly favor the establishment of buttonbush over other species due to seed longevity.

- 132** HALSE, RICHARD R.\* AND KATHY MERRIFIELD. Department of Botany and Plant Pathology, 2082 Cordley Hall, Oregon State University, Corvallis, OR 97331-2902—*A floristic survey of Bruno Mire in the central Cascade Range, Oregon.*

Bruno Mire is a 12 hectare sedge/grass-dominated wetland with a mat-forming aquatic bryophyte layer surrounded by a second-growth fir/hemlock/spruce forest at an elevation of 1224 m on the west slope of the Cascade Range. From 1991 through 1999, we surveyed the flora in all habitats and substrates within the area surrounded by the high water table, including all those in open water, marsh, and upland islands. Vascular plants were represented by 41 families comprising 119 species in 88 genera. The largest family representations were Cyperaceae (4 genera, 15 spp.), Poaceae (7 genera, 10 spp.), Asteraceae (7 genera, 10 spp.), Rosaceae (8 genera, 9 spp.), and Ericaceae (5 genera, 8 spp.). Bryophytes were represented by 38 families comprising 65 species in 43 genera. The largest family representations were Mniaceae (4 genera, 10 spp.), Brachytheciaceae (4 genera, 7 spp.), Hylocomiaceae (4 genera, 6 spp.), Dicranaceae (2 genera, 5 spp.), and Scapaniaceae (1 genus, 4 spp.). The variety of habitats within Bruno Mire is such that the floristic diversity exceeds those of Torrey Lake Mire and Crater Lake Sphagnum Bog in the central and southern Oregon Cascades.

- 133** HANNAN, GARY L. Department of Biology, Eastern Michigan University, Ypsilanti, MI 48197—*Phenotypic gender modification in *Platystemon californicus* (Papaveraceae), a wind-pollinated, self-incompatible annual.*

Current sex allocation theory assumes that a trade-off exists between allocation to male versus female reproductive effort because a limited pool of resources is available for reproduction. Expected fitness gains derived from investment of resources in each sex differ among pollination mechanisms, mating systems, and plant sizes (including architecture). *Platystemon californicus* is a self-incompatible, wind-pollinated annual plant exhibiting strict modular growth and extreme variability in numbers of stamens, pollen grains, carpels and ovules within flowers, providing an opportunity to detect results of selection for shifts in phenotypic gender in plants from diverse habitats, of different sizes and at different developmental stages. Number of male and female reproductive structures per flower exhibited significant variation among 41 populations. Comparisons of field versus garden-grown plants from seven populations indicated that numbers of male and female structures were mostly genetically based. Theory predicts that wind-pollinated species should

allocate an increased proportion of resources to male function as plants become larger. I found that flowers of larger plants had more stamens, carpels, and ovules and produced more pollen than did flowers of smaller plants. However, the only difference in relative allocation to male vs. female structures was for the ratio of stamens to ovules per flower; larger plants had more stamens per ovule than did smaller plants. Earliest flowers on a plant generally had fewer stamens, carpels and ovules than did later flowers, but relative numbers of flower parts did not differ significantly with developmental stage (although trends toward increasing maleness were found). Although *P. californicus* is extremely variable in floral construction within and among populations and among plant size categories within populations, the patterns of phenotypic gender modification inferred by current theory were not found.

- 134** HAWKINS, TRACY S. School of Biological Sciences, University of Kentucky, Lexington, KY 40506 and Hazard Community College, Jackson, KY 41339—*A vegetation transect of the south slope of Pine Mountain, Kentucky: changes since E. Lucy Braun and chestnut blight.*

Forest composition and structure were determined on a 68-ha tract on the south slope of Pine Mountain, Kentucky, in 1997. Data collected from 28 0.04-ha plots were summarized as importance values. Canopy compositions were compared with those described by E. Lucy Braun (*The American Midland Naturalist* 16: 517-565, 1935) prior to the peak of chestnut blight (*Cryphonectria parasitica*). No significant change has occurred in canopy composition on the xeric SSE dip slope. *Pinus echinata* and *P. rigida* have persisted as co-dominants, and *Quercus prinus* has remained an important component in the canopy. In mesic sites, canopy composition has remained stable; however, near the crest of the mountain *Acer rubrum* has replaced *Castanea dentata* and assumed secondary importance to *Liriodendron tulipifera*. On the ESE aspect of the dip slope, where *C. dentata* made up one third of the pre-blight canopy, forest gaps were filled by *Q. coccinea* and *Q. velutina*, which now have a higher importance value than that of the pre-blight oak dominants (*Q. alba*, *Q. prinus*). Except for the absence of *C. dentata*, canopy components of the forest communities have remained relatively unchanged during the past 65 years; however, the loss of *C. dentata* initiated changes in the relative importance of these species in the forest community. Further, in all sampling sites the contribution of existing canopy species to importance values for the sapling/small tree and shrub/woody seedling strata is less than that of fire-sensitive species (*A. rubrum*, *Nyssa sylvatica*, *Sassafras albidum*), suggesting future changes in these post-blight forest communities.

- 135** HIDAYATI<sup>1</sup>, SITI, N.\*, JERRY, M. BASKIN<sup>1</sup>, AND CAROL, C. BASKIN<sup>1, 2</sup>. <sup>1</sup>School of Biological Sciences, University of Kentucky, Lexington, Kentucky 40506; and <sup>2</sup>Department of Agronomy, University of Kentucky, Lexington, Kentucky 40546—*Dormancy-breaking and germination requirements for seeds of Symphoricarpos orbiculatus (Caprifoliaceae).*

Fruits (drupes) of *Symphoricarpos orbiculatus* Moench ripen in autumn and are dispersed from autumn to spring. Seeds (true seeds + fibrous endocarp) are dormant at maturity, and they have a small, linear-shaped embryo that is underdeveloped. In contrast to previous reports, the endocarp and seed coat of *S. orbiculatus* are permeable to water; thus, seeds do not have physical dormancy. No fresh seeds germinated during 2 wk of incubation over a 15/6-35/20°C range of thermoperiods in either light (14 h photoperiod) or constant darkness; neither GA<sub>3</sub> nor cold stratification alone overcame dormancy. One hundred percent of the seeds incubated in a simulated summer → autumn → winter → spring sequence of temperature regimes germinated, whereas none of those subjected to a winter → spring sequence did so. That is, cold stratification is effective in breaking dormancy only after seeds first are exposed to a period of warm temperatures. Likewise, embryos grew at cold temperatures only after seeds were exposed to warm temperatures. Thus, the seeds of *S. orbiculatus* have nondeep complex morphophysiological dormancy. As a result of dispersal phenology and dormancy-breaking requirements, in nature most seeds that germinate do so the second spring following maturity; a few may germinate the third spring. Seeds can germinate to high percentages under *Quercus* leaf litter and while buried in soil; they have little or no potential to form a long-lived seed bank.

- 136** JAMESON, ANNEMARIE. Department of Biology, University of Miami, P.O. Box 249118, Coral Gables, FL 33124-0421—*Spatial pattern analysis of Torchwood in south Florida.*

In order to further our understanding of the habitat requirements an endangered butterfly, I undertook a study to determine the spatial patterning of a Rutaceous tree with a neotropical distribution. Torchwood, *Amyris elemifera* L., is considered to be the primary larval food plant of an endangered butterfly subspecies with an Antillean distribution, the Schaus swallowtail, *Heraclides* (= *Papilio*) *aristodemus ponceanus*. Patchiness in plant communities can provide the underlying habitat structure for a specialist herbivore on both a land-

scape and population level. Determining the scale of the spatial patterning for torchwood can aid us in determining the minimum scale at which models of the butterfly's habitat must be based, as well as providing a cell size for multivariate models of both butterfly and host plant habitat. Two term local quadrat variance (TTLQV) as described by Dale (1999) in *Spatial Pattern Analysis in Plant Ecology* was used to address the question, at what scale(s) is torchwood aggregated in the tropical hardwood hammocks of south Florida? The unit measured was contiguous 5 meter square quadrats. The data recorded is mapped locations of stems at each of two life stages, seedlings (< breast height) and reproductive individuals (>breast height). In TTLQV, the average squared difference between a block and the adjacent block is calculated for a range of block sizes,  $b$ . Peaks in the plot of the variance,  $V3(b)$  against block size are indicative of scales at which the species is aggregated. Preliminary results collected in Crocodile Lakes National Wildlife Refuge, North Key Largo Florida, indicate that *Amyris elemifera* is strongly aggregated at distances between 20 and 25 meters.

- 137** KLIPS, ROBERT A. Department of Evolution, Ecology, and Organismal Biology, The Ohio State University at Marion, 1465 Mt. Vernon Ave., Marion OH 43302—*Inbreeding depression is variable among populations of rose mallows (Hibiscus species, Malvaceae).*

The reduced fitness of progeny produced from selfing is an evolutionary force that helps shape the mating system of many self-compatible plant species. The rose-mallows (genus *Hibiscus* section *Muenchhusia*) bear large self-compatible hermaphroditic flowers that bloom for one day and possess simultaneously mature anthers and stigmas. An insect visitor is required for pollination and they have a mixed mating system. In tests to determine whether inbreeding depression may have influenced the maintenance of features that foster outcrossing, progeny produced by inbreeding were compared to progeny derived from outcrossing in several populations of two *Hibiscus* species: *H. grandiflorus*, which is restricted in distribution to the southeastern Atlantic and Gulf coasts, and the widespread *H. moscheutos*. Both taxa exhibited inbreeding depression in two components of fitness expressed later in the life-cycle: seed germination (in a few instances only), and (more frequently) progeny growth. The populations that were more strongly affected by inbreeding tended to be the more southerly ones, suggesting that the more northerly ones may have gone through bottlenecks and so been purged of the deleterious alleles and/or the beneficial polymorphisms as they re-established the region following glacial retreat. The selfing rate of one Ohio *H. moscheutos* population was estimated to be 0.44 using introduced plants with a foreign electrophoretic genotype. Inbreeding depression appears likely to be maintaining floral features which result in a substantial fraction of outcrossed offspring. A related study is underway of variation in inbreeding depression among populations of another rose-mallow, *Hibiscus laevis*, that differ in their ability to self-pollinate autonomously.

- 138** KOPTUR, SUZANNE\* AND JOHN HENRY GEIGER. Department of Biological Sciences, Florida International University, Miami, FL 33199—*Pollination of Byrsonima lucida (Malpighiaceae) in southern Florida.*

*Byrsonima lucida* is the only member of the Malpighiaceae native to subtropical Florida, and occurs in pine rockland habitat on the Miami Rock Ridge and in the Lower Keys. Its flowers have oil glands that produce rewards for specialized pollinators, bees in the genus *Centris* (Anthophoridae). *Centris errans* is endemic to southern Florida (Dade and Monroe Counties), while *C. lanosa* has a wider distribution throughout Florida and the Caribbean. The plants flower from February - April, usually preceding the appearance of the bees (often a month later). Early flowers do not produce fruit, and bagging experiments have shown that pollination is necessary for fruit set. We predicted that *B. lucida* would be likely to show negative effects of the extensive habitat destruction and fragmentation that pine rocklands have undergone; its specialized pollinators might disappear from the small, isolated patches of intact habitat left after development. Surprisingly, the bees are present in most of the fragments studied, and the plants fruit at these sites (though somewhat less successfully than those in pristine Everglades sites). It appears that home landscape plantings that include several ornamental Malpighiaceae, as well as native plants, may have helped to support the specialized pollinators in the matrix between natural habitat fragments.

- 139** LI, XIAOJIE\* AND STEVEN A. FENNIMORE. Department of Vegetable Crops, University of California, Davis, c/o USDA ARS, 1636 East Alisal Street, Salinas, CA 93905—*Temporal changes in germinability and light response of seeds of six common weed species.*

Freshly-matured seeds of *Amaranthus retroflexus*, *Capsella bursa-pastoris*, *Lamium amplexicaule*, *Spergula arvensis*, and *Urtica urens* (collected on 29 Oct.-3 Nov., 1999) and of *Portulaca oleracea* (collected on 21 Sep., 1999) were (1) incubated for 3 mo at approximated prevailing soil (5 cm below surface) temperatures



of arable lands in Salinas, CA, with long (10 hr daily) or short (< 2 min weekly) exposure to light (Experiment 1); or, (2) subjected to natural temperature conditions by burial at a depth of 5 cm in the field or dry-storage in paper bags in a non-heated warehouse room (Experiment 2). For Experiment 2, after 1.5 and 3 mo, seeds were incubated for 14 d in the same manner as described above to detect temporal changes in germinability and light response. Results showed that short light exposure did not satisfy the germination requirement of freshly dispersed seeds of any species except *A. retroflexus*. Following burial, seeds of *U. urens* and *A. retroflexus* germinated to significantly lower percentages after long exposure compared to short exposure, whereas those of *C. bursa-pastoris*, *L. amplexicaule*, and *S. arvensis* responded indifferently to the light exposure conditions and those of *P. oleracea* retained their absolute dependence on long exposure for germination. At approximated prevailing soil temperatures, newly-matured seeds of all species, except *P. oleracea* (with a percent germination of  $76 \pm 2$ ), exhibited low germinability (ca. 0-11%), which increased significantly after burial in soil. Compared to burial, dry-storage essentially resulted in similar germination responses to the light conditions but with significantly lower percent germination for all species.

**140** MACMILLAN, PAUL C.\* AND LINDSAY M. BETZ. Department of Biology, Hanover College, Hanover, IN 47243—*Twenty-five years of forest succession in southeastern Indiana.*

In April 1974, a major tornado traveled across Jefferson County in southeastern Indiana and caused extensive damage to the Happy Valley forest adjacent to Hanover College. Nearly all canopy trees were destroyed, thus creating a natural experiment in forest succession. The pre-tornado forest was an *Acer saccharum*-*Aesculus glabra* community with a stem density of 512 trees/ha. In the fall of 1974, the forest was surveyed on three transects across the valley; the northern and central transects were in the most damaged area, the southern transect was in the less-damaged area. Following the tornado, the most common trees were *Acer saccharum*, *Quercus* sp., and *Fraxinus americana*. The forest was resurveyed along the same transects 7, 15, 20, and 25 years after the tornado. Changes in stem density and basal area will be reported.

**141** MCLEITCHIE, D. NICHOLAS. School of Biological Sciences, 101 Morgan Building, University of Kentucky, Lexington, KY 40502—*Sex-specific life histories and population sex ratios in the dioecious liverwort Marchantia inflexa.*

Unisexual, female- or male-biased populations are common among dioecious bryophytes and the demographic causes of such biases are unclear. Life history studies can be valuable in understanding the contribution of each life history stage to a population sex ratio, yet few studies use this approach. We chose to study the liverwort *Marchantia inflexa* to investigate the potential effect of various stages/traits on population sex ratio. Across *M. inflexa*'s distribution range, herbarium data suggest female-biased sex ratios. Field studies in Trinidad & Tobago suggest an overall 1:1 sex ratio within a single watershed, however, patches can be single-sex, bisexual or without sex expression. We investigated sex-specific survival of asexual propagules (lab), clonal expansive traits (greenhouse) and patterns of sex expression (field & greenhouse). We found that neither sex had a consistent advantage. Females had higher propagule survival, lower propagule production and higher growth rates. Sex expression tended to occur first in males then in females. These patterns suggest that focusing on any single stage or trait can result in erroneous conclusions as to the demographic causes of sex ratio biases. Thus, studies on population sex ratio biases should incorporate multiple traits and stages.

**142** MCMASTER, ROBERT T. Department of Botany, Connecticut College, New London, CT 06320—*Ecology and population biology of Ophioglossum pusillum in New England.*

*Ophioglossum pusillum*, the northern adder's-tongue (Ophioglossaceae), is a small, inconspicuous fern of wetlands and moist meadows. Once common throughout the northeastern U.S., it has declined dramatically in recent decades. Historical records exist from 90 Massachusetts towns, yet today it is known from only seven localities in the state. It is listed as endangered or threatened in MA and in a number of other states. This study sought to relocate historical records in Massachusetts, examine the population biology of extant populations, and make management recommendations. Five populations were located in summer 1991. Starch gel electrophoresis revealed no genetic variation in plants from four Massachusetts populations. One New Hampshire population showed possible variation. Low variability may be a result of the reproductive biology of the species which readily self-fertilizes and expands vegetatively. While low genetic variability may explain the decline of the species, habitat loss is a clear factor in some sites. In fact, genetic variability may not be as important in this early successional species as the ability to spread rapidly and disperse to new habitat as conditions change.

- 143** MICHELANGELI, FABIAN A. L.H. Bailey Hortorium, Department of Plant Biology, Cornell University, Ithaca, NY 14853—*Ant-protection against herbivory and evolution of myrmecophytism in the genus *Tococa* (Melastomataceae).*

*Tococa* is a neotropical genus of small trees and shrubs, composed of about 45 species, 2/3 of which have symbiotic association with ants. The ants inhabit domatia that develop at the base of the leaf blade or the apex of the petiole. Natural history observations and field experiments were carried out in order to study the characteristics of this association. Ants from at least 7 different genera from 3 different subfamilies were found inhabiting the domatia of *Tococa*. Depending on their behavior, the inhabiting ants can be characterized as timid or aggressive. The different types of behavior are not associated with the host species, but with the surrounding environment. Neither there are co-specific associations between the ants and the different species of *Tococa*. Ant exclusion experiments in ant-bearing *Tococa* demonstrated that both timid and aggressive ants protect their host plants against potential herbivores, by both warding off scouts of leaf-cutter ants and removing the eggs of Lepidoptera and Coleoptera. The presence of stem and petiole trichomes seems to be critical for the establishment of ant colonies, since their removal often results in the ants vacating their host plant. Employing a previously obtained phylogeny of the genus *Tococa*, it was possible to determine that ant domatia, and thus myrmecophytism, have evolved at least twice within the genus. Secondary losses of domatia have also occurred. These losses can be associated with the life history and habitat of the species lacking domatia. The presence of stem pubescence has predated the evolution of ant domatia in both instances within *Tococa*.

- 144** MILLER, J. S. University of Arizona, Department of Ecology & Evolutionary Biology, Biological Sciences West, #310, 1041 East Lowell, Tucson, AZ 85721—*The evolution of gender dimorphism in *Lycium* (Solanaceae).*

Gender dimorphism has evolved at least twice in the Solanaceous genus *Lycium*. In the North American dimorphic species, male-sterile plants (i.e., females) have flowers with a long style equal to or slightly exerted from the corolla tube and abortive anthers, while perfect-flowered plants (i.e., hermaphrodites) have a style of variable length with a set of long, fertile anthers equal to or exerted from the mouth of the corolla tube. Several important characters associated with the evolution of gender dimorphism are highlighted and discussed in the context of the evolution of gender dimorphism. In this group, polyploidy appears to have triggered the evolution of gender dimorphism by disrupting the self-incompatibility system, leading to inbreeding depression and invasion by male-sterile mutants.

- 145** PASCARELLA, JOHN B. Department of Biology, Valdosta State University, Valdosta, GA 31698—*Causes and consequences of reproductive isolation between two sympatric *Gelsemium* species.*

Prezygotic barriers to hybridization were examined for two sympatric *Gelsemium* (Loganiaceae) species, *G. sempervirens* and *G. rankinii*, occurring in the southeastern U.S. Two populations in Lowndes County, Georgia were studied in 1999 and 2000. Both species have similar floral biologies and share pollinator species, with the apid bee *Habropoda laboriosa* the most important visitor to both species. Differences in temporal flowering patterns appear to be limiting potential hybridization events, with *G. sempervirens* flowering from late January to late March and *G. rankinii* flowering from late March to mid April. A consequence of this divergence in flowering time is much lower fruit set ratios in *G. sempervirens* than *G. rankinii*. This low fruit set is attributed to two factors: 1) colder temperatures limit the activity of pollinators of *G. sempervirens* but do not limit those of *G. rankinii*; 2) the proportion of males vs females of *Habropoda laboriosa* visiting *Gelsemium* flowers is more strongly male biased for *G. sempervirens* and males are less effective pollinators than females. One consequence of this lower fruit set may be the longer flowering period and greater flower production in *G. sempervirens*.

- 146** PETERSON<sup>1</sup>, PAUL M.\*<sup>1</sup>, MONES ABU-ASAB<sup>2</sup>, STANWYN G. SHETLER<sup>1</sup>, AND SYLVIA STONE ORLI<sup>1</sup>. <sup>1</sup>Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington, DC 20560-0166 and <sup>2</sup>Section of Ultrastructural Pathology, Laboratory of Pathology, National Cancer Institute, Bethesda, MD 20894—*Earlier plant flowering as a response to global warming in the Washington, DC, area.*

Evidence for global warming is inferred from the onset of earlier flowering times in plants from the Washington, DC, area. First-flowering times over a 29 year period were examined for 100 plant species representing 43 families of angiosperms. The trend of average first-flowering times for all plants/year for 100

species shows a significant decrease of -2.4 days over the 29-year period. When 11 species that exhibited later first-flowering times were excluded from the data set, the remaining 89 showed a significant decrease of -4.5 days. Trends for earlier-flowering species ranged from -0.2 to -46 days, while those for later-flowering species ranged from +0.3 to +10.4 days. Onset of earlier flowering in these 89 species is inversely correlated with local changes in minimum temperature ( $T_{\text{MIN}}$ ). Our results are concordant with other studies where warmer air temperatures and higher CO<sub>2</sub> levels have lead to advancement of the average annual growing season.

- 147** PIGLIUCCI, MASSIMO\*, HEIDI POLLARD, AND MITCHELL CRUZAN. Department of Botany, University of Tennessee, Knoxville, Tn 37996-1100—*Comparative studies of reaction norms in Arabidopsis: evolution of response to coarse and fine grained environmental variation in Scandinavian haplotypes.*

There is general agreement that we need a better understanding of how historical processes contribute to patterns of variation in phenotypic plasticity within and among species; however, the evolution of reaction norms has rarely been addressed from within an explicitly phylogenetic comparative framework. Furthermore, the simultaneous evolution of traits in response to environmental variation characterized by different grains (coarse and fine from the standpoint of the organism being considered) is also amenable to phylogenetic comparative studies which have not been attempted so far. In this paper we compare the reaction norms to foliage shade (changes in light quality, spatially fine-grained environmental variation) and photoperiod (day-length, spatially coarse-grained environmental variation) in several haplotypes of *Arabidopsis thaliana* and of two closely related species, *A. arenosa* and *A. lyrata* subsp. *petraea*, from Scandinavia. We found that across-environment means evolved continuously and very rapidly within this group, while plasticity changed only rarely and especially between the outgroups and *A. thaliana*. Character means evolved largely independently of each other, while trait plasticities were highly integrated, as predicted by the adaptive plasticity hypothesis for response to foliage shade (the so-called “shade avoidance” syndrome). We found evidence of strong constraints across environmental factors (daylength and foliar shade) for some traits directly related to life history, but otherwise largely independent evolution of the reaction norms of many traits in response to either daylength or light quality. Some of the observed patterns can be explained by a combination of shared ecological circumstances and an underlying genetic constraint due to the fact that an overlapping battery of photoreceptors perceive both aspects of light availability.

- 148** PITTAM<sup>1</sup>, SHERRY KAY\*, FRANK JOSEPH HANUS<sup>2</sup>, AND KEN FERSCHWEILER<sup>3</sup>. <sup>1,2</sup>Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, USA, <sup>3</sup>Northwest Alliance for Computational Science and Engineering, 218 Alumni Center, Oregon State University, Corvallis, OR 97331, USA—*Plugging in: what we have learned in making scientific databases available on the World Wide Web.*

Communication of research information to biological consultants, government agency planners, conservation biologists, academic researchers, private land owners, and the general public has become a major goal of both the research community and granting agencies. The internet has become the method of choice for this distribution of scientific data. The data can be rapidly transported, displayed or visualized with graphical content, can be made selectively available with different levels of access to the public or to research colleagues and can even be rendered downloadable. The data range from systematic studies of plants and fungi, to floristic studies, to synoptic keys. Working with academic and government researchers we have developed Web deliverable query pages against robust high-performance database management systems. The pages are interactive, attractive, and easy to use by scientists and the general public; yet, can perform complex queries involving, in some cases, many tables of data. We will explore in this paper the results of studies with users of disparate skill levels e.g. scientists within a discipline and the general public, including secondary school students. We will detail the success we have had teaching students and faculty in the biological sciences, to build and maintain their own sites without learning arcane programming or database languages. We will also provide suggestions, guidelines and pitfalls to consider in the early planning of your database design to insure ease and efficiency of data retrieval. And finally we will discuss issues of security and sensitivity of data that must be addressed when making your data available to the public.

- 149** POTTER, DANIEL\* AND FANGYOU GAO. Department of Pomology, University of California, Davis, CA 95616—*Black, English, Royal, or Paradox? - developing molecular markers for walnut (*Juglans*) species, cultivars, and hybrids.*

The most important rootstock in the California walnut industry is Paradox, which refers to the offspring of a California black walnut pollenized by an English walnut (*Juglans regia*). Paradox was developed by Luther

Burbank, who did not distinguish between Northern (*Juglans hindsii*) and Southern (*J. californica*) California black walnut. Although it is generally accepted that Paradox designates hybrids between *J. hindsii* and *J. regia*, the name is commonly applied to any black walnut - English walnut hybrid. Moreover, due to gene flow among black walnut species, the genealogy of Paradox hybrids may also include species such as *J. major* and *J. nigra*. Since the nuts from which Paradox seedlings are grown are collected from wild trees, their genetic backgrounds are not generally known. In conjunction with a large study aimed at evaluating Paradox hybrids from different industry sources, we have been working on developing molecular markers that can be used to infer the parentage (maternal black walnut species and paternal English walnut cultivar) of individual Paradox seedlings. Chloroplast (*trn* gene spacers) and nuclear (ITS) DNA sequences have been useful for distinguishing species and PCR-based screens have been developed based on these sequence differences. ISSR markers have been used to distinguish cultivars. Our results indicate that, among industry Paradox sources, there is considerable genetic contribution from species other than *J. hindsii*. The markers developed in this study also have applications in verifying cultivar identification and genealogy and in investigating the parentage of other hybrids, such as Royal hybrids, designated by Burbank as the hybrid between eastern (*J. nigra*) and California black walnut.

**150** RUVINSKY, JESSICA\* AND DAVID ACKERLY. Department of Biological Sciences, Stanford University, Stanford, CA 94305-5020—*Adaptive phenotypic plasticity in Mimulus guttatus*.

Physiology and morphology of *Mimulus guttatus* vary with water level. Under flooded conditions, root to shoot ratio is significantly higher and photosynthetic rate and conductance are significantly lower than at field capacity. Is this phenotypic plasticity adaptive? Plants were grown from seed in the greenhouse under two water levels. At 5, 7 and 10 weeks from emergence, a subset of the plants was switched into the other environment (high water into low water and vice versa). The third switch resulted in a crossover in fitness between the switched and control plants: within each environment, the plants whose early environmental cues corresponded to their ultimate environment had a higher fitness than those responding to "incorrect" early cues. This provides evidence that plasticity in response to water level is adaptive in this species. The time courses of root to shoot ratio, leaf area ratio, specific leaf area, reproductive allocation, maximum photosynthetic rate and instantaneous water use efficiency were followed, and fitness responses are interpreted in terms of changes in these traits over time.

**151** TRIPP, BRADLEY B. AND JOHN C. MOORE.\* Department of Biological Sciences, University of Northern Colorado, Greeley, CO 80639—*Food webs in saxicolous lichens (Xanthoparmelia spp.) a comparison of lichen, litter, and soil microhabitats*.

We examined the effect of productivity and elevation on micro-fauna communities within saxicolous lichens (*Xanthoparmelia* spp.), adjacent litter, and soil habitats. Productivity was indexed by lichen colony size (cm<sup>2</sup>). Species diversity in the three habitat types was calculated. Lichen communities were significantly different than litter and soil microhabitats ( $p < 0.05$ ). Bacterial, fungal, protozoan (flagellates, amoebae, ciliates), and nematode densities were significantly lower than that of litter and soil. While tardigrades, rotifers, mites (mesostigmatid, and cryptostigmatid), and diplopoda densities were significantly higher than adjacent litter and soil microhabitats. For example, mean tardigrade density in lichens was 10.39 per gram dry weight, while litter density was 0.98/gdw and soil density was 0.47/gdw. Total mean micro-arthropod density in lichens was 5.347.91/gdw, while the means were 1.562.06/gdw and 1.24+1.53/gdw for litter and soil respectively. There was no significant differences in collembola and prostigmatid mite densities. Neither productivity nor elevation appeared to influence species diversity within lichen communities. Lichen colony size was not correlated with micro-fauna density. We present a food web that describes the community within saxicolous lichen of the genus *Xanthoparmelia* in Colorado. Additional micro-fauna included thrips, ants, symphylans, dipterians, pseudoscorpions and beetles. While further research needs to be conducted, it does not appear that saxicolous lichens are distinct communities but rather they represent elements of both adjacent litter and soil communities. They may represent both sources and sinks of these organisms to adjacent microhabitats.

**152** WALCK, JEFFREY L.<sup>1\*</sup>, NOBUO OKAGAMI<sup>2</sup>, AND SITI N. HIDAYATI<sup>3</sup>. <sup>1</sup>Department of Biology, Middle Tennessee State University, Murfreesboro, TN 37132; <sup>2</sup>Faculty of Horticulture, Chiba University, Matsudo 271-8510, Japan; <sup>3</sup>School of Biological Sciences, University of Kentucky, Lexington, KY 40506—*Germination ecophysiology of the Asian Osmorhiza aristata (Apiaceae), and comparison with its North American congeners*.

*Osmorhiza aristata* is a herbaceous polycarpic perennial that grows primarily from Japan, through southern China, to the Himalayas. It is related closely to the central and eastern North American species *O. claytonii*



and *O. longistylis*. Together, the distribution of the three species represents an example of the well-known Asian-North American pattern of disjunction. Requirements for dormancy-break and embryo growth were determined for seeds of *O. aristata* collected in Japan during summers 1998 and 1999. Embryos in fresh seeds were 0.48 mm long, and they had to grow to 9 mm before the radicle emerged from the mericarp. Embryo growth and germination occurred during cold stratification at 5 C, which was the optimum temperature for germination. A warm (30/15 C) stratification pretreatment was not required for seed germination at 5 C, and gibberellic acid (GA<sub>3</sub>) did not substitute for cold stratification. Thus, *O. aristata* seeds have deep complex morphophysiological dormancy (MPD). In contrast, seeds of *O. claytonii* and *O. longistylis* have nondeep complex MPD, i.e., they require warm followed by cold stratification to germinate and GA<sub>3</sub> overcomes dormancy (Baskin & Baskin 1984, 1991). The type of MPD in seeds of *O. aristata* is identical to that in seeds of western North American populations of *O. berteroi* (*chilensis*) and *O. occidentalis* (Baskin et al. 1995). Although closely-related, Arcto-Tertiary relict congeners often exhibit high morphological similarity (stasis), the taxa may differ vastly in their physiological traits, such as seed dormancy.

- 153** WATSON, MAXINE A.\* AND CYNTHIA S. JONES. Department of Biology, Indiana University, Bloomington, IN 47405—*Developmentally-dependent interactions between mayapple, Podophyllum pelatum L. (Berberidaceae) and its associated mycorrhizal fungi.*

Plant-mycorrhizal interactions are generally considered to be examples of a mutualism in which both plant and mycorrhizal fungi benefit. Plants gain increased access to soil nutrients, particularly phosphorus, while mycorrhizal fungi gain access to the carbon fixed by plants. However, there are exceptions to this pattern. Numerous workers have noted that some plants shed mycorrhizal fungi when soil nutrients are supplemented, suggesting that under nutrient rich conditions, the costs to the plant of maintaining the symbiosis outweigh the benefits. In such systems the symbiosis is facultative. Much less is known about plant-mycorrhizal fungi interactions in woodland as opposed to grassland, prairie or agricultural systems. Here we report the nature and properties of the symbiosis in mayapple, *Podophyllum pelatum* L. (Berberidaceae), a long-lived perennial of the eastern deciduous forest floor. Our data indicate that the mayapple-fungal interaction is facultative; addition of soil phosphorous reduces the intensity of colonization of mayapple roots by mycorrhizal fungi. Of greater interest, we find that not all roots are equally colonized. Roots at young rhizome nodes contain few if any mycorrhizal fungi. Fungal loads increase to their highest level at two to four year old nodes before dropping again. The pattern of soil phosphate depletion mirrors the pattern of mycorrhizal fungi distribution, with the greatest depletion of soil P observed under the most heavily colonized nodes. Hypotheses relating to the regulation of plant-mycorrhizal fungal interactions will be discussed.

- 154** WATSON, MAXINE A.\*, CYNTHIA S. JONES, AND YING LU. Department of Biology, Indiana University, Bloomington, IN 47405—*Variation in the expression of developmental and phenological traits in mayapple, Podophyllum pelatum L. (Berberidaceae).*

Plants' programs of development can be considered evolved traits. If this is correct, then we should be able to detect variation among clones in developmental traits and demonstrate that this variation leads to fitness differences. Here we report variation in three developmental traits: timing of shoot emergence and senescence and the timing of shoot type determination. We demonstrate significant variation among colonies for all three traits. A reciprocal transplant experiment in the field goes on to demonstrate that the timing of emergence and senescence has both a genetic and environmental component. Variation in emergence and senescence date should effect clonal resource dynamics while variation in the timing of shoot type determination should effect how both short and long term environmental variation influences the demographic trajectory and, hence, fitness of different clones. Further reciprocal transplant experiments are needed to demonstrate genetic variation in the timing of shoot type determination.

- 155** WEEKLEY, CARL W.\* AND TAMMERA RACE. Plant Ecology Lab, Archbold Biological Station, Lake Placid, FL 33852—*The breeding system of Ziziphus celata Judd and D. Hall (Rhamnaceae), a rare endemic shrub of the Lake Wales Ridge, Florida: implications for recovery.*

While the rarity of an endangered plant species can seldom be ascribed to its breeding system, knowledge of its breeding system may be critical to its recovery. The federally-listed endangered *Ziziphus celata*, a woody clonal shrub endemic to xeric upland habitats of the Lake Wales Ridge in central Florida, is known from only five populations, four of which are sterile and perhaps uniclinal. Altogether only eleven genotypes of *Z. celata* have been identified, based on allozyme electrophoresis. We conducted field experiments, including hand-pollinations of bagged flowers, over a four year period to determine the breeding system of *Z.*

*celata*. We found that it is an obligate outcrosser and that some genotypes appear to be cross-incompatible. Determination of cross-compatibility is complicated by the high percentage of seed abortion and by the presence of parthenocarpic fruit. Germination trials and seed dissections are therefore required to confirm cross-compatibility. While eleven of 44 test crosses performed to date have yielded fruit, we have obtained germinants from only four crosses. Our objective is the identification of cross-compatible genotypes to be used for the genetic enhancement of sterile populations and the creation of new fertile populations. The translocation of compatible mating types to create reproductively viable populations is essential for the recovery of *Z. celata*.

- 156** WONG, THEODORE G.\* AND DAVID D. ACKERLY. Department of Biological Sciences, Stanford University, Stanford, CA 94305-5020—*How sensitive should plants be to cues? Theoretical studies of plastic reproduction schedules.*

We explore relationships among bet-hedging, phenotypic plasticity, and the reliability of environmental cues with respect to the reproductive allocation schedule in annual plants. The optimal schedule of biomass allocation between reproduction and vegetative growth has been shown to be bang-bang in constant environments and graded in unpredictable environments – a bet-hedging strategy. We summarize genetic-algorithm studies which show that the optimal graded schedule is in fact a weighted combination of the within-season fecundity-maximizing strategies for each of the season-lengths possible in the environment. Each season-length's contribution is a function of its probability, so the degree of optimal gradedness directly reflects the degree of environmental unpredictability. We then develop an analytical model of allocational plasticity which compares fitness between the optimal allocation given an environmental distribution and that given the same distribution but conditioned on the state of an environmental cue. The adaptiveness of plasticity is upper-bounded by an information-theoretic measure of cue reliability: the mutual information of the cue and the environmental state. Simulations confirm that the probability that plastic allocators invade a bet-hedging population increases with cue reliability and that the form of the probability function is that of the mutual-information function. Finally, we discuss the evolution of the complexity of plants' environmental sensitivity and some ecological implications of degrees of perceptual complexity.

## Contributed Posters

- 157** BELL<sup>1</sup>, TIMOTHY J.\*, MARLIN BOWLES<sup>2</sup>, JENNY MCBRIDE<sup>2</sup>, AND KAYRI HAVENS<sup>3</sup>. <sup>1</sup>Department of Biological Sciences, Chicago State University, Chicago, IL, 60628; <sup>2</sup>Morton Arboretum, Lisle, IL, 60532; and <sup>3</sup>Chicago Botanic Garden, Glencoe, IL, 60022—*Viability analysis of a restored population of the federal threatened Pitcher's Thistle (Cirsium pitcheri) in Illinois.*

Pitcher's thistle (*Cirsium pitcheri*) is a federal threatened monocarpic herbaceous perennial of the western Great Lakes shoreline dune habitats. The plant is self-compatible, with little allozyme variation across its range. Population maintenance of this species depends on cohort replacement and recolonization of successional habitat maintained by shoreline processes. Succession also eliminates populations, while disturbances can either eliminate or create new habitat for populations. These dynamics require metapopulation persistence, in which local populations avoid simultaneous extinction by reacting independently to landscape-scale disturbances and colonizing newly formed habitats. Our population restoration in former Illinois habitat along Lake Michigan comprises 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. Spontaneous seedlings from flowering plants are now replacing these artificial cohorts, and the first flowering of these plants occurred in 1998. Morphological, demographic, and genetic (as shown by RAPDs) differences occur between geographically different seed sources, with Indiana plants having larger cotyledons and greater growth, survivorship and reproduction in the restoration. The restored Illinois population is now in its seventh year with nearly 150 plants, but population growth rate ( $\lambda$ ) is less than 1. Stage structured demographic analysis projects cohort sizes, number of spontaneous seedlings and, or, translocations, and amount of flowering needed to sustain population viability. For example, the minimum number of translocated seedlings needed to achieve a positive growth rate is twice the number of currently observed spontaneous seedlings.

- 158** BERTIN, ROBERT I.\* AND GREGORY M. GWISC. Biology Department. Holy Cross College, Worcester, MA 01610—*Sex expression and gynodioecy in Solidago (Asteraceae).*

Roughly 3% of flowering plants are gynodioecious, with individual plants bearing both female and bisexual flowers. Little attention has been paid to the adaptive significance of this sexual system, which is particularly

prevalent in the Asteraceae. Here we investigated one hypothesized advantage of having two flower types, namely that the arrangement permits flexibility in allocation of resources to male and female reproductive functions. We examined several perennial, gynomonoecious members of the genus *Solidago*. These plants produce small heads consisting of several female flowers, each bearing a single small petal, surrounding several bisexual disk flowers. We carried out greenhouse experiments in which we varied one or more of three environmental variables: light, nutrients and water, and/or examined heads in different positions on the plants or produced on different dates. The effects of these variables on the proportion of female flowers were modest to none. Specifically, significant effects were found for light in 0 of 3 species, for nutrients in 2 of 4 species, for water in 0 of 1 species, for position in 1 of 3 species and for date in 1 of 1 species. Because of the small number of significant effects and their modest magnitude, we conclude that the presence of two flower types in goldenrods is probably not advantageous in allowing flexibility in allocation of resources to male and female functions. It seems likely that this sexual system has been more important either in providing for pollinator attraction or in reducing pollen-pistil interference.

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CARTER, CHRISTY TUCKER\* AND IRWIN A. UNGAR. Department of Environmental and Plant Biology, Ohio University, Athens, Ohio, 45701 USA—*Germination response of *Spergularia marina* to seasonal changes in temperature and light.*

Seeds of *Spergularia marina* were collected in October, 1998, from an inland salt marsh in Rittman, Ohio, to test for seasonal change in germination responses to different temperature regimes and light vs dark treatments. To allow for exposure to natural temperature and moisture conditions, seeds contained in polyester bags were buried outdoors at the Ohio University greenhouse during November, 1998. Fresh seeds and seeds harvested monthly were tested for germinability. Four replicate petri dishes each containing 25 seeds were exposed to four alternating (12-h night/12-h day) temperature regimes (5/15°C, 5/25°C, 15/25°C, and 20/35°C) with a 12-h dark/12-h light photoperiod (20  $\mu\text{mol m}^{-2}\text{s}^{-1}$ ) for 20 days. An identical set of replicates was exposed to the same temperature regimes, but instead received 24-h dark for 20 days. Means  $\pm$ SE were calculated monthly for each temperature and a two-way ANOVA and Bonferroni post-hoc test were performed on arcsin square root transformed data. We found that no fresh seeds germinated in light or dark treatments. For seeds exposed to 24-h dark, less than 4% germinated at any temperature for any given month. From the two-way ANOVA and Bonferroni tests, germination responses at all temperatures were found to be significantly different ( $P < 0.0001$ ) with seeds in the 5/15°C temperature regime demonstrating the greatest and those at 20/35°C the lowest germination. Length of burial was also found to significantly ( $P < 0.0001$ ) influence germination and there was a significant ( $P < 0.0001$ ) interaction between temperature and length of burial. Except for 20/35°C, germination increased in the remaining three temperature regimes over the 12 month period. *Spergularia marina* seeds had both primary and conditional dormancy, but did not demonstrate a secondary dormancy. Seeds are probably inhibited from germinating in the field when they are buried and during the summer when temperatures are high and often exceed 35°C.

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DANLEY, KIMBERLY, TIFFANY ISAKSEN, NICOLE GARDNER, PAULA RANDALL-YOHO\*, AND LOREEN ALLPHIN. Department of Botany and Range Science, Brigham Young University, Provo, UT 84602—*Spatial distribution and sexual dimorphism in dioecious *Atriplex garrettii* Rydb.*

*Atriplex garrettii* Rydb. is a diploid, dioecious member of the Chenopodiaceae family with a known male specific genetic marker. Sex determination in this species appears to be genetically controlled with a 1:1 segregation of sexes. In harsh environments, some species exhibit a male biased sex ratio. However, *A. garrettii* exhibits unbiased sex ratios in its natural populations. This study assessed whether spatial segregation of sexes occurs within populations. Other studies have shown that in populations which exhibit differential spatial distribution of sexes, females prevail in resource rich microhabitats while males prevail in resource poor sites. Three populations of *A. garrettii*, growing in dry, sandy soils along the Colorado river near Moab, Grand County, Utah, were assessed for spatial segregation of sexes within populations. One hundred individuals per population were randomly selected using the point quarter method. Sex was recorded for all individuals and their nearest neighbors. Microenvironmental parameters (soil moisture, soil pH, etc.) were assessed for each sampled individual. Plant height and foliar crown diameter were measured to determine if males of *A. garrettii* are larger than females. Xylem water potential of each individual was assessed using a pressure chamber to determine if there was differential water stress in females and males. Degree of parasitism/pathogenic infection was measured for all individuals and compared between sexes.

- 161** DENTON, RENEE GENEVIEVE\* AND RAYMOND D. RATLIFF. Forestry Sciences Lab, Pacific Southwest Research Station, 2081 E. Sierra Ave., Fresno, CA 93710—*Ecology and Management of Trifolium Bolanderi Gray. in the Central Sierra Nevada.*

*Trifolium bolanderi* Gray. (Fabaceae) is a narrow endemic restricted to meadows of the central Sierra Nevada of California extending from Yosemite National Park to north of the King's River. It occurs within a narrow elevational band from 2134 m to 2165 m. The type location is Westfall meadow in Yosemite National Park. Commonly called Bolander's clover, it is federally designated by the U.S. Fish and Wildlife Service as a 'species of concern'. *Trifolium Bolanderi* occurs on grazed forest ranges, and its sensitive categorization influences land use planning. Species Ecology—Reasons for its limited distribution were investigated. According to park and forest records (1990), there were only 20 meadows with known populations. Ratliff and Denton (1993) examined 81 sites within 32 meadows, 10 meadows of which were protected from livestock grazing. Sites having the target species were compared to those without it. In terms of plant associations, soils, hydrology, ground cover, and other micro-climatic site factors for meadows, no biological reasons were reported (Ratliff and Denton 1993). Grazing Management—A study was initiated to evaluate hypothetical response to defoliation. Clipping treatments were applied in situ, at two clipping heights, 3cm and 6 cm. Clipping treatments simulated grazing use: early season, season-long, deferred, and deferred rotation grazing. One control plot per meadow was used. Plots were circular 1/8 square meter, surrounded by a buffer, and caged from herbivore use. Pre-clipping plant height was set a priori at 8cm. Treatments continued every two weeks through the growing season and were repeated over years. Twenty-two morphological parameters are being evaluated. Above-ground responses include average stem length, growth form, leaf length and number of flowers per head. Below ground responses include number of active shoots from the crown, crown diameter and length of the tap root. Statistical analysis will employ a mixed-model ANOVA.

- 162** FINER, MATTHEW S\* AND MARTIN T MORGAN. School of Biological Sciences, , Washington State University, , Pullman, WA, 99163—*Geitonogamy and the evolution of inflorescence design in Asclepias speciosa.*

Geitonogamy has the unique distinction of having the ecological properties of outcrossing, but the genetic consequences of selfing. We investigate the potential of geitonogamy as a selective force in the evolution of inflorescence design in *Asclepias speciosa*. We conducted 1,092 hand outcross pollinations (6 per individual) on two treatments, one covered in pollinator-excluding bridal veil before and after pollinations and the other left open to experience the consequences of natural rates of self-pollinations. The bagged treatment had significantly higher female fitness than the open treatment, providing strong evidence that natural rates of self-pollination significantly reduce fruit set in *A. speciosa*. Results were consistent in both undisturbed and fragmented populations, suggesting geitonogamy may be independent of population size. Fruit set data provides evidence that geitonogamy, and not resource limitation, may limit female success. We will also look at the effect of inflorescence-unit size on geitonogamous pollinations in natural populations. We will manipulate umbels in the field to create five treatments ranging in size (5, 15, 25, 35, 45 flowers per umbel), and then measure effects of size on pollen export and selfing rate with AFLP analysis of inserted pollinia. This will be the most direct study of pollen export and geitonogamy in a natural population conducted to date.

- 163** HAYWARD, JAMES L.\* AND DENNIS W. WOODLAND. Biology Department, Andrews University, Berrien Springs, MI 49104-0410—*Plant diversity and ecology of Protection Island, Washington.*

Protection Island, Washington, is located at the southeast end of the Strait of Juan de Fuca in the rain shadow of the Olympic Mountains (approximate rainfall=41 cm/year). The 160-hectare island contains one of the largest breeding colonies of seabirds and harbor seals (*Phoca vitulina*) in the Pacific Northwest. In 1988 most of the island was designated as the Protection Island National Wildlife Refuge. While Protection Island's habitat structure has changed little since George Vancouver's 1792 description of the island, published information on its flora consists only of incidental remarks appended to faunal studies. As part of a long-term assessment of Protection Island's biodiversity, vascular plants were collected from 1997-2000. During June-August 1999, plant diversity and density were sampled in 311 randomly-selected, 1 x 1-m quadrats along 15 transects. Introduced species accounted for 42% of the 106 species collected overall, and for 55% of 20 species of grasses. Exotics accounted for most of the grassland cover. Field bindweed (*Convolvulus arvensis*) and Canada thistle (*Cirsium arvense*) were particularly invasive. Snowberry (*Symphoricarpos albus*) was common along north-facing slopes. Two small forested areas, dominated by Douglas fir (*Pseudotsuga menziesii*), were commonly bordered by Douglas maple (*Acer glabrum*), Pacific madrone (*Arbutus menziesii*), ocean spray (*Holodiscus discolor*), and Nootka rose (*Rosa nutkana*). Weedy species dominated the sparsely-



vegetated nesting areas of rhinoceros auklets (*Cerorhinca monocerata*) and glaucous-winged gulls (*Larus glaucescens*). A vegetation map of the island was created using ground-truthed, aerial photographs. A species-association matrix highlights correlations among species distribution patterns. Results from this study have raised questions about the impact of previous agricultural practices, real estate development, and fire prevention on the island's grassland community. They have also led to hypotheses about plant/nesting-bird interactions and about the value of controlled burns of the island's grassland areas. These hypotheses are currently being tested.

- 164** JALONEN, JYRKI A.\* AND ILKKA VANHA-MAJAMAA. CW-405, Department of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada—*Understorey vegetation response to alternative forest harvesting methods in southern boreal forests.*

New forestry practices are being implemented in the hope of achieving ecological sustainability, but little is known of their effects on biota. We investigated stand level effects of five different felling methods on mature boreal *Picea abies* forest understorey vegetation in southern Finland. We hypothesized that vegetation response depends on the level of disturbance, i.e., intensity of the felling method. There were eight one hectare sized replicates of the five treatments, which were as follows: a) control, 100 % retention; b) single-tree selection system felling, 70 % dispersed retention; c) gap felling, with and without (n=3) site preparation, 50 % aggregated retention in three patches/ha; d) retention felling, 10 % retention, three clusters of trees/ha and d) clear felling, 0 % retention. Vegetation was sampled before the treatments and during two following years. The immediate response of the understorey vegetation to the level of retention was linear. Bryophyte species richness decreased significantly in selection system, 10 % retention and clear felling, but remained at the pre-treatment level in gap felling and control. Bryophyte cover decreased significantly with all studied retention levels except control, most prominently in clear and 10 % retention felling. Vascular plant cover decreased significantly in all studied retention levels, including control, but species richness only with 10 and 0 % retention levels. During the second post-treatment year, a significant decrease in bryophyte cover was observed in gap felling with site preparation, apparently due to the disturbance caused by the preparation, while no further decrease was observed in the other treatments. On the contrary, species number and cover of bryophytes and vascular plants increased slightly in 10% retention felling and clear felling due to the invasion of early successional species. The 10% retention and clear felling did not differ from each other in terms of vegetation response. Apparently the residual tree groups were too small to provide shelter for late successional vegetation in or outside of residuals.

- 165** JAMESON, ANNEMARIE. Department of Biology, University of Miami, P.O. Box 249118, Coral Gables, FL 331240-0421—*Feeding trials of Giant Swallowtail larvae on Rutaceae in south Florida.*

Specialist herbivores are linked to their host plants through a variety of mechanisms from oviposition cues, to cues to feed on the host the larval herbivore finds itself, to non-tolerance of a host once feeding is initiated. In order to examine the diet breadth of the Giant Swallowtail, *Papilio* (= *Heraclides*) *cresphontes*, in south Florida, I examined survival and development time of larvae to pupation on both the host plants on which eggs were laid and of an alternate host plant that I switched eggs to. Giant Swallowtails range from North America through northern South America, where they specialize on the family Rutaceae. There were three control groups (larvae raised on their natal host plant): *Casimiroa edulis*, *Zanthoxylum fagara*, and *Z. coriaceum*, hereafter referred to CE, ZF and ZC. There were two treatment groups: ZF to CE, and ZC to ZF. Survival in the control groups was either nearly complete (CE and ZF) or an utter failure (ZC). In the treatment groups, survival was complete on ZC, and nearly complete on CE. Among larvae in the control groups, larvae raised on CE took significantly less time to develop than that raised on ZF. When I switched eggs from ZF to other plants, the mean number of days to develop reflected that change. Eggs switched to CE pupated after a time intermediate to those raised on a natal plant of ZF or CE. It is interesting to note that the longest development time is that of larvae switched to a palatable plant (ZF) from one they fail to accept as a host (ZC). Additionally, while CE is exotic in Florida, its range includes other portions of the Giant Swallowtail's range. It appears that host plant usage in the Giant Swallowtail is genetically determined, likely as a result of all three mechanisms.

- 166** MORRISON, JANET A. Department of Biology, The College of New Jersey, P.O. Box 7718, Ewing, NJ 08628-0718—*Dogwood decline in the urban New York Botanical Garden Forest.*

Much of the forest in the eastern United States exists as fragments surrounded by urbanizing development, yet little explicit attention has been paid to plant ecology in forests embedded in an urban matrix. In the 16

ha old-growth New York Botanical Garden Forest, in Bronx, NY, many native tree species exhibit decline and/or lack of recruitment. *Cornus florida* shows distinct symptoms of decline that may be due to dogwood anthracnose disease, age-related senescence, and/or environmental stress. In order to investigate spatial factors often associated with disease, such as host density and distance from the forest edge, I characterized spatial patterns of symptoms and mortality from 1995 to 1998, using GIS with positional data from a sub-meter accurate GPS. Most dogwoods in the forest were mature; only 2% had DBH < 3 cm in 1998 and no seedlings were found in either year. In both years the fungal pathogen *Discula destructiva* was present. Nearly all trees showed some symptoms (lower branch and twig die-back, conidiomata on leaves, leaf blotch). Of 219 trees found alive in 1995, 12% were dead by 1998, 80% were alive, but another 8% were not relocated. Dead trees had a smaller DBH on average, suggesting that older trees were not more likely to die. No clear spatial pattern was evident for symptoms, but there were patterns for mortality. Only one of the 41 trees at or close to the forest edge (within 15 m) died. The 81 trees within 2 m of another dogwood were also less likely on average to die (only 8.6%). So, the interior of this urban forest appears to present a challenge to isolated young dogwoods in particular. At the observed mortality rates, and without recruitment, the interior of the NYBG Forest may lose half of its dogwood trees by 2013.

- 167** PERONI, PATRICIA A.\*, JAMES W. WHITE, ALLISON A. CALDWELL, LAURAN HALPIN, AND ADAH WALKER. Department of Biology, Davidson College, Davidson, NC 28036-1719—*Dark induced secondary dormancy in seeds from a Silene latifolia meta population.*

Habitat heterogeneity may influence the germination phenology of seed crops if the environments that seeds experience upon dispersal differ in their ability to induce secondary dormancy. We initiated germination trials for seeds from two populations of *Silene latifolia* in light (14 hr photoperiod) and dark conditions at 22 C in growth chambers (2 chambers per light treatment), and found significantly lower percent germination in the dark environment than the light treatment after 1 wk. When we subsequently exposed ungerminated seeds from the dark treatment to a 14 hr photoperiod, mean cumulative percent germination for these replicates after two wk (1wk dark, 1 wk light) was lower than the mean percent germination of seeds in the light treatment after 1 wk. Cumulative percent germination for seeds initially exposed to dark conditions plateaued after 2 wk in the light. At this time, cumulative percent germination of these seeds was significantly lower than that recorded for replicates that entered germination trials in the light at the same time the dark treated seeds were exposed to light. We conclude that our dark treatment initiated secondary physiological dormancy in a large percentage of seeds. Treatment with gibberellin (100 ppm) failed to break this dormancy. Stratification at 4 C for 1 mo broke dormancy for a fraction of the viable seeds that remained ungerminated. These results suggest that a large percentage of buried *S. latifolia* seeds may be unable to germinate immediately upon exhumation, although field investigations will be necessary to fully explore this potential effect of seed burial.

- 168** STEHLIK, IVANA\* AND ROLF HOLDEREGGER. Institute of Systematic Botany, University of Zurich, Zollikerstr. 107, CH-8008 Zurich, Switzerland—*Spatial genetic structure and clonal diversity of Anemone nemorosa in late successional deciduous woodlands of Central Europe.*

We tested whether established populations in similar environmental conditions exhibit similar or varying spatial genetic structures by comparing populations of the long-lived, early-flowering plant species *Anemone nemorosa* L. in late successional deciduous woodlands of Central Europe. A standardized sampling strategy was used to collect thirty ramets from each of 20 populations. Genotypes of the samples were determined by allozyme electrophoresis. Genetic variation and clonal diversity were high compared with other clonal species. Most (95 %) of the sampled ramets had unique multilocus genotypes with only 22 multilocus genotypes occurring more than once. No recurring multilocus genotype occurred in more than one population. Fixation indices (mean over 14 loci) in the populations ranged between 0.08 and 0.56 (grand mean = 0.21) confirming that the breeding system in *A. nemorosa* is predominantly outcrossing or mixed-mating. Limited gene flow among populations ( $N_m = 0.62$ ) was reflected by high population differentiation ( $G_{ST} = 0.29$ ) and low genetic identities among populations. A non-significant correlation between these identities and geographic distances was detected (Mantel test). Spatial autocorrelation (Moran's I) showed no significant differences in genetic structures between populations under similar environmental conditions. Samples taken less than 0.5 m apart from each other were genetically more closely related than to more distant samples, but similarity of genotypes only decreased slightly with further increase in distance. The high levels of genetic variation found in populations of *A. nemorosa* are probably due to repeated seedling recruitment and the outcrossing or mixed-mating breeding system, whereas vegetative propagation and short-distance seed dispersal may contribute to the positive genetic autocorrelation observed at a small spatial scale.

- 169** UNGAR, IRWIN A.\* AND M. AJMAL KHAN. Department of Environmental and Plant Biology, Ohio University, Athens, Ohio 45701—*Effect of bracteoles on the seeds of two species of Atriplex*.

A comparison was made to determine the effects of bracteoles on the germination response of a salt marsh annual *Atriplex prostrata* and a salt desert perennial *Atriplex griffithii*. Attached bracteoles did not inhibit the germination of *A. prostrata* but completely inhibited the germination of *A. griffithii* seeds. The presence of detached bracteoles of *A. griffithii* in petri dishes with seeds also inhibited germination. Water soluble extracts from bracteoles of both species indicated that they contained up to 132 g/kg total salts in *A. griffithii* and 87 g/kg total salts in *A. prostrata*. The water potential of dissolved substances in bracteoles extracts was  $-15.2 \pm 0.17$  MPa for *A. griffithii* and  $-12.1 \pm 0.74$  for *A. prostrata*. The ash content of bracteoles on a dry weight basis was  $28.7 \pm 0.4\%$  for *A. prostrata* and  $30.0 \pm 0.3\%$  for *A. griffithii*. Soluble salts are inhibitory to the germination of both species and the presence of relatively high concentrations of total salts in bracteoles may explain the reduced germination in *A. griffithii*. Germination of seeds of the perennial *A. griffithii* may also be mechanically inhibited by the presence of persistent bracteoles, whereas, the annual *A. prostrata* has ephemeral bracteoles that may serve to limit germination in the fall but they are not present during the normal spring germination period. Bracteoles may play a significant role in the dispersal of seeds by water since seeds enclosed in bracteoles remained floating longer than seeds with the bracteoles removed.

- 170** VALENTINE, LORI\*, HAROLD BERNINGHAUSEN, AND DARLENE SOUTHWORTH. Department of Biology, Southern Oregon University, Ashland, OR 97520—*Mycorrhizae on Quercus garryana at Whetstone Savanna in Southern Oregon*.

*Quercus garryana*, Garry oak or Oregon white oak, is the dominant vegetation on the western edge of the Agate Desert, an alluvial fan capped with shallow clay loam over a cemented hardpan. The landform exhibits patterned ground with mounds and vernal pools. The oaks are associated with *Ceanothus cuneatus* and with native and exotic grasses. In preparation for a study of the biocomplexity of common mycorrhizal networks among oaks and grasses, we are examining the morphotypes of mycorrhizae on *Quercus garryana*. We sampled soil cores at distances half way to the canopy edge, at the canopy edge, and outside the canopy and have identified four morphotypes of ectomycorrhizae including extensive *Cenococcum*. Where *Cenococcum* dominates, few other morphotypes are found. In addition, endomycorrhizae with intraradical hyphae and vesicles also occur. Infection rates are 10-32% with lowest rates on roots under vernal pools and highest rates in areas of canopy overlap. Funded by NSF Grant DEB-9981337.

- 171** WEBER, DARRELL J., WILFORD M. HESS\*, BULQUES GUL, M. AJMAL KHAN, AND SAM ST. CLAIR. Department of Botany and Range Science, Brigham Young University, Provo, Utah, 84604 and Department of Botany, University of Karachi, Karachi Pakistan—*Halophytic fungi from an inland salt playa of the Great Basin*.

The Great Basin area in the Western United States has no natural river drainage. As a result of the water evaporation in the valleys, the soils are high in salts. In some valley regions the high salt content of the soil (5%) limits plant growth to a few halophytic plants. Desert conditions exist during much of the growing season and when the rains come shallow saline pools form in depressed areas. In a salt playa near Goshen, Utah, fungi were isolated from four zones; the bottom of the salt playa, the zone where *Salicornia* grows, the salt grass *Distichlis* zone, and the least saline tall grass area. Fungal cultures were obtained and were evaluated for their salt tolerance. The salinity of the soil in the zones ranged from 2% to 15%. Most of the fungi isolated were *Aspergillus* species although *Penicillium* was also common. Of the 22 fungal isolates, 15 isolates were able to grow on PDA with 16% to 22% NaCl. The spores of these 15 fungal isolates were able to germinate in 20% NaCl. All of the fungal isolates grew well on PDA that had 30% glucose and no salt.

- 172** WHITE, JAMES W.\*, PATRICIA A. PERONI, DAVID E. MCCAULEY, AND CHRISTOPHER M. RICHARDS. Department of Biology, Davidson College, Davidson, NC 28036-1719; Department of Biology, Vanderbilt University, Nashville, TN 37235—*Effects of inbreeding and light treatments on the germination responses of Silene latifolia seeds*.

Colonizing populations often experience inbreeding. This inbreeding may influence the ability of these populations to establish successfully if the mass or germination behavior of inbred seeds differs from that of outbred seeds. As part of a larger investigation into the effects of seed banks on colonization in a *Silene latifolia* meta population located in southwestern Virginia, we created outbred and F1 and F2 inbred lines

of seeds. Mean seed mass varied significantly among maternal families within breeding treatments, but did not differ significantly among the three breeding treatments. To determine if germination cues or rates differed among the three treatments, we conducted germination trials at 22 C in two light (14 hr photoperiod) and two dark growth chambers. The effects of breeding and light treatments on percent germination and germination rates will be discussed

- 173** WHITTEMORE-OLSON, A. A.\*, A. MOSIER, AND JOHN C. MOORE. Department of Biological Sciences, University of Northern Colorado, Greeley, CO 80639—*Effects of elevated atmospheric carbon dioxide on micro-arthropod populations of the Shortgrass Steppe*.

We studied the effects of doubled atmospheric CO<sub>2</sub> concentration on the density and diversity of microarthropods of the Shortgrass Steppe of the Pawnee National Grasslands in Colorado. Samples were extracted from soil cores taken from three ambient CO<sub>2</sub> chambers, three doubled CO<sub>2</sub> chambers and three control plots. The treatments were established in the spring of 1997 and the first year's data was collected after the first full growing season, in the fall of 1998. In all, we collected 18 soil cores per year or two cores per chamber or plot, each of which was separated into five depths. The total microarthropods for combined depths, found in the first year, equaled 744 in the ambient CO<sub>2</sub> chambers, 523 in the control plots and 670 in the doubled CO<sub>2</sub> chambers. While the total microarthropod densities were similar across treatments, the numbers of cryptostigmatid, astigmatid, mesostigmatid and prostigmatid mites began to show differences by functional groupings. The cryptostigmatid mites had the highest densities in the ambient chambers and control plots. The doubled CO<sub>2</sub> chambers had higher densities of predatory prostigmatid mites. The populations did not demonstrate significant treatment effects but did have significant treatment by depth interactions. The aggregation of mite populations to lower soil horizons was apparent.

- 174** WILSON, CHESTER E.\* AND ERIN L. BRASSIL. Biology Department, University of St. Thomas, St. Paul, MN 55105—*Variation in fluctuating asymmetry among genotypes of Glechoma hederacea*.

Fluctuating asymmetry is a measurement of non-directional deviation from bilateral symmetry. Variation in floral and vegetative symmetry between genets of creeping charlie (*Glechoma hederacea*) would indicate developmental differences in the shape of flowers and leaves. Floral samples were collected from a 1/2 square mile area during two summer seasons. Leaf samples were collected from the same area during one summer season. No difference in asymmetry exists among genets for floral traits, but asymmetry of vegetative traits differs significantly among genets. The degree of fluctuating asymmetry in vegetative traits displays strong positive spatial autocorrelation. This suggests that the potential for phenotypic plasticity differs greatly between floral and vegetative traits. Quantitative genetic studies are underway in order to determine the relative importance of environmental and genetic contributions to the genotypic differences.

## VII. Genetics Section

### Contributed Papers

- 175** ALLPHIN, LOREEN\*, TATE TISCHNER, KEVIN CHASE†, JIM ORF‡, FRED ADLER†, AND KARL G. LARK†. \* Department of Botany and Range Science, Brigham Young University, Provo, UT 84602, †Department of Biology, University of Utah, Salt Lake City, UT 84112, ‡Department of Agronomy and Plant Science, University of Minnesota, St. Paul, MN 55108—*Genetics of seed abortion and reproductive traits in soybean, Glycine max (L.) Merr., I.*

Genetic basis of embryo abortion in *Glycine max* was analyzed using a large Recombinant Inbred (RI) population. RI lines (including three replicates), parental lines (Minsoy & Noir 1) and "Check" cultivars were planted in hill plots. Fifty fruits from each hill were analyzed for reproductive, quantitative traits (number of ovules per pod, number of filled seeds per pod, seed/ovule, and developmental stage and position of abortions). Parental lines differed significantly for traits. Average values for the RI population were intermediate between the parents. Some segregants had high frequencies of four ovules or seeds per pod, whereas parents and "Checks" did not. There was a positive correlation between yield and ovules per pod and between seed number and ovules per pod. No correlation was observed between variation in pod size and seed/ovule. If abortion occurred within a pod there was a greater probability that another abortion would



occur at the same developmental stage. Most abortions fell in the first position within the fruit. Abortions were observed at all developmental stages, but primarily occurred at two of four stages. Six significant QTLs were associated with reproductive traits. QTLs accounted for 36% of the variation in ovule or seed number. Two QTLs were involved in interactions with another locus.

- 176** DATWYLER, SHANNON L.\* AND ANDREA D. WOLFE. Department of Evolution, Ecology and Organismal Biology, Ohio State University, Columbus, OH 43210-1293—*Assessment of ISSR band homology by southern hybridization with implications for data analysis and microsatellite development.*

Despite numerous recent studies using inter-simple sequence repeat (ISSR) markers, there have been no comprehensive studies examining homology among ISSR fragments. In this study, we are assessing homology among ISSR fragments by southern hybridization. Thirty two taxa, representing a wide sampling among the Lamiales, with a focus on *Penstemon* subg. *Dasanthera* were chosen for study. Three ISSR primers representing different repeat motifs have been used for DNA amplification. Southern blots were performed for all three primers of interest. Probes for southern hybridization were generated from three taxa (*Penstemon cardwellii*, *Hyobanche glabrata*, and *Scrophularia scopoli*) for all three primers by PCR cloning. Each ISSR band was hybridized separately to the appropriate primer blot and visualized using the ECL non-radioactive labeling kit. Preliminary data suggest that comigrating fragments represent homologous fragments among closely-related taxa, but homology assessment is more complicated among distantly-related taxa. In addition, some ISSR bands have been demonstrated to hybridize with multiple bands generated by the same primer, especially among closely-related taxa. This could be the result of tandemly-repeated SSRs of the same di- or trinucleotide repeat. Comparisons are being made for genetic diversity statistics estimated including all bands visualized using ethidium bromide-stained agarose gels and only bands that are determined to be independent based on southern hybridization. In addition, a new strategy for developing microsatellite loci from ISSR fragments will be discussed.

- 177** DUFF, R. JOEL\*, MARK DAVIS, AND ANGELA BOYLE. Department of Biology, University of Akron, Akron, OH 44325-3908—*The fate of conserved ribosomal DNA and protein coding gene clusters during the evolution of land plant mitochondrial genomes.*

The mitochondrial DNAs of flowering plants are the largest and most complex of any eukaryotes. One approach to better understanding the complex behavior of this genome exhibited by higher plants is to identify changes in genetic structure and composition of this genome across the landscape of land plant evolution. A comparison of the genomes of *Arabidopsis* and Maize with *Marchantia* reveals that very few gene clusters have been conserved during land plant evolution. Presently we have examined two gene clusters that are conserved among most eukaryotic mitochondrial DNA genomes but which have been disrupted in the flowering plant genomes. These gene clusters include the ribosomal DNA cistron and *rps12-rps7* genes. The ribosomal DNA cistron of *Marchantia* consists of the following genes in the order: SSU, two tRNAs, 5S, two tRNAs, and LSU. In flowering plants only the SSU and 5S, without the transfer RNAs, remain linked. A survey of land plants using PCR primers designed to amplify both the SSU-5S and 5S-LSU gene regions reveals that the entire ribosomal cistron is present in representatives of all the main lineages of land plants except gymnosperms and angiosperms. Further, based on nucleotide sequences of selected samples and sizes of PCR products it is likely that the two tRNAs found between the SSU and 5S of *Marchantia* were lost in the common ancestor of the gymnosperms. The *rps12-rps7* gene cluster is conserved among the same organisms as the entire rDNA cistron but is also found among the gymnosperms surveyed and thus appears to have been lost in the ancestor of the angiosperms. The distribution of the linkage of *nad3* and *rps12* previously reported among gymnosperms and angiosperms will be discussed in the context of the *rps12-rps7* data.

- 178** KORPELAINEN, HELENA. Department of Biosciences, Division of Genetics, P.O. Box 56, 00014 University of Helsinki, Finland—*The evolutionary processes of chloroplast and mitochondrial genomes differ from those of nuclear genomes.*

The replication and partitioning of chloroplast and mitochondrial genomes to daughter cells at cell division occur in a flexible manner, unlike in the case of nuclear genomes. Many of the genes present in the prokaryotic endosymbionts that became chloroplasts and mitochondria have been lost or transferred to the nucleus of the host, where they have joined the stringent genetic system of the nuclear genome, including also sexual recombination and more efficient DNA repair. However, genes retained within the cytoplasmic organelles can be involved in selection processes both within and among individuals. In the case of heter-

oplasmy, which is attributed to mutations or biparental inheritance, within-individual selection on cytoplasmic DNA may provide a mechanism by which to adapt rapidly. The persistence of genes in cytoplasmic genomes indicates that chloroplast and mitochondrial genomes can be maintained in the process of evolution. The inheritance of cytoplasmic genomes is not universally maternal (e.g. about one-third of the angiosperm genera seem to display biparental chloroplast inheritance to some degree) and, therefore, unlikely to be a mere consequence of the asymmetry in gamete sizes. The presence of inheritance patterns other than the strictly maternal pattern indicates that different strategies have been adopted among different organisms.

- 179** MORRISON, LAURA A.\*, LISELE CREMIEUX, ROBERT S. ZEMETRA, OSCAR RIERA-LIZARAZU, AND CAROL MALLORY-SMITH. Department of Crop & Soil Science, Oregon State University, Corvallis, OR 97331-3002; Department of Plant, Soil & Entomological Sciences, University of Idaho, Moscow, ID 83844-2339—*Gene flow in the crop-weed complex of wheat* (*Triticum aestivum* L.) and *jointed goatgrass* (*Aegilops cylindrica* Host).

Jointed goatgrass (*Aegilops cylindrica* Host - CD genomes), a wild tetraploid wheat, was introduced into North America as a contaminant of wheat seed brought from Eastern Europe in the late 1800's and early 1900's. Since its introduction, it has become a serious crop weed in fields where hexaploid bread wheat is grown (*Triticum aestivum* L. - ABD genomes). Hybridization is common among members of the wheat complex, having played an important role in the evolution of this allopolyploid group. Wheat and jointed goatgrass share only the D genome. Therefore, hybrids are considered to be sterile, a fact supported by the identification of a gametocidal sterility system in jointed goatgrass (Endo, 1988). However, large numbers of partially female fertile hybrids are being found in the jointed goatgrass infested wheat fields of the Pacific Northwest. Studies of experimental material and hybrids collected in Oregon now suggest that neither hybridization nor seed production is a rare event. Preliminary genetic analyses using SDS-PAGE of the high molecular weight glutenin seed proteins, microsatellite (SSR) markers, and genomic *in-situ* hybridization suggest the development of a crop-weed complex via introgressive hybridization. To date, evaluation of hybrid material supports the possibility of a two-way introgression with both species capable of serving as the female parent. Wheat field populations appear to be a diverse mix of F<sub>1</sub> and backcross (BC) hybrid generations. Work with experimental wheat x jointed goatgrass BC hybrids, with either species as the recurrent male parent, shows a rapid move to fully fertile, self-pollinating hybrids. The wheat-jointed goatgrass weed complex offers a model system for studying introgressive hybridization within the agricultural ecosystem. It also offers a timely opportunity to study gene flow risk in advance of the release of transgenic wheat.

- 180** PRICE, H. JAMES\*, M. NURUL ISLAM-FARIDI, AND DAVID M. STELLY. Department of Soil and Crop Sciences, Texas A&M University, College Station, TX 77843-2474—*Molecular cytogenetic mapping of sorghum chromosome 1*.

Fluorescent in situ hybridization (FISH) of cloned probes provides a powerful tool for the integration of recombination, physical and cytogenetic maps. As part of a sorghum genomics project we have assigned the position of eight cloned DNA sequences to chromosome 1 of *Sorghum bicolor*. The probes used included a centromere-associated repeat, 28S-18S rDNA, a corn pollen-expressed *Adh* cDNA-selected sorghum bacterial artificial chromosome (BAC), and five RFLP-selected sorghum BACs. With the exception of the centromere-associated sequence and the 28S-18S rDNA, the probes produced FISH sites at the ends of the chromosome. The BACs selected from probes used to map two adjacent RFLP loci produced FISH signals at opposite ends of the chromosome. Over 85% of the physical length of this chromosome corresponded to approximately 12 map units separating the two RFLP loci. This indicates that most of the recombination and the loci of the ca. 120 cM RFLP map are located at the ends of the chromosome. Research supported by the Texas Advanced Technology and Research Program (grant 999902-090 to HJP and DMS), the Texas Agricultural Experiment Station, and the Texas A&M University Office of University Research.

- 181** RICHARDSON, ADJOA O.\*, QUI-YUN (JENNY) XIANG, AND CHUANZHU FAN. Department of Biological Sciences, Idaho State University, Pocatello, ID 83209—*Microsatellite analysis of the hybrid zone in the Buckeye Genus Aesculus L. (Hippocastanaceae)*.

Introgressive hybridization plays an important evolutionary role in plants. However, studies of the genetic structures of natural hybrid zones are often hindered by the lack of sensitive molecular markers. We employed the highly sensitive genetic markers from microsatellite loci to 1) define the genetic structure of a broad hybrid zone in *Aesculus* L. involving *A. pavia* and *A. sylvatica* and 2) to test previous hypotheses derived from allozyme and ISSR data. Using PCR, eight pairs of microsatellite primers developed specifically for

Aesculus were used to amplify eight microsatellite loci of populations representing pure parental species and hybrids. The genotype of each locus was determined for each individual using an ABI-377 automated DNA sequencer with GeneScan version 3.1 and the data obtained analyzed with Genotyper version 2.0. Our preliminary results indicated that these microsatellite loci are highly polymorphic. Multiple alleles that differ in one to more than 15 nucleotides were found for these loci. The loci contain unambiguous species-specific alleles that can be used as species-specific markers. These species-specific markers from the parental species were combined in the hybrid populations. The results from the microsatellite analysis are congruent with previous data from morphology, allozyme, and ISSR in suggesting the existence of introgressive hybridization in the hybrid zone, and most hybrids in the zone represent latter hybrid generations.

- 182** TISCHNER, TATE\*, LOREEN ALLPHIN, KEVIN CHASE†, JIM ORF‡, AND KARL G. LARK†. \*Department of Botany and Range Science, Brigham Young University, Provo, UT 84602, †Department of Biology, University of Utah, Salt Lake City, UT 84112, ‡Department of Agronomy and Plant Science, University of Minnesota, St. Paul, MN 55108—*Genetics of seed abortion and reproductive traits in soybean, Glycine max (L.) Merr., II.*

Based on the results given in a previous abstract, a more extensive study was performed to assess the genetic basis of seed abortion and reproduction in soybean. For this study, reproductive data were obtained from two replications of three different RI populations derived from the three parents Minosy, Noir 1 and Archer grown under typical agronomic conditions. This study surveyed a more extensive list of reproductive parameters (number of nodes per plant, nodal length, number of fruits per node, nodal position of fruits, number of fruits/plant, number of ovules per pod, number of filled seeds per pod, seed/ovule, and developmental stage and position of abortions). In addition, a variety of agronomic traits (seed number, seed weight, total yield, leaf shape, oil content of seeds, number of flowers per plant, protein content of seed, etc.) were measured in the same experiment. All reproductive and agronomic traits were compared with three existing genetic linkage maps of genotypes from these RI populations. Quantitative trait loci (QTLs) responsible for the variation in reproductive traits were identified and also analyzed for interactions with other QTLs. These results were compared with data (given in previous abstract) obtained from different environmental conditions (Utah vs. Minnesota).

- 183** WAITT, DAMON E.\*, SARAH HOFFMAN, AND JOCYLEN FOURNET. Department of Biology, Southwestern University, Georgetown, TX 78626—*Meristic variation in wild and cultivated populations of Phlox drummondii.*

To determine the extent to which natural populations vary in levels of developmental instability, meristic variation was assessed in fourteen wild populations of *Phlox drummondii* growing in central Texas. There were significant differences among populations in the percentages of flowers that exhibited an abnormal number of sepals and anthers, but not petals or stigmatic lobes. Of the four whorls, stigmatic lobes varied the most with 4.5% of the flowers exhibiting an abnormal number. Overall, 8.2% of the 5,022 flowers scored had at least one anomalous flower. In a separate greenhouse study, five cultivars and three natural populations of *P. drummondii* were grown simultaneously to determine the extent to which the domestication process has influenced meristic variability. Cultivars exhibited significantly greater floral formula variation in all four whorls compared to their wild progenitors. As with the survey of wild populations, stigmatic lobes varied the most with 17% of the flowers exhibiting an abnormal number of lobes in the cultivated populations.

- 184** WALL, DENNIS P.\* AND JOSH T. HERBECK. Department of Integrative Biology &, University and Jepson Herbaria, University of California, Berkeley, Berkeley, CA 94720—*Codon Usage in Green Plants: an Analysis Using rbcL.*

We have constructed a composite phylogeny of 92 green plant taxa with representatives from all major clades to examine the level and degree of codon usage for the gene *rbcL* and to search for potential links between primary and secondary levels of organization. *rbcL* encodes the large subunit of RUBISCO, an important enzyme in photosynthesis. Such functional importance predicts that changes in primary genetic substructure, and perhaps secondary structure and enzymatic efficiency should be infrequently tolerated. Specifically, this conservation predicts that changes in codon bias and usage should occur infrequently, if at all. We have tested this claim and found it to be largely false. Instead the degree of codon bias among green plant lineages shifted in correspondence with phylogeny. One notable finding was a major transition to decreased codon bias at the boundary between spore plants and seed plants. The codon bias cannot be explained by overall genome composition bias, and must have other explanations, related to selection. Codon preference also changed among green plant lineages, but these changes were most often homoplasious. However, the shifts

in preference were predominantly to G or C ending codons, indicating possible biochemical canalization. To search for mechanisms that may explain these changes, we examined the relationship between the degree of bias and rates of Kn/Ks substitutions in *rbcL*. Lower Kn/Ks ratios were correlated with higher codon bias, indicating tracking of preferred codons within amino acid families. These data support the hypothesis that codon bias and usage are under selective pressure. In general, our study identifies how comparative analyses of genetic organization may help clarify the mechanisms linking genes, proteins, and patterns of microevolution. Our study also indicates that usage of nucleotide sequence alone for phylogenetic reconstruction may be overly simple; consideration of how the selective environment may effect phylogenetic results is critical.

- 185** WHITKUS, RICHARD\* AND TIMOTHY K. LOWREY. Department of Biology, Sonoma State University, Rohnert Park, CA 94928-3609 and Department of Biology, University of New Mexico, Albuquerque, NM 87131—*Genetic marker diversity in Hawaiian and Cook Island Tetramolopium (Asteraceae)*.

*Tetramolopium* is a genus of sub-shrubs with an Australasian-Polynesian distribution. The Hawaiian and Cook Islands species represent a monophyletic group of three clades, each recognized by morphological and ecological characteristics and hypothesized to represent products of adaptive radiation. The genetic diversity of this group was assessed using RAPD and isozyme genetic markers, and compared with a previous nuclear RFLP analysis of 38 loci. This report represents the first study using these three markers in island plants. Twenty isozyme loci and 126 RAPD markers were surveyed for known populations. Overall diversity is very low ( $<0.22$ ), following the general pattern observed in insular species, and confirming the extremely low diversity for *Tetramolopium* in comparison to all other studies. RFLP and RAPD marker diversity is similar while allozyme diversity is markedly lower. There is greater differentiation among species within sections than among sections. Analyses of all three marker sets do not agree with morphology/ecology based clades. The coefficient of genetic differentiation ( $G_{ST}$ ) over all species ranges from 0.558 for RFLP to 0.787 for allozymes and 0.858 in the RAPD data, indicating a high degree of genetic differentiation among species. The results show that allozyme data underestimate the total amount of genetic diversity present. The high  $G_{ST}$  values are what would be expected as a result of genetic drift in small isolated insular populations. The low overall genetic diversity coupled with the lack of congruence between the morphological and genetic differentiation firmly establishes that the group has undergone recent and rapid adaptive radiation. These results suggest that conservation efforts in this genus need to focus on preserving all species since they each harbor a distinct set of genetic diversity.

- 186** ZAHN, LAURA M. Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721—*Population dynamics of the gynodioecious Bouteloua chondrosioides (Spruce-top grama)*.

*Bouteloua chondrosioides* (Poaceae) is a perennial, gynodioecious, Chloridoid grass with both diploid ( $2N=20$ ) and polyploid ( $2n=40$ ; 80) populations that vary in levels of male sterility. *B. chondrosioides* was initially considered to be hermaphroditic; however Reeder and Reeder in 1966 described a male sterile form that makes aborted anthers (MA form) not visible to the naked eye. This form has been observed in all populations surveyed to date. A second, independently segregating form of male sterility has also been recently identified. This form makes stamens of reduced size that contain no pollen grains (MS form). Both forms have been found in all Texas and Arizona populations observed. No correlation between ploidy levels and levels of male sterility has been observed. In this talk I will outline evidence from work performed to date supporting the hypothesis that the transmission of male sterility in the gynodioecious *Bouteloua chondrosioides* appears to be primarily determined by cytoplasmic male sterility.

## Contributed Posters

- 187** CYRIL, JENITH\*, GARY POWELL, AND WM. VANCE BAIRD. Departments of Horticulture and Biological Sciences, Clemson University, Clemson, SC 29634—*Cloning and characterization of fatty acid desaturase genes from bermudagrass (Cynodon spp)*.

All plants are exposed to environmental stress at some time during their life cycle. Plants respond to such stress by regulating the expression of genes ultimately responsible for synthesis of compounds that help in adapting to the stress. Cold temperature is an important stress affecting crops in the U.S. Some plants are more tolerant to low temperature stress than others, and many of these "acclimate" to withstand previously



lethal low temperatures. Acclimation is a naturally occurring physiological process in many temperate perennial plants. In addition to synthesis of compounds like osmolytes and cryoprotectants, the degree of unsaturation of membrane lipid fatty acids contributes to the ability of these plants to withstand prolonged exposure to low temperature. Bermudagrass is a warm season turfgrass, which shows an increase in the synthesis of the tri-unsaturated fatty acid, linolenic acid during cold-acclimation. In addition, there is concomitant decrease in the amount of the di-unsaturated fatty acid linoleic acid. There are cultivar-specific differences in the timing and magnitude of these changes, but the basic pattern is the same. We are currently cloning the omega-3 and omega-6 desaturase genes, of the fatty acid biosynthetic pathway leading to linolenic acid. We used a PCR-based cloning method, with degenerate primers, to clone members of the omega-3 and omega-6 desaturase gene families. Gene family sizes will be determined by genomic Southern blot analysis. Full-length cDNA clones will be obtained by rapid amplification of cDNA ends (RACE). A genomic library, in lambda EMBL3, will be screened to obtain the full-length gene clones. Expression patterns of the desaturase genes in different tissues/organs, during cold acclimation, also will be investigated.

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GAILING, OLIVER\*, FRANK R. BLATTNER, AND KONRAD BACHMANN. Department of Taxonomy, Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Gatersleben, Germany—*Isolation of closely linked markers for the evolutionary reduction of inner microsporangia within the asteracean genus Microseris.*

The reduction of inner (adaxial) pollen sacs (microsporangia = MS) is a common derived character for the three asteracean species *Microseris bigelovii*, *M. pygmaea* and *M. elegans*. The genetic of this reduction was determined in the F6 inbred population of an interspecific cross between *M. douglasii* with 4 MS and *M. bigelovii* with 2 MS by the cosegregation with molecular markers (AFLPs). One major gene and four modifying genes could be mapped as quantitative trait loci (QTLs). Three of those modifying genes had only an effect on the homozygous recessive (2 MS) genotyp of the major gene. 2 MS were produced only if at least 5 alleles of those modifying genes determined the 2 MS phenotype. We isolated one plant with the heterozygous genotype of the major gene and the homozygous recessive 2 MS genotype in all the modifying genes. The 87 offspring of this plant showed a visible 3:1 segregation in normal fertile plants with 4 MS and small sterile plants with 2 MS in a more or less homozygous genetic background. Thus AFLP markers closely linked with the MS locus can be isolated. In order to test many markers in respect of their cosegregation with the MS locus, DNA bulks of 10 plants with the 2 MS phenotype and 10 plants with the 4 MS phenotype will be screened with about 1000 AFLP primer combinations. After having tested 444 Eco/ Mse primer combinations the MS locus could be mapped in an intervall of 4 Centimorgan between two flanking markers. Those markers will be transferred into codominant SCARs (Sequence Characterized Amplified Regions). Recombinants between those markers can be used to narrow the F7 population of about 2000 plants that segregate for the MS locus to about 160 plants for the fine mapping. With the isolation of markers closely linked to the MS gene (or the gene itself) we have the tools to explain the evolution of this diagnostic character in detail.

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LIU, XIANAN\*, AHMED BAHIELDIN, EL-SAYED HASSANEIN, MOHAMED EL-DO-MYATI, SHERIF EDRIS, AND WM. VANCE BAIRD. Horticulture Department, Clemson University, Clemson, SC 29634-0375; and Department of Genetics, Faculty of Science, Ain Shams University, Cairo, Egypt—*Identification and characterization of genes from sunflower (Helianthus annuus L.) that are regulated by drought or osmotic stress.*

Negative effects on the water status of plants is one of the most common and deleterious stresses experienced by wild and cultivated plants throughout the world. Sunflower is the second most important edible oil crop on a worldwide production basis. In the middle-east, insufficient water or irrigation of sunflower using salt-contaminated water from rivers or reservoirs is a major problem for field establishment and final crop production. Our project is designed to identify, clone and characterize gene sequences regulated in response to water stress (e.g., drought and/or salinity). We employed the differential-display reverse transcriptase polymerase chain reaction (DD-RT-PCR) methodology to accomplish our objectives. To date five drought-regulated and ten salinity-regulated gene sequences have been cloned. These represent genes that are either induced *de novo*, up-regulated or down-regulated in response to water stress, and preliminary evidence shows that individual transcripts may be present in all tissues/organs or expressed specifically in roots, shoots or leaves. Sequence analysis has tentatively identified genes for at least five clones: guanylate kinase (Cap1-U), an enzyme important in second messenger signaling pathways; selenium binding protein (Gap1-D), also implicated in ABA-response; activator-encoded transposase (Cap2-U), an essential factor for the mobility of Ac-like elements; polyprotein (RSG10-U), a retrotransposon-associated reverse transcriptase-like

sequence; and LytB (VC2-D), a pneumococcal murein hydrolase important in cell-division. Current efforts focus on acquiring full-length cDNA and genomic clones, identifying and characterizing their *cis*-acting regulatory elements and *trans*-acting factors, precisely defining expression patterns on a tissue and temporal basis, and determining the *in vivo* biochemical/physiological function of the proteins encoded by each gene clone.

- 190** WILLIAMS, JOSEPH H., JR.\*, WILLIAM E. FRIEDMAN, AND MICHAEL L. ARNOLD. 1, 3: Department of Genetics, University of Georgia, Athens, GA 30602; 2: Department of EPO Biology, University of Colorado, Boulder, CO 80309—*Interspecific pollen competition in a diploid-polyploid hybrid zone in birch (Betula)*.

Among flowering plants, females often have little control over the genetic relatedness of pollen deposited on stigmas. Yet embryo sacs in many such species are rarely approached by more than one pollen tube, regardless of the original pollen load size. Thus, post-pollination/pre-fertilization events are critical to mate choice and reproductive isolation. We studied early post-pollination barriers in *Betula papyrifera* ( $2n = 2x = 28$ ) and *B. occidentalis* ( $2n = 6x = 84$ ). These wind-pollinated species form a broad hybrid zone in the northern Great Plains/Rocky Mountains, USA. A 3-fold difference in DNA content of gamete nuclei between these two species allowed us to determine the paternity of individual pollen tubes growing within female reproductive tissues. We tracked their developmental fate in conspecific, heterospecific, and mixed-species crosses. This enabled us to quantify the contribution of both male x male interactions and male x female interactions to reproductive isolation in a natural population. We found no evidence for strong male x male interactions. Instead, strong early post-pollination barriers such as pollen tube incompatibility, slower pollen tube growth, and aberrant cell cycle progression of the generative cell revealed the presence of favorable or unfavorable male x female interactions. In mixed-species pollinations, such barriers resulted in almost complete conspecific siring bias, as determined by an allozyme-based paternity analysis. This result was not due to differential embryo abortion. Strong selection on interspecific male x female interactions will act to restrict variation for mate recognition traits in  $F_1$  hybrids, and thus can be an important determinant of later-generation processes such as introgression and hybrid speciation.

## VIII. Historical Section

### Symposium: Botany in the age of Mendel: A symposium in honor of the centennial of the rediscovery of Mendel, and the 50th year anniversary of the publication of G. L. Stebbins' *Variation and Evolution in Plants*

- 191** SMOCOVITIS, VASSILIKI BETTY. Dept. History, 4131 Turlington Hall, University of Florida, Gainesville, FL 32611—*Botany in the Age of Mendel: A Symposium in Honor of the Centennial of the Rediscovery of Mendel, and the 50th Year Anniversary of the Publication of G.L. Stebbins's Variation and Evolution in Plants*.

This symposium is devoted to an examination of the impact of the rediscovery of Mendel and the consequent relationship between the new science of genetics and botany. Papers in this session highlight the contributions of individuals like E.B. Babcock, G. Ledyard Stebbins and Barbara McClintock and explore the varied institutional settings for the new science in agricultural, horticultural, as well as academic environments. The session is organized in honor of the centennial year of the rediscovery of Mendel by three individuals Hugo de Vries, Carl Correns, and Eric Von Tschermak and in honor of fiftieth anniversary of the book that integrated genetics with a range of botanical sciences by G. Ledyard Stebbins titled *Variation and Evolution in Plants*.

- 192** JONES, DAVID A. Dept. Botany, PO Box 118526, 220 Bartram Hall, University of Florida, Gainesville, FL 32611-8526—*Plant Genetics at Rothamstead, Cambridge and the "John Innes," 1856-1960*.

In 1919, R.A. Fisher was hired to discover whether the accumulated records of some 70 years of agricultural research at Rothamstead would yield more information than had been possible in the absence of a qualified statistician. It never fails to impress biology students - and indeed statisticians - to learn, or be reminded, that

the Analysis of Variance, arguably the most powerful technique in statistical analysis, was invented by Fisher to analyze field experiments, some of which used different varieties of wheat, beans, clovers, grasses, and mangel wurzels. The new techniques were soon recognized to be of fundamental importance for determining the best designs for experiments in basic research and Fisher, himself, used them to lay the foundation of Biometrical Genetics. Similarly, much research on horticultural plants at the John Innes Horticultural Institution yielded fundamental genetical principles. Led by C.D. Darlington, mitosis and meiosis were sorted out; breeding work with cherries and primroses forced study of the gametophytic and sporophytic incompatibility systems; attempts to breed a yellow sweetpea were partly behind research on the genetics and chemistry of flower pigments, this last being pioneering work in chemotaxonomy and genecology. The 'John Innes' formulae for seeding and potting composts were invented to overcome the inconsistent germination of seeds and establishment of young plants. In 1944, Fisher returned to Cambridge determined to start the first undergraduate degree in Genetics in the UK. During his time there the system of tristylly in *Lythrum salicaria* was clarified both theoretically and by breeding work in Fisher's own garden; the Hfr mating type in *E. coli* was discovered (by L. L. Cavalli-Sforza) and the journal *Heredity* was founded by Fisher and Darlington - using their own money to launch it. In the Botany School, initially by D. G. Catcheside, the mating systems, mechanisms of recombination, gene conversion and biochemical genetics of fungi were being studied.

**193** KASS, LEE B. L.H. Bailey Hortorium, Cornell University, Ithaca, NY 14853 and Natural Sciences, Elmira College, Elmira, NY 14901—*Barbara McClintock, \*Botanist, Cytologist, Geneticist*.

"Botany in the Age of Mendel" suggests the importance of classifying biologists as Botanists or even Mendelians. Many researchers who considered themselves botanists, zoologists, or physiologists, would today be thought of as Geneticists. Barbara McClintock, who is currently identified as a geneticist, was starred in the research subject Botany, in her biographical sketch in the Biographical Dictionary, AMERICAN MEN OF SCIENCE, 1944. The subject, Botany, was one of twelve principle sciences of which the editors chose "men" whose work was supposed to be the most important. The star meant that the entrant was one of the leading students of science of the United States. The first professional organization McClintock is affiliated with is the Botanical Society of America. In 1944, McClintock was elected to the National Academy of Science's Section of Botany. Other notable members of the National Academy of Science, who might currently be considered Geneticists or Molecular Biologists, are A.F. Blakeslee, R.A. Brink, G.W. Beadle, R.E. Clausen, Max Delbruck, E.M. East, and L.J. Stadler, but all were elected to the Academy's Section of Botany. In 1957, McClintock received the Botanical Society of America's Merit Award for Distinguished Achievements in Contributions to Advancement of Botanical Sciences. I will describe McClintock's undergraduate and graduate education as a "Botanist." That preparation, so essential to an understanding of Mendelian heredity in plants, led to the achievements for which she was awarded the Nobel Prize in 1983. I will demonstrate McClintock's role as advisor and Instructor of Botany at Cornell University and as Assistant Professor of Botany at the University of Missouri.

**194** KIMMELMAN, BARBARA. School of General Studies, Philadelphia University (formerly Philadelphia College of Textiles and Science), Schoolhouse Lane and Henry Ave., Philadelphia, PA 19144—*"Playing Catch-Up? An Institutional Interpretation of Mendel's Two Receptions, 1865-1900"*.

Given that the fate of most scholarly productions at most times is to be ignored, a greater problem than Mendel's original "neglect" is why his work was ever resurrected. A classic explanation is that Mendel was "ahead of his time," and that during the next thirty-five years the scientific world "caught up" with him. This explanation has invoked chiefly the intellectual aspects of science; historians have pointed to the discoveries in cytology, development, and evolution that enabled scientists in 1900 to conceptually process Mendel's work. Having scrutinized the circumstances surrounding the rediscovery, I offer an alternative institutional version of the game of "catch-up." Mendel's recent biographers have stressed his rather unique training and background, which combined physics, evolution, and intracellular plant physiology with experience in agricultural breeding. Between 1865 and 1900, the number of both educational and research institutions dedicated to scientific agriculture dramatically expanded, in Europe and even more so in the United States. This produced a swelling profession of scientifically educated agricultural breeders, with a constellation of preparation and interests more similar to Mendel's than were those of his contemporaries who enjoyed state support and permanent academic structures available to support their work. I argue that it is the growth of such scientific agricultural institutions that accounts both for the rediscovery of Mendel's work and for its largely positive reception in 1900.

- 195** KLEINMAN, KIM J. c/o Archives, Missouri Botanical Garden, Box 299, St. Louis, MO 63166-0299—*Genetics at the Missouri Botanical Garden*.

The Missouri Botanical Garden provides an interesting case study for the introduction of Mendel's ideas in the first decades of the Twentieth Century. The Garden, then and now strives to three not always perfectly complementary goals: research, display, and education. Thus, in this period, it was the site of work in plant physiology, plant pathology, and taxonomy as well as plant breeding. The products of the horticultural research helped make the grounds a national attraction. And the Garden ran both the Henry Shaw School of Botany at Washington University and a School for Gardening that trained horticulturists and landscape architects. Interest in Mendel at the MBG ultimately culminated in Edgar Anderson becoming "Geneticist to the Garden" in 1922. This paper traces both the background to Anderson's appointment and his work in the 1920s.

- 196** SMOCOVITIS, VASSILIKI BETTY. Dept. History, 4131 Turlington Hall, University of Florida, Gainesville, FL 32611—*Plant Genetics after Mendel: E.B. Babcock, G. Ledyard Stebbins and the Genus Crepis*.

This paper explores the efforts of two Berkeley geneticists E. B. Babcock and G. Ledyard Stebbins to understand the genetic basis of evolutionary change in the complex plant genus, *Crepis*. The paper introduces us to an important research project that has been neglected by historians. Begun in the nineteen-teens, the project on the genetics and systematics of the genus *Crepis* (and its relatives) was meant to emulate the success of the *Drosophila* genetics research program that was orchestrated by Thomas Hunt Morgan at Columbia University and later at the California Institute of Technology. The project was in fact Babcock's dream of finding an easily tractable model organism that would integrate genetics with systematics, but that would also resolve some persistent problems in plant genetics that remained unexplained after Mendel. The paper traces the history of the articulation of the polyploid complex and ends with the publication of Babcock's *Genus Crepis* in 1947. The paper additionally locates Babcock and Stebbins in the agricultural context of the University of California, Berkeley, and Babcock's pioneering efforts to create one of the first departments of genetics in the United States.

## Contributed Papers

- 197** MCCOURT, RICHARD M.\*, EARLE E. SPAMER, ALFRED E. SCHUYLER, AND MER-EDITH A. LANE. Academy of Natural Sciences, Philadelphia, PA 19103—*Saving an American Treasure: Restoring the Herbarium of the Lewis and Clark Expedition*.

One of the remarkable results of the expedition of Meriwether Lewis and William Clark in 1803-1806 was their extensive collection of western North America's flora. The collections, mostly by Lewis, were the first extensive sampling of vegetation in the western territories newly acquired by the United States from France. Despite the loss of some specimens on the trail and subsequent to Lewis's return from the expedition, a large number of plant specimens were presented to President Thomas Jefferson, the scientific mentor of the expedition. Today, after nearly two centuries and a circuitous path through the hands of a number of botanists at institutions in the U.S. and England, the bulk of the collection (226 specimen sheets) resides in the Lewis and Clark Herbarium of the Academy of Natural Sciences in Philadelphia. More than a third of the Lewis and Clark herbarium is type material, which includes three state flowers (Montana, Idaho, and Oregon) and a state grass (Montana). With the bicentennial of the Lewis and Clark Expedition approaching in 2003-6, we have assessed restoration needs of the collection. The condition of the specimens varies widely, from fragmentary to nearly intact plants in excellent shape. Ongoing efforts include repairs to sheets and specimens, re-housing specimens in custom archival holders and cabinets, and upgrading environmental conditions in storage rooms. In response to growing public interest in the Lewis and Clark Herbarium, a database and a series of digitized images of specimens will be made available to scientists, students, and the general public via the internet and print publications, as well as museum display. This restoration project is funded by federal grant from the Save America's Treasures Program of the National Park Service and the Institute for Museum and Library Services, to be matched by funding from private donors.



## IX. Paleobotanical Section

### Contributed Papers

- 198** AXSMITH, BRIAN J.\*, MICHAEL KRINGS, AND THOMAS N. TAYLOR. Department of Biological Sciences, University of South Alabama, Mobile, AL 36688, Department of Ecology and Evolutionary Biology, and Natural History Museum and Biodiversity Research Center, University of Kansas, Lawrence, KS 66045—*A filmy fern from the Upper Triassic of North Carolina.*

A new assemblage of pteridophyte remains from the Upper Triassic Pekin Formation of North Carolina is believed to represent the earliest unequivocal Mesozoic record of the Hymenophyllaceae (filmy ferns). The collection includes numerous fronds and frond fragments, one of which is attached to a rhizome. Individual fronds were bipinnate, delicate, and up to 20 cm long. Pinnae are alternately arranged and widely positioned, giving the frond an open appearance. Pinnules are segmented with each segment characterized by one to several rounded to elongate lobes, each of which is vascularized by a single vein. Laminae are represented by inconspicuous, light brown stains on the matrix that may be suggestive of a membranaceous organization. Most of the lobes are fertile, and each bears a marginal sorus consisting of 5 - 8 sporangia radially or helically arranged on a short receptacle that is situated at the base of a shallow, funnel-shaped indusium. Sporangia appear to be attached by short, thick sporangial stalks, or may be sessile. Although this fossil lacks the deep tubular or bivalved indusium like those of the extant representatives of *Trichomanes* and *Hymenophyllum*, the soral morphology is similar to that of early developmental stages common to both indusial types. The new specimens are compared with other Mesozoic fossils attributed to the Hymenophyllaceae.

- 199** BORGARDT, SANDRA J.\*, KEVIN C. NIXON, AND WILLIAM L. CREPET. L. H. Bailey Hortorium, Cornell University, Ithaca, NY 14853—*A Turonian inflorescence bearing perigynous flowers of a lower rosid affinity.*

The outcrops of the Raritan Formation, of the Late Cretaceous in New Jersey (Turonian, ca. 90 mybp), have been particularly rich in charcoallified plant remains from diverse lineages, including ferns, conifers, Ericales, Magnoliales, Caryophyllaceae, Clusiaceae, Hamamelidaceae, and Triuridaceae. A new fossil taxon is represented by several fossils including part of an inflorescence. The flowers are small (1.8mm high by 1.5mm wide) and have half-inferior ovaries. Each ovary is composed of two basally fused carpels. There are two distinct stigmas, and dehiscence is biaxial apical. The flowers have ten stamens or staminodia in a single whorl. Based upon attachment scars, there appear to be five tepals in a single whorl arranged on the rim of the hypanthium. One flower has retained an incurved, clawed tepal. Pollen grains are small (ca. 10-15  $\mu$ m). They occur as clumps on the stigmas, carpels and "staminodes". Pollen is tricolpate with no apparent endoaperture and coarsely scabrate colpus membranes. Pollen morphology, ovary dehiscence pattern, carpel number, and the presence of a hypanthium suggest a lower rosid affinity (e.g., Hamamelidaceae, Cunoniaceae, Saxifragales).

- 200** COOPER, ERIN E.\* AND JEFFREY A. MYERS. Department of Earth and Physical Sciences, Western Oregon University, Monmouth, OR 97361—*Paleoclimate of the middle Eocene John Day Gulch Flora, central Oregon.*

Leaf physiognomic data from the 45-44 Ma John Day Gulch Flora, Clarno Formation, indicate that central Oregon experienced a frost-free, warm subtropical climate with high, non-seasonal rainfall during the middle Eocene. These data were used to test two hypotheses to explain climatic cooling trends during the middle Eocene. The traditional model (Wolfe, 1992), proposes that the John Day Gulch Flora grew during a late Eocene "Late Eocene Cool Interval", which was followed by a return to near-tropical conditions in the latest Eocene. An alternative hypothesis (Myers, 1996; Manchester et al, 1998) proposes that the John Day Gulch Flora a series middle to late Eocene cooling steps. Morphologic/anatomical (physiognomic) analysis of the leaves of extant woody dicot assemblages provides quantitative information about climate that can be applied to ancient leaf floras. Two leaf physiognomic approaches, Climate Leaf Analysis Multivariate Program - CLAMP (Wolfe, 1993) and Leaf Litter Analysis (Greenwood, 1992), were used to estimate the paleoclimate of the middle Eocene John Day Gulch Flora. The CLAMP method and the Leaf Litter Analysis yield essentially identical MAT estimates of 17.5°C and 17.8°C, respectively (+/- ~ 1°C), compared to the ~13°C CLAMP MAT estimated from the flora by Wolfe (1992). This leaf physiognomic MAT estimate, combined

with new age information, indicate that the John Day Gulch assemblage grew under climate conditions similar to estimates from other assemblages of the Clarno Flora, and refute the hypothesis that John Day Gulch assemblage grew during a late Eocene cool interval.

- 201** CROSS, AUREAL T.\* AND MYUNG SUK YI. Department of Geological Sciences, Michigan State University, East Lansing, MI 48824-1115 and Department of Geology, Yonsei University, 134 Shinchon-dong Seochemun-Gu, Seoul, 120-749, Korea—*K-T boundary hiatus, Wasatch Plateau environs, Utah, U.S.A.*

Stratigraphic distribution of palynomorphs in the Price Canyon and the Wasatch-Gunnison Plateau region, central Utah are reviewed. Three floristic assemblages have been documented, indicating a late Campanian, Maastrichtian, and Lower and Upper Paleocene age for the stratigraphic units in the Price Canyon section. A hiatus (erosional or non-depositional) of several million years duration separates mid-Maastrichtian from early to middle Paleocene strata. Similar gaps in mammalian and reptilian faunas in successive strata of the Wasatch and Gunnison Plateau regions are in accord with the stratigraphic breaks in the palynological record. During early Price River-early North Horn Formation time, palynological data demonstrate the presence of coastal margin, fluvial plain, and braid plain sedimentary environments. Inland lake sedimentation, alternating with broad floodplain environments, indicate interrupted stream-floodplain deposition during early middle Paleocene. Later Paleocene and early Eocene environments were characterized by expanded lake and playa deposition. Stratigraphic deposition of vertebrate fossils in similar strata in the Wasatch and Gunnison Plateau areas, including titanosaurid, ceratopsian, and tyrannosaurid dinosaurs, lizards, crocodilians, and turtles, are present in the lower and middle portions of the North Horn Formation. Above this, mammalian faunas characterize North Horn strata up to about 90 m below the contact with the Flagstaff Limestone Formation. The earliest Paleocene strata are characterized by condylarth-dominated faunal assemblages.

- 202** DILCHER, DAVID L.\*, ANA FLORA MANDARIM-DE-LACERDA, ALCINA M.F. BARRETO, AND MARY E.C. BERNARDES-DE-OLIVEIRA. Florida Museum of Natural History, University of Florida, Gainesville, FL 32611-7800; Departamento de Biologia Animal e Vegetal, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil, 20550-900; Departamento de Geologia, Universidade Federal de Pernambuco, Recife, PE, Brazil, 05422-970—*Selected fossils from the Santana Formation, Chapada do Araripe, Brazil.*

Collections from Universidade de São Paulo (USP), Universidade Federal de Pernambuco (UFPE), Universidade Guarulhos (UnG) and Universidade Rural do Cariri (URCA) have been examined to provide a survey of the nature of the plants preserved in the lithographic limestone of the Crato Member of the Santana Formation. The Crato Member is basal in the Santana Formation and considered to be middle Aptian in age. The depositional environment is considered to be lacustrine preserving numerous well-known invertebrates, vertebrates and ichnofossils associated with palynomorphs and megafossils. The diversity of megafossil plant remains includes several different types of plants, many of which are also found as palynomorphs in the sediment. Some small herbaceous appearing plants have roots and stems with leaves attached similar to some species of *Schizoneura*. *Isoetes*-like clusters of sporophylls and leaves are associated with a small stem and a unique vegetative fern axis with doubly compound leaves are present. One small trilobed conifer scale occurs in these sediments. More common fossils are the Gnetales such as *Ephedra*-like stems, some bearing leaves and some bearing bracts enclosing seeds, as well as various types of isolated leaves. The other common gnetalian fossils are *Welwitschia*-like winged seeds, seedlings bearing two seed-leaves and isolated young leaves. Four angiosperm leaf types are represented by one leaf each and each one having a distinct form and venation. An angiosperm follicle, several winged fruits and a cluster of three large petals are also present.

- 203** DOYLE, JAMES A. Section of Evolution and Ecology, University of California, Davis, CA 95616—*Congruence of molecular phylogenies and the Early Cretaceous angiosperm record.*

Although molecular phylogenetic analyses refute morphological cladistic inferences that angiosperms are related to Gnetales and leave angiosperm outgroup relationships as unclear as ever, they provide increasingly strong evidence on rooting of the angiosperms, with *Amborella*, Nymphaeales, and a clade including Illiciaceae, Trimeniaceae, and *Austrobaileya* as the first three branches of the angiosperm tree, possibly followed by Chloranthaceae. These results suggest that previously reported similarities between pre-Albian angiosperms and these taxa are more significant than originally recognized, whether as confirmation of molecular results or as evidence that the Early Cretaceous radiation may be close to the origin of crown-group angiosperms. Similarities between Aptian leaves and the presumed basal lines include chloranthoid teeth and variable

stomata, as noted by Upchurch. According to molecular phylogenies, the first angiosperms had columellar exine structure, and a reticulate tectum arose soon after, whereas the supposedly primitive granular and “atectate” exines of Magnoliales are derived. This is further evidence against the homology of granular exine structure in Bennettitales, Gnetales, and angiosperms. Thus the reticulate-columellar monosulcates that dominate Hauterivian, Barremian, and Aptian angiosperm pollen floras need not have been preceded by long phase with granular monosulcates. Hauterivian verrucate monosulcates described by Hughes as “CACTI-SULC”, which resemble pollen of *Amborella*, could represent the pre-reticulate stage. Molecular trees imply that ascidiate rather than plicate carpels are ancestral, and exotestal seeds are common in the basal lines; this is consistent with the abundance of such carpels and seeds in the oldest Cretaceous mesofloras described by Friis and others. Groups appearing in the Albian belong to more deeply nested “magnoliid” clades and the first few lines of eudicots in molecular phylogenies (Ranunculales, Nelumbonaceae, Platanaceae, Buxales).

## 204

DUNN, MICHAEL T. Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701—*A new species of Pachytosta from the Upper Pennsylvanian Finis Shale of Texas.*

As part of an ongoing study of Late Paleozoic terrestrial plants preserved in marine environments, a number of specimens of permineralized ovules of medullosan seedferns have been discovered in the Virgilian (Gzhelian), Finis Shale near Jacksboro, Texas. Age assessment of the strata is based on ammonoid biostratigraphy. Twenty of these specimens are exceptionally well preserved by limonite and pyrite permineralization. These specimens have been analyzed from wafers and cellulose acetate peels, to provide detailed information about external form, as well as internal cellular anatomy. Analysis of the ovules suggests that they represent a new species of *Pachytosta*. The specimens conform to *Pachytosta* in the presence of three angled symmetry of the integument with three secondary ribs, and a stalked nucellus free from the integument except at the base; a single vascular strand enters the base of the ovule, and subsequently branches into discrete bundles in the nucellus. As in all species of *Pachytosta*, this species has a three layered integument consisting of an innermost endotesta, a middle sclerotesta, and an outermost sarcotesta. Unlike previous reports of *Pachytosta*, in this species, the sarcotesta forms six approximately isomorphic exterior longitudinal lobes that usually extend from the micropylar end to the chalaza. Cells of the sarcotesta are homogenous, elongated, radially aligned, and form a single layer. Unexpectedly, the integument is apparently un-vascularized. This new species expands the range of variation within *Pachytosta*. In addition, these specimens from strata dated by marine biostratigraphy, represent the youngest known occurrence of this genus and thereby extend the known biostratigraphic range of *Pachytosta*.

## 205

ERWIN, DIANE M.\* AND HOWARD E. SCHORN. Museum of Paleontology, University of California, Berkeley, CA 94720-4780—*Floristic revision of the Eocene Thunder Mountain megaf flora of Idaho.*

The middle Eocene (46-45 Ma) Thunder Mountain flora of central Idaho represents a rare, well-dated upland mixed conifer forest from North America. As such, it has some of the earliest occurrences and associations of Tertiary conifers and angiosperms in the US western interior. Despite being newly published, the Thunder Mountain flora contains numerous misidentifications, taxonomic and nomenclatural problems that continue to misrepresent and obscure the fossil record of many taxa. Preserved as compression/impressions the fossils are from two sites: the upper Road Locality (lacustrine shale) and the stratigraphically lower Dewey Mine site (carbonized stream-borne debris in coarse to finer-grained sandstone). Study shows the type of *Larix leonardii* is a more likely a spruce, two axes identified as *L. leonardii* are fern rhizomes, and the new species *Pinus baileyi*, *Abies deweyensis*, and *Chamaecyparis edwardsii* are fragmentary and at best identifiable to genus. *Potamogeton* is an insect wing, the Dewey Mine *Populus* is five overlapping conifer needles, *Mahonia deweyensis* is indistinguishable from specimens referred to *M. reticulata* and *M. simplex*, and *Salix* shows no natural margin with venation too poorly preserved to describe. *Spiraea idahoensis* at Dewey Mine has a toothed margin in the distal half of the leaf, the lower half entire, yet the margin of the holotype of *S. idahoensis* is fully toothed. *Typha* is a piece of bark and the *Nymphaeites* root scar is an iron-stained sedimentary structure. The megafossil occurrences of *Pseudotsuga* and *Cephalotaxus* are equivocal. Although *Thuja* is not present in the Thunder Mountain megaf flora, there is a new undescribed cupressoid plant that morphologically resembles the southern hemisphere *Libocedrus* in the Road florule. We present these and other taxonomic changes that more accurately reflect the floristic composition of the Thunder Mountain flora, stressing accurate identifications are critical for understanding the evolutionary and biogeographic histories of taxa.

- 206**      FIELDS, PATRICK F.\* AND RALPH E. TAGGART. Department of Botany and Plant Pathology, Michigan State University, East Lansing, MI 48824-1312—*Neogene western North American Nelumbo, Nuphar, and Nymphaea megafossils.*

Neogene megafossil floras of western North America occasionally include remains of leaves, petioles, rhizomes, and roots of Water Lily and Water Lily-like plants. Most of this material has been assigned to the form genus "*Nymphaeites*". Recent systematic revisions of numerous fossil assemblages has led to a better understanding of leaf and rhizome morphology, and suggests that much of this material can be reliably assigned to extant genera in the Nymphaeales. As revised, specimens are more properly referable to: *Nelumbo*, *Nuphar*, or *Nymphaea*. *Nelumbo* is known from nearly complete remains in Reynolds Basin, Id. and as rhizomes in the Stinking Water, Or. flora. It is distinguished by rhizomes with swollen root-bearing nodes, and large centrally peltate (peltate central), orbicular leaves. *Nuphar* is known from leaves in Trout Creek, Or. and possibly from Eastgate, Nv. It is distinguished by bi-convex leaf scars on the rhizome, and deeply cordate, ovate to oblong leaves with a prominent midrib and pinnate venation. While *Nymphaea* is known from leaves and rhizomes from Sonoma, Ca., Trapper Creek and Weiser, Id., Buffalo Canyon, Eastgate, Esmeralda, and Middlegate, Nv., Mascall, Stinking Water, Succor Creek, and Trout Creek, Or. It is distinguished by oval leaf scars along the rhizomes and cordate or off-centered peltate (peltate eccentric), orbicular to ovate leaves, with a faint midrib and weakly pinnate to radial venation. Further, pollen assignable to the Nymphaeaceae is known from Reynolds Basin, Id. and Succor Creek, Or.

- 207**      HERMSEN, ELIZABETH J.\*, WILLIAM L. CREPET, AND KEVIN C. NIXON. L.H. Bailey Hortorium, Cornell University, Ithaca, NY 14853—*A new fossil saxifragoid from the Upper Cretaceous of New Jersey.*

A new fossil flower from the Old Crossman Clay Pit locality of the Raritan Formation (Upper Cretaceous, Turonian, ~90 million years BP), Sayreville, New Jersey, is described from charcoaled, three-dimensionally preserved specimens. The flower is minute in size, perfect, and pentamerous except for the gynoecium, which is composed of only two carpels. The sepals are triangular in shape and basally connate forming a hypanthium; trichomes occur on both surfaces of the sepals. Three overlapping petals preserved in one specimen and petal scars present in others indicate that the corolla is composed of five petals with imbricate aestivation. The androecium is composed of five staminodes or stamens with relatively long, ribbonlike filaments; anthers are currently unknown. The bicarpellate ovary is either semi-inferior or inferior with two locules and axile placentation. Although there are two free styles, the stigmas are fused forming a single stigmatic platform. A swollen ring located on top of the ovary and surrounding the base of the styles is interpreted as a nectary disk. Based on the pentamerous flower plan with bicarpellate gynoecium, inferior or semi-inferior ovary position, and especially the presence of free styles with fused stigmas, this fossil has affinities with the modern genus *Itea*, typically placed within the Saxifragaceae *sensu lato*.

- 208**      HERNANDEZ-CASTILLO, GENARO RODRIGO. Department of Environmental and Plant Biology, Ohio University, Athens, OH, 45701—*Use of multivariate analysis in reconstructing fossil conifers.*

The fossil record of conifers is characterized by fragmentary remains of simple organs with cryptic characters. There is also a wide range of variation from branch to branch on the same plant. Therefore, meaningful species delimitation is extremely difficult for many fossil conifers, particularly Paleozoic conifers. Different authorities often assign the same specimen to different species, and the same authority may assign the same specimen to different species at different times. A large number of Upper Pennsylvanian conifer specimens from the 7-11 mine in Columbiana, Co., Ohio are preserved by a combination of coalified compression and pyrite permineralization. These specimens display features of external morphology, cuticular characters and internal anatomy, and can all be assigned to a single species with a high degree of confidence. The confident recognition of this single species allows us to record ranges of variation for a large number of characters, and to recognize differences that result from variables such as ontogeny, taphonomy, and/or different positions on the plant. Several multivariate methods have been employed to interpret similarities and differences resulting from each of these variables. Principal Component Analysis (PCA), Discriminant Function Analysis (DFA), and Cluster Analysis (CA) have been used to compare the features of different specimens. Individual specimens are best characterized by leaf length and width, angle of divergence, and diameter of vegetative shoots. Differences in these characters are correlated with shoot length and diameter. Angles of divergence in leaves seem to be a consistent feature among all the specimens. Such characters may explain differences among fossil conifer specimens due to biological or taphonomic variables, and they may be valuable for reliably distinguishing among species.



- 209** KLAUVINS, SHARON D. Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66045—*Anatomically preserved gymnosperms from the Late Devonian of Ireland.*

Within the last forty years, understanding of the early radiation of the gymnosperms has been greatly augmented by the description of numerous gymnospermous reproductive structures from the Late Devonian and Early Carboniferous. While a great deal of data have been amassed from anatomically preserved specimens from the Early Carboniferous, most specimens identified from Late Devonian sediments have been based on compression fossils. A suite of disarticulated gymnospermous specimens has been recovered from Late Devonian (latest Famennian) sediments from Hook Head, County Wexford, Ireland. Three different types of ovules, a pollen organ, and vegetative axes are anatomically preserved in pyrite and fusain. Two of the ovules have not been previously described and the third represents a new report of *Hydrasperma* Long. The two new ovules are radially symmetrical with four integumentary lobes. Both types of ovules display hydrasperman reproduction. The larger of the two ovules possesses an integument composed of three distinct layers, a feature not previously described for Devonian gymnosperms. The pollen organ is comprised of a cluster of four microsporangia, the organization of which is consistent with lyginopterid pteridosperms. Scanning electron micrographs of the vegetative axes show tracheid wall thickening patterns, which include scalariform-bordered pits, circular-bordered pits, and crowded pitting. These new ovules increase the total number of anatomically preserved ovules from the Devonian to five and the total number of ovules known from the Devonian to thirteen. The known diversity of gymnosperms in the latest Famennian suggests that future efforts in understanding the origin of this group should focus on Frasnian or even Givetian sediments.

- 210** LEOPOLD, ESTELLA B. Botany Department, University of Washington, Seattle WA 98195—*How well do pollen corroborate Eocene leaf taxa?—Florissant Formation, Colorado, a case study.*

The Florissant Fossil Beds National Monument, Colorado, provides a diverse record of megafossil taxa. Some 110-112 species of vascular plants described by Harry D. MacGinitie and studied by Steven Manchester are based on close botanical scrutiny in search of nearest living relatives. A pollen and spore study of the sediments attempted to check modern pollen for affinity with all these identifications on the generic and family level to determine if fossil microspores matching these leaf identifications can be found. Twenty of the 38 families of vascular plants identified from fossil leaves are corroborated by pollen and spores. Of the 84 genera, some 26 have been found in the microfossil record. The 23 genera that microfossil evidence adds to the flora include several new families not previously identified at Florissant: among these are Selaginellaceae, Schizaeaceae, Elaeagnaceae, Rhoipteleaceae, Ericaceae, Onagraceae, Chenopodiaceae, Eucommiaceae. Further, a member of the Fremontodendreae has verified the family Sterculiaceae. Three new conifer taxa of the Pinaceae are added to the flora (*Tsuga*, an extinct *Cedrus* type and *Pseudotsuga/Larix*). A strong bias in favor of wind-pollinated plant types is apparent: For example, we can identify affinities with about 3/4 of the wind-pollinated genera with matching pollen or spores, but only 1/3 of the genera that are known to be insect-pollinated types producing low to medium amounts of pollen. The pollen assemblage strengthens the impression that the flora is of warm temperate to sub-tropical in aspect, reminiscent of the summer-moist vegetation of Tamulipas, and Monterrey, in northeastern Mexico.

- 211** LITTLE, STEFAN A.\* AND RUTH A. STOCKEY. Department of Biological Sciences, University of Alberta Edmonton, AB T6G 2E5 Canada—*Reconstructing aquatic angiosperms from the Middle Eocene Princeton chert: Decodon allenbyensis.*

Aquatic Lythraceae remains were first recognized in the Princeton chert by Cevallos-Ferriz and Stockey in 1988 with the description of fruits and seeds of *Decodon allenbyensis*. Recently large numbers of roots, stems and leaves have been identified along with the fruit and seed remains from layer #43 in the chert. Fossils come from the Allenby Formation (Middle Eocene) near Princeton, BC. Specimens of the vegetative remains thought to belong to *D. allenbyensis* were studied using the cellulose acetate peel technique in an attempt to reconstruct the whole plant. Roots and stems show diffuse porous wood with vessels that are solitary or in radial multiples of two to five with numerous tyloses. Heterogenous rays vary from one to at least five cells wide. Secondary phloem with clusters of thick-walled fibers is preserved in some axes. Most of the roots and some stems show distinctive concentric layers of thin walled lacunate phellem, characteristic of submerged aquatics. Tissue of this type has been described in *Ammannia* L., *Lythrum* L. and *Decodon verticillatus* L. (Ell.) of Lythraceae. Leaves, roots, stems, seeds and inflorescence axes of *D. verticillatus* have been studied using paraffin techniques and scanning electron microscopy and were closely compared

to these remains in the chert. Anatomy of *D. allenbyensis* suggests that these plants were growing under submerged conditions with fluctuating water levels at the edge of a shallow water system.

- 212** LIU, ZHAO HUA\*, GENE MAPES, AND GAR W. ROTHWELL. Department of Environmental and Plant Biology, Ohio University, Athens OH 45701, U.S.A.—*Taxonomic diversity among Late Pennsylvanian conifers at Hamilton, Kansas.*

The Late Pennsylvanian flora at Hamilton, KS has yielded approximately three thousand conifer specimens including leafy shoots, pollen cones, ovulate cones, ovules and seeds, and decorticated stems that show a wide range of variation in structural features and preservational modes. These specimens display characters of external morphology, internal anatomy and cuticular detail, and are interconnected in various combinations of organs that provide a large number of characters for formulating and testing hypotheses of taxonomic diversity. These include the morphological and cuticular characters used in classical fossil conifer studies, as well as new information on anatomical and developmental variation, and reproductive biology. Based on our analyses of vegetative shoots, pollen cones, pollen, ovulate cones and ovules/seeds we have identified intergrading combinations of characters for individual organs. When the characters of organs that are in organic attachment are included, these combined analyses allow us to test our hypotheses of taxonomic diversity using multivariate techniques and cladistic methodologies.

- 213** MANCHESTER, STEVEN R. Paleobotany Laboratory, Florida Museum of Natural History, Gainesville FL 32611-7800—*Leaves and fruits of Aesculus antiquorum (Newberry) Iljinskaya (Sapindales) from the Paleocene of North America.*

*Aesculus* has been reported previously from Tertiary deposits of the Northern Hemisphere based on isolated leaflet impressions, but corroborative data from complete, palmately compound leaves and from reproductive organs has been scarce. It is now possible to confirm this genus in the Paleocene of North America based on combined evidence from complete leaves, fruits and seeds. Fossil leaflets from the Paleocene of North Dakota, Montana and Wyoming that were previously assigned to the Juglandaceae as *Carya antiquorum* Newberry were transferred to *Aesculus* by Iljinskaya in 1968 based on her assessment of fossil leaflets described and illustrated in the literature. However, this transfer was largely overlooked by North American workers. Recently discovered complete, palmately compound leaves and associated trivalved fruits from the Fort Union Formation of North Dakota and Wyoming confirm that the fossils represent *Aesculus*. Each leaf has a long petiole with an expanded base and bears three to five obovate, sessile leaflets with finely serrate margins. Fruits are preserved as three-dimensional impressions in siltstone in association with these leaves at three localities: Little Bitter Creek and Rock Springs, Wyoming, and Trenton Hill, North Dakota. The fruits are trivalved, globular loculicidal capsules with spiny ornamentation. Globular seeds sometimes remain attached to the valves. Silicified seeds found with the leaves at Almont, North Dakota, correspond in seedcoat anatomy to extant *Aesculus*. The spiny ornamentation on the fruit valves matches that of *A. glabra* (eastern North America) and *A. hippocastanum* (eastern Europe); all other extant species are smooth or verrucate. The fossil species differs from extant Asian species by its spiny fruits, and its sessile, somewhat asymmetrical leaflets. These fossils indicate that the extant genus was already established by the late Paleocene in North America, complementing foliage remains from the Paleogene of Spitsbergen and Kamchatka and predating the Oligocene occurrences from mainland Europe.

- 214** MAPES, GENE\*, KEQIN SUN, MICHAEL KRINGS, GAR W. ROTHWELL, AND ROYAL H. MAPES. Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, U.S.A.; China University of Geosciences, Beijing 100083, China; Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence KS 66045, U.S.A.; Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, U.S.A.; Department of Geological Sciences, Ohio University, Athens, OH 45701, U.S.A.—*The earliest occurrence of Medullosa.*

The medullosan pteridosperms are a common group of early seed plants that extend from the Lower Carboniferous to the Permian of North America and Europe. The earliest occurrence of the genus *Medullosa* is from the Mississippian Fayetteville and Imo Formations of Arkansas, which are equivalent to the uppermost Lower Carboniferous (Namurian A) in Europe. Four specimens of permineralized stems with diverging leaf traces have been discovered, and these represent a previously undescribed species with features that are characteristic of vine-like growth architecture. Specimens range up to 40 cm long and 2-3 cm in diameter. The number of vascular segments ranges from two to eight, with relatively equal development of centripetal and centrifugal secondary xylem. In cross sections the vascular segments vary from circular to oval to

tangentially elongated, as they anastomose from level to level. The stelar zone is surrounded by a thin zone of periderm and primary cortex. Cross sections reveal that the primary cortex is subdivided into leaf bases in differing stages of divergence, and this indicates helical phyllotaxis. Within the cortex, vascular bundles, resin canals and sclerenchyma form the typical *Myeloxylon* histological configuration for species of *Medullosa*. Leaf traces to a single frond are produced over an extended vertical distance along the stem, and are relatively large at the level of separation from the stele. Traces subdivide further in the leaf base. In cross sections of the stem, traces from each protoxylem sympodium consistently diverge in two directions at the same level. This produces two emission areas in each cylinder of secondary vascular tissues. These stems represent the earliest occurrence of the genus *Medullosa*, and are stratigraphically equivalent to the earliest records of the family Medullosaceae.

- 215** MCMANUS, H. A.\*, E. L. TAYLOR, T. N. TAYLOR, AND L. D. BOUCHER. Department of Ecology and Evolutionary Biology and Natural History Museum-Biodiversity Center, University of Kansas, Lawrence, KS 66045; Department of Biology, University of Nebraska-Omaha, Omaha, NE 68182—*An Enigmatic Axis from the Triassic of Antarctica*.

An axis with a complex vascular system is detailed from Middle Triassic silicified peat of the Fremouw Formation of Antarctica. The diameters of the four specimens identified range from 1.2 to 2.2 cm; the longest specimen is approximately 12 cm. In transverse section, the vascular system of the silicified axis is divided into approximately 10 to 16 arms, which extend almost to its periphery. The vascular segments are embedded in parenchyma and occur as single traces or as segments connected in the center of the axis. These segments anastomose at varying levels within the axis. Ground tissue is located in the center of each segmented arm and consists of parenchyma and small diameter tracheids which are presumed to represent primary xylem. Secondary xylem borders this central ground tissue and extends completely around the segmented arms. A cambial zone is located external to the secondary xylem with poorly preserved secondary phloem to the outside. Traces are given off by the segments near the periphery of the axis; these consist of radially arranged secondary xylem, some with apparent external periderm. The anatomy of this axis most closely resembles the vascular tissue arrangement of plants belonging to the Cladoxylales (Devonian-Lower Carboniferous), but the anatomical differences, in addition to the stratigraphic age, preclude formal assignment to this or other orders.

- 216** MITRA, MADHUMI AND JAMES E. MICKLE.\* Department of Natural Sciences, University of Maryland Eastern Shore, Princess Anne, Md 21853, Department of Botany, North Carolina State University, Raleigh, NC 27695—*Aquilapollenites in the early Campanian of eastern North America*.

The Late Cretaceous period witnessed the rapid radiation of angiosperms along with the development of microfloral provinces namely Normapolles in eastern North America and Europe and *Aquilapollenites* in western North America and Asia. The Tar Heel Formation of the Black Creek Group has been assigned an Early Campanian age based on invertebrate faunal and palynological data. Samples from Goldsboro and Tar River localities of the Tar Heel beds showed the abundant occurrence of two western *Aquilapollenites* species in addition to diverse Normapolles grains. Based on these earlier studies, it was unclear whether the occurrence of grains of this western element at the Goldsboro and Tar River localities was due to *Aquilapollenites*-producing plants being present or to long distance dispersal. To resolve the controversy of occurrence of *Aquilapollenites* in the east, this study was expanded to other localities of the Tar Heel Formation including those that yielded *Aquilapollenites*. A total of 103 samples from Elizabethtown, Goldsboro, Ivanhoe, Lock, Tar River and Willis Creek localities of the Tar Heel Formation were investigated for palynomorphs. Most of these samples yielded rich assemblage of Normapolles grains. Species of *Basopollis*, *Complexiopollis*, *Labrapollis*, *Plicapollis*, *Pseudoplicapollis*, *Trudopollis*, and tetraporate Normapolles were reported from all the localities. Samples from the other localities did not yield *Aquilapollenites* grains. The lack of grains at the other localities and in additional samples from the original localities in this study suggests that occurrence of *Aquilapollenites* grains is more likely to be due to long distance dispersal of the western element during the Campanian.

- 217** MYERS, JEFFREY A. Department of Earth and Physical Sciences, Western Oregon University, Monmouth, OR 97361—*Unique vegetation from the Eocene Cordilleran uplands*.

The ~38-35 Ma Cedarville Flora, NE California, is a unique leaf-dominated impression flora intermediate between "Boreotropical" Paleogene vegetation and Metasequoia-dominated "Arctotertiary" vegetation of the early Oligocene Northwest. The assemblage grew at ~1000 m paleoelevation on the seaward slope of

the Paleogene Cordillera, in biogeographic connection with both upland interior and lowland coastal vegetational sources. Cedarville evergreen broadleaved taxa (eg. Annonaceae, Magnolia, Meliosma, Quercus, Schizandra) while not diverse, closely resemble species from Eocene Oak-Laurel vegetation of the Northwest lowlands. Deciduous broadleaved taxa (eg. Alnus, Cedrelospermum, Cercidiphyllum, Decodon, Parrotia, Plafkeria, Platanus exaspera, Pterocarya, Ulmus) are conspecific with or similar to taxa from the latest Eocene Florissant Flora, Colorado, and Oligocene Bridge Creek Flora, central Oregon. With the exception of Rosaceae (seven species) however, diverse "Arctotertiary" lineages that distinguish Bridge Creek-type assemblages (eg. Aceraceae, Betulaceae, Tiliaceae, etc.) are absent or represented by one species in the Cedarville Flora. At Cedarville, the combination of moderate elevation and maritime climate (cool summers, moderate winters, and copious, non-seasonal precipitation) permitted the intergradation of "Boreotropical" lineages from lowland coastal vegetation and "Arctotertiary" lineages from the interior Cordillera. The Cedarville Flora documents both the early westward migration of seasonally-adapted microthermal lineages, and the adaptation of megathermal "Boreotropical" lineages to increasingly cool and seasonal climate.

- 218** NAGALINGUM, NATHALIE S\*, ANDREW N DRINNAN, STEPHEN MCLOUGHLIN, AND RICHARD LUPIA. School of Botany, The University of Melbourne, Parkville, Victoria, Australia, 3052; School of Geology and Geophysics, University of Oklahoma, Norman, OK, USA 73072—*Patterns of pteridophyte evolution and diversification in the Cretaceous of southern Gondwana.*

Palynological data provide an informative record of pteridophyte history because spores are sampled from habitats beyond the immediate area of deposition. This data complements macrofossil data about local fluvial and lacustrine taxa. Palynological data is recorded as dispersed spores and pollen in numerous Cretaceous studies of Australian and Antarctic sediments, bore cores and wells. Once compiled into a database these records can potentially form a large and comprehensive data set for examining patterns of pteridophyte biogeography and evolution during the Cretaceous. The Cretaceous North American palynofloras exhibit a decline in abundance and diversity of ferns that coincides with the evolution and later overwhelming floristic dominance of angiosperms. However, patterns of fern evolution have yet to be investigated for the Southern Hemisphere continents of Gondwana. We present the results of the analysis of Australian and Antarctic palynomorphs from over 100 references showing changes in fern abundance, diversity and distribution.

- 219** OTTO, ANGELIKA\*, WILLIAM C. REMBER, AND BERND R. T. SIMONEIT. 1,3 College of Oceanic and Atmospheric Sciences, Oregon State University, Corvallis, OR 97331; 2 College of Mines and Earth Resources, University of Idaho, Moscow, ID 83444—*Chemical characteristics of five fossil conifer species from the Miocene Clarkia Flora, Emerald Creek, Idaho, USA.*

The excellent preservation of plant macrofossils of the Miocene Clarkia flora, Emerald Creek, Idaho, USA, allowed the analysis of the extractable chemical compounds of five fossil conifer species. Foliar branches and cones of *Cunninghamia chaneyi*, *Glyptostrobus oregonensis* and *Taxodium dubium* (Taxodiaceae) and foliar branches of *Metasequoia occidentalis* (Taxodiaceae) and *Calocedrus* sp. (Cupressaceae) have been extracted with organic solvents, and the extracts have been analyzed as is and derivatized using gas chromatography-mass spectrometry. Generally, the extracts from foliar branches and cones of the same species showed similar extract patterns while the extracts from different species yielded different extract compositions. Several sesqui- and diterpenoids that probably originate from the resins have been identified. Most of the terpenoids have been degraded during diagenesis, but some compounds have been preserved unaltered. An aliphatic alcohol, n-nonacosan-10-ol, that occurs in the waxes of extant conifers was present in the foliage of all investigated fossil conifers. Furthermore, all conifer species contained the diterpenoids ferruginol and 6,7-dihydroferruginol which are known from extant species of Cupressaceae, Taxodiaceae and Podocarpaceae. The fossil conifer species showed characteristic diterpenoid patterns which in part match the compounds that have been found in related extant species. In *Taxodium dubium* some terpenoids (sugiol, ferruginol methylether, isochamaecydine) have been identified which also occur in extant *T. distichum*. *Glyptostrobus oregonensis* contains terpenoids similar to *Taxodium dubium*, but lacks ferruginol methylether. *Cunninghamia chaneyi* is characterized by two diterpenoids (hinokiol, hinokione) that have also been identified in the extracts of extant *C. lanceolata*. Specific terpenoids have not been observed in the foliar branches of *Metasequoia occidentalis*. Extracts of *Calocedrus* sp. (Cupressaceae) contain totarol which is known from numerous extant species of Cupressaceae and Podocarpaceae, but has been described only from one species of the Taxodiaceae (*Cryptomeria*).



- 220** PIGG, KATHLEEN B.\* AND MARIA TCHEREPOVA. Department of Plant Biology, Arizona State University, Box 871601, Tempe, AZ 85287-1601—*Taxonomic, phytogeographic and ecological significance of the Yakima Canyon flora (middle Miocene, Washington state, USA).*

The middle Miocene Yakima Canyon flora (15.6 Ma) of central Washington state is one of the few Neogene fossil localities with anatomically preserved seed, fruit and vegetative remains. The detailed morphological and anatomical features preserved in these fossils have allowed us to recognize plants at several infrageneric levels, including section, subsection and extant species. Phytogeographic relationships and ecological associations can also be resolved to varying degrees. The presence of *Woodwardia virginica* (Blechnaceae), essentially identical to the modern Virginia chain fern of eastern North America, illustrates species longevity, well-known among homosporous ferns. Its occurrence with *Osmunda wehrlii* (subgenus *Osmunda*) and a small onocleoid fern demonstrates that fern community associations in the Miocene were quite similar to those today. *Quercus hiholensis* is assignable to subgenus *Quercus*, section *Quercus*, and represents a white oak with developmental features that suggest annual fruit maturation, a highly derived feature within the genus, was established by the Miocene. Petrified *Liquidambar* infructescences showing features of section *Liquidambar*, provide the first evidence of fruit anatomy for this genus that today has a highly disjunct Asian-North American distribution. Conifers present include abundant taxodiaceous remains and *Pinus foisyi* (subgenus *Pinus*, section *Pinus*, subsection *Oocarpae*), which is most similar to modern California closed cone pines based on leaf and ovulate cone anatomy. In addition to other typical Miocene floristic elements such as Vitaceae, Cornaceae, and Rosaceae, the Yakima flora contains several fruits and seeds (cf. Rhamnaceae, Zygophyllaceae and Lythraceae) that probably represent extinct genera. The Yakima Canyon flora thus documents anatomy for plants of the widespread temperate flora of the middle Miocene during its maximum geographical distribution.

- 221** PIGG, KATHLEEN B.\* AND WESLEY C. WEHR. Department of Plant Biology, Arizona State University, Box 871601, Tempe, AZ 85287-1601; Burke Museum of Natural History and Culture, University of Washington, Seattle, WA 98195—*Trochodendron (Trochodendraceae) from the early middle Eocene Republic Flora, Washington, USA.*

*Trochodendron* (Trochodendraceae) is documented from the early middle Eocene (49-50 Ma) Republic flora of Washington state, USA, based on distinctive leaves, an inflorescence and an isolated fruit. Leaves are morphologically similar to Miocene and extant *Trochodendron*, but demonstrate basally actinodromous venation like that of the extant sister genus *Tetracentron* rather than pinnate venation characteristic of the single extant species of *Trochodendron*. This new *Trochodendron* thus has venation that appears evolutionarily intermediate between these two genera as previously known and retains the palmate condition thought to be primitive within the Hamamelideae as a whole. Leaves are simple, symmetric, 3-8 cm long x 1.5-5 cm wide with an acute apex and acute to cuneate base, with exstipulate, striate, deeply caniculate petioles. Venation includes 2-3 pairs of lateral primaries, a marginal vein and up to three secondaries that diverge at angles of 40-45 degrees. Weak intersecondary veins anastomose at right angles into widely and irregularly spaced orthogonal reticulate tertiary veins. Leaves typically have an unlobed crenate margin with numerous small appressed chloranthoid (papillate) teeth in the apical portion of the lamina, while more basal portions are entire. Reproductive structures are quite similar to those of Miocene and extant forms. An infructescence specimen consists of a single woody axis 3.2 cm long and 16-23 mm wide that bears fruits on striated pedicels. Fruits have an acute base and truncate apex and sometimes show evidence of persistent recurved styles. Occurring in the same beds, is the extinct infructescence *Nordenskioldia* (Trochodendraceae) and its associated leaf *Zizyphoides* that show similarities to those of Paleocene and Neogene relatives in North America, Europe and Asia. The presence at Republic of both a distinctive *Trochodendron* plant and *Nordenskioldia* and *Zizyphoides* remains demonstrates that the Trochodendraceae, today known exclusively from Asian endemics, was undergoing rapid diversification in the Eocene of western North America.

- 222** REMBER, WILLIAM C.\*, ANGELIKA OTTO, AND BERND R. T. SIMONEIT. <sup>1</sup>Department of Geology, University of Idaho, Moscow ID 83844, <sup>2</sup>College of Oceanic and Atmospheric Sciences, Oregon State University, Corvallis OR 97331—*Morphology of Cunninghamia chaneyi from the Middle Miocene Clarkia flora northern Idaho.*

The occurrence of *Cunninghamia chaneyi* from the middle Miocene sediments of the former Lake Clarkia in Northern Idaho is the last known occurrence of this genus in the geologic record of North America. *Cunninghamia chaneyi* has been reported on the basis of foliar branches from the Oligocene Rujada, Lyons and Bridgecreek floras of Oregon and the Oligocene Gumboot flora of southwestern Washington. These resemble the extant *C. lanceolata*. The *C. marquettii* from the Haynes Creek flora of east central Idaho more

closely resembles *C. konishii*. Both *C. protokonishii* from the middle Miocene of Japan and *C. europaea* from the later Miocene of Poland also resemble *C. konishii*. The *C. miocenica* that has been described from the Oligocene and Miocene of central Europe is thought to be intermediate between the two extant species. The *Clarkia Cunninghamia chaneyi* is represented at four localities by well preserved compressions and impressions of foliar branches, rarely single needles, seed cones and pollen cone fascicles. The foliar branches are similar to those found beneath arboretum trees of *C. lanceolata*. The needles are slightly smaller in both width and length than those of the extant species. The size of the cones and cone fascicles of the fossils is identical to that of the extant *C. lanceolata*. However the shape of the cone bracts, the reduced cone scales and the seed attachment scars are some what different from that of the extant species. Most significantly, stomatal bands on the fossil species are half as wide as those on the extant species. The excellent preservation allowed analysis of extractable chemical compounds from foliar branches and cones of *Cunninghamia chaneyi* from Clarkia. Several mono-, sesqui- and diterpenoids have been identified in the extracts. The sesquiterpenoid pattern is similar to that described from the resin of *C. miocenica* from Central Europe.

- 223** RETALLACK, GREGORY JOHN. Department of Geological Sciences, University of Oregon, Eugene, Oregon, 97403-1272—*Peltaspermaceous affinities of "Dicroidium" callipteroides from the earliest Triassic, basal Narrabeen Group, Australia.*

The earliest Triassic, Coal Cliff Sandstone (basal Narrabeen Group) forming roof shales to the latest Permian Bulli Coal in the Southern Coalfield of New South Wales, Australia, contains a low-diversity flora of ferns, lycopsids, conifers, and seed ferns, that survived the greatest mass extinction of all time at the Permian-Triassic boundary. Only one taxon of seed fern is known from this flora, and its affinities have been unclear until recent discovery of its reproductive organs. The leaves are coriaceous, bipinnate and bipinnatifid, and its terminal unipinnate rachides show multiple dichotomies of the rachis. These leaves were referred by John Townrow to "*Thinnfeldia*" *callipteroides*", based on type material from the Early Triassic, Sakamena Group of Madagascar. However, the stomatal apparatus of the leaves is cyclocytic with papillate subsidiary cells, distinct from the doubly cyclocytic non-papillate subsidiary cells of Middle to Late Triassic *Thinnfeldia*, and identical to the stomatal apparatus of *Lepidopteris*. Despite this cuticular similarity, Mary White has used rachis dichotomies as a character to transfer these leaves to "*Dicroidium*" *callipteroides*. Newly discovered ovulate fructifications of this taxon consist of branching systems of peltate ovular heads each with about 10 distinct marginal lobes, referable to the genus *Peltaspermum*. In a large collection of these fructifications no more than 2 ovules were seen per head, although it is possible that other ovules abscised. Microsporophylls also were found, and are still under investigation, but are also compatible with peltasperm rather than corystosperm affinities. This taxon of seed fern shows affinities with European and Russian Permian peltasperms, and probably invaded Gondwanaland from the north during earliest Triassic postapocalyptic greenhouse. Peltasperms are plausible ancestors of corystosperms such as *Dicroidium*, which first appears higher within the Narrabeen Group (upper Bulgo Sandstone) in the Southern Coalfield of New South Wales.

- 224** RILEY, MICHAEL G.\* AND RUTH A. STOCKEY. Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada, T6G 2E9—*A new aquatic angiosperm with a floating rosette of leaves from the St. Mary River Formation of southern Alberta.*

Three hundred specimens of a new aquatic angiosperm have been excavated from the Upper Cretaceous deposits of the St. Mary River Formation (Maastrichtian) of southern Alberta, Canada. Plants are compression/impressions and are represented primarily by isolated leaflets found in grey siltstones and fine-grained sandstones. These sediments probably represent a sudden overbank flood. The remains of 13 complete or partial rosettes of this dicot have been identified in the grey siltstones. Growth habit is similar to that described for *Quereuxia* (= *Trapago*) *angulata* from the same locality. The leaves of the new plant, however, are more than twice the size of those of *Q. angulata* and the largest rosettes measure at least 16 cm in diameter. Leaves are opposite, simple at the first two nodes from the apex, and compound with three leaflets for at least four nodes below. Blades of leaves or leaflets are symmetrical, obovate, microphyllous with obtuse to rounded apices and bases. The margin is unlobed and crenate. Five to seven primary veins enter from the petiole/petiolule exhibiting reticulate actinodromous to pinnate, craspedodromous branching. Primary veins are thicker near the base and weaker near the apex and show deflections near the leaflet tip. Secondary veins branch dichotomously and thin toward the margin. Tertiary veins are random reticulate with quaternaries forming irregular areolae. Leaves were probably aerenchymatous and fleshy with the abaxial epidermis being preserved on several specimens. Teeth appear to have been chloranthoid or rosoid. Rosettes are attached to a vertical axis, the largest being at least 11 cm in length. The rosettes were probably floating on the surface on a shallow pond or oxbow lake. These plants are found in the same deposits as *Quereuxia angulata* and the two species shared the same habitat.

- 225** SCHECKLER 1, STEPHEN E.\*, DONNA L. LINDSAY POSTNIKOFF 2, AND ERIC J. CHAMEROY 1. 1. Department of Biology, Virginia Polytechnic Institute & State University, Blacksburg, VA 24061-0406 and , 2. Department of Geological Sciences, University of Saskatchewan, Saskatoon, SK, CANADA S7N 5E2—*Late Devonian forests with the first large trees* (Archaeopteris).

Aneurophyte progymnosperms are common shrubs of an early Late Devonian (basal Frasnian Oneonta Fm.) flora from a quarry near Ashland, New York. Floristic census of the marine bay-fill/prodelta deposits at the lowest quarry bench shows that the regional flora was dominated by aneurophytes (80-85%) with *Tetraxlopteris* the commonest of these (plus *Triloboxylon* & *Proteokalon*). Lesser components include cladoxylalean trees and vines (*Pseudosporochnus* & *Rhymokalon*), the progymnosperm tree *Archaeopteris* (*Callixylon zaleskyi* and *A. macilenta*) and a few scarce lycopsids (*Archaeosigillaria*). Delta progradation established vegetated floodplains with sandy paleosols on this site within 4 m upsection. Farther upsection, paleosols are commoner, thicker, and mud-dominated. The floor of the uppermost quarry bench exposes about 1 ha of horizontal paleosol from which we uncovered six small test plots that show stump bottom casts, root penetration zones, and other depositional features of this floodplain soil. Shrink/swell slickensides, many with root penetrations, characterize this vertisol. XRD and SEM analyses show a combined kaolinite/smectite signature, illite (derived from smectite?), and an absence of caliche carbonate, which suggest a savanna-like paleoclimate. Larger stumps are more widely spaced while smaller root zones are closer and clustered farther away from the larger stumps. The ratio of large to small stumps/root masses corresponds to our gross floristic census and suggests that this floodplain paleosol exposure is representative of the regional vegetation of this time on the Catskill Delta. Except for *Archaeopteris*, these were short-lived taxa, which implies considerable successional turnover. This mixed community, was rapidly re-organized, however, by the world-wide spread of *Archaeopteris*, a large tree with a much branched, leafy, and shade producing crown, and decline then extinction of aneurophytes, small xeromorphic shrubs with high light tolerance. Nearby quarries of slightly younger strata show greater domination by *Archaeopteris*, which reaches nearly 95% of biomass by mid Frasnian time.

- 226** SCHERER, JACQUELINE\*, GARLAND R. UPCHURCH, JR., GREG H. MACK, AND MARGARET J. KNAUS. Department of Biology, Southwest Texas State University, San Marcos, TX 78666, and Department of Geological Sciences, New Mexico State University, Las Cruces, NM 88003—*Foliar physiognomic estimates of climate for the latest Cretaceous: comparative sensitivity to transfer function.*

Estimates of climate derived from the foliar physiognomy of modern vegetation indicate that, for modern test sites, the calculated climates can differ from actual climates and are sensitive to the equation used to quantify the leaf/climate relationship (or transfer function). To determine how estimates of past climates can vary in response to transfer function, we analyzed a latest Cretaceous (Maastrichtian) leaf assemblage from the Jose Creek Member of the McRae Formation, southern New Mexico, in part because of its relevance to climatic change across the Cretaceous-Tertiary boundary. The Jose Creek assemblage represents probable *in situ* leaf litter preserved in volcanic ash and was derived from vegetation growing in well-drained soil. The analyzed assemblage consists of 132 specimens of dicot leaves belonging to 43 species, which are associated with a comparable number of ferns, conifers, and thermophilic monocots belonging to at least 10 species. Estimates of mean annual temperature (MAT) and mean annual precipitation (MAP) were made using published univariate and multivariate transfer functions derived from the CLAMP database of Wolfe or regional floras. Calculations were made using raw physiognomic data and data adjusted to account for the overrepresentation of small leaves in modern leaf litter. Calculated MAT for the Jose Creek assemblage generally ranges from 16-21°C, with multivariate transfer functions tending to give cooler values than univariate transfer functions. Calculated MAP ranges from under 800 to over 1500 mm per year, with an average of 1100 mm. Variation in calculated temperature and precipitation, relative to the mean of all estimates, can exceed  $\pm 35\%$ , underscoring the potential bias introduced by choice of transfer function. However, the range of values is congruent with more qualitative estimates of climate derived from fossil soils and plant life form, which indicate warm moist conditions and above-freezing cold-month means for the Jose Creek Member.

- 227** SCHORN, HOWARD E.\* AND DIANE M. ERWIN. Museum of Paleontology, University of California, Berkeley CA 94720-4780—*The impression record history and ecological diversification of Pseudotsuga Carriere (Pinaceae) in western North America during the later half of the Cenozoic.*

Douglas-fir [*Pseudotsuga menziesii* (Mirb.) Franco] is the state tree of Oregon. It is appropriate that the geologically oldest macrofossil record of the genus is also from Oregon; the ~32 Ma Rujada site southeast



of Eugene. Revision of the North American impression fossils indicate that only 7 of the 27 (26%) literature citations are correctly assigned to *Pseudotsuga*. A previously unrecognized specimen from Cartwright Ranch, Idaho is added. These eight occurrences are all within the present geographic range of extant *Pseudotsuga* in western North America. The genus is known from Miocene and younger horizons of Japan. Records from Europe are considered equivocal. The North American impression fossils can be segregated into three forms on the basis of the size of the ovulate cone and/or winged seed; large, intermediate and small. Based on climatic analyses of the associated dicotyledonous paleofloras, these three forms occurred in three different climatic settings. It is inferred that these occurrences are expressions of ecologically driven evolutionary trends. The earliest record, a large winged seed form near extant *P. macrocarpa* from the early Oligocene of Oregon, is inferred to be the least derived *Pseudotsuga*. It was adapted to a mean annual temperature centered on  $\sim 13^{\circ}\text{C}$ , an intermediate mean annual range of temperature centered on  $\sim 22^{\circ}\text{C}$ , with  $\sim 150$  cm precipitation distributed through a seven plus month growing season; this condition is typical for the bulk of the least modified species of extant Northern Hemisphere conifers. Through time, *Pseudotsuga* adapted to dryer, and both cooler or warmer, climates. The large seed form adapted to dryer-warmer. An intermediate-sized form from the late middle Miocene was dryer-cooler. The small-sized *P. menziesii* type is known from the middle Miocene on in dryer, but both cooler and warmer settings. The history of *Pseudotsuga* viewed in the present framework demonstrates a dynamic adaptive history.

- 228** SCHWAB, HEIDI C.\*, RUTH A. STOCKEY, AND CHARLES E. SCHWEGER. Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9, Department of Anthropology, University of Alberta, Edmonton, AB T6G 2E9—*Ovulate cones of Picea from the Lower Pliocene Ch'ijee's Bluff, Yukon Territory, Canada.*

Large numbers of ovulate cones resembling *Picea* Dietrich were recovered from the Lower Pliocene sediments of Unit One of Ch'ijee's Bluff on the Porcupine River, Yukon Territory, Canada. Fourteen structurally preserved cones were sectioned using glycol methacrylate and bioplastic embedding techniques for anatomical study. Cones are cylindrical with a slightly tapering apex, 6.7 to 11.2 cm long, 1.9 to 2.8 cm in diameter. Pith and cortex are parenchymatous with scattered sclerenchyma in the middle and outer cortex. Bract and ovuliferous scale traces arise separately from the axis stele with a series of adaxial resin canals. The ovuliferous scale has a V-shaped trace at its origin while the bract trace is terete and accompanied by two resin canals. Five to six resin canals in the ovuliferous scale extend into the abaxial scale sclerenchyma. Bracts are keeled, 6.1-7.3 mm long, with a thin, tapered apex. Elongate, winged seeds are borne in pairs on the adaxial scale surface. Cones were compared anatomically to *Picea breweriana* S. Wats., *P. glauca* (Moench.) Voss, *P. engelmannii* (Parry) Engelm., and the fossil taxa *P. anadyrensis* Krystofovich and *P. banksii* Hills and Ogilvie. The Yukon cones most closely resemble *Picea glauca*, but differ in the number of resin canals per scale, shape of the ovuliferous scale trace in transverse section, number of ovuliferous scales per cone, bract length, and amount of sclerenchyma in the cortex of the cone axis. These cones represent a new species of *Picea* that could easily be confused with *P. glauca* which occurs in east central Alaska based on anatomical evidence. Our results point out the importance of anatomical sectioning in the documentation conifers from the late Tertiary of the Yukon and Alaska where similar cones have been recovered.

- 229** STROTHER, PAUL K. Weston Observatory of Boston College, Department of Geology & Geophysics, 381 Concord Road, Weston MA 02493—*The cryptospore record indicates a Cambrian origin for land plants.*

Cryptospore tetrads and dyads have been recovered from Middle Cambrian strata in Arizona (Bright Angel Shale) and eastern Tennessee (Rogersville Shale). Although many tetrads are irregular in their configuration, small tetrahedral tetrads similar to *Tetrahedraletes grayae* strengthen the likelihood that these are meiotic tetrads from spore-bearing embryophytes. It is now possible to trace a cryptospore history from the Middle Cambrian to the Devonian. Late Cambrian tetrads are known from at least three sites in North America. The Cambro-Ordovician record in Europe and North Africa is characterized by the monads, *Attritasporites* and *Virgatasporites*. Middle Ordovician deposits in Saudi Arabia and the Prague Basin contain dyads, tetrads and other cryptospores, including spore clusters and cuticle-like fragments. The Caradoc is marked by evolutionary stasis, based on Charles Wellman's study of the type region in the UK. Uppermost Ordovician and lower Silurian strata contain diverse and widespread cryptospore assemblages. Cryptospores continue to diversify through the Homerian (middle Silurian) origin of tracheophytes and decline in abundance in the Early Devonian as trilete spores begin to dominate terrestrial assemblages. Although some membrane-enclosed cryptospores have been attributed to possible freshwater chlorophytes that have strayed into estuarine waters, the bulk of morphological evidence points clearly to an embryophytic affinity for these fossils. The



affinities of even the earliest cryptospore tetrads are with hepatics and anthocerophytes. Since rhyniophytoids are the only plants (living or extinct) known to produce dyads normally in sporangia, dyads also stand as a proxy for the embryophytes. (To propose otherwise requires the retention of dyad sporogenesis from a hypothetical charophycean ancestor.) Thus, cryptospores continue to serve as a proxy for early land plants that have yet to reveal a macro or mesophyte record. It now seems plausible that embryophytes occupied terrestrial habitats throughout the entirety of the Paleozoic.

- 230** TAGGART, RALPH E. AND AUREAL T. CROSS.\* Department of Botany and Plant Pathology, Michigan State University, East Lansing, MI 48825—*Ecological dynamics of Eocene Lake Florissant, Colorado.*

The Late Eocene (34 Ma) volcanoclastic deposits of the Florissant Fossil Beds National Monument (Colorado) contain abundant well-preserved remains of plants and a wide range of insect taxa. Paleoecological analysis of the deposits, based on integration of palynological, stratigraphic, and geochemical data, suggest that the Florissant ecosystem was subject to chronic ecological stress. The terrestrial vegetation was commonly devastated by holocaustic fires, most of which probably originated in drier communities on surrounding slopes. Precipitation was marginal, relative to the high rate of evaporation, and lake water levels fluctuated over a wide range. During low-water intervals the lake water was highly alkaline, limiting aquatic biodiversity. This is consistent with the fine preservation of fossil plant and insect material and the general absence of an indigenous lacustrine fauna. One drop in lake level lasted for several centuries, permitting the establishment of a redwood/red cedar-dominated forest on the former lake bottom. A subsequent rise in lake level resulted in the permineralization of the bases of the standing trees, today represented by the numerous petrified stumps throughout the Monument area.

- 231** TAYLOR, THOMAS N.\*, EDITH L. TAYLOR, MICHAEL KRINGS, AND HANS KERP. Department of Ecology and Evolutionary Biology, and Natural History Museum and Biodiversity Research Center, University of Kansas, Lawrence, KS 66045; Abt. Paläobotanik am Geologisch-Paläontologischen Institut, Westfälische Wilhelms-Universität Münster, Hindenburgplatz 57, D-48143 Münster, Germany—*Reconstruction of the climbing late Paleozoic seed fern Pseudomariopteris busquetii.*

Vine- to lianallike growth habits have to date been documented for a number of late Paleozoic pteridosperm taxa; only a few scrambling and/or climbing taxa, however, have been reconstructed in detail. *Pseudomariopteris busquetii* (Zeiller) Danzé-Corsin, emend. Krings et Kerp, a (?callistophytalean) taxon that was quite common in the European late Paleozoic, was a medium-sized, vine- to lianallike plant with slender stems to which small bipartite fronds were attached. The growth habit of *P. busquetii* is reconstructed, based on compression material from the Upper Carboniferous of France and Lower Permian of Germany. *P. busquetii* utilized two different strategies to both anchor and support the plant body. Most specimens possess specialized climber hooks developed from apical extensions of the pinna axes, indicating that the fronds were used to attach the plant. A few specimens suggest that the stem may also have had some capacity for attachment. In the absence of suitable supports, however, *P. busquetii* may also have grown in thickets in which the individual plants supported each other. The reconstruction of *P. busquetii* presented here depicts a growth form which was apparently widely distributed among mariopterid pteridosperms. Several gross-morphological features, which are characteristic of *P. busquetii* and important for our understanding of its growth form, have also been documented for other mariopterid taxa. Based on local abundance in the fossil record, mariopterid pteridosperms may have played an important role in some of the Upper Carboniferous and Lower Permian coal swamp forest ecosystems. They may have represented part of a rather vigorously growing, sprawling, scrambling and/or climbing type of vegetation that may be structurally comparable to vegetation often found at edges or in disturbed areas (e.g., treefall gaps) of contemporary forest ecosystems.

- 232** TAYLOR, WILSON. Department of Biology, University of Wisconsin-Eau Claire, Eau Claire, WI 54701—*Ultrastructural variability of lower Paleozoic trilete spores.*

Continuing investigations of early land plant spore wall ultrastructure are beginning to reveal a considerable degree of diversity, despite a limited number of taxa defined at the level of the light microscope. Previous analyses of in situ cryptospore monads showed several ultrastructural types within a single taxon, *Laevolancis divellomedium*. A similar situation seems to exist with some dispersed trilete spores (e.g., *Ambitisporites*). Variable characteristics of these trilete spores include the relative thickness of the proximal and distal walls, the nature of the presumed proximal suture, and the number of sublayers comprising the wall. Thus far, no lamellae have been identified in any dispersed trilete spore. These trilete spores are from geographically

diverse locations (eastern US, eastern Canada, central US, eastern Europe and Saudi Arabia), range in age from Middle Ordovician to Upper Silurian, and have different degrees of thermal maturity. Therefore, much additional work will need to be done to determine the extent to which these factors are contributing to the apparent structural diversity. Although broad categories of ultrastructural types will no doubt ultimately become apparent, as yet, many dispersed spore taxa seem to represent heterogeneous assemblages.

- 233** TIFFNEY, BRUCE H.\* AND NORMAN WANG. Geological Sciences and College of Creative Studies, University of California, Santa Barbara, CA 93106—*Seeds of Rhododendron from the Eocene of California.*

*Rhododendron* is known from seeds in the Paleocene of England. All other reports, including those from North America, are based on fossil leaves, many of poor quality. In addition, the foliar characters of fossil *Rhododendron* may mimic those of the leaves of several genera of Fagaceae, requiring great care in identification. Thus, pre-existing reports of Tertiary age North American *Rhododendron* require verification. We report seeds clearly assignable to *Rhododendron* from the La Porte Flora of Northern California. This flora has been dated by whole rock  $^{238}\text{U}/^{205}\text{Pb}$  methods at 33.2 Ma (corrected), placing it in the Early Oligocene, but the climatic affinities of the flora suggest that it is pre-deterioration and thus likely of Late Eocene age. Thus, *Rhododendron* had achieved at least a Euramerican distribution by the Eocene. *Rhododendron* seeds fall into three morphological categories which bear some association with the higher order systematic divisions of the genus. Our investigation suggests that the variability of seed morphology is such that identification to lower taxonomic groupings is not possible.

- 234** TOMESCU, ALEXANDRU MIHAIL FLORIAN. Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701—*The seed fern Lyginopteris in the Mississippian of North America.*

The seed fern *Lyginopteris* is described from Upper Mississippian (middle Chesterian - Namurian A) shales in northwestern Arkansas. The pyritized stem is 29 cm long and slightly compressed; the diameter is about 11 x 5 mm. Seven leaf bases diverge at intervals of 2 to 5.5 cm. A *Lyginopteris*-type rachis with a paired vascular bundle is also preserved. The cauline primary bundles are mesarch and positioned at the margin of the pith. They form a eustele with five sympodia. The secondary xylem includes numerous rays. The vascular cambium and phloem are incompletely preserved. The inner cortex consists of thin-walled parenchyma cells. The outer cortex shows the characteristic *Dictyoxylon* structure of *Lyginopteris*. Coprolites produced by plant tissue decomposers were observed in different tissues of the stem. The study of the leaf trace divergence necessitated the use of a deformation model to help reconstructing the original position of the cauline bundles in the compressed stele. Phyllotaxis of the specimen approaches 2/5. The cauline bundles divide radially and the leaf traces diverge from the stele at very low angle, extending through five internodes before entering the leaf bases. They follow a slightly dextrorse coiling pattern upward. The leaf traces become bilobed but do not divide; in the leaf bases they acquire a butterfly shape. A characteristic feature of the specimen is the presence of a sclerotic bundle adaxial to the diverging leaf trace. The bundles accompany each leaf trace from its emergence in the cortex and along its whole trajectory to the leaf base. In contrast to previously described *Lyginopteris* stems, there are no capitate epidermal glands. These features suggest that the specimen could belong to a new species. This new occurrence of *Lyginopteris* confirms the North American distribution of the genus and emphasizes that it was not restricted to Western Europe.

- 235** WHEELER, ELISABETH A.\* AND STEVEN R. MANCHESTER. Department of Wood and Paper Science, North Carolina State University, Raleigh, NC 27695-8005; Florida Museum of Natural History, University of Florida, Gainesville, FL 32611—*Survey of the diverse middle Eocene wood assemblage of the Clarno Formation, northcentral Oregon.*

A diverse assemblage of silicified woods occurs in the type area of the Clarno Formation in north central Oregon, USA. These woods occur as predepositionally abraded fragments along with abundant fruits and seeds in tuffaceous sediments at the Nut Beds locality in the Clarno Unit of John Day Fossil Beds National Monument. A comprehensive investigation of these woods, involving the thin-sectioning and analysis of more than 500 specimens, has resulted in the recognition of about 70 distinct taxa—making it the richest Eocene wood assemblage so far known. Although the diversity of woods at the Nut Beds apparently is not as high as that of fruits and seeds (ca 175 species), the woods document some new families for the flora and provide improved insight into the composition of this thermophilic assemblage. At least fifty of Nut Beds wood types are referable to extant family. Among these, some have anatomy diagnostic of particular modern genera (e.g., *Alangium*, *Meliosma*, *Prunus*); others represent extinct genera (e.g., *Clarnoxylon*—Jug-

landaceae, *Triplochitioxylon*—Malvaceae s.l.); but most are stereotypic genera, i.e., cannot be assigned to an extant genus because their combination of features occurs in more than one extant genus (e.g., *Magnoliaceoxylon*, *Maloidoxylon*). We recognize the following families based on woods from the Nut Beds: Aceraceae, Anacardiaceae, Annonaceae, Araliaceae, Betulaceae, Cercidiphyllaceae, Cornaceae, Eupteleaceae, Fagaceae, Flacourtiaceae, Hamamelidaceae, Juglandaceae, Lauraceae, Leguminosae, Magnoliaceae, Malvaceae, Moraceae, Platanaceae, Rosaceae, Sabiaceae, Sapindaceae, Ulmaceae, Vitaceae, Palmae, Ginkgoaceae, Pinaceae, Taxodiaceae.

- 236** WILDE, VOLKER\*, HERBERT FRANKENHAEUSER, AND BIRGIT NICKEL. 1st and 3rd author: Forschungsinstitut Senckenberg, Palaeobotanik, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, 2nd author: Naturhistorisches Museum Mainz/Landessammlungen fuer Naturkunde Rheinland-Pfalz, Reichklarastr. 10, 55116 Mainz, Germany—*A chloranthaceous inflorescence with pollen in situ from the Middle Eocene of Germany.*

Some Middle Eocene localities in Germany (e.g. Geiseltal, Messel, Eckfeld) have yielded a great number of exceptionally well preserved plant remains such as leaves, seeds/fruits, flowers/inflorescences with pollen in situ, and dispersed pollen. Combining the different taphocoenoses, reconstruction of the minor-scale differentiation of the Middle Eocene vegetation of Central Europe is possible to a certain degree. A complex inflorescence of undoubtful chloranthaceous affinity was recently found in Eckfeld. It is now covering a major gap in the reliable fossil record of that primitive angiosperm family which has been for the first time recorded even in the Lower Cretaceous. *Emmapollis* is a genus for dispersed pollen which are well known from the Central European Tertiary. Various botanical interpretations have previously been offered for these quite characteristic grains, already including chloranthaceous affinities. The new inflorescence from Eckfeld is clearly showing *Emmapollis*-type grains in-situ preserved within the anthers. This is now unequivocally proving their chloranthaceous affinities. Therefore the new fossil may be regarded as a missing link in the stratigraphic distribution of Chloranthaceae, and in the assignment of a certain type of dispersed pollen.

## Contributed Posters

- 237** BARKSDALE, LISA. Stonerose Interpretive Center, Republic, WA 99166—*Utilization of amateurs in the development of the Stonerose Museum fossil collection.*

The Stonerose Fossil Site in Republic, Washington with its wide variety of Eocene flora and its more limited Eocene fauna is often the scene of hectic but purposeful activity. Students of all ages, tourists, scientists, families, and rock hounds search for that perfect example of that rare or not-so-rare fossil. The curator and her assistants maintain a careful watch on the activities on the site and control over the removal of the fossils. Visitors are limited to three fossils per day. Unidentified or exceptional specimens of fossils are kept for scientific analyses or added to the Stonerose collection. In the last ten (10) years 70,000 visitors have found thousands of fossils and have taken great pride in their contribution to science, and they feel particularly rewarded if their "treasure" has been retained for further study. One of the major functions of the Center is to educate the visitors of the importance of science and scientific methodology. On all levels amateurs contribute to the success of Stonerose. From the Board of Directors to those who are participating in a stratigraphic study to sophisticated "amateurs" who have contributed their collections to the Center, Stonerose is the beneficiary of amateur activity. Funding is a community effort involving county, city, and private resources, as well as the activities of the Stonerose Center itself. Although the curator works closely with the State of Washington's Burke Museum of Natural History and Culture and museums and scientists throughout the world own and study Republic fossils, it is amateurs who provide the "fire" for the engine that makes Stonerose run.

- 238** BUECHLER, WALTER K. Boise, ID 83705—*Estimating polyploidy levels from cell size in Salix leaves.*

Leaf material from 41 herbarium specimens representing 31 *Salix* taxa was examined for correlation between polyploidy levels and size of petiole epidermal cells and stomatal guard cells. The species included most of the polyploidy levels encountered in contemporary *Salix* ( $2n = 38, 76, 114, 152, 190$ ). Petiole epidermal cell size allowed a clear distinction between diploids and tetraploids. The same was true for guard cell size if comparisons were made only within sections or within groups of closely related sections. Polyploidy levels higher than tetraploid could be estimated to  $\pm 2 - 4x$ . The data suggest that cell size may depend also, to

a minor degree, on climate. Some cultivars that were transplanted from high to lower altitudes showed exceptionally large cell sizes; such specimens should be excluded from reference data. Contrary to chromosome counts where live material is necessary, these cell size methods can be used on herbarium material and on well-preserved fossil specimens (the epidermis of the petiole is often the only organically preserved part of a leaf remain). Cell size methods are also suitable to scan large numbers of living plants for deviations in chromosome numbers, because preparation and measuring procedures are relatively simple. The petiole cell size method was applied to 14 fossil *Salix* leaves from the Late Miocene Pickett Creek flora (Idaho). *Salix succorensis* Chaney and Axelrod, *S. inquirenda* Knowlton, *S. wildcatensis* Axelrod, *S. desatoyana* Axelrod, and two undetermined specimens were found to be diploid. The result for *S. wildcatensis* is of particular interest because its closest modern relative, *S. lasiolepis* Benth., is tetraploid. The objective of future studies is to estimate the age of some polyploid complexes in *Salix* by fossil evidence.

- 239** FREILE, DEBORAH\* AND MELANIE DEVORE. Geology, Berry College, Mt. Berry, GA 30149, Department of Biological and Environmental Sciences, Georgia College and State University, Milledgeville, GA 31061-0490—*Utility of petrographic thin section analysis of fossil plant material and associated sediments in taphonomic studies: An example from the Oligocene of Texas.*

Petrographic thin sections of the late Oligocene Catahoula Formation in Huntsville, TX show well preserved plant fragments including some with clear indications of permineralization. The plant fragments show primarily a reddish-brown low grade thermal maturation. Authigenic feldspar crystals, some within the organic fragments, are clearly visible. Other cements include chert and quartz. The highly variable lithology of the samples indicates the potential of a multiple provenance rock. Some grains are clearly volcanic in origin (including clear examples of volcanic glass clasts), others are clearly detrital (principally subrounded quartz and chert grains), while a few other quartz grains show the characteristic undulose extinction patterns of metamorphic quartz. The rock samples are either finely parallel laminated, very fine to fine grained, angular to subangular, and moderately sorted OR wavy laminated, fine to medium grained, subangular to subrounded, and moderately to well sorted. Accessory minerals include feldspars-exhibiting good twinning, altered micas, zeolites and nascent stage glauconitic globules. Some specimens show cementation by opal and clays; probably related to the diagenesis of volcanic ashes into silica and smectite. The Catahoula Fm. has been described as a primarily terrigenous, fluvial, deltaic, marginal unit. The presence of glauconite is an indication of shelf (60-550m depth) marine environments and/or a transgressive episode. The late Oligocene was a time of transgression after a period of lowest (-200 to -350 m relative to present) sea level. The rapid rise of sea level at the end of the Oligocene, increased erosion and sedimentation to the shelf, and catastrophic flooding events may all have contributed to the unusual circumstances in which glauconite is preserved as authigenic crystals within quartz grains and cements within the plant fragments. This contradicts previous descriptions suggesting that the fine laminations present in some members of the formation represent a terrestrial, oxbow lake, fluvial environment.

- 240** KESTER, PAUL R. Department of Geological Sciences, University of Washington, Seattle, WA 98195—*Tracking the radiation and regional extinctions of the genus Cunninghamia (Taxodiaceae).*

The genus *Cunninghamia*, family Taxodiaceae, is now distributed in the mixed mesophytic forests of southeastern China and the mixed coniferous-deciduous hardwood forests of Taiwan. Currently, three species of *Cunninghamia* are recognized: *C. konishii*, native to the mountainous northern region of Taiwan, and *C. lanceolata* and *C. unicanaliculata*, native to southeastern China. Despite the limited number of species and their restricted geographical distribution, *Cunninghamia* has an extensive paleobotanical record. Earliest fossil records of *Cunninghamia* are found in the Yuanbaoshan Formation, of Inner Mongolia. The age is assigned to middle early Cretaceous (Hauterivian-Barremian). By the middle Eocene, *Cunninghamia* was distributed in both western North America and western Europe. Early Paleogene fossils from the Eureka Sound Group, Ellesmere and Axel Heiberg Islands in the Canadian Arctic (paleolatitudes of 75-80° N) indicates migration via both the Bering and the North Atlantic Land Bridges by the late Paleocene (Thanetian). *Cunninghamia* became extinct in both North America and Europe by the end of the Miocene. The present distribution of the genus is limited to regions of mean annual temperature (MAT) of 15° to 19° C and mean annual precipitation (MAP) exceeding 1500 mm. Its limited distribution is a result of continual global cooling since the Eocene thermal maximum.



- 241** RATZEL, STEPHEN R.\*, GAR W. ROTHWELL, ROYAL H. MAPES, GENE MAPES, AND LARISA A. DOGUZHAEVA. Department of Environmental and Plant Biology, Ohio University, Athens OH 45701, U.S.A.; Department of Geological Sciences, Ohio University, Athens OH 45701, U.S.A.; and Paleontological Institute, Russian Academy of Sciences, Moscow 117868, Russia—*Pityostrobus* in the Lower Cretaceous of southwestern Russia.

A species of *Pityostrobus* (*P. milleri* Falder et al.) recently was described from calcareous nodules recovered from shallow marine sediments of Lower Cretaceous (latest Aptian: Clansenian) age located east of the Black Sea in the Caucasus Mountains in southwestern Russia. Nodules of this type also contain conifer needles, filiclean frond members, wood fragments, gastropods, bivalves, and an extremely rich assemblage of well preserved cephalopods. Additional collecting at this locality has yielded a second new species of this extinct ovulate cone genus assignable to the Pinaceae. The incomplete cone measures 8 cm long and 3.4 cm wide. The cone axis is 5 mm in diameter, with a parenchymatous pith that displays scattered sclerids. The cylinder of wood is discontinuous and does not show a growth ring. The tiny bract is united with the scale except at the tip. Bract and scale traces diverge from the stele independently, and the bract trace extends to near the tip of the organ. Resin canal architecture is distinct, but similar to that of *Larix*, *Pseudotsuga* and *Picea*. Ovules display a distinctly undulating surface of the integument on the side that faces the ovuliferous scale. This new species adds further to our knowledge of the explosive diversification of Pinaceae during Early Cretaceous time.

- 242** SMITH, SELENA Y.\* AND RUTH A. STOCKEY. Department of Biological Sciences, University of Alberta, Edmonton, Alberta T6G 2E9—A permineralized *Pityostrobus* cone (Pinaceae) from the Cretaceous of British Columbia.

One cylindrical abraded cone specimen, 2.8 cm in diameter and at least 3.0 cm long, has been found in a calcareous concretion from the Cretaceous Oyster Bay Formation (Late Campanian) of Vancouver Island, British Columbia. The cone was sectioned and peeled using the cellulose acetate peel technique. Sclerenchymatous pith is surrounded by a ring of separate secondary xylem bundles that lack resin canals. Numerous dilating resin canals occur in the inner parenchymatous cortex. The thick, sclerenchymatous outer cortical zone is covered in a dense ramentum of trichomes. Trichomes are also found on ovuliferous scale and bract bases. Vascular traces to ovuliferous scales and bracts arise independently. The bract is keeled with a terete trace and two lateral resin canals. Ovuliferous scales are sclerotic with resin canals adaxial, abaxial, and in between the vascular strands. A prominent interseminal ridge occurs between the two winged seeds of each scale. Seeds have a ridged sclerotesta; and nucellus, megagametophyte, and embryos with eight cotyledons are preserved. Cone structure most closely resembles the fossil pinaceous genus *Pityostrobus*. The unique features of this cone distinguish it from the known species of *Pityostrobus* and extant Pinaceae and emphasize the rapid evolution and diversification of the family Pinaceae that occurred during the Cretaceous.

- 243** TIDWELL, WILLIAM D.\*, LEITH S. TIDWELL, DEBRA L. MICKELSON, DAN S. CHANEY, AND AMANDA L. HANSEN. Department of Botany and Range Science, Brigham Young University, Provo, UT 84602, Department of Earth Sciences, University of Colorado at Boulder, CO 80309, Department of Paleobiology, NMNH Smithsonian Institution, Washington D.C. 20560—A new flora from the Lower Permian Cedar Mesa Sandstone near Canyonlands National Park, Utah.

A new flora consisting of both compression-impressions and petrifications occurs in the shales and sandstones of the Lower Permian Cedar Mesa Sandstone near Canyonlands National Park, approximately 48 km (30 miles) northwest of Monticello in southeastern Utah. A preliminary analysis has identified among the compression-impressions species of *Calamites*, *Sphenopteris*, and a fertile pectopterid, that may be a new taxon. Two species of *Dadoxylon* and one of *Cordiaxylon*, based on its pith, have been noted among the petrified remains, although other types of stems are likely present as well. Many of the petrifications are relatively large, including logs that appear to have been washed together into a fairly large logjam. The most abundant members of the flora are numerous pectopterid leaves, often with intact fronds, and petrified logs. This flora constitutes one of the few known floras of this age in the American Southwest.

- 244** TIDWELL, WILLIAM D.\*, SIDNEY R. ASH, AND LEITH S. TIDWELL. Department of Botany and Range Science, Brigham Young University, Provo, UT 84602 and Department of Earth and Planetary Sciences, University of New Mexico, Albuquerque, NM 87131—Two new species of *Charliea* from Pennsylvanian - Permian strata of New Mexico and Utah.

Two new species of *Charliea* Mamay (1990), originally described from the Upper Pennsylvanian Kinney Brick quarry east of Albuquerque, NM, have been collected from two additional localities in the western

United States. *Charliea* n. sp. A is from the Lower Permian Red Tanks Member of the Madera Formation at the Carrizo Arroyo locality west of Albuquerque and *C.* n. sp. B from the lowermost Pennsylvanian Manning Canyon Shale in central Utah. *Charliea* was defined as having linear-oblong pinnae incised to form 2-4 nearly equal lobes, and having a rather broad, oblique attachment. The venation is simple, parallel, dichotomously branched and terminates in the lobed margins. Slight modifications in the generic diagnosis are necessary before these new species can be included in *Charliea*. The new species differ from the genotype *C. manzanitana* Mamay from the Kinney quarry in pinna shape and size, position of the greatest pinna width, and the smaller number of veins entering the lobes. Based on the ages of the new species, *Charliea* appears to have existed throughout the Pennsylvanian into the Lower Permian in the western United States.

- 245** WANG, XIN\* AND DAVID DILCHER. Paleobotany Lab, Florida Museum of Natural History, University of Florida, Gainesville, FL32611-7800—*Study of Ternstroemites Leaves and Their Relationships With Living Gordonia*.

*Ternstroemites* leaves are frequently found in Eocene Claiborne age clay deposits in Western Kentucky and Tennessee. The present study was focused upon anatomical and morphological analysis of the fossil leaf *Ternstroemites* and leaves of the living plant, *Gordonia lasianthus*. This analysis consists of leaf form, size, margin, venation, cuticle characters (including stomata, trichomes and epidermal cells) of the fossil and modern leaves. Reports of *Gordonia* have been made based upon fruits and seeds preserved in the same clay deposits from which *Ternstroemites* leaves have been found. Therefore we applied a rigorous comparison of leaf characters to see if the fossil leaves also demonstrate close similarities of numerous characters to the living genus *Gordonia*. The character sets of the fossil and living leaves appear similar. As a result of its ancient history, *Gordonia* is distributed today Southeast Asia, southeast North America, Central America and north South America. Changes in paleoatmosphere concentration of carbon dioxide can also be observed from the stomatal index data of the fossil leaves.

## X. Phycological Section

### Contributed Papers

- 246** FREDERICQ, SUZANNE AND JUAN M. LOPEZ-BAUTISTA.\* Department of Biology, University of Louisiana at Lafayette, Lafayette, LA 70504-2451—*Phylogeny, biogeography and life history evolution in the red algal family Phyllophoraceae (Gigartinales)*.

Red algae are exceptional for the great diversity in reproductive morphology and for their complex life histories. In particular, the family Phyllophoraceae, consisting of ~100 species worldwide, stands out in exhibiting a wide spectrum of unique life history types that makes it unusually interesting for assessing the phylogenetic importance of reproductive traits relative to classification criteria. Type of life history and position of the reproductive structures on the plant body have traditionally formed the basis for separating eleven genera in the Phyllophoraceae; however, phylogenetic analyses inferred from three sets of DNA sequences [chloroplast-encoded *rbcL*, nuclear large-subunit ribosomal RNA gene (LSU), and internal transcribed spacer regions (ITS) of nuclear ribosomal DNA], instead indicate a lack of correlation between type of life history and phylogenetic relationships among the established taxa. This lack of correlation dramatically challenges all of the traditional taxonomy. The study will answer the question which morphological features and which aspects of life history evolution can be used as meaningful indicators of phylogenetic relationships in the Phyllophoraceae. The results will also be addressed in light of global biogeographic hypotheses for the family. (Supported by NSF DEB-9903900 and LA BoRSF(1999-2000)-RD-A-50)

- 247** LEWIS, LOUISE A. Ecology & Evolutionary Biology, University of Connecticut, Storrs, CT 06269 USA—*Molecular diversity of green algae from biotic crust communities*.

Biotic crusts are communities of microorganisms such as algae, fungi, and bacteria, that together with lichens and bryophytes, aggregate soil in semi-arid and arid habitats world-wide. A survey of biotic crust algae from several biotic crust sites in western North America is currently underway. One aspect of this project is to assess the diversity of green algae from the soil samples, using both morphological and molecular data. At present, there are over 200 isolates of green algae in hand. Based on morphological, the isolates have been provisionally assigned to genera in three green algal classes: the Charophyceae, Chlorophyceae, and Trebouxiophyceae. A small proportion of the isolates have been sequenced thus far. Phylogenetic analyses using

the molecular data can be used to demonstrate that the phylogenetic diversity of the desert green algae is very high. In addition, a significant proportion of the isolates are not closely related to published sequences of other green algae. In each of the Classes, there appear to be distinct clades of desert algae. Most interesting is the association of clades of desert algae to aquatic sister taxa. These pairs of taxa offer an interesting comparison between aquatic and desert taxa with regard to physiological adaptations to desert-living. A project to explore possible physiological adaptations is underway.

## Contributed Posters

- 248** LOPEZ-BAUTISTA, JUAN M.\*, DONALD KAPRAUN, DEBRA A. WATERS, AND RUSSELL L. CHAPMAN. Department of Biology, University of Louisiana at Lafayette, Lafayette, LA, 70504 (Lopez-Bautista), Department of Biological Sciences, University of North Carolina, Wilmington, NC (Kapraun), Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803 (Waters and Chapman)—*Nuclear DNA quantification and the life cycle in Cephaleuros parasiticus (Trentepohliales, Chlorophyta)*.

Microspectrophotometry with the DNA-localizing fluorochrome DAPI was used to quantify nuclear DNA content in eight species representing three genera of the subaerial green algal order Trentepohliales (Chlorophyta). Comparisons of mean fluorescence intensity (If) values of algal nuclear genomes to those of chicken erythrocytes (RBC) resulted in an estimate of 1.1-4.1 pg for the algae. DNA levels in *Cephaleuros parasiticus* Karsten for 2C nuclei in gametophytic phase closely approximate 50% of the 4C values in the sporophytic phase, confirming previous observations based on culture and ultrastructural studies on the presumptive sexual life cycle in this genus. The alternation of generations in this species was not indicated in the original description by Karsten or in any subsequent studies. Genome quantification data for eight trentepohlialean taxa suggest a doubling sequence for nuclear DNA contents. This phenomenon might reflect the presence of a polyploid series in the order Trentepohliales

## XI. Physiological Section

### Contributed Papers

- 249** GURALNICK, LONNIE J.\*, MAURICE SB KU, GERALD E. EDWARDS, VINCENT R. FRANCESCHI, AND BRANDON HOCKEMA. Department of Biology, Western Oregon University, Monmouth, OR 97361, School of Biological Sciences, Washington State University, PO Box 644236, Pullman, WA 99164, University of Florida IFAS, Citrus Res and Education Ctr, 700 Experiment Station Rd, Lake Alfred, FL 33850—*Induction of the CAM pathway in the C4 plant, Portulaca grandiflora*.

*Portulaca grandiflora* is a herbaceous annual of the family *Portulacaceae*. It exhibits a Kranz anatomy typical of C4 species but *Portulaca* shows some degree of succulence. Research has shown that *Portulaca* shows a diurnal acid fluctuation typical of CAM-cycling. Under well-watered conditions, PEP carboxylase was localized in the leaf mesophyll tissue but when water-stressed, PEP carboxylase was found throughout the water storage tissue of the leaf. Stems also showed an increase in the PEP carboxylase signal when water-stressed. During water stress, the water storage tissue collapses, presumably transferring water to the bundle sheath, which remain turgid during the 10 days of water stress. Immunoblot analyses of protein gels were done for NADP-ME, and PEP carboxylase. We found a slight decrease in the proteins of the C4/CAM pathway in the leaves of *Portulaca*. The stem showed increases in the proteins of the CAM pathway when water stressed which included a new isoform of NADP-ME. These results demonstrate for the first time, that the stems of *Portulaca* are an inducible CAM tissue. The stem may play a supporting role for the leaves during water stress since our experiments showed that the stem during 10 days of water stress, lost only ~5% of its relative water content. Under water stress conditions, a measure of the true rate of photosynthesis (Photosystem II activity; JO2) showed an increase in the late afternoon when compared to control plants. Two factors may account for this; one, an increase in the CO2 released from decarboxification in the water storage tissue giving the leaf an internal source of carbon dioxide, and two, an increase in the Mehler peroxidase reaction. Our results reveal differences between *Portulaca grandiflora* and other, non-succulent C4 plants, *Amaranthus cruentus* and *Zea Mays*, which show a decline in JO2 after 4 days of water stress.

- 250** ALOKAM, SUNEETHA\*, CHENDANDA C CHINNAPPA, AND DAVID M REID. Department of Botany, University of Calgary, Calgary, AB T2N1N4, Canada—*Red/Far red light-mediated shade avoidance stem elongation response and anthocyanin accumulation in alpine and prairie ecotypes of Stellaria longipes*.

The ratio of red light (R) to far red (FR), R/FR light varies greatly between different environments. Plants perceive this variation in the quality of light through phytochromes and regulate their growth and development in response to these signals. We compared the shade avoidance stem elongation response and anthocyanin accumulation between alpine (1D) and prairie ecotypes (7B) of *Stellaria longipes* under varied R/FR ratios of 0.7 and 1.9 while all other environmental conditions were maintained at uniform levels. The prairie ecotype considered to be the shade avoider showed a high degree of stem elongation in response to R/FR 0.7 than under R/FR 1.9 as compared to alpine ecotype. Correlation between the effect of varied R/FR light on anthocyanin levels and Phenyl alanine ammonia lyase (PAL) activities were also studied: 1) The levels of anthocyanin in 7B, as compared to 1D, were significantly higher under high R/FR light and under reduced R/FR both 1D and 7B showed almost the same levels of anthocyanin; 2) Etiolated 7B plants when transferred to both high and reduced R/FR conditions showed highest PAL activity at 48h. There was no significant difference in PAL activity under varied R/FR light; 3) Etiolated 1D plants also showed similar trends with highest activity at 48h, however the overall PAL activity under both reduced and high R/FR light was significantly less as compared to 7B. These results indicate that varied R/FR light causes significant difference in the stem elongation and accumulation of anthocyanin but not in PAL activity.

- 251** FAN, SHUGUO\*, CHENGYE LIANG, AND HONGXIAN LIU. South China Institute of Botany, Academia Sinica, Guangzhou 510650, P. R. China—*Somaclonal male sterile mutants and their expressions in male sterile rice (Oryza sativa L.) somaclones*.

Young panicles from five rice varieties, Zhenshan 97A (WA type cytoplasmic male-sterile (CMS) line, indica), Hongyuan A (HL type CMS line, indica), Baoyuan A (BT type CMS line, indica), Nongken 58s (photoperiod-sensitive genic male-sterile rice (PGMR), japonica) and W6154s (thermo-sensitive genic male-sterile rice (TGMR), indica), were cultured on different media. 10 cases of male-sterile variants in three rice varieties, Hongyuan A, Baoyuan A and W6154s were found. Abortive pollen of rice could be classified into four types: pollen free type (PFT), typical abortion type (TAT), spherical abortion type (SpAT) and stained abortion type (StAT). The phenomenon that type of pollen abortion could change from one to another through tissue culture was found in rice somaclones in R1 generation. Male-sterile variants in R1 generation were crossed with ten typical maintainer lines and restorer lines (Zhenshan 97B, Erjiuai 4B, Hongyuan B, Baoyuan B, Taiyin 1, Minghui 63, Ce 64, IR24, IR26 and IR36) to investigate the restoring and maintaining relationship of these male-sterile variants. The main results were as follows: The restoring and maintaining relationship of one typical abortion type (TAT) variant in R1 regenerated plants which derived from Baoyuan A (coded 28-18) was the same as that of WA type. The variant had been backcrossed with their maintainer lines for five generations, and kept sterile all along. Four male-sterile variants, which derived from Hongyuan A (one was coded 24-1, StAT; the other was coded S14-1, TAT) and Baoyuan A (one was coded 28-5, SpAT; the other was coded 28-19, TAT), kept sterile continuously for five generations when they were backcrossed with the ten parents stated above. The other five male-sterile variants, which derived from Hongyuan A (coded 24-5), Baoyuan A (coded 28-35) and W6154s (coded WP-1, WP-2 and WS) turned into fertility with a lot of fertile pollens and more than 80% self seed set rate when they were crossed with the ten parents stated above.

- 252** STRAUB, PETER F. Biology Program, The Richard Stockton College, Pomona, N.J. 08240-0195—*Construction of a putA -GUS reporter gene for insertion in the nitrogen fixing symbiont Bradyrhizobium japonicum*.

To study the effects of drought induced proline accumulation in soybean nodules on the resident nitrogen fixing bacteria (*B. japonicum*), a reporter gene was constructed by fusing ca.1 kb of upstream region of a cloned *B. japonicum* putA gene with a  $\beta$ -glucuronidase (GUS) reporter gene (with the technical assistance of Dr. T. Sutliff). The GUS gene was cloned into a new *Xba*I site that was made by site directed mutagenesis of the putA start codon. A spectinomycin resistance gene was cloned in to complete the expression cassette. The expression cassette, in pBluescript, was tested in *E. coli* by incubation of cells with and without 250 mM proline followed by assay with the chromogenic substrate X-Gluc. GUS activity was consistently higher in the proline treated samples indicating the reporter construction was expressing. The expression cassette was then isolated by restriction digest, blunted and linkerized with *Not*I linkers and cloned into the *B. japonicum* insertion plasmid pAY19, prepared by *Hind*III digestion and linkerized with *Not*I. The plasmid pAY19



directs chromosomal insertion into a non-coding region of the *nifDK* locus. This work will compliment previous *putA* insertional knockout mutants in the symbiont that have been shown to affect seed yield under drought in the whole plant by allowing the *putA* gene activity to be monitored *in vivo* without disrupting bacteroid proline concentrations as in the case of the knockout mutants.

## Contributed Posters

- 253** BOTHWELL, BRYAN, CHERYL L. LOVELESS, RAYMOND R. BARD, AND MICHAEL D. SNOW.\* Department of Chemistry and Physics, Department of Biology, University of Portland, Portland, OR 97203—*Monoterpene levels in Douglas-fir needles in relation to needle midge infestation.*

The Douglas-fir Needle Midge (*Contarinia pseudotsugae*) is a serious pest of Douglas-fir Christmas trees in the Pacific Northwest. In this study, levels of monoterpenes were measured in needles of current (1999) and previous year's (1998) growth from infested and uninfested branches of Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) trees. Samples were taken at approximately bi-monthly intervals from May through October. Monoterpenes were identified and quantified using gas chromatography/mass spectroscopy. Nine monoterpenes occurred regularly in all trees. Beta-pinene was the most prevalent compound in all samples. Total terpenes were higher in 1998 age-class needles than the 1999 age-class needles in the early season. Camphene and bornyl acetate were higher in uninfested needles than in infested 1999 age-class needles. These two compounds are known to decrease budworm larval growth and may be important in influencing needle midge host choice.

- 254** FAN, SHUGUO\*, CHENGYE LIANG, AND HONGXIAN LIU. South China Institute of Botany, Academia Sinica, Guangzhou 510650, P. R. China—*Identification of restoring and maintaining relationship of male sterile variants of rice (Oryza sativa L.) cultured in vitro.*

Pollen free type (PFT) genic male-sterile (GMS) line Nanguangzhan had turned into WA type-like CMS line. The restoring and maintaining relationship of NT1 and NT2 (two typical abortion type male sterile variants from Nanguangzhan somaclones) was similar to that of WA type. NT1 had been backcrossed with its maintainer lines for 10 generations and kept sterile all the way. This might be the first report of this kind of mutant derived from somaclones of rice which had turned into CMS from GMS. There were four typical abortion type (TAT) variants in R1 regenerated plants which derived from Minghui 63 (coded S11-14), IR26 (coded 26-9-15-7), Zhenshan 97B (coded B2-9-15-4), and Baoyuan A (coded 28-18), whose restoring and maintaining relationship was the same as that of WA type. These variants had been backcrossed with their maintainer lines for five generations, and kept sterile all the way. The restoring and maintaining relationship of one of TAT variants which derived from Minghui 63 (coded S10-2) was completely different from that of WA type, HL type and BT type, viz. S10-2 was crossed with IR24, IR26, IR36, Ce 64, Taiyin 1 and Minhui 63 and kept sterile; while it was crossed with Zhenshan 97B, Erjiuai 4B, Hongyuan B and Baoyuan B and turned into fertility, both pollens and seeds were fertile. S10-2 had been back-crossed with its maintainer lines for five generations, and kept sterile all along. Five male-sterile variants, which derived from IR26 (coded 26-9-24-11, TAT), Hongyuan A (one was coded 24-1, stained abortion type (StAT); the other was coded S14-1, TAT) and Baoyuan A (one was coded 28-5, spherical abortion type (SpAT); the other was coded 28-19, TAT), kept sterile continuously for five generations when they were backcrossed with 10 fertile parents (Zhenshan 97B, Erjiuai 4B, Hongyuan B, Baoyuan B, IR24, IR26, IR36, Ce 64, Taiyin 1 and Minghui 63).

- 255** FAN, SHUGUO\*, CHENGYE LIANG, AND HONGXIAN LIU. South China Institute of Botany, Academia Sinica, Guangzhou 510650, P. R. China—*In vitro mutation of rice (Oryza sativa L.) from GMS to CMS.*

Pollen free type (PFT) genic male-sterile (GMS) line Nanguangzhan had turned into wild abortive (WA) type-like cytoplasmic male sterile (CMS) line. The restoring and maintaining relationship of NT1 and NT2 (the two typical abortion type (TAT) variants derived from Nanguangzhan somaclones) was similar to that of WA type, viz. the restorer lines and maintainer lines of WA type were also fit for NT1 and NT2. NT1 had been backcrossed with its maintainer lines for ten generations and kept sterile all the way. This might be the first report of this kind of mutant derived from somaclones of rice which had turned into CMS from GMS.

- 256** HAY, JORDAN O.\*, MIGUEL PINEROS, LEON V. KOCHIAN, AND ROGER M. SPAN-SWICK. Department of Plant Biology, U.S. Plant, Soil and Nutrition Laboratory, Cornell University, Ithaca, NY 14853—*Isolation of rice aleurone protoplasts and whole cell patch clamping.*

Very little is known about the physiology of sucrose transport into developing rice grains. While the post-phloem unloading sucrose transport pathway has been described in detail, quantitative studies of sucrose uptake including the role of membrane transport are lacking. This has limited our understanding of carbon partitioning and the control of rice yield. We are interested in studying the sucrose-proton cotransport system that has been reported as being expressed in rice endosperm. Based on previous reports that the aleurone layer is symplastically isolated from the phloem, we chose to investigate sucrose-proton cotransport in rice aleurone cells. Aleurone protoplasts were isolated from *Oryza sativa* aleurone peels using standard cell wall degradation enzymes. Very high osmolarity, 0.8-1 M mannitol or sorbitol, was essential for obtaining high yields of 5,000-30,000 viable protoplasts/10 grains. Protoplasts were 20-40  $\mu\text{m}$  in diameter and had granular cytoplasm. These traits were consistent with previous reports on rice aleurone layer morphology and were confirmed after our study of grain anatomy using light microscopy. The aleurone protoplasts proved to be a system amenable to whole cell patch clamping. We formed high resistance seals (3 Giga-ohms) without difficulty and assessed whole cell currents from protoplasts bathed in solutions containing different levels of  $\text{K}^+$ . The whole cell conductance of these cells was dominated by an instantaneous outward current as well as a slow developing, time dependent inward current. Future experiments, designed for modeling rice yield, include testing the suitability of this aleurone whole cell system for quantitative studies of sucrose-proton cotransport.

- 257** PEREIRA-NETTO, ADAUCTO B.\*, JULIANA M. MENESTRINA, ANA MARIA A. CARNEIRO LEO, AND MARCELO IACOMINI. 1Dept. of Botany-SCB-University of Parana; 2 Dept. of Biochemistry-SCB-University of Parana; 3 Dept. of Animal Morphology and Physiology-University of Pernambuco—*A novel lysine-rich arabinogalactan with regulatory effects on carrot (*Daucus carota*) cells growth and differentiation.*

Arabinogalactan-proteins (AGPs) are a class of proteoglycans found in cell secretions and plasma membranes. Attention is currently focused on their structure and their potential role in plant cell growth and development. An acid arabinogalactan has previously been shown to be the major component of the cashew nut tree (*Anacardium occidentale*) gum exudate [Menestrina, J.M. et al., 1998 (Phytochemistry, 47: 715-721)]. Steric exclusion chromatography revealed that this arabinogalactan has a molecular weight of  $11.2 \times 10^3$  of which 0.5 % (w/w) consists of protein. Analysis of the amino acid composition of the polysaccharide protein moiety showed that it has a high lysine content (82.1%), a low serine (9.5%) and alanine (2.2%) content, and also undetectable amounts of proline or hydroxyproline. Significant ( $p=0.05$ ) reduction on the number of somatic embryos, regardless differentiation stage, was found for carrot (*Daucus carota*) cells grown in a culture medium enriched with this arabinogalactan. However, no significant change on the number of somatic embryos, at the cotyledonary stage, was found for carrot cells grown in this arabinogalactan-enriched culture medium. No significant ( $p=0.05$ ) difference was found for fresh weight of carrot cells grown in the arabinogalactan-enriched culture medium. However, significant reduction on the cells's fresh weight was noticed when the cells were grown in a culture medium containing a sulfated (D.S. = 1.13) form of the arabinogalactan. Based on these results, we hypothesize that the hydroxyprolin, serine, and alanine-rich protein moiety, which characterizes AGPs, is not a requirement for the arabinogalactans to be able to change the plant cell growth (fresh weight) or differentiation (embryogenetic potential) pattern.

## XII. Phytochemical Section

### Contributed Papers

- 258** JOHNSON, EMANUEL L. AND STEPHEN D. EMCHE.\* USDA ARS Weed Science Laboratory PSI, Bldg 001 Rm 329 , Beltsville, MD 20705-2350 USA—*Transgenic Plants: A source for medicinal plants.*

Tropane alkaloids are a class of secondary metabolites occurring in several solanaceous and Erythroxylum plant species. The alkaloid family includes several important compounds that have both positive and negative effects on the mammalian and insect nervous systems, and for commercial purposes, are plant derived. Leaf

waxes and polyphenols are major bearers that inhibit protoplast isolation from leaves of alkaloid bearing taxons of *Erythroxylum* which are useful for electrochemical fusion to produce transgenic plants. In this study several digestion enzymes were used to overcome these barriers to obtain ideal protoplasts for electrochemical fusion. The most efficient was a combination of Cellulase (2%), Hemicellulase (1%) and Macerace (1%) in a 0.7 M mannitol and 0.01 M MES osmoticum (pH 5.8). Young leaves were harvested from four tropane bearing *Erythroxylum* taxons and thoroughly washed in a 10% bleach solution, rinsed  $3 \times$  in de-ionized water, cut into 1 mm strips and placed into petri dishes for digestion at 24°C. The enzymes and osmoticum above were used for the digestion. Leaves during digestion were agitated for 3 hr at 45 rpm and thereafter, digestion continued for 5 hr. After digestion, the osmoticum and free protoplasts were filtered, to remove debris, centrifuged and separated by sucrose density gradient. Digestion yielded a cell density of  $\sim 8.0 \times 10^5$ . For electroporation, volumes of 20  $\mu$ l of protoplasts were placed in BTX electroporation chambers and 'pearl chained' for 20 sec at 20 V, and fused at 120 V for 10  $\mu$ s. Within the microscopic field of view (200 $\times$ ), an average of 15 protoplasts could be viewed with 5 to 7 successful fusions. There were  $\sim 6000$  protoplasts per slide or 2,400 fusions and the rate of fusion was 40%. Vector incorporation, transgenic growth and development and metabolites are currently being monitored for herbicide activity and useful medicinal products.

**259** JOHNSON, EMANUEL L.\*, WALTER F. SCHMIDT, AND DONALD COOPER. USDA ARS, Bldg 001 Rm 329, 10300 Baltimore Ave, Beltsville, MD 20705-2350—*Flavonoids as chemotaxonomic markers for cultivated Amazonian Erythroxylum*.

Purported *Erythroxylum coca* var. *ipadu* Plowman (E. c. var. *ipadu*; Amazonian coca) leaves were harvested from fields in Colombia, South America (S. A.) during the months of October, November and December, 1997 to: (i) determine if their flavonoid profiles were complementary to those of our collection and (ii) determine if the leaf flavonoids could be indicative of kinship to a specific taxon(s) of cultivated *Erythroxylum*. Polar methanolic extracts from leaf tissue of Amazonian coca harvested from fields in Colombia S. A., were assayed by HPLC, GC-MS, LC-MS and <sup>1</sup>H NMR to determine the flavonoid profile and O-conjugation of aglycones. These leaf extracts afforded eight O-conjugated flavonoids: two O-conjugates of taxifolin, one O-conjugate of quercetin, two, O-conjugates of eriodictyol three, O-conjugates of kaempferol. Present also in leaf tissue of Amazonian field grown E. c. var. *ipadu*, but lacking in leaf tissue from our collection was an O-ethyl ester typically found in E. c. var. *coca*, kaempferols and an O-7-rutinoside commonly encountered in the E. novogranatense taxons. Flavonoids in our collection of Amazonian coca, previously obtained from Colombia, S. A., contained five O-conjugated derivatives of taxifolin and an O-conjugated quercetin. Thus, the leaf flavonoids of the taxon differ not only between species but also within taxons. The flavonoids of E. c. var. *ipadu* (Amazonian coca) currently under cultivation in fields in Colombian are a mixture of those present in E. c. var. *coca*, E. c. var. *ipadu* and E. n. var. *truxillense*, whereas the flavonoids present in our living collection of E. c. var. *ipadu* are derivatives of E. c. var. *coca*. Our data strongly suggest that Amazonian coca (E. c. var. *ipadu*) currently under cultivation in Colombian fields is a genetic hybrid between E. c. var. *coca* and E. n. var. *truxillense*. We propose that this hybridization occurred after the late 1970's.

**260** SEILER, GERALD J. USDA, Agricultural Research Service, Northern Crop Science Laboratory, P.O. Box 5677, Fargo, ND 58105—*Concentration of Saturated Palmitic and Stearic Fatty Acids in Achene Oil of a Population of Wild Helianthus annuus*.

The present trend in human diets is to decrease the consumption of the saturated fatty acids, palmitic and stearic fatty acids. Studies have shown that consumption of high levels of saturated fats increases the risk of cardiovascular diseases. Vegetable oils are the principal source of fats in many diets. Sunflower oil, which is fourth in production among vegetable oils in the world, contains 6.5% palmitic and 4.5% stearic acids. In an effort to reduce saturated fats in sunflower oil, a survey of wild annual *H. annuus* populations was undertaken to identify potentially useful populations with low palmitic and stearic fatty acids (less than 7% combined). Achene oil of one population of wild *H. annuus* from Holmquist, SD had a palmitic acid level that averaged 3.9% with a range of 2.8 to 4.3%, while stearic acid averaged 1.9% with a range of 1.5 to 2.2%. The combined 5.8% palmitic and stearic acids is almost 50% lower than the present level of these fats in sunflower oil. The level of saturated fatty acids observed in the population remained low when plants were grown in the greenhouse under uniform conditions. In the greenhouse, palmitic acid averaged 4.0%, while stearic acid averaged 1.9%. This would indicate that palmitic and stearic acids have a genetic base with the potential for selection and incorporation into cultivated sunflower to lower the present level of saturated fats in sunflower oil.

### XIII. Pteridological Section / American Fern Society

#### Symposium: Biology and conservation of the Ophioglossaceae: A tribute to Warren “Herb” Wagner

- 261** FARRAR, DONALD R.\*, CINDY L. JOHNSON-GROH, AND WARREN D. HAUKE. Department of Botany, Iowa State University, Ames, IA 50011; Department of Biology, Gustavus Adolphus College, St. Peter, MN 56082; Department of Biology, Denison University, Granville, OH 43023—*Biology and conservation of the Ophioglossaceae—A tribute to Warren “Herb” Wagner.*

The Ophioglossaceae possess a suite of characters that long ago prompted speculation on their possible descent from Paleozoic Coenopterid ferns. The combination of vascular cambium (*Botrychium*), collateral vascular bundles, non-circinnate venation, single annual leaf cleft into fertile and sterile segments, underground apex with preformed leaves, simple, fleshy, hairless mycorrhizal roots and long-lived subterranean gametophytes suggest a lineage separate from the remainder of ferns. Many of these plants possess remarkably low intraspecific genetic diversity, perhaps due to underground fertilization, and perhaps allowed by their mycorrhizal relationship. Despite low genetic variability, *Botrychium* species appear to have undergone recent and continuing speciation. Aspects of Ophioglossaceae morphology, phytogeography, speciation, and systematic relationships will be presented in the first half of the symposium. Ecology and conservation issues will be presented in the second half. Subtle species differences in morphology, combined with small size, irregular appearance above ground, and rarity of many of the species, present daunting challenges in conservation management. Spore germination, gametophyte growth, fertilization and juvenile sporophyte stages occur below ground. Current analyses of critical underground stages are increasing our understanding of population dynamics in *Botrychium*. Reviews of Ophioglossaceae floristics and conservation needs in North America conclude the symposium.

- 262** AHLENSLAGER, KATHLEEN E. Colville National Forest, Colville, WA 99114—*Conservation of rare plants on public lands.*

Managers of public lands are charged with conserving rare plants, but information about the basic life history and ecology of these plants is lacking. Each federal and state land agency has distinct mandates and regulations under which it manages public lands. Federal and state botanists assist in planning and implementing a variety of diverse projects on these lands, including timber harvest, grazing, mining, road-building, and recreation. These specialists survey project areas, report rare plant sightings to state Natural Heritage Programs, analyze projects for effects, propose mitigation measures, and monitor rare plant populations. As budgets to carry out this work continue to decrease, managers and academics need to coordinate our efforts to prioritize work and establish long-term population monitoring in order to understand each species' response to environmental variation and habitat management.

- 263** FARRAR, DONALD R. Department of Botany, Iowa State University, Ames, IA 50011—*Evolution and speciation in Botrychium.*

Allozyme studies of *Botrychium* have revealed several surprising and seemingly contradictory facts: 1) diploid species have remarkably low genetic variability, and 2) heterozygous individuals within populations are extremely rare, but 3) genetic differentiation between species is high, equaling that between species of most fern genera. Low genetic variability in species and lack of heterozygotes most likely result from sexual reproduction via intragametophytic selfing that is promoted by the underground habitat of the bisexual gametophytes. If this has always been true of *Botrychium*, then how did inbreeding ancestors with low genetic variability generate the variation to produce the current well-differentiated species. The expected continuous variation among progeny of such species over time must have been recently fragmented into precursors of today's species. Habitat fragmentation by Pleistocene glaciation in the high latitude/high elevation habitats typical of *Botrychium* is a likely cause of recent speciation events. In *Botrychium* subgenus *Botrychium* allotetraploid species outnumber diploids nearly 2 to 1, and many are widespread and considerably more variable genetically and morphologically than their diploid parents. Allotetraploids may be favored because of their greater variability inherited through multiple origins and enhanced through differential gene silencing.



- 264** FARRAR, DONALD R.\* AND FLORENCE S. WAGNER. Department of Botany, Iowa State University, Ames, IA 50011; Department of Biology, University of Michigan, Ann Arbor, MI—*An overview of the Ophioglossaceae.*

Are Ophioglossaceae really derived from coenopterid ferns? What is their relationship to other ferns? What is the origin of their morphological peculiarities? To what extent is morphology related to habitat and mycorrhizal associations? These questions have perplexed pteridologists for over a century of study of this enigmatic group of plants. In this presentation we introduce aspects of morphology, growth habit, and ecology that give rise to these questions. We also present overviews of the group's taxonomy, cytology, and phyto-geography to set the stage for detailed presentations that follow. These studies illuminate the unique contributions of the Ophioglossaceae to the study of pteridophyte evolution and conservation.

- 265** HAUKE, WARREN D. Department of Biology, Denison University, Granville, OH 43055—*Phylogeny of the Ophioglossaceae based on molecular and morphological characters.*

Phylogenetic relationships among genera of the Ophioglossaceae are controversial because morphological/anatomical features have been interpreted differently by various researchers. To construct a phylogeny of the family, I sequenced the protein encoding gene *rbcL* and the non-coding spacer region *trnL-F* from approximately 40 species representing the range of diversity of the family. In addition, I analyzed cladistically morphological/anatomical characters from the same taxa to provide an independent comparison to the molecular phylogeny. All three data sets supported two major clades within the family, an ophioglossoid lineage and a botrychioid lineage. *Helminthostachys* is sister to a monophyletic *Botrychium s.l.*, in which *Botrychium s.s.* is sister to *Sceptridium*, and *Botrypus* is paraphyletic. Though relationships within *Ophioglossum s.l.* were not well resolved, *Cheiroglossa* and *Ophioderma* appear to be sister taxa, and *Ophioglossum s.s.* may be paraphyletic.

- 266** HOEFFERLE, ANN M. Northern Ecological Services, Inc., P.O. Box 54, Reed City, MI 49677—*Impacts of aerial leaf removal on subsequent year reappearance and size of leaves of the daisy leaf moonwort (Botrychium matricariifolium) and the triangle moonwort (Botrychium lanceolatum var. angustisegmentum).*

The impacts of aerial leaf (trophophore and sporophore) removal on reappearance and trophophore size the following year was studied in two species of moonworts (*Botrychium* subgenus *Botrychium*). Aerial leaves of *B. matricariifolium* and *B. lanceolatum angustisegmentum* were removed either before spore release in the spring or after spore release in the late summer. Leaf removal did not have an impact on the percent re-emergence of leaves the following year, regardless of the time of removal. Aerial leaf removal before spore release also had no impact on the size of leaves (i.e. length and width of trophophore and the length of the basal pinna) produced the following year. However, in plants having their leaves removed after spore release, the size of the next year's leaves were significantly smaller than control plants of the same year. This suggests that some of the energy expended in the maturation of spores may need to be recovered from the above-ground structures in order to produce the same size aerial leaf the next year. Removing the above-ground leaf before sporulation allows the plant to retain sufficient energy reserves to produce the same size leaf the following year.

- 267** JOHNSON-GROH, CINDY, L., LAURA SCHOESSLER\*, CHANDA RIEDEL, AND KRISSA SKOGEN. Department of Botany, Gustavus Adolphus College, 800 W. College Ave., St. Peter, MN 56082—*Underground distribution and abundance of Botrychium gametophytes and juvenile sporophytes.*

A significant portion of the life history of *Botrychium*, the gametophyte and juvenile sporophytes stages, are spent underground. Experiments were conducted to determine the distribution and abundance of underground structures of eight species of *Botrychium*. Soil samples were collected in a 200 m<sup>2</sup> area, sieved through a series of soil sieves and then processed using a centrifugation technique separating out the lighter plant material. The underground distribution of *Botrychium* is clumped and not regularly distributed. Only 30% of the samples processed contained underground structures. The gametophytes of *B. campestre* are most abundant followed by *B. mormo* with 2021 and 700 gametophytes/m<sup>2</sup> respectively. *B. montanum* and *B. fenestratum* also have relatively high abundances of 580 and 480 gametophytes/m<sup>2</sup>. *B. virginianum* and *B. gallicomontanum* were the least abundant at 70 and 10 gametophytes/m<sup>2</sup>. *B. campestre* and *B. gallicomontanum* both produce vegetative propagule (gemmae) but there was no apparent correlation with this character and abundance of gametophytes underground. The "underground structure bank" is the source of juvenile

plants that will eventually emerge and sustain the populations. The underground bank greatly exceeds in number the visible aboveground portion of the population. Its size and health is critical to sustain the aboveground reproductive portion of the population.

**268** JOHNSON-GROH, CINDY. Department of Biology, Gustavus Adolphus College, 800 W. College Ave., St. Peter, MN 56082—*Population dynamics of Botrychium*.

The 2000 field season represented the fourteenth year of monitoring several species of *Botrychium* populations in Minnesota, Iowa, Oregon, and Alaska. A total of 37 plots have been monitored annually including over 2600 individual tagged plants. Populations fluctuate independently within and between plots as well as between years and between plots at different sites. These differences reflect microsite differences such as soil moisture, herbivory, or mycorrhizae. Fire, herbivory, herbicide and timber harvest have an immediate impact on the above-ground sporophytes. The long-term effect of these factors on below-ground structures (gametophytes and juvenile sporophytes) appears to be buffered by the large bank of underground structures. Monitoring reveals populations are fairly resilient and rebound following perturbations though it may take several years. Using what we know about the species biology we can model population responses to natural and man-made perturbations. The model resulting from this analysis predicts greater stability of populations than might be concluded from monitoring above-ground plants. This is a consequence of having a large proportion of the population existing in underground stages. Even catastrophic elimination of all the underground gametophyte and sporophyte stages does not inevitably lead to population extinction because of the importance of the spore bank. Despite highly variable above-ground population fluctuations, below-ground stages provide *Botrychium* populations with a high degree of buffering against local extinction.

**269** MATULA, COLLEEN F. USDA, Ottawa National Forest, Bessemer, MI 49911—*Conservation status of Botrychium in the Upper Great Lakes*.

In the Upper Great Lakes Region of the United States, the *Ophioglossaceae* are represented by 2 species of *Ophioglossum* and 18 species of *Botrychium*. In the latter there are 13 species of moonworts (subgenus *Botrychium*), 4 species of grapeferns (subgenus *Sceptridium*) and *B. virginianum*, the rattlesnake fern in subgenus *Osmundopteris*. Of these, 13 species are state-listed as endangered, threatened, or of special concern. In Minnesota *B. gallicomontanum*, *B. oneidense* and *B. pallidum* are listed state endangered; *B. lanceolatum*, *B. lunaria* and *B. rugulosum* are listed as state threatened; and *B. campestre*, *B. minganese*, *B. mormo* and *B. simplex* are listed state special concern. In Wisconsin, *Botrychium lunaria* and *B. mormo* are state endangered; and *B. campestre*, *B. minganese*, *B. oneidense*, *B. rugulosum*, and *B. spathulatum* as state special concern. In Michigan, *Botrychium acuminatum* is state endangered; *B. campestre*, *B. hesperium*, *B. mormo* are state threatened; and *B. pallidum* is state special concern. Conservation measures in the Upper Great Lakes Region have varied among the agencies within the states. The similarities have been in the form of inventory, monitoring rare occurrences and identifying local distributions. Some agencies have developed protection measures by leaving buffers adjacent to rare populations. In Minnesota, various population studies of *Botrychium mormo* were conducted by science professionals from federal agencies. The Forest Service is conducting a 5 year study of *Botrychium mormo* habitat that have had some forest canopy removal. Also in Minnesota, a population viability assessment for *Botrychium mormo* in the three states was conducted in 1997 assessing distribution, potential threats and research needs. In Michigan, the Pictured Rocks National Lakeshore is developing strategies to lessen the impact of exotic species invasion that would potentially affect rare populations of the *Botrychium* species that occur on the dunes. Overall, information exchange across agencies and states is helping to resolve key management concerns.

**270** MONTGOMERY, JAMES D. Ecology III, Berwick, PA 18603—*Conservation Status of the Ophioglossaceae in the Northeast*.

In the northeast region of the United States the *Ophioglossaceae* are represented by 12 species of *Botrychium* and 3 species of *Ophioglossum*. *Botrychium* includes 6 species of moonworts (subgenus *Botrychium*), 5 species of grapeferns (*Sceptridium*), and rattlesnake fern (*Osmundopteris*). No species is federally listed as threatened or endangered. Five species of *Botrychium* and all 3 species of *Ophioglossum* are listed as endangered, threatened or vulnerable in one or more states. All of these represent species at or near their geographic range limits. Some are probably more common than recognized because of their small size and the disappearance of the single leaf produced in a year due to herbivory.

- 271** STENSVOLD, MARY CLAY. U.S.D.A. Forest Service, Alaska Region, 204 Siginaka Way, Sitka, Alaska 99835—*The conservation status of Ophioglossaceae in southern Alaska.*

In southern Alaska the Ophioglossaceae are represented by one species of *Ophioglossum* and eight named species of *Botrychium*. In the latter there are six species of moonwort ferns (subgenus *Botrychium*), one grapefern (subgenus *Sceptridium*), and *B. virginianum*, the rattlesnake fern in subgenus *Osmundopteris*. In addition, there are three distinct undescribed species and several unusual moonworts not clearly fitting known taxa. The State of Alaska does not maintain a threatened and endangered species list, but the U.S. Forest Service is mandated to manage habitats to maintain viable populations of plants; therefore *Botrychium* is afforded protection on National Forest System lands. Habitat disruption resulting from off-road vehicle use and trampling are currently the greatest human-caused threat to *Botrychium*. Several *Botrychium* occupy sandy beach-beach meadow habitat, and this habitat is used by an increasing number of off-road vehicles, resulting in *Botrychium* habitat degradation. Only after the taxonomy, distribution and habitat needs of *Botrychium* are better understood, and the various landowners cooperate in land use management, will we be able to effectively deal with *Botrychium* conservation issues across southern Alaska.

- 272** WATKINS, JR., JAMES E.\* AND J. DAN PITTILLO. Iowa State University, Department of Botany, 353 Bessey Hall, Ames, IA, 50011. Western Carolina University, Department of Biology, 132 Natural Sciences Bldg., Cullowhee, NC 28723—*The Conservation Status of Ophioglossaceae in the Southeastern United States.*

In the Southeastern region of the United States (Virginia west to S Illinois and Arkansas) the Ophioglossaceae are represented by six species of *Ophioglossum*, ten species of *Botrychium*, and a single species of *Cheiroglossa*. In the genus *Botrychium* there are three species of moonworts (subgenus *Botrychium*), five species of grapeferns (subgenus *Sceptridium*) and *B. virginianum*, the rattlesnake fern in subgenus *Osmundopteris*. Of these, 12 species are state-listed as endangered, threatened or of special concern. These include *B. lunarioides* listed as special concern in Alabama, Florida, Mississippi, and Louisiana; *B. bitermum* threatened in Illinois; *B. jenmanii* of historical distribution in Alabama and Virginia, special concern in Louisiana, significantly rare in North Carolina, and threatened in Tennessee; *B. multifidum* endangered in Illinois, significantly rare in Virginia, and candidate in North Carolina; *B. oneidense* of special concern in Tennessee, significantly rare in Virginia, and candidate in North Carolina; *B. lanceolatum* significantly rare in North Carolina and threatened in Virginia; *B. matricarifolium* of special concern in Tennessee, significantly rare in North Carolina, and endangered in Illinois; *B. simplex* listed as historical in Virginia, candidate in North Carolina and endangered in Illinois; *O. crotalophoroides* of special concern in Tennessee and significantly rare in North Carolina; *O. englemannii* of special concern in Alabama and Georgia; *O. petiolatum* historical in Virginia; and *Cheiroglossa palmata* as federally endangered and imperiled in Florida. Special problems regarding the conservation of these are discussed

- 273** WHITTIER, DEAN P. Department of Biology, Vanderbilt University, Nashville, TN 37235—*Gametophyte and young sporophyte development in the Ophioglossaceae.*

Gametophytes of the Ophioglossaceae are tuberous, nonchlorophyllous, nonphotosynthetic, and subterranean. They are parasitic on mycorrhizal fungi which invade their tissues. It is difficult to study these gametophytes in their underground habitat because they are rarely found. Recent work has been done in axenic culture because it offers the opportunity to investigate their development and reproduction for extended periods of time. Depending on the species, the spores germinate after two weeks to several months in the dark. Usually, germination is inhibited by nitrate and promoted by ammonium. The gametophytes remain in the 4-5 celled stage in culture if sugar is not available. Sugar replaces the need for a fungus under these conditions. Normal gametophyte morphology occurs in culture on a nutrient medium containing minerals, including ammonium, and sugar without the fungus. Mature gametophytes of this family can be cylindrical, spherical, tongue-shaped, or bean-shaped and they develop antheridia before becoming bisexual. The gametangia are adjacent to each other which may contribute to the inbreeding known for *Botrychium*. Although gametophytes of some species may mature in less than a year after spores are released in nature or sown in culture, it has been reported that other species may take 20 years to form embryos. In culture, the fastest gametophyte maturation is about 8 months with *Ophioglossum crotalophoroides*. Normal embryo development produces a root that emerges from the gametophyte prior to the first leaf. In axenic culture, young sporophytes of *Botrychium jenmanii* can form one root and three leaves 15 months after the spores were sown. However, after fertilization in some species, a delay in the emergence of a leaf above the soil of 5 or more years can occur because several roots or rudimentary leaves are formed by the young sporophytes.

- 274** ZIKA, PETER\* AND KATHLEEN E. AHLENSLAGER. Herbarium, Department of Botany, University of Washington, Seattle, WA 98195-5325; Colville National Forest, Colville, WA 99114—*Conservation status of Ophioglossaceae in the western United States.*

In the western region of the contiguous United States the Ophioglossaceae are represented by three species of *Ophioglossum* and twenty-two described species of *Botrychium*. In the latter there are twenty species in the moonwort subgenus *Botrychium*, *B. multifidum* in the grapefern subgenus *Sceptridium* and *B. virginianum*, the rattlesnake fern, in the subgenus *Osmundopteris*. This region supports the greatest number of moonwort species in the world, including at least two species as yet undescribed. Because of morphological diversity within species and sometimes subtle differences between species, the moonworts present challenging taxonomic problems. A number of Ophioglossaceae species are listed as endangered, threatened or of special concern in one or more states. Special problems regarding the conservation of rare Ophioglossaceae in the western US are discussed.

## Contributed Papers

- 275** CESKA, ADOLF\* AND OLDRISKA CESKA. Conservation Data Centre, British Columbia Ministry of Environment, P.O. Box 9344, Victoria, BC, Canada V8W 9M1—*Isoetes minima* A.A. Eaton (Isoetaceae) - an overlooked terrestrial quillwort of the Pacific Northwest.

*Isoetes minima* was described from a single collection made by Wilhelm Suksdorf from Spangle near Spokane, WA, and until recently, the only authentic material of this taxon has been the type specimen. On the same collecting trip, Suksdorf collected copious material of *Isoetes howellii* that looked superficially the same as the type of *I. minima*. Based on this limited material, N.E. Pfeiffer reduced *I. minima* into a variety of *I. howellii*. The Flora of North America followed Pfeiffer and redefined this variety to include any small plants of *I. howellii* with small megaspores. Several years ago, we found several large populations of *I. minima* in Wenatchee Mountains, WA, and in 1996 this species was also found in south-central British Columbia. *Isoetes minima* differs from *I. howellii* by having small, spiny megaspores and by sporangia that completely lack velum. Ecologically, *I. minima* occupies the most extreme habitats among the western North American terrestrial *Isoetes* species. It grows in periodically wet depressions in *Artemisia tridentata* sagebrush with *Hesperichon pumilus*, *Lewisia pygmaea*, and *Floerkea proserpinacoides* as accompanying species.

- 276** CRANFILL, RAYMOND. Department of Integrative Biology, University & Jepson Herbaria, University of California, Berkeley, CA 94720—*Has ecological specialization driven a fundamental phylogenetic split in the Polypodiales?*

Notwithstanding significant progress in our understanding of the relationships of basal pteridophytes, the phylogeny of derived leptosporangiate ferns, the Polypodiales, remains enigmatic. Although demonstrably monophyletic, the deeper branching patterns within the group remain uncertain and highly controversial. Accordingly, I conducted an analysis of 40 genera representing each major lineage of Polypodiales based on a combination of three molecular data sets (*rbcL*, *rps4* and *nad5*). Although results are preliminary in view of limited taxon sampling, several interesting observations emerge. The basal position of the denstaedtioid ferns is unperturbed. From this group a monophyletic clade of pteridoid ferns is derived, characterized by the loss of a true indusium and the migration of sporangia back from the laminar margin along the veins. Also derived from this group is an as yet unnamed monophyletic clade of ferns in which the indusium is retained but which is also characterized by a migration of the sorus from a marginal to medial position. The indusiate clade is divided into an asplenioid group and an unnamed sister group that is further divided into two unnamed groups, each with good phylogenetic support. The first group is characterized by the presence of mostly linear, indusiate sori; a fundamentally terrestrial habit; and often strongly dimorphic leaves. The second group is characterized by having round sori, which in several subclades become exindusiate; a more or less epilithic to epiphytic habit; and monomorphic leaves in basal clades which often become strongly dimorphic in epiphytic lineages. The relationship of groups within the second clade suggests a directed diversification related to increasing specialization for the epiphytic habit, while epiphytism is absent from the first clade entirely.



- 277** FARRAR, DONALD R.\* AND JAMES E. WATKINS. Department of Botany, Iowa State University, Ames, IA 50011—*Morphological differentiation through differential gene silencing in the allotetraploid derivatives of Botrychium lunaria X B. lanceolatum—a partial confirmation of the hypothesis of Werth and Windham.*

An allotetraploid species, with two sets of homoeologous gene loci, can lose the function of genes from one of its diploid parents at any given locus without deleterious loss of gene product. This silencing of gene loci can be visualized through enzyme electrophoresis when the gene products of the parental diploid species migrate differentially and one of these contributions is clearly missing in the allotetraploid. Werth and Windham postulated that extensive gene silencing over time could produce evolutionary change in allotetraploids including divergent evolution between genetically isolated lines. *Botrychium* species present a model for testing the possibility of morphological divergence of allotetraploid lines through differential gene silencing. *Botrychium lunaria* and *B. lanceolatum* each display a number of unique allozymes revealing them as the unquestionable parents of the widespread tetraploid *B. pinnatum*. Recently discovered *B. "alaskense"* is equally unquestionably a tetraploid product of the same parental diploids, yet it is quite distinct morphologically from *B. pinnatum*. Allozyme patterns show these taxa to be differentially silenced at 50% of the loci examined in which silencing is detectable.

- 278** GRANT, JASON R. Institut de botanique, Laboratoire de phanérogamie, Université de Neuchâtel, ch. de Chantemerle 18, Neuchâtel 2007, Switzerland—*The genus Botrychium (Ophioglossaceae) in the interior of Alaska - Herb Wagner's final conquest.*

During an on-going floristic project in the interior of Alaska, numerous accessions of *Botrychium* were made and sent to Warren Herb Wagner for identification. Several of these were of such interest that during the summer of 1999, Herb and Florence Wagner came to Fairbanks where we spent a week collecting moonworts. At least five species were identified including *Botrychium lanceolatum*, *B. lunaria*, *B. minganense*, *B. pinnatum*, and a new species. This new species, appears to be related to *B. pinnatum* and *B. boreale*. At present, there doesn't appear to be any need for concern for the habitats of these species, as all seem to thrive best in recently disturbed sites as revegetating river sandbars, maintained lawns, long-fallow agriculture fields, and especially in ditches and along sides of highways. In the interior of Alaska, *Botrychium lunaria* is the most commonly encountered species with *B. minganense* following soon thereafter. The new species is abundant where found. *Botrychium lanceolatum*, *B. pinnatum*, and the second putative new species are infrequently encountered within the large populations of *B. lunaria*, *B. minganense* and the new species. The Wagner's trip to Alaska represents one of Herb's last field exercises. A photographic travelogue of the trip, of these moonworts and other pteridophytes of the interior of Alaska will be presented.

- 279** HAUFLER, C. H.<sup>1\*</sup>, T. HILDEBRAND<sup>1</sup>, P. HAMMOND<sup>2</sup>, J. P. THERRIEN<sup>1</sup>, AND C. WALTERS<sup>1</sup>. <sup>1</sup> Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS, <sup>2</sup>University of California Botanical Garden, San Francisco CA—*New insights concerning the origin of Polypodium scolieri and its ongoing hybridization with sympatric congeners.*

With its thick, leathery leaves, reticulate venation, and large sori, *Polypodium scolieri*, located in a narrow band along the Pacific coast of North America, is perhaps the most distinctive member of the cosmopolitan *P. vulgare* species complex. Although early studies based on morphology and chromosomes were able to develop hypotheses about the relationships among some elements of this complex, no close alliances to *P. scolieri* could be proposed. Combining data from *rbcL* and *trnL* DNA sequences with isozymic analyses suggests that *P. scolieri* is a recently evolved species that is closely allied to and sympatric with *P. californicum* and *P. glycyrrhiza*. Alternatively, because isozyme data indicate that *P. scolieri* is quite distinct from its sympatric neighbors, hybridization between these lineages may have led to chloroplast capture prior to range expansion of *P. scolieri*. Adding further intrigue is that *P. scolieri* contrasts strikingly with its congeners in having never been implicated in the origin of allotetraploid derivatives. As early as 1951, Manton suggested that *P. scolieri* could be forming hybrids with neighboring polypods, but she was sufficiently unsure of the morphology to request, "a purer sample of *P. scolieri*," before stating positively that hybrids had been discovered. Since that time, others have suggested that *P. scolieri* might be involved in hybridization, but no solid evidence has been obtained. Using isozyme techniques, we have detected little or no infraspecific variation across the range of the species. We have been able to confirm that *P. scolieri* is hybridizing with neighboring *P. californicum* and/or *P. calirhiza*. Individuals that appear to be intermediate in morphology contain isozyme marker alleles from two putative lineages. We are currently characterizing these hybrids further and studying the dynamics of this interesting population and species.

- 280** HOOT, SARA B.\*, W. CARL TAYLOR, AND E. WAGNER. Department of Biological Sciences, University of Wisconsin, Milwaukee, WI 53201 and Botany Department, Milwaukee Public Museum, Milwaukee, WI 53233—*Species delimitation and hybrid origins in North American Isoëtes based on LEAFY intron data.*

Sequences from the second intron of a homolog of *LEAFY*, a meristem identity gene, are highly variable in *Isoëtes* and other plants (including flowering plants). The *LEAFY* data is approximately four times more variable than ITS sequences in *Isoëtes* and is useful at both the species and population level. For species delimitation, we have identified numerous substitutions and indels that characterize the North American species of *Isoëtes*. For example, *I. echinospora* has virtually identical sequences for populations from such distant locations as Iceland, Maine, Wisconsin, and Montana. In contrast, while two populations of *I. melanopoda* from Mississippi and Louisiana are very similar, a third population from Arkansas differs at numerous sites, indicating a cryptic species. For determining parental origins of hybrids and allopolyploids, we cloned the intron region to separate the sequences originating from the parental species. Using this method, we were able to enter the two hybrid sequences into an extensive data set of North American species to identify the putative parents. For example, intron sequences from both *I.X eatonii* (a known diploid hybrid) and *I. riparia* (an allotetraploid) have virtually identical sequences with the putative parental species (*I. engelmannii* and *I. echinospora*). The sequences of the allotetraploid, *I. louisianensis*, are not similar to any of the North American species. One sequence is weakly supported as sister to a clade consisting of *I. tegetiformans*, and *I. lithophila*. The other sequence is sister to a clade consisting of *I. virginica*, *I. melanopoda*, and *I. echinospora*.

- 281** HOUSTON, HEATHER J.\* AND TOM A. RANKER. Department of Environmental, Population and Organismic Biology, University of Colorado, Boulder, CO 80310-0334—*Population genetics of Sadleria cyatheoides (Blechnaceae), a Hawaiian endemic.*

Population genetic analyses were conducted on the endemic Hawaiian fern *Sadleria cyatheoides* (Blechnaceae) using Amplified Fragment Length Polymorphisms (AFLPs). Populations were examined to reveal levels and patterns of genetic diversity within and among populations and within and among islands of the Hawaiian archipelago. DNA was extracted from frozen isozyme grindate and utilized in the AFLP technique to allow greater discrimination between individuals. When compared to data obtained for the same individuals with isozyme electrophoresis, finer patterns of genetic structure were evident with AFLPs.

- 282** KORALL, PETRA\* AND PAUL KENRICK. Department of Botany, Stockholm University, SE-106 91 Stockholm, SWEDEN, Department of Palaeontology, The Natural History Museum, Cromwell Road, London SW7 5BD, United Kingdom—*Phylogeny of Selaginellaceae based on the plastid gene rbcL: congruence and incongruence with morphology.*

Selaginellaceae are a cosmopolitan family of heterosporous lycopods that originated during the Paleozoic Era. We present a phylogeny of the group based on *rbcL* gene sequences from a representative sample of living species, currently standing at approximately 10% (63 taxa). Monophyly of some widely recognised groups is upheld (*Selaginella*, *Tetragonostachys*, and *Articulatae*), but others are shown to be paraphyletic (*Stachygynandrum*, *Heterostachys*, and *Ericetorum*). We present an evaluation of some of the morphological data used in previous classifications. Leaf dimorphism correlates poorly with the major divisions in the family. However, some of the new groups recognised on molecular criteria are shown also to have distinctive morphological characteristics (e.g., patterns of rhizophore development, megaspore wall ultrastructure). Megaspore wall ultrastructure is singled out as one characteristic that might be of exceptional utility in calibrating the phylogenetic tree. Our results have implications for the interpretation of xerophytic strategies within the family. "Resurrection plants" appear to have evolved at least three times.

- 283** MEHLTRETER, KLAUS<sup>1</sup>\* AND MÓNICA<sup>2</sup> PALACIOS-RIOS. Instituto de Ecología, A.C., <sup>1</sup>Departamento Ecología Vegetal, <sup>2</sup>Departamento Sistemática Vegetal, Apartado Postal 63, Xalapa 91000, Veracruz, México—*Phenological studies on Acrostichum danaeifolium Langsd. et Fisch. (Pteridaceae, Pteridophyta) on a Caribbean mangrove site of Mexico.*

Why does only a few studies on fern phenology exist? Perhaps this is the consequence of 3 prejudices: 1. Slow growth, 2. No growth or fertility rhythms as it is believed that ferns grow only under continually favorable humid conditions, and 3. Independence of pollinators for fertilization and animal vectors for their dispersal. Results of these study clearly prove that all 3 prejudices are not true for the mangrove fern *Acrostichum danaeifolium*. A population of 30 individuals was observed along a transect during one year in

La Mancha (19°36'00"N, 96°22'40"W), Veracruz, Mexico. The climate is hot and humid with a dry season from November to March. Mean annual temperatures fluctuate between 22-26°C and annual precipitation varies between 1200-1500 mm. The study site is some 300 m from a brackish water lagoon, in the understory of the mangroves, dominated by *Avicennia germinans* (Avicenniaceae), where *Acrostichum danaeifolium* forms populations of 28,000 individuals per hectare. Phenological measurements were done biweekly. Individual daily leaf growth can reach up to 6-8 cm during the rainy season and slows down to 4 cm during the dry season, while the number of new buds and leaves shows little variation. Plants have a mean number of 8-10 sterile leaves, develop 1-2 leaves per month and the age of sterile leaves is around 9 to 12 months. The population was composed of 35 % of mature plants, which produce 1-3 fertile leaves only during the rainy season. Fertile leaves are alive for 2-3 months, so that there are no fertile plants during the dry season. Living gametophytes were present during the whole year, but especially abundant during the end of the dry season.

**284** NOTIS, CHRISTINE. Department of Botany, Iowa State University, Ames, IA 50011—*Sperm longevity and swimming distance in ferns.*

The goal of this study is to determine the maximum longevity and swimming distance of fern sperm in liquid media of differing pH and solute concentration. This information is relevant to determining gametophyte population densities necessary for intergametophytic crossing. Species used in the study included *Lygodium japonicum*, *Macrothelypteris torressiana*, *Pteridium aquilinum* and *Asplenium pinnatifidum*. For determinations of longevity, culture-grown male or bisexual gametophytes were submersed in the test solution in a microscope depression slide. After five minutes the gametophytes were removed leaving only the sperm that had been released into the medium. The solution was then checked every 15 minutes to determine whether sperm remained active. Results indicate that sperm are capable of swimming for over two hours. Longevity decreased with increasing acidity for the species tested. Additional species are being tested and swimming distances are being calculated.

**285** SAHASHI, NORIO. Department of Biology, School of Pharmaceutical Sciences, Toho university, Funabashi, Chiba 274-8510, Japan—*A New Combination of the Ophioglossaceae Using Palynological and Morphological Studies on the Old World.*

Phylogenetic relationships among the genera of the Ophioglossaceae sensu lato are controversial from the viewpoints of morphological and anatomical features. However, I demonstrated mainly from the spore morphological studies of the Ophioglossaceae on the Old World. I concluded that the Botrychiaceae (includes *Botrychium* s.lat. and *Helminthostachys*) is composed of five genera, *Botrychium* (divided into 2 sections), *Sceptridium* (divided into 2 sections), *Botrypus* (divided into 2 sections), *Japanobotrychium* and *Helminthostachys*. Moreover, Ophioglossaceae sensu strict consists of two genera, *Ophioglossum* and *Ophioderma*. A key to the genus according to spore morphology is as follows; Spores subtriangular, or often rounded triangular in polar view, with almost projective basic ornamentations: Botrychiaceae. Spores tuberculate to verrucate, or often extervermiculate: *Botrychium*. Spores rugulo-reticulate with fine granules, or beset with irregularly fine projections: *Sceptridium*. Spores convolute or often uniting to form reticulate with finely striate: *Japanobotrychium*. Spores coarsely and largely verrucate with fine granules: *Botrypus*. Spores reticulum-like pattern, thin ridges decorated with delicate projections: *Helminthostachys*. Spores rounded triangular or globose in shape, with mostly depressed basic ornamentations: Ophioglossaceae. Spores usually globose, foveolate to foveo-reticulate, or often reticulum-like pattern: *Ophioglossum*. Spores large and rounded triangular in polar view, usually foveolate to reticulum-like pattern: *Ophioderma*.

**286** SCHUETTE, S.W.\*, A.R. MADEN, D.P. WHITTIER, AND K.S. RENZAGLIA. Department of Plant Biology, Southern Illinois University, , Carbondale, IL 62901 , Department of Biology, Vanderbilt University, Nashville, TN 37235—*Ultrastructure of the spermatozoid of Diphasiastrum digitatum.*

The ultrastructure of motile cells provides valuable information in assessing phylogenetic relationships among lycophytes. In continuation of our studies of spermatogenesis, we examined the ultrastructure of spermatozooids of *Diphasiastrum digitatum*. The mature sperm cell is obovoid, biflagellated, and contains relatively little cytoplasm. The elongate nucleus occupies most of the cell and contains large spherical inclusions. A multilayered structure wraps laterally around the anterior of the nucleus and is subtended by a single mitochondrion. The two adjacent basal bodies are staggered and slightly skewed from parallel. The flagella emerge from the same side of the multilayered structure and coil at least twice around the cell in parallel. A wide spline of 150-200 microtubules encases most of the diameter of the nucleus. At the posterior of the cell, a

short but wide spline shank supports a large starch-laden plastid. Numerous small mitochondria are abundant in this region. To illustrate architectural relationships among cellular entities, we will present a three-dimensional reconstruction of the mature spermatozoid of *Diphasiastrum*. This cell has specific features in common with sperm cells of *Lycopodium*, *Huperzia*, *Phylloglossum*, and *Lycopodiella*. Phylogenetic relationships among these taxa will be evaluated by analyses of data derived from male gametogenesis.

- 287** SMITH, ALAN R.\*, HARALD SCHNEIDER, BARBARA S. PARRIS, CHRISTOPHER H. HAUFLER, TOM A. RANKER, JAMES P. THERRIEN, AND JENNIFER M. O. GEIGER. University Herbarium, University of California, Berkeley, CA 94720; Fern Research Foundation, 21 James Kemp Place, Kerikeri, Bay of Islands, New Zealand; Department of Ecology and Evolutionary Biology University of Kansas, Lawrence, KS 66045; University Museum Herbarium, University of Colorado, Boulder, CO 80309—*Phylogeny of Grammitidaceae and Polypodiaceae inferred from two large data sets: rbcL and morphology.*

Recent studies utilizing nucleotide sequence data have indicated that Grammitidaceae and Polypodiaceae form a monophylum, in which the monophyletic Grammitidaceae are nested in a paraphyletic Polypodiaceae. This hypothesis is tested with an enlarged rbcL data set and a new morphological data set. Nearly all proposed genera of Grammitidaceae and Polypodiaceae are included with one or more representatives in both data sets. The two data sets utilize the same taxa and are analyzed both separately and combined. Our analyses reveal monophyletic groups within both families (and the relationships among Grammitidaceae and Polypodiaceae). Several disputed genera in both families are shown to be polyphyletic or paraphyletic, e.g. *Grammitis*, *Microgramma*, *Microsorium*, and *Polypodium*, but many monophyletic units correspond with previously proposed genera, e.g. *Campyloneurum*, *Pecluma*, and *Prosaptia*. Several large clades have biogeographical continuity, being restricted to either the Paleotropics or Neotropics. The entire group probably had an Old World origin, whereas Grammitidaceae are sister to New World Polypodiaceae. However a number of genera have attained pantropical distribution, presumably in their relatively short history. Important changes in the classification are outlined. The phylogenetic results are compared with traditional taxonomic units based on morphological characters, and conflicts are discussed. Both families are primarily tropical/subtropical epiphytes, and some morphological characters may reflect adaptation to similar habitats. Such similarities cause conflicts in the recognition of natural groups with traditional and phylogenetic methods. The rbcL data set is used to recognize convergent characters and evolutionary trends in epiphytic plants.

- 288** SÁNCHEZ-BARACALDO, PATRICIA. Department of Integrative Biology, and University and Jepson Herbaria. University of California, Berkeley, CA 94720—*A recent radiation of Neotropical fern genera in pramo ecosystems.*

There are two traditionally recognized fern genera in the Neotropics that together form a monophyletic group, *Jamesonia* and *Eriosorus*. Molecular phylogenetic studies suggest that neither genus is a natural group and that several lineages with “jamesonia” morphology have undergone a fairly recent radiation, approximately 3-5 million years ago, in pramo ecosystems. “Jamesonia” is unique among the ferns in its highly modified vegetative and ecological characteristics. Some of the most outstanding morphological features of this genus are: 1) indeterminate growth, 2) xeromorphic and coriaceous leaves, and 3) extremely reduced pinnae. A robust phylogeny was generated based on sequence data of the External Transcribed Spacer (ETS) and the Internal Transcribed Spacers (ITS) of 18s-26S rDNA, and the plastid coding region and spacer of the rps4 gene. Several conclusions can be made about the evolutionary history and biogeographic patterns of the eriosorus-jamesonia complex such as: 1) ‘jamesonia’ was found to be polyphyletic, having arisen independently at least three times, 2) two well supported clades can be recognized, roughly corresponding to the Northern vs. Southern Andes, and 3) the sister taxon of the Andean radiation was found to be in Brazil, *Eriosorus myriophyllus*. Character evolution studies indicate a sharp ecological shift in the evolution of “jamesonia’s” ecological preferences. In addition, there is a repetitive trend towards pinnae reduction and indeterminate growth, perhaps correlated with the extreme environmental factors prevailing in Neotropical pramo ecosystems. The independent lineages of “jamesonia” provide the first examples of recent adaptive radiations in the ferns.

- 289** TAYLOR, W. CARL\* AND SARA B. HOOT. Botany Department, Milwaukee Public Museum, Milwaukee, WI 53233 and Department of Biological Sciences, University of Wisconsin, Milwaukee, WI 53201—*Evolutionary relationships and biogeography of Isoetes based on nucleotide sequences.*

Nucleotide sequences from the internal transcribed spacer (ITS) region of nuclear ribosomal DNA and the *atpB-rbcL* spacer region of the chloroplast genome were used to resolve species relationships of *Isoetes* from



a worldwide perspective. Basic diploid species from North and Central America, Europe, Africa, Asia, and Australasia were included. A well-supported, putatively Gondwanian clade consisted of *I. stellenbosiensis* and *I. capensis* of South Africa, *I. coromandelina* of India, and *I. panamensis* of Costa Rica. Results demonstrated a close, well-supported relationship of the Asian taxa (*I. kirkii* of New Zealand, *I. drummondii* of Australia, and *I. taiwanensis*). North American species of *Isoetes* are not monophyletic. Two western North American species (*I. nuttallii* and *I. orcuttii*) were found in a well-supported clade consisting of European and African species. The remaining, weakly resolved North American clade of 15 species included *I. mexicana* and *I. storkii* of Costa Rica. The two species from Costa Rica (*I. panamensis* and *I. storkii*) and two species from Spain (*I. setacea* and *I. velata*) were not closely related, appearing in widely divergent clades. The resulting phylogeny and the number of substitutions and indels supporting the branches suggest that some clades are of relatively ancient origin, whereas others (the weakly resolved North American clade) are much more recent.

- 290** THERRIEN, JAMES P.\* AND CHRISTOPHER H. HAUFLE. Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66045—*Phylogeny and biogeography of Selaginella subg. Tetragonostachys based on nuclear ribosomal ITS sequence data.*

*Selaginella* subg. *Tetragonostachys* is a group of ca. 50 widely distributed species that exhibit a number of putative adaptations to xeric environments. Morphologically, the subgenus includes taxa with thickened, isophyllous microphylls, tetrastichous sporophylls, and in several species, the presence of vessels. Previous phylogenetic analyses based on rbcL sequence data strongly supported the monophyly of this subgenus, but failed to adequately resolve relationships within the group. To address open questions of phylogenetic relationships, nuclear ribosomal internally transcribed spacer (nrITS) sequences were obtained from 44 ingroup taxa and 6 outgroups. Maximum parsimony analysis of the data yielded several well supported clades. The resulting tree topology exhibits patterns that are consistent with classic Tertiary relictual distributions. There is strong support for a clade comprised of taxa from southern Africa, Madagascar, and India - land masses previously united in a larger assemblage. Further vicariant relationships include an eastern US, western US, Asian clade, again with strong bootstrap support. Moderate support is also obtained for a clade of species within section *Arenicolae*, comprised of taxa distributed in the southwestern US, southeastern US, and northern Africa. In addition, several of the clades correspond well with morphological characters traditionally considered indicative of sister group relationships. These include such features as red pigmented microphylls, readily fragmenting stems, dimorphic sporophylls, and the prostrate, incurling habit. The overall pattern from the nrITS phylogeny suggests that speciation in *S. subg. Tetragonostachys* may be attributed primarily to vicariant events, rather than to long distance dispersal.

- 291** THERRIEN, JAMES P.\*, MICHAEL D. WINDHAM, AND CHRISTOPHER H. HAUFLE. Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66045, Utah Museum of Natural History, University of Utah, Salt Lake City, UT 84112—*Hybridization and putative allotetraploid speciation in Selaginella subg. Tetragonostachys.*

Hybridization and polyploid speciation are well documented evolutionary mechanisms in plants. Although taxa derived through such reticulate processes occur in nearly every major lineage of pteridophytes, including the homosporous lycopods and heterosporous quillworts, to date there have been no confirmed cases of hybridization or allopolyploid speciation in the related genus *Selaginella*. Recent fieldwork in the southwestern US has revealed examples of hybridization among taxa within *S. subg. Tetragonostachys*. Hybrids between the strongly divergent species *S. arizonica* and *S. rupincola* initially were identified based on intermediate morphologies and abortive sporangia. Confirmatory isozyme data support at least two independent hybridization events and suggest that the hybrids are triploid, resulting from crosses between tetraploid *S. rupincola* and diploid *S. arizonica*. In addition, nrITS sequences diagnostic for both *S. arizonica* and *S. rupincola* are present in the hybrid, and were obtained via sequencing multiple clones of the hybrid nrITS PCR product. Whereas the two nrITS sequences in the hybrid are clearly derived from the parental nrITS sequences, they exhibit moderate degrees of divergence from the parental sequences. Hybrids between *S. arizonica* and *S. eremophila*, closely related members of section *Eremophilae*, also have been documented. Some of these plants produce well-formed spores, and isozyme banding patterns suggest that certain populations entirely consist of stabilized tetraploids. Owing to the similarity in nrITS sequences for the putative parents, nrITS sequence data do not fully aid in resolving parentage in this hybrid. If confirmed by additional markers, the *S. arizonica* X *S. eremophila* hybrid would represent the first documented example of allotetraploid speciation in *Selaginella*.

- 292** WATKINS, JR., JAMES E.\* AND DONALD R. FARRAR. Iowa State University, Department of Botany, 353 Bessey Hall, Ames, IA 50011—*Biosystematic investigation of the rare, disjunct, rockhouse fern* *Thelypteris pilosa* var. *alabamensis* (*Thelypteridaceae*: *Stegnogramma*).

*Thelypteris pilosa*, has been recognized as the sole member of the subgenus, *Stegnogramma*, in the new world. This taxon is common throughout central and southern Mexico, Guatemala and Honduras, and exhibits an intriguing temperate disjunction in Alabama. Past taxonomic studies have suggested that the Old World *T. pozoii* is closely allied to *T. pilosa* adding these taxa to the list of Asian - American disjuncts. A significant amount of morphological variation exists in the Mexican taxa and it is unclear whether these differences are due to phenotypic plasticity or genetics. Two regionally sympatric morphotypes, terrestrial with deltate fronds and epipetric with lanceolate fronds occur throughout Mexico. These two types have been described as var. *major* and var. *pilosa* respectively. A more distinct type, described as var. *alabamensis*, is endemic to north Alabama rockhouse habitats and has been reported from only a single county. Data on ecology, gametophyte biology, crossing studies, spore morphology, and molecular biology question the varietal distinction of the Mexican material but support the elevation of *T. pilosa* var. *alabamensis* to specific status under the proposed name of *T. burksiorum*. Insights into the origin and taxonomic affinities of the Old and New World species are presented.

## Contributed Posters

- 293** MEHLTRETER, KLAUS\*, JOSÉ G. GARCÍA-FRANCO, AND ALEJANDRO FLORES-PALACIOS. Instituto de Ecología, A.C., Departamento Ecología Vegetal, Apartado Postal 63, Xalapa 91000, Veracruz, México—*Microhabitat preferences of trunk epiphytes in a cloud forest of Mexico, with special reference to ferns.*

Aim of this study was to investigate microhabitat preferences of epiphytes in relation to trophophytes and to exposition and location on the trunk. The study site is a cloud forest fragment, located in a river gorge in central Veracruz (19°30'N, 96°59'W) at 1550 m altitude. There, annual precipitation is 1440 mm and the average temperature is 18.0°C. Trees were marked at the end of the rainy season along four transects of 30 m length, running perpendicular to the river. All 100 trees within 2.50 m distance of the transect were checked for trunk epiphytes between 0-1.50 m height. Frequency and cover for each epiphyte species were estimated with a modified scale of Braun-Blanquet, for three ranks of 50 cm height and for the river and mountain exposed side. Most abundant tree species were the angiosperms *Arachnothryx capitellata* (Rubiaceae), *Clethra mexicana* (Cyrillaceae) and *Liquidambar styraciflua* (Hamamelidaceae), and the tree ferns *Alsophila firma* and *Cyathea divergens* (both Cyatheaceae), the latter two with highest cover rates of epiphytes. Most abundant epiphyte species were *Trichomanes capillaceum*, *Trichomanes reptans* (Hymenophyllaceae) and *Peperomia quadrifolia* (Peperomiaceae). Strongest microhabitat preferences were found between *Trichomanes capillaceum* and both tree fern species, while *Peltapteris peltata* was exclusively present on angiosperm trees. Also *Trichomanes reptans* occurred mostly on different angiosperm trees, and finally *Peperomia quadrifolia* was indifferent in relation to trophophytes. Some epiphyte genera showed preferences for only one of the tree fern species: *Asplenium* (Aspleniaceae) and *Elaphoglossum* (Lomariopsidaceae) were significantly more frequent on *Alsophila firma*, while *Syngonium* (Araceae) was more represented on *Cyathea divergens*. Species diversity of epiphytes was higher on the river exposed side and increased from the lower to the higher trunk sites, while the species coverage decreased.

- 294** WILLISTON, PATRICK\* AND PAULA BARTEMUCCI. Department of Botany, University of British Columbia, Vancouver, British Columbia, V6T 1Z4—*The Ophioglossaceae of British Columbia.*

The Ophioglossaceae is a unique family of small, inconspicuous, and often rare ferns with 16 species in British Columbia. This paper summarizes what is known about the Ophioglossaceae in British Columbia and draws attention to the lack of information regarding their taxonomy and ecology within the region. Species associations within the family are discussed and localities with high species richness are noted. This paper contains an illustrated key to the Ophioglossaceae of British Columbia and includes descriptions, distribution maps, habitat information, and rarity status for each species. Pertinent questions for future research and conservation are suggested.

**XIV. Systematics Section / American Society of Plant  
Taxonomists / International Association for Plant Taxonomy  
Symposium (BSA Systematics Section / ASPT): Historical biogeography  
of the Northern Hemisphere**

- 295** MANOS, PAUL S.\* AND MICHAEL J. DONOGHUE. Department of Botany, Duke University, Durham, NC 27708-0338, Harvard University Herbaria, 22 Divinity Avenue, Cambridge, MA 02138—*Historical biogeography of the Northern Hemisphere symposium abstract.*

The phylogeography of the Northern Hemisphere represents one of the great challenges to understanding the interaction of Earth history and biological diversification. Although floristic similarities between the disjunct areas of Laurasia are striking, it has become increasingly clear that phylogenetic hypotheses are needed to resolve the dynamic history of vicariance throughout the Cretaceous and Tertiary. One of the major advances towards further understanding phylogeographic connections around the Northern Hemisphere has been the significant increase in the number of phylogenies for disjunct taxa. By the summer of 2000 phylogenies for as many as 70 relevant taxa will be available for consideration, allowing the search for general patterns in area cladograms. The goals of this symposium are: 1) to assemble and help coordinate the activities of investigators working from various perspectives on reconstructing angiosperm distributions around the Northern Hemisphere; 2) to explore the use of modern methods in analytical biogeography in synthesizing knowledge of geographic patterns around the Northern Hemisphere; and 3) to evaluate phylogenetic hypotheses for temporal congruence in the context of fossil data and current theories regarding geological and climatic changes.

- 296** DONOGHUE, MICHAEL J.\*, CHARLES D. BELL, AND JIANHUA LI. Harvard University Herbaria, 22 Divinity Avenue, Cambridge, MA 02138 and Department of Ecology and Evolutionary Biology, Yale University, New Haven, CN 06511, Arnold Arboretum of Harvard University, Jamaica Plain, MA 02130—*Reconciling phylogeographic patterns around the Northern Hemisphere.*

Traditional vicariance analyses of the Northern Hemisphere are destined to be confusing by virtue of mixing splitting events that occurred at different times. To avoid this problem it would be wise to sort phylogenies according to lineage divergence times and then analyze subsets of trees that are relevant to the same time period/vicariance events. As a starting point in this sorting process, we recognize two major tracks around the Northern Hemisphere: an Atlantic track characterized by species in China, Europe, and southeastern North America, and a Pacific track involving China, Japan, often western North America, and eastern North America. Here we concentrate on our recent analyses of clades showing the Pacific track. All possible patterns of relationship involving North America, Japan, and China appear among the groups we have considered. North American species are most closely related to Japanese species in *Hamamelis* and *Viburnum* sect. *Pseudotinus*. North American species are linked with one or more Chinese species in *Triosteum* and *Buckleya*, to the exclusion of the Japanese species. In *Torreya* it appears that the Chinese and Japanese species form a clade to the exclusion of the North American species. These differences either imply different vicariance events in different time periods, or differential responses to the same vicariance events coupled with extinction. We explore both possibilities, bringing estimated divergence times to bear on the problem when possible.

- 297** FRITSCH, PETER W.\* AND CYNTHIA M. MORTON. Department of Botany, California Academy of Sciences, Golden Gate Park, San Francisco, CA 94118 and Department of Botany and Microbiology, Auburn University, Auburn, AL 36849—*Phylogeny of the Styracaceae based on four data sets: implications for the historical biogeography of the northern hemisphere and amphi-Pacific tropical disjunctions.*

About 120 plant taxa exhibit amphi-Pacific tropical disjunctions, i.e., endemism in both tropical America and tropical east Asia. The number is inexact because many amphi-Pacific disjuncts have distributions that overlap to some extent with north-temperate patterns of disjunction. This overlap and the presence of north-temperate fossils of currently amphi-Pacific tropical groups suggest that amphi-Pacific tropical disjunctions follow a boreotropical historical pattern with subsequent expansion or relictualism in tropical areas, as opposed to a southern route of migration. However, phylogenetic estimates, which would otherwise provide a test of this idea, are lacking for most amphi-Pacific tropical groups. We used phylogenetic data from the

Styracaceae to test the idea of a boreotropical link between north-temperate and amphi-Pacific tropical disjunctions. We compared and ultimately combined the data from previous morphological phylogenetic studies with those from three molecular data sets (*rbcL* and *trnL* spacer/intron of chloroplast DNA, and the ITS region of nuclear ribosomal DNA) to 1) estimate the phylogeny through total evidence and 2) infer the biogeographic history of the family in the context of the fossil record. Results generally support a boreotropical pattern as the best explanation for the current and fossil distribution of the Styracaceae. The phylogeny supports an eastern Asian origin for the family and the large, monophyletic genus *Styrax*, with *Styrax* secondarily derived in South America, likely from southern North American ancestors. The phylogenetic data support a rare and geohistorically problematic [eastern north America + eastern Asia][western North America + western Asia] pattern within the north-temperate section of *Styrax*. Morphology suggests that the eastern Asian-eastern North American genus *Halesia* is monophyletic, but ITS and *trnL* analyses group the Asian species of *Halesia* with the strictly Asian genus *Rehderodendron*. Other amphi-Pacific tropical groups now need phylogenetic study to assess the generality of the boreotropical pattern detected in the Styracaceae.

- 298** LAVIN, MATT\*, MARTIN F. WOJCIECHOWSKI, MICHAEL J. SANDERSON, AND ADAM RICHMAN. Department of Plant Sciences, Montana State University, Bozeman, MT 59717, and Section of Evolution and Ecology, University of California, Davis, CA 95616—*Molecular biogeography of temperate and tropical legumes in North America.*

Temperate deciduous forests have been the focus of northern hemisphere biogeographical studies, yet the origins of the floristic elements in these forests stem in part from tropical deciduous forests that pervaded northern latitudes during the early Tertiary. The legume family Fabaceae may provide some insight into the fate of the early elements in North American deciduous forests. Most did not radiate into the temperate deciduous forests, but rather remained in the seasonally deciduous tropical forests that migrated southward with the global cooling of the late Tertiary. Most of the temperate largely herbaceous diversity in legumes seems to have migrated in from the Old World during the late Tertiary rather than have evolved in situ in North America from tropical, woody ancestors. We illustrate the early Tertiary North American pattern with tropical legume groups including Robinia and close relatives, as well as the dalbergioid legumes. The late Tertiary to Quaternary North American pattern is illustrated with temperate legumes including Hologalegina and Gleditsia. For tropical lineages, a molecular clock based on nuclear rDNA ITS/5.8S sequences is calibrated with an early Tertiary Caribbean vicariance event for the endemic Greater Antillean radiations Poitea and Pictetia.

- 299** MANCHESTER, STEVEN R.\* AND BRUCE H. TIFFNEY. Paleobotanical Laboratory, Florida Museum of Natural History, Gainesville, FL 32611-7800; Department of Geological Sciences, University of California, Santa Barbara, CA 93106—*Paleobotanical data and the phylogeographic history of holarctic angiosperm clades.*

A clear understanding of the phytogeographic history of angiosperms in the Northern Hemisphere requires integration of data from both living and fossil plants. Attempts to reconstruct phytogeographic history based exclusively on modern distribution patterns are prone to error, because there are numerous instances of genera with holarctic paleobotanical distribution that are today confined to one or two continents. Centers of diversity have changed over time, undermining attempts to place centers of origin in areas of current high diversity. There has sometimes been a temptation to view the earliest known fossil representatives of a clade as an indication of the place of origin; however, this method is biased by the differential availability of pertinent stratigraphic sequences on different continents. Perhaps the most informative method is to conduct phylogenetic analyses of all the available fossil and extant representatives of a given clade and examine the sequence of geographic dispersal events indicated by the most parsimonious trees. The choice of taxa for such investigations should be based in part on the richness and quality of paleontological data. Carefully documented whole plant reconstructions of fossil species, providing characters from foliage, stem anatomy, flower, fruit, seed, and/or pollen morphology, provide the best opportunities for the successful integration of fossil and modern taxa in phylogenetic analyses. Preliminary investigations illustrate varied patterns of intercontinental dispersal, but two of the more common are: Asian-North American diversification with subsequent dispersal to Europe (e.g., *Acer*, *Aesculus*, *Eucommia*, *Paliurus*), North American-European diversification with subsequent dispersal to Asia (e.g., *Nyssa*, *Platycarya*, *Tilia*, *Ulmus*). Greater resolution of the directions and timing of dispersal events throughout the Northern Hemisphere will require intensive investigations of taxa with excellent fossil records, with attention to both vegetative and reproductive morphological characters, complemented by molecular-based phylogenetic analyses of the living representatives.



- 300**    MANOS, PAUL S.\* , ALICE M. STANFORD, AND MICHAEL J. SANDERSON. Department of Botany, Duke University, Durham, NC 27708, Division of Science & Math. University of the Virgin Islands, 2 John Brewers Bay, St. Thomas, VI 00802, and Section of Evolution and Ecology, University of California, Davis, CA 95616—*Phylogenetic patterns of disjunct Fagales: tracking the history of north temperate and subtropical forests.*

An improved understanding of the phylogenetic history of the Fagaceae and Juglandaceae, two widespread members of the expanded Fagales clade, suggests several patterns of vicariance throughout the Tertiary of the Northern Hemisphere. The rich fossil record for these families also provides essential temporal data for calibrating phylogenies and comparing divergence times among apparently similar patterns of vicariance. At least 4 genera of Fagaceae (*Castanea*, *Fagus*, *Lithocarpus* and *Quercus*) and two genera of Juglandaceae (*Carya* and *Juglans*) have disjunct distributions amenable to biogeographical analysis. Fagaceae show a successional pattern of discontinuity, perhaps starting with an ancient disjunction within *Trigonobalanus*. More species-rich genera such as *Fagus*, *Quercus*, and *Lithocarpus* continue to support a center of origin in south east Asia with subsequent migration to western North America. Disjunction within the evergreen genus *Lithocarpus* (SE Asia-W N. Amer.) may suggest an exchange during warmer periods of the Eocene. In contrast, a close relationship between *Fagus grandifolia* (NA) and south east Asian species rather than Eurasian species supports a deciduous connection via the Bering Land Bridge. Fossil data also confirm the presence of *Fagus* in the Miocene of western North America. More recent connections, possibly via the Bering Land Bridge, but with the reverse pattern of migration, are indicated by the trans-continental white oaks (*Quercus* sect. *Quercus* s.s.). For Juglandaceae, disjunctions within *Carya* and *Juglans* appear to have occurred at different times: *Carya* shows no evidence of trans-continental disjunction at the sectional level, whereas *Juglans* shows one recent example within the butternut species group. In order to temporally discriminate among apparently similar vicariant patterns, divergence times were calculated with maximum likelihood methods that assume a molecular clock and alternative methods that permit constrained rate variation. Randomization tests were used to assess confidence intervals on divergence times, permitting rigorous tests of the sequence of biogeographic events.

- 301**    TIFFNEY, BRUCE H.\* AND STEVEN R. MANCHESTER. Department of Geological Sciences, University of California, Santa Barbara, CA 93106 and Paleobotanical Laboratory, Florida Museum of Natural History, Gainesville, FL 32611—*Physical Influences on Phytogeographic Continuity in the Northern Hemisphere Tertiary.*

The phylogeographic patterns of Northern Hemisphere angiosperms reflect the dynamic interplay between plate tectonics, climate and terrestrial biota during the last 100 Ma. Barriers including oceans, mountains, deserts, day length, available precipitation, and seasonal temperature influenced the dispersal, genetic isolation, and evolutionary diversification of terrestrial plants and their dependent animals. The major physiographic barriers to early Tertiary land organisms were oceanic, restricting exchange to higher latitudes between Eastern Asia and North America (The Bering Land Bridge) and North America and Europe (The North Atlantic Land Bridge). Europe and Asia were separated by the Turgai Strait. While boreal climate was relatively warm, winter day length may have posed an added barrier at the more northerly latitudes. Global cooling near the end of the Eocene introduced the further barrier of continental climates hosting herb-dominated biomes in midcontinental North America and Eurasia, aided locally by the growth of the Rockies (North America), the Alpine Orogeny (Europe), and the retreat of the Turgai Strait (Eurasia). By the Late Tertiary, continued tectonism, including the rising Himalayan Mountains, increased the intensity of seasonal changes. The Pleistocene ice ages further restricted intercontinental exchange to cool-temperate and Arctic forms, while decimating warm-temperate and subtropical clades in Europe and North America. The basic geological and paleoclimatological evidence for these environmental changes is now relatively well known. However, several finer-scale questions remain unanswered. Does short winter day length really pose a barrier to evergreen plants in warm northerly latitudes? Did ephemeral migration routes allow brief pulses of biotic exchange during climatic transitions, e.g., allowing warm-temperate elements to move between Europe and Asia in the middle Tertiary? What is the role of herbs in early Tertiary floras, where they are generally poorly represented?

- 302**    WEN, JUN. Department of Biology, Colorado State University, Fort Collins, CO 80523—*The evolution of eastern Asian and eastern North American plant disjunctions: overview and perspectives from phylogenetic studies.*

The eastern Asian and eastern North American plant disjunction is a classical biogeographic pattern. This pattern was first noticed by Linnaeus in 1750 and elaborated by Asa Gray in a series of papers between

1840 to 1878. Approximately 65 genera of flowering plants are confined to eastern Asia and eastern North America. Previous studies reported a high level of morphological similarity among the disjunct species and many intercontinental species pairs were proposed. Morphological stasis has been suggested to be common among these disjuncts. Recent phylogenetic analyses confirm the close affinity of taxa in most disjunct genera, but few intercontinental sister-species relationships have been detected. Several disjunct taxa are polyphyletic or paraphyletic, suggesting that the morphological similarities in these groups may be attributable to convergence or symplesiomorphies. Subtropical and tropical taxa (e.g., in *Aralia*) may be nested within the temperate disjuncts, suggesting the need to examine the eastern Asian - eastern North American disjunction in the context of global biogeography. Phylogenetic patterns and results from morphometric analyses in *Aralia*, *Corylus*, *Osmorhiza*, *Panax*, and *Prunus* support morphological stasis of the eastern Asian and eastern North American disjuncts via either evolutionary constraints or convergence.

- 303** XIANG, (JENNY) QIU-YUN\* AND DOUGLAS E. SOLTIS. Department of Biological Sciences, Idaho State University, Pocatello, ID 83209-8007—*Phylogenetic Patterns and Divergent Times of Disjunct Taxa: Insights into Historical Biogeography of Angiosperms in the Northern Hemisphere*.

One of the most fascinating aspects of angiosperm biogeography in the Northern Hemisphere is the intercontinental disjunct distribution of closely related species. Analyses of phylogenetic relationships and divergence times are crucial in seeking possible explanations for the origins of various disjunct patterns. Molecular phylogenetic analyses of diverse plant taxa with clades disjunctly distributed in eastern Asia, eastern North America, western North America (e.g., *Trillium*, *Cornus*, *Boykinia*, *Tiarella*, *Trautvetteria*, *Thermopsis*, *Aralia* sect. *Aralia*, *Calycanthus*, *Asarum*, *Staphylea*), and taxa also found in one or more of the following areas: Europe, western Asia, and South America in addition to eastern Asia and North America (e.g., *Aesculus*, *Chrysosplenium*, *Gleditsia*, *Styrax*, *Astragalus*, *Nuphar*, and *Rubus*) revealed similar phylogenetic patterns: the North American species form a monophyletic group sister to the eastern Asian or the Eurasian species, with the old world species basal and the South American species appearing in derived positions. Vicariance-Dispersal analyses suggested that 1) many taxa diversified in eastern Asia and then spread from the old-world to the new-world; 2) The modern disjunctions are mostly the result of vicariance following dispersal and geographical isolation; 3) vicariance events within North American or Eurasian continent occurred subsequent to that between the two continents; and 4) disjunct distributions in South America are due to long-dispersal from North America or from eastern Asia. Analyses of divergence times using molecular clocks indicated that disjunct species from different genera diverged at different geological times (Oligocene to recent) with most of the eastern Asian-eastern North American species analyzed diverged from the late Miocene to the Quaternary. These data suggested that the congruent geographic distributions and phylogenetic pattern exhibited by these disjunct taxa represent “pseudocongruence”.

## Symposium (IAPT / ASPT / BSA Systematics Section): New frontiers in plant systematics: The next 50 years

- 304** ELISENS, WAYNE\* AND TOD STUESSY. Department of Botany and Microbiology, University of Oklahoma, Norman, Oklahoma 73019; Department of Higher Plant Systematics and Evolution, Institute of Botany, University of Vienna, Vienna A-1030, Austria—*New frontiers in plant systematics: the next 50 years. Introduction*.

The past 50 years in plant systematics have seen an unbelievable increase in types of data collected, methods of data analysis, and different philosophical perspectives. These years have taken us essentially from the age of the “New Systematics” in the mid 1940s to what we now might call “Comprehensive Systematics” that utilizes many different kinds of data and requires sophisticated computer programs for finding meaningful relationships among plant taxa. We have transitioned through phenetics and into cladistics, and have moved from emphasis on cytological and cytogenetic data into secondary products followed by isozymes and recently into DNA. We have also learned how to track these data and relationships better, and hence informatics has come of age. We have changed from being mostly single investigators working isolated on our own favorite groups to collaborating with people from diverse laboratories. The role of the single expert in taxonomic groups is diminishing. Through all these changes, we begin to worry about the proper role of nomenclature and whether our rules for naming are keeping pace with present demands for flexibility, efficiency and information content. The challenge for us in this symposium is to attempt to look at what is

happening today and then to go beyond these frontiers into the next 50 years. In view of the spectacular changes that this past half-century has witnessed, what directions are likely to develop into the future? What should our priorities be? Are there underdeveloped opportunities that we profitably should be exploring now? What dangers and pitfalls lie ahead? It also must be remembered that plant diversity is steadily declining world-wide. In short, in view of these challenges, where are we and where are we going in plant systematics?

- 305** HEYWOOD, VERNON H. Centre for Plant Diversity & Systematics, School of Plant Sciences, The University of Reading, Reading RG6 6AS, UK—*Floristics and monography - an uncertain future?*

Like much of the rest of taxonomy, both floristics and monography, two of its principal outputs, are being subjected, albeit slowly, to the dramatic changes in concepts and methodology that are affecting other parts of these fields. After a number of false starts, electronic web-based preparation and publication of floristic and taxonomic projects, in the form of continually updated information systems and databases, are beginning to replace conventional time- and information-limited Floras and, to a lesser extent, monographs. Coincidental with these developments, the value of floristics is being questioned by some biologists on the grounds of its lack of scientific objectivity and its weakening of systematics as a scientific endeavour, while at the same time its fundamental importance, under the guise of completing the inventory of biodiversity, is being emphasized by other biologists and by the Convention on Biological Diversity and the Global Taxonomic Initiative. Other important developments that will affect the way in which floristics and monography are pursued, is the questioning of the continuing relevance of the Linnaean hierarchical structure of biological classification and proposals to replace it with a phylogenetic structure, and proposals to adopt phylogenetic species concepts. Both of these, however scientifically justified, would drastically affect the accessibility of the units of taxonomy to a large number of non-specialist users. In contrast to this, we are beginning to see in taxonomy policy-making, an increasing sensitivity to societal and ethical concerns that characterize 'post-normal science', including the recognition of the need to command strong public identification such as response to user needs and concerns, and an acceptance that floristic and taxonomic work cannot be pursued as open-ended, long-term enterprises, because of the time limit imposed by human activities in destroying the very resource base of biodiversity that it is aimed at studying.

- 306** KELLOGG, ELIZABETH A. Department of Biology, University of Missouri-St. Louis, St. Louis, MO 63121—*Genetics of character evolution.*

Rapid advances in plant genomics and in developmental genetics are providing new tools for plant systematists. Understanding the developmental and genetic basis of morphology will help to understand homology and character state delimitation, and to suggest the sorts of selective pressures that might have been responsible for diversification. A developmental genetic framework has been used to investigate macroevolution in the grasses, in which major morphological change has often involved change in the position of developmental programs (heterotopy), possibly via ectopic gene expression. Heterotopy may have been responsible for 1) long-short cell alternation in the leaf epidermis of the grasses and their sister genus, *Joinvillea*; 2) diversification of function of C-class genes in the grass flower, and possibly suppression of portions of the perianth; 3) acquisition of perianth-like characteristics in leaf-like inflorescence organs; 4) formation of staminate flowers in the panicoid grasses; and 5) repeated origin of C4 photosynthesis in multiple lineages. Not all macroevolutionary changes fit this model. For example, the novel morphology of the grass embryo can be described as a change in timing of development (heterochrony) rather than a change in position. As our understanding of morphological characters improves in coming years, it will be intriguing to see if other morphological novelty is created by simply moving old genes to new places.

- 307** MCNEILL, JOHN. Royal Ontario Museum, Toronto, and Royal Botanic Garden, Edinburgh, EH3 5LR, Scotland, UK—*Botanical nomenclature: on the threshold of major change?*

The binomial system of botanical nomenclature has existed for almost 250 years, the principle of a taxon having a single correct name determined on the basis of priority of publication was formalized almost 150 years ago, and the type method for the application of scientific names of plants has had international acceptance for almost 75 years. In this historic time-frame, do the next 50 years hold any prospect of change, and indeed is any change possible or even desirable? The requirement of botanical nomenclature to provide a stable, unambiguous reference system for plant information implies an inherent conservatism of rules and procedures - even the smallest change to the *Code*, however beneficial it may be in general, is virtually certain to have some destabilizing effect. Despite this truism, it is suggested that the next few years will see quite major change. Bionomenclature provides the mechanism for communication about the elements of

taxonomy and for those who perceive these solely, or even primarily, in terms of phyletic lineages, a more or less revolutionary phyletic nomenclature is probably indicated. But when the elements of taxonomy seek to reflect the greatest information on patterns of biodiversity, bionomenclature will continue to communicate the general information content of taxa effectively, only if it evolves to take fuller advantage of the opportunities of the electronic age. The historical tendency to improve the rules of nomenclature by continuous “tinkering” with the *Code* needs to give way to a recognition that stability and simplicity are key requirements of users of names (amongst whom professional biologists are a relatively small minority), and that web access to authoritative lists will generally be their preferred approach to answering the nomenclatural questions that arise in their study and use of plants, animals and micro-organisms.

**308** SCHAAL, BARBARA A. Department of Biology, Washington University, St. Louis, MO 63130—*Plant population biology and systematics.*

Traditionally population genetics and systematics have been separate fields, with distinct conceptual frameworks, tools, and statistics. Hennig drew a clear distinction between the reticulate genealogical relationships among individuals and populations on one hand, and the hierarchical phylogenetic relationships among divergent species or taxa on the other. For many plant species, such distinctions blur. The genetic structuring of plant populations is strongly affected by phylogenetic history, and the phylogenetic relationships among species are frequently confounded by gene migration between species. The identification of molecular markers that vary within species, as well as reductions in costs and time associated with DNA sequencing have set the stage for a blending of the two fields. Haplotype variation at a non-recombining locus can be historically ordered to produce a gene genealogy. Genealogical analysis coupled with the theoretical framework of coalescence theory can be used to estimate the roles of migration, founder effects and range expansion during the formation and subsequent establishment of species. Such studies hold great promise for understanding the interplay of phylogenetic history and population level process in shaping distinct evolutionary lineages.

**309** SOLTIS, PAMELA S. School of Biological Sciences, Washington State University, Pullman, WA 99164—*Molecular phylogenetics and beyond.*

Plant molecular systematics has been transformed during the past 15 years through the combined application of molecular techniques and phylogenetic methodology. During this brief window in time, molecular data have become increasingly sophisticated and increasingly easy to obtain. The ease with which molecular data are currently generated provides both opportunities and challenges for molecular systematics. These include (1) choices of DNA regions for analysis, including the development of nuclear genes appropriate for phylogeny reconstruction at a number of hierarchical levels and whole-genome comparisons, particularly of the chloroplast genome; (2) data handling, including the development and refinement of phylogenetic methodologies for analysis of many samples and methods for storage and retrieval of both data sets and trees; (3) integration of molecular and other types of data; (4) use of molecular-based phylogenetic trees for analyses of morphological, biochemical, and molecular characters; and (5) extension of phylogenetic/historical methodologies not only for analysis of population dynamics but also for analysis of gene histories, both across taxa and within gene families.

**310** SYTSMA, KENNETH J.\* AND J. CHRIS PIRES. Department of Botany, University of Wisconsin, Madison, WI 53706—“*You say you want a (Re)volution*”: *(Re)inventing Systematics.*

The end of the 20th century has seen the emergence of major and exciting new directions and tools in plant systematics - literally a revolution or re-invention of systematics. In summarizing these advances as reviewed in part by the previous speakers, the reciprocal impact of systematics to other biological and/or evolutionary fields is examined - these including communication of biodiversity, conservation biology, ecology, developmental biology, population genetics, genomics, and molecular biology. Although plant systematic biology is increasingly ‘borrowing’ from these fields, in return these fields are to some extent being shaped, enriched, or even re-invigorated with this interaction. But we do not “borrow” these tools wholecloth but only in parts, we often ask different questions with those tools and subsequently influence those other disciplines. But what is in store for the next 50 years of systematics? A more thorough revolution for systematics, in our view, would not be making phylogeny/monophyly, for example, “central” to systematics (since that is merely one way to do history from many ways to do history); instead a more radical revolution would be a return to the pluralism of Clausen, Keck and Hiesey - who modeled ecotypes, morphotypes, phylotypes. The CKH system failed because systematists then and now want to have “one system” - perhaps it is time to explore other systems. The new systematics would be not reifying parsimony or ML - but rather, chal-



lenging tree-like representations and evolving a “meta theory” that links dynamically these webs of disciplines. The model organism of the future may not be *Arabidopsis* but complex chimeric organisms like lichens; the genomic projects are showing that at some level we are all chimeric.

- 311** WILSON, HUGH D. Department of Biology Herbarium, Texas A&M University, College Station, TX 77843-3258—*Informatics: new media and paths of data flow.*

The international community of Systematic Botany is in the process of entering a networked, digital environment that, after initial development over the past 5 years, will dominate all aspects of scientific activity in the future. Emerging new technologies are transforming the Internet into a global neural network that presents Systematic Botany, and Science in general, with future prospects that include remarkable opportunity and significant challenge. The products of Systematic Botany, previously generated locally as static, hardcopy documents, can now be presented as collaborative enterprises from distributed centers as high-content, dynamic data resources that are constantly updated and refined. In addition, these products can be made available to a global user community in multiple forms that can be targeted for different user groups. The emerging Internet standard of ‘usage equals value’ could place the products of Systematic Botany in a position to draw public interest, usage, and - most importantly - support. However, opportunities inherent in the coming ‘digital transition’ will not be realized if traditional, hardcopy-based, perspectives on collaboration, peer review, publication and ‘ownership’ are retained. Scientific communities that are able to recognize new potentials and respond by establishing appropriate interactive protocols will enhance and advance their discipline in this new environment. They will also work to insure, via interaction and content review by professionals, that information available to the public is of the highest scientific quality.

### **Symposium (ASPT / ABLs / AFS / BSA Teaching Section): Scientific outreach for the next millennium**

- 312** WOLFE, ANDREA D. Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, OH 43210—*Symposium: Scientific outreach for the next millennium.*

Scientists and scientific institutions are sometimes labeled as ‘ivory towers’ that are isolated from the real world. As university and college educators, scientists often interact with students who believe that science is too hard for them to learn, or students claim they’ve never been good in science and math when faced with a suboptimal grade. Television and video-based media present scientists as “mad” or wacky, and scientific techno-babble sensu the Star Trek industry is what many viewers interpret as a normal depiction of science as a process. To present science in a user friendly environment without undermining the essence of science, it is necessary to make an effort to bring science to the public in a palatable format. Scientific outreach can be achieved on multiple levels that reinforce one another. For example, scientists can interact with the media to help reporters understand important concepts so that the information can be translated into jargon that has less “techno-babble” than what can be easily understood by nonscientists. Scientists can also interact with the public through the development of educational websites, public lectures, and by volunteering their time to youth organizations or K-12 programs. Research institutions such as museums, botanical gardens, and the like develop programs to educate the public on scientific issues. This symposium presents scientific outreach as different levels of opportunities from the perspective of scientists, educators, institutions, and the media.

- 313** ANDERSON, GREGORY J. Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269-3043—*Professional societies and promotion of the biological sciences: Will this be the “Century of Biology?”*

Science has enjoyed unprecedented public support for the past half century. Now, in the face of increasing loss of biodiversity and continuing environmental degradation, there are serious questions regarding renewal of the endangered species laws, passage of environmental legislation, and surprisingly, in this new millennium, a successful campaign based on fear and misinformation has revived an anti-evolution sentiment. Organized support for legislative science appropriations, curricular reforms and enhancement of the image of science and scientists is well developed in chemistry, physics, geology, the medical sciences and molecular biology. In organismal and integrative biology, advocacy of the field comes primarily from individuals and volunteer committees. Although the latter are important and significant activities, this ad hoc advocacy means

that effective, full time, coordinated, professional public advocacy for our fields is minimal. To be effective at this critical time, we have to empower our professional societies to commit to such public advocacy or face continuing erosion of public and governmental support.

- 314** DIETRICH, BILL. Science Reporter, The Seattle Times, Seattle, WA—*Science for People Who Don't Like Science: The Perspective of a Journalist and Novelist.*

The greatest era of scientific discovery in history is being witnessed by a population that by some measurements is largely scientifically illiterate. With science and technology driving philosophy and commerce, the scientific community needs to find ways to sustain a dialogue with the public when popular culture often portrays scientists as vain and hubristic villains and science itself as frighteningly complex. Simplified language, common sense questions, the humanization of research, gee-whiz facts, humor, hands-on education and a head-on acknowledgement of moral and ethical issues can all help ordinary people become engaged with science. If scientists want robust public support of science, they need to understand where laymen are coming from and meet them at least halfway. Suggested strategies will be offered.

- 315** HILL, RICHARD. Science Writer, The Oregonian, Portland, Oregon—*Scientists and Journalists: Worlds in Collision?*

Researchers and reporters often seem to be living in separate universes, with conflicts often arising between the two professions. But they share a curiosity and healthy skepticism about the world around them. How can they collaborate better to ensure that the public better understands science and scientists?

- 316** WOLFE, ANDREA D. Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, OH 43210—*In the Trenches: Scientific Outreach from the Perspective of a Working Scientist.*

Scientific outreach is an effort made by scientists to share information about their research with nonscientists. Examples of outreach from a botanical perspective may include (but are not limited to): workshops or seminars for K-12 teachers, local horticultural societies, garden clubs, nature clubs, schools or businesses; special events for the general public (e.g., nature hikes, wild flower workshops); newspaper columns or op-ed articles; freelance articles in newspapers, on the internet, and in horticultural or popular science magazines; taxon-oriented websites or books that are aimed at a general audience; TV spots; legislative testimony; or legal defense of rare or endangered plant species. Working scientists have a unique opportunity to share the excitement of discovery with the public. The process of scientific outreach enriches the scientist and facilitates a dynamic teaching environment that is a natural extension of the academic paradigm.

## Contributed Papers

- 317** ALBACH, DIRK C.\* AND MARK W. CHASE. Botanisches Institut der Universität Wien, Rennweg 14, 1030 Vienna, Austria, & Jodrell Laboratory, Royal Botanic Garden Kew, Richmond, Surrey TW9 3DS, U. K.—*Phylogeny of Veroniceae based on ITS-sequence-analysis - A comparison with morphology, biochemistry, and chromosome number.*

The genus *Veronica* includes about 200 species occurring throughout the Northern Hemisphere. Several genera have been split from *Veronica* in the last hundred years, such as shrubby *Hebe* from New Zealand or *Pseudolysimachion* with long corolla tubes. An analysis of ITS-sequence data for 70 taxa including 37 species of *Veronica* and several segregate genera neither supports the monophyly of *Veronica* in the widest sense nor the monophyly of *Veronica* as used today. According to our analysis, the tribe Veroniceae is monophyletic including *Veronica*, the “*Hebe*-complex”, *Paederota*, *Pseudolysimachion*, *Synthyris* (and *Besseya*), *Veronicastrum*, *Wulfenia*, and *Lagotis*. The genus *Veronica* is split into at least four clades with the Australasian species of the “*Hebe*-complex” and the genera *Synthyris*, *Paederota*, and *Pseudolysimachion* being nested within *Veronica*. The relationship between these clades, however, is not well supported. The intraspecific classification of *Veronica* so far has been mostly based on inflorescence morphology. The most important character for that matter is the presence or absence of a terminal inflorescence. Character state changes, however, seem to be more common than formerly assumed. Other characters will, therefore, be more important taxonomically in the future. Biochemical characters may be important in that sense, but they are also interesting for pharmaceutical reasons with several species of the tribe used in folk medicine. The

analysis of ITS-sequence data underlines especially the value of chromosome numbers in the taxonomy of *Veronica*. A comparison of the ITS phylogeny with chromosome numbers reveals well supported groups showing a constant chromosome number with only few exceptions. The inferred phylogeny of *Veronica* and related genera does not only have serious implications for the taxonomy of the group but also for its biogeography and spread of the tribe in the tertiary.

- 318** ALEXANDER, JASON A.\*, AARON LISTON, AND STEVE POPOVICH. Department of Botany & Plant Pathology, 2082 Cordley Hall, Oregon State University, Corvallis, OR 97331-2902; P.O. Box 265, Shoshone, ID 83352-0265—*The conservation genetics of Astragalus oniciformis*.

The genus *Astragalus* (Fabaceae) in North America is composed of nearly 400 species. Most *Astragali* in the western United States are annual or perennial herbs and are noted as “pioneer” species that grow in xeric habitats left vacant after the retreat of the last Ice Age. *Astragalus oniciformis* Barneby is a xerophyte of the sagebrush deserts of central Idaho. It is a narrow endemic of the upper Snake River Plains where it inhabits stabilized, aeolian sand deposits over Quaternary basalt flows. The demography of this species is well known, however the genetic variation of this species has never been documented. The objective of this study was to determine the levels and distribution of genetic variation within and among populations of *Astragalus oniciformis*. Several populations in the eastern portion of its range are isolated from the western populations by an eight mile long, inhospitable, basaltic lava flow. The eruption occurred 3600 years ago. The eastern populations will be analyzed to determine if they have significantly differentiated from the western, more contiguous populations. Inter-simple sequence repeats (ISSR) were chosen as the marker used to assess genetic variability. Eight populations, chosen from throughout the distribution of the species, were selected for their accessibility, density of individuals, and large population size. Levels of genetic variation, genetic similarity, and degree of population differentiation will be investigated. Populations that exhibit high levels of genetic variation and/or differentiation will be identified as a priority for conservation.

- 319** ALICE, LAWRENCE A.\* AND DUSTIN K. CONOVER. Department of Biology, Biotechnology Center, and Center for Biodiversity Studies, Western Kentucky University, Bowling Green, KY 42101—*Systematics of Rubus (Rosoidae; Rosaceae) based on nuclear ribosomal ITS and chloroplast trnK intron DNA sequences*.

We used DNA sequences from the nuclear ribosomal internal transcribed spacer (ITS) region and the chloroplast *trnK* intron, including the *matK* gene, to test monophyly and infer phylogenetic relationships of *Rubus* and its subgenera. Our ITS and *trnK* data sets include 17 species representing eight of the 12 *Rubus* subgenera, *Dalibarda repens*, and using *Fallugia* as an outgroup. Separate and combined parsimony analyses suggest that *Rubus* is paraphyletic because *Dalibarda* nests within it although bootstrap support is low. A clade including 12 of the species (excluding *Dalibarda repens*, *Rubus pedatus*, *R. chamaemorus*, *R. deliciosus*, and *R. odoratus*) is apparent in both the ITS and *trnK* analyses, and gains strong support (95%) in the combined analysis. This suggests that unarmed and primarily herbaceous, simple-leaved species are ancestral in *Rubus*. Within the clade of 12 species, several relationships are well supported in both separate and combined analyses. One includes four species of North American blackberries (subgenus *Rubus*) and another is the relationship between *R. crataegifolius* of subg. *Idaeobatus* and *R. trifidus* of subg. *Anoplobatus*. These results indicate that subg. *Anoplobatus* is polyphyletic because *R. trifidus* is more closely related to *R. crataegifolius* than to *R. odoratus* + *R. deliciosus* which form part of the basal complex in *Rubus*.

- 320** ALICE, LAWRENCE A.\*, GERASSIMO G. BORNEO, AND KHIDIR W. HILU. Department of Biology, Western Kentucky University, Bowling Green, KY 42101 and Department of Biology, Virginia Tech University, Blacksburg, VA 24061—*Systematics of Chloris (Chloridoideae; Poaceae) and related genera: evidence from nuclear ITS and chloroplast matK sequences*.

We used DNA sequences from the nuclear ribosomal internal transcribed spacer (ITS) region and the chloroplast gene *matK* to examine generic circumscriptions and infer phylogenetic relationships of the grass genus *Chloris* (Chloridinae: Chloridoideae: Chloridoideae) and several related taxa. Our ITS and *matK* data sets include 36 and 29 species, respectively, and represent at least 13 genera plus three outgroups from the tribe Eragrostideae. Independent and combined analyses of both data sets firmly suggest that *Chloris* is polyphyletic and should be redefined. However, a clade containing 7-11 *Chloris* species, *Enteropogon dolichostachys*, and *Lintonia nutans* is strongly supported by bootstrap values of 99%. Thus, it appears that *Lintonia nutans* of subtribe Pommereullinae and *Enteropogon dolichostachys* should be included in *Chloris*. Species treated

either as a separate genus (*Eustachys*) or as a subgenus of *Chloris* (except for *C. retusa*) form a monophyletic group that is distinct from *Chloris* and weakly associated with a clade comprising *Cynodon* + *Brachyachne*. The relationships among *Eustachys*, *Cynodon-Brachyachne*, and *Chloris* are not clear based on either data set alone or the combined analysis due to an internal polytomy. Additional taxa that have been treated in *Chloris* and as separate genera, such as *Trichloris* and *Oxychloris*, are distinct in these analyses and should be retained. This study forms the phylogenetic foundation for a taxonomic revision of *Chloris*.

- 321** ALLAN, GERARD J.\*, ELIZABETH A. ZIMMER, AND WARREN W. WAGNER. Laboratory of Molecular Systematics, National Museum of Natural History, Smithsonian Institution, Washington, DC 20560—*Biogeographic relationships between western North American and Mediterranean floras: insights from molecular phylogenetic studies of tribe Loteae (Fabaceae)*.

Mediterranean regions are some of the most unique and biologically fascinating areas on the face of the Earth. Corresponding largely to the Cape region of South Africa, central Chile, southwest and southern Australia, California and the borders of the Mediterranean Sea, these five regions exhibit remarkable similarities in climate, topography and flora and fauna. How similarities in the flora and fauna arose, however, has been a question of considerable interest and debate. The discovery of the underlying phylogenetic relationships of organisms inhabiting these areas can lead to an increased understanding of their evolution and diversification. In this study, we investigate the biogeography of two groups of morphologically similar plant taxa that occupy two different mediterranean regions: western North America and mediterranean Eurasia. Taxa of the two groups were sequenced for the ITS1, 5.8S and ITS2 regions of nuclear ribosomal DNA and their phylogenetic relationships were estimated using parsimony. We are also investigating the phylogenetic utility of the *trnL* region of cpDNA. Evidence based on ITS, however, suggests that the largest taxon, *Lotus*, is not monophyletic, but is composed of separate western North American and Eurasian clades. This suggests that the morphological similarities observed between Old and New World *Lotus* are either the result of convergence or are symplesiomorphic. Mapping of the character "region" onto the phylogeny suggests a complex biogeographic scenario involving multiple dispersals from Eurasia to western North America, followed by back dispersal to Eurasia. This dispersal pattern suggests a series of multiple, intercontinental dispersals that involve not only *Lotus*, but the Eurasian taxon *Coronilla* as well. These results provide insight into the evolution of morphological similarities in tribe Loteae, and yield a preliminary framework for assessing the biogeography of other temperate legume taxa occupying disjunct mediterranean regions

- 322** ALLEN, GERALDINE A.\*, DOUGLAS E. SOLTIS, AND PAMELA S. SOLTIS. Department of Biology, University of Victoria, Victoria, B.C. V8W 3N5, Canada; Division of Life Sciences, Washington State University, Pullman, WA 99164—*Phylogeny, biogeography and character evolution of Erythronium (Liliaceae)*.

The fawn-lilies (*Erythronium*) are a group of spring-flowering bulbous plants that are distributed widely in both Eurasia and North America, and reach their greatest diversity (18 of 28 species) in western North America. We carried out phylogenetic analyses of species from all geographical regions based on ITS and partial matK DNA sequences. Our results indicate that *Erythronium* is of Old World origin and is closely related to *Tulipa*, and that the species of eastern and western North America belong to separate clades that may have become established independently in the New World. Several morphological and ecological features of this group, including mottled leaves, vegetative propagation by bulb offsets, and adaptation to high-elevation environments, appear to have arisen more than once. Although some of these features have historically been used as a basis for infrageneric classification of the fawn-lilies, it seems likely that they reflect adaptation of individual species or groups to specific habitats.

- 323** ANDREASEN, KATARINA\* AND BRUCE G. BALDWIN. Jepson Herbarium and Department of Integrative Biology, University of California, Berkeley, CA 94720—*Phylogeny, unequal evolutionary rates, and biogeography in the western North American genus Sidalcea (Malvaceae)*.

Results of phylogenetic analyses of 18S-26S nuclear ribosomal DNA ITS (Internal Transcribed Spacer) and ETS (External Transcribed Spacer) sequences lead us to reject the previously suggested hypothesis of monophyly for the annual species of *Sidalcea* (Malvaceae), a western North American genus comprising ca. 25 species of annuals and perennials. Based on the rDNA data, we conclude that the annual habit arose at least three times, probably as an adaptation to seasonally dry habitats. Among the perennials, *S. oregana* and *S. malviflora* are the most heterogeneous species (with numerous subspecific taxa) and each appears to be



polyphyletic. Comparisons of evolutionary rates between perennial and annual lineages in *Sidalcea* establish that both ITS and ETS have evolved significantly faster in the annuals than in the perennials. Roush's (1931) hypothesis that the perennial species *S. hickmanii* and *S. malachroides* represent basally divergent groups within *Sidalcea* is upheld by our rDNA trees (although *S. stipularis*, discovered subsequent to Roush's study, represents an additional basally divergent lineage). Roush's (1931) suggestion that the genus spread northward from Mexico along two major routes (through the Rocky Mountains and the Sierra Nevada foothills) is not congruent with our results. Of ca. 20 rare or endangered taxa in *Sidalcea*, those corresponding to basally divergent lineages (i.e., *S. hickmanii*, *S. keckii*, *S. malachroides*, and *S. stipularis*) are well diagnosed by rDNA mutations. Others, e.g., the endangered *S. nelsoniana* (in the *S. oregana* clade), cannot be distinguished from more common, closely related taxa using ITS and ETS sequences.

**324** ASMUSSEN, CONNY B.\*, MARK W. CHASE, AND MICHAEL ZANIS. Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3DS, UK—*Nuclear 26S rDNA and systematics of monocotyledons.*

The most comprehensive phylogenetic study of monocotyledons based on DNA sequences includes 100 of the 102 currently recognized families (APG 1998) and is based on a combined analysis of *rbcL*, *atpB*, and 18S (Chase et al. 2000). This phylogeny is well resolved and well supported, except for the higher level inter-relationships among some orders. Separate analyses of the plastid genes, *rbcL* and *atpB*, result in well resolved strict consensus trees, whereas an analysis of the nuclear 18S gene gives a far less resolved consensus tree. Furthermore, the composition of a number of clades in the 18S topology differs from those of the plastid gene topologies. It is therefore important to add another nuclear DNA region to the three-gene data set, to gain further confirmation for the plastid DNA topologies and higher bootstrap support for the ordinal clades. Only a few studies have used the 3400 base pair long 26S gene for cladistic analyses, and we explore the phylogenetic information from this nuclear ribosomal DNA region. The results presented are based on the first 1200 base pairs, which contain six of the 12 expansion segments. These sequences could be aligned easily across monocot families, except for a few highly variable areas of the expansion segments. The 26S region produced about the same number of parsimony informative characters as *rbcL* and *atpB*, and more informative characters than 18S. The strict consensus tree resulting from cladistic analysis of 26S sequences is comparable to the well resolved strict consensus trees of *rbcL* and *atpB*, and much better resolved than the 18S consensus tree. The 26S topology largely recovered the clades present in the previous analyses of *rbcL*, *atpB*, and combined *rbcL*, *atpB*, and 18S. Many smaller clades received high bootstrap support, but most major clades had less than 50% support.

**325** BAILEY, C. DONOVAN\* AND JEFF J. DOYLE. L.H. Bailey Hortorium, Cornell University, 462 Mann Library, Ithaca, NY 14853—*Species boundaries in Sphaerocardamum (Brassicaceae): Integrating multiple data sources.*

As currently circumscribed, *Sphaerocardamum* (Brassicaceae) contains eight species that are endemic to limestone soils of Mexico's Chihuahuan desert. Populations of *Sphaerocardamum* are small, scattered, and difficult to find, which has resulted in poor representation of the genus in herbaria. Previous authors have considered the current species limits relatively tentative and the present project was developed to address the species boundaries within the genus as part of a systematic study of *Sphaerocardamum* and its relatives. Field studies were conducted to obtain new material from known localities as well as from regions of the Chihuahuan desert from which *Sphaerocardamum* had not been previously collected. Data from crossing studies, DNA sequences (chloroplast *trnL* intron - *trnL/F* spacer, nrDNA ITS, and *pistillata* intron 1), flow cytometry, meiotic chromosome counts, and morphology were generated to address these problems. The results suggest that the genus should be reduced from eight species to a maximum of four and that some interspecific gene flow may have occurred. The results identify that these are diploid taxa with genome sizes ranging from 0.35-0.42 pg/2C. The genome sizes match species boundaries based on morphological and molecular data.

**326** BAILEY†, C. DONOVAN\*, ROBERT A. PRICE‡, AND JEFF J. DOYLE†. †L.H. Bailey Hortorium, Cornell University, 462 Mann Library, Ithaca, NY 14853. ‡Department of Botany, University of Georgia, 2502 Miller Plant Science Bldg, Athens, GA 30602-7271—*Monophyly of the Halimolobine Brassicaceae.*

*Halimolobos*, *Mancoa*, *Pennellia*, and *Sphaerocardamum* are New World Brassicaceae genera with their greatest species diversity in Mexico. The familial classification for these genera has been controversial. Our higher level studies, using DNA sequence data from *ndhF* and *trnL* intron, suggested that some species of

these genera represent a monophyletic group. The goal of the present study was to test the monophyly of the group and their relationships relative to one another with additional species samples and data sources. Data were generated from three independent loci (chloroplast *trnL* intron - *trnL/F* spacer, nrDNA ITS, and *pistillata* intron 1) and morphology for 26 of their currently recognized 48 species. The difficulties associated with incorporating these data into total evidence analyses are discussed and our strategy is presented. Separate and total evidence analyses identify a monophyletic core group of *Halimolobos*, *Mancoa*, *Pennellia*, and *Sphaerocardamum* species that is closely related to members of the Arabidopsoid lineage. In addition, the results suggest that *Pennellia* and *Sphaerocardamum* are monophyletic but that *Halimolobos* and *Mancoa* are polyphyletic. Silique characteristic appear to be highly plastic within the lineage while characteristics of the corolla, seeds, and trichomes are relatively stable.

- 327** BALDWIN, BRUCE G.\* AND BRIDGET L. WESSA. Jepson Herbarium and Department of Integrative Biology, University of California, Berkeley, CA 94720—*Molecular phylogenetic evidence for major lineages of helenioid Heliantheae (Compositae)*.

Results of phylogenetic analyses of nuclear 18S-26S rDNA ITS-region sequences for representatives of all but four recognized genera of helenioid Heliantheae (i.e., Helenieae s. lat.) and various members of Heliantheae s. str. and Eupatorieae help to clarify major lineages in the clade corresponding to Heliantheae s. lat. plus Eupatorieae. Most subtribes of helenioid Heliantheae circumscribed by Robinson (1981) correspond closely with ITS clades. Polygeneric subtribes of helenioid Heliantheae that appear to be monophyletic based on ITS data include Flaveriinae s. Turner and Powell (1977), Madiinae s. Carlquist (1959), and Peritylinae s. Robinson (1981). Chaenactidinae s. Robinson (1981) is polyphyletic but most members of the group are encompassed within only four ITS clades. Based on the ITS data, Heliantheae s. str. and Eupatorieae represent clades nested among clades of helenioid Heliantheae, as previously suggested. Loss of receptacular bracts appears to have occurred rarely during radiation of Heliantheae s. str.; only one of the epaleate taxa that we sampled (*Trichocoryne*) was placed within the ITS clade corresponding to Heliantheae s. str., a principally paleate group. We conclude that receptacular bracts were acquired independently in the ancestors of Heliantheae s. str. and Madiinae. We also conclude that pappi of bristles have evolved in various lineages of helenioid Heliantheae and often have received too much weight in circumscriptions of suprageneric taxa. Multiple examples of extreme dysploidy from high ancestral chromosome numbers in helenioid Heliantheae are evident from the phylogenetic data. Bidirectional ecological shifts between annual and perennial habits and repeated origins of woodiness from herbaceous ancestors also must be concluded for helenioid Heliantheae. Based on modern distributions of taxa and evident phylogenetic patterns, the most recent common ancestor of Heliantheae s. lat. and Eupatorieae probably occurred in southwestern North America (including northern Mexico). Baeriinae, Madiinae, and the  $x = 19$  "arnicoid" taxa may share a common Californian ancestry.

- 328** BARBER, JANET C.\*, JAVIER FRANCISCO-ORTEGA, ARNOLDO SANTOS-GUERRA, KATHRYN TURNER, AND ROBERT K. JANSEN. Section of Integrative Biology, School of Biological Sciences, University of Texas, Austin, TX 78712; Dept. of Biological Sciences, Florida International University, University Park, FL 33199; Jardin de Aclimatacion de La Orotava, Puerto de la Cruz, Tenerife, Canary Islands, E-38400, Spain—*Origin of Macaronesian Sideritis L. (Lamiaceae) inferred from sequences of two non-coding regions of chloroplast DNA*.

*Sideritis* L. (Lamiaceae) comprises approximately 150 species of annuals and perennials distributed chiefly in the Mediterranean region. Twenty-four of these are woody perennials endemic to the Macaronesian archipelagos of Madeira and the Canary Islands. An earlier study used a chloroplast DNA restriction site approach to elucidate the pattern of evolution within and among the islands. In an effort to determine the continental origin of the insular group, we sequenced the *trnL* intron and the *trnT-trnL* intergenic spacer of the chloroplast genome. Sampling included seven island taxa, drawn from all three sections of the Macaronesian subgenus *Marrubiastrum*, and 29 continental taxa representing the remaining four sections that comprise the continental subgenus *Sideritis*. The two perennial continental sections form strongly supported clades, but there is little resolution within the groups. While the Macaronesian subgenus *Marrubiastrum* is monophyletic, its sections are not; this finding agrees with the results of the earlier cpDNA RFLP study. The cpDNA sequence data identified *Sideritis cossoniana*, an annual species from Morocco, as the closest continental relative of the Macaronesian group. Preliminary analyses of ITS sequences for the same taxa corroborate this relationship, which contrasts with the hypothesis of earlier workers who suggested that the insular taxa were most closely related to eastern Mediterranean species of the genus. This study provides

further evidence for the evolution of woodiness in insular taxa descended from herbaceous continental ancestors.

- 329** BARBER<sup>1</sup>, JANET C.\*, JAVIER FRANCISCO-ORTEGA<sup>2</sup>, ARNOLDO SANTOS-GUERRA<sup>3</sup>, AND ROBERT K. JANSEN<sup>1</sup>. <sup>1</sup>Section of Integrative Biology, School of Biological Sciences, University of Texas, Austin, TX 78712; <sup>2</sup>Dept. of Biological Sciences, Florida International University, University Park, Miami, FL 33199; <sup>3</sup>Jardín de Aclimatación de La Orotava, Puerto de la Cruz, Tenerife, Canary Islands, E-38400, Spain—*Evolution of Sideritis L. (Lamiaceae) in Macaronesia based on an analysis of chloroplast and nuclear datasets.*

In an earlier study, we used a chloroplast DNA restriction site approach to elucidate evolutionary patterns within *Sideritis* L. subgenus *Marrubiastrum* (Lamiaceae). This assemblage of 24 species comprises one of the largest endemic groups in Macaronesia. The subgenus contains a wide array of life forms which are found in all ecological zones present in the Macaronesian archipelagos of Madeira and the Canary Islands. A unique characteristic of the group is its high level of aneuploidy, a feature rare in oceanic island plants. We undertook a second analysis of the insular taxa using sequences of the internal transcribed spacers (ITS) of nuclear ribosomal DNA in order to test the patterns revealed by the chloroplast phylogeny. Placement of several taxa in the earlier cpDNA RFLP analysis suggested that hybridization may have been important in the evolution of the group. Populations of *S. canariensis* from three different islands appeared in three different places in the cpDNA tree, and infraspecific taxa of two other species were also split up. Our nuclear-based analysis provides support for an interpretation of hybridization. The three populations of *S. canariensis* are sister to each other in the ITS phylogeny, as are the subspecies of *S. cretica* and *S. gomerae* that were split in the chloroplast tree. If incongruence between the two datasets is non-significant, we will conduct rigorous analyses on a combined dataset to test the hybridization hypothesis and to further characterize evolutionary patterns within Macaronesian *Sideritis*.

- 330** BARKMAN, TODD J., JOEL R. MCNEAL, GORDON CHENERY, AND CLAUDE W. DE-PAMPHILIS.\* Department of Biology and Institute of Molecular Evolutionary Genetics, Pennsylvania State University, University Park, PA 16802 and Montgomery Bell Academy, Nashville, TN 37205—*Evolutionary genomic analyses converge on basal angiosperm phylogeny.*

Plant evolutionary genomic analyses have the greatest potential to reveal phylogeny when congruent evidence is obtained independently from the plastid, mitochondrial, and nuclear genomes with all methods of analysis. Incongruent genomic compartment estimates were obtained in analyses of previously assembled multigene data sets for basal angiosperms due in part to a combination of suboptimal outgroup choice, phylogenetic noise, and incorrect homology assignment. In spite of these potential sources of systematic error, method of analysis had the strongest effect on the results obtained. In this study, results are presented from combined analyses of 3 mitochondrial (*cox1*, *atpA*, *matR*), 2 plastid (*rbcL*, *atpB*) and 1 nuclear gene (18S) that suggest Amborella+ Nymphaeales as the first-branching angiosperm lineage. Individual genomic compartments and most methods of analysis estimated the Amborella+Nymphaeales topology with high support. Surprisingly, unweighted parsimony alone estimated Amborella-only as the first branching angiosperm, but support for this result was low after noise reduction. Ancestral character state reconstructions differ between the two topologies and profoundly affect inferences about angiosperm evolution. Relative Apparent Synapomorphy Analysis (RASA)-based data exploration was a critical step involved in these analyses and illustrated the advantage of evaluating data prior to formal phylogenetic study.

- 331** BARKMAN, TODD J., JOEL R. MCNEAL, NELSON D. YOUNG, AND CLAUDE W. DE-PAMPHILIS.\* Department of Biology and Institute of Molecular Evolutionary Genetics, Penn State University, University Park, PA 16802 and Department of Biology, Trinity University, San Antonio, TX 78212—*Multiple origins of parasitism within angiosperms.*

Phylogenetic origins of parasitic angiosperm lineages have been difficult to study using DNA sequence data used previously because plastid genes and 18S rDNA may be lost or evolve at greatly accelerated rates making inferences uncertain. We present results of a large-scale sequencing study of conserved mitochondrial genes present in all plants regardless of their photosynthetic status. *cox1* and *atpA* sequences were obtained from every order of angiosperm (recognized by APG, 1998), including every widely recognized hemi- and holoparasitic family. Phylogenetic analyses unambiguously place 12 major parasitic lineages within the context of angiosperm phylogeny. Origins of Balanophoraceae and Mitrastemonaceae are still uncertain and await further sampling. Several of the parasites appear to have arisen within lineages of plants they parasitize. This completely unexpected result suggests cases of adelophoparasitism or horizontal gene transfer from host to parasite.

- 332** BATES, PAUL L.\*, JAMES R. ESTES, AND LINDA E. WATSON. School of Biological Sciences, University of Nebraska, 348 Manter Hall, Lincoln, NE 68588-0118; Department of Botany, Miami University, Oxford, OH 45056—*Phylogenetic relationships in the Artemisia ludoviciana complex (Anthemidae/Asteraceae)*.

The *Artemisia ludoviciana* complex is a widely distributed group of herbaceous perennial species that occur in western North America from the Aleutian Islands to Jalisco in Central Mexico, which includes approximately 18 taxa. Evolutionary relationships within the group are unresolved due to continuous variation within the complex, perhaps as a result of hybridization and polyploidy. Previous work on the group yielded two mutually exclusive hypotheses of polyploid origin: allopolyploidy vs. autopolyploidy. We initiated a study to determine the mode of polyploid origin in the group and to construct a phylogeny for the group. We are using ITS and ETS nrDNA sequences to infer phylogenetic relationships and ISSR analyses to reveal polyploid origin. Data gathered to date will be discussed.

- 333** BAYER, RANDALL J.\*, DAVID G. GREBER, AND NEIL H. BAGNALL. Australian National Herbarium, Division of Plant Industry, CSIRO, Canberra, ACT, 2601, Australia—*A phylogenetic reconstruction of Australian Gnaphalieae (Asteraceae) based on four chloroplast and nuclear sequences*.

The Gnaphalieae are a group of sunflowers that have their greatest diversity in Australia, South America, and Southern Africa and are represented in the Northern hemisphere by relatively few genera. The objective of this study was to reconstruct a phylogeny of the Gnaphalieae in Australia using sequence data from three chloroplast DNA sequences, the *trnL* intron, *trnL/trnF* intergenic spacer, *matK* and one nuclear sequence, the external transcribed spacer (ETS) of nrDNA. The primary aim was to test the monophyly of the Australian endemic subtribe Angianthinae. Results indicate that two genera, *Cratystylis*, and *Isoetopsis* should be excluded from the Gnaphalieae. *Cratystylis* aligns with the Plucheeae and *Isoetopsis* allies with the Astereae. In most trees *Pterygopappus*, the only member of subtribe Loricariinae in Australia, comprises a clade that is sister to the remainder of the Australian Gnaphalieae. The base of the Australian Gnaphalieae is comprised primarily of genera of woody shrubs or subshrubs of subtribe Cassiniinae, such as *Ozothamnus* and *Cassinia*, from eastern Australia. Annual western Australian genera, such as *Gnephosis* and *Angianthus* of subtribe Angianthinae, dominate the derived clades. However, the Australasian subtribe Angianthinae is non-monophyletic, as are Australasian members of the Cassiniinae, and the genus *Myriocephalus*. Nevertheless, there is general agreement between our molecular analysis and that of morphology, particularly in the terminal branches of the trees.

- 334** BEARDSLEY, PAUL M.\* AND RICHARD G. OLMSTEAD. Botany Department, University of Washington, Seattle, WA, 98195—*A phylogenetic analysis of the genus Mimulus and tribe Mimuleae (Lamiales)*.

Species of *Mimulus* are important models for the study of plant evolution, population biology, and genetics. However, the phylogenetic relationships among species of *Mimulus* are not clear, nor is the relationship of *Mimulus* to other genera in the tribe Mimuleae or the position of this group to other families of Lamiales. The monophyly of the tribe and the seven major sections within *Mimulus* were tested using sequences of the nuclear ITS and ETS regions and the chloroplast leucine tRNA (*trnL*) intron and the intergenic spacer between *trnL* and *trnF*. Data from over 110 taxa indicate that the genera *Leucocarpus*, *Hemichaena*, *Berendtia*, *Lancea*, and the taxonomically isolated *Phryma* are derived from within *Mimulus*. The Australian genera *Glossostigma* and *Peplidium* are also derived from within *Mimulus*, indicating a second regional diversification of *Mimulus* in Australia (ca. 20 species), in addition to the recognized diversification in western North America. Within *Mimulus*, sections *Diplacus*, *Erythranthe* (plus *M. parishii*), and *Simiolus* (minus *M. gemmiparus*) are monophyletic. Sections *Mimulus*, *Eunanus*, *Oenoe*, *Paradanthus*, and *Mimulastrum* are paraphyletic.

- 335** BEILSTEIN, MARK\* AND IHSAN AL-SHEHBAZ. Department of Biology, University of Missouri Saint Louis, Saint Louis, MO 63121 and Missouri Botanical Garden, Saint Louis, MO 63110—*Toward a Phylogeny of the Brassicaceae (Cruciferae)*.

The Brassicaceae (Cruciferae) is the largest family of the diverse order including the mustard oil glycoside-producing plant families. Morphological evidence (e.g., the presence of tetradynamous stamens, cruciform corolla, radially symmetric flowers, and characteristic fruit often with a false septum dividing it into two locules) and recent molecular phylogenetic studies support the monophyly of Brassicaceae. Nonetheless, relationships within the family remain problematic. Previous classification schemes for the family relied



heavily on fruit characters to determine generic and tribal boundaries. Published preliminary molecular data show that fruit characters are highly homoplastic and that groups based on these features often do not reflect phylogeny. As a result, current generic circumscriptions in Brassicaceae make it difficult to identify putatively monophyletic terminal clades appropriate for sampling at the familial level. Recent molecular work at the generic and tribal levels suggests that the traditionally circumscribed tribe, Brassiceae, as well as a narrowly circumscribed Lepideae are monophyletic. We suggest that trichome morphology may be useful in delimiting monophyletic groups of genera in Brassicaceae. For example, the genera *Alyssum*, *Arabidopsis*, *Arabis*, *Draba*, and *Lesquerella* share branched trichomes and may form one putatively monophyletic group, while *Armoracia*, *Barbarea*, *Cardamine*, *Nasturtium* and *Rorippa* are either glabrous or have simple trichomes, forming another putatively monophyletic group. By integrating current molecular knowledge with detailed morphological investigations, we present a series of hypotheses of evolution in the family, testable using current molecular techniques. Furthermore, we discuss the importance of trichome morphology in predicting relationships in Brassicaceae.

- 336** BERGGREN<sup>1</sup>, SCOTT THOMAS\*, SANGTAE LEE<sup>2</sup>, AND JUN WEN<sup>3</sup>. <sup>1,3</sup>Department of Biology, Colorado State University, Fort Collins, CO 80523 USA, , <sup>2</sup>Department of Biology, Sungkyunkwan University, Suwon 440-746, Korea—*Phylogenetic studies in the Amygdaloideae (Rosaceae) using ITS and ndhF sequences.*

The relationships among the members of the economically important subfamily Amygdaloideae (Rosaceae) are in need of a phylogenetic reappraisal. Sequences of the ITS regions of nrDNA and the *ndhF* gene of cpDNA were employed to reconstruct the phylogeny of the subfamily, and evaluate the traditional classification schemes of this group. The two data sets are congruent in several aspects: (1) the genera *Prunus* s.l. and *Maddenia* form a monophyletic group, with *Maddenia* being nested within *Prunus*; (2) *Exochorda* (traditionally placed in subfamily Spiraeoideae) is closely allied with the Amygdaloideae; (3) two major clades are recognizable within *Prunus*: one consisting of the subgenera *Amygdalus* and *Prunus*, and the other containing the subgenera *Cerasus*, *Laurocerasus*, and *Padus* (including *Maddenia*); and (4) a few members of the subgenus *Cerasus* (*Prunus besseyi* and *P. tomentosa*) are placed within the clade consisting of subgenera *Amygdalus* and *Prunus*, suggesting that subgenus *Cerasus* is polyphyletic. The two analyses differ in the placement of the core cherry group (subgenus *Cerasus*) and the position of *Maddenia*. The combined analysis has a higher resolution within *Prunus* and places *Maddenia* sister to *Prunus* s.l. Traditionally, *Maddenia* has been separated from *Prunus* because of the calyx lobes (10 as opposed to 5 in most *Prunus*) and unisexual flowers. This study suggests the need for further evaluation of the phylogenetic position of *Maddenia*.

- 337** BERRY, PAUL E.\*, AUSTIN R. MAST, WILLIAM H. HAHN, AND KENNETH J. SYTSMA. Department of Botany, University of Wisconsin, Madison, WI 53706—*Evaluation of sectional delimitations in Fuchsia (Onagraceae) using chloroplast and nuclear DNA sequence data.*

Recent morphologically-based treatments of *Fuchsia* (Onagraceae) recognize 105 species in 11 sections. This study examines the monophyly of the sections and intersectional relationships using sequence data from the ITS region of nuclear ribosomal DNA and two chloroplast DNA regions (the *rpl16* intron and *trnL/F* spacer). The study uses 45 accessions representing 35 *Fuchsia* species in all 11 sections and four species in two outgroup genera, *Circaea* and *Hauya*. Relationships common to the nrDNA and cpDNA results include the following: Monotypic section *Pachyrrhiza* from Peru is sister to (nr), or nested in (cp), the large and generally monophyletic Andean section *Fuchsia*. Sections *Jimenezia* and *Schufia* are sister to the third small-flowered Central American section *Encliandra* (cp) or to members of the large-flowered Central American section *Ellobium* (nr). Coastal Chilean section *Kierschlegeria* is sister to south temperate Andean and southeastern Brazilian section *Quelusua*. The remaining sections (Andean *Hemsleyella*, Central American *Ellobium*, and South Pacific *Skinnera* and *Procumbentes*) are monophyletic (except *Ellobium* in nr results), but their relationships to other sections are not strongly supported with the character sampling. The small flowered *Fuchsia verrucosa* from northern South America clearly does not belong in section *Fuchsia*, appearing sister to section *Encliandra* (cp) or sister to section *Hemsleyella* (nr). The Hispaniolan *Fuchsia triphylla* is nested in the mainly Andean section *Fuchsia* (nr), but in the cp results it is sister to the apetalous section *Hemsleyella*. With these data and additional molecular and morphological sampling, we hope to obtain greater basal resolution and address biogeographical questions such as: 1) Are the two South Pacific sections sister to the nine American sections?, 2) Are sections *Quelusua* and *Kierschlegeria* from southern South America basal-most among the American species?, and 3) what are the closest relatives to the Central American sections?

- 338** BLATTNER, FRANK R. Department of Taxonomy, Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Gatersleben, Germany—*Phylogenetic analysis of Hordeum based on intron sequences of nuclear phospholipase D.*

The genus *Hordeum* L. (barley genus) occurs with about 32 species in temperate climates in most parts of the world. *Hordeum* is divided in four mostly morphologically defined sections. Four basic genomes were described within *Hordeum* species (H, I, X, Y) that, however, do not correspond to the sections of the genus. To elucidate phylogenetic relationships in *Hordeum*, intron 3 of the nuclear phospholipase D gene was used to analyze species and genome relationships in the genus, together with several closely related outgroup species. The intron sequences provide sufficient informative positions to analyze species relationships, making phospholipase D a suitable nuclear marker gene for phylogenetic inference.

- 339** BOGLER, DAVID J.\* AND JAVIER FRANCISCO-ORTEGA. Research Center, Fairchild Tropical Garden, 11935 Old Cutler Rd, Miami, FL 33156—*Phylogeny of the cycads (Cycadales) based on chloroplast DNA gene spacers and ITS rDNA sequences.*

The results of a DNA sequencing study of cycads conducted at the new molecular systematics laboratory at Fairchild Tropical Garden are presented and assessed with reference to previous phylogenetic analyses and classification schemes based on morphology and anatomy. Cycads are an ancient group of gymnosperms that were abundant and widely distributed during the Mesozoic, but are now largely confined to isolated tropical and subtropical regions. The 11-12 genera of cycads currently recognized are thought to comprise a monophyletic group, classified as a single order, the Cycadales, which is divided up into three or four families. Analysis of several chloroplast (trnL intron, trnS-trnG, psbB-psbF, atpB-rbcL) and nuclear gene (ITS2) spacer sequences suggests a number of relationships, some of which were inferred by previous morphological studies, some of which are new. The sequences of *Cycas* are the most divergent among cycads, suggesting the longest isolation. *Dioon* is relatively isolated from the other genera, and contains two major clades. *Stangeria* does not appear closely related to *Bowenia*, but does seem to have an affinity with *Zamia* and *Microcycas*. *Lepidozamia* is more closely related to *Encephalartos* than to *Macrozamia*. Sequence variation among the species of *Ceratozamia* is low. *Microcycas* and *Zamia* are closely related.

- 340** BOHS, LYNN. Department of Biology, University of Utah, Salt Lake City, UT 84112—*Slicing up the Solanums: major lineages and morphological synapomorphies.*

Analyses of molecular data from chloroplast ndhF and nuclear ITS sequences have identified six to seven major clades within the genus *Solanum* (Solanaceae). For the most part, these clades do not conform to the traditional *Solanum* subgenera. Exceptions to this pattern are the aneuploid Australasian subgenus *Archaeosolanum* and the majority of species in the spiny subgenus *Leptostemonum*, each of which appear to form monophyletic groups. Closely related to subgenus *Leptostemonum* are the non-spiny sections *Brevantherum*, *Extensum*, *Lepidotum*, *Geminata* (including *Holophylla* pro parte), *Gonatotrichum*, *Pachyphylla*, and *Cyphomandropsis*. *Solanum* *allophyllum* and the spiny species *S. wendlandii* form a clade within this group which may either be basal in *Leptostemonum* or placed outside the spiny *Solanums*. Woodiness and branched hairs are commonly found in members of this larger clade. *Solanum* sections *Solanum*, *Parasolanum*, *Dulcamara*, *Jasminosolanum* and *Holophylla* pro parte form another discrete clade composed of taxa placed by D'Arcy (1991) in subgenera *Minon*, *Potatoe*, and *Solanum*. The potatoes (section *Petota*) comprise a clade with the tomatoes (section *Lycopersicum*) and members of sections *Anarrichomenum*, *Basarthrum*, *Etuberosum*, *Juglandifolium*, *Regmandra*, *Pteroidea*, and *Herpystichum*, uniting taxa of subgenera *Potatoe* and *Bassovia*. The African non-spiny taxa represented by *S. terminale*, *S. quadrangulare*, and *S. aggregatum* in this analysis form an isolated clade within the genus. The genera *Normania* and *Triguera*, notable for their unusual morphology and distribution, are nested within *Solanum* and constitute a well-supported clade with no clear relationship to other *Solanum* groups. These data allow *Solanum* to be cleaved into several well-supported subgeneric units, some of which are diagnosable by morphological synapomorphies.

- 341** BORSCH<sup>1</sup>, THOMAS\*, KHIDIR W. HILU<sup>2</sup>, VOLKER WILDE<sup>3</sup>, CHRISTOPH NEINHUIS<sup>1</sup>, AND WILHELM BARTHOLOTT<sup>1</sup>. <sup>1</sup>Botanisches Institut und Botanischer Garten, Friedrich-Wilhelms-Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany; <sup>2</sup>Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061; <sup>3</sup>Forschungsinstitut Senckenberg, Paläobotanik, Senckenberganlage 25, 60325 Frankfurt a.M., Germany—*Phylogenetic analysis of noncoding chloroplast DNA sequences reveals Amborella as basalmost angiosperm.*

A highly resolved phylogeny of basal angiosperms was inferred from sequences of the trnT-L- and trnL-F-spacers and the trnL-intron. A robust alignment was obtained, although it was complicated by the recognition

of a large number of indels, mostly simple direct repeats ranging from 3-10 bp. About 30% of the aligned positions had to be excluded from analysis because of too high variability. Conifers and *Ginkgo* were used as outgroups. *Gnetum* shows such a high sequence divergence that no part of the trnT-F-region could be aligned with conifers, *Ginkgo*, or angiosperms. The ingroup comprises 35 taxa to represent all major lineages of basal angiosperms. In parsimony analysis, *Amborella* appears as sister to all other angiosperms examined. A Nymphaeales-clade (Nymphaeaceae plus Cabombaceae) and an *Austrobaileya-Illicium-Schisandra*-clade diverge next. These results are in agreement with recent phylogenies based on multiple coding regions. Bootstrap and decay support for the majority of nodes in the trees of the trnT-trnF-analysis was found to be high, and phylogenies obtained from separate versus combined analyses of the two spacers and the intron were largely congruent. Patterns of molecular evolution in the trnT-F-region are analyzed in order to elucidate these unexpected findings.

- 342** BOYD, AMY E. Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721—*Geographic variation in morphology and pollinator taxa in Macromeria viridiflora*.

*Macromeria viridiflora* (Boraginaceae), a perennial species that occurs as isolated populations on the Sky Islands of southwestern North America, displays geographic variation in floral morphology that may be related to pollinator variation. Analysis of morphometric data from eight sites across the range of the species shows significant among-population variation in 19 out of 20 vegetative and floral traits measured. Flower size variation is particularly strong and follows a latitudinal cline, with flowers being much larger in the southern part of the range and smaller in the northern part of the range. Observations also indicate differences in floral visitors between northern and southern populations. While flowers in all populations were visited by hummingbirds, the large-bodied hummingbirds visiting plants in the southern regions are not present in the northern regions, where flowers are visited by hummingbirds with nearly half the body size and much shorter bills. This difference in body size of pollinators mirrors the geographic variation in flower size in *M. viridiflora*, suggesting that pollinator-mediated selection may be acting upon the species. Floral variation will also be placed into a phylogenetic context to determine the historical direction of change in flower size.

- 343** BUSS, CRAIG C., THOMAS G. LAMMERS\*, AND ROBERT R. WISE. Department of Biology and Microbiology, University of Wisconsin Oshkosh, Oshkosh, WI 54901—*Systematic implications of seed coat morphology in Cyanea and allied genera of Lobelioideae (Campanulaceae)*.

Recent surveys of seed morphology in Lobelioideae (Campanulaceae) by Murata (1992, 1995) have led to a taxonomic revision of *Lobelia* L. and demonstrated the utility of such data in understanding systematic relationships within the subfamily. We have examined via scanning electron microscopy 52 additional seed accessions, emphasizing genera in which no species or only one species was examined by Murata. Foremost among these was the Hawaiian endemic *Cyanea* Gaudich., which comprises 75 species, only one of which (*C. kunthiana* Hillebr.) was examined by Murata. We examined 25 accessions, representing all major clades in the published phylogeny of the genus inferred from chloroplast DNA (cpDNA) restriction site analysis. Most were characterized by Type C morphology (the type reported by Murata for *C. kunthiana*), including species formerly segregated as *Rollandia* Gaudich., thus supporting synonymization of that genus. However, the species comprising the *C. angustifolia*-clade [sect. *Delisseoideae* (Hillebr.) Rock, s. str.] within the "Purple-fruited Clade" have a unique seed type with prominent bump-like lignose thickenings on the testa, thus offering a morphological marker for this molecularly-defined clade. We also examined seeds of the related Hawaiian endemics *Brighamia* H. Mann (both species) and *Delissea* Gaudich. (2 of 10 species) and found a second testal pattern (characterized by prominent transverse ridges) not reported by Murata. This supports the sister-status of these genera, a relationship originally revealed in the cpDNA phylogeny. The pattern observed in the *C. angustifolia*-clade appears to be intermediate between the *Brighamia-Delissea* pattern and Murata's Type C, supporting earlier hypotheses that *C. angustifolia* and its relatives lie nearest the ancestry of the genus.

- 344** BUTTERWORTH, CHARLES A. AND ROBERT S. WALLACE.\* Department of Botany, 353 Bessey Hall, Ames, IA 50011-1020—*Phylogenetic studies of the Cactus genus Mammillaria Haw. using chloroplast DNA sequence data*.

The genus *Mammillaria* (Cactaceae subfamily Cactoideae) comprises around 170 species of low growing cacti possessing tuberculate stem morphologies, distributed throughout Mexico, the Caribbean, northern

South America and the southern USA. Generic delimitation is difficult, morphologically due to close relationships with *Neolloydia*, *Coryphantha*, *Ortegocactus* and *Escobaria*. A number of infra-generic classifications of *Mammillaria* have been proposed, and although based primarily on morphological data, they are largely incongruent. Preliminary chloroplast DNA sequence data suggest that *Mammillaria*, as currently circumscribed is not monophyletic, and that previously proposed infra-generic classifications need to be re-evaluated. This paper presents results from chloroplast DNA sequence data aimed at assessing the generic boundaries of *Mammillaria* and its infra-generic classification.

- 345** CAMERON, KENNETH M.\* AND CHENGXIN FU. The Lewis B. & Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458 USA; Laboratory of Plant Systematics, Department of Biology, Zhejiang University, Hangzhou 310029, China—*Untangling the catbriers: phylogenetic studies in Smilacaceae*.

Smilacaceae are a family of monocotyledons typically characterized by climbing habit, reticulate leaf venation, paired tendrils on the petioles, unisexual flowers with six stamens, and superior ovaries found throughout the world. Deviations from this generalized description of growth form and floral morphology have led to the division of Smilacaceae into at least two different families, two subfamilies, seven different genera, and five sections within the largest genus, *Smilax*. In particular, taxa with either fused perianth, more than six stamens, or herbaceous habit have been difficult to classify. Moreover, the affinity of the family among monocots has been a matter of debate. Current treatments of Smilacaceae based partly on molecular evidence recognize three genera: *Smilax*, *Heterosmilax*, and *Rhipogonum* positioned near Philesiaceae and Liliaceae. Our cladistic analyses of 61 taxa using 51 morphological characters show that *Heterosmilax*, *Pseudosmilax*, *Oligosmilax*, *Pleiosmilax*, and *Nemexia* are monophyletic clades embedded within *Smilax* itself and that *Rhipogonum* is a monophyletic sister genus. Within *Smilax*, the erect woody habit has evolved from climbers on several occasions, but herbaceous species are monophyletic and those with inflorescence of more than one umbel also share a common ancestor. Preliminary DNA sequence data derived from the trnL-F intergenic spacer conflict with the morphological trees and support the view that *Heterosmilax* is sister to *Smilax* with *Rhipogonum* sister to this pair. These molecular data are limited and weakly supported, however, and continued sampling with more variable gene regions is required before the catbriers can be fully untangled.

- 346** CANTINO, PHILIP D.\* AND MICHAEL J. DONOGHUE. Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, Harvard University Herbaria, 22 Divinity Ave., Cambridge, MA 02138—*Objectives and progress of the PhyloCode project*.

The PhyloCode, a code of phylogenetic nomenclature, has been in development since 1997. A preliminary draft will soon be available on the Internet (<http://www.ohio.edu/phylocode/>), probably by the time of this meeting. It is hoped that many members of the systematics community will examine and comment on it. Changes will undoubtedly be made in response to public input before the code goes into operation several years from now. Phylogenetic nomenclature is designed to name the parts of the tree of life by explicit reference to phylogeny. The PhyloCode will facilitate the naming of clades and promote clear communication about phylogeny. The need for a more efficient system for naming clades has recently become critical because of the dramatic and escalating improvement in our knowledge of phylogeny. The PhyloCode will make it possible to name clades as they are discovered, without changing the names of other clades. It will also allow those who favor monophyletic taxonomy to name the clades they wish to name without being required to name groups they do not accept. The PhyloCode is designed for concurrent use with the ICBN, ICZN, etc. The first edition of the PhyloCode will govern only the naming of clades, but the intent is to add rules governing species names in the future.

- 347** CAYOUE<sup>1</sup>, JACQUES\*, PAUL M. PETERSON<sup>2</sup>, BRUCE COULMAN<sup>3</sup>, AND YASAS FERDINANDEZ<sup>3</sup>. <sup>1</sup>Eastern Cereal and Oilseed Research Centre, Agriculture and AgriFood Canada, Ottawa, ON, K1A 0C6, Canada; <sup>2</sup>Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington, DC 20560-0166; <sup>3</sup>Saskatoon Research Centre, Agriculture and AgriFood Canada, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada—*Morphological, cytological, and molecular characterization of the Bromus ciliatus complex (Poaceae: Bromeae)*.

The *Bromus ciliatus* L. complex consists of diploids and tetraploids from throughout North America with considerable morphological variation. To determine levels of variability we have sampled 32 populations of this complex from eastern and western Canada, California, and Arizona. Important morphological characters that vary within this complex are pubescence (presence/absence and density) on the basal sheaths, nodes,



and lemmas, and glume length. Morphological and cytological data from these populations and from herbarium specimens suggest that at least three groups are involved. One group (*B. ciliatus sensu stricto*) from throughout the range of the complex seems to consist of diploid individuals. Another group (*B. richardsonii* Link) consists of tetraploid individuals occurring in the Rocky Mountains from Alaska to southern California with isolated populations found in the Cypress Hills of southern Saskatchewan and Alberta. A peculiar combination of characters seems to distinguish a third group that is sympatric with the other two groups in Arizona and New Mexico. A detailed molecular characterization using RAPD markers to determine genomic relationships and genetic diversity within this complex has yielded valuable information. A discriminate analysis of all available characters will be presented.

- 348** CHANDLER, GREGORY T.\*, RANDALL J. BAYER, AND MICHAEL D. CRISP. Centre for Plant Biodiversity Research, Australian National Herbarium, GPO Box 1600, Canberra, ACT, 2601, Australia—*Molecular revision of Gastrolobium (Fabaceae: Mirbelieae), using the matK 5' intron, external transcribed spacer and psbA-trnH intergenic spacer.*

*Gastrolobium* (Fabaceae: Mirbelieae) is a genus of legumes that is endemic throughout southwest Western Australia. This genus is important economically, as it produces Sodium monofluoroacetate (a.k.a. 1080) and is of particular interest to farmers, as many deaths to sheep and cattle have been attributed to it in the past. There has been controversy over the generic delimitation of *Gastrolobium*, particularly in regard to the closely related genera *Brachysema*, *Jansonia*, *Nemcia*, and *Oxylobium*. Some morphological variation exists between the genera, but none of them can be readily separated by reliable characters, but rather by a suite of characters that overlap significantly between genera. Also, presence of 1080 was used as a secondary character to separate *Gastrolobium* and *Nemcia*, but fluoroacetate has been found in some species of *Nemcia*. Current studies using molecular tools (using the psbA-trnH intergenic spacer and the trnK 5' intron from chloroplast DNA and ETS from ribosomal nuclear DNA) have shown these genera to be very paraphyletic. *Gastrolobium* includes not only *Nemcia*, but also *Jansonia* and *Brachysema*, and one species of *Oxylobium*, *O. lineare*. The phylogenetic relationships revealed in this study within *Gastrolobium sensu lato* will lead to a recircumscription of genera in this complex, and lead to the reevaluation of evolutionary traits in this group, particularly fluoroacetate.

- 349** CHASE, MARK W., VINCENT SAVOLAINEN\*, KEI TAKAHASHI, DOUGLAS E. SOLTIS, AND PAMELA S. SOLTIS. Jodrell Laboratory, Royal Botanic Gardens, Kew TW9 3DS UK; Institute of Molecular Evolutionary Genetics, The Pennsylvania State University, PA 16802 USA; Department of Botany, Washington State University, Pullman, Washington 99164-4238 USA—*Large-scale phylogeny of flowering plants I: simple tree-building methods work better.*

Large-scale molecular phylogenies have been thought to be non-tractable due to computer limitation (extensive searches), resulting in the need for years of CPU time or a parallel computing environment. Using simulated and real 3-gene data sets for ca. 150 angiosperms, we evaluated various tree-building algorithms. We used minimum evolution (neighbor-joining with corrected distances), no swapping or NNI and TBR swapping with maximum parsimony, and maximum likelihood. We compared tree lengths versus topological distances of individual searches to the best trees (viz. combined tree with real data and model tree in simulations). We found that the simplest tree-building algorithms (e.g. fast swapping) performed equally well or better compared to other methods. These results imply that large-scale phylogenies can be built easily and accurately without extensive computer power. It also explains why incorrect trees are built when not enough data are used, no matter how complex and time-consuming the tree-building methods employed.

- 350** CHASSOT, PHILIPPE. Institut de Botanique, Université de Neuchâtel, Emile Argand 11, 2007 Neuchâtel, Suisse—*Phylogenetic position of the genus Swertia (Gentianeaceae) in the subtribe Swertiinae.*

The genus *Swertia* consists of ca 130 species and is nearly cosmopolitan in its distribution. However, most of the species occur in temperate regions of the Northern Hemisphere. The circumscription of the genus is still debated, mainly because many morphological traits such as pollen and seed ornamentation, or various floral structures, are shared with species of closely related genera of *Gentianeae-Swertiinae* (e.g. *Frasera*, *Lomatogonium*, *Halenia* and *Veratrilla*). Moreover, at the infrageneric level, only partial and controversial classifications have been attempted. To clarify the evolutionary history of *Swertia*, we analyzed phylogenetically non-coding nrDNA (ITS) and cpDNA (trnL-F) sequences of a broad range of taxa representing nearly all the morphological and biogeographical diversity of the genus *Swertia*, and of taxa belonging to 9 closely related genera. These genera are scattered among *Swertia* species in the phylogenetic tree, suggesting

that they should be viewed as sister groups of paraphyletic lineages of *Swertia*. Owing to the highest species diversity and the occurrence of taxa with the presumed ancestral characters, the mountains of southwest China are thought to be the cradle of subtribe *Swertiinae*. Our phylogenetic tree brings also some light on the biogeographic processes associated to the species radiation resulting in the actual diversity of taxa.

- 351** CHATROU, LARS, VINCENT SAVOLAINEN\*, MARK W. CHASE, MARTYN POWELL, AND YIN-LONG QIU. Jodrell Laboratory, Royal Botanic Gardens, Kew TW9 3DS UK; Department of Botany, University of Massachusetts, Amherst, MA 01003-5810 USA—*Large-scale phylogeny of flowering plants 2: the faster the better*.

It has been thought that higher-level taxonomic phylogenetic studies focusing on ancient cladogenesis events would be better recovered using slow-evolving genes, thereby avoiding multiple hits and homoplasies. Furthermore, the distinction of “slow versus fast” has long been confusing: lower numbers of variable sites and lower frequency of change at variable sites being have both been used when referring to slowly-evolving genes. Hillis has addressed both issues using simulations of a 232-taxon 18S rDNA tree, and showed that rapidly-evolving characters should perform better in phylogeny reconstruction, providing that enough variable sites are used. Using a six-gene data set (atpB, atp1, rbcL, matR, matK, and 18S rDNA, from mitochondrial, plastid and nuclear genomes) for basal angiosperms, we evaluated Hillis’ expectations and reached the same conclusion. Rapidly-evolving genes (i.e. those with more variable sites) performed the best (e.g. matK), indicating that large-scale phylogenetic analyses of plants will benefit from sequencing “fast” genes. Contrary to what is generally assumed, none of these regions differs much with respect to the frequencies of change at variable sites (i.e. variable positions are all evolving at similar rates).

- 352** CHUMLEY, TIMOTHY W.†\*, JOSÉ L. PANERO†, STERLING C. KEELEY‡, AND ROBERT K. JANSEN†. †Section of Integrative Biology, School of Biological Sciences, University of Texas at Austin, Austin, TX 78712; ‡Dept. of Botany, University of Hawaii, 3190 Maile Way, Honolulu, HI 96822-2279—*A phylogeny of the Ecliptinae (Asteraceae: Heliantheae) as inferred from internal transcribed spacer (ITS) sequences, and the origin of Lipochaeta*.

As part of a study looking at relationships within the Hawaiian endemic genus *Lipochaeta* DC., a phylogenetic analysis of the subtribe Ecliptinae s. s. (Asteraceae: Heliantheae) using sequences of the internal transcribed spacer (ITS) region of nuclear ribosomal DNA was conducted to explore the potential polyphyly of the genus. Two well supported clades were found. A clade containing the “core Ecliptinae” (*Wedelia*, *Zexmenia*, *Oyedaea*, and *Elaphandra*) agrees with results of a previous cpDNA restriction site study, although topological relationships within the clade and its placement in the tree are not well supported by bootstrapping. A much more robust clade consisting of *Wulffia*, *Perymenium*, *Wollastonia*, *Melanthera*, and *Lipochaeta* shows a sister relationship between *Wollastonia* and *Melanthera*, and these are sister to *Lipochaeta*. While some previous workers have suggested independent origins of the two sections of *Lipochaeta* from possibly different wedelioid ancestors, *Lipochaeta* appears to be monophyletic. An expanded sampling of genera in the subtribe is currently in progress.

- 353** CLARKE, H. DAVID\* AND VICKI FUNK. Department of Botany, Smithsonian Institution, Washington, DC 20560—*Analyzing checklists and using collections data to investigate plant diversity: An examination of five florulas from northeastern South America*.

Five plant checklists from areas on and adjacent to the Guiana Shield were analyzed and used to test hypotheses of the emergent properties of the flora of northeastern South America. Checklists of Iwokrama, Mabura Hill, and Kaieteur Falls (all three in Guyana), Central French Guiana, and Reserva Ducke near Manaus, Brazil, which have only recently been made available, were compiled and synonymized. Data from checklists provide an attractive alternative to transect or plot data because they are based on rigorously determined plants of all habit types rather than the sterile vouchers of tree species often used in plot or transect studies. Descriptive data were compiled for the checklists regarding diversity, overlap, and endemism. Rankings of diversity at the family level was subjected to Kendall’s coefficient of concordance of ranks test and Spearman rank correlation coefficients to evaluate similarities among the five sites. A UPGMA dendrogram was created from data for the presence or absence of species shared by two or more sites. The results indicate greater similarity of the three sites in Guyana and also of Central French Guiana with Reserva Ducke, supporting a model of plant distributions determined by the presence or absence of sandstone substrates rather than disjunct between the Guiana Highland and low elevation areas of the Guiana Shield. Relatively little overlap was found even between adjacent areas with very similar abiotic environments,

indicating that plant diversity will not necessarily be protected by conserving representative areas selected on the basis of general characteristics.

- 354** COLUMBUS, J. TRAVIS\*, MICHAEL S. KINNEY, MARIA ELENA SIQUEIROS DELGADO, AND ROSA CERROS TLATILPA. Rancho Santa Ana Botanic Garden, Claremont, CA 91711—*Homoplasy, polyphyly, and generic circumscription: the demise of the Boutelouinae (Gramineae: Chloridoideae)*.

In 1986 Clayton and Renvoize (Kew Bull., Addit. Ser. 13: 1-389) assembled 16 genera into the Boutelouinae, one of their four subtribes in tribe Cynodonteae (Gramineae: Chloridoideae). However, evidence we have gathered from morphology (including lemma micromorphology), leaf blade transverse anatomy, cytology, and nuclear and chloroplast DNA sequences indicates that the subtribe, and indeed the tribe, is polyphyletic. *Aegopogon* and *Schaffnerella* appear closely related to genera in tribe Eragrostideae—*Pereilema* and *Lycurus*, respectively. The affinities of *Melanocenchris* and *Neobouteloua* remain uncertain, as is the case for the clade comprised of the sister taxa *Hilaria* and *Pleuraphis* (often treated as a single genus, as by Clayton and Renvoize). The remaining 12 Boutelouinae genera form a monophyletic group, but the largest genera—*Bouteloua* s.s. and *Chondrosium*—are not monophyletic. Considering our much-improved knowledge of relationships, the features in common to the 12 genera, and the practical issue of identification, we advocate that the group be treated as a single genus (*Bouteloua* s.l.). The many generic synonyms are testament to the wide range of variation in inflorescence form—including sexual dimorphism and branch persistence/abscission—displayed by *Bouteloua*. The evidence shows that some architectures have evolved in parallel, notably the *Chondrosium*-like staminate inflorescence of species scattered in several lineages. The long and erroneous affiliation of *Aegopogon* with *Bouteloua*, especially the *Cathestecum* group of species, can be owed to homoplasy. Remarkable is the convergence in inflorescence form between *Aegopogon* and the *Cathestecum* group: spikelets three per branch, the lateral two reduced; branches short, pendulous, and deciduous; lemma 3-awned. Although macromorphology has generally served us well in the classification of grasses and other plants, other sources of data are necessary to detect cases of homoplasy and to ensure that the units of classification best reflect phylogeny.

- 355** CONTI, ELENA\* AND SYLVIA KELSO. Institute for Systematic Botany, , University of Zurich, 8008 Zuerich, SWITZERLAND, , Colorado College, Colorado Springs, CO, 80907, USA—*Phylogenetic relationships and character evolution in Primula L.: Results from ITS sequences*.

The main goals of this research are to reconstruct the intrageneric phylogeny of the genus *Primula* based on both nuclear and chloroplast DNA sequences and to use the resulting phylogenies to elucidate the evolution of breeding systems, morphological characters, chromosome number, and biogeographic distribution in the genus. In this paper we present the results of a pilot study based on the nuclear ribosomal Internal Transcribed Spacer (ITS) region. ITS sequences from 21 taxa produced a number of variable characters sufficient to resolve relationships among sections. The resulting phylogeny confirmed the monophyly of sections *Auricula* and *Aleuritia*. Sections *Armerina*, *Proliferae*, *Crystallophlomis*, *Parryi*, and *Auricula*, with a base chromosome number of  $x = 11$ , and sect. *Aleuritia*, with a base chromosome number of  $x = 9$ , formed two well supported clades. The ITS topology also suggested that leaves with revolute vernation, previously believed to be a derived state, might represent the ancestral condition in *Primula*, with later reversals to the involute condition. Finally, this initial ITS tree lent preliminary support to the proposed role of the widespread, diploid and heterostylous *P. mistassinica* as having given origin to the polyploid, homostylous *P. incana* and *P. laurentiana*.

- 356** COSTELLO, ANNEMARIE\* AND TIMOTHY J. MOTLEY. The Lewis B. and Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458, Biology Department, New York University, 100 Washington Square East, New York, NY 10003—*Molecular systematics of Tetraplasandra, Munroidendron, and Reynoldsia sandwicensis (Araliaceae) and the evolution of superior ovaries in Tetraplasandra*.

*Tetraplasandra*, *Munroidendron*, and *Reynoldsia sandwicensis* are Hawaiian members of a complex of closely related genera in the Araliaceae that also includes *Gastonia* and the extra-Hawaiian species of *Reynoldsia*. Generic limits in the *Tetraplasandra* complex have been hazy and phylogenetic relationships within the genera have been uncertain. Systematic relationships within the Hawaiian group are presented here based on parsimony analysis of separate and combined data sets of nucleotide sequences from ITS 1 and 2 and 5S-NTS nuclear ribosomal DNA. Results of the analyses indicate that *Tetraplasandra*, *Munroidendron*, and

*Reynoldsia sandwicensis* are monophyletic and *Reynoldsia* is paraphyletic. Both the ITS and 5S-NTS data sets support two major clades: a *Munroidendron*/*Reynoldsia sandwicensis* clade and a *Tetraplasandra* clade, but are discordant in relation to the monophyly of *Tetraplasandra*. Based on the 5S-NTS analysis, *Tetraplasandra* is paraphyletic, and the data support treating *Tetraplasandra*, *Munroidendron*, and *Reynoldsia sandwicensis* as a single genus. The ITS results support maintaining *Tetraplasandra* as a distinct genus from *Reynoldsia* and *Munroidendron*. The combined analyses are congruent with ITS results, resolving *Tetraplasandra* as a monophyletic genus. All of the analyses support combining *Reynoldsia sandwicensis* with *Munroidendron* and treating *Reynoldsia sandwicensis* separate from *Reynoldsia* species outside Hawaii. *Tetraplasandra gymnocarpa* is the only Araliaceae with a completely superior ovary, and in *T. kawaiensis* it is partially superior. Together, they form a well-supported clade within the Hawaiian complex, supporting the hypothesis that in *Tetraplasandra* superior ovaries evolved from an inferior-ovary ancestor. Research is underway to include a morphological data set; to be analyzed both independently and in combination with the molecular data sets.

- 357** CRANFILL, RAYMOND. Department of Integrative Biology, University and Jepson Herbaria, University of California, Berkeley, CA 94720-2465—*Phylogenetic utility of plastid ribosomal protein S4 (rps4) in land plants.*

Nadot and colleagues (1994) were first to demonstrate that nucleotide sequences of chloroplast ribosomal protein S4 (*rps*) were phylogenetically informative. In spite of early promise, *rps4* has been largely ignored since. Comprehensive analysis of sequences drawn from over 200 representatives of all extant lineages of embryophytes demonstrates that this neglect is unwarranted. For a plastid gene, *rps4* exhibits a remarkable degree of nucleotide substitution rate heterogeneity. The gene can be divided into five regions based on nucleotide substitution rate. Slowly evolving first (5' end), last (3' end) and middle regions exhibit substitution rates similar to *rbcL*, and may be functionally constrained. The two regions flanking either side of the middle region evolve at a much faster rate. Furthermore, these regions are prone to insertion and deletion, with some insertions exceeding 140 bp's. Both insertions and deletions can be phylogenetically informative, either individually or in groups and sometimes define large clades with long evolutionary histories (e.g., euphyllophytes, moniliforms (ferns + horsetails), polypodiaceous ferns, and yew-conifers). Further phylogenetic information can be culled from the spacer region immediately adjacent to the 3' end of the gene. This region is highly variable in length with different size classes characteristic of different major clades of land plants. The spacers of the three "bryophyte" clades, lycopsids and most seed plants are short (generally <50 bp), whereas those of the moniliforms are considerably longer (generally >300 bp). The spacer region evolves at a rate similar to ITS in ferns and angiosperms and is generally useful for detecting radiations occurring during the Tertiary (i.e., within "families" of tracheophytes). Although *rps4* is significantly shorter (and thus provides fewer characters for analysis) than phylogenetically comparable plastid genes, such as *rbcL* or *atpB*, the phylogenetic resolving power of *rps4* is often greater, providing both fuller and more well supported resolution of radiations occurring from the Devonian to the early Tertiary.

- 358** CRAWFORD, DANIEL J.\*, DONALD H. LES, ELIAS LANDOLT, REBECCA T. KIMBALL, AND JOHN D. GABEL. Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, OH 43210-1293; Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269-3043; Geobotanisches Institut ETH Zürichbergstrasse 38, , CH-8044, Zürich, Switzerland—*A phylogenetic study of the genus Wolffia (Lemnaceae).*

The genus *Wolffiella* (Hegelm.) Hegelmaier, together with the genus *Wolffia* Horkel ex Schleid., comprise the subfamily Wolffiodeae of the Lemnaceae (duckweeds). Prior to the treatment of Landolt in 1986, species had been transferred between the genera, and several segregate genera were recognized in this subfamily. Problems with generic delimitation were the result of the few morphological characters available in these very small and simple flowering plants, and the relative taxonomic significance assigned features. The most recent treatment of *Wolffiella* by Landolt recognized nine species in three sections, and he described a new species in 1992. The present phylogenetic study of *Wolffiella* includes more than 4,600 characters, including flavonoid chemistry, morphology, anatomy, allozymes, and DNA sequences from two chloroplast genes and three chloroplast introns. A parsimony analysis of our data provide strong support for the monophyly of *Wolffiella* as recognized by Landolt. The two sections *Wolffiella* and *Stipitatae* likewise enjoy 100% bootstrap support. Landolt recognized two major lineages within the genus, one consisting of sect. *Wolffiella* and another comprised of sect. *Stipitatae* and the monospecific sect. *Rotundae*. There is 100% bootstrap support for these two groups. Within sect. *Wolffiella*, the three species *W. gladiata*, *W. lingulata*, and *W. olbonga*



are close morphologically, have high genetic identities at allozyme loci, and appear to result from recent speciation. They form a highly derived clade within the section, which is concordant with recent divergence. The three species of sect. *Stipitatae* and sect. *Rotundae*, which form one of the two major clades in the genus, show high similarities at allozyme loci, suggesting relatively recent speciation in this strictly African lineage. The phylogeny suggests that the radiation of *Wolffiella* was from southeastern Africa into South America, and ultimately to North America.

- 359** DATWYLER, SHANNON L.\* AND ANDREA D. WOLFE. Department of Evolution, Ecology and Organismal Biology, Ohio State University, Columbus, OH 43210-1293—*Evolutionary and biogeographic relationships among the woody-anthered Penstemons (Scrophulariaceae)*.

*Penstemon* subg. *Dasanthera* (Scrophulariaceae) is a small group comprising 17 taxa distributed at high elevations in western North America. The subgenus is characterized by a woody habit and lanate pubescence on the anther surfaces. Hybridization has played a significant role in the evolution of the subgenus. Phylogenetic and biogeographic relationships within subg. *Dasanthera* are being examined using nrITS and *matK* sequence data. Sequence divergence is very low for both ITS (mean=0.0086) and *matK* (mean=0.0046). However, these data suggest that subg. *Dasanthera* represents the earliest divergence in *Penstemon*. Furthermore, the monophyly of the subgenus is supported. Both data sets suggest an origin of *Penstemon* in the northern Rocky Mountains, followed by westward migration and radiation of subg. *Dasanthera* in the Cascade and Sierra Nevada Mountains. These data are insufficient for resolving relationships among the Cascade/Sierra *Dasanthera* penstemons. To examine evolutionary relationships among the *Dasanthera* penstemons, inter-simple sequence repeat (ISSR) have been utilized to examine species relationships. Five primers were surveyed for 128 individuals representing all species of *Penstemon* subg. *Dasanthera*. A neighbor joining tree was produced using a similarity matrix constructed from Dice's coefficient. In addition, the potential for use of ISSR fragments in cladistic analyses have been examined. This study suggests the utility of ISSR markers for examining evolutionary relationships and patterns of introgression among closely-related taxa.

- 360** DENTON, AMY L.\* AND BENJAMIN D. HALL. Department of Botany & Plant Sciences, University of California, Riverside CA 92521 and Departments of Botany and Genetics, University of Washington, Seattle WA 92521—*Adaptive radiation of elepidote rhododendrons in the post-Miocene Himalaya: evidence from RNA polymerase III intron sequence data*.

*Rhododendron* subg. *Hymenanthus* (ca. 400 species) comprises 24 taxonomic subsections, 23 of which occur only in southeastern Asia. The combined forces of tectonic uplift and monsoon-driven erosion have shaped the terrain of the Himalaya and the adjacent mountainous Salween-Mekong-Yangtze river system. A nearly perfect overlap exists between this region of high geological relief and that of maximum species-richness in subg. *Hymenanthus*. New habitat creation resulting from rapid uplift of the Tibetan plateau and ensuing changes in monsoonal patterns, river basin connectivity and glaciation provides a plausible explanation for the occurrence of rapid rhododendron speciation in this area. Paleoclimatic and paleobotanical evidence argues that during the mid-Eocene, when the Indian and Asian plates first collided, rhododendrons were present only at high latitudes. In contrast to the modern ranges of the subsections described above, no members of *Rhododendron* subsect. *Pontica* are found in the Himalayan region. Instead, species are distributed in Turkey, eastern North America and the Pacific rim. To study the origin and tempo of speciation of elepidote rhododendrons, we sequenced a 1200 bp intron in *RPC1*, encoding the largest subunit of RNA polymerase III, from 22 Sino-Himalayan species and all 12 *Pontica* rhododendrons, and carried out a phylogenetic analysis. The inferred tree strongly supports a vicariance hypothesis of rhododendron distribution. Subsect. *Pontica* rhododendrons are basal and form two clades: a Eurasian group and a Beringian group. The non-*Pontica* Asian rhododendrons form a monophyletic assemblage, sister to the Eurasian subsect. *Pontica* rhododendrons. Clock-like evolution of the *RPC1* gene within *Rhododendron* permits several key nodes in the phylogeny to be dated by fossils or paleogeological events. This suggests a rapid post-Miocene diversification of rhododendron species after the Himalayan orogeny had begun and may signify an adaptive radiation in response to habitat expansion. Our data also suggest that several other recognized elepidote subsections do not constitute natural groups.

- 361** DICKINSON, TIMOTHY A.<sup>1,2\*</sup>, RODGER C. EVANS<sup>2</sup>, AND CHRISTOPHER S. CAMPBELL<sup>2</sup>. (1)Center for Biodiversity & Conservation Biology, Royal Ontario, Museum, 100 Queen's Park, Toronto, CANADA M5S 2C6 and Botany Department, University of Toronto, 25 Willcocks Street, Toronto, CANADA M5S 3B2; (2)Department of Biological Sciences, Deering Hall, University of Maine, Orono ME 04469-5722 U.S.A.—*Phylogenetic relationships between Crataegus and Mespilus (Rosaceae subf. Maloideae) based on rDNA sequence variation*.

Results from work on a phylogeny of the genus *Crataegus* suggest a possible re-evaluation of the status of *Mespilus*. *Crataegus* and *Mespilus* share a number of wood anatomical and morphological features that set

them apart from most other members of Rosaceae subfamily Maloideae. Data for single species of each genus from rDNA internal transcribed spacer regions (ITS1, ITS2) likewise have shown *Crataegus* and *Mespilus* to be sister genera, in a clade with *Amelanchier*, *Peraphyllum*, and *Malacomeles*. We report now on sequence variation in ITS1, 5.8S rDNA, and ITS2 in a sample of *Crataegus* species representing most of the 15 sections of the genus, and both species of *Mespilus* (Eurasian *M. germanica* L. and the Arkansas endemic *M. canescens* Phipps). For outgroups we have used *Amelanchier*, *Malus*, and *Pyrus*. The medlar, *M. germanica*, appears to be nested within *Crataegus*; preliminary results suggest that *M. canescens* could be of hybrid origin. Results may also cast light on relationships between stamen-number morphotypes in North American sections of *Crataegus*.

**362** DOWNIE, STEPHEN R. Department of Plant Biology, University of Illinois, Urbana, IL 61801—*Tribes and clades within Apiaceae subfamily Apioideae: the contribution of molecular data.*

This paper synthesizes the results of some 25 molecular systematic investigations carried out by numerous researchers over the past six years as they pertain to elucidating the higher level relationships within Apiaceae (Umbelliferae) subfamily Apioideae. Here a variety of molecular characters has been considered, including the comparative sequencing of chloroplast genes (*rbcL* and *matK*) and introns (*rpl16*, *rpoC1*, and *rps16*) and the nuclear ribosomal DNA ITS region. Restriction site mapping of the chloroplast genome has also been performed, with these data revealing unprecedented variation in size and position of the inverted repeat. On the basis of these phylogenetic studies and consistent with all available molecular evidence, ten major lineages within the subfamily are erected or confirmed as monophyletic. These are referred to as tribes Aciphyllae, Bupleureae, Careae, Echinophoreae, Heteromorphae, Oenantheae, Pleurospermeae, Pyramidoptereae, Scandiceae, and Smyrnieae. Tribe Scandiceae includes subtribes Daucinae, Scandicinae, and Torilidinae. Caucalideae sensu Heywood is not monophyletic, containing elements of subtribes Daucinae and Torilidinae. Seven additional groups, such as the *Angelica*, *Apium*, *Arracacia*, *Heracleum*, and *Pimpinella* clades, and the apioid superclade, are also recognized but have yet to be treated formally. Relationships among the major clades comprising the apioid superclade are equivocal; moreover, within this superclade several genera are of uncertain phylogenetic placement. Tribe Heteromorphae is sister to all other apioid taxa investigated, with Bupleureae, Pleurospermeae, the *Komarovia* clade, and Oenantheae comprising successively more distantly branching lineages. Apioideae, upon the inclusion of the saniculoid genus *Lagoecia* and the exclusion of the subsaharan African endemic genera *Polemanniopsis* and *Steganotaenia*, are monophyletic and sister to subfamily Saniculoideae. Subfamily Hydrocotyloideae, however, are polyphyletic, with the *Azorella* clade (*Azorella*, *Bolax*, and *Eremocharis*, and possibly *Bowlesia* and *Klotzschia*) sister to Apioideae plus Saniculoideae. These molecular data provide the framework from which future revisionary and evolutionary studies within subfamily Apioideae can proceed.

**363** DR. BOYLE, TATIANA G. Sustainable Ecosystems Institute, 0605 SW Taylors Ferry Rd. Portland OR 97219—*On the comparative analysis of the Pacific Northwest - Northeast Floras.*

The floristic researches of the Pacific Northwest and Northeast are being continued. The are focused on the determination of floral-genetic links of the largest terrestrial phyto-formations of Northern Asia and Northern America on the instance of northeastern - northwestern Pacific. The comparison of possible ways of the floras transformation with strengthening of human impact has been undertaken. Some of the preliminary results are the following. The large disjunction once formerly connected ranges of common or close related flora taxa for the Pacific's North East - North West are appear obvious with consideration the northern hemisphere flora multi-complex and are confirmed existing paleobotanical data. Especially that similarity is shown on instance of tertiary relicts, rare and endangered plant species and also the taxa which isolation and origination were furthered by transformations going on in Pleistocene. Ecological conditions and floristic compositions of the plant communities in habitat sites of common or close related species in the considered phyto-formations are not always identical. With anthropogenic impact the vector of quality composition recombination of similar local floras depends on series of factors. Among those current meso-climats and the levels of substrate multi- complex sustainability play the leading role. The changes of quality composition of close related floras in both regions caused by non-natural factors lead to origination of poor plants communities compositions with weak and unstable genetic potential and lose of natural floral-genetic links and similarities between studied regions as well.

- 364** ELISENS, WAYNE\*, MIA MOLVRAY, PAUL KORES, AND CLAUDE DEPAMPHILIS. Department of Botany & Microbiology, University of Oklahoma, Norman, OK 73019 and Department of Biology, Pennsylvania State University, University Park, PA 16802—*ITS sequence variation among climbing snapdragons (Veronicaceae): implications for delimiting genera and evaluating crossing data.*

The 20 North American species comprising subtribe Maurandyinae have been treated in four to seven genera and are noteworthy for exhibiting a diversity of floral morphologies 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 ingroup and four outgroup species were analyzed for nucleotide variation among nrDNA ITS sequences. Parsimony analyses result 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, two main clades with moderate levels of support are delineated: *Maurandya* + *Epixiphium* + *Holmgrenanthe* and *Mabrya* + *Lophospermum*. Biogeographic analyses suggest a basal diversification in arid habitats with a subsequent radiation into more mesic habitats in southern Mexico and Guatemala. The frequently segregated monotypic genera *Epixiphium* and *Holmgrenanthe* are characterized by long branch lengths and the lowest indices of crossability in the group. Species previously segregated in *Mabrya* appear paraphyletic, supporting their merger in an expanded *Lophospermum* and consistent with their moderate levels of 'intergeneric' hybrid fertilities. The highest indices of crossability and interfertility are found in species of *Maurandya* and *Lophospermum* that have the closest topological placement on ITS trees.

- 365** ENDRESS, PETER K.\* AND ANTON IGRSHEIM. Institute of Systematic Botany, University of Zurich, Zurich, Switzerland—*Floral structure of Amborella, the earliest branching extant angiosperm.*

In 1999 the monotypic genus *Amborella* was identified as the earliest branching extant angiosperm, based on multiple gene analyses by several research groups. *Amborella* flowers are small (c. 4 mm diameter), functionally unisexual but with a bisexual organization (in female flowers one or two sterile stamens are present outside of the gynoecium), with spiral phyllotaxis, with c. 8-13 inconspicuous tepals (more in male than in female flowers), with 12-22 stamens in male flowers, and mostly 5 carpels in female flowers. The flower base forms a flat cup, which tears irregularly when the flower opens. The stamens have a short filament and a triangular anther with four bulging pollen sacs forming two thecae that open by a longitudinal slit (not by valves), and a short connective protrusion. The carpels are pronouncedly ascidiate, and they have a secretory stigma with irregular pluricellular protuberances. The stigmas are contiguous in the early phase of anthesis, forming an extragynoecial compitum. Each carpel has a single, median, pendant, orthotropous, bitegmic, crassinucellar ovule. The ventral slit is not postgenitally fused but closed by secretion; however, the inner surfaces are contiguous and form a narrow slit. For an evolutionary evaluation it will be important to compare the floral structure of *Amborella* with that of other extant early-branching angiosperm lineages that recently have been identified.

- 366** ENDRESS<sup>1</sup>, MARY E.\*, BENGT SENNBLAD<sup>2</sup>, RAYMOND W. J. M. VAN DER HAM<sup>3</sup>, SIWERT NILSSON<sup>4</sup>, KURT POTGIETER<sup>5</sup>, LAURE CIVEYREL<sup>6</sup>, MARK CHASE<sup>7</sup>, JEFFREY JOSEPH<sup>7</sup>, MARTYN POWELL<sup>7</sup>, DAVID LORENCE<sup>8</sup>, ANTON IGRSHEIM<sup>9</sup>, AND VICTOR A. ALBERT<sup>10</sup>. <sup>1</sup>Institute of Systematic Botany, University of Zurich, Zurich, Switzerland; <sup>2</sup>Department of Systematic Botany, Uppsala University, Uppsala, Sweden; <sup>3</sup>Nationaal Herbarium Nederland, Leiden, Netherlands; <sup>4</sup>Palynological Laboratory, Swedish Museum of Natural History, Stockholm, Sweden; <sup>5</sup>Department of Plant Biology, University of Illinois, Urbana, Illinois, U.S.A.; <sup>6</sup>Laboratoire d'Ecologie Terrestre, Université Paul Sabatier, Toulouse, France; <sup>7</sup>Royal Botanic Gardens, Kew, Richmond, Surrey, United Kingdom; <sup>8</sup>National Tropical Botanical Garden, Lawai, Hawaii, U.S.A.; <sup>9</sup>Institute of Botany, University of Vienna, Vienna, Austria; <sup>10</sup>Botanical Laboratory, University of Copenhagen, Copenhagen, Denmark—*Arils, wings, and other sneaky things: coming to terms with the Alyxieae (Apocynaceae).*

Tribal delimitation in the Apocynaceae has traditionally been based on fruit and seed characters. These were especially important in the basalmost subfamily, Rauvolfioideae (usually called "Plumerioideae"), where the flowers are often superficially similar, with relatively unspecialized organs and few distinguishing morphological characteristics. Results of various, mostly molecular, studies in recent years, however, suggest that the fruit-based classifications did not yield monophyletic groups. Here we focus on one such group of the Rauvolfioideae, which has usually been treated as a tribe called the "Rauvolfieae" or "Alyxieae", and

characterized by having drupaceous fruits. This study is based on a combined analysis from five data sets, including four genes (*matK*, *rbcL*, *trnL* intron and *trnL*-F spacer) and 54 morphological characters. In the consensus trees from each individual data set the bulk of the genera fall within two clades, which have been re-circumscribed as *Alyxieae* and *Vinceae*. In the combined matrix consensus tree the traditional “*Alyxieae*” is polyphyletic, with genera dispersed over 4 separate clades. This exemplifies the ease with which fruits may switch back and forth from dry to fleshy and/or dehiscent to indehiscent, or seeds independently evolve similar structures to aid in dispersal in response to selective pressures. It also bodes ill for delimitation of higher taxonomic categories based on traditional fruit and seed characters elsewhere in the family, and should serve as a warning in other families in the Gentianales as well, such as *Rubiaceae*, where fruit characters have played an important role in classification. Combining morphological and molecular methods allows us to glimpse how much more intricate the evolutionary pathways are than previously imagined and provides a groundwork on which to study character evolution.

- 367** ESSIG, FREDERICK B.\*, JAMES R. GAREY, AND JONATHAN M. SLOMBA. Department of Biology - SCA 110, University of South Florida, Tampa, FL 33620—*The infrageneric classification of Clematis (Ranunculaceae)*.

The infrageneric classification of the large, cosmopolitan genus, *Clematis* (*Ranunculaceae*), has been based on minor differences in vegetative and inflorescence morphology, along with flower size, shape and color. The most comprehensive global classification recognizes 26 infrageneric taxa, including the sometimes segregated genera *Archiclematis*, *Naravelia* and *Clematopsis*, but many of the 250-300 species are uncertainly placed or unplaced within this system. A more sound basis for classification, based on seedling morphology, reproductive compatibility, and a reevaluation of a number of vegetative and floral characters, was suggested by earlier work. A major feature of a new classification would be the division of at least the bulk of the genus into two subgenera, one exhibiting classical epigeal germination and alternate seedling phyllotaxy, and the other exhibiting a type of hypogeal germination and opposite seedling phyllotaxy. The proposed major divisions of the genus are being tested with a phylogenetic study based on DNA sequence data, which will be expanded as part of the development of a comprehensive new classification. We have so far extracted DNA from 18 taxa broadly representative of the genus and are PCR amplifying the nuclear ribosomal RNA internal spacer and a noncoding region located between the *trnT* and *trnF* genes of the chloroplast genome. Preliminary results of that study will be presented.

- 368** EVANS, RODGER C. AND CHRISTOPHER S. CAMPBELL.\* Department of Biological Sciences, University of Maine, Orono, ME 04469—*A multigene tree of the Rosales*.

The recently published analysis of *atpB*, *rbcL*, and 18SrDNA sequences (Soltis et al. 1999. *Nature* 402:402) strongly supports monophyly of the Rosales. This order contains about 6300 species in 9-11 families, all of which except *Moraceae* and *Rosaceae* have fewer than 1500 species. These genes place *Rosaceae* as sister to the remainder of the order, which consists of a trichotomy of *Rhamnaceae*, the weakly supported pairing of *Elaeagnaceae* + *Barbeyaceae*, and the well supported suborder *Urticineae*. *Ulmaceae* is the first branch within *Urticineae*, and *Urticaceae* is sister to a weakly supported assemblage of *Moraceae* + (*Cannabaceae* + *Celtidaceae*). In an attempt to clarify relationships within the Rosales, we use three chloroplast DNA sequences - portions of the *matK* and *ndhF* genes and the *trnL* region - that are more rapidly evolving than *atpB*, *rbcL*, and 18SrDNA. Our three genes total about 4400 aligned nucleotide sites, and our sample is nearly identical to the 18 genera in the combined *atpB*-*rbcL*-18SrDNA study. With sequences from *Fabaceae* as an outgroup, our three genes recover nearly the same topology as the *atpB*-*rbcL*-18SrDNA study, although there is less support for deeper branches in the Rosales tree, and the trichotomy is weakly resolved with the *Rhamnaceae* as sister to the *Urticineae*. The combined analysis of over 9000 aligned sites from *atpB*, *rbcL*, 18SrDNA, *matK*, *ndhF*, and *trnL* produces the same topology as the *atpB*-*rbcL*-18SrDNA study, including the trichotomy, but adds support to the *Elaeagnaceae*-*Barbeyaceae* and *Moraceae*-*Cannabaceae*-*Celtidaceae* clades. This topology provides a context for studies of character evolution in this morphologically diverse order.

- 369** EVANS, RODGER C.\* AND CHRISTOPHER S. CAMPBELL. Department of Biological Sciences, University of Maine, Orono, ME 04469-5722—*The polyploid origin of a large clade: Nuclear Granule-Bound Starch Synthase (GBSSI or waxy) gene sequences support a spiraeoid ancestry of the Maloideae (Rosaceae)*.

Base chromosome number (X) is 7, 8, or 9 in most members of *Rosaceae* except the *Maloideae* (X = 17). The base number of 17 plus molecular and morphological data support the inclusion in *Maloideae* of *Ka-*



*geneckia*, *Lindleya*, and *Vauquelinia* ( $X = 15$ ), which were traditionally assigned to the polyphyletic “Spiraeoideae.” The base number of 17 has long been interpreted as evidence of either allopolyploidization involving ancestral Amygdaloideae ( $X=8$ ) and “Spiraeoideae” ( $X=9$ ) or polyploidization within ancestral “Spiraeoideae”. To investigate the origin of Maloideae, we cloned and sequenced 941 bp from nine exons in the 5' portion of GBSSI. We sampled 13 genera of Maloideae (including *Kageneckia*, *Lindleya*, and *Vauquelinia*) plus genera of Rosaceae that previous studies have shown to be closely related to the Maloideae. Our analysis supports a close relationship between our Maloideae sample and  $X = 9$  *Porteranthus* (“Spiraeoideae”) of the southeastern United States. Maloideae have four GBSSI paralogues, two (GBSSI-1 and GBSSI-2) from a duplication prior to the origin of Rosaceae and two from a duplication within each Maloideae clade (GBSSI-1A and B; GBSSI-2A and B). Multiple clones of *Porteranthus* nest within either Maloideae GBSSI-1 or 2 and are weakly linked to GBSSI-1A or GBSSI-2A. Monophyly of Maloideae-*Porteranthus* clades is supported by bootstrap values approaching 100%, loss of the sixth intron in all GBSSI-1 sequences, alignability of introns between genera, and numerous non-molecular characters. Our results are consistent with a polyploid origin involving only members of a lineage that contained the ancestors of *Porteranthus*. Under this hypothesis, the subfamily originated in North America, and the high Maloideae chromosome number arose via aneuploidy from  $X = 18$ .

- 370** FAN, CHUANZHU\*, JENNY QIU-YUN XIANG, AND RICHARDSON ADJOA. Department of Biological Sciences, Idaho State University, Pocatello, Idaho 83209-8007—*Phylogenetic Relationships of Cornus L. Inferred from Nuclear DNA Sequences.*

Previous phylogenetic analyses of *Cornus* using cpDNA data and morphological characters suggested different relationships within the genus. Independent data sets containing sequences from nuclear 26S and ITS1-5.8S region of rDNA were generated for *Cornus* L. to test the phylogenetic hypotheses based on chloroplast DNA and morphological data. The obtained 26S rDNA sequences were easily aligned with few gaps consisting of 3465 bp, but sequences from the ITS1-5.8S region were difficult to align unambiguously among subgroups of the genus. Phylogenetic analyses of these sequence data were conducted using PAUP4.0b4. Results from 26S rDNA sequences suggested relationships among subgroups congruent with those inferred from cpDNA data. That is, the dwarf dogwoods and the big-bracted dogwoods are sisters, which in turn, the sister of the cornelian cherries. The blue- or white-fruited dogwoods form a clade sister to this red-fruited. However, results from the ITS1-5.8S region suggested different relationships within the red-fruited dogwoods (i.e., the dwarf dogwoods are sister to the cornelian cherries).

- 371** FERGUSON, CAROLYN J.<sup>1</sup>\* AND BARBARA A. SCHAAL<sup>2</sup>. <sup>1</sup>Herbarium and Division of Biology, Kansas State University, Manhattan, KS 66506-4901, <sup>2</sup>Department of Biology, Washington University, St. Louis, MO 63130-4899—*Genetic relationships and variation in populations of Phlox pilosa and P. divaricata (Polemoniaceae) in the Ozarks.*

Phylogenetic relationships of eastern North American *Phlox* L. are complicated, and many studies have suggested this may be due in part to hybridization. Recently developed molecular phylogenies (based on markers from the nuclear and chloroplast genomes) showed patterns of incongruence consistent with hypotheses of hybridization, although other causes of incongruence were not ruled out. To explore the potential evolutionary role of hybridization in *Phlox*, we are investigating genetic relationships and variation in populations of two species, *P. pilosa* L. and *P. divaricata* L., in and near the Ozark highlands of the central United States. *Phlox pilosa* exhibits striking morphological variation in the Ozarks, and a distinct subspecies is recognized, *P. pilosa* subsp. *ozarkana* (Wherry) Wherry. Given that *P. pilosa* and *P. divaricata* occasionally come into local contact and hybridize, it is intriguing to ask whether introgression has occurred between these species in the Ozark region, potentially contributing to the variation observed within *P. pilosa*. A phylogeographic approach to this question is presented, and preliminary gene trees based on regions of low-copy number nuclear genes are discussed, along with some of the challenges of developing and interpreting these trees. In addition, development of microsatellite markers is underway, and these methods are outlined. The microsatellite data will yield information on population genetic structure for comparison with the gene genealogies. Overall, this approach of carefully examining genetic data at the population level and interpreting that information within a larger phylogenetic context will provide insights that lead to an improved understanding of the evolutionary processes at play in *Phlox*.

- 372** FERGUSON, DIANE M.\* AND TAO SANG. Department of Botany and Plant Pathology, Michigan State University, East Lansing, MI 48824—*Testing hypotheses of hybrid speciation in peonies (Paeonia; Paeoniaceae) using the low-copy nuclear gene alcohol dehydrogenase (Adh).*

DNA sequence data from the low-copy nuclear gene alcohol dehydrogenase (*Adh*) were used to test the putative hybrid origin of several diploid and tetraploid species of peonies belonging to *Paeonia* section

*Paeonia* (Paeoniaceae). Two paralogous loci (*Adh1* and *Adh2*), duplicated prior to the diversification of *Paeonia* species, were amplified with locus-specific primers and cloned for one or more accessions from each species. All distinct clone copies were included in a single simultaneous parsimony search for each locus. *Adh1* and *Adh2* support that several tetraploid species, including the “arietina” species group (*P. arietina*, *P. humilis*, *P. officinalis*, *P. parnassica*), *P. peregrina*, and *P. banatica*, are of allopolyploid origin. After the initial hybridization event, tetraploid peonies may have gone on to speciate and further hybridize, creating new species such as *P. officinalis*. For putative hybrid diploids, distinct sequences were found at the *Adh2* locus for *P. emodii*, and *Adh1* sequence polymorphism was detected for *P. japonica* and *P. obovata*. This may imply that heterozygosity resulting from hybridization can be maintained at a nuclear locus but homogenized at the other following genome rearrangement in a diploid hybrid. Overall, *Adh2* corroborates many of the findings based on *Adh1*; however, the tempo of gene duplication and deletion at that locus is much more dynamic than *Adh1*, with many pseudogenes found in several species.

**373** FREID, ETHAN. Department of Botany, Miami University, Oxford, OH 45056—*Leaf anatomy of the tribe Coccolobeae (Polygonaceae)*.

Leaf anatomy, including leaf clearings, of *Antigonon*, *Brunnichia*, *Coccoloba*, *Muehlenbeckia*, and *Podopterus* was investigated. These genera have historically been united within the tribe Coccolobeae. Twelve anatomical features were compared among 39 species. Despite many similarities in cell types and venation patterns, a number of interesting trends were apparent. Variation among the genera involves the presence of tanniferous idioblasts, prismatic crystals, collenchyma, sclerenchyma, and hypodermal layers. Leaf clearing data was not conclusive at the intrageneric level but was instructive in differentiating species within *Brunnichia* and *Podopterus*. Additionally, in *Coccoloba diversifolia* the relationship between leaf morphology and leaf anatomy was investigated. The data supports previous hypotheses that the variation in leaf shape is partially due to varying levels of sunlight.

**374** FREID, ETHAN. Department of Botany, Miami University, Oxford, OH 45056—*Stem and nodal anatomy of the tribe Coccolobeae (Polygonaceae)*.

Stem and nodal anatomy of *Antigonon*, *Brunnichia*, *Coccoloba*, *Muehlenbeckia*, and *Podopterus* was investigated. These genera have historically been united within the tribe Coccolobeae. Seventeen anatomical features were compared among 19 species. Two groups of character states were identified as significant. First, the width of the band of sclerenchyma fibers correlates with the presence of an endodermoid layer. Second, two patterns of leaf trace divergence are present. Species either have traces that diverge simultaneously or have the main trace diverge initially followed by the lateral traces. Furthermore, the lateral leaf trace pathway is either perpendicular to the stem and the traces fuse together before entering the petiole or the trace pathway is parallel to the stem and the traces enter the petiole independently. The patterns of leaf trace divergence and the pathway of traces to the petiole are stable at the generic level.

**375** FREID, ETHAN. Department of Botany, Miami University, Oxford, OH 45056—*Stem, node, petiole, and leaf anatomy of Coccolobeae (Polygonaceae) and its systematic implications*.

Stem, node, petiole, and leaf anatomy of *Antigonon*, *Brunnichia*, *Coccoloba*, *Muehlenbeckia*, and *Podopterus* was investigated. These genera have historically been united within the tribe Coccolobeae. The tribe is interesting to study because the genera form a heterogeneous group of taxa with either winged achenes or drupes and habits that include vines, lianas, shrubs, and trees. Forty anatomical features were compared across 39 species. Despite many similarities among the genera a number of interesting patterns were observed. Anatomical trends that were observed include variation in the presence of a stem endodermoid layer, sclerenchyma, leaf trace divergence, and leaf trace pathways. Petiole anatomy revealed differences in the vascular bundle arrangement, and the presence of tanniferous idioblasts, and endodermoid layers. In leaves, there was variation in the presence of tanniferous idioblasts, prismatic crystals, leaf hypodermal layers, as well as variation in venation patterns at the species level in *Brunnichia* and *Podopterus*. The data suggests that Coccolobeae may not be a cohesive evolutionary unit and contains genera that would be best placed in other tribes.

**376** FREUDENSTEIN, JOHN V.\*, DIANA M. SENYO, AND MARK W. CHASE. Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, OH 43212; Department of Biological Sciences, Kent State University, Kent, OH 44242; Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3DS—*Phylogenetic implications and comparative utility of 26S and ITS2 sequences in Orchidaceae*.

As the nuclear portion of a multigene analysis of relationships in Orchidaceae, ITS2 and the first 1200 bp of the 26S locus were sequenced in over 60 genera from the family. Alignment of the 26S segment was

straightforward, while that of ITS2 was less so. Regions within ITS2 varied with respect to base substitution and indel rate, presumably reflecting secondary structure relationships in the molecule. Equally weighted parsimony analysis of these data yielded two most parsimonious trees, the consensus of which is well resolved. While analysis of the 26S sequences alone gave a moderately resolved tree, addition of the ITS2 data increased resolution and branch support, particularly among closely related groups. Five subfamily-level assemblages are resolved, corresponding to Vanilloideae, Cypripedioideae, Orchidoideae (including Spiranthoideae), and Epidendroideae. Tribal level groups are apparent, and jackknife analysis indicates that while most of these groups are well supported, the relationships among them often are not. This is particularly true among groups within Epidendroideae, where branch lengths are typically short. This is the same pattern seen in other molecular and morphological data sets and is interpreted to reflect a rapid radiation of epidendroid groups. Basal clades in Epidendroideae include Neottieae, *Elleanthus*, *Triphora* and *Tropidia*, with more derived groups including an Asian clade corresponding to Podochileae, as well as a monophyletic Maxillarieae. The patterns are highly congruent with those obtained from plastid and mitochondrial sequence data.

**377** FUERTES AGUILAR, JAVIER\*, BELÉN GUTIÉRREZ LARENA, AND GONZALO NIETO FELINER. Real Jardín Botánico, CSIC. 28014 Madrid, Spain—*Reticulate evolution along an altitudinal gradient in Armeria (Plumbaginaceae) inferred from ITS, cpDNA, and morphology.*

Reproductive barriers between different species of *Armeria* are mostly external, leading to extensive hybridization. We have studied two molecular markers in populations from Sierra Nevada, an E-W aligned massif in Southeast Spain reaching 3500 m, where four taxa occur at different altitudes under several ecological conditions. These are *A. splendens*, *A. filicaulis* ssp. *nevadense*, *A. villosa* ssp. *bernisii*, and *A. filicaulis* ssp. *trevenqueana*. Forty populations (with at least five individuals per population) were sampled for ITS1-5.8S-ITS2 and chloroplast trnL-trnF spacer sequences. Morphologically, the four taxa are easily distinguished not only using qualitative characters but also quantitative, as revealed by a principal components analysis based on twenty characters. The ITS sequences are represented in the area by one common ribotype present in all samples regardless of their taxonomic identification. Additionally, at least two other ribotypes, differing on three nucleotide positions plus a 1-bp indel, are present in the area. Despite the occurrence of concerted evolution in the genus, these additional ribotypes occur in some individuals of the two putative hybrid taxa (*A. filicaulis nevadense* and *A. villosa bernisii*), besides the common ribotype. In contrast, *A. splendens*, occurring on alpine meadows, bears a single ribotype. In the cpDNA, sequences from trnL-F intergenic spacer display a haplotype variability independent from ITS and morphology. Six different haplotypes are found within the massif, their distribution being correlated with the altitude. While *A. splendens* populations show a single haplotype, *A. villosa bernisii* shows four different haplotypes across the massif. Our results are consistent with the hypothesis that *A. filicaulis nevadense* and *A. villosa bernisii* have a hybrid origin. *A. splendens*, or an immediate ancestor, seems to be one of the parental taxa.

**378** GABEL, JOHN D.\*, DONALD H. LES, W. ALAN CHARLTON, AND ALLEN J. COOMBES. Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269-3043; Department of Biological Sciences, Manchester University, Manchester, M13 9PT, UK; The Sir Harold Hillier Gardens and Arboretum, Jermyns Lane, Ampfield, Romsey Hampshire, SO51 0QA, England, UK—*Phylogeny of Azara (Flacourtiaceae).*

Although Flacourtiaceae are often thought of as a highly artificial family, the genus *Azara* has long been recognized as a natural group. *Azara* is the only genus in Flacourtiaceae to possess foliar stipules which provide a unifying synapomorphy for the taxon. Major taxonomic treatments of Flacourtiaceae have placed *Azara* in the tribe *Flacourtieae* along with such genera as *Flacourtia*, *Dovyalis*, *Idesia*, *Olmediella* and *Xylosma*. However, interspecific relationships in *Azara* have been poorly elucidated. Gilg (1925) placed *Azara* species into three sections (*Microazara*, *Celastrazara*, and *Euazara*) which were defined using leaf and stamen characters. The most recent monograph by Sleumer (1977) also recognized three species groups within the genus, but these were not formally named. Sleumer defined these groups using a combination of inflorescence, floral and leaf characters. Our phylogenetic study combines nuclear and chloroplast DNA sequences to investigate interspecific relationships in *Azara*, and also to evaluate its relationship to other members of the tribe *Flacourtieae*. We sequenced the complete ITS region and trnL (chloroplast DNA) intron for 12 of the 13 *Azara* species, five other genera of tribe *Flacourtieae*, and from *Scolopia* (tribe *Scolopieae*). Outgroup sequences (Salicaceae) were obtained from GenBank. Overall, we find the groups delimited by Sleumer (1977) to be supported by both molecular data sets with one slight modification to recognize *A. microphylla* as a separate, monotypic group. Molecular data are also largely congruent with preliminary analyses of morphological characters in the genus and tribe.



- 379** GERNANDT, DAVID S., AARON LISTON\*, AND DANIEL PIÑERO. Instituto de Ecología, Universidad Nacional Autónoma de México, México D.F. 04510, Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon 97331—*Nuclear ribosomal DNA internal transcribed spacer region polymorphism and its implications for phylogenetic inference in Pinus subsection Cembroides.*

*Pinus* subsection *Cembroides* (the pinyon pines) is a group of palaeo- and neo-endemics confined to the western United States and Mexico. Both ancient, and recent speciation are apparent causes of taxonomic disagreement in the group. We used nuclear ribosomal DNA internal transcribed spacer (ITS) region sequences to reconstruct a molecular phylogeny for subsection *Cembroides* and representative species from other subsections of *Pinus*. The ITS1 is approximately 2.6 Kb in *Pinus*, thus providing more variable sites for phylogenetic reconstruction than typically expected for the ITS region. Restriction digests of ITS region amplified either directly from genomic preparations or from clones revealed polymorphism within individuals. ITS pseudogenes were detected by examining the rate and pattern of substitution, and by a relaxation of secondary structure. Although pseudogenes could be distinguished and removed from the phylogenetic analysis, inclusion of multiple clones that were not pseudogenes resulted in topological conflicts that we attribute to deep coalescence of paralogous copies. ITS polymorphism may limit the utility of the ITS for phylogenetic reconstruction among closely related species in *Pinus*. However, agreement with cpDNA phylogenies at the level of subsection and above suggests that the ITS is useful for higher level phylogeny in the genus.

- 380** GIUSSANI, LILIANA M., J. HUGO COTA-SANCHEZ\*, FERNANDO ZULOAGA, AND ELIZABETH A. KELLOGG. Instituto de Botanica Darwinion, Buenos Aires, Argentina; and Department of Biology, University of Missouri-St. Louis, St. Louis, MO 63121—*A molecular phylogeny of the subfamily Panicoideae (Poaceae) using ndhF sequences.*

The grass subfamily Panicoideae includes over 3000 species, approximately 500 of them in the polymorphic and polyphyletic genus *Panicum*. We have used full-length sequences of the chloroplast gene *ndhF* to determine the phylogeny of the group. The final data set includes sequences of 102 panicoids plus 6 outgroups; of these 79 sequences are new to this study. The Panicoideae are monophyletic, supporting all previous molecular and morphological studies. The subfamily is divided into three strongly supported clades, representing groups with the same chromosome base number: the Andropogoneae ( $x=10$ ),  $x=10$  Paniceae and  $x=9$  Paniceae; the first two may be sister taxa, but this result is not strongly supported. The point of origin of C4 photosynthesis is ambiguous, and varies among and within strongly-supported clades. The PCK and the NAD-ME C4 subtypes each originated once and are unreversed synapomorphies for the *Urochloa*-clade and for *Panicum* subgenus *Panicum*, respectively. All other C4 species are NADP-ME and lack an outer bundle sheath; despite their biochemical and anatomical similarity, these do not form a monophyletic group. *Panicum* subg. *Panicum* is unrelated to the other subgenera of *Panicum*. *Panicum maximum*, the sole species in *Panicum* subg. *Megathyrsus* is better placed in *Urochloa*, as suggested by earlier authors. *Panicum* subg. *Agrostoides*, subg. *Phanopyrum* and possibly also subg. *Dichantherium* are polyphyletic. *Paspalum* is paraphyletic, with *Thrasya* derived from within it. All genera with bristles in the inflorescence (*Setaria*, *Pennisetum*, *Cenchrus*, *Paspalidium*) form a clade. Previously defined subtribes are not monophyletic, but some clades in the phylogeny are similar to those in morphological cladograms.

- 381** GIVNISH, THOMAS J.\*, GREG BEAN, AND KENNETH J. SYTSMA. Department of Botany, University of Wisconsin, Madison, WI 53706—*Phylogeny, floral evolution, and patterns of inter-island dispersal in Clermontia (Lobeliaceae) in Hawaii based on ISSR variation.*

Present-day *Clermontia* apparently represents the residuum of a relatively recent radiation from a relatively old lineage sister to the much larger genus *Cyanea*. *Clermontia* species differ dramatically in flower shape, color, and form, with several taxa having petaloid sepals. Roughly half the species are restricted to single islands, mainly Maui and Hawai'i at the young end of the Hawaiian chain. Taxa diverge little from each other in cpDNA restriction site or ITS sequences, and previous attempts to reconstruct phylogeny in this group have been largely unsuccessful. Here we present a well-resolved phylogeny based on a cladistic analysis of ISSR variation. As we had previously predicted, the most early divergent species among the present-day taxa is *Clermontia fauriei* of Kaua'i, the oldest tall island. The next species to diverge was *Clermontia persicifolia*, the only species restricted to O'ahu, the second oldest tall island. Our data are consistent with the origin of *Clermontia* on Kaua'i or some older, now eroded island, with subsequent dispersal down the chain toward younger islands. These data are also consistent with hybridization and with relatively extensive gene flow, perhaps occasioned by *Clermontia*'s dependence on vagile, forest-edge birds for fruit dispersal. Our phylogeny supports one, or at most two, origins of petaloid sepals, and at least one



loss of this apparent homeotic mutation. Floral tube length appears to have evolved rapidly. A cladistic reanalysis of morphological data yields almost no resolution of evolutionary relationships.

- 382** GIVNISH, THOMAS J.\*, J. CHRISTOPHER PIRES, SEAN W. GRAHAM, KENDRA C. MILLAM, THOMAS B. PATTERSON, TIMOTHY M. EVANS, ERIC H. ROALSON, AND KENNETH J. SYTSMA. Department of Botany, University of Wisconsin, Madison, WI 53706; Department of Biological Sciences, University of Alberta, Edmonton Alberta, T6G 2M7; Rancho Santa Ana Botanical Garden, Claremont, CA 91711; and Department of Botany, Hope College, Holland MI 49423—*Phylogeny of the monocotyledons based on ndhF sequence variation, with special emphasis on relationships within and among commelinoids, lilioids, and asparagoids.*

Many higher-level relationships within and among major monocot lineages remain unresolved or poorly supported in analyses based on sequence variation in *rbcL*, *atpB*, and 18S rDNA. We attempted to resolve some of these ambiguities by assembling a large number (ca. 200) of sequences of the large, rapidly evolving, chloroplast-encoded *ndhF* gene. Parsimony analyses resolved all major clades of monocotyledons, using *Acorus* as an outgroup. Within the traditionally difficult commelinoids, several sister-group relationships were resolved. *Hanguana* was sister to Zingiberales, and the latter was fully resolved: Zingiberaceae-Costaceae sister to Cannaceae-Marantaceae, and Musaceae-Heliconiaceae sister to Lowiaceae-Strelitziaceae. Dasypogonoids were closely related to Commelinales, and both were sister to Zingiberales/Hanguana near the base of the commelinoids, near Arecaceae. Rapateaceae was the closest relative of Poales and allied orders; Mayacaceae was sister to Bromeliaceae. Asparagales was resolved as the sister group to the commelinoids. Within the asparagoids, Themidaceae was sister to a large lineage including Agavaceae, Hyacinthaceae, Hostaceae, and Anthericaceae. Liliales was sister to the commelinoid-asparagoid clade. Within the lilioids, Calochortaceae and Liliaceae (both sensu Tamura) were monophyletic sister groups. *Clintonia-Medeola* was sister to Liliaceae s.s., while *Tricyrtis* was sister to *Calochortus*. Stemonoids formed a grade at the base of the commelinoids-asparagoids-lilioids; the alismatids were sister to all monocots sampled, excluding *Acorus*. Sequence variation in *ndhF* provides an additional, powerful set of molecular data with which to explore relationships and evolutionary patterns within the monocotyledons.

- 383** GIVNISH, THOMAS J.\*, KENDRA C. MILLAM, AND KENNETH J. SYTSMA. Department of Botany, University of Wisconsin, Madison, WI 53706—*Phylogenetic relationships and evolutionary patterns in Bromeliaceae based on ndhF sequence variation.*

Among commelinoids, bromeliads display low rates of chloroplast sequence evolution. However, the large, rapidly evolving, chloroplast-encoded *ndhF* gene displays useful amounts of sequence variation for phylogenetic reconstruction. We obtained 17 new *ndhF* sequences for major bromeliad groups unsampled in previous surveys to present a more complete picture of evolution in this important Neotropical group. Parsimony analysis using members of Poales as outgroups indicated that *Mayaca* is sister to Bromeliaceae. The family itself appears to have arisen in the ancient Guayana Shield, based on the presence at its base of a grade of genera (*Brocchinia*, *Lindmania*, *Connellia*) restricted to that region. Subfamily Tillandsioideae is monophyletic, and also appears to have arisen in the Guayana Shield, based on its being nested between the basal grade and another clade (*Brewcaria*, *Navia*, "*Brocchinia*" *serrata*) restricted to that region, and based on the present-day occurrence of the two basal tillandsioid genera (*Catopsis*, *Glomeropitcairnia*) partly or wholly in areas adjacent to the Guayana Shield. The xeric clade (*Abromeitiella*, *Deuterocohnia*, *Dyckia*, *Encholirium*, *Hechtia*) characterized by tough, succulent leaves and CAM photosynthesis, is closely related to *Pitcairnia*; both groups are sister to a clade composed of *Puya* and the subfamily Bromelioideae. The *ndhF* phylogeny implies two major migrations from the ancestral Guayana Shield, giving rise to Tillandsioideae and to Bromelioideae embedded within a grade of genera formerly assigned to subfamily Pitcairnioideae. The pitcairnioids are highly paraphyletic and appear to represent five distinct clades: *Brocchinia*, *Lindmania-Connellia*, *Brewcaria-Navia*-"*Brocchinia serrata*", the xeric clade + *Pitcairnia*, and *Puya*. Epiphytism appears to have arisen several times in the family, in basalmost *Brocchinia*, in tillandsioids, and in bromelioids. Cushion plants at high elevations in the Andes (*Abromeitiella*, *Deuterocohnia*) appear to have evolved from lowland forms adapted to severe drought.

- 384** GOFFINET, BERNARD\* AND A. JONATHAN SHAW. Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs CT, 06269 and Department of Botany, Duke University, Durham NC, 27708—*Dung and carcasses, the ultimate habitat within the dung-moss family (Splachnaceae)? Answers from a phylogenetic study based on cp DNA sequence data.*

Seventy species distributed among 7 genera currently compose the family Splachnaceae. Although many species are restricted to dung or other animal remains for a substrate, others are terricolous or epiphytic.

Coprophilous species exhibit a series of “adaptations” to their unique habitat: they produce chemicals that attract insects that look for dung to lay their eggs; the sterile tissue below the sporangium is expanded allowing for insects to land on the sporophyte; they produce small sticky spores; their capsule wall contracts upon drying and the spores are continuously pushed up to the mouth of the sporangium by a pseudocolumella subtending the spore mass. Entomochorous taxa (i.e., those that use insects to disperse their spores) have traditionally been considered derived within the family, with *Splachnum* representing the ultimate product of this evolutionary trend. Here we present phylogenetic analyses of sequences of two chloroplast loci (trnL-trnF and rps4) for about 100 accessions, including exemplars of all genera considered closely related to the Splachnaceae. Maximum parsimony and likelihood analyses yield topologies wherein *Splachnum* is resolved sister to a clade comprising all remaining taxa. Within the latter, *Tetraplodon* whose species are all thought to be entomophilous too, is sister to the Taylorioideae. *Brachymitrium*, the sole genus lacking any feature associated with entomophily, and occurring primarily in epiphytic habitat, composes the most derived lineage. Most noticeable is the recurrent association of anemophilous (using wind for spore dispersal) and entomophilous species. Based on these results it is hypothesized that entomophily was acquired early in the evolutionary history of the Splachnaceae and subsequently lost multiple times. This scenario would suggest that although highly specialized taxa may be evolutionary dead ends, that they offer a source for subsequent evolution of less specialized taxa, and thus may play in a significant part in the diversification of these lineages.

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GRAHAM, SEAN W\*, HARDEEP RAI, PATRICK REEVES, HEATH O'BRIEN, AND RICHARD OLMSTEAD. Dept. of Biological Sciences, University of Alberta, Edmonton AB, Canada T6G 2E9; Dept. of Botany, University of Washington, Seattle WA 98195—*Inference of seed plant phylogeny from multiple chloroplast genes.*

The reconstruction of seed plant relationships is recognized as one of the most difficult problems in plant systematics. A range of studies using various lines of evidence from morphology and molecules have given different and often strongly conflicting results. It is not clear, for example, whether the Gnetales represent the extant sister group of the flowering plants (the “anthophyte hypothesis”). Recent molecular studies suggest that they are instead closely related to (or even nested within) the conifers. The root of the seed plants, and the issue of gymnosperm monophyly, are likewise unclear. Long-branch attraction appears to be a major problem in seed plant phylogenetic inference, and may be partly responsible for the strongly discordant results from different studies. We have sampled large amounts of DNA sequence data from a variety of slowly evolving chloroplast genes, across taxa that span the major lineages of the seed plants, in order to try to explore these issues. The impact of long-branch attraction and of different levels of gene and taxon sampling on seed plant phylogenetic inference will be addressed.

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GRANT1, JASON R.\* AND LENA STRUWE2. 1 Laboratoire de phanérogamie, Institut de botanique, Université de Neuchâtel, ch. de Chantemerle 18, 2007 Neuchâtel, Switzerland, 2 The Lewis B. & Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458 USA—*Morphological evolution and neotropical biogeography in Macrocarpaea (Gentianaceae: Helieae).*

The genus *Macrocarpaea* consists of 50-60 species of herbs, shrubs (some epiphytic), and small trees restricted to the neotropics. The majority of its species are distributed in mid- to upper-elevation rain or cloud forests in the Andes. Additional species occur in the mountains of southeastern Brazil, the Guayana Highlands, Central America, and the Greater Antilles. A monographic treatment of the genus based on over 1500 herbarium specimens on loan from over 40 different herbaria has been initiated. Nomenclature problems will be resolved, dozens of new species will be described, and dubious taxa will be confirmed. *Macrocarpaea* is one of only a few genera among that gentians that have hairy leaves in some species. Scanning electron microscopy studies of indumentum anatomy will be evaluated and presented. Large micromorphological variation can also be found in seed and pollen anatomy, as well as in macromorphological characters. Species level cladistic analyses based on ribosomal 5s-NTS and nuclear ITS (internal transcribed spacer) sequences are presented and will eventually be combined with morphological data. Preliminary molecular data suggests that within the distribution area of the genus, the most ancestral lineages are present in the peripheral regions (i.e. Brazil and the Caribbean), with the Andean species representing more recent and more species-rich radiations.

**387** GUALA, GERALD F. Keeper of the Herbarium, Fairchild Tropical Garden Research Center, 11935 Old Cutler Rd., Miami, FL 33156 USA—*Lessons from the Virtual Herbarium*.

The Fairchild Tropical Garden is building the first truly virtual herbarium on the web at ([www.ftg.fiu.edu](http://www.ftg.fiu.edu)). Unlike other herbaria that may be putting up text-only databases or selections of type photos, we are providing an integrated text database of ALL of our specimens with a high resolution photo of the complete specimen and a high resolution scan of the label. This allows researchers to gather distribution data and check identifications on the WWW at a greatly reduced cost and effort. It already contains more than 30,000 specimens including all of our Cycad, Palm and Florida specimens and is expanding rapidly. The resource has been built using a simple, efficient and streamlined process that employs inexpensive and widely available hardware and widely compatible software. We have also designed the software and data entry protocol specifically for unskilled volunteer labor with automatic error checking and constrained and very simple data entry procedures. Specimens are geocoded by volunteers in remote localities over the WWW and automatically checked for reasonable accuracy based on independently entered data. Several key lessons have been learned through the building of this resource and they will be shared with audience. Highlights include error checking and avoidance, personnel management, ghosts of botanists past, ghosts of herbarium workers past, getting the data to the web, getting the data checked, distributed data entry and error checking, protecting sensitive data and geocoding on the web.

**388** HALL, JOCELYN C.\* AND KENNETH J. SYTSMA. Department of Botany, University of Wisconsin, Madison, WI 53706—*Solving the riddle of Californian Cuisine: phylogenetic relationships of capers and mustards*.

The pantropical family Capparaceae comprises approximately 40 genera and 800 species. Capparaceae are well suited for systematic and evolutionary inquiries. Not only are Capparaceae in need of cladistically based phylogenetic hypotheses, but the diversity of floral form exhibited by the group make the family a model system to examine evolution of floral forms. It has been almost universally agreed that Capparaceae have a very close phylogenetic relationship with Brassicaceae, including the model species *Arabidopsis thaliana*. Recent morphological and molecular analyses indicate that *Cleome* (Capparaceae) are more closely related to Brassicaceae than to other Capparaceae. However these studies have sampled a maximum of four taxa from Capparaceae and typically have used only two. The goal of this study was to clarify the relationships between these two families by using evidence from DNA sequences of two regions of the chloroplast, *ndhF* and *trnL-trnF*, and by increasing sampling of Capparaceae to include most traditionally circumscribed groups. We sampled over 10 genera of Capparaceae, 10 species of Brassicaceae, and outgroups chosen from previous analyses of Capparales. Three monophyletic groups were supported: Brassicaceae, Cleomoideae, and Capparidoideae, the last two clades corresponding to subfamilies of Capparaceae. Within the Capparaceae, *Capparis* is paraphyletic. This is not surprising given that more than one-half of the species of this family are placed in two genera, *Capparis* and *Cleome*; suggesting that plants with extreme morphological traits have been segregated out. Surprisingly, the genus *Forchhammeria* (Capparaceae) appears to be either sister to the rest of the Capparaceae and Brassicaceae clade or sister to other families in the Capparales such as Pentadiplandraceae. The chloroplast DNA phylogeny is used to assess floral character evolution within Capparaceae and Brassicaceae. New nomenclatural possibilities of naming Brassicaceae and Capparaceae will be evaluated based on these data.

**389** HARDY, CHRISTOPHER R.<sup>1,2\*</sup>, ROBERT B. FADEN<sup>3</sup>, JERROLD I. DAVIS<sup>1</sup> AND DENNIS WM. STEVENSON<sup>2,1</sup>. <sup>1</sup>L.H. Bailey Hortorium, Cornell University, Ithaca, NY 14853-4301, <sup>2</sup>New York Botanical Garden, Bronx, NY 10458-5126, and <sup>3</sup>Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington, DC 20560-0166—*A phylogenetic and developmental approach to understanding androecium evolution in the subtribe Dichorisandrinae (Commelinaceae)*.

Cladistic studies (morphology + molecules) and developmental studies were used to gain insight into the evolution of androecial characters in the neotropical subtribe Dichorisandrinae, tribe Tradescantieae (Commelinaceae), which consists of *Cochliostema* (2 spp.), *Dichorisandra* (25+ spp.), *Geogenanthus* (5 spp.), *Siderasis* (2-3 spp.), and a fifth, soon-to-be-described genus (ca. 6 spp.). Within the subtribe, there is a tendency towards reduction from six fertile stamens per flower to five or three. This tendency is particularly strong in the clade (*Geogenanthus* (*Cochliostema*, undescribed genus)). The number of fertile stamens in *Cochliostema* and the undescribed genus is consistently three, although there is considerable variation in expression of the three remaining members of the androecium. Developmental studies in these two genera reveal that three staminodes are usually initiated in the same manner as the fertile stamens but, at anthesis,

they vary among species from being relatively large and showy to vestigial. Developmental studies in *Geogenanthus*, in which the fertile stamens may be either five or six, reveal that in flowers with five stamens, the missing stamen is either not initiated or is early-abortive and vestigial in the mature flower. In addition, although the number of stamens is usually constant for any given species, there is some infraspecific variability in *Geogenanthus*.

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HILU, KHIDIR W\*, THOMAS BORSCH<sup>2</sup>, JENS ROHWER<sup>3</sup>, CHRISTOPH NEINHUIS<sup>2</sup>, TRACEY SLOTTA<sup>1</sup>, BIRGIT GEMEINHOLZER<sup>4</sup>, MICHAEL WINK<sup>4</sup>, AND LAWRENCE A. ALICE<sup>5</sup>. <sup>1</sup>Department of Biology, Virginia Tech, Blacksburg, VA, 24061; <sup>2</sup>Botanisches Institut und Botanischer Garten, Universität Bonn, Germany; <sup>3</sup>Institut für Spezielle Botanik, Johannes Gutenberg Universität, 55099 Mainz, Germany; <sup>4</sup>Institut für Pharmazeutische Biologie, INF 364, 69120 Heidelberg, Germany; <sup>5</sup>Department of Biology and Biotechnology Center, Western Kentucky University, Bowling Green, KY, 42101—*Insight into the evolution of angiosperms: evidence from matK sequences.*

We analyzed DNA sequences of the plastid gene *matK* to infer phylogenetic relationships among angiosperms. Our sample includes seven monocot families (Anthericaceae, Asparagaceae, Convallariaceae, Juncaceae, Poaceae, Restionaceae, and Trilliacae) and 19 dicot families (Amborellaceae, Anthospermataceae, Brassicaceae, Calycanthaceae, Ericaceae, Fabaceae, Hamamelidaceae, Hernandiaceae, Illiciaceae, Lauraceae, Loganiaceae, Magnoliaceae, Monimiaceae, Nymphaeaceae, Paeoniaceae, Rosaceae, Rubiaceae, Saxifragaceae, and Scrophulariaceae). The tree is rooted with three families of conifers (Pinaceae, Cupressaceae, and Taxaceae) plus *Gnetum* (Gnetaceae). Including all species (*Amborella* and *Illicium* are missing the 5' one-third of the gene), the angiosperms are strongly supported as monophyletic. The base is a polytomy of six lineages: *Amborella*, *Illicium*, monocots, Nymphaeales, magnoliids, and tricolpates. Magnoliaceae are sister to all other members of the Magnoliid complex sampled. Saxifragales species form a clade with the rosids that is sister to the asterid clade. When *Amborella* and *Illicium* are excluded from the analysis, a single most parsimonious tree is recovered with a CI of 0.47 and an RI of 0.70 excluding uninformative characters. This tree shows Nymphaeales (bootstrap of 100%) as sister to the other angiosperms; the latter are divided into two large clades with the magnoliids (99%) sister to the tricolpates (97%). Additionally, the Nymphaeales are supported by a 12-bp insertion, the monocots by a different 12-bp insertion, and the tricolpates by a 9-bp deletion.

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HILU, KHIDIR W.\* AND LAWRENCE A. ALICE. Department of Biology, Virginia Tech, Blacksburg, Virginia, 24061, and , Department of Biology, Western Kentucky University, Bowling Green, Kentucky, 42101—*Addressing and raising new systematic questions in the Chloridoideae (Poaceae) with matK sequence data.*

Monophyly, origin and systematics of the subfamily Chloridoideae have long been debated. We present evidence from the plastid *matK* gene sequences of 74 species representing 55 genera and all tribes, and from extensive outgroup survey to address these questions. The monophyly of the Chloridoideae and its origin from an arundinoid group with C<sub>4</sub> photosynthesis are unequivocally ascertained by this study. Rooted with the arundinoid *Centropodia*, a basal polytomy was observed among *Triraphis schlecteri* and three strongly supported clades labeled A, B, and C. Clade A comprises the Pappophoreae, Uniolineae, and three Eragrostideae genera; clade B includes most representatives of subtribe Sporobolinae, *Spartina*, *Zoysia*, and some *Eragrostis*; and clade C encompasses the remaining taxa. The two largest tribes Eragrostideae and Chloridoideae are polyphyletic. Uniolineae, Orcuttieae and Triodiinae form strongly supported monophyletic entities. The taxonomic status of other tribes is discussed. Two large genera, *Chloris* and *Eragrostis*, do not appear monophyletic. A repeated pattern of segregation of Old World from New World taxa is evident. The results provide a framework for further detailed studies at the tribal and generic levels to reach a comprehensive systematic treatment of the Chloridoideae.

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HOGGARD, GLORIA, RON HOGGARD, MIA MOLVRAY, AND PAUL KORES.\* Department of Botany-Microbiology and Oklahoma Biological Survey, University of Oklahoma, Norman, OK 73019—*A phylogenetic analysis of Gaura (Onagraceae) based on ITS sequence data.*

*Gaura* is a small genus found in southern Canada, eastern and central United States, Mexico and Guatemala. Its center of distribution is within Texas. Raven and Gregory's monograph of the genus (1972) formed the basis for a cladistic analysis by Carr, Crisci and Hoch in 1990. In these treatments the 21 species of *Gaura* were assigned to eight sections. Four of these sections, (*Campogaura*, *Gauridium*, *Schizocarya*, *Xenogaura*) were monotypic. The remaining four sections (*Gaura*, *Pterogaura*, *Stipogaura*, *Xerogaura*) encompassed 17



species. In the cladistic analysis by Carr et al., section *Gauridium* is sister to the other seven sections within the genus, and the sections *Xerogaura* and *Gaura* are not monophyletic. We compared this morphologically-based phylogeny to one based on DNA sequence data from the nuclear ribosomal internal transcribed spacer region (ITS). A total of four outgroup taxa and 18 species of *Gaura* were included in this analysis. Our molecular phylogeny of *Gaura* supports five of the sections proposed by Raven & Gregory (*Campogaura*, *Pterogaura*, *Schizocarya*, *Stipogaura*, and *Xerogaura*), but the remaining three sections are problematic. Section *Xenogaura* is embedded within section *Gaura*, and the status of section *Gauridium* is uncertain. Our results indicate that this section is either sister to section *Gaura* or should be included within it. Thus, *Gaura mutabilis*, the sole representative of section *Gauridium*, may actually be one of the more derived species within *Gaura* and not the most basal member of the genus as suggested by Carr et al.

**393** HORN, JAMES W. Department of Botany, Box 90338, Duke University, Durham, NC 27708—*Phylogeny, biogeography, and patterns of morphological evolution in Hibbertia (Dilleniaceae).*

The largely Australian genus *Hibbertia*, containing ca. 150 species, has been characterized in the literature as containing a far greater amount of morphological variation with respect to floral bauplan, growth habit, and range of ecological adaptations than perhaps any other group of similar taxonomic rank. A familial-level phylogenetic analysis of Dilleniaceae utilizing sequences of the chloroplast gene *rbcL* strongly supports the monophyly of *Hibbertia* as currently conceptualized. Simultaneous maximum parsimony analysis of three data sets—cpDNA (*rpl16* intron), nrDNA (ITS 1-2), and morphology—resolves two major clades within the genus that, with at least two notable exceptions, mirrors the morphological dichotomy of species with actinomorphic versus zygomorphic androecia and gynoecia. *Hibbertia* from the isolated, Mediterranean-climate region of southwestern Western Australia are largely clustered into a few large clades embedded within a grade of taxa indigenous to the eastern states of Australia. Western Australian species from these different clades frequently occur sympatrically, with different clusters of species found throughout the many vegetation types occurring in this part of the continent. In the extensive sclerophyllous shrublands (kwongan) occurring on nutrient-poor sands, sympatric *Hibbertia* species may show striking convergence on similar ericoid leaf forms, yet each co-occurring species will possess fundamentally different floral bauplans that are characteristic of its respective clade. This pattern of diversification is consistent with the concept of “leapfrogging” adaptive radiations put forth by Chase and Palmer (1997).

**394** ICKERT-BOND, STEFANIE, M. Department of Plant Biology, Arizona State University, Tempe, AZ 85287-1601—*Micromorphological and cytological patterns among New World species of Ephedra L. (Ephedraceae).*

As part of an ongoing systematic study of New World *Ephedra*, 29 taxa were sampled for micromorphological, cytological, and ovule ontogenetic variation. *Ephedra* grows as dioecious much-branched shrubs, climbers or trees with small opposite or whorled scale- to needle-like leaves in arid regions of the New and Old World. Species are characterized by ovulate strobili with dry membranous, winged or fleshy bracts; lance pyriform to ovoid seeds; microsporangiate strobili with inaperturate, non-saccate, polyplicate pollen; and a base chromosome number  $x = 7$ . A combination of newly recognized and reevaluated features of potential taxonomic value includes: micromorphology of stem and seed cuticle, leaf venation, tubillus variation and features of ovule ontogeny. Stomata of *Ephedra* are haplocheilic, monocyclic and tetracytic and occur in furrows, which alternate with non-stomatiferous bands. Species vary in stomatal opening shape, number of stomatal rows per furrow, epidermal cell shape, position of cuticular flanges, and shape of papillae. Seed coat variation exhibits three distinct types: 1) striate and papillate, 2) striate, and 3) striate and reticulate. Leaf venation patterns may be bi- or trifasciculate. Phyllotaxy determines the number of ovules per strobilus, while a reduction in ovule number has also taken place in some decussate (e.g., *E. antisiphilitica*) and trimerous (e.g., *E. trifurca*) taxa. Natural interspecific hybridization and polyploidization are thought to play a role in the evolution of New World ephedras. Cuticular characters confirm the position and parentage of the two interspecific hybrids, *E. × arenicola* and *E. × intermixta* as described by H. C. Cutler. Chromosome numbers are available for 15 species. Of the New World taxa examined, 40 % are diploid, 13.3 % are polyploid and 46.7 % are both diploid and polyploid. These patterns are further tested against O. Stapf's long-standing classification system.

**395** INGRAM, AMANDA L.\* AND JEFF J. DOYLE. L. H. Bailey Hortorium, Cornell University, Ithaca, NY 14853—*Polyploid origin of Eragrostis tef: evidence from the waxy locus.*

*Eragrostis tef* (Zucc.) Trotter (Poaceae) is an allotetraploid cereal crop cultivated primarily in Ethiopia and Eritrea. Of the approximately 350 species in *Eragrostis*, a total of thirteen potential diploid and polyploid

progenitors have been proposed to be the sources of *tef*'s genome, but rigorous tests of these competing hypotheses have not been performed. We are using sequence data from a 1250 bp region of the *waxy* locus (granule-bound starch synthase; GBSSI), a low-copy nuclear gene, to test the hypotheses of *tef*'s origins. We have amplified 2 partial and 4 complete exons and 5 introns from this locus, and have sampled homoeologous copies of the gene in the polyploid taxa. Preliminary results from cladistic analyses of *waxy* sequences support the widely held notion that *tef* is a domesticate of *E. pilosa*, a widespread and morphologically similar allotetraploid.

**396** JENKINS, PHILIP D. Herbarium, 113 Shantz, University of Arizona, Tucson, AZ 85721—*Systematics of Browallia Linnaeus (Solanaceae, Cestroideae), inferences from morphological data.*

*Browallia* Linnaeus (Solanaceae, Cestroideae) is native to the New World tropics and subtropics. Taxonomists first grouped *Browallia* and morphologically similar genera within the Salpiglossideae, which were considered advanced in Solanaceae because of their derived characters. Recent evidence indicates that Salpiglossideae is paraphyletic within the subfamily Cestroideae and perhaps Cestroideae is primitive in Solanaceae, and that *Browallia* seems more closely allied with the large, widespread genus *Cestrum*. Morphological evidence, analyzed phylogenetically and using multivariate techniques, implies that there are five species of *Browallia*. The generic boundaries of *Browallia* and the monotypic sister group *Streptosolen jamesonii* (Benth.) Miers are doubtful. *Streptosolen*, erected out of *Browallia* in 1850, is here resubmerged. The species recognized are *Browallia acutiloba* Segástegui & Díos, *B. americana* Linnaeus, *B. eludens* R. K. Van Devender & P. Jenkins, *B. jamesonii* Benth., and *B. speciosa* Hooker. Four *Browallia* have limited distributions: three in the South American Andes and one disjunct in southwestern North America. The fifth, *Browallia americana*, is widespread and introduced throughout the tropics of the New and Old Worlds. It exhibits variable characters in the Andes of Peru, but less so elsewhere, especially where it is likely introduced. Morphological evidence suggests that the origin of the group is Andean, and that the genus is diverging, but that diversification does not warrant recognition of all the species previously described. *Browallia eludens*, with its disjunct range, poses interesting questions about the biogeographical history of the group. It has a more northern range where seasonally freezing temperatures occur. It appears to be a seasonal ephemeral with larger seeds than the tropical *Browallia*, that the seeds are viable for a number of years, and that the plants may be largely autogamous.

**397** JOHNSON, LEIGH A. Department of Botany and Range Science, Brigham Young University, Provo, UT 84602—*Sinister speciation: elucidating phylogeny and taxonomy in a cryptic species complex in Polemoniaceae.*

*Gilia sinistra* remains one of the more enigmatic species of Polemoniaceae. Formally recognized in the early 1900's, this small-flowered plant was afterward considered synonymous with *G. capillaris*. A larger-flowered form was also later described as a subspecies of *G. leptalea*. These two forms were united under the name *Gilia sinistra* in 1993. Concomitantly, all three of the above species were circumscribed in a new section of *Gilia*, section *Kelloggia*. Cohesive in gross morphology but variable in geographic distribution and breeding systems, the species of section *Kelloggia* provide an interesting model for exploring patterns of diversification among a putatively monophyletic group. Isozyme analyses of 24 populations, however, reveal unexpected divergence within *Gilia sinistra*. Analyses of chloroplast and nuclear DNA sequences also reveal this remarkable divergence. Instead of a monophyletic group, section *Kelloggia* comprises three distinct lineages, all with affinities to *Navarretia*. *Gilia leptalea* and *G. capillaris* form one lineage, and *G. sinistra* occurs in two well-separated lineages. The geographic distribution of the morphologically cryptic races of *G. sinistra* were determined from sampling DNA sequences from over 30 populations throughout its range. The proper application of the specific epithet to one of these races was determined by scrutiny of micromorphological characters among these populations and the nomenclatural type. Combined, these data suggest possible reticulate evolution in the origin of at least one of the *sinistra* lineages. These data also favor the recent realignment of the kelloggioid *gilia*s in *Navarretia*, rather than in *Allophyllum* as also recently proposed. Although these "gilia"s are readily distinguished in gross morphology from both genera, corroboration of morphological and molecular data argue for expanding the concept of *Navarretia* to include these species—but not as a single, exclusive section within this genus.

**398** KELCH, DEAN G.\* AND RAYMOND CRANFILL. University and Jepson Herbaria, University of California, Berkeley, CA 94720—*Seed plant phylogeny: the yew-conifers and a farewell to the anthophyte hypothesis.*

Recent discussions of relationships within seed plants have focussed on the correct placement of the Gnetales. Some phylogenetic conclusions based on DNA sequence data have placed this group as sister to conifers or

even within the conifers. Contrary to this, phylogenetic analysis of sequence data from the chloroplast gene *rps4* places Gnetales as sister to all other living seed plants. Bootstrap support for this result is increased by adding *rbcL* and 18S rDNA sequence data to the analysis. Angiosperms comprise a branch located between Gnetales and other living seed plants. The paraphyly of living anthophytes (Gnetales and angiosperms) contradicts the anthophyte theory, but also modifies significantly the interpretation of character evolution deduced from trees presenting Gnetales as coniferophytes. Within conifers, there is robust support for Pinaceae as sister to other conifers, followed by an Araucariaceae/ Podocarpaceae clade. The crown group includes Cupressaceae s.l., *Cephalotaxus*, *Sciadopitys*, Taxaceae, and Torreyaaceae. This group of “yew-conifers” is also found in trees based on *rbcL* and 18S rDNA. The *rps4* gene proves useful at the level of seed plant family relationships, but also includes more variable regions that have utility between genera.

- 399** KELCHNER, SCOT A. Australian National Herbarium, CSIRO Plant Industry, G.P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA—*Alignment and analysis of noncoding cpDNA sequences: implications of molecular evolution for phylogeny estimation.*

Noncoding chloroplast DNA sequence comparison has become a popular tool for systematics studies at low taxonomic levels. But earlier expectations of random, unconstrained, and independent nucleotide evolution in such regions have not been validated by research results. Mutation in noncoding cpDNA may be largely dependent on sequence structure and pattern, resulting in nonindependent and predictable sequence evolution. Mechanisms of molecular evolution described in these regions include slipped-strand mispairing, stem-loop secondary structures, minute and moderate-sized inversions associated with secondary structures, intramolecular and extra-regional recombination, and nucleotide substitutions. Detection of mutational mechanisms contributing to inferred mutations can enhance the alignment of insertions and deletions and the assessment of nucleotide and indel homology. The manner of noncoding cpDNA evolution described here has several important repercussions for phylogenetic analysis, effecting all levels of methodology by invalidating underlying assumptions. Unique evolutionary characteristics of noncoding cpDNA may eventually prove no more difficult to assimilate than related phenomena occurring in genic DNA; perhaps a reasonable course for now is to identify probable mutational processes evident in a data set, and carefully modify existing phylogenetic analysis procedures to more accurately reflect the underlying mutational model.

- 400** KELCHNER, SCOT A.\*, RANDALL J. BAYER, ROBERT J. CHINNOCK, MICHAEL D. CRISP, AND JUDY G. WEST. Centre for Plant Biodiversity Research, CSIRO Plant Industry, G.P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA—*A data partition analysis of noncoding sequence evolution in Bontia and Myoporaceae.*

The monotypic genus *Bontia*, endemic to the Caribbean, is the extreme outlier of a primarily southern-hemisphere Old World family, the Myoporaceae. Ninety-five percent of the 250 species of Myoporaceae sensu R. J. Chinnock (in press) are endemic to Australia. Only six species in the family occur north of the equator; of these, all but *Bontia daphnoides* are locally distributed in the western Pacific. Is the evolutionary history of *Bontia* truly shared with Myoporaceae, or has it descended instead from the family's probable sister lineage, the Leucophylleae (Scrophulariaceae) of Mexico and Central America? We examined the possibility that *Bontia* is indeed an outlying member of the Myoporaceae by sequencing the *rpl16* intron of the chloroplast genome for 60 taxa representing all major morphological lineages within the family, and representatives of probable outgroups that include the Leucophylleae. The sequence data were partitioned based on the probable secondary structure of the Group II intron; partition categories were defined as stem, loop, and interceding sequence. Relative rate of base change per partition was estimated using the method of Vawter and Brown (1993). The method does not assume rate constancy and allows for base composition bias between taxa and secondary structure components; therefore, relative rates of substitution can be compared between sequence partitions to study the amount of mutation occurring in stem, loop, and interceding sequence. We present the results of this partition study and the phylogeny estimate based on this data set. In this topology, Myoporaceae is monophyletic, Leucophylleae is sister to Myoporaceae, and *Bontia* is derived from within Myoporaceae. The results suggest that the distribution of *Bontia* is due to dispersal from an Australian ancestral lineage.

- 401** KIM, KI-JOONG\*, GYE-SOOK HA, AND HAE-LIM LEE. Department of Biology, Yeungnam University, Kyeongsan, Kyeungbuk, Korea 712-749—*Introgressive hybridization between native and introduced species of Taraxacum.*

*Taraxacum officinale* complex was introduced from Europe into Korea about a hundred years ago. This species widely occurs on Korean peninsula and take over the habitats of native species of *Taraxacum* and

increasingly common in open habitats. *Taraxacum officinale* complex produce more abundant apomictic seeds than native species, however, some populations also show facultative sexual reproduction. Native species consist of diploid, triploid, and tetraploid and show a series of facultative sexual reproduction. In order to measure the degree of gene flow between native and introduced species, we analyzed the maternally inherited chloroplast DNA markers and biparentally inherited nuclear DNA markers from 130 populations of *Taraxacum*. Nuclear ITS tree show the morphologically circumscribed species boundaries both in native and introduced species. However, cpDNA trees was substantially different from that of nuclear rDNA and show mixed patterns between European and Asian species. The results suggest that the introgressive hybridizations are relatively common between native and introduced species of *Taraxacum*. The unidirectional introgression from introduced species into native species is one of major driving force to extinction of native populations. Hybridizations are relatively rare among native species because of disjunctive distribution.

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KRON, KATHLEEN A.\*, E. ANN POWELL, AND JAMES L. LUTEYN. Department of Biology, Wake Forest University, Winston-Salem, NC 27109-7325; New York Botanical Garden, Bronx, NY 10458-5126—*Molecular systematics of Macleania and Psammisia and their relationship to other members of Vaccinieae.*

*Macleania* and *Psammisia* are two genera of blueberries found primarily at higher elevations throughout the Neotropical cordillera. These genera have been considered closely related to each other and distinct from other tropical Vaccinieae based on features of the androecium. As part of a revision of these taxa, a molecular systematic study was performed using nuclear ribosomal internal transcribed spacer (nrITS) and the chloroplast gene *matK* for 29 species of *Macleania* and *Psammisia* (i.e., about 30% of the taxa currently recognized within the genera) and selected Vaccinieae. Analyses of the combined data indicate that most of the taxa currently within *Macleania* and *Psammisia* form a clade. (Exceptions to this are *Macleania megabracteata* and *Psammisia urichiana* which consistently fall outside the group.) However, branch lengths are very short at the base of this clade and therefore bootstrap support for the group is below 50%. *Macleania* and *Psammisia* are both paraphyletic in this study. The results indicate that *Macleania* is, for the most part, derived from within *Psammisia*. *Psammisia dolichipoda* and *Ps. sodiroi* are indicated as sister and this relationship has strong bootstrap support. These two species represent the “globosa” subgroup within *Psammisia*. However, the results of this study do not support any of the other species groups suggested in previous studies for either *Macleania* or *Psammisia*. This study suggests that *Macleania* and *Psammisia* are closely related but that neither is monophyletic as currently recognized. Further resolution of species relationships is likely to require a more variable data source. Larger scale analyses based on combined analysis of *matK*, ITS and the chloroplast *trnT-L* spacer indicate that *Macleania* and *Psammisia* fall within a large clade that includes other Neotropical genera such as *Satyria* and *Sphyrrosperrum*.

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LARA-CABRERA, SABINA I.\* AND DAVID M. SPOONER. USDA, Agricultural Research Service; Department of Horticulture, University of Wisconsin, Madison, WI 53706—*Morphological and microsatellite variation of Mexican diploid wild potato species.*

*Solanum* L. section *Petota* Dumort., the potato and its wild relatives, contains over 200 wild species distributed from the southwestern United States to south-central Chile. Most of these species grow in the Andes, but the United States, Mexico, and Central America contain about 30 taxa of diploids, tetraploids, and hexaploids. Chloroplast DNA restriction site data show 13 of these 30 taxa to form a clade containing only diploid species, but there is low resolution within this clade. In addition, some of these 13 taxa are similar morphologically and may not be valid species. In preparation for a monograph of sect. *Petota* from this region, we are analyzing members of this clade with phenetic analysis of morphological data, and two nuclear markers with the potential to show better resolution than chloroplast DNA restriction site data. Morphological data show extensive overlap of putative “species-specific” characters, but most species can be supported by multivariate techniques (except *S. cardiophyllum* subsp. *ehrenbergii*, *S. nayaritense*, and *S. stenophyllidium* that remain problematical). We here also report on one nuclear marker, mapped microsatellites developed in *Solanum tuberosum*, chosen because of their hypervariable nature. Preliminary data, using ten microsatellite markers distributed over seven chromosomes, strongly cluster some species (e.g., *S. jamesii*) but other morphologically different species cluster together, despite analyses of data as alleles or as each microsatellite variant as unrelated characters. There is considerable controversy regarding mutation processes of microsatellites and the best analytical method for phylogenetic studies. Interestingly, scoring each microsatellite variant as unrelated characters did a “better” job of clustering taxa. Our results suggest that microsatellites have reduced utility to analyze the United States, Mexican, and Central American diploid species.



- 404** LEE, JOONGKU\*, BRUCE G. BALDWIN, AND LESLIE D. GOTTLIEB<sup>1</sup>. Jepson Herbarium and Department of Integrative Biology, University of California, Berkeley, CA 94720. <sup>1</sup>Section of Evolution and Ecology, University of California, Davis, CA 95616—*A molecular phylogenetic study of Stephanomeria and related North American genera (Compositae-Lactuceae) based on 18S-26S nuclear rDNA ITS sequences.*

Phylogenetic analysis of rDNA ITS sequences shows that all of the western North American genera of Lactuceae with a base chromosome number of  $n = 8$ , including *Stephanomeria* Nutt., *Munzothamnus* P. H. Raven, and *Rafinesquia* Nutt., constitute a monophyletic group. *Stephanomeria*, with 17 annual and perennial species, forms a single clade and is more closely related to *Rafinesquia* than to *Munzothamnus*. *Munzothamnus* contains a single perennial species endemic to one of the Californian Channel Islands and has been previously placed both within *Stephanomeria* and within *Malacothrix*; our results suggest it is an ancient lineage best recognized as a distinct genus. *Rafinesquia* contains two annual species in California and the adjacent deserts and its close relationship to *Stephanomeria* was not previously recognized. The results also show that *Stephanomeria spinosa* (Nutt.) Tomb, which was transferred to *Stephanomeria* from *Lygodesmia* D. Don, is the sister group of either *Rafinesquia* or *Stephanomeria* or both and probably is best treated as a monotypic genus, *Pleiocanthus* Rydb. Two perennial species, *Stephanomeria pauciflora* (Torr.) A. Nelson and the tetraploid *S. parryi* A. Gray, are closely related to each other and appear to be more closely related to the six annual species than to the other perennials.

- 405** LES, DONALD H.\*, DANIEL J. CRAWFORD, ELIAS LANDOLT, JOHN D. GABEL, AND REBECCA T. KIMBALL. Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269-3043; Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, OH 43210; Geobotanisches Institut ETH, Zürichbergstrasse 38, CH-8044, Zürich, Switzerland—*Phylogenetic relationships in Lemnaceae Dumortier, the duckweed family.*

Duckweeds (family Lemnaceae) comprise a distinctive group of diminutive, aquatic monocotyledons which have been difficult taxonomically because of their cosmopolitan distribution, extreme reduction and miniaturization. As currently circumscribed, the Lemnaceae comprise 38 species in five genera which include the world's smallest angiosperms. Taxonomic studies in the 19th and 20th centuries by Schleiden, Hegelmaier, Thompson and Daubs began to clarify generic and species limits in the family, but did little to evaluate either intergeneric or interspecific phylogenetic relationships. Only within the last 15 years have detailed phylogenetic hypotheses been presented for Lemnaceae by Landolt. With few conspicuous morphological characters to serve as phylogenetic markers, molecular data have been applied to duckweed taxonomy since the 1960's when McClure studied flavonoids intensively in the family. Recently, the three senior authors have undertaken a major study to ascertain interspecific phylogenetic relationships by analyzing data sets encompassing a wide range of characters. We present results of phylogenetic analyses of more than 4,600 characters, including data from morphology and anatomy, flavonoids, allozymes and DNA sequences from chloroplast genes (*rbcL*, *matK*) and introns (*trnK*, *rpl16*). With exception of flavonoids, all data are reasonably congruent; yet even flavonoid data contribute to nodal support in combined analyses. Using parsimony, our data yield a single, well-resolved, maximum parsimony tree with most nodes supported by bootstrap values exceeding 90%. Only one major topological disparity exists between cpDNA based trees and those obtained from nuclear encoded genes such as allozymes (*Lemna japonica* exhibits characteristics of a hybrid origin, which was hypothesized previously by Landolt). Our studies support the taxonomic recognition of five monophyletic duckweed genera (*Landoltia*, *Lemna*, *Spirodela*, *Wolffia*, *Wolffiella*), and present specific hypotheses of interspecific relationships among all 38 known extant species. As a consequence, Lemnaceae are now among the most thoroughly understood angiosperm families from a systematic standpoint.

- 406** LEVIN, RACHEL A.\*, ROBERT A. RAGUSO, AND LUCINDA A. MCDADE. Department of Ecology & Evolutionary Biology, University of Arizona, Tucson, AZ 85721—*The relationship between floral fragrance, phylogeny, and hawkmoth-pollination in Nyctaginaceae.*

It is known that floral scents attract pollinator service for plants, and differences in floral fragrances are thought to be related to pollinator type. We have examined the relationship between floral fragrance and hawkmoth-pollination within a phylogenetic context. The genera *Selinocarpus*, *Acleisanthes*, and *Mirabilis* (Nyctaginaceae) are predominantly hawkmoth-pollinated. Through headspace floral scent collections and GC-MS analysis we found that these species have complex floral fragrance profiles. Interestingly, the fragrance composition appears strongly associated with phylogenetic relationship. This suggests that hawkmoths are

attracted to a variety of floral volatiles, and as a result may constrain the evolution of floral fragrance less than has been previously thought.

- 407** LEWIS, CARL E.\* AND JEFF J. DOYLE. L. H. Bailey Hortorium, Cornell University, Ithaca, NY 14853—*Low-copy nuclear genes for phylogenetic research in the palm family.*

Low-copy nuclear genes are a potential source of new phylogenetic information in the palm family. We describe two genes that resolve relationships at various taxonomic levels within the family. Malate synthase, a glyoxylate cycle enzyme, appears to be encoded by a single-copy gene in palms. Exon sequences from the malate synthase gene are alignable across the family and with sequences from outgroup taxa, and are useful for resolving relationships among major clades of palms. Malate synthase intron sequences are alignable across the palm subfamily Arecoideae and provide phylogenetic resolution among its genera. Two copies of the gene encoding phosphoribulokinase, a pentose phosphate pathway enzyme, appear to be present in palms. Sequences of one phosphoribulokinase paralogue have been useful for a species-level phylogeny of the genus *Hyophorbe*. The malate synthase and phosphoribulokinase genes may also be useful sources of data for studies in other groups of plants.

- 408** LITTLE, DAMON P. L.H. Bailey Hortorium, Cornell University, Ithaca, NY 14853—*Phylogenetic relationship and monophyly of Cupressus and Chamaecyparis (Cupressaceae): molecular and organismal evidence.*

Most 19th and early 20th century works treated *Chamaecyparis* Spach as an infrageneric taxon within *Cupressus* L. (Cupressaceae). In recent works *Cupressus* and *Chamaecyparis* are recognized as separate genera on the basis of a single constant character: the presence of vermiform (a.k.a. trabeculate) thickenings on the pits of leaf transfusion tracheids in *Cupressus* and the absence of such thickenings in *Chamaecyparis*. Other characters commonly used to circumscribe these taxa (e.g. the configuration of the ovulate cone, the anatomy of the seed, the timing of embryo development) are not constant within each genus, largely due to the conflicting suite of characters observed in *Chamaecyparis nootkatensis* (D. Don) Spach. As a result of limited taxon sampling and/or the reliance on composite terminals, the monophyly of these genera in the Cupressaceae was not tested by previous phylogenetic efforts. The monophyly of *Cupressus* and *Chamaecyparis* is tested with a simultaneous cladistic analysis of organismal data and *rbcL* sequences. Organismal data, including morphology, anatomy, biochemistry, and embryological development, comprise ca. 50% of the informative characters in the combined matrix. Preliminary analysis suggests that, as currently circumscribed, *Cupressus* and *Chamaecyparis* are not monophyletic.

- 409** LIVSHULTZ, TATYANA. L.H. Bailey Hortorium, 462 Mann Library, Cornell University, Ithaca, NY 14853—*Systematics and evolution of ant-leaves in the genus Dischidia (Asclepiadaceae).*

The genus *Dischidia* comprises approximately 80 species of succulent epiphytic vines native to Southeast Asia. The genus is divided into three sections based on leaf morphology: section *Dischidia* with laminar leaves, section *Conchophylla* with shell-shaped leaves, and section *Ascidifera* with pitcher-leaves. Many species of all three sections frequently occur in the nests of arboreal ants, and ants use the leaves of section *Ascidifera* and section *Conchophylla* as nesting sites. Both shell- and pitcher-leaves develop via differential growth of the adaxial and abaxial leaf surfaces, leading to the hypothesis that pitcher-leaves evolved from shell-leaves via increased curvature of the leaf during development. I present combined cladistic analysis of morphology and sequences of the second intron of the nuclear gene *Leafy*. The results support the monophyly of *Dischidia* s.l. and the sister-group relationship of *Dischidia* and *Hoya*. The segregate genera *Dischidiopsis*, *Oistonema*, *Conchophyllum*, and *Leptostemma* should be included in *Dischidia* s.l. while the monotypic genus *Micholitzia* should be excluded. The analysis also shows that *Dischidia* species which have both alternate and opposite phyllotaxy form a clade, a grouping which has never been formally proposed. Section *Conchophylla* plus section *Ascidifera* form a monophyletic group, consistent with the evolution of pitcher-leaves from shell-leaves.

- 410** LOWREY, TIMOTHY K.\*, CHRISTOPHER J. QUINN, RACHAEL K TAYLOR, RAYMUND CHAN, REBECCA KIMBALL, AND JAN C. DE NARDI. Department of Biology, University of New Mexico, Albuquerque, NM 87131, School of Biological Science, University of New South Wales, Sydney, NSW 2052, Australia, Jepson Herbarium and Department of Integrative Biology, University of California, Berkeley, CA 94720, USA—*Molecular, morphological and biogeographical reassessment of relationships within the Vittadinia group of Astereae (Asteraceae).*

*Vittadinia* Rich. and *Tetlopium* Cass. (Asteraceae; Astereae) are two Austral-Pacific genera that have long been recognized as being closely related, having been variously merged and segregated by different authors.

The two genera encompass diverse morphologies as well as broad and unusual distributional patterns. A number of other genera in the region have also been implicated as being related. We present the results of a reassessment of the phylogenetic relationships within the Pacific taxa of *Tetramolopium* and among the Austral-Pacific *Vittadinia-Tetramolopium* group of genera using molecular and morphological data. Morphological and ITS (internal transcribe spacer) sequence data for 40 species of *Camptacra*, *Kippistia*, *Minuria*, *Peripleura*, *Tetramolopium*, and *Vittadinia*, as well as one semi-herbaceous species of Australian *Olearia*, were subjected to cladistic analysis, separately and together. Results show both datasets exhibit marked homoplasy indicating why generic delimitation in the group has been historically problematic. This homoplasy may be the result of past intergeneric hybridization and/or convergence/parallelism among the taxa in similar arid environments in Australia. *Minuria*, *Peripleura* and *Tetramolopium* are paraphyletic as currently defined. *Tetramolopium vagans* from Australia appears to represent an undescribed genus. *Kippistia suae-folia* and *Peripleura diffusa* fall within the affinity group of *Minuria* species. *Vittadinia* and the remaining species of *Tetramolopium* and *Peripleura* form a strong affinity group. The distribution of indels and the combined analysis each provide evidence that the Hawaiian and Cook Island species of *Tetramolopium* are descended from New Guinea species. The combined analysis also suggests that the Cook Island species is sister to the Hawaiian clade. *Olearia arguta* shows no close affinity with either of the arborescent species of *Olearia* used to root these analyses. Further studies are needed to clarify the relationships of other taxa (particularly in New Guinea) not included in this study that have been linked to the *Vittadinia-Tetramolopium* group.

- 411** LUTZONI, FRANCOIS\*, PETER WAGNER, AND VALERIE REEB. Department of Botany, The Field Museum, Chicago, IL 60605—*Integrating ambiguously aligned regions of DNA sequences in phylogenetic analyses without violating positional homology.*

Phylogenetic analyses of non-protein coding nucleotide sequences such as ribosomal RNA genes, internal transcribed spacers (ITS) and introns are often impeded by regions of the alignments that are ambiguously aligned. These regions are characterized by the presence of gaps and their uncertain positions no matter which optimization criteria are used. This problem is particularly acute in large scale phylogenetic studies and when aligning highly diverged sequences. Accommodating these regions, where positional homology is likely to be violated, in phylogenetic analyses has been dealt with very differently by molecular systematists and evolutionists, ranging from the total exclusion of these regions to the inclusion of every position regardless of ambiguity in the alignment. We present a new method that allows the inclusion of ambiguously aligned regions without violating homology. This three-step procedure consists first of delimiting homologous regions of the alignment containing ambiguously aligned sequences. Second, each ambiguously aligned region is unequivocally coded as a new character that replaces its respective ambiguous region. Third, each of these coded characters is subjected to a specific step matrix to account for the differential number of changes (summing substitutions and indels) needed to transform one sequence to another. The optimal number of steps included in the step matrix is the one derived from the pairwise alignment with the highest similarity and the lowest number of steps. In addition to potentially enhancing phylogenetic resolution and support, by integrating previously nonaccessible characters without violating positional homology, this new approach can improve branch length estimations when using parsimony.

- 412** LUTZONI, FRANCOIS\*, MARK PAGEL, AND VALERIE REEB. Department of Botany, The Field Museum, Chicago, IL 60605 USA. School of Animal and Microbial Sciences, University of Reading, Whiteknights, Reading RG6 6AJ UK. Department of Biological Sciences, University of Illinois at Chicago (M/C 066), Chicago, IL 60607 USA—*Contribution of the lichen symbiosis to the diversification of ascomycetes: A new approach to determining confidence levels for ancestral character states.*

The acceptance by the mycological and lichenological communities, more than 12 years ago, that basidiomycetes tightly associated with green algae or cyanobacteria are lichens, simultaneously established, for the first time, that lichens (including both asco- and basidiolichens) are derived from multiple independent origins. Because approximately one-fifth of all known fungi are lichenized and more than 98% of the diversity of lichens is within the ascomycetes, one crucial question remains to be answered: How many independent origins of lichens took place during the evolution of the ascomycetes? To address this question we have sequenced a 1 kb and a 1.4 kb fragment at the 5' end of the small and large subunits of the nuclear ribosomal DNA, respectively, for 54 species representing 31 orders of ascomycetes. The combined maximum parsimony analysis revealed two equally most parsimonious trees. The ancestral character states (lichenized versus non-lichenized) were reconstructed for every node using maximum likelihood. The confidence levels for each of

the ancestral character states were estimated by reconstructing the evolution of lichenization on a large number of trees randomly sampled within the confidence envelope surrounding the best trees.

**413** MAGALLÓN, SUSANA A. Section of Evolution and Ecology, University of California, Davis, CA 95616—*Extinct and extant Hamamelidoideae: phylogeny and character evolution.*

The members of Hamamelidaceae have unambiguously been documented to belong to the Saxifragoid clade, within the core eudicots. Although the monophyly of the family has not been firmly established, the monophyly of subfamily Hamamelidoideae is confirmed by several independent phylogenetic studies. Insights about the early history of Hamamelidoideae have been provided by the flowers of *Archamamelis* (Santonian-Campanian, Sweden), and *Allonia* (late Santonian, Georgia, U.S.A.). A third, recently discovered flower, *Androdecidua*, from the late Santonian of Georgia, provides further information about morphological diversity within Hamamelidoideae. *Androdecidua* has two pentamerous androecial whorls, in which the stamens of the outer whorl have bisporangiate anthers, resulting from the absence of the adaxial pollen sac of each theca. A phylogenetic analysis was conducted to obtain explicit information about relationships within Hamamelidoideae, particularly the affinity of fossil genera, and about character evolution. The analysis included 38 taxa, comprising members of Hamamelidaceae, representatives of the Saxifragoid clade, and outgroups from the basal eudicot grade, and was based on 57 characters of floral form. The strict consensus of 42 most parsimonious trees resolves *Archamamelis* and *Hamamelis* as sister taxa, whereas *Androdecidua* and *Allonia* are nested within a monophyletic Loropetalinae. The obtained phylogenetic hypothesis suggests that the strap-like, circinate coiled petals, which characterize some genera of Hamamelidoideae, evolved twice; a specialized stomium configuration that results in a distinctive mode of anther dehiscence evolved once, but was subsequently lost, and stamens with bithecal anthers evolved at least two times. The highly nested placement of fossil taxa suggests that the main evolutionary lineages within Hamamelidoideae had evolved by the late Santonian. Considering that the oldest records for core eudicots are from slightly older strata (Turonian), it appears that morphological and taxic diversification proceeded quickly during the initial evolution of Hamamelidoideae, and subsequently remained stable.

**414** MAGALLÓN, SUSANA A.\*, MICHAEL J. SANDERSON, JAMES A. DOYLE, AND MARTIN F. WOJCIECHOWSKI. Section of Evolution and Ecology, University of California, Davis, CA 95616—*Estimate of the age of the angiosperm crown group derived from integrated analysis of molecular and paleontological data.*

Previous estimates for the age of the angiosperms derived from molecular clock models, although in conflict with one another, have generally implied that angiosperms originated long before their first appearance in the stratigraphic record (Early Cretaceous). We estimate the age of the angiosperms by integrating new data and new methods of analysis. Taxa were sampled from all major clades of extant land plants. Sequences of two highly conserved chloroplast genes, *psaA* and *psbB*, were used as primary data. A data set of combined *psaA* and *psbB* sequences for 54 genera of land plants was used to obtain hypotheses of relationships through parsimony analysis. Gnetales are resolved as the sister taxon of all other seed plants if codon positions are weighted equally (Tree 1), or alternatively, as the sister taxon to Pinaceae within a monophyletic gymnosperm clade if 1st and 2nd codon positions are given greater weight (Tree 2), in accordance with their much lower substitution rates. Substitution models for synonymous and non-synonymous sites were obtained through a likelihood approach in which a molecular clock was enforced. Temporal calibration was achieved by fixing the time of divergence between *Marchantia* and all other land plants at 450 Ma (Late Ordovician). Based on data from non-synonymous sites, the angiosperm crown group is dated as 144 Ma, according to Tree 1, and as 133 Ma, according to Tree 2. These preliminary estimates are closer to ages derived from the fossil record than published estimates, but confidence intervals are broad enough to include some previous dates. Subsequent analyses will incorporate methods for estimating divergence times assuming heterogeneous rates of molecular evolution, and temporal calibrations that include minimum ages for several nodes, obtained from reliably identified fossil taxa. These analytical approaches are expected to provide a narrower estimate for the age of the angiosperm crown group.

**415** MALCOMBER, SIMON T.\* AND ELIZABETH A. KELLOGG. Missouri Botanical Garden, PO Box 299, Saint Louis, MO 63166-0299 and Department of Biology, University of Missouri, Saint Louis, MO 63121—*Gaertnera (Rubiaceae): a rapid radiation based on sequence data from three nuclear DNA sequence data sets.*

*Gaertnera* (Gaertnereae, Rubiaceae) is a well-defined genus of approximately 70 species, with a paleotropical distribution encompassing Western Africa, Madagascar, Mascarenes, Sri Lanka and Southeast Asia. In ad-



dition to its wide geographical range, the genus also exhibits a large degree of morphological diversity, and is one of only twelve angiosperm genera in which dioecy has evolved from distylous ancestors. Prior to testing predictions from two alternative hypotheses for the evolution of dioecy in ancestrally distylous taxa it is necessary to reconstruct a phylogenetic estimate for the genus. Molecular phylogenetic estimates for *Gaertnera* are presented based on sequence data from 30-40 species for three nDNA markers; ITS (Internal Transcribed Spacer), *Tpi* (Triose phosphate isomerase) and *PepC* (Phosphoenolpyruvate carboxylase). Counter to our expectations based on the morphological differences and geographical separation between the sampled species, all markers reconstruct a rapid radiation for the genus. A combined analysis of all three markers will be discussed, in addition to molecular clock estimates for the divergence time of *Gaertnera* from its South American sister taxon, *Pagamea*.

- 416** MANSION, GUILHEM. Institute of Botany, University of Neuchâtel, Emile Argand 11, 2007 Neuchâtel, Switzerland—*Phylogenetic position of the north and central american species of Centaurium (Gentianaceae) based on molecular data and chromosome numbers: evidence of an old-world origin.*

The genus *Centaurium* (Gentianaceae) consists of about 50 species, mostly annuals or biennials, distributed in two main regions of diversification. In the Mediterranean area, diploid to hexaploid species occur whereas in the western part of North America and Mexico only polyploids species are found. We have investigated the phylogenetic relationships within this group for almost all the species using sequences of nrDNA (ITS) and cpDNA (trnL-F region). Moreover, we have stated a large survey of the chromosome numbers of different population of the New World species. Phylogenetic analysis strongly supports the existence of at least five geographic groups and suggest a pattern of colonization from Eurasia to California followed by a migration in Texas and Mexico. The caryological survey of the American species comfort the evolutive scenario inferred from molecular markers. New chromosome numbers for several species were also found. In addition, our study provides some evidences of regular hybridization process among different *Centaurium* species followed by polyploidization. These results suggest that amphiploidy is involved in the diversification of the genus as a speciation process. Finally, this work will result in a systematic revision of the known classification of the whole genus.

- 417** MAST, AUSTIN R.\* AND THOMAS J. GIVNISH. Department of Botany, University of Wisconsin, Madison, WI 53706—*Historical biogeography of Banksia and Dryandra (Proteaceae) in Australia's Southwest Botanical Province.*

Sixty-three of the seventy-nine species of *Banksia* and all ninety-three species of *Dryandra* are restricted to Australia's Southwest Botanical Province. The Province - isolated from the rest of the continent by Australia's arid middle - is one of the world's great centers of floristic endemism (80% of the 4000 native species are endemic). Our cpDNA and nrDNA sequence data strongly support the paraphyly of *Banksia* with respect to a monophyletic *Dryandra*. *Dryandra* and the lineage of southwestern banksias from which it arose appear to form the largest documented radiation of plants wholly restricted to the region. We examined the historical processes generating this diversity by (1) defining areas of endemism and then (2) using cladistic biogeography to identify relationships among these areas. We analyzed presence/absence data for >130 taxa of *Banksia* and *Dryandra* in 170 50 km x 50 km cells using clustering and ordination techniques, as well as parsimony analysis of endemism. Cells with the greatest diversity of *Banksia* and *Dryandra* center around the northern and southern sandplains (as has been shown for *Banksia* alone by Byron Lamont). When areas of endemism are plotted onto the cladograms, we see at the broad scale several migrations (dispersal and/or vicariance with subsequent extinction) of ancestral taxa from the southern to the northern sandplains. Within *Banksia*, migrations in the reverse direction appear largely limited to range expansions of widespread species. At a finer scale, we are examining the importance of the Stirling and Barren Ranges (southern sandplains) and the Mt. Lesueur region (northern sandplains) as local refugia during climatic fluctuations.

- 418** MAYER, MICHAEL S.\*, JON P. REBMAN<sup>1</sup>, AND LAURA M. WILLIAMS. Department of Biology, University of San Diego, 5998 Alcalá Park, San Diego, CA 92110-2492 and <sup>1</sup>Department of Botany, San Diego Natural History Museum, Balboa Park, P.O. Box 121390, San Diego, CA 92112-1390—*Confirmation and characteristics of the hybrid origin of Opuntia prolifera through RAPD analyses.*

*Opuntia prolifera*, the Coastal Cholla, is common to the coastal sage scrub community extending from Ventura County, California to El Rosario, Baja California. On the basis of morphological intermediacy, *O. prolifera* is suspected to have originated through hybridization between *O. alcahes* and *O. cholla*, both species

of coastal and inland deserts of Baja California and Baja California Sur. For an independent test of this hypothesis, we screened populations of *O. prolifera* and the putative parents for RAPD banding patterns. In order to exclude other potential parents and to distinguish species-specific RAPD bands we included *O. bigelovii*, *O. ganderi*, *O. tesajo*, and *O. wolfii* in the screening. The results provide abundant support for the hybridization hypothesis as well as insight into various features of the process. Twenty-nine primers revealed 44 bands shared only between *O. prolifera* and just one of the two putative parents. Unique bands are rare (=2) in *O. prolifera* compared with *O. alcahes* (=19) or *O. cholla* (=23). Lack of marker asymmetry within and among populations of *O. prolifera*, which is triploid, is consistent with a single diploid-level hybridization event. Trends in the degree of band sharing between *O. prolifera* and its putative parents suggest a central Baja California origin of the species.

- 419** MCCAULEY, ROSS A.\* AND HARVEY E. BALLARD. Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701—*Systematics, biogeography, and evolutionary trends in the North American species of Froelichia (Amaranthaceae)*.

As it is currently circumscribed, *Froelichia* Moench. is a genus of 15-20 species of annual and perennial herbs and shrubs which inhabit dry plains and coastal areas of the tropical and subtropical western hemisphere and temperate North America. This group is closely related to *Gomphrena* (Globe Amaranth) and *Alternanthera* (Chaff Flower), both planted ornamentally in North America. As a portion of a full generic revision of this group, the identity and distribution of the North American species are considered using a series of morphological and molecular datasets. Preliminary analysis suggests there are four distinct species, *F. interrupta* (L.) Moq. in central and northern Mexico, *F. arizonica* Thornber ex Standley in northern Mexico and the American Southwest, *F. gracilis* (Hooker) Moq. native to Texas and now naturalized over a wide range, and *F. floridana* (Nutt.) Moq., a species exhibiting wide varietal variation in regions of the Great Plains and southeastern United States. Evidence is also presented for the recognition of *F. floridana* var. *pallescens* Moq., a form from central Florida described by Moquin-Tandon in 1849 but not recognized by later authors.

- 420** MCDADE, LUCINDA A.\*, THOMAS F. DANIEL, AND KATHERINE M. RILEY. Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721; Department of Botany, California Academy of Sciences, Golden Gate Park, San Francisco, CA 94118; Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721—*Phylogenetic relationships within the enigmatic tribe Justicieae (Acanthaceae)*.

We used molecular sequence data from the nuclear ribosomal internal transcribed spacers and from the intron and spacer of the trnL-trnF chloroplast region to study phylogenetic relationships within the large (ca. 2000 species), wide-ranging, and taxonomically difficult tribe Justicieae (Acanthaceae). Analysis of the combined data set provides a highly resolved hypothesis of relationships, much of it strongly supported. Justicieae are strongly supported as monophyletic; within the tribe, five lineages and one paraphyletic grade are related as follows: [*Pseuderanthemum* Lineage (Isoglossinae {*Tetramerium* Lineage [multiple clades of Old World "justicioids" (Diclipterinae + New World "Justicioids")])}). Many aspects of this phylogenetic hypothesis are supported by morphological and cytological data, and some conform to earlier classifications of the group. There are, however, a number of novelties. Notably, the large genus *Justicia* (ca. 700 species) is not monophyletic; the Old World members form a grade and the New World members are monophyletic only if a number of other genera are included. The strongly supported sister group relationship between Diclipterinae and the New World "Justicioid" Lineage is novel, and we cannot identify non-molecular synapomorphies confirming this relationship. *Rhinacanthus*, a "justicioid" (i.e., *Justicia* and morphologically similar genera) by all but phylogenetic criteria, is strongly supported as the basal member of Diclipterinae and cytological evidence confirms this placement. The *Pseuderanthemum* Lineage is only modestly supported as monophyletic and may represent a series of basal lineages. These plants are marked by having four staminal elements (four stamens or two stamens plus two staminodes), a plesiomorphic condition for all Acanthaceae. Additional evidence (both taxa and characters) will be necessary to resolve this uncertainty, as well as to determine the phylogenetic status of Old World "justicioids." Our analysis also provides considerable resolution within lineages.

- 421** MCMAHON, MICHELLE\* AND LARRY HUFFORD. School of Biological Sciences, Washington State University, Pullman, WA 99164-4236—*Phylogeny of Amorpeae (Fabaceae: Papilionoideae) based on DNA sequences from the chloroplast trnK intron, including the matK gene*.

Floral evolution in the legume tribe Amorpeae (eight genera, c. 240 species) has involved dramatic changes in the number, shapes, and positions of floral organs, including an unusual corolla-androecium synorgani-

zation. To study floral evolution in the tribe, we have reconstructed the phylogeny of the group, sampling heavily from genera for which we have morphological evidence that calls monophyly into question. Our preliminary results indicate that there are two major lineages, one consisting of three genera (*Dalea*, *Marina*, *Psorothamnus*) and the other of four (*Parryella*, *Eysenhardtia*, *Errazurizia*, *Amorpha*); the placement of monotypic *Apoplanesia* is uncertain. The first of these major clades includes floral diversity encompassing limited variation in the “papilionoid” floral form, but includes all cases of the corolla-androecium synorganization. The second clade includes a surprising level of diversity in petal number and floral symmetry. *Psorothamnus* is paraphyletic due to the placement of dalea-like *P. emoryi* as sister to *Dalea* plus *Marina*. *Marina* is supported as monophyletic, however *Dalea* is not. *Dalea filiciformis* shares many morphological characteristics with *Marina* and our results show that it is well supported as the sister group to *Marina*. The underused non-coding regions of the *trnK* intron (i.e., outside the coding region for *matK*) provided many variable and informative sites for resolving these relationships. Our well supported phylogeny of Amorpheae at the generic level provides a firm basis for refining classification of the tribe and analyzing processes generating floral diversity.

- 422** MCNEAL, JOEL R.\* AND CLAUDE W. DEPAMPHILIS. Department of Biology and Institute of Molecular Evolutionary Genetics, Penn State University, University Park, PA 16802—*Origin and molecular systematics of the parasitic plant genus Cuscuta (dodder).*

The genus *Cuscuta* is composed of a large number of morphologically similar stem parasitic vines. They produce minute, scale-like leaves with flower structure that is often only discernable microscopically. The morphological reduction of *Cuscuta* has historically rendered them a taxonomically difficult group, although most authorities have agreed they are allied to Convolvulaceae (Morning Glories). Even molecular systematic approaches have proven confounding, as the chloroplast and nuclear genes most often used in broad phylogenies have been shown to evolve at accelerated rates in parasitic plants, sometimes leading to incorrect phylogenetic inferences. Mitochondrial gene and intron sequences have revealed a sister relationship of *Cuscuta* to members of Convolvulaceae rather than suggesting *Cuscuta* is nested within the family. A Nuclear ITS phylogeny provides insights into the relationships between the three traditionally recognized subgenera of *Cuscuta* along with a more detailed interspecific phylogeny. These relationships have a significant impact on the understanding of the evolution of parasitism and photosynthesis in *Cuscuta*.

- 423** MOLVRAY, MIA\*, PAUL KORES, STEVE HOPPER, AND ANDEW BROWN. Oklahoma Biological Survey and Department of Botany & Microbiology, University of Oklahoma, Norman, OK 73019; Kings Park Botanical Garden, Perth, WA, Australia; and Division of Conservation and Land Management, Perth, WA, Australia—*A phylogenetic analysis of the subtribe Caladeniinae (Orchidaceae): Based on ITS sequences.*

The largest subtribe of Diurideae is Caladeniinae, which has a predominantly Australian distribution. As circumscribed by Dressler, the subtribe included ten genera, a number that has grown to fourteen in recent treatments. The status of the four segregate genera, *Praecoxanthos*, *Drakonorchis*, *Elythranthera*, and *Cyanicula*, has been questioned by some authors. The current study assessed the monophyly of Caladeniinae, the segregate genera, and the genus *Caladenia* itself. Three genera that have been included in the subtribe, *Leporella*, *Lyperanthus* and *Rimacola*, should be excluded from Caladeniinae based on sequence data. Our study supports the removal of *Praecoxanthos* from *Caladenia*, as suggested by Hopper and Brown on the basis of morphological characters. *Praecoxanthos* is sister to a clade composed of *Glossodia*, *Elythranthera*, *Cyanicula*, *Caladenia*, and *Drakonorchis*. *Elythranthera* is well-supported and appears sister to *Glossodia*. *Cyanicula* is likewise very well-supported and is sister to *Caladenia* s.str.. *Drakonorchis*, on the other hand, is embedded within the more derived species of *Caladenia*. Like some members of Drakaeinae, *Drakonorchis* has a thynnid wasp pseudocopulation pollination syndrome, showing that this complex suite of adaptations has evolved more than once within Diurideae.

- 424** MORRIS, JULIE A.\* AND JOHN V. FREUDENSTEIN. <sup>1</sup>Department of Biological Sciences, Kent State University, Kent OH 44242 <sup>2</sup>Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, OH 43212—*A systematic study of the North American Yellow Lady's Slipper orchids.*

The North American Yellow Lady's Slipper Orchids (*Cypripedium*) and their relatives present a large amount of variation that has remained intractable to study of morphological characters alone. In this study, the group was investigated using inter-simple sequence repeat (ISSR) markers and morphometric analysis of floral structures. Samples were collected from multiple populations of *C. parviflorum* and *C. pubescens* from across

their ranges, as well as from populations of *C. kentuckiense*, *C. candidum* and *C. montanum*. One population of *C. californicum* was included as an outgroup. Individuals were scored for the presence or absence of bands for 8 ISSR primers, and the data were analyzed cladistically using parsimony, and phenetically using UPGMA and neighbor-joining. Twenty-six floral characters were measured and analyzed using principal component analysis; lip shape was quantified using a truss approach. Populations of *C. pubescens* and *C. parviflorum* are intermixed in all of the analyses with very few patterns correlated with morphological differences. Some patterns seem to relate to geographical distributions. This could mean either that these morphologies have arisen independently multiple times, or that they were perhaps largely distinct in the past, but continue to exchange genes when in proximity. Populations of *C. kentuckiense* fall out in two clades associated with two different populations of *C. pubescens*. This could also be due to convergent evolution or occurrences of secondary hybridization. In each of these cases we favor the secondary gene flow hypothesis. The distinctness of the white lady's slippers, *C. candidum* and *C. montanum*, from the rest of this clade is well supported.

- 425** MORT, MARK E.\*, DOUGLAS E. SOLTIS, PAMELA S. SOLTIS, JAVIER FRANCISCO-ORTEGA, AND ARNOLDO SANTOS-GUERRA. Department of Biological Sciences, Eastern Illinois University, Charleston, IL 61920; School of Biological Sciences, Washington State University, Pullman, WA 99164; Department of Biology, Florida International University, Miami, FL 33199; Jardín de Aclimatación de la Orotava, Puerto de la Cruz, Tenerife, Canary Islands, Spain—*Phylogenetics and evolution of Aeonium (Crassulaceae) and related genera on the Canary Islands.*

The Macaronesian clade (Crassulaceae) includes four genera, *Aeonium*, *Aichryson*, *Greenovia*, and *Monanthes*, that are largely endemic to the Canary Islands. The monophyly of this clade has been supported based on phylogenetic analyses of Crassulaceae; however relationships within this clade remain uncertain. To resolve relationships within this clade, parsimony analyses were conducted on DNA sequences from several chloroplast regions (*trnL-trnF*, *psbA-trnH*, and *matK*), the internal transcribed spacers, and morphology (*Aeonium* only). Phylogenetic analyses of these data sets recover three major clades. Congruence tests were conducted on each of these data sets as well as the topologies resulting from our initial parsimony analyses. Several incongruent taxa were pruned from the cpDNA data set; a combined data set was constructed; and parsimony analyses were repeated. These analyses again recovered three clades. The monophyly of *Aichryson* and *Greenovia* was supported; however, *Aeonium* is monophyletic only if *Greenovia* is included in this genus. *Aeonium*, the largest genus of Canary Island Crassulaceae, comprises species that are highly diverse in growth form, including rosette trees, candelabrum shrubs, highly-branched shrubs, and woody rosettes. In addition, species of *Aeonium* are also diverse in habit (perennial and perennial monocarpic species) and physiology, with CAM, C<sub>3</sub>, and CAM-C<sub>3</sub> intermediate photosynthesis present in the genus. Analyses of stable isotopes of carbon were conducted from field collected leaf material to determine the degree of physiological variation present in *Aeonium*. The evolution of growth forms, habit, and physiology was investigated using our phylogenetic hypothesis for this genus. These analyses suggest that two subclades of *Aeonium* comprise taxa with similar growth forms, whereas two subclades contain taxa that display a wide range of growth form diversity. Monocarpy has arisen a minimum of four times in the genus. The ancestral physiological condition for *Aeonium* is C<sub>3</sub> photosynthesis, with at least three origins of CAM photosynthesis.

- 426** MÜLLER<sup>1</sup>, KAI\*, THOMAS BORSCH<sup>1</sup>, LAURENT LEGENDRE<sup>2</sup>, STEFAN POREMBSKI<sup>3</sup>, AND WILHELM BARTHOLOTT<sup>1</sup>. <sup>1</sup>Botanisches Institut und Botanischer Garten, Friedrich-Wilhelms-Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany; <sup>2</sup>Laboratoire de Biologie et Physiologie Végétales, Université de Reims Champagne-Ardenne, Moulin de la Housse - B.P. 1039, 51687 Reims Cedex 2, France; <sup>3</sup>Institut für Biodiversitätsforschung, Allgemeine und Spezielle Botanik, Universität Rostock, Wismarsche Straße 8, 18051 Rostock, Germany—*A phylogeny of Lentibulariaceae based on sequences of matK and adjacent non-coding regions.*

The carnivorous angiosperm family Lentibulariaceae comprises about 280 species in 3 genera (*Utricularia*, *Pinguicula*, *Genlisea*) and is of nearly worldwide distribution. It belongs to the order Lamiales within eusterids. From representatives of Lentibulariaceae and different outgroup taxa of the Lamiales the whole *trnK* intron including the *matK* gene was sequenced. The size of the *matK* coding region in Lentibulariaceae ranges between 1521 and 1581 bp. Size differences are caused by indels from 3 - 36 bp, which accumulate in the first half of the gene. The length of the noncoding region adjacent to the 5' end of *matK* is 729 - 780 bp, and of the region adjacent to the 3' end 305 - 330 bp. Sequence variability within Lentibulariaceae is



23% for the coding region as compared to 27% for the noncoding region. For the large 5' noncoding region a robust alignment was obtained, whereas the short 3' region could not be aligned all over due to high numbers of indels. Parsimony analyses based on substitutions and carried out independently for the *matK* gene and the long 5' noncoding region yielded identical, well resolved phylogenies with high bootstrap and decay support. The *matK* indels appear to be highly informative phylogenetically and seem to be much less homoplastic than substitutions. Lentibulariaceae appear monophyletic and *Byblis* is resolved as closest relative. Within Lentibulariaceae, *Pinguicula* diverges first and its species appear as a terminal clade on a long branch. *Genlisea* is sister to *Utricularia* with quite similar branch-lengths within the topology of the *Genlisea-Utricularia*-clade.

- 427** NEINHUIS, CHRISTOPH\*, KHIDIR, W. HILU, AND THOMAS BORSCH. Botanisches Institut und Botanischer Garten, Universität Bonn, Germany, Institute of Biology, Virginia Tech. University, Blacksburg, USA—*Systematics of Aristolochiaceae: Molecular Evidence*.

Aristolochiaceae comprises some 600 species occurring worldwide with concentration in tropical and subtropical regions. The family belongs to a basal angiosperms clade consisting of Piperaceae, Saururaceae, and Lactoridaceae; the latter is either nested in or sister to Aristolochiaceae. Although Aristolochiaceae is generally split into subfamilies Asaroideae and Aristolochioideae, strong disagreement exists in systematic relationships at the generic level. This is particularly true for *Pararistolochia* and *Isotrema*, although they can be recognized by several morphological synapomorphies. We present a phylogeny based on trnT-trnF for Aristolochiaceae. The two subfamilies are well supported with *Saruma* and *Asarum* being sister groups. *Pararistolochia* and *Isotrema* form well supported monophyletic clades, with *Endodeca* sensu Huber being closely related to *Isotrema*. The morphologically unique, monotypic *Holostylis* nests within the South American species of "Howardia" sensu Huber. Based on a broad sampling of outgroup taxa (e.g., Saururaceae, Piperaceae, Austrobaileaceae, Amborellaceae) we also allow to look for close relatives of the Aristolochiaceae. Special attention was paid to the problem of an presently unresolved position of *Lactoris fernandeziana*. The outgroup results of this study show Piperaceae and Saururaceae forming a monophyletic group with *Lactoris* at its base and confirming this grade being sister to Aristolochiaceae.

- 428** NICKOL, MARTIN G. Botanisches Institut und Botanischer Garten, Christian-Albrechts-Universität, Kiel, D-24098, Germany—*Flower morphology and floral ecology of Plumbaginaceae*.

Within Plumbaginaceae adaptations to maritime habitats led to significant morphological and physiological features. Focussing on the characters of the bisexual flowers their morphological features and distinctive change during anthesis can also be interpreted as adaptations to the microclimatic conditions and the pollinator abundance in the mainly coastal environment of the different species. Even within the genera *Armeria* and *Limonium* (Armerioideae) a great variety in special floral features influencing pollination efficiency has developed, e.g. heterostyly and polymorphic pollen grains. These morphological patterns can not be interpreted solely as autapomorphic characters strongly influenced by actual environmental conditions, but moreover including the phylogenetic relationships of and within genera.

- 429** NICKRENT, DANIEL L. 1\*, CHRISTOPHER L. PARKINSON 2, JEFFREY D. PALMER 2, AND R. JOEL DUFF 3. 1 Department of Plant Biology and Center for Systematic Biology, Southern Illinois University, Carbondale, IL, USA 62901-6509, 2 Department of Biology, Indiana University, Bloomington, IN USA 47405, 3 Department of Biology, University of Akron, Akron OH USA 44325-3908—*Parsimony and likelihood analyses of genes from all three subcellular genomes strongly support major land plant phylogenetic relationships*.

The evolution of land plants from green algal ancestors has long been a topic of interest to botanists and has more recently taken on special interest given results from molecular phylogenetic analyses. Parsimony and likelihood analyses were conducted on a data set comprising chloroplast *rbcL*, and nuclear, chloroplast, and mitochondrial small-subunit (SSU) rDNA (6095 total characters) from all major land plant lineages. Significant bootstrap support was obtained for 1) hornworts as sister to the remaining embryophytes, 2) a sister-group relationship between mosses and liverworts, and 3) monophyly of vascular plants, lycophytes, pteridophytes, seed plants, and angiosperms. In contrast to the other genes, mitochondrial SSU rDNA analyzed alone recovered essentially the same topology as the multigene tree and had the lowest level of homoplasy. The tree topology obtained here is highly congruent with previous cladistic analyses of morphological characters, thus strongly suggesting that the same phylogenetic pattern is being tracked.

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NYFFELER, RETO\* AND URS EGGLI. Harvard University Herbaria, Cambridge, MA 02138; Sukkulanten-Sammlung, CH-8002 Zurich, Switzerland—*Phylogenetic relationships and diversification of the columnar and globular cacti of Chile (Cactaceae - Cactoideae)*.

For Chile Hunt (1999; CITES Cactaceae Checklist) recognizes 11 genera and about 80 species of Cactoideae (Cactaceae), of which six genera (*Austrocactus*, *Copiapoa*, *Corryocactus*, *Eriosyce* s.lat., *Eulychnia*, and *Neowerdermannia*) and about 65 species are traditionally regarded as closely related and referred to the tribe Notocacteae (Barthlott & Hunt 1993; Families and Genera of Flowering Plants). Molecular phylogenetic analyses based on chloroplast DNA markers (*trnK* intron, *matK*, *trnL-trnF* intron and spacer), however, reveal that these genera in fact are members of three different major clades of Cactoideae. *Austrocactus*, *Eulychnia*, and *Corryocactus* are related to basically West Andean representatives of the tribes Browningieae (excl. *Browningia*) as well as the Central and North American Hylocereeae, and Pachycereeae. *Copiapoa* represents a distinct basal lineage within Cactoideae without any obvious close relatives. Finally, *Eriosyce* and *Neowerdermannia* are related to the East Andean genus *Parodia* s.lat. These findings indicate that the various similarities in different types of growth forms and related vegetative characters in the two most diverse Chilean genera, *Copiapoa* and *Eriosyce*, represent striking convergences. Biogeographically the cactus flora of Chile falls into two distinct parts with minimal overlap, (1) a narrow strip along the coast of the central and northern half of the country, comprising the coastal cordillera as well as some of the major inland valleys, and (2) the W slopes of the main cordillera of the extreme NE of the country. Representatives of the former area are *Austrocactus*, *Copiapoa*, *Echinopsis*, *Eriosyce*, and *Eulychnia*, while the genera *Browningia*, *Corryocactus*, *Neowerdermannia*, *Oreocereus*, and *Weberbauerocereus* are only present in the latter area. The exception to the rule is *Haageocereus* which is present with one representative in each of the two areas and *Echinopsis atacamensis* which occurs in area 2.

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OCHOTERENA, HELGA\* AND MARK PITKIN SIMMONS. L.H. Bailey Hortorium, Cornell University, Ithaca, NY 14853—*Justification and methods for incorporating gap characters in sequence-based phylogenetic analyses*.

We discuss the theoretical arguments for, and implications of, the different methods of treating gaps in phylogenetic analyses. We consider alignment (making hypotheses of primary homology) and tree searches (testing hypotheses of primary homology) to be logically independent steps in phylogenetic analysis. Although both operations may be incorporated into a single step, they need not be. Gaps do not occur in organisms and therefore cannot be directly observed. However, gaps are as much a part of the pattern of aligned sequences as bases are. Because this aligned pattern is used to code characters for tree searches, the informative variation from gaps should be incorporated along with base characters into tree searches. We argue that gaps are properly coded as separate, equally-weighted, presence/absence characters (not 5th character states for nucleotides or 21st character states for amino acids). Although gaps are alternative forms of aligned positions, gaps are not alternative forms of positions that do not exist in organismal sequences. In addition to evidence that contiguous gap positions originate as single indel events, the parsimony criterion favors the interpretation of coding contiguous gap positions as single characters because of the co-occurring pattern. In consequence of these arguments, we propose two methods by which gaps coded as characters can be implemented in tree searches. Simple indel coding, in which all gaps are coded as separate binary characters, is easy to implement but does not utilize all available information and can cause ambiguous optimizations of gap characters. Complex indel coding, in which non-overlapping gaps are coded as separate binary characters and overlapping gaps that share a common terminus (or are subsets of longer gaps) are coded as separate multistate characters in step matrices, is harder to implement but allows all available information to be utilized.

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OCHOTERENA, HELGA. L. H. Bailey Hortorium, 462 Mann Library, Cornell University, Ithaca, NY, 14853—*Phylogeny and character evolution in Hintonia (Rubiaceae) and related taxa*.

The systematic position of the genus *Hintonia* Bullock within Rubiaceae has been controversial. Cladistic analyses of the chloroplast ribulose biphosphate carboxylase-oxygenase large subunit (*rbcL*) DNA sequences including a wide range of taxa from within and outside Rubiaceae have been conducted. These studies suggest that *Hintonia* is related to genera belonging to the *Portlandia* group forming a monophyletic clade that also includes members of the Chiococceae and Catesbaeae tribes in addition to *Exostema* (Pers.) Humb. & Bompl. Previous classifications do not entirely reflect the relationships suggested by the *rbcL* analyses. A combined analysis including *rbcL* and morphology provides the basis for the interpretation of the evolution of characters traditionally used in the taxonomy of the family. These characters include life form, presence/

absence of raphides, flower arrangement, flower aestivation, unit of pollen dispersal, texture of the fruit, pattern of fruit dehiscence, and presence/absence of a wing on the seed. A morphological cladistic analysis with a greater sampling of the taxa likely to be related to *Hintonia* provides further evidence for the interpretation of the phylogenetic relationships of these genera and the evolution of additional characters. These characters include: pattern of wax deposition in the leaves, point of insertion of the stamens in the corolla, pollen aperture number and type, placentation and placenta characters, seed orientation and seed coat characters. The morphological studies suggest that only three species endemic to Mexico and Guatemala should be recognized within *Hintonia*.

- 433** OLMSTEAD, RICHARD G.\*, PHILIP D. CANTINO, BRENDAN LEPSCHI, AND PATRICK A. REEVES. Department of Botany, University of Washington, Seattle, WA 98195 USA, Dept. Environmental & Plant Biology, Ohio University, Athens, OH 45701 USA, Australian National Herbarium, GPO Box 1600, Canberra, ACT, 2601, Australia, Department of Botany, University of Washington, Seattle, WA 98195 USA—*A molecular systematic study of the Prostantheroideae (Lamiaceae), including Chloantheae (formerly Verbenaceae).*

As part of our ongoing molecular systematic research into the phylogeny of the Lamiales, we have conducted an investigation of the hypothesis put forward by Cantino that the Australian endemic labiate tribe Westringieae (= Prostanthereae) and the Australian endemic verbenaceous tribe Chloantheae together form a monophyletic group, which also included Tectona (Verbenaceae/Viticoideae sensu Briquet). The evidence for this postulated relationship comes from a cladistic analysis of morphological and anatomical characters, in which members of these two groups come out adjacent to each other in an unrooted tree. A total of 58 sequences was analysed, including the 24 sequences representing Chloantheae and Westringieae, along with 33 sequences representing species from throughout the Lamiaceae (including *Spartothamnella*) and related families. The results provide strong support for monophyletic groups comprising Chloantheae, Westringieae, and those two clades combined (Prostantheroideae). *Tectona* is not found to belong to this group. *Spartothamnella* is found to not belong with the Prostantheroideae, but belongs in Teucroideae. It is sister to another Australian endemic, *Oncinocalyx*, and together they are sister to the New Zealand endemic *Teucrium*. These three taxa, all formerly assigned to Verbenaceae, are most closely related to *Teucrium*, traditionally assigned to Lamiaceae.

- 434** PARK, SEON-JOO\*, ELISA KOROMPAI, JAVIER FRANCISCO-ORTEGA, ARNOLDO SANTOS-GUERRA, AND ROBERT JANSEN. Section of Integrative Biology, University of Texas, Austin TX 78712—*Phylogenetic relationships of Tolpis (Asteraceae: Lactuceae) based on ndhF sequence data.*

*Tolpis* includes approximately 12-20 species distributed primarily in Europe, Middle East, and Africa with most species (10) confined to the Macaronesian archipelagos of the Azores, Madeira, Canary Islands, and Cape Verde Islands. Although there has been considerable effort to resolve generic circumscriptions and relationships among genera of the tribe Lactuceae, much controversy still remains regarding these taxonomic issues for *Tolpis*. Phylogenetic analyses of the chloroplast encoded gene *ndhF* were performed using 36 species from 28 genera of Lactuceae and outgroup taxa from the five other tribes of Cichorioideae. The sampling included most previously suggested generic relatives of *Tolpis* and seven species of *Tolpis* from Africa, Europe, and Macaronesia. The *ndhF* phylogeny indicates that *Tolpis* is not monophyletic because two continental species, *T. capensis* from south-central Africa and Madagascar and *T. staticifolia* from central and southeast Europe, do not occur in the strongly supported core *Tolpis* clade. This result is in agreement with recent suggestions based on macromorphology and palynology that these two species should be excluded from *Tolpis*. *Tolpis capensis* is sister to *Taraxacum* and *T. staticifolia* is nested within the genus *Crepis*. The *ndhF* tree also indicates that the core *Tolpis* clade is an isolated lineage that is not related to any of the previously suggested genera of Lactuceae. Relationships among the five examined core *Tolpis* species are fully resolved in the *ndhF* tree. The three examined island species occur in two different clades suggesting either multiple colonizations or a single origin and subsequent recolonization of the continent. Resolution of the origin of the island endemics will require additional taxon sampling and the use of more variable molecular markers.

- 435** PARK, SEON-JOO\*, JAVIER FRANCISCO-ORTEGA, ARNOLDO SANTOS-GUERRA, JOSE PANERO, AND ROBERT JANSEN. Section of Integrative Biology, University of Texas, Austin TX 78712—*Implications of chloroplast DNA variation for the evolution of the Macaronesian Endemic genus Pericallis (Asteraceae, Senecioneae).*

*Pericallis* includes 14 species endemic to the archipelagos of the Azores, Canary Islands, and Madeira. Species in the genus occur in all five ecological zones except the high altitude desert and they exhibit

considerable variation in growth form and floral biology. We have examined cpDNA restriction site variation for all species of *Pericallis* and several closely related continental genera. We detected 135 parsimony informative restriction site changes among the 403 variable sites using 22 restriction enzymes. The cpDNA data produce highly resolved and well supported trees which are largely congruent with previous trees generated from nuclear ITS data. We plotted both growth form (woody versus herbaceous), ecology, and island distribution on the combined tree from both markers. Two evolutionary trends are evident from these comparisons. First, there have been at least two independent origins of woodiness in the island endemics from a herbaceous continental ancestor. Second, inter-island colonization between similar ecological zones on different islands is the major avenue of evolution, a pattern that we have observed previously in several other Macaronesian endemics.

- 436** PELL, SUSAN K.\* AND LOWELL URBATSCH. Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803—*Evaluation of evolutionary relationships in Anacardiaceae using matK sequence data.*

Anacardiaceae, the cashew family, comprises ca. 600 species in 80 genera. It is a primarily pantropical family with approximately equal representation in Africa, South America and Southeast Asia. Anacardiaceae is most well known for its edible fruits and seeds, contact dermatitis-causing species, and lacquer plants. Recent studies have indicated that the most widely used classification, Engler's 1883 treatment consisting of five tribes (Anacardieae, Dobineae, Rhoeae, Semecarpeae, and Spondiadeae), is artificial. In order to develop a clearer picture of the circumscription of the tribes within Anacardiaceae, a phylogeny has been constructed from DNA sequence data of the chloroplast gene *matK*. Preliminary sequence data support earlier molecular and morphological/anatomical studies that found two, rather than five, lineages within the family. Establishing the root of the Anacardiaceae is an essential part of determining the intrafamilial relationships. Numerous authors have recognized Burseraceae as sister to Anacardiaceae, a relationship supported by Gadek et al.'s *rbcL* DNA sequence data from a few representatives (three Burseraceae and 7 Anacardiaceae) of each family. This interfamilial relationship will be investigated in more detail via *matK* sequence data from numerous representatives of Burseraceae and Anacardiaceae.

- 437** PERRET, MATHIEU\*, ALAIN CHAUTEMS, RODOLPHE SPICHIGER, AND VINCENT SAVOLAINEN. Conservatoire et Jardin botaniques, Geneva, CH 1292, Switzerland; Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, United Kingdom—*Floral diversification and speciation in Sinningieae inferred from phylogenetic analysis of plastid and nuclear cpGS gene sequences.*

The tribe Sinningieae (neotropical Gesneriaceae) comprises three genera (*Sinningia*, *Paliavana* and *Vanhouttea*) with a total of 75 species exhibiting bee, moth, hummingbird and bat pollination syndromes. The phylogeny of all species was inferred using five plastid non-coding DNA regions (*atpB-rbcL*, *trnT-trnL*, *trnL-trnF*, *trnS-trnG*, *rpl16*) and the nuclear-encoded chloroplast glutamine synthetase (*ncpGS*). Molecular cloning of *ncpGS* PCR products and infraspecific samplings revealed sequence variation within one third of the species. Allelic polymorphism of *ncpGS* and comparison between trees obtained from *ncpGS* gene and plastid regions combined were used to infer putative introgression events among Sinningieae. Based on a species-level phylogeny, evolution of floral morphology and nectar reward chemistry were reconstructed. Frequent parallelisms and reversals in pollination syndromes were observed. Specific sugar chemistries in nectar were found in species with bat and moth syndromes, whereas no significant difference in nectar composition were found in bee and hummingbird-pollinated species, thereby facilitating multiple shifts between these latter syndromes. Comparison of geographic area overlaps between sister species indicate that allopatric speciation was most common, with subsequent phenotypic changes and adaptations to pollinators.

- 438** PLUNKETT, GREGORY M.<sup>1\*</sup>, PORTER P. LOWRY II<sup>2</sup>, AND JONATHAN M. EIBL<sup>1</sup>. <sup>1</sup>Department of Biology, Virginia Commonwealth University, Richmond, VA 23284-2012, and <sup>2</sup>Missouri Botanical Garden, St. Louis, MO 63166-0299—*Phylogenetic relationships of Schefflera and Polyscias: non-monophyly in the two largest genera of Araliaceae.*

Over the past several decades, taxonomic re-alignments in Araliaceae have resulted in a dramatic expansion in the size of the two largest genera, *Schefflera* (~650 spp.) and *Polyscias* (~130 spp.). As currently circumscribed, these genera now represent nearly two thirds of the species diversity in the family. The large size (relative to other araliad genera) and mostly Gondwanan distribution of both *Schefflera* and *Polyscias* make these genera good model systems for a variety of diversification studies, including the study of speciation rates and biogeographic patterns. Although taxonomic systems have often been used as the basis for



such studies, it is now widely accepted that robust phylogenetic reconstructions are needed to test alternative evolutionary hypotheses. Preliminary data based on the internal transcribed spacers (ITS) of nuclear ribosomal DNA suggest that neither *Schefflera* nor *Polyscias* is monophyletic, a finding that will have important implications for both taxonomic and diversification interpretations. More specifically, ITS data suggest that *Schefflera* is polyphyletic, forming at least three (and perhaps many more) unrelated clades within Araliaceae. These clades do, however, exhibit geographic structuring (and in some cases form sister groups with other araliad taxa from the same geographic region). The data also suggest that *Polyscias* is paraphyletic; no fewer than six additional genera (*Reynoldsia*, *Tetraplasandra*, *Munroidendron*, *Arthrophyllum*, *Gastonia*, and *Cuphocarpus*) are derived from within a broad *Polyscias sensu lato* clade. As in *Schefflera*, the several groups of *Polyscias s. lat.* are geographically structured, with one broad subclade centered on Madagascar (and the Indian Ocean basin in general), and several additional subclades centered in the Pacific. Preliminary biogeographic analysis suggests these clades may have been derived from repeated dispersal events from Australasia.

- 439** PORTER, J. MARK\* AND LEIGH A. JOHNSON. Rancho Santa Ana Botanic Garden, 1500 North College Avenue, Claremont, CA 91711. Botany and Range Science, 451 WIDB, Brigham Young University, Provo, UT 84602—*Age and diversification and their implications for historical biogeography of Polemoniaceae.*

A small monophyletic family of approximately 360 species, Polemoniaceae are most diverse in the New World. Historical discussions of diversification of this family have relied upon (1) classification as recapitulating phylogeny and (2) major lineages of the family corresponding roughly to Arcto-tertiary or Madro-tertiary elements. The combination of quantitative phylogenetic (maximum likelihood) methodologies and new fossil evidence provide a framework to test these hypotheses of diversification. Phylogenetic estimates, based on chloroplast (*matK*, *trnL-F*) and nuclear (nrITS) DNA sequences, while supporting some relationships suggested by recent classification, refute the implied pattern of diversification. Molecular clock estimates, using the three genic regions and the fossil *Gilisenium hueberi* as a calibration point, infer that nearly all of the diversification, resulting in present day genera, occurred during the mid-Tertiary (58-35 MYBP). Indeed, the common ancestor of the so-called “temperate group” may date to 100 MYBP or earlier, during the Cretaceous. We further show that present day distributions and ecological preferences may be misleading in their implications for historical origins of lineages within Polemoniaceae.

- 440** POTGIETER, K\*, J ROVA, E WALLANDER, V.A ALBERT, AND L STRUWE. Molecular & Integrative Physiology, University of Illinois, Urbana, IL 61801—*Large molecular trnL intron phylogeny of the Gentianales.*

This trnL intron derived phylogeny of the Gentianales represents the most extensive and most evenly sampled study of the group, or any angiosperm order for that matter, to date. Past systematic work using morphological and/or molecular sequence data did not effectively resolve interfamilial relationships within the Gentianales. Increased taxon sampling may effectively distribute phylogenetic signal more evenly and thereby improve resolution of the major families at all levels within the order. Roughly 500 accessions were sampled from major tribes of the Strychnaceae, Loganiaceae, Gelsemiaceae, Gentianaceae, Apocynaceae s.l., and Rubiaceae. Members of the Oleaceae, Scrophulariaceae, and more distally related genera were included as outgroups. Apocynaceae s.l. comes out in the most derived position and has a sister group relationship with a clade consisting of Strychnaceae-tribe Strychneae and Loganiaceae s.str. Gelsemiaceae is supported as a distinct family and is unresolved along with Strychnaceae-tribe Antonieae and Rubiaceae. Surprisingly, Gentianaceae is in the basalmost position; it is also the only family (except for tribes Antonieae and Spigeliaceae in the Strychnaceae) that lack alkaloids. Most of the traditional families in the Gentianales appear to be monophyletic, except for Strychnaceae and Loganiaceae.

- 441** PRATT, DONALD B.\* AND LYNN G. CLARK. Department of Botany, Iowa State University, Ames, IA 50011-1020—*Amaranthus rudis and A. tuberculatus—One species or two?*

*Amaranthus rudis* and *A. tuberculatus*, the waterhemp, are an important weedy, dioecious species pair, the identification of which historically has been much confused. Morphological examination reveals a large number of pistillate intermediates that fit neither species and that staminate plants have not been well characterized. Principal components analysis of isozyme data of waterhemp collected from throughout the species' ranges shows that populations segregate along a single geographic continuum that does not correspond with the original morphological species designations. A single species, *Amaranthus tuberculatus* (Moq. ex DC.) J. D. Sauer, is proposed.

- 442** PRINCE, LINDA M.\* AND W. JOHN KRESS. National Museum of Natural History, Department of Botany MRC-166, Smithsonian Institution, Washington, DC 20560—*Phylogenetic relationships among genera of the prayer plant family (Marantaceae) based on chloroplast DNA sequence data.*

The Marantaceae are a cohesive but taxonomically difficult group. The genera appear well-defined with few changes in circumscription over the recent decades. Relationships among the genera are poorly understood. The latest treatment above the rank of genus was that of Loesener in 1930, dividing the genera into two tribes based on the number of fertile locules. Andersson provided an informal treatment of the family in 1980, dividing the genera into five groups plus five genera of uncertain affinity based on a number of morphological characters. We sequenced the chloroplast *matK* gene plus flanking non-coding spacers and the *trnL* to *trnF* spacer region for 85 ingroup taxa representing 28 of the 31 currently recognized genera in the family. Additional sequences for 9 outgroup taxa representing the 7 other families of Zingiberales were included in the analyses. Our data do not support either of the above classifications although some of Andersson's groups are supported in part. A number of genera appear paraphyletic or polyphyletic based on our results including *Phrynium*, *Calathea*, and *Schumannianthus*. We evaluate the strength of the morphological features used for previous classifications and propose a provisional classification of Marantaceae.

- 443** PRYER, KATHLEEN M.\*, HARALD SCHNEIDER, ALAN R. SMITH, PAUL G. WOLF, RAYMOND C. CRANFILL, JEFFREY S. HUNT, AND SEDONIA D. SIPES. Department of Botany, The Field Museum, Chicago, IL 60605; University Herbarium, University of California, Berkeley, CA 94720; Dept. of Biology, Utah State University, Logan, UT 84322—*The closest living relative to seed plants: insights from four genes and morphology.*

Extant vascular plants comprise free-sporing "pteridophytes" (lycophods, Psilotaceae, *Equisetum*, and ferns) and seed plants (gymnosperms and angiosperms). The evolution of vascular plants is mostly a 470-million-year history of pteridophytes and gymnosperms, which ultimately led to the domination of our terrestrial ecosystems by angiosperms 100 million years ago. Pteridophytes traditionally are depicted as having various paraphyletic relationships to seed plants and are often thought of as "intermediate evolutionary grades" of relatively minor significance in early land plant evolution. Phylogenetic estimates based on single genes and/or morphology yield weak evidence for the divergence and relationships among these major groups of vascular plants. This is not entirely surprising given that, with the exception of angiosperms, they all evolved in the Paleozoic and had diverged by the late Devonian (ca. 400 mya). The long independent history of each of these lineages ensures that resolving their relationships is not likely to be revealed by a single data set. Data from four genes (*rbcL*, *atpB*, *rps4*, nrSSU) and morphology was tested for congruence and results from the combined analysis strongly corroborate several weak inferences made from single data set trees. However, the clear resolution provided by the combined analysis for a basal dichotomy between seed plants and all other (non-lycophyte) "pteridophyte" lineages is novel. This result differs remarkably from most topologies found in the separate analyses for each of the five data sets. Robust support for Psilotaceae + Ophioglossaceae, as well as relationships among basal fern groups will also be discussed.

- 444** RANKER, TOM A.\*, KENDRA A. MINGO, CHRISSEN E. C. GEMMILL, AND WINONA CHAR. University Museum & EPO Biology, University of Colorado, Boulder, CO, 80309; SMILE Program, Oregon State University, Corvallis, Oregon 97331-3510; Centre for Biodiversity and Ecology Research, Dept. of Biological Sciences, University of Waikato, Hamilton, New Zealand 2001; Honolulu, HI—*Systematics and classification of Hawaiian Sesbania (Fabaceae).*

Populations of *Sesbania* in Hawaii exhibit a classic situation found among many Hawaiian plant taxa in that there is much morphological variation across populations but the variation for any single trait appears as a cline. Such apparent clinal variation has led to conflicting classifications in *Sesbania* with from one to seven species being recognized by various workers. We have employed data from isozymes, DNA sequence variation (SSCP of ITS-nrDNA), and morphology in multivariate analyses and phylogenetic analyses to address the following questions: 1) Are populations of Hawaiian *Sesbania* a monophyletic group? 2) Can the different populations be discriminated from each other multivariately? 3) Do individual populations or groups of populations represent discrete, multiple evolutionary lineages? 4) What are the phylogeographic relationships of populations/taxa? 5) What are the implications of our results for the classification of Hawaiian *Sesbania*? Preliminary results suggest the following: Hawaiian populations of *Sesbania* are a monophyletic group; some single populations and some groups of populations are distinct and non-overlapping for various combinations of data and they may represent discrete lineages; the data support the recognition of at least the following

taxa, here listed as informal names based on the work of Char: “polihaliensis”, “kauensis-intermedia”, “manaensis”, “tomentosa-Maui”, “tomentosa-Hawaii”. Even when all populations of Hawaiian *Sesbania* are treated as a single species, this is a rare taxon. The classification proposed here suggests that Hawaiian *Sesbania* is a complex of extremely rare and endangered species.

- 445** RAUBESON, LINDA A\*, MARY E COSNER, ANDREA OESTREICH, AND ROBERT K JANSEN. Department of Biological Sciences, Central Washington University, Ellensburg, WA 98926 and Section of Integrative Biology, University of Texas, Austin TX 78713—*Molecular characters in phylogeny reconstruction: A comparison of nucleotide data and chloroplast genome structural changes.*

We are using nucleotide sequence data from three chloroplast genes (*atpB*, *matK* and *rbcL*) as well as chloroplast genome structural mutations to study evolutionary relationships in the Campanulaceae *sensu stricto*. Our work to date focuses on 18 representative taxa. In addition to elucidating phylogenetic relationships among the organisms, we are interested in investigating genome structural evolution in the family. Approximately seventy-two different structural mutations have been identified in the eighteen genomes including examples of inversions, gene losses, duplications, insertions and possibly transpositions. We will use the three nucleotide sequence data sets to develop a hypothesis of Campanulaceae phylogeny and then use the DNA sequence results to develop models of chloroplast genome structural evolution. Relative to most other land plants, Campanulaceae chloroplast genomes have experienced an unusually high amount of structural change. This presents an opportunity to better understand the mechanisms leading to structural mutation. In addition, Campanulaceae provides an opportunity to compare the effectiveness of structural data versus sequence data in phylogeny reconstruction. In our initial comparisons, consistency indices were higher in the structural data regardless of the method of character scoring or weighting used in parsimony analyses. Other measures also favored structural data. Plus the structural data produced similarly resolved trees. In Campanulaceae, the structural data provide many characters without high levels of homoplasy. Our comparisons suggest that chloroplast genome structural data is an important adjunct to other data sets in groups where such markers are available.

- 446** REE, RICHARD H.\*, MICHAEL J. DONOGHUE, AND DAVID E. BOUFFORD. Harvard University Herbaria, 22 Divinity Ave., Cambridge, MA 02138—*Plant diversity of the Hengduan Mountain region of China.*

The Hengduan Mountains, located east of the Himalayan range, form a dramatic series of north-south trending valleys and ridges extending from 1000 to over 7000 meters in elevation. This region and the surrounding area may contain as much as 40% of China's plant diversity, and is especially rich in endemic species. Several groups are extraordinarily diverse in the region, including *Rhododendron*, *Saussurea*, *Cremanthodium*, *Gentiana*, and *Primula*. For these reasons, and owing to ecological pressures imposed by human activity, this region is considered one of 24 biodiversity hotspots worldwide, and one of only three in the north temperate zone. Our recent NSF-sponsored (DEB-9705795) expeditions to the Hengduan region have yielded over seven thousand collections of macrofungi, bryophytes, and vascular plants. A database of information on these specimens, including elevation and GPS-based coordinate data, habitat information, field observations, images, and tissue available for DNA and anatomical analyses, is now available via the Harvard University Herbaria web site (<http://www.herbaria.harvard.edu>). Specimens collected on these expeditions have enabled detailed study of several groups that are particularly diverse in this region, including discomycete fungi, Dipsacales, *Brassicaceae*, *Corydalis*, and *Pedicularis*.

- 447** ROALSON, ERIC H. Rancho Santa Ana Botanic Garden and The Claremont Graduate University, 1500 N. College Ave., Claremont, CA 91711—*Molecular phylogenetic studies in Carex section Acrocystis (Cyperaceae): evidence from nuclear Adh and ITS genic regions.*

*Carex* section *Acrocystis* (Cyperaceae) traditionally has included ca. 45 species. Recent studies have suggested that a “core” group of *Acrocystis* species forms a monophyletic group, while other species are more closely related to other sections. This core group includes all North American *Acrocystis* species and some but not all Eurasian members. Taxonomists have recognized several species complexes in North American *Acrocystis*, with several “orphan” species not dealt with in these species complexes. The complexes that have been defined include the “*Carex pensylvanica* complex,” the “*Carex nigromarginata* complex,” the “*Carex deflexa* complex,” and the “*Carex umbellata* complex”. Taxa not included in these complexes are *Carex novae-angliae*, *C. turbinata*, *C. leucodonta*, *C. communis*, *C. globosa*, *C. brainerdii*, and *C. serpenticola*. How these complexes and orphan species are related has not been addressed explicitly, and none of the

North American species have been explicitly compared with Eurasian or South American members of *Acrocystis*, with few exceptions. The study presented here explores relationships within North American members of *Carex* section *Acrocystis* and related Eurasian species and addresses biogeographic patterns of diversification using nuclear *Adh* genic regions and the nrDNA ITS region.

- 448** RUSSELL, ADRIENNE D. Department of Biology, San Diego State University, San Diego, CA 92182—*Phylogeny and morphology of Chorizanthe and related taxa (Polygonaceae: Eriogonoideae)*.

The subfamily Eriogonoideae is a diverse group of shrubs, herbaceous perennials, and annuals that is characterized by the absence of sheathing leaf stipules (ocrea), and the presence of a whorl of inflorescence bracts subtending each inflorescence node and a whorl of involucre bracts subtending each flower or cluster of flowers. The majority of taxa in the subfamily are aligned with one of two large genera, *Eriogonum* (wild buckwheat, ~240 spp.) and *Chorizanthe* (spineflower, 40 N. American spp.). The remaining 15 genera in the subfamily are small, largely monotypic taxa. Relationships within *Chorizanthe* and within the Eriogonoideae were examined through parsimony analysis of 93 taxa using 80 non-molecular characters. The analysis included 42 species of *Chorizanthe*, 40 additional members of the Eriogonoideae, and eleven out-group taxa representing Polygonaceae and Plumbaginaceae. The objectives of this study were to assess (1) monophyly of *Chorizanthe*, (2) interspecific relationships within *Chorizanthe*, and (3) intergeneric relationships within the subfamily Eriogonoideae. Data presented are from studies of vegetative morphology, inflorescence structure, floral and fruit morphology, and palynology. Morphological character evolution is discussed as it pertains to classical and revised (phylogenetic) definitions within the eriogonoid taxa. The study points to extensive variation in floral and inflorescence morphology in the subfamily Eriogonoideae and recognizes the high level of homoplasy in this group of specialized annuals and related perennials. In addition, newly discovered variation in pollen ultrastructure of *Chorizanthe* species will be presented.

- 449** SALYWON, ANDREW. Department of Plant Biology, Arizona State University, Tempe, AZ 85287—*A revision of Mosiera (Myrtinae: Myrtaceae)*.

*Mosiera* is a New World genus of approximately 12 species of trees and shrubs that occur primarily in tropical dry, deciduous or partially deciduous forests, mainly in the Caribbean. Two species occur in eastern and southern Mexico, one of these also occurring in Guatemala, and only one species occurs in South America (Brazil). Ecologically, *Mosiera* appears to be restricted to gypsum, limestone or serpentine soils. Only one species, *M. longipes*, is widely distributed throughout the Caribbean, the other species are generally narrowly endemic. The center of diversity of the genus is in eastern Cuba which corresponds to the center of botanical diversity of the Antilles as a whole. Described by Small in 1933, the boundaries of *Mosiera* have never been adequately defined until recently. *Mosiera* has a combination of characters which cause it to be superficially similar to other genera (i.e., *Anamomis* or *Eugenia* of the subtribe Eugeniinae or *Myrtus* or *Psidium* in the subtribe Myrtinae). The genus was first comprehensively described in 1992 by Landrum, however, to date only three species have been systematically treated and no objective phylogeny for the genus or the American Myrtinae has yet been proposed. Seed coat characters in combination with floral characters are useful in classifying taxa in the American Myrtinae. This revision confirms and expands this assertion. Preliminary sequence data from the ITS region of nrDNA of the American Myrtinae supports a closer relationship of *Mosiera* to *Psidium* than to *Myrtus* and *Calycolpus*. In addition, two different copies of the ITS region are present in several genera of Myrtinae.

- 450** SANG, TAO\*, SONG GE, BAO-RONG LU, AND DE-YUAN HONG. Department of Botany and Plant Pathology, Michigan State University, East Lansing, MI 48824; Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing 100093; Genetic Resources Center, International Rice Research Institute, 1099 Manila—*Phylogeny of rice genomes*.

The rice genus, *Oryza* (Poaceae), comprises 23 species and nine recognized genome types. Clarification of phylogenetic relationships of rice genomes is critical for effective utilization of the wild rice germplasm. By generating and comparing two nuclear genes (*Adh1* and *Adh2*) trees as well as a chloroplast gene (*matK*) tree of all rice species, phylogenetic relationships among the rice genomes were inferred. Origins of the allotetraploid species, which constitute more than one third of rice species diversity, were reconstructed based on the *Adh* gene phylogenies. Genome types of the maternal parents of allotetraploid species were determined based on the *matK* gene tree. The phylogenetic reconstruction largely supports the previous recognition of rice genomes. It further revealed that the EE genome species is most closely related to the DD genome



progenitor that gave rise to the CCDD genome. Three species of the CCDD genome may have originated through a single hybridization event and their maternal parent had the CC genome. The BBCC genome species had different origins and their maternal parents had either a BB or CC genome. A new genome type, HHKK, was recognized for *O. schlechteri* and *Porteresia coarctata*, suggesting that *P. coarctata* is an *Oryza* species. Phylogenetic relationship of the AA genome, which contains cultivated rice, is further investigated with additional nuclear gene markers.

- 451**      SAWYER, NEIL W.\*, DONALD H. LES, AND GREGORY J. ANDERSON. Biological Sciences, University of Wisconsin - Whitewater, Whitewater, WI, 53190—*Systematics of Deprea and Larnax (Solanaceae)*.

Problems with the classificatory status of *Deprea* and *Larnax* and their affinities with other genera have persisted. Nuclear and plastid molecular sequence data were used in cladistic analyses, both separately and combined with morphological data, to clarify the relationships between *Deprea* and *Larnax* and among these and related genera. Results provided by ITS-2 nrDNA sequence data, especially in combined analysis with morphology, served to clearly delineate *Deprea* and *Larnax*, and to support the transfer of *D. glabra* and its sister species *D. sylvarum* to *Larnax*. The trnL intron cpDNA sequence data was conserved, evolving predominately by insertion/deletions. Results from the trnL data provided evidence that *Athenaea* is the closest sister to *Withania* and that neither are closely related to *Deprea* or *Larnax* as has been suggested by morphology. Based on divergence patterns observed among the trnL sequences, *Brachistus* appears to be closely related to *Witheringia* and these genera more closely related to *Physalis* than to any other genera included in this study. These data further suggest that a *Saracha/Vassobia* clade is sister to *Deprea* and *Larnax*. Based on these findings, *Deprea* and *Larnax* will be treated as distinct. Further, *D. glabra* and *D. sylvarum* will be transferred to *Larnax*.

- 452**      SCHATZ, GEORGE E.<sup>1</sup>, CHRISTOPHER BIRKINSHAW<sup>2</sup>, PORTER P. LOWRY II<sup>1,3\*</sup>, FALY RANDRIANTAFIKA<sup>2</sup>, AND FIDISOA RATOVOSON<sup>2</sup>. <sup>1</sup>Missouri Botanical Garden, P.O. Box 299, St. Louis, MO 63166-0299; <sup>2</sup>Missouri Botanical Garden, Madagascar Research and Conservation Program, B.P. 3391, Antananarivo 101, Madagascar; <sup>3</sup>Laboratoire de Phanérogamie, Muséum National d'Histoire Naturelle, 16 rue Buffon, 75005 Paris, France—*Endemic plant families of Madagascar: integrating taxonomy and conservation*.

Madagascar's eight endemic plant families (Asteropeiaceae, Didymelaceae, Didiereaceae, Kaliphoraceae, Melanophyllaceae, Physenaceae, Sarcolaenaceae, and Sphaerosepalaceae) comprise 19 genera and ca. 100 species. These taxa are truly the "most endemic of the endemics" among the island's remarkably rich flora (ca. 12,000 spp., ~85-90% endemic) and are thus of exceptional conservation importance. An outdated taxonomic framework for most genera and insufficient knowledge of the distributions, ecology and conservation status of many species have precluded making sound recommendations for their protection. Updated revisions now provide refined species circumscriptions and documented distributions as a basis for classifying species according to modified IUCN "risk of extinction" categories. Using GIS technology, herbarium collections are mapped with respect to protected areas, bioclimatic zones, geological substrates, vegetation types, and human population density; field studies then focus on species of conservation importance (e.g., with restricted ranges or absent from protected areas) to gather data on the number of sub-populations, area of occupancy and extent of occurrence, regeneration, presence/absence in protected areas, and predicted future population trends. Analyses of 29 species in three families (Asteropeiaceae, Melanophyllaceae and Sphaerosepalaceae) show that at least 18 are currently classified as "threatened"; GAP analysis indicates that 7 of these have never been recorded in a protected area. Preliminary data on all ca. 100 species in the endemic families confirm this trend, and permit the identification of several critical areas for their conservation, many of which fall outside the current network of parks and reserves.

- 453**      SCHUETTPELZ, ERIC J.\* AND SARA B. HOOT. Department of Biological Sciences, University of Wisconsin, Milwaukee, WI 53201—*Phylogeny and biogeography of Anemone (Ranunculaceae) in the Southern Hemisphere based on molecular data*.

Although *Anemone* is found primarily in the Northern Hemisphere, several species exist in the temperate or montane regions of the Southern Hemisphere. Nuclear ITS and chloroplast *rbcL-atpB* spacer sequences have resolved the relationships between and among some Northern Hemisphere and Southern Hemisphere species. The resulting phylogeny, which is largely congruent with a tree based on chloroplast restriction site data, suggests a variety of dispersal patterns. Several species in the Southern Hemisphere conform to a pattern typical of a Gondwanan distribution: species from South Africa (*A. caffra*, *A. knowltonia*) and Tasmania (*A.*

*crassifolia*) are found in the same clade. Another Southern Hemisphere species from Kenya (*A. thomsonii*), is sister to a Mediterranean species (*A. blanda*), indicating a north-south dispersal event. More intriguing still is the close affinity between a New Zealand endemic (*A. tenuicaulis*) and species from the Northern Hemisphere (e.g. *A. dichotoma*), suggesting dispersal along an island chain with subsequent extinction of all ancestral species.

- 454** SCHULTZ, JOANNA\*, LEIGH JOHNSON, AND CAROLYN FERGUSON. Lewis-Clark State College, Division of Natural Sciences, Lewiston, ID 83501, Brigham Young University, Department of Botany and Range Science, Provo, UT 84602, Washington University, Department of Biology, St. Louis MO 63130—*Phlox idahonis* (*Polemoniaceae*): *Morphologic and molecular approaches to conservation*.

*Phlox idahonis* Wherry (Idaho Phlox) is presently a category one candidate for listing under the Endangered Species Act (ESA). This ranking indicates that *P. idahonis* is critically imperiled due to extreme rarity causing vulnerability to extinction. Previous studies of *P. idahonis* suggest the species evolved via a vicariant event following the Rocky Mountain orogeny, with the species closest relatives distributed in the eastern and Midwestern United States. However, since its first collection and subsequent description, the species has received little systematic attention. Additionally, it has been suggested the species is an ornamental *Phlox* introduced from the eastern United States in the early 1900's. The taxonomic status and evolutionary relationships of *P. idahonis* to other members of the genus *Phlox* remain elusive. *Phlox idahonis* is therefore an excellent example of a species considered for federal ranking before the taxonomic status of the taxon has been definitively established. Our studies reveal that *P. idahonis* is morphologically allied with *P. subsect. Ovatae* of the eastern and Midwestern United States. However, the species falls within the range of morphologic variability of *P. subsect. Longifoliae*, comprising species of western United States distributions. Sequencing of the internal transcribed spacer (ITS) region of rDNA reveals that *P. idahonis* is most closely related to *P. subsect. Longifoliae*, notably *P. longifolia*. These results support *P. idahonis* as an Idaho endemic and recommend federal listing under the ESA.

- 455** SCHWARZBACH, ANDREA E.\* AND LOREN H. RIESEBERG. Department of Botany, Indiana University, Bloomington, IN 47405—*Multiple origins of a diploid hybrid species*.

*Helianthus anomalus* is a well characterized diploid hybrid species occurring in several geographically isolated sand dune habitats in Utah and Arizona. The parental species *H. annuus* and *H. petiolaris* can be found in the same area but show different habitat preferences. *Helianthus annuus* prefers heavy clay soils whereas *H. petiolaris* can be found on drier sandy soils. Endemic dune species often are characterized by avoidance of long-distance dispersal. *Helianthus anomalus* displays many characters that seem to follow this rule, e.g. large achene weight and non-shattering of fruits. We conducted a phylogeographic study to reconstruct the historical biogeography of this dune species and we also examined the possibility of recurrent hybrid origin using cpDNA-CAPS and nuclear SSR markers. At least seven populations of each species and 12 individuals per population were sampled and a haplotype tree was reconstructed. Our molecular data support poor long-distance dispersal capabilities and suggest several independent origins of the hybrid species *H. anomalus* on different dune systems.

- 456** SENTERIS<sup>1</sup>, ANNE E.\*, DOUGLAS E. SOLTIS<sup>1</sup>, PAMELA S. SOLTIS<sup>1</sup>, MICHAEL ZANIS<sup>1</sup>, SANGTAE KIM<sup>2</sup>, JAMES D. THOMPSON<sup>1</sup>, AND ELIZABETH A. ZIMMER<sup>3</sup>. <sup>1</sup>School of Biological Sciences, Washington State University, Pullman, WA 99164, <sup>2</sup>Seoul National University, Seoul, Korea, <sup>3</sup>Laboratory of Molecular Systematics, Smithsonian Institution, Washington D.C. 20560—*Phylogenetic relationships among eudicots based on a combined data set of four genes: rbcL, atpB, 18S rDNA, and 26S rDNA*.

Relationships among core eudicot clades (the asterid, rosid, Caryophyllales, Santalales, Berberidopsidales, and Myrothamnaceae/Gunneraceae clades) remain one of the last major questions of deep-level phylogeny in the angiosperms. To resolve these relationships, we assembled a large data set of entire 26S ribosomal DNA sequences for approximately 250 angiosperms. The 26S rDNA is just under 3.4 kb in length and consists of conserved core areas, as well as more rapidly evolving expansion segments. Because of its length and regions with different evolutionary rates, it appears to be highly useful for resolving relationships at this level. We constructed several different data sets and analyzed them using parsimony: 1) 26S rDNA sequences were added to the existing 567-taxon matrix (Soltis et al.), 2) a smaller data set was constructed for only those angiosperms for which all four genes were available. We also used a compartmentalization approach,

reconstructing ancestral sequences for major clades. Our preliminary analyses provide additional support for the major core eudicot clades and the relationships of early-branching eudicots.

- 457** SENYO, DIANA M. AND JOHN V. FREUDENSTEIN.\* Department of Biology, Kent State University, Kent, OH 44242, Dept. of Evolution, Ecology and Organismal Biology, Ohio State University, Columbus OH 43212—*A molecular phylogeny of Corallorhiza (Orchidaceae) and related genera.*

*Corallorhiza* Gagnebin (Orchidaceae) comprises eleven species of leafless, rootless, mycotrophic orchids. Closely related genera (*Aplectrum*, *Cremastra*, and *Oreorchis*) all possess leaves and roots. Because morphological synapomorphies for *Corallorhiza* are all loss characters, additional evidence for its monophyly was sought with molecular characters; these data were also used to study relationships among the species of *Corallorhiza* and among genera of the Corallorhizinae. The ITS region of nuclear ribosomal DNA and the chloroplast gene *matK* were sequenced for multiple accessions of *Corallorhiza* (representing 8 of 11 spp.), *Aplectrum* (1 of 1 sp.), *Cremastra* (2 of 2 spp.), and *Oreorchis* (1 of 16 spp.). *Govenia* and *Coelia* were used as outgroups in the parsimony analysis. ITS data suggest that the relationships among the genera are *Aplectrum* (*Cremastra* (*Oreorchis*, *Corallorhiza*)), while *matK* differs in the positions of *Aplectrum* and *Cremastra*. Molecular data also support the monophyly of *Corallorhiza*. Relationships among the species are congruent with previous phylogenetic hypotheses based on plastid RFLP patterns. *Corallorhiza bentleyi*, a newly described West Virginian species, is sister to a small-flowered accession of *C. striata* from southern Mexico. Since previous analyses provided evidence of deletions in the plastid genome in *Corallorhiza*, we investigated this more finely by amplifying a segment of the chloroplast genome that includes the gene *psbA* in *Corallorhiza* and outgroups. The size of this segment is ca. 2150 bp in *Govenia*, 2050 bp in *Aplectrum*, 2250–2350 bp in *Cremastra*, and 2000 bp in *Oreorchis*. Within *Corallorhiza* it appears that both insertions and deletions have occurred, with sizes ranging from 2300 bp among larger flowered *C. striata* to 1750 bp in *C. bentleyi* and its sister *C. striata* accession. Other species exhibit less pronounced variation, but multiple accessions of a species often exhibit the same segment length.

- 458** SIMMONS, MARK PITKIN\* AND HELGA OCHOTERENA. L.H. Bailey Hortorium, Cornell University, Ithaca, NY 14853—*Effects of gap characters on sequence-based phylogenetic analyses.*

We assess the effects of gap characters on phylogenetic analyses and the relative levels of homoplasy of gap and base characters from a selection of published sequence-based matrices. Our results, based on structural rDNA, internal transcribed spacer (ITS) of rDNA, intron, and exon sequence-based matrices, demonstrate that: 1) gap characters can represent a considerable portion of the potential phylogenetic information in sequence-based matrices; 2) gap and base characters have similar levels of homoplasy; 3) including gap characters in sequence-based matrices often changes the tree topology and/or resolution of the most-parsimonious trees; and 4) including gap characters in sequence-based matrices often increases branch-support values. These empirical results, in combination with the theoretical bases given for using gap characters and rigorous methodologies with which to code gap characters, strongly support the use of gap characters in phylogenetic analyses that include sequence data from structural rDNA, ITS of rDNA, intron and/or exon regions. Our results suggest that longer gaps are not necessarily better phylogenetic characters than shorter gaps.

- 459** SIMMONS, MARK PITKIN\*, VINCENT SAVOLAINEN, CURTIS C. CLEVINGER, ROBERT H. ARCHER, AND JERROLD I. DAVIS. L.H. Bailey Hortorium, Cornell University, Ithaca, NY 14853; Jodrell Laboratory, Molecular Systematics Section, Royal Botanic Gardens, Kew, Richmond Surrey TW9 3DS, United Kingdom; Department of Botany, University of Texas, Austin, Texas 78713; National Herbarium, National Botanical Institute, Private Bag X101, Pretoria 0001, Republic of South Africa—*Phylogeny of the Celastraceae inferred from morphology and nuclear and plastid loci.*

Phylogenetic relationships within the Celastraceae were inferred from a simultaneous analysis of morphological characters and sequence-based characters from the 5' end of 26S nuclear ribosomal DNA, the first exon of phytochrome B, *rbcL*, and *atpB*. Two genera previously assigned to the Celastraceae, *Forsellesia* and *Goupia*, are resolved as members of the Crossosomataceae and the Goupiaceae, respectively. *Lepuropetalon* and *Parnassia* (Saxifragaceae) are resolved as members of an early-derived lineage within the Celastraceae. The Stackhousiaceae are resolved as a monophyletic group nested within the Celastraceae. *Canotia* is supported as the sister group of *Acanthothamnus* within the Celastraceae. *Maytenus* sensu lato is resolved

as a polyphyletic assemblage with *Gymnosporia* and *Tricerma* derived from different lineages. *Maytenus* sensu stricto remains an unnatural genus that needs to be re-circumscribed. *Cassine* sensu stricto, endemic to South Africa, is supported as distinct from the large, widely-distributed genus *Elaeodendron*. *Kokoona* and *Lophopetalum* are resolved as “transitional genera” between the Celastraceae sensu stricto and the Hippocrateaceae. *Plagiopteron* (Plagiopteraceae) is supported as closely related to *Hippocratea* sensu lato. The Hippocrateaceae (including *Plagiopteron* and *Lophopetalum*) are supported as a monophyletic group nested within the Celastraceae. The classifications of the Celastraceae sensu stricto and the Hippocrateaceae by Loesener and Hallé, respectively, are not supported. Arils appear to have two independent origins within the Celastraceae and have been variously modified into mucilaginous pulp, seed wings, or lost.

- 460** SIMMONS, SARAH L.\* AND JOSE L. PANERO. School of Biological Sciences, Section of Integrative Biology, University of Texas, Austin, TX 78712—*Phylogeny and biogeography of Staphyleaceae (DC.) Lindl.*

The family Staphyleaceae is a small dicotyledonous family of trees and shrubs consisting of three genera, *Staphylea*, *Euscaphis*, and *Turpinia*, totaling approximately 50-60 species and distributed across both the old and new world. No revision exists for the family or any of its component genera. The distribution of Staphyleaceae and the fact that the three genera are primarily delimited on the basis of fruit type has led to some interesting questions about the monophyly of the genera. We initiated a study to address this problem using sequence data from one nuclear (ITS 1 and 2) and three chloroplast (the *psbA-trnH*, *matK-trnK* and *trnT-trnL*) regions. All recognized species of Staphyleaceae were sampled, as well as related genera. Results from comparative studies based on sequence data revealed relationships quite different from those supported by morphology. Results from this analysis suggest that traditional generic groupings are polyphyletic and a re-evaluation of the delimitation of the genera is necessary. Data gathered to date and the biogeographic history of Staphyleaceae as constructed from molecular sequence, morphological and fossil data will be discussed.

- 461** SLOTTA, TRACEY A. B.\* AND DUNCAN M. PORTER. Biology Department, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061—*Phylogenetic analysis of Iliamna (Malvaceae) using the internal transcribed spacer (ITS).*

The eight species of *Iliamna* have a taxonomically complex history. Since its conception in 1906, the genus was not recognized for some time, several species were placed into other genera, and the status of a few species was questioned. Six species are located in western North America and two are found isolated to the east. Species in *Iliamna* are very similar morphologically with only a few characters distinguishing several as separate entities. The need for systematic study became apparent since all but one species is considered rare or endangered and the differentiation between two endangered species, *I. corei* and *I. remota*, was unclear in a previous study using RAPDs. Of the western species, four overlap in distribution (*I. crandallii*, *I. grandiflora*, *I. longisepala*, and *I. rivularis*) and their recognition as independent species has been questioned. The focus of this study was to develop a phylogeny for *Iliamna* using sequences from the Internal Transcribed Spacer Region in order to determine the biogeographical and evolutionary history. Cladistic analyses were performed and the resulting phylogeny is presented. *Iliamna* forms a well-supported clade distinct from related genera and is monophyletic. Three well-supported groups are formed. One contains representatives from the Pacific Northwest and forms the base of the genus. Another contains all of the remaining species with the third clade nested therein. This last clade contains the two eastern species, *I. corei* and *I. remota*, but there is little to support the divergence of these taxa as distinct species. Unfortunately, there is not enough variability in the ITS region to separate the western species *I. crandallii*, *I. grandiflora*, *I. longisepala*, and *I. rivularis* as distinct species either. The ITS data does provide information that brings new insight to the origination of the genus and its distribution, yet further work remains to resolve the uncertainties.

- 462** SMALL, RANDALL L. Department of Botany, The University of Tennessee, Knoxville TN 37996—*Phylogenetics of Hibiscus section Furcaria (Malvaceae) based on nuclear Adh and ITS sequences.*

*Hibiscus* section *Furcaria* (Malvaceae) includes 100+ species distributed pantropically, with major centers of diversity in Africa, Australia, and the New World. The section includes ten extant diploid ( $n = 18$ ) species, nine of which are primarily African, and one New World species (*H. costatus*). In addition to the diploid species there are several allopolyploid lineages ranging from tetraploid to decaploid. Most of the extant diploid species, and several allopolyploid species have previously been cytogenetically characterized and



placed into “genome groups” based on chromosome pairing behavior in F1 hybrids. Despite these strong foundational data, however, no phylogenetic studies have been performed in this group. Accordingly, the monophyly of the diploid genome groups and the relationships among them are currently unknown. Further, the affiliation of two of the diploid species, *H. berberidifolius* and *H. costatus*, are unclear. Finally, the origins of, and relationships within and among groups of allopolyploid species have yet to be extensively analyzed. To begin to address these questions DNA sequence data has been generated from several nuclear single-copy alcohol dehydrogenase (*Adh*) genes, as well as from the ITS region of nuclear ribosomal DNA. Preliminary results suggest that at least one of the genome groups may not be monophyletic. Further, the placement of the sole New World diploid, *H. costatus*, indicates that it is most closely related to the African G-genome diploid, *H. sudanensis*. The relative utilities of *Adh* and ITS sequences will be discussed, as will the origins and relationships of selected allopolyploid species.

- 463** SMITH, JAMES F\* AND TERRY A. BATEMAN. Department of Biology, Boise State University, Boise, ID, 83725—*Genetic differentiation of rare and common varieties of Eriogonum shockleyi (Polygonaceae) in Idaho using ISSR variability.*

Idaho populations of *Eriogonum shockleyi* are taxonomically divided into two varieties. These are *E. shockleyi* var. *packardae*, which is endemic to Idaho, and the typical variety is widespread in the western United States. Recent morphological investigations of *E. shockleyi* in Idaho have identified potentially reliable morphological characters for field identification of the subspecific taxa. This paper investigates the genetic basis for the separation of the two varieties of *E. shockleyi* using ISSR markers. Although there were some morphological differences found between the populations that correlated with the two varieties, there were no molecular markers identified in this study to distinguish between them. Morphological measurements obtained in the field indicate that although a population may have an overall average morphology that defines the variety, some individuals in nearly all populations have putative diagnostic characters that define the other variety. The morphological characters used to distinguish the two varieties are most likely the result of environmental variability and could result from differences in precipitation and soil water retention. Alternatively, high levels of outcrossing through pollen flow could be obscuring selection for morphological characters at particular sites.

- 464** SMITH, R. ALAN\*, DIANE M. FERGUSON, TODD J. BARKMAN, AND CLAUDE W. DEPAMPHILIS. Department of Biology, Vanderbilt University, Nashville, TN 37235 and Department of Biology and Institute of Molecular Evolutionary Genetics, Penn State University, University Park, PA 16802, and Department of Botany and Plant Pathology, Michigan State University, East Lansing, MI 48824—*Molecular phylogenetic evidence for the origin of Lennoaceae: A case of adelphoparasitism in the angiosperms?*

Lennoaceae are a small family of root parasites endemic to Mexico and the southwestern United States. These plants are non-photosynthetic and exhibit a reduction of morphological features which makes systematic placement difficult. Earlier studies of Lennoaceae based on floral and pollen morphology have suggested relationships with Boraginaceae, “Hydrophyllaceae,” or Verbenaceae. Molecular evidence is presented from all three genomic compartments to test these hypotheses. The plastid gene *rps2*, the mitochondrial genes *cox1* and *atpA* and the nuclear ITS region were sequenced and subjected to phylogenetic analysis. Preliminary results indicate that a monophyletic Lennoaceae is most closely related to Ehretioideae, a subfamily of Boraginaceae. This subfamily contains host plants of Lennoaceae, indicating a possible case of adelphoparasitism, the first such association suspected among the angiosperms. Further investigation should resolve this question and determine the closest extant relative of Lennoaceae among this group.

- 465** SPJUT, RICHARD W. World Botanical Associates, P.O. Box 2829, Laurel, MD 20709-0829—*A phytogeographical analysis and classification of leaf characteristics of Taxus (Taxaceae).*

A phytogeographical analysis of leaf character data will be presented to show that *Taxus* is least variable in North America and NW Himalayas, and most diverse in SW China. Characters include the number of cells across a marginal zone without papillae, and number of stomata rows/band. Leaf characteristics will be discussed for three species groups typified by *T. baccata*, *T. wallichiana*, and *T. sumatrana*, and their subdivisions. Most European specimens have a *baccata* type (8-10 stomata rows/band bordered by a marginal zone of 4-7 smooth cells followed by 7-22 papillose cells), and less often a *canadensis* type (4-9 stomata rows/band bordered by 8-24 smooth cells and 0-12 papillose cells); the latter includes a *cuspidata* subtype that differs by papillose cell walls. Specimens from E Asia have the *canadensis* and *cuspidata* types, but often with more stomata, which range from 7-13(-16) rows/band. Northwest Himalayan specimens have the

*baccata* type with 5-9 stomata rows/band, and show less variation in leaf length and phyllotaxy. All three types occur in the Caucasus Mountains, but most specimens there appear similar to those in Europe. From the E Himalayas to SW China, and in North America, occurs the *Wallichiana* Group. Its leaves usually have a uniformly papillose undersurface with a relatively narrow marginal border of smooth cells, 0-7 (-10) cells across. The epidermal cells are distinctly angular in transverse sections, and stomata show geographical differences, 7-21 rows/band in Asia, and 4-11 rows/band in North America. A *Chinensis* Subgroup, mostly in central China, Indonesia and Philippines, differs by rounded epidermal cells (x-sect.) that are sometimes less papillose on the ventral midrib. The *Sumatrana* Group, which is common in SE China, especially below 2,000 m, has a broad margin of cells bordering stomata bands, from 8-36 cells across, and often a truncate midrib.

- 466** SPJUT, RICHARD W. World Botanical Associates, P. O. Box 2829, Laurel, MD 20709-0829—*The morphological relationships of Taxus canadensis (Taxaceae) in North America and Eurasia.*

*Taxus canadensis* has been generally recognized as a low shrub in NE North America. Its leaf papillae are confined to stomata bands, sometimes seen only along stomatal ridges. Stomata are mostly in 5-7 (-9) irregular rows/band with the higher counts from coastal and northern regions. These characteristics, and the elliptically shaped epidermal cells in leaf x-sections, indicate a closer affinity to yews of Europe than to other yews of North America. Three varieties are differentiated by arrangement of branchlets and leaves. Examples will be shown from different geographic regions. The typical variety, a low shrub that spreads by layering, has equally divided branchlets and two-ranked leaves. Similar specimens have been collected from shrubs and trees in Morocco, Madeira, France, Sweden, Estonia, Caucasus Mountains, and are evident in fossils described from Tertiary deposits in Europe. Their leaves differ slightly by more prominent papillae that often extend into the marginal zone; however, a fossil described by Z. Kvacek from a Miocene deposit in Bohemia is more similar to American than European plants. Variety *minor*, occasionally collected in North America and Madeira, differs by unequally divided branchlets with erect leaves. A third variety, based on *T. baccata* var. *adpressa* (= *T. tardiva*), is generally known in horticulture; however, wild forms are evident in specimens from Iowa (U.S.A.), Norway, Sweden, Slovenia, and a fossil from a Pliocene deposit in Bohemia. Other related plants include tree forms in Europe, Vietnam and Sichuan, and shrub forms in England, SE Russia, and Japan. Although shrub and tree forms of *Taxus* are often parapatric in E Asia and W North America, it would seem that the shrub form in E North America has survived more by vegetative reproduction, while the tree form has largely vanished.

- 467** STANFORD, ALICE M.\* AND CLIFFORD R. PARKS. Division of Science and Mathematics, University of the Virgin Islands, St. Thomas, VI 00802, and CB#3280, Biology, University of North Carolina, Chapel Hill, NC 27599-3280—*Phylogeny of Castanea (Fagaceae) based matK sequence data.*

The current range of *Castanea* Mill., a Tertiary disjunct genus with about seven species, includes eastern and western Asia, Europe, and eastern North America. The similarity between the forests of eastern Asia and eastern North America has been of interest to botanists since the time of Linnaeus. The disjunct taxa involved are hypothesized to have undergone restriction of a formerly continuous range during the Tertiary period, nearly 15 million years ago. At that time a global cooling and drying trend forced temperate forests to migrate southward. We sequenced cpDNA region matK and its surrounding spacers for all seven *Castanea* species, and the sequence data were used to construct a phylogenetic hypothesis for the genus. Percent sequence divergence between species of *Castanea* varies from 1.6 to 4.0%. Phylogenies generated by this work indicate that the previously proposed intrageneric classification systems within *Castanea* do not reflect the evolutionary relationships of the constituent species. Mapping the distribution of these plants onto the phylogenies generated by this study supports a complicated biogeographic history for this disjunct genus. The distribution of these plants has been thought to be the result of a simple range restriction, but our data support a more complicated history of repeated migrations, resulting from a combination of geographic and climatic factors.

- 468** STEELE, K. P.\*, L. YANG, M. SABIR, AND M. F. WOJCIECHOWSKI. Department of Biology, California State University, Hayward, CA 94545, and Section of Evolution and Ecology, University of California, Davis, CA 95616—*Phylogenetic relationships of the tribes Trifolieae and Vicieae (Fabaceae) using sequences of Mendel's stem length gene, Le.*

The nuclear gene *Le*, the original stem length gene studied by Gregor Mendel, encodes 3B-hydroxylase, a key enzyme in the gibberellic acid biosynthetic pathway. Nucleotide sequences of this single copy nuclear

gene were used for phylogenetic analyses of representatives of genera traditionally included in the Trifolieae and Viciae, with representatives of tribes Cicereae and Galegeae used as outgroups. This gene consists of two exons of approximately 1.1 Kb with a large intron of about 544 bp. Exon sequences are sufficiently conserved to be useful for analyses of genera within these two tribes. Intron sequences are useful only for analyses within genera. Consistent with our earlier results from analyses of *matK* sequences for these taxa, *Medicago*, as defined by floral characters associated with an explosive pollination syndrome, forms a well-supported monophyletic group distinct from that formed by *Melilotus* which is nested within *Trigonella*. *Trifolium* is basal to the remainder of Trifolieae (excepting *Parochetus*). Within Viciae *Vicia* is basal to *Pisum* and *Lathyrus*. Phylogenetic analyses of these sequence data provide a framework to consider hypotheses about the evolution of trifoliate leaves and floral and fruit characteristics in these clades.

- 469** STEELE, K.P.\*, E. TIZON, R.C. EVANS, C.S. CAMPBELL, AND M.F. WOJCIECHOWSKI. Department of Biology, California State University, Hayward, Department of Biological Sciences, University of Maine, Orono, and Section of Evolution and Ecology, University of California, Davis—*Sister group relationships of Fabaceae and Rosaceae: phylogenetic relationships of Eurosids I.*

Sister group relationships of the large, important flowering plant families Fabaceae and Rosaceae are uncertain. Recent studies (e.g. Angiosperm Phylogeny Group, Ann. Missouri Bot. Gard. 85:531-553; Soltis et al., 1999, Nature 402:402-404) find strong support for including Fabales and Rosales within the Eurosoid I group, which also includes Cucurbitales and Fagales. Fabales consists of four families, with the Polygalaceae, Surianaceae, Quillajaceae each suggested as the sister group to the Fabaceae. Rosaceae are currently seen as the sister group to the remainder of the Rosales. Nucleotide sequence data from the chloroplast *matK* gene are used for phylogenetic analyses of representatives of most families of Eurosoid I with the primary aim of resolving the sister group relationships of Fabaceae and Rosaceae. Preliminary results indicate strong support for Eurosoid I and less support for relationships among its four orders. *matK* sequence data do, however, appear to provide sufficient characters to help resolve relationships within Rosales and Fabales.

- 470** STEFANOVIC, SASA\* AND RICHARD G. OLMSTEAD. Department of Botany, University of Washington, Box 355325, Seattle, WA 98195, USA—*Molecular systematics of Convolvulaceae inferred from cpDNA sequences.*

Convolvulaceae are a large family, comprising approximately 50-60 genera with some 1600-1700 species, the members of which present a rich diversity of morphological characteristics and ecological habitats. Previous efforts to systematize this diversity without a cladistic phylogenetic framework have disagreed on the circumscription of the family as well as tribal composition and relationship. In order to circumscribe the family and assess the relationships among its major lineages, a broad data set was constructed, containing representatives of all ten recognized tribes of Convolvulaceae plus representatives of putatively related families within Asteridae. This is done by using four chloroplast regions: *rbcL*, *atpB*, *psbE-J* operon, and *trnL-trnF* intron/spacer. The results indicate that Convolvulaceae are sister to Solanaceae, with 100% bootstrap support for each family and the clade comprising both families. Two of the three groups that have been proposed previously as segregate families, *Cuscuta* and *Dichondreae*, are nested within the Convolvulaceae in this analysis, and the third, *Humbertia*, is the sister to all other members of the family. The exact position of *Cuscuta* could not be ascertained, but some alternatives were rejected with confidence. The study identified several distinct monophyletic groups, some of which correspond to earlier ideas. Close relationships of tribes Hildebrandtieae with Cresseae and Ipomoeae with Argyreieae (forming Echinoconieae) were confirmed. The polyphyly of Poraneae and Erycibeae is first reported in this study.

- 471** STEHLIK, IVANA\*, JOHANN JAKOB SCHNELLER, AND KONRAD BACHMANN. Institute of Systematic Botany, University of Zurich, Zollikerstrasse 107, CH-8008 Zurich, Switzerland—*Molecular evidence for nunatak survival of the high-alpine plant *Eritrichium nanum* within the Central Alps.*

Two main possibilities of glacial survival of the mountain flora of the European Alps during the Quaternary have been proposed: the tabula rasa and the nunatak hypotheses. *Eritrichium nanum* (L.) Gaudin (Boraginaceae) is a perennial cushion plant occurring at high elevations of the Central Alps and having a preference for extreme habitats. It belongs to a group of high-alpine plants, for which in-situ glacial survival on nunataks has been suggested. By investigating 20 populations of *E. nanum* from potential nunatak and refugial regions using AFLPs, substantial genetic differences between populations from the Central Alps and populations from peripheral refugia in the Southern Alps were detected, excluding the latter as potential sources for the

recolonization of the Central Alps after glaciation. Genetic variation was hierarchically structured (AMOVA), and three genetically separated regions could be identified in the Central Alps. Two of these, the Penninic and Rhaetic Alps, correspond to narrow nunatak regions formerly proposed in the biogeographic literature. Populations from the Lepontic Alps formed a third, separate genetic group. Genetic correlation (Mantel test) was highest within populations, showing a modest decline among populations within specific nunatak regions and a negative correlation outside the radius of the 'genetic influence' of specific nunatak regions. The present demonstration of in-situ glacial survival in *E. nanum* could be exemplary for the Quaternary history of other alpine plants, especially those occurring at high elevations and in similar habitats as *E. nanum*.

- 472** STRUWE, LENA\* AND VICTOR A. ALBERT. Cullman Program, The New York Botanical Garden, Bronx, NY 10458, Botanical Institute, Copenhagen University, Gothersgade 140, DK-1123 Copenhagen K, DENMARK—*Mycotrophic, non-chlorophyllous Voyria placed in Gentianaceae*.

The genus *Voyria* (Gentianaceae) consists of 19 tropical species of small, non-chlorophyllous and herbaceous mycotrophs. The genus shows extensive variation in pollen morphology, stem anatomy, and flower and seed morphology. Previous sequencing of the chloroplast derived *trnL* intron for over 100 gentians and *Voyria* failed to place the genus inside the family or even the order Gentianales due to extreme sequence divergence. Several new ribosomal 18S sequences show *Voyria* to be placed among the basal clades of the Gentianaceae. Nuclear ITS (internal transcribed spacer) sequences have also been produced and will be analyzed together with an earlier published morphological data set including all species in the genus. The ribosomal data does not appear particularly divergent relative to other gentians, whereas the ITS sequences differ markedly among presumably closely related taxa. Evolution of complete or partial mycotrophy has evolved at least three times independently in the Gentianaceae, and this will be discussed in a phylogenetic context.

- 473** STRUWE, LENA\* AND VICTOR A. ALBERT. Cullman Program, The New York Botanical Garden, Bronx, NY 10458, Botanical Institute, Copenhagen University, Gothersgade 140, DK-1123 Copenhagen K, DENMARK—*Supermerous corollas, fleshy fruits, and pantropical biogeography in Anthocleista, Fagraea, and Potalia (Gentianaceae)*.

The woody and fleshy-fruited genera *Anthocleista*, *Fagraea*, and *Potalia* (Gentianaceae) are tree- or shrub-like tropical gentians previously associated with Loganiaceae. Molecular data from *rbcL*, *matK*, and the *trnL* intron (along with morphological and phytochemical evidence) has shown that this group is deeply nested inside Gentianaceae. Specific relationships of the group are to lineages of herbaceous and dry-fruited genera that are more basally placed, implying secondary derivations of tree-like habit and fleshy fruits in the family. *Anthocleista* and *Potalia* also diverge from the usual gentian floral bauplan in having supermerous corollas and staminal parts (being 8-16-merous). SEM studies have revealed multiplication of corolline and staminal primordia based on an initially 4-merous primordia area. *Anthocleista*, *Fagraea*, and *Potalia* also appear to lack postgenital fusion of carpels, which is typical for other gentians. The congenitally fused carpels in these genera may have predisposed evolution of their fleshy, indehiscent fruits. Preliminary results from nuclear ITS (internal transcribed spacer) sequences show the three genera to be monophyletic, with African-Malagasy *Anthocleista* sister to American *Potalia*, and with Asian-Australian-Pacific *Fagraea* as the sister to this pair. This is in contradiction to an earlier morphology-based cladistic study, which showed a paraphyletic *Fagraea*. Morphology-based species level results in *Potalia* show white-sand, narrowly endemic species from central Amazonia to be most basally placed, and species from Central America, Guianas, and non-white-sand Amazonian areas in more derived positions. This supports the hypothesis that lowland white-sand areas in the Neotropics may be relictual areas that harbor many ancestral and phylogenetically divergent plant lineages.

- 474** SUN, FENG-JIE\*, STEPHEN R. DOWNIE, AND RONALD L. HARTMAN. Department of Plant Biology, University of Illinois, Urbana, IL 61801 and Department of Botany, University of Wyoming, Laramie, WY 82071—*A phylogenetic study of Cymopterus and related genera*.

Since the early 19<sup>th</sup> century, there has been considerable confusion concerning the proper delimitation of the genus *Cymopterus* (Apiaceae; Umbelliferae) and its relationship to putatively allied genera *Aletes*, *Harbouria*, *Lomatium*, *Musineon*, *Neoparrya*, *Orogenia*, *Pteryxia*, and *Shoshonea*. Regarding *Cymopterus*, extremes in treatment range from the recognition of many generically distinct elements (such as, *Pseudocymopterus*, *Podistera*, *Oreoxis*, *Pteryxia*, and *Glehnia*) to one large genus with multiple subgenera and sections. Currently, some 35 species are recognized within *Cymopterus*. These plants are largely endemic to western North America. They are all herbaceous perennials, frequently caespitose and xerophytic in habit, and usually occur in elevated habitats. Our major goal is to produce an explicit phylogenetic hypothesis for *Cymopterus* using



anatomical, morphological, and molecular evidence. To date, we have obtained sequence data from the nuclear rDNA ITS region as well as the chloroplast *rps16* intron, *trnL* intron, and the *trnF-trnL-trnT* intergenic spacer regions. Anatomical and morphological data have also been procured, with emphasis placed on the taxonomically problematic species *Pseudocymopterus montanus*, *Pteryxia terebinthina*, and *Cymopterus acaulis*. While our results are preliminary, the molecular data suggest that *Aletes*, *Cymopterus*, *Lomatium*, *Musineon*, and *Oreoxis* are each not monophyletic, as currently circumscribed. The analyses of morphological data suggest that *Pseudocymopterus montanus* cannot be divided into infraspecific taxa. Moreover, the separation of *Pteryxia terebinthina* varieties *albiflora* and *californica*, and the separation of *Cymopterus acaulis* varieties *acaulis* and *fendleri*, are not supported.

- 475** SYTSMA, KENNETH J., JEFFREY MORAWETZ\*, J. CHRIS PIRES, AND CLIFFORD W. MORDEN. Department of Botany, University of Wisconsin, Madison, WI 53706; Department of Botany, University of Hawaii-Manoa, HI 96822—*Phylogeny of the Urticales based on three molecular data sets, with emphasis on relationships within Urticaceae.*

The traditional Urticales (Ulmaceae, Celtidaceae, Cannabaceae, Moraceae, Urticaceae, and Cecropiaceae) is one of the more controversial orders in terms of family circumscriptions and both inter- and intra-familial phylogenetic relationships. Recent molecular evidence has clarified its position as a monophyletic assemblage within a now expanded Rosales, with close relationships to an unresolved group including Barbeyaceae, Dirachmaceae, Rhamnaceae, and Elaeagnaceae. Although the Ulmaceae has now been demonstrated to be sister to the rest of the urticalean lineage with both morphological and molecular data, the circumscription and relationships of the other families has remained unclear and controversial. The majority of morphological analyses have concluded either that (1) Celtidaceae, Cecropiaceae, Moraceae, and Urticaceae should be combined as one family, or (2) at least Moraceae and Urticaceae should be merged; the placement of Cannabaceae being largely unknown. Analyses now based on *rbcL*, *ndhF*, and *trnT-trnL* spacer sequences strongly support monophyly of each of the families Moraceae and Urticaceae (with Cecropiaceae) and the polyphyletic nature of Cecropiaceae with Poikilospermum at least imbedded within Urticaceae. There is both strong sequence and indel support for the placement of Cannabaceae within Celtidaceae. The different molecular data are congruent in indicating polyphyly for the tribe Moreae and the isolated position of Maclura within Moraceae, and that a number of tribes within Urticaceae are either paraphyletic or polyphyletic. Some of this discrepancy is due to the unusual placements of some Hawaiian Urticaceae, most notably Touchardia. The robust molecular results for major portions of the phylogenetic history of the urticalean clade permit reinterpretation of morphological, anatomical, and ecological features in the group as well as suggest changes in classification and nomenclature.

- 476** SÁNCHEZ-BARACALDO, PATRICIA\* AND ROBERT P. GURALNICK. Department of Integrative Biology, University of California, Berkeley, CA 94720—*Multifaceted Heterochrony: Evolution, development, and ecological covariates of leaf morphology in Neotropical ferns.*

Developmental shifts are the proximate causes of morphological evolution, and these shifts themselves have been theorized to be driven by ecological factors. Here we present a case study showing the interplay between evolution, development, and environment using Andean Neotropical ferns. Our focus is a comparison of the shape and number of pinnae along a rachis for the *Eriosorus-Jamesonia* complex with a known and well corroborated phylogeny. Species of “*eriosorus*”, a basal paraphyletic group, are characteristically found at lower elevations in sheltered, shady, and xeric environments. “*Jamesonia*”, a polyphyletic collection of derived clades, is found at high elevation environments ranging from open, humid, xeric, exposed to grassy habitats, and has been derived independently at least three times. “*Jamesonia*” pinnae have a highly modified morphology compared to “*eriosorus*”. “*Eriosorus*” has relatively few highly plicate leaves, and this “plicate-ness” increases along the rachis from younger to older leaves. “*Jamesonia*” has many simple, almost oval-shaped leaves that do not appear to change shape along the rachis. We empirically document these heuristic patterns using two methods: 1) eigenshape analysis, in order to construct ontogenetic shape trajectories for the pinnae, and 2) Chi-square analysis to test whether pinnae number has increased or decreased through phylogeny. Our preliminary results suggest a trend of truncation of the shape trajectories, such that the older pinnae of “*jamesonia*” resemble the youngest pinnae of “*eriosorus*”. Furthermore, based on our count data, there has been an opposite, meristic trend towards greater number of leaves in “*jamesonia*”. Thus shape trajectories have been truncated but leaf number increased possibly demonstrating pedomorphosis via neotony. An obviously correlated and perhaps causal factor is the environment. Although “*jamesonia*” is polyphyletic, in each case a similar morphology has evolved, perhaps in response to high levels of insolation, strong winds, and temperatures ranging from 12 °C to -2 °C.

- 477** SÁNCHEZ-KEN, JORGE GABRIEL.\* AND LYNN G. CLARK. Department of Botany, Iowa State University, 353 Bessey Hall, Ames, IA, 50011-1020—*Overview of the subfamily Centothecoideae (Poaceae)*.

The subfamily Centothecoideae s.s., distributed worldwide in the tropical and subtemperate regions, comprises 10 genera (Bromuniola, Calderonella, Centotheca, Chasmanthium, Chevalierella, Lophatherum, Megastachya, Orthoclada, Pohlidium and Zeugites). It was defined originally by embryo formula (P+PP and F+PP), tessellation of the leaf-blades, pseudopetiolate leaves, small herbaceous habit, and forest habitat, as well as by the differentiation of the mesophyll into palisade and spongy tissue, but its cohesiveness was questionable and its relationships were uncertain. In the last two decades, certain other genera (Cyperochloa, Danthoniopsis, Gouldochloa, Gynierium, Spartochloa, and Thysanolaena) have been segregated from other subfamilies and placed in or suggested as members of the centothecoid clade; a sister relationship between the centothecoids in the broad sense (including these genera) and the Panicoideae also has been inferred. These findings were based mainly on molecular data and some morphological data also, although at present there is no morphological synapomorphy that supports the centothecoids as monophyletic. Consequently, the position of these genera with respect to the centothecoids, and the circumscription of the centothecoid clade itself, remain uncertain. We present a preliminary morphological and anatomical comparison of the Centothecoideae s.s. and the putatively related genera, as well as a preliminary phylogenetic analysis using molecular and morphological data. According to the morphoanatomical data, leaf anatomy in cross section, the venation of the leaf blades, and the arrangement of the unisexual florets in the spikelets are likely to be the most informative features.

- 478** TANK, DAVID C.\* AND TAO SANG. Department of Botany and Plant Pathology, Michigan State University, East Lansing, MI 48824—*The glycerol-3-phosphate acyltransferase gene in Paeonia (Paeoniaceae): molecular evolution and phylogenetic utility*.

The nuclear encoded glycerol-3-phosphate acyltransferase gene (GPAT) has been found to be single copy in a number of angiosperm families. In this study we investigated the phylogenetic utility of the GPAT gene in determining the interspecific relationships of the angiosperm genus *Paeonia*. An approximately 2.3 kb fragment of the GPAT gene was amplified, cloned, and sequenced from all diploid and selected tetraploid species of *Paeonia*. The GPAT gene may exist as a single copy in some species of *Paeonia*, but constitutes a small gene family in others. Two distinct genomic clones of *P. anomala* containing the GPAT gene have been characterized and suggest that the gene underwent an ancient duplication followed by the formation of a pseudogene in one copy. Blast sequence similarity analysis suggests that the GPAT pseudogene may contain a large retrotransposon-like insertion that could have triggered the pseudogene formation. The rate of evolution of the GPAT gene was determined to be greater than that of the nuclear ITS region in *Paeonia*, demonstrating the potential of the GPAT gene to be used in resolving low-level taxonomic relationships of angiosperms. When compared to existing gene phylogenies, such as the cpDNA *matK* gene, nuclear ITS region and the alcohol dehydrogenase genes, the GPAT gene phylogeny yielded additional insights into the relationships within *Paeonia*.

- 479** TREMETSBERGER, KARIN, TOD STUESSY\*, ROSE SAMUEL, AND CARLOS BAEZA. Department of Higher Plant Systematics and Evolution, Institute of Botany, University of Vienna, Vienna A-1030, Austria; Departamento de Botanica, Universidad de Concepcion, Concepcion, Chile—*High levels of genetic variation and multiple origins for newly established populations of Hypochaeris tenuifolia (Asteraceae) on Volcan Lonquimay, Chile*.

As with newly formed oceanic islands, new volcanic areas on continents also provide an opportunity to examine populational phenomena during arrival and early establishment of plant species. Of special interest is the degree of genetic variance in these early colonizers, as they contain genetic resources that fuel, in part, future populational differentiation and eventual speciation. It is predicted that new populations in open ash fields should (1) result from limited numbers of propagules from geographically adjacent areas, and (2) contain reduced genetic variation in comparison with source populations. *Hypochaeris tenuifolia* (Asteraceae), confined to high elevation volcanic peaks (1750-2400m) along the southern Andes between 35-39 degrees S, was selected to test these predictions. A new volcanic cone, La Navidad, erupted on the flank of Volcan Lonquimay, Chile, on 25 Dec 1988, spreading lava and ash along well documented routes. During 1999 and 2000, we analyzed using AFLP markers 11 populations (20-30 plants in each) of *H. tenuifolia* in two transects on Volcan Lonquimay, including newly ashed slopes and undisturbed *Araucaria* forests, and compared these data with those from 30 additional populations throughout the range of the species. The results show a surprisingly high level of genetic variance in pioneer populations as well as connections to many different

source areas. It appears that biological attributes of species, in this case dispersal capability, can be more important than biogeographic parsimony in defining genetic characteristics of colonizing species in island-like habitats.

- 480** TRUSTY, JENNIFER L.\*, DAVID J. BOGLER, ARNOLDO SANTOS-GUERRA, RICHARD G. OLMSTEAD, AND JAVIER FRANCISCO-ORTEGA. Department of Biology, Florida International University, University Park, Miami, FL 33199, and, Fairchild Tropical Garden Research Center, 11935 Old Cutler Road, Miami, FL 33156—*Tracing the origin of the Macaronesian endemic genus *Bystropogon* (Lamiaceae)*.

Attempts to trace the origin of organisms on islands is frustrated by the major morphological changes that often occur following long distance dispersal and speciation. The Canary Islands exemplify how island environments influence speciation. The unique flora of the Canary Islands includes approximately 600 endemic species with at least 23 endemic genera that represent 40% of the native plant species of these islands. A molecular phylogenetic study based on chloroplast and nuclear DNA regions suggest that the ancestor of the Macaronesian endemic genus *Bystropogon* (Lamiaceae) arrived from the New World. These results provide further molecular evidence for a floristic link between the Macaronesian Islands and the New World previously shown in *Sedum* (Crassulaceae) and *Pericallis* (Asteraceae). Our results also provide an initial phylogeny within the Mentheae tribe and will help to resolve the intergeneric relationships and evolutionary history of this tribe.

- 481** UHINK, CHRISTIAN H. Botanisches Institut und Botanischer Garten, Christian-Albrechts-Universität, D-24098 Kiel, Germany—*Molecular phylogeny and evolutionary trends in Plumbaginaceae JUSS.*

The Plumbaginaceae are commonly divided into two subfamilies, the Staticioideae and the Plumbaginoideae. These groups are sometimes treated as two separate families. Recent molecular studies confirm this assumption. Based on this molecular phylogeny more genera will be analyzed. In addition other molecular marker systems will be included for further investigations within the family. With the background of the molecular data sets the families variety in morphological and physiological characters, especially in adaptation to the mostly dry or salt-influenced habitats, can be investigated in an evolutionary context. Plumbaginaceae are nearly worldwide distributed. Molecular data can also be helpful to explain their biogeography.

- 482** VANDEN HEUVEL, BRIAN DAVID\* AND C. RANDAL LINDER. Integrative Biology Section, The University of Texas at Austin, Austin, TX 78712—*A Molecular Phylogeny for *Cercocarpus* H.B.K. (Rosaceae) using the External Transcribed Spacer of the Nuclear Ribosomal Repeat.*

*Cercocarpus* H.B.K. (Rosaceae) has undergone three revisions, each varying widely in the ranks assigned to taxa and the number of species. Discrepancy among revisions is due primarily to a continuum of morphological variation within and between taxa. We have developed a molecular phylogeny to address this discrepancy. The ITS region of the nuclear ribosomal repeat contained insufficient phylogenetically informative sequence variation, so we developed the external transcribed spacer (ETS) of the nuclear ribosomal repeat. The ETS has more informative variation than the ITS and a unique central region which has shown to be an important marker within this group. The correct taxonomic affiliation of *C. traskiae*, California's rarest tree, will also be addressed.

- 483** VAZQUEZ, M. LUCIA\*, JEFF J. DOYLE, AND KEVIN C. NIXON. L. H. Bailey Hortorium, 462 Mann Library, Cornell University, Ithaca NY 14853—*Paralogous ITS loci in Mexican red oak species (*Quercus* section *Lobatae*) and their implications in phylogeny reconstruction.*

In contrast to European and US oak species, there are no molecular studies addressing the relationships of the diverse Mexican taxa. In this study we use the ITS-1 and -2 regions to study the phylogeny of red oaks (*Quercus* sect. *Lobatae*), focusing on Mexican and selected North American species. Previous studies addressing the phylogeny of oak species using ITS have reported results from only one putatively orthologous ITS locus. Utilizing additional species, we found that PCR amplification of the ITS-1 and -2 regions resulted in products of several sizes for some Mexican oak species. Two of these products have been characterized: one of them is about 600 bp and the other is approximately 500 bp long. A comparison of our sequences with those from previous studies indicates that most of the published sequences are most similar to our 600 bp copy. Analyses of our sequences from the 500 bp copy show regions of similarity to the 600 bp copy,

however, there is an average divergence of 15% between those copies. Since multiple ITS loci have been reported for some angiosperm taxa and unexpected phylogenies have been obtained in some previous oak studies, the possibility of finding other ITS paralogues in *Quercus* should not be ruled out.

- 484** WALLACE, LISA E. Department of Evolution, Ecology, and Organismal Biology, Ohio State University, Columbus, OH 43210—*The significance of population size on reproductive success and genetic variability in the Eastern Prairie White Fringed Orchid*, *Platanthera leucophaea*.

*Platanthera leucophaea* (Orchidaceae) is a federally threatened species that is adapted to mesic prairies east of the Mississippi River. Populations have been declining rapidly due to the encroachment of competing weedy species. Studies were initiated to examine differences in reproductive success and genetic variability in populations of variable size. Seed viability was assessed among selfed, hand-outcrossed, and naturally pollinated flowers in a large population (greater than 5,000 flowering individuals) and a smaller more typical population (fewer than 75 flowering individuals). In the large population, seeds and capsules produced from selfing weighed nearly half as much as those resulting from hand-outcrossing or natural pollinations. Additionally, selfed capsules contained relatively few healthy seeds while hand-outcrossed and naturally pollinated capsules had significantly higher levels of viable embryos. In contrast, seed viability in the smaller population did not differ significantly among any of the pollination treatments. These preliminary data suggest that the large population is adapted to outcrossing and experiences inbreeding depression as a result of selfing while the small population has a history of inbreeding. Theory predicts that inbred populations should contain less genetic variability than outcrossed populations. However, populations of varying size were found to have comparable levels of variability at allozyme and RAPD loci. Additionally, most of the variation resides within populations, suggesting high levels of interpopulation gene flow or recent divergence from a common ancestral population. Potential implications for the management of *P. leucophaea* populations are considered.

- 485** WALLACE, ROBERT S. Department of Botany, Iowa State University, Ames, IA 50011-1020—*Taxonomic placement of morphologically anomalous genera of Cactaceae subfamily Cactoideae*.

Several genera within the subfamily Cactoideae of the Cactaceae have historically been taxonomically problematic, due to the difficulty of confidently classifying them within the tribal groups of Buxbaum and the subsequent recent variations on his classification for the subfamily. Parallelisms, character loss, and nebulously-defined tribal boundaries have contributed to this confusion, thereby rendering modern intergeneric classification schemes less robust. Forthcoming taxonomic revisions of the cactus family require the assignment of these unusual genera within a defined tribal classification. Specifically, these studies have been conducted to evaluate the evolutionary affinities of the genera *Deamia* Britton and Rose, *Eulychnia* Philippi, *Harrisia* Britton, *Stetsonia* Britton and Rose, and *Uebelmannia* Buining among others. To provide additional data to assist with tribal placement of these problematic genera, variation in several molecular markers from the plastid genome were used. Maximum parsimony estimates of phylogenetic relationships for representatives of all major tribal lineages within the subfamily Cactoideae were determined and used to elucidate the position of the problematic genera. Phylogenies inferred from these new data are used in concert with morphological characters to determine the closest evolutionary relationships for these genera. These studies will ultimately suggest whether new morphological definitions of evolutionarily-related generic groups need to be established to reflect a revised tribal classification.

- 486** WALLANDER, EVA. Botanical Institute, Göteborg University, P. O. Box 461, SE 405 30 Göteborg, Sweden—*Phylogenetic relationships among the Ashes of the world*, *Fraxinus* (Oleaceae).

The genus *Fraxinus*, the Ashes, in Oleaceae, consists of about 50 tree and shrub species. The most recent classification of the genus by Lingelsheim (1920) identified two sections: Ornus (subsections Euornus and Ornaster), and Fraxinaster (subsections Dipetalae, Pauciflorae, Sciadanthus, Melioides, and Bumelioides). Ornus is characterized by terminal inflorescences, insect pollinated Euornus have showy petalous flowers and wind pollinated Ornaster are apetalous. The species of section Fraxinaster are wind pollinated and characterized by apetalous flowers in lateral inflorescences (except *F. dipetala* that has two petals). The two main subsections Melioides and Bumelioides differ in that both calyx and corolla are wanting in Bumelioides. In an attempt to establish phylogenetic relationships among all species of *Fraxinus*, DNA sequences from the nuclear ITS region in 94 specimens, representing 43 of the 49 presently recognized taxa of the genus, were analyzed by cladistic methods. The result shows that three major and two smaller clades can be distinguished, roughly corresponding to Lingelsheim's subsections, but relationships between them depend



heavily on the choice of outgroup: (1) Old World subsection Bumelioides, including North American *F. nigra* as sister to *F. mandshurica* and *F. platypoda*. *F. xanthoxyloides*, in monotypic *Sciadhanthus*, is sister to Bumelioides. (2) New World subsection Melioides and *F. cuspidata*. (3) Xerophytic New World Pauciflorae. (4) *F. dipetala*, in monotypic Dipetalae, is joined by *F. anomala* and *F. quadrangulata* in a strongly supported clade, sister group to the rest of *Fraxinus* in some of the trees. (5) Section Ornus is clearly monophyletic, but its subsection Euornus is paraphyletic because subsection Ornaster is derived from it. Section Fraxinaster, as circumscribed by Lingelsheim, is paraphyletic no matter how the cladograms are rooted. Thus, in *Fraxinus*, wind pollination appears to be ancestral and insect pollinated species are derived, and within the insect pollinated group, adaptations to wind pollination have evolved again.

- 487**      WANG, XIAO-QUAN, DAVID C. TANK\*, AND TAO SANG. Laboratory of Sytematic and Evolutionary Botany, Institute of Botany, the Chinese Academy of Sciences, Beijing 100093, China, , Department of Botany and Plant Pathology, Michigan State University, East Lansing, MI 48824—*Phylogeny and divergence times in Pinaceae: evidence from three genomes.*

In Pinaceae, the chloroplast, mitochondrial, and nuclear genomes are paternally, maternally, and biparentally inherited, respectively. Examining congruence and incongruence of gene phylogenies among the three genomes should provide insights into phylogenetic relationships within the family. Here we studied intergeneric relationships of Pinaceae using sequences of the chloroplast *matK* gene, the mitochondrial gene encoding subunit 5 of NADH dehydrogenase (*nad5*), and the low-copy nuclear gene encoding 4-coumarate : coenzyme A ligase (4CL). The 4CL gene may exist as a single copy in some species of Pinaceae, but constitutes a small gene family with two or three members in others. Duplication and deletion of the 4CL gene occurred at a tempo such that paralogous loci are maintained within but not between genera. Exons of the 4CL gene have diverged approximately twice as fast as the *matK* gene and five times more rapidly than the *nad5* gene. The partition-homogeneity test indicates that the three data sets are homogeneous. A combined analysis of the three gene sequences generated a well resolved and strongly supported phylogeny. The combined phylogeny, which is topologically congruent with the three individual gene trees based on the Templeton test, is likely to represent the organismal phylogeny of Pinaceae. This phylogeny agrees, to a certain extent, with previous phylogenetic hypotheses based on morphological, anatomical, and immunological data. Disagreement between the previous hypotheses and the three-genome phylogeny suggests that morphology of both vegetative and reproductive organs has undergone convergent evolution within the pine family. The strongly supported monophyly of *Nothotsuga longibracteata*, *Tsuga mertensiana*, and *Tsuga canadensis* on all three gene phylogenies provides evidence against previous hypotheses of intergeneric hybrid origins of *Nothotsuga longibracteata* and *Tsuga mertensiana*. Divergence times of the genera were estimated based on sequence divergence of the *matK* gene, and they correspond well with the fossil record.

- 488**      WEESE, TERRI L.\* AND LEIGH A. JOHNSON. Department of Botany, North Carolina State University, Raleigh, NC 27695 and Department of Botany and Range Science, Brigham Young University, Provo, UT 84602—*Taxonomic limits and phylogenetic affinities of Saltugilia: molecular and morphological support for generic recognition apart from Gilia.*

*Saltugilia* first received formal taxonomic status in 1954 as a section of *Gilia*, and initially included five species in two species groups: *Gilia splendens*, *G. caruifolia*, and *G. australis*, and *G. leptalea* and *G. capillaris*. The latter two species were subsequently removed to their own section of *Gilia* before ultimately being removed from the genus. *Gilia stellata* and *G. scopulorum* were included in section *Saltugilia* in 1959, and a sixth species, *G. yorkii*, was added in 1999. Previous analyses of nuclear ITS and chloroplast *matK* DNA sequences suggest *Gilia splendens*, *G. caruifolia*, and *G. australis* form a lineage independent of the true *gilia*s. Additional DNA analyses and morphological characterization concur, providing support for elevating *Saltugilia* to generic status. As here circumscribed, *Saltugilia* includes *S. splendens*, *S. caruifolia*, *S. australis*, and an unnamed species. *Gilia stellata*, *G. scopulorum*, and *G. yorkii* are retained in *Gilia*. *Saltugilia* is characterized morphologically by a verrucate seed coat and combination of chainlike trichomes on the leaves and short, flat-topped, multicellular glands in the inflorescence. Comprising an apparent incipient species complex, the four species within *Saltugilia* are distinguished primarily by floral features and distribution. They show little molecular differentiation in the loci we sampled. Two chloroplast haplotypes are distinguished, but these do not entirely reflect taxonomic or geographic boundaries.

- 489** WHEELER, JOHN A.\*, DENNIS P. WALL, KIRSTEN JOHANNES, AND BRENT D. MISHLER. University Herbarium, Jepson Herbarium, and Department of Integrative Biology, University of California, Berkeley, CA 94720-2465—*Congruence and convergence in the moss family Calymperaceae: phylogenetic analysis of two chloroplast genes (rbcL and rps4) and Morphology.*

Morphological homoplasy is reputed to be prevalent in plants, perhaps especially in mosses and other haploid-dominant 'bryophytes'. The Calymperaceae is a diverse and ecologically important family of mosses in the tropics that has proven difficult to place phylogenetically and circumscribe taxonomically; single characters are not often definitive and supra-specific taxa are mostly defined by tenuous combinations of morphological features. Using morphological characters, as well as sequence data from the plastid-encoded genes *rbcL* and *rps4*, we reconstructed a phylogenetic framework in which to explore character evolution in the Calymperaceae and putative relatives, particularly, the origin and evolution of a distinctive leaf anatomy seen most prominently in *Leucobryum* and similar taxa. This generalized 'leucobryoid' leaf type contains living green cells that are covered with empty dead hyaline cells. We showed that a monophyletic Calymperaceae can only be defined by including several leucobryoid genera within the traditional family; in fact, our topologies confirm that the leucobryoid leaf architecture evolved independently at least four times within our taxon sample. The phylogenetic patterns probably denote both convergence and parallelism. When mapped to the phylogenies (using several different quantitative comparative methods), coarse habitat characterizations of sampled leucobryoid taxa appear to falsify previous adaptive hypotheses and yet provide no obvious clues about why this leaf architecture might be favored. If one considers all the various extant moss taxa with hyalocyst-dominated architectures then there might conceivably be one common denominator: their respective oligotrophic habitats.

- 490** WHITLOCK, BARBARA A. Harvard University Herbaria, Cambridge, MA 02138—*Phylogenetics of Byttneria and Ayenia (Sterculiaceae or Malvaceae s.l.): Biogeography and evolution of growth form in a large group of tropical woody plants.*

The genera *Byttneria* and *Ayenia* (Sterculiaceae or Malvaceae s.l.) are characterized by their unusual fly-pollinated flowers, with five petals that are clawed at the base and apically adnate to the top of the staminal column. The only character that consistently can be used to distinguish these two genera from each other is the number of anther thecae (two in the pantropical *Byttneria* and three in the exclusively neotropical *Ayenia*). Although basic construction of the flowers remains remarkably constant, habit and leaf morphology show extraordinary variation. Phylogenetic analyses of chloroplast DNA sequences indicate that *Ayenia* is monophyletic and nested within paraphyletic *Byttneria*. These results have important implications for the evolution of stamen number and further demonstrate the plasticity of this character within Byttnerioideae. This study contributes to a growing body of empirical work that examines the biogeography of tropical plants in a phylogenetic context. In the case of *Byttneria* and *Ayenia*, changes in growth form coincide with radiations into new geographical areas and habitats.

- 491** WILSON, BARBARA L.\*, RICHARD BRAINERD, MANUELA HUSO, KELI KUYKENDALL, DANNA LYTJEN, BRUCE NEWHOUSE, NICK OTTING, AND PETER ZIKA. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331—*The Carex Working Group, an example of cooperative taxonomy.*

The dwindling support from academia and government funding agencies for primary plant taxonomy is a concern for both academic taxonomists and practical field botanists. Given this funding climate, an alternative approach was used by the *Carex* Working Group in Oregon. This group of students and professional botanists reviewed the classification of *Carex* in Oregon, discovering species new to the state, rediscovering a population missing for over a century, describing a new species, and publishing maps of the 128 Oregon *Carex* taxa. The work was supported by academic botanists and the herbarium at Oregon State University. Although most of the work was done by dedicated volunteers, funding from private and government agencies supported databasing and field work expenses.

- 492** WILSON, BARBARA. Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon 97331—*Recent developments in fescue taxonomy in the Pacific Northwest.*

Although botanists have studied the Pacific Northwest Flora for a century and a half, primary taxonomy of community-dominant fescue grasses (*Festuca* spp.) has been confused. Recently, their taxonomic status, identification, and ranges have been clarified. *Festuca roemerii*, rather than the similar *F. rubra* or *F. ida-*

*hoensis*, is the native dominant fescue in upland grasslands west of the Cascade Range and Sierra Nevada, from SW British Columbia to central California. *Festuca roemerii* in the California Floristic Province has been recognized as a taxonomic variety. Sheep Fescue (*F. ovina*) is not native to North America. The most commonly planted "Sheep Fescue" cultivar in the Pacific Northwest originated from *F. valesiaca* X *F. callieri* stock. It is not native to North America. It is persisting and locally spreading, and will complicate fescue identification as it becomes naturalized. Taxonomy of the rarer grasses *F. howellii* (= *F. elmeri*) and *F. washingtonica* has also been studied.

**493** WILSON, HUGH D. Department of Biology Herbarium, Texas A&M University, College Station, TX 77843-3258—*Botanical informatics and full text indexing, compression, and retrieval.*

Active centers of systematic research are moving, as the computer revolution proceeds, to transfer raw taxonomic data (specimens, checklists, floras, manuals) to digital form. While this process has involved work with complex, expensive database management software in the past, emergence of the Internet as a global medium for information flow has stimulated the development, in the public domain, of relatively simple full-text indexing and retrieval systems for text, images, and textual images. These new systems allow content providers to work in a familiar, text-based environment to create information-rich documents (checklists, manuals, monographs, specimen databases) using standard, commercial microcomputer software (word processing, spreadsheet, database). Base document files, under full control and continuous update by those responsible for the data, are then converted to compressed, full text indices which are "full-text" in the sense that every word in the text is indexed and queries operate only on the index to do the searching. Conversion to 'document database' from original documents can be a simple, quick process for updating and correcting the data resource that involves no contact with either hardware or software specialists. Systems produced by the Texas A&M Bioinformatics Working Group and now online will be used to demonstrate procedural steps and advantages of full text indexing, compression, and retrieval of botanical data.

**494** WOLF, STEVEN J. Department of Biology, California State University Stanislaus, Turlock, CA 95382—*Teaching, research and collaborative applications of Internet based video conferencing.*

Although traditionally used for face to face real-time meetings, video conferencing programs that support application sharing may also be used for a wide variety of teaching, research and collaborative applications. As the phrase implies, "application sharing" involves synchronous, remote sharing of applications, files, or literally anything on a host computer. For example, many clients could simultaneously work on a central host database, without having the program installed on their computer. Likewise, collaboration on publications could be in real-time, rather than by passing multiple revisions back and forth. Teaching applications include guest lectures by experts on a particular subject, viewing live microscope images from another site, and/or remote collaboration with students. For example, rather than explaining how to perform a spreadsheet function, an instructor could remotely perform that function on the student's computer. For the systematics community, one of the most exciting applications could be remote examination of herbarium specimens. Using an inexpensive video capture board and standard video camera or CCD camera, full size screen images of herbarium specimens and/or microscope images may be broadcast, in real-time, and with viewer interaction, over the Internet. Although this technique is not viewed as a substitute for critical, hands-on examination, many routine examinations, comparisons and verifications could be made this way. For example, a cursory, remote examination by a specialist might quickly validate or invalidate a determination or new endangered species record. Hardware, software and technical requirements for remote collaboration and image sharing, as well as a proposal for a central systematics video conferencing server will be discussed.

**495** WOLFE, ANDREA D.\*, CHRISTOPHER P. RANDLE, AND SHANNON L. DATWYLER. Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, OH 43210—*Phylogeography and character evolution of the genus Penstemon (Scrophulariaceae).*

The 275 species of *Penstemon* are distributed in North America from Alaska to Guatemala and coast-to-coast, exclusive of the Canadian shield. The area of richest species diversity is the Intermountain Region and the area of lowest diversity lies east of the Rocky Mountains. *Penstemon* has been divided into six subgenera. The primary morphological characters defining subgenera are anther dehiscence and pubescence patterns. We used nrITS sequence data to reconstruct the phylogeny of *Penstemon*. The strict consensus tree was used to assess biogeographic and taxonomic relationships, the evolution of anther dehiscence and pubescence, the shift from bee- to bird-pollination syndromes, and evolution of polyploidy. Our results suggest an origin of

*Penstemon* in the Rocky Mountains, a subsequent migration to the west early in the history of the genus followed by migration throughout the Intermountain region, the southwest and finally east of the Rocky Mountains. Our results also suggest that anther characters are insufficient to define subgenera and that bird-pollination and polyploidy have originated independently numerous times in *Penstemon*.

- 496** WON, HYOSIG\* AND SUSANNE S. RENNER. Department of Biology, University of Missouri-St. Louis, St. Louis, MO 63121—*Why so many dioecious species in Siparunaceae (Laurales)?*

Siparunaceae are tropical evergreen shrubs or trees, composed of 2 genera and ~70 species. Different from other families in Laurales, which show diverse mating systems, flowers of Siparunaceae are strictly unisexual, with plants monoecious or dioecious. More than 60 species are dioecious, while 12 species are monoecious. A few morphological characters covary with mating system. To trace the evolution of dioecy in Siparunaceae, we reconstructed a phylogeny using cpDNA trnL-trnF IGS and nrDNA ITS sequences, and diverse outgroups. The phylogeny strongly supports monophyly of Siparunaceae and evolution of dioecy from monoecy within Siparuna. Dioecious *Glossocalyx* is placed as sister to all other Siparunaceae, while the dioecious Siparuna species form a clade nested higher up in the tree. This phylogeny is congruent with the geographical distribution of Siparunaceae; monoecious species are distributed in the Amazonian lowland, while most dioecious species are found at higher altitudes in the Andes. Relatively small sequence divergences among the dioecious species and their geographical distribution suggest rapid speciation of dioecious populations with changes in ecological conditions.

- 497** YOUNG, NELSON D.\*, CAROLINE YOON, AND MITRA AZODI. Department of Biology, Trinity University, San Antonio, TX 78212—*Speciation by allopolyploidy in Castilleja: the case of C. dissitiflora*.

*Castilleja dissitiflora* N. Holmgren is a montane species, endemic to central Nevada, and a tetraploid ( $2n=48$ ). It is thought to be a genomic allopolyploid descendant of a cross or crosses between *C. linariifolia* Benth. ( $2n=24$ ) and *C. applegatei* Fernald ssp. *pinetorum* (Fernald) Chuang & Heckard ( $2n=24$ ). This hypothesized relationship is based on the fact that *C. dissitiflora* is intermediate between the two putative parents in floral morphology and overall aspect. Although currently, *C. dissitiflora* is only sympatric with one putative parent, *C. linariifolia*, the other putative parent, *C. applegatei* ssp. *pinetorum* approaches it to within 200 km on the west and north of its range. It is commonly held that allopolyploids are most successful when the parents are not close relatives, for if they are, tetrasomic inheritance may generate unbalanced gametes. Although the two putative parents are both in subgenus *Castilleja*, *C. linariifolia* is in section *Castilleja*, whereas *C. applegatei* is in section *Viscidulae*. The phylogenetic relationship among sections of *Castilleja* can reveal just how close or distant these two sections are. Sequences of the plastid *trnK* intron and nuclear ITS are used along with morphology and new chromosome counts to assess the validity of the hypothesized allopolyploidy. A skeletal phylogeny of the genus *Castilleja* is used to determine the degree of relationship between the sections with the two putative parent species. *Castilleja* is a member of the newly redefined Orobanchaceae.

- 498** ZEREGA (1,2), NYREE J. CONARD\*, DIANE RAGONE (3), AND TIMOTHY J. MOTLEY (1). 1) The Lewis B. and Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458, 2) Biology Department, New York University, 100 Washington Square East, NY, NY 10003, 3) National Tropical Botanical Garden, 3530, Papalina Road, Kalaheo, Kauai, HI 96741—*Artocarpus phylogenetics and AFLP genetic fingerprinting of breadfruit cultivars* *Artocarpus altilis*.

The genus *Artocarpus* (Moraceae) includes approximately 50 species native to the tropics of Southeast Asia and the Pacific. Many of the species are utilized locally for their fruit, seeds, and/or timber while two are cultivated circumtropically for their fruit and seeds (breadfruit, *A. altilis* and jackfruit, *A. heterophyllus*). Despite the economic importance of *Artocarpus* species, no phylogenetic analysis of the genus has been undertaken. A phylogenetic hypothesis would be useful for identifying close relatives of the cultivated species in the genus, studying character evolution, and for setting an evolutionary framework for more detailed species level studies such as the work on breadfruit presented here. Breadfruit is a staple crop harvested for either its starchy fruit or proteinaceous seeds. It has been cultivated and improved upon by human selection for millennia in the Pacific Islands, and today hundreds of seedless and seeded cultivars exist. Up to three possible species have been distinguished by various authors to represent the breadfruit. *Artocarpus altilis* (Parkinson) Fosberg (synonym: *A. communis*) has been used to encompass a wide range of morphological



variation. However, this variation has also been considered to include two additional species, *A. camansi* and *A. mariannensis* based on fruit surface and leaf characters. Morphological evidence for hybridization between *A. altilis* and *A. mariannensis* also exists from Micronesia where their ranges overlap. A preliminary *Artocarpus* phylogeny has been generated based on parsimony analysis of nucleotide sequence data from the internal transcribed spacers (ITS1 and 2). The results indicate that *Artocarpus* is a monophyletic group. The analysis also supports the recognition of three distinct breadfruit species and provides molecular support for hybridization between *A. altilis* and *A. mariannensis*. Further investigations into breadfruit relationships are also in progress using AFLPs (Amplified Fragment Length Polymorphisms) to address biogeographic, taxonomic, and conservation issues.

- 499** ZJHRA, MICHELLE L. Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85720—*Preliminary findings of evolutionary and ecological aspects of cauliflory.*

Coleeae, a tribe of Bignoniaceae endemic to Madagascar is characterized by cauliflory with approximately half its species exhibiting this trait. Cauliflory arises in parallel with a treelet habit and may persist with further shifts in habit. The role of scent, as well as different floral and fruit characters will be discussed in the context of the evolution of cauliflory as will the homology of different forms of cauliflory. In the Coleeae cauliflory appears to be driven by lemur dispersal and may be key to the remarkable diversity of this group.

## Contributed Posters

- 500** BAIRD, GARY I. Department of Botany and Range Science, Brigham Young University, Provo, UT 84602—*A phylogenetic assessment of *Chrysothamnus* Nutt. (Asteraceae, Astereae).*

The genus *Chrysothamnus* Nutt. is comprised of a group of asteraceous shrubs distributed throughout the western United States but with a center of diversity on the Colorado Plateau. The most well-known, widely distributed and studied species is *C. nauseosus* (Pall.) Britton. This singular taxon tends to dominate most informal concepts of the genus as a whole. Recent phylogenetic studies of the tribe Astereae, using cpDNA restriction site data, have placed *C. nauseosus* as either sister to or within the genus *Ericameria* Nutt. This is a position long supported by morphological and chemical analyses and as a natural consequence has precipitated the transfer of *C. nauseosus* into *Ericameria*. None of the other species of *Chrysothamnus* have been included in these recent phylogenetic studies, yet there is morphological and chemical data to suggest that at least *C. viscidiflorus* (Hook.) Nutt. and possibly some of the other core *Chrysothamnus* species are not closely related to *Ericameria* but are phylogenetically allied to *Petradoria* Greene and its sister taxa within the subtribe Solidagininae. This apparent phylogenetic contradiction within *Chrysothamnus* would suggest that the genus is polyphyletic, as generally construed. The purpose of the current study is to test the monophyletic nature of *Chrysothamnus* and resolve its putative phylogenetic relationships using DNA sequence data, in addition to morphological data.

- 501** BARKWORTH, MARY E.\*, KATHLEEN M. CAPELS, AND LINDA A. VOROBİK,. Intermountain Herbarium, Department of Biology, Utah State University, Logan, UT 84322-5305; Intermountain Herbarium, Department of Biology, Utah State University, Logan, UT 84322-5305; University Herbaria, University of California, Berkeley, CA 94720-2465 and Department of Botany, University of Washington, Seattle, WA 98195-5325—*The Manual of Grasses for North America: Progress Report.*

The Manual of Grasses for North America will be an identification manual for North America's grasses. Its geographic coverage comprises the continental U.S., Canada, and Greenland, plus the French islands of St. Pierre and Miquelon. It includes many ornamental and experimental species in addition to the species that are native to or established in the region. The original goal for the Manual project was publication of a book similar in concept to that of Hitchcock's Manual of Grasses of the United States. This is still our first goal, one that we can realistically hope to meet in 2003, if we obtain adequate funding. There is, however, increasing interest in having the Manual made available over the Internet. It is relatively simple, but time-consuming, to make the text, illustrations, and maps available as static files over the Internet, and we have begun to do so, the major limitation being funding. The files would, however, have greater value if they were used as the foundation of a Web site designed to maintain the currency of the information they contain in a manner that encourages participation by all qualified individuals. We are exploring means for accom-

plishing this goal while keeping our focus on attainment of the primary goal, completion of the print version. The poster will summarize the status and funding of the project as of July 1, 2000.

- 502** BELL, CHARLES D.\* AND MICHAEL J. DONOGHUE. Harvard University Herbaria, 22 Divinity Avenue, Cambridge MA, 02138 and Department of Ecology and Evolutionary Biology, Yale University, New Haven, CN 06511—*Dipsacales phylogeny based on chloroplast DNA sequences.*

Ten new DNA sequences of the 5' end of the chloroplast *ndhF* gene, along with 5 new *rbcL* sequences, were obtained for taxa representing Caprifoliaceae, Valerianaceae, and Dipsacaceae. These were combined with 31 published *ndhF* sequences, as well as published *rbcL* sequences and morphological characters. Phylogenetic relationships were estimated using parsimony and maximum likelihood methods. Trees inferred from all datasets and methods are in strong agreement with previous hypotheses based on morphology, *rbcL*, and combined datasets (M. Donoghue, T. Eriksson, P. Reeves, and R. Olmstead, manuscript in review). There is strong support for the monophyly of traditional Dipsacales and for Adoxaceae (including *Viburnum*, *Sambucus*, and *Adoxa*) and Caprifoliaceae (including Morinaceae, Valerianaceae, and Dipsacaceae). The new sequences also provide additional support for lineages within Adoxaceae and Caprifoliaceae. For example, *Tetradoxa* and *Sinadoxa* are related to *Adoxa*, and Linnaeae are monophyletic and united with a clade including Morinaceae, Valerianaceae, and Dipsacaceae. We also generated sequence data from several additional chloroplast genes to help resolve phylogenetic relationships within Morinaceae (*Morina*, *Acanthocalyx*, and *Cryptothladia*) and Caprifoliaceae (*Leycesteria*, *Lonicera*, *Symphoricarpus*, and *Triosteum*).

- 503** BLARER, ALBERT\*, DAN NICKRENT, HANS BÄNZIGER, PETER K. ENDRESS, AND YIN-LONG QIU. Institute of Systematic Botany, University of Zurich, Zollikerstr. 107, CH-8008 Zurich, Switzerland—*Phylogenetic relationships among genera of the parasitic family Rafflesiaceae s.l. based on nuclear ITS and SSU rDNA, mitochondrial LSU and SSU rDNA, atp1, and matR sequences.*

We analyzed the sequences of nuclear ITS and SSU rDNA, and mitochondrial *atp1*, *matR*, and LSU and SSU rDNA (total length about 9000 bp) from 13 species and 9 Genera of Rafflesiaceae s.l. Separate and combined phylogenetic analyses of these six data sets gave consistent results. They identified four clades that were previously recognized as Rafflesiaceae s.s., Apodanthaceae, Cytinaceae, and Mitrastemonaceae. Furthermore, based on expanded unpublished analyses with other angiosperms, Mitrastemonaceae do not form a monophyletic group with the other Rafflesiaceae s.l. *Bdallophyton* forms a clade with *Cytinus*.

- 504** BLATTNER, FRANK R.\*, DIRK FISCHER, NIKOLAI FRIESEN, SVEN POLLNER, AND KONRAD BACHMANN. Department of Taxonomy, Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Gatersleben, Germany—*Molecular markers in Allium, range of application and taxonomic consequences.*

DNA polymorphisms are the markers of choice for the identification and characterization of plants. They are an integral part of the plant and they are not subject to environmental modification. There are relatively reliable generally applicable methods to obtain large samples of markers from any species of plant. However, each marker system samples a different fraction of the genome and therefore has a different resolving power, range of applicability and probability of homology. Standard measures (e.g., genetic distance) are dependent on the marker system and on the group under study. Taxa of similar rank may differ greatly in the variability of molecular marker systems. This is illustrated with examples from the genus *Allium*. At the IPK, a unique living collection of about 300 species of the genus, many collected at type localities, and a large collection of accessions of the cultivated species has been studied with a range of molecular markers: isozymes, RAPDs, ITS-sequences, PCR-RFLPs of variable regions of chloroplast DNA, and genome in situ hybridization (GISH). Molecular marker studies have necessitated changes in the subgeneric classification of the genus but have confirmed the monophyly of most sections within subgenera. The origin of various cultivated groups has been elucidated, especially where material of native origin was available, since garden-grown *Allium* are very liable to genetic introgression. Introgression in nature between species from various sections has been demonstrated. Microsatellite primers have been developed for the characterization of individual accessions of *Allium cepa* and for molecular genetic mapping experiments.

- 505** BOYD, STEVE. Herbarium, Rancho Santa Ana Botanic Garden, Claremont, CA 91711—*Vascular flora of the Liebre Mountains, Western Transverse Ranges, California.*

The Transverse Ranges, with their east-west orientation, are one of southern California's most prominent physiographic features, and contain large tracts of intact, biologically diverse, public trust lands. Areas such

as these are critical for meeting societal goals of preserving California's natural heritage, but long-term conservation requires development of a baseline account of the resources being managed. Although much of the Transverse Ranges border the Los Angeles Basin, California's most densely populated region, published floristic accounts of the component ranges are surprisingly scarce. This study represents a preliminary floristic account of the Liebre Mountains region, and includes the results fieldwork conducted over a nine year period (1990-1999), as well as review of collections housed in the herbarium of Rancho Santa Ana Botanic Garden (RSA-POM) and elsewhere. The Liebre Mountains form a discrete unit within the western portion of the Transverse Ranges, and are geographically and floristically transitional to the San Gabriel Mountains, Inner Coast Ranges, Tehachapi Mountains, and Mojave Desert. A total of 1,010 vascular plant taxa was recorded from the range, representing 104 families and 400 genera. The ratio of native vs. nonnative elements of the flora is 4:1, similar to that documented in other areas of cismontane southern California. The range is noteworthy for the diversity of *Quercus* taxa and associated oak-dominated vegetation, and represents the southern limit of the foothill woodland flora characteristic of ranges bordering California's Central Valley. A total of 32 sensitive plant taxa (rare, threatened or endangered) was recorded from the range.

- 506** CHANDERBALI, ANDRE\*, HENK VAN DER WERFF, AND SUSANNE S. RENNER. Missouri Botanical Garden, St. Louis, MO 63166 and Department of Biology, University of Missouri-St. Louis, St. Louis, MO 63121—*Historical biogeography of neotropical Lauraceae*.

Phylogenetic relationships among Lauraceae, inferred from sequence variation in the chloroplast and nuclear genomes, suggest an early Gondwanan and Laurasian division. Descendants of the Gondwanan lineage form a minor element in the neotropical Lauraceae flora. Most neotropical diversity instead is accommodated in a large terminal clade that is nested within a paraphyletic assemblage of Laurasian lineages. Within this terminal clade, South American lineages form derived branches relative to clades restricted to Central America. This supports the morphology-based hypothesis of Rohwer and Kubitzki (1993) of a northern hemisphere origin and immigration into South America of part of the neotropical Lauraceae stock. But when did this immigration take place? The presence of African species of *Ocotea* near the base of the neotropical clade indicates that the initial southward movement occurred when terrestrial migration into Africa was also possible. Molecular clock estimates of the divergence of South American from Central American Lauraceae place the event at ~70 MYBP. This would be consistent with a Late Cretaceous invasion of South America—either from Central America via the Proto-Antilles arc or from Africa—followed by extensive radiation during the isolation of South America from the Upper Cretaceous to the Pliocene.

- 507** CHARI, JEANNIE AND PAUL WILSON.\* Department of Biology, California State University, Northridge, CA 91330-8303—*Factors limiting hybridization between *Penstemon spectabilis* and *Penstemon centranthifolius**.

Speciation involves the origination of reproductive isolating mechanisms, such as a difference in pollinators, incompatibility between pollen tubes and stylar tissue, or poor growth of hybrid seedlings. We studied reproductive isolating mechanisms in a natural sympatric population of *Penstemon spectabilis* and *Penstemon centranthifolius* where natural  $F_1$  hybrids occurred at very low frequency. We compared conspecific crosses, backcrosses and heterospecific crosses in terms of pollen germination, pollen tube growth, fruit set, seed set, and seed weight. When *P. spectabilis* was the recipient, heterospecific crosses had reductions in pollen tube growth, fruit set, seed set, and seed mass. When *P. centranthifolius* was the recipient, heterospecific crosses had reduced pollen grain germination, and they set nearly no fruit. Backcrosses were generally intermediate between conspecific and heterospecific crosses, at least when differences were significant. In this system, partial pollinator specificity also contributes to maintaining the species boundary, and we are currently quantifying the performance of conspecific, backcross, and  $F_1$  offspring.

- 508** CLAUSING, GUDRUN\* AND SUSANNE S. RENNER. Institut fuer Spezielle Botanik, University of Mainz, D-55099 Mainz; Department of Biology, University of Missouri-St. Louis, MO 63121—*Phylogenetic relationships and character evolution in Melastomataceae*.

Melastomataceae are a tropical eudicot family of about 156 genera and 4500 species. Melastome androecium and fruit evolution are little understood due to controversial hypotheses about family circumscription and intra-family relationships. Our poster presents a phylogenetic hypothesis for Melastomataceae and their closest relatives, Memecylaceae, Crypteroniaceae, Alzateaceae, Rhynchocalycaceae, Oliniaceae, and Penaeaceae, based on combined *rbcL*, *ndhF*, and *rpl16* sequences and parsimony, minimum evolution, and maximum likelihood reconstructions. Fifty-six exemplars, representing the 13 traditional tribes and three subfamilies,

Astronioideae, Melastomatoideae, and Memecyloideae (= Memecylaceae DC.), were sequenced, with additional denser taxon sampling for *ndhF*. Memecylaceae are sister to Melastomataceae, and *Pternandra*, a SE Asian genus of 15 species, is the first-branching Melastomataceae. This placement of *Pternandra* has low bootstrap support (72%), but agrees with its melastome-like leaf venation. The next deepest split is between the SE Asian Astronieae, with anthers opening by slits, and the remaining melastomes, which have anthers opening by pores. Morphological implications of the phylogeny concern stamen connective appendages, loss of anther endothecia, the evolution of poricidal dehiscence, and switches between berries and capsules.

- 509** CROSS, HUGH B.\* AND TIMOTHY J. MOTLEY. The Lewis B. and Dorothy Cullman Molecular Systematics Program, The New York Botanical Garden, Bronx, New York 10458. And Center for Environmental Research and Conservation, Columbia University, New York, New York 10027—*Molecular systematics of Hawaiian Peperomia*.

*Peperomia* is a large pantropical genus of more than 1000 species. The genus is represented by 25 species in Hawaii, of which 22 are endemic. A previous study of Hawaiian *Peperomia* hypothesized that the present distribution of species is the result of three or four independent colonization events to the archipelago. Many morphological characters used for delineation of the species are quantitative, and therefore it has been difficult to determine relationships among *Peperomia* species based solely upon the morphology. Nucleotide sequence data from the nuclear ribosomal ITS and 5S-NTS loci were obtained from Hawaiian *Peperomia* as well as from several Pacific and South America species. Cladistic analyses of the molecular data indicate that: (1) the Hawaiian *Peperomia* are of Pacific ancestry and originally colonized the older northwestern islands, and (2) the Hawaiian species form a monophyletic group. Species relationships are still not well resolved among the Hawaiian *Peperomia*, which may be the result of past and present hybridization events. However, this study was able to resolve some general patterns, but further research incorporating more variable molecular data will be required to completely resolve the phylogenetic relationships among the Hawaiian taxa.

- 510** DEVORE, MELANIE L. Department of Biological and Environmental Biology, Georgia College and State University, Milledgeville, GA 31061—*Tectonism and its impact on the biogeography of South America*.

Biogeographical patterns observed in floras are the result of a number of historical factors. Biogeographers have viewed tectonic events as significant historical factors influencing patterns of species richness, endemism, and biotic history based on phylogenetic analyses. In many cases, biogeographers consider tectonic events in the context of major plate movements resulting in continental separation, convergence and generalized orogenic events. Other phenomena associated with major plate movements, as well as motions of smaller "microplates", have also had a considerable impact on the evolution of major groups and development of biota. In particular, plant evolution and floras of South America have been strongly influenced by tectonic events on several scales. Microplate movements have played a significant role in the continental evolution of both the northern and southern margins of the continent. Hot spots and their associated aseismic ridges have also influenced the development of floras on both the eastern and western margins of South America. Finally, recent studies have indicated that the main Andean deformation consisted of a series of events starting in the Jurassic (Andes of Colombia-Ecuador) and continuing into the present. These events have resulted in segmenting the 9000 km mountain range into seven sections. Each section has a distinct orogenic history of its own. The potential impact of these events on biota was examined using both distribution data and phylogenies of selected angiosperm groups. Although we think of the evolution of older groups being influenced by tectonics, younger families (e.g. Asteraceae and Calyceraceae) also have histories tied with tectonic events.

- 511** GOULD, KATHERINE R.\* AND MARK C. TEBBITT. Science Department, Brooklyn Botanic Garden, Brooklyn, NY 11225—*Morphological and molecular variation in Helianthemum dumosum (Cistaceae), a rare coastal heathland taxon, and its widespread relative, H. canadense*.

The taxonomic status of *Helianthemum dumosum*, the rare and endangered Bushy Rockrose, was investigated using morphological and molecular methods. *Helianthemum dumosum* has a highly restricted range, found mainly on coastal heathland habitat in southern New England (especially Cape Cod, Nantucket, and Martha's Vineyard) and Long Island, NY. However, it is often confused with the geographically widespread and sympatric close relative, *H. canadense*, and morphological intermediates between the two have been found. We searched for taxon-specific molecular markers and evidence of hybridization and introgression between the two using the high-resolution fingerprinting technique of intersimple sequence repeats (ISSRs). We per-



formed multivariate statistical analyses and a comparative cladistic analysis between the ISSR data and morphological data. Preliminary results indicate that a pattern of clinal variation between the two taxa exists.

- 512** GROSE, SUSAN O.\* AND RICHARD G. OLMSTEAD. Department of Botany, University of Washington, WA 98195—*Phylogenetic Analysis of Crescentieae and Tabebuia s.l. (Bignoniaceae)*.

Bignoniaceae have been shown to be one of the four most abundant and diverse families in several different neotropical ecosystems. Recent phylogenetic studies based on cpDNA sequences have shown Bignoniaceae to be monophyletic, and indicated that one of the largest tribes, the Tecomeae is paraphyletic. In addition, one group of Tecomeae including *Tabebuia* s.l. appears to be paraphyletic, having given rise to tribe Crescentieae. We have expanded our molecular phylogenetic studies based on *ndhF* to include increased sampling of *Tabebuia* s.l. and Crescentieae to examine this relationship further. This relationship, proposed by Alwyn Gentry, is surprising because *Tabebuia* is characterized by dehiscent fruits, non-cauliflorous inflorescences and bird or insect pollination, while Crescentieae is distinguished by cauliflory, indehiscent fruits and bat pollination. *Tabebuia* s.l. has a center of diversity in the Greater Antilles (mainly Cuba) with a smaller proportion of species occurring in mainland Central and South America while the Crescentieae have a primarily mainland Central American distribution.

- 513** HOOPER, ELISABETH A.\* AND POLLY HIGGINS. Department of Biology, Truman State University, Kirksville, MO 63501—*A preliminary investigation into the origin of the Pale Purple Coneflower, Echinacea pallida (Asteraceae), using allozyme and ISSR markers*.

The pale coneflower, *Echinacea pallida* (Nutt.) Nutt., is a conspicuous member of the tallgrass prairie community in the eastern Great Plains, USA. In 1968, McGregor published a taxonomic revision of the *Echinacea* based on extensive morphological, cytological, and biosystematic data. McGregor revealed that unlike most species in the genus, which are diploid, *E. pallida* was a tetraploid. He also suggested that *E. pallida* might be an allotetraploid derived from the two diploid species, *E. sanguinea* Nutt. and *E. simulata* McGregor. The former occurs in eastern Texas, western Louisiana, and southwestern Arkansas; whereas the latter is nearly restricted to southeastern Missouri. All species are similar morphologically, and the most conspicuous difference between the diploids and the tetraploid is pollen color (bright yellow in the diploids and bright white in the tetraploid). Last summer, we collected leaf samples from roadside populations of all three taxa to try to test McGregor's hypothesis on the origin of *E. pallida*. Starch gel electrophoresis was used to assay each taxon for allelic variability. In particular, we looked for unique genetic markers in the putative parental taxa that might be inherited and expressed co-dominantly in the allotetraploid. While we have found differences in allelic frequencies among taxa, and interesting allozyme profiles in the tetraploid, we have not found unique marker alleles in the diploids. Although allozyme data generated thus far appear to be insufficient for answering our original question, we are now testing whether ISSR (inter-simple sequence repeat) markers can shed light on the evolutionary origin of *E. pallida*.

- 514** HUANG, MINGJUAN\*, JOHN V. FREUDENSTEIN, AND DANIEL J. CRAWFORD. Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, OH 43210—*Phylogenetic relationships of the Caryopteris-Trichostema complex (Lamiaceae) based on ndhF sequence data*.

The so-called *Caryopteris-Trichostema* complex consists of these two genera and several monotypic or very small genera. *Trichostema* is North American where all other taxa are Asiatic. The complex has been problematic taxonomically, and Cantino in particular, has questioned the monophyly of *Caryopteris*. A molecular phylogenetic study of the complex was carried out using sequences from the chloroplast *ndhF* gene. The monophyly of *Trichostema* is strongly supported in the molecular phylogeny and three major clades are present in the genus. The lineages correspond closely to groupings recognized by Harlan Lewis, with the notable exception of *T. brachiatum*. Implications of the placement of this species in the molecular phylogeny will be discussed relative to the evolution of annuality and base chromosome number. The *ndhF* phylogeny suggests that *Caryopteris* is polyphyletic. Section *Caryopteris* is strongly supported as monophyletic and is sister to *Trichostema*. The monotypic genus *Amethystea* is nested within the complex and is closely related to the above group of *Trichostema* and *Caryopteris* s.s.. Section *Pseudocaryopteris* (*C. bicolor* and *C. paniculata*) appears to be a natural group, thus supporting its elevation from the sectional to generic level as proposed by Cantino et al. (1998). *Caryopteris divaricata*, characterized by its porate pollen and delimited as the monotypic genus *Tripura* by Cantino, is sister to *Pseudocaryopteris* in a moderately supported clade. *Caryopteris nepetifolia* and *C. terniflora* form a strongly supported group together with *Schnabelia*, providing

additional evidence to support the transfer of the former two species of *Caryopteris* to the genus *Schnabelia*. *Rubiteucris* is well supported as sister to *Schnabelia* rather than to the rest of *Caryopteris*. These results are largely congruent with relationships inferred from ITS sequence data, but provide better resolution.

- 515** LEE, NAM SOOK, YOUNGBAE SUH, SUNGHEE YEAU, AND SANGTAE LEE.\* Department of Biological Science, Ewha Womans University, , Seoul, Korea 120-750—*The Morphological and genetic analyses of Korean Adonis*.

*Adonis amurensis* is the only species traditionally known in Korea. The identity has been doubted because of its conspicuous geographical variations. This morphological and genetic study revealed that the Korean *Adonis* comprises three species. Morphologically *A. amurensis*, is well distinguished from the others by having the bifurcated main axis of pinnately compound leaves, no branch of the stem, and similar to longer sepals than petals, whereas *A. pseudoamurensis* having about 5 petals and the acute tip of dissected pinnae is distinguished from *A. multiflora* having 8 petals and the acuminate tip. Genetic variations based on 19 isozyme loci revealed that *A. multiflora* was distinguished from the others by *Tpi*, whereas *A. amurensis* from *A. pseudoamurensis* by *Mdh*. The least amount of genetic variability was found in *A. multiflora*. On the basis of chromosome number, *A. ramosa* which was once reported does not seem to exist in Korea.

- 516** LEE, SANGTAE, CHUNGHEE LEE, YOUNGBAE SUH, SUNGHEE YEAU, AND NAM SOOK LEE.\* Department of Biological Science, Sungkyunkwan University, Suwon 440-746 Korea—*Pollen morphology of the genus Adonis L. (Ranunculaceae) in Korea*.

To elucidate the taxonomic identities of Korean *Adonis*, the pollen morphology of 18 (14 Korean, 3 Japanese, and 1 Chinese) populations were studied with light and scanning electron microscopes. The populations were grouped as follows: Type I. *A. amurensis* (Korea: Choongnyong Mt., Chunma Mt., Juksang Mt., and Jumbong Mt.): Foveolae elongate, small, 27-40 per 49 $\mu$ m<sup>2</sup>, 2-3(5) aligned; echinae 0.9-1.24 $\mu$ m length and 2-4/49 $\mu$ m<sup>2</sup>. Type II. *A. ramosa* (Japan: Tashiro): Foveolae round, large and 20/49 $\mu$ m<sup>2</sup>, rarely aligned; echinae 0.8 $\mu$ m high and 4/49 $\mu$ m<sup>2</sup>. Type III. Foveolae round to elongate, small to large, 23-55/49 $\mu$ m<sup>2</sup> sometimes aligned; echinae 0.31-0.74 $\mu$ m high and 6-17/49 $\mu$ m<sup>2</sup>. Subtype 1. *A. multiflora* (Korea: Kwanumsa and Yorimok; Japan: Ryonuma): Echinae 6-8/49 $\mu$ m<sup>2</sup>, 0.35-0.59 $\mu$ m in length, 0.44-0.81 $\mu$ m in width, L/W=0.73-0.80; foveolae 27-40/49 $\mu$ m<sup>2</sup>, similar sized. Subtype 2. *A. pseudoamurensis* (Korea: Jangbong Ir., Dukjuk Ir., Palgong Mt., Naesosa, Kwanchon, Euryoung, and Keryong Mt.; Japan: Nishi-yoshino-mura; China: Kirin): Echinae 6-17/49 $\mu$ m<sup>2</sup>, 0.31-0.74 $\mu$ m in length, 0.24-0.79 $\mu$ m in width, L/W=0.84-1.29; foveolae 23-55/49 $\mu$ m<sup>2</sup>, size variable.

- 517** LI, JIANHUA\*, DAVID E. BOUFFORD, AND MICHAEL J. DONOGHUE. Arnold Arboretum of Harvard University, 125 Arborway, Jamaica Plain, MA 02130; Harvard University Herbaria, 22 Divinity Avenue, Cambridge, MA 02138—*Phylogenetics of Buckleya (Santalaceae) based on ITS sequences of nuclear ribosomal DNA*.

*Buckleya* Torr. (Santalaceae) is a hemi-parasitic shrubby genus with two species in China, one in Japan, and one in the southeastern United States. Phylogenetic relationships among these species are controversial and have not been tested using molecular data. In this study we used sequences of the internal transcribed spacer region of nuclear ribosomal DNA to test previous phylogenetic hypotheses. Two sister species pairs are well supported: *B. distichophylla* plus *B. graebneriana*, and *B. lanceolata* plus *B. henryi*. Sequence differences and morphological characters support the recognition of *B. lanceolata* and *B. henryi*. Sequence divergence between *B. distichophylla* and *B. graebneriana* is twice as high as that between *B. lanceolata* and *B. henryi*. These results are most consistent with the treatment proposed by Carvell and Eshbaugh (1982). Biogeographically, one of the Chinese species (*B. graebneriana*) is most closely related to the eastern North American species (*B. distichophylla*), while the other Chinese species (*B. henryi*) is allied with the Japanese species (*B. lanceolata*). Maximum likelihood analyses do not reject clock-like evolution of nrDNA ITS spacers in *Buckleya*, and divergence times may date to the Late Miocene and Pliocene.

- 518** LUTZ, ANDREW W.\* AND ANDREA D WOLFE. Department of Evolution Ecology and Organismal Biology, Ohio State University, 1735 Neil Avenue, , Columbus, OH 43210—*Population genetics of the endemic species, Penstemon caryi Pennel*.

*Penstemon caryi* (Scrophulariaceae) is an endemic of the Big Horn Mountains of Wyoming and the Pryor Mountains of Montana. The species is endemic to exposed limestone outcrops that occur infrequently throughout the region. Nine populations were collected from The Nature Conservancy's Tensleep Preserve

in Wyoming. Five inter-simple sequence repeat (ISSR) markers were used to evaluate genetic diversity found within and among populations of *P. caryi*. Results from this study, in conjunction with results from a reproductive ecology study, will be used to determine conservation strategies for the species on Nature Conservancy lands.

- 519** MEEROW, ALAN W.\* AND DEIRDRE A. SNIJMAN. USDA-ARS-SHRS, 13601 Old Cutler Road, Miami, FL 33158 and Compton Herbarium, National Botanic Institute, Kirstensbosch, Rhodes Drive, Newlands, Cape Town, South Africa—*Phylogeny of Amaryllidaceae tribe Amaryllideae based on nrDNA ITS sequences.*

Tribe Amaryllideae of the Amaryllidaceae is endemic to Africa with the exception of the pantropical *Crinum*. It is sister to the rest of the family in trees generated by plastid sequences. We present the results of cladistic analyses of nrDNA ITS sequences for 30 species representing all genera of the tribe, using *Scadoxus puniceus* as outgroup. Six trees are found with equal weights imposed on the data, three with successive weighting. The consensus trees of both analyses are identical. *Boophane* is unresolved in relation to the rest of the tribe, which may be due to the outgroup used. *Agapanthus* is the preferred outgroup for this analysis, but we have been unable to obtain ITS sequences for any *Agapanthus* sp. *Amaryllis* is sister to all of the other genera, which form two clades conforming to Snijman and Linder's subtribes Amaryllidinae (less *Boophane*) and Crininae (less *Amaryllis*). *Crossyne* is the first branch of the Amaryllidinae, within which *Hesseea* (less *H. bruce-bayeri*) is resolved as sister to *Brunsvigia*. *Strumaria* is monophyletic only if *Carpolyza* is treated as a *Strumaria* or several species are transferred to *Carpolyza*, and *Hesseea bruce-bayeri* is transferred to *Strumaria*. *Nerine* is sister to *Strumaria*. Within Crineae, *Ammocharis*, *Cybistetes*, and *Crinum baumii* form a sister clade to an otherwise monophyletic *Crinum*. The results are contrasted with Snijman and Linder's cladistic analysis based on morphological data, with which the gene trees are only partially congruent.

- 520** MERMELL, LESLY P.\* AND TINA J. AYERS. Department of Biological Sciences, Box 5640, Northern Arizona University, Flagstaff, AZ 86011-5640—*Use of nrITS sequence data for phylogenetic analysis of the Lysipomia sphagnophila (Campanulaceae) species complex.*

All members of the genus *Lysipomia* (Campanulaceae) are endemic to high elevations (~3,000 m) of the Andean mountain chain of South America, making this genus a unique member of the bellflower family. *Lysipomia sphagnophila* along with a small number of additional species appeared to form a monophyletic group within this genus in a preliminary phylogenetic analysis based on ITS sequence data. Due to a high degree of morphological similarity, species and subspecies delimitations within this complex remain tentative. nrITS sequence data may aid in clarifying species and subspecies relationships as well as in determining the possible monophyly of this group. ITS data may also be useful in a biogeographical interpretation of this complex including aspects such as species origin and subsequent radiation. Sequences for the entire ITS and accompanying 5.8S region of nrDNA were obtained for all members of this complex by direct double-stranded sequencing of PCR amplified DNA. Results of this phylogenetic analysis will be presented.

- 521** MEYER, KARSTEN\* AND SUSANNE S. RENNER. Institut fuer Spezielle Botanik, University of Mainz, D-55099 Mainz; Department of Biology, University of Missouri-St. Louis, St. Louis, MO 63121—*Long distance dispersal in Melastomeae: from South America to Africa to Madagascar and SE Asia.*

Melastomeae are pantropically distributed and comprise ~550 spp. in the New World, including the 13 spp. of *Rhexia* in North America, 170 spp. in Africa, 70 in Madagascar, and 50 spp. of *Melastoma* and *Osbeckia* in SE Asia and tropical Australia. The monophyly of Melastomeae is strongly supported by combined rbcL, ndhF, and rpl16 cpDNA sequences analyzed under maximum likelihood, distance, and parsimony criteria. Melastomeae are closest to Microlicieae, a clade currently appearing endemic in the neotropics. Melastomeae-type seeds have been reported from the Early Miocene of Eurasia (~20 MYBP), while the oldest records for the family are Paleocene (~60 MYBP) pollen grains from Colombia and leaves from North America. A molecular phylogeny of Melastomataceae (Clausing and Renner, submitted) shows Melastomeae branching off relatively late and paleotropical Melastomeae forming a clade within neotropical Melastomeae. This suggests a relatively recent neotropical origin of Melastomeae, followed by dispersal to North America, Africa and Europe, Madagascar, SE Asia, and Australia. Molecular clock estimates, using rbcL and ndhF genetic distances calibrated with the fossils, imply a mid-Tertiary age for the separation between Central American and North American genera, and arrival and dispersal of *Melastoma* and *Osbeckia* in SE Asia from Africa/Madagascar during the Pliocene.

- 522** MIONE, THOMAS. Biological Sciences, Central Connecticut State University, New Britain, CT 06050-4010, U.S.A—*Jaltomata (Solanaceae) of Costa Rica: species delimitation using morphological and ITS sequence variation.*

The genus *Jaltomata*, widespread in Latin America, is noteworthy because: 1) the corolla form is extremely variable among the 50 species, being rotate, tubular or campanulate, 2) flowers of most species are protogynous, exhibiting post-anthesis filament elongation immediately followed by anther dehiscence, 3) berries of most species are consumed, and 4) red floral nectar is produced by some Andean species. Although *Jaltomata* ranges from 40 to 2,900 m of elevation in Costa Rica where it occupies diverse habitats, botanists have recognized only a single species, *J. procumbens* (Cav.) J.L. Gentry in the country. Recent field work suggests that the diversity present in Costa Rica would be better reorganized as three or four species, including *J. procumbens* and *J. repandidentata* (Dunal) Hunz. *Jaltomata repandidentata* is uniquely characterized by heteranthery, sigmoid filaments and curved styles, but has been overlooked in Costa Rica until now. Species are delimited through the use of comparative morphology, and ribosomal ITS sequences obtained in the laboratory of Donald Les at the University of Connecticut.

- 523** MISHKIN, MIRAMANNI, SALLIE J HERMAN\*, AND LINDA A RAUBESON. Department of Biological Sciences, Central Washington University, Ellensburg, WA 98926—*Genetic diversity of a rare buttercup.*

*Ranunculus triternatus* occurs as a few isolated populations in Washington, Oregon, Utah, and Nevada. We are using RAPDs to measure genetic diversity among 25 individuals of one population from the Columbia Hills Preserve near Goldendale, WA. We are also examining 25 individuals from one population of the widespread sagebrush buttercup, *Ranunculus glaberrimus*. This will allow the diversity of the isolated species to be compared to its widespread congener. In our early analyses, each RAPD primer tested shows at least one band unique to each species. So far more variation has been detected among individuals of *R. triternatus* than among individuals of *R. glaberrimus*.

- 524** MOODY, MICHAEL L\* AND DONALD H LES. Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269-3043—*Phylogenetic relationships in Myriophyllum (Haloragaceae).*

Phylogenetic analyses of data from the plastid genes *rbcL* and *matK* were conducted using parsimony and maximum likelihood methods to assess the monophyly of the genus *Myriophyllum* (Haloragaceae) and the relationships among the species. *Myriophyllum* is an aquatic genus that consists of approximately 40 species with the greatest species diversity centered in Australia. Relationships among many aquatic plants have been notoriously difficult to assess due to their often convergent and highly plastic vegetative morphology and structurally reduced flowers. All of these factors have made it difficult to determine species limits and relationships among *Myriophyllum*. *MatK* and *rbcL* have been highly informative in delimiting relationships among species of *Myriophyllum*. Our results indicate two well supported clades in the genus. One clade consists predominantly of plants with eight stamen flowers, the other predominately four stamen flowers. A clade of North American endemics (Schindler's Subgenus *Tessaronia*) is also well supported. Currently, the cpDNA data support a monophyletic *Myriophyllum*; although more inclusive sampling among all genera in the family will be needed. Recently acquired material of Haloragaceae genera and additional species of *Myriophyllum* from Australia are currently being processed for inclusion in expanded analyses.

- 525** MOORE, LAURA A.\*, RASHMI PANT, AND STEVE BOYD. Herbarium, Rancho Santa Ana Botanic Garden, Claremont, CA 91711—*Fruit dimorphism and dispersal in Pterostegia drymarioides.*

*Pterostegia drymarioides* Fischer & Meyer is a monospecific taxon in the Polygonaceae (subfamily *Eriogonoideae*; tribe *Pterostegieae*). First described from horticultural specimens in St. Petersburg (Leningrad), Russia, it is a monoecious, sprawling, wirey annual with fan-shaped leaves resembling those of *Drymaria* (Caryophyllaceae), hence the specific epithet. The range of *Pterostegia* extends from Baja California, Mexico northward through California, including off-shore islands, and eastward into parts of Nevada, Arizona, and Utah. Traditionally, the fruit of *Pterostegia* has been characterized as an achene loosely invested by an involucre bract that is highly modified into a somewhat gibbous winged structure. Examination of plants in the field in southern California, and subsequently, herbarium specimens from throughout the range of the taxon, reveal the presence of two distinct fruit types produced on the same plant: the typical winged fruit, and a nutlet-like fruit in which the involucre bract is not inflated and closely invests the mature achene. To



our knowledge, fruit dimorphism has not been reported previously for *Pterostegia*. Our study characterized the variation in fruit morphology using SEM. We hypothesized that the winged fruit are more readily dispersed by wind than the nutlet-type fruit. This was tested experimentally and notable differences in distance dispersed were recorded. Common garden trials were conducted to test for differences in germination rate between winged and nutlet fruit.

- 526** OESTREICH, ANDREA\*, LINDA A RAUBESON, MARY E COSNER, AND ROBERT K JANSEN. Department of Biological Sciences, Central Washington University, Ellensburg, WA 98926 and Section of Integrative Biology, University of Texas, Austin, TX 78713—*Campanulaceae systematics based on four chloroplast DNA markers*.

We have completed an analysis of 18 genera of Campanulaceae sensu stricto based on nucleotide sequences from the chloroplast genes, *rbcL* and *atpB*, and on chloroplast genome structural mutations. The combined analyses generate a well-resolved and supported tree that has several interesting biogeographic implications. For example, the topology of the tree supports an Asian rather than a Southern Hemisphere origin of the family. The three Asian genera sampled, *Codonopsis*, *Cyananthus* and *Platycodon*, occur in a basal position in the tree whereas the Southern Hemisphere genera form a strongly supported derived clade. Also, *Musschia*, a Macronesian endemic, is linked to the Southern Hemisphere taxa. In terms of phylogenetic implications, the cpDNA tree corresponds well with the distribution of two major pollen types in the Campanulaceae but corresponds poorly with previous suggestions of intrafamilial relationships. Although major intrafamilial patterns are well supported, the relationships among the north temperate genera remain unresolved with the current cpDNA data. Therefore, we are adding data from a third chloroplast gene, *matK*. We will analyze all four data sets together to further resolve our phylogenetic hypotheses.

- 527** POLANS, NEIL O.\*, JEFFERY A. NELSON, AND DAYLE E. SAAR. Department of Biological Sciences and Plant Molecular Biology Center, Northern Illinois University, Dekalb, IL 60115—*Phylogenetic studies of pea comparing different data sets*.

*Pisum* is often divided into three wild species, *fulvum*, (northern and southern) *humile* and *elatius*, in addition to the cultivated *sativum*. In this study, pea taxa representing both wild populations and cultivated accessions are scored for morphological characters, allozymes, RAPDs and ITS sequences. The relatively small number of morphological characters and allozymes precisely organize the species into traditional taxonomic groupings, perhaps in part reflecting the role morphology plays historically in pea classification. A much larger RAPD data set supports several of these same groupings. *P. fulvum* is clearly the most distinct of the pea taxa, while *humile*, *elatius* and *sativum* form a monophyletic group. RAPD trees, however, often show the southern *humile* populations forming a clade that is distinct from *elatius*, *sativum* and even northern *humile*. These results may support previous studies which suggest that northern *humile* may be the sister taxon to *sativum*. The current study presents only modest support for northern *humile* as the single closest relative of the domesticated pea. Additionally, a very small number of polymorphic ITS sites actually places northern *humile* further from *sativum* and reemphasizes the close affinity among all the non-*fulvum* peas. ISSR data are presently being collected to provide yet another measure of relationship among these taxa. Comparisons among all the data sets are also being made, and particularly the informativeness of increasing the number of RAPD markers.

- 528** PRINCE, LINDA M. Department of Botany MRC 166, National Museum of Natural History, Smithsonian Institution, Washington, D.C. 20560—*Additional evidence of monophyly, paraphyly, and polyphyly in genera of Theaceae*.

Recent investigations of DNA sequence data for representatives of Theaceae (sensu stricto = Theoideae of Cronquist) identified several paraphyletic or polyphyletic genera yet significant questions remained due to taxon sampling issues and to the low level of sequence divergence of the previously sampled DNA regions (*rbcL* and *matK* plus partial flanking spacers). New data using nuclear (ITS and *rpb2* intron 23) and chloroplast intergenic spacer (*trnL* to *trnF*) regions are providing increased resolution and higher statistical support for many nodes. Despite differences in taxon sampling, the overall topologies from separate analyses of each of the five data sets are congruent and identify three major clades: *Stewartia* + *Hartia*, *Gordonia* (sensu lato, pro parte) + *Franklinia* + *Schima*, and close *Camellia* relatives [*Camellia*, *Polyspora*, *Laplacea* (sensu stricto, pro parte), *Tutcheria*, etc.]. *Camellia* relatives comprise approximately 75% of the genera (sensu stricto) and 80% of the species in this family. The *trnL* to *trnF* intergenic spacer provides almost the same resolution as either of the previous chloroplast data sets in roughly one quarter to one fifth the number of bases sequenced. The smaller fragment is much easier to amplify from herbarium DNA samples allowing

several critical taxa to be added to the study. ITS sequence data is being used to investigate relationships in the *Hartia* + *Stewartia* clade. It provides moderate bootstrap support for the monophyly of both *Hartia* and *Stewartia*. The *rpb2* intron data set is being used to address relationships in the *Camellia* relatives clade. It provides moderate bootstrap support for the monophyly of each of the *Camellia* relatives thus far sampled (*Camellia*, *Laplacea*, and *Polyspora*), however this remains the largest and least resolved clade of Theaceae.

- 529** RANDLE, CHRISTOPHER PATRICK. Department of Evolution, Ecology and Organismal Biology, Ohio State University, Columbus, OH 43202—*Biosystematics of Harveya Hook. (Orobanchaceae): preliminary studies.*

*Harveya* is a genus of root holoparasites in Orobanchaceae, distributed throughout southern Africa. Preliminary studies of herbarium material indicate that 19-25 species of *Harveya* inhabit South Africa, the center of diversity for this genus. Morphometric analysis of herbarium material was performed to establish species boundaries and morphological characters have been used to generate a preliminary phylogeny of this genus. Future work will involve inclusion of molecular data into phylogenetic analysis, a monograph based on natural groupings, and investigation of the evolution of photosynthetic loci in this holoparasite.

- 530** RENNER, SUSANNE S.\* AND ANDRE CHANDERBALI. Department of Biology, University of Missouri-St. Louis, MO 63121 and The Missouri Botanical Garden, St. Louis, MO 63166—*What is the relationship among Hernandiaceae, Lauraceae, and Monimiaceae, and why is this question so difficult to answer?*

Molecular phylogenetic studies have found that Hernandiaceae, Lauraceae, and Monimiaceae sensu stricto form a monophyletic group, here referred to as the HLM clade. Due to a paucity of phylogenetically informative substitutions relationships among the three families have remained unclear. We analyzed a total of 2,808 aligned nucleotides from a plastid intron, three spacers, and a portion of the nuclear 26S rDNA gene in a dense sample of HLM genera, using four outgroups with differing substitution rates. Despite obtaining single best topologies with maximum likelihood, minimum evolution, and parsimony approaches, family relationships remained as poorly supported as in the previous molecular studies. Exploration of the data indicates that varying substitution rates across lineages or sites, insufficient taxon sampling, fast evolving outgroups, or biased base composition are unlikely to explain the difficult reconstruction. Exclusion of the longest-branched taxa, such as the hemiparasite *Cassytha*, which is nested in Lauraceae, certain Hernandiaceae, and outgroups, had no effect on family relationships. To resolve HLM relationships one could add some of the basal genera sequenced here to the existing five-gene data set of Qiu et al. (1999) to increase taxon sampling density. Alternatively, and this is the strategy we will pursue, one can sequence low-copy nuclear genes for key HLM genera to sample "faster" genes.

- 531** ROBERTS, ROLAND P.\* AND LOWELL E. URBATSCH. Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, 70803—*Phylogenetic investigations of the Ericameria complex (Astereae, Asteraceae).*

Systematic and evolutionary studies of *Ericameria* based largely on morphological and cytological data have resulted in dramatically different phylogenetic concepts. *Ericameria* has been treated as a section of *Haplopappus* and as a distinct genus. At various times, species in the genus *Chrysothamnus* have been transferred to *Ericameria*. Additional proposals suggest that all species of *Chrysothamnus*, and species previously residing in *Haplopappus* sections *Asiris*, *Macronema*, and *Stenotopsis* be treated as *Ericameria*. Furthermore, the genus *Xylothamnia* was established to accommodate certain species that were once part of *Ericameria*. Inferred relationships based on DNA sequence data from a few representative taxa are not entirely in keeping with existing assumptions but provide the basis for additional hypotheses. For example, *Chrysothamnus viscidiflorus* forms a clade including *Solidago petiolaris* and *Sericocarpus tortifolius*, while *Tracyina*, *Ragiopappus*, and *Pentachaeta* form a clade with a representative species of *Ericameria*. This study proposes to investigate, in more detail, phylogenetic relationships of this complex using DNA sequence data from both nuclear and chloroplast markers. Preliminary data suggest that the ITS and ETS regions and the 3' *trnK* intron will provide information useful for phylogenetic reconstruction.

- 532** SHIH, BING-LING<sup>1,2\*</sup>, YUEN-PO YANG<sup>1</sup>, AND SHU-MIAW CHAW<sup>2</sup>. <sup>1</sup>Department of Biological Sciences, National Sun Yat-Sen University, Kaohsiung 80424; <sup>2</sup>Institute of Botany, Academia Sinica, Taipei 11529, Taiwan—*Origin of a Rhododendron hybrid in alpine Taiwan: evidence from nuclear and chloroplast phylogeny.*

In Taiwan the two Taiwan endemic species, *Rhododendron pseudochrysanthum* and *R. hyperythrum*, are sympatric in the northeastern and central alpine ridges. A natural hybrid putatively originated from these

two species was recognized based on field observations and morphological studies. In its leaf-shape, the hybrid resembles the putative parents but with the lower surface being gray to brownish indumentum, which is intermediate between those of the former parent (sparse gray) and the latter (dense rust-brown). Six additional taxa represent other three subgenera of *Rhododendron* were also sampled, and nuclear ITS as well as chloroplast maturase K (cp matK) sequences were employed to examine relationships between the hybrid and its proposed parents. The ITS-based analyses strongly supported that the hybrid originates from interbreed of parental populations in Mt. Nanhu, and the hybrid origin is likely very recent. Indels found in the ITS provided reliable information as to the possible parental parent. We are in the process of assembling the cp matK data. A more thorough assessment as to the maternal and parental parents will be presented.

- 533** SHOCKEY, KARA M.\* AND MICHAEL A. VINCENT. Department of Botany, Iowa State University, Ames, IA 50011—*A revision of the Trifolium polymorphum (Fabaceae) species complex.*

In the most recent monograph of the genus *Trifolium*, Zohary and Heller circumscribe *Trifolium polymorphum* in a broad sense, describing the species as occurring in Texas, Arkansas and Louisiana as well as southern Peru and Chile to the coastal areas of southern Brazil and Argentina. This broad distribution suggested that the species was actually a species complex composed of more than one species. A morphological study of the species complex revealed that several species can easily be circumscribed, and these morphologically distinct entities also have distinct geographical distributions. These include a northern Chilean-North American species, several others from western South America, as well as several from southern and southeastern South America.

- 534** SOZA, VALERIE L. <sup>1</sup>\*, STEVE BOYD<sup>1</sup>, AND ANDREW C. SANDERS<sup>2</sup>. <sup>1</sup>Herbarium, Rancho Santa Ana Botanic Garden, Claremont, CA 91711, and <sup>2</sup>Herbarium, Department of Botany and Plant Sciences, University of California, Riverside, CA 92521—*Phytogeographic “black holes” in southern California botany, a geographic information systems (GIS) model based on herbarium collections of two representative genera, Camissonia and Salvia.*

Our knowledge of plant distribution remains forever incomplete. New species are discovered and described, range extensions are documented for known taxa, and geographical areas remain to be explored and catalogued. This phenomenon holds particularly true in California; with approximately 6300 described taxa, it is home to about one-quarter of all plant species found in the United States and Canada. Yet many physiographic areas in California remain virtual “black holes” in botanical exploration, areas that have received little or no attention by botanical collectors. Attention to these areas is critical in the face of growing urbanization and other anthropogenic change, especially, within southern California. Despite publication of various floras and checklists for areas throughout southern California, the flora is not entirely known and a general decline in collecting activity and academic interest in floristic botanical issues has occurred. In an attempt to identify potential phytogeographic “black holes” in southern California, historical and recent collections of two representative genera were databased and mapped into a Geographic Information Systems (GIS) using ArcView. *Camissonia* and *Salvia* were selected as model taxa because they are widely distributed, generally common, and frequently collected. Taxon name, locality, collection date, collector and collection number, and latitude/longitude coordinates were recorded for herbarium specimens from several institutions in California, primarily Rancho Santa Ana Botanic Garden. Latitude and longitude coordinates in most cases were extrapolated from locality information given on specimen labels, using topographic maps. For this project, southern California was defined as including the ten counties from Santa Barbara, Kern, and Inyo southward. Useful information displayed in the GIS product included overall collection intensity within southern California and within specific geographical areas, collection intensity by dates, distribution of specific taxa, and collection activity by various collectors. Key regions of southern California warranting floristic attention were identified.

- 535** SPJUT, RICHARD W. World Botanical Associates, P. O. Box 2829, Laurel, MD 20709-0829—*A revised taxonomic key to the species and varieties of Taxus (Taxaceae).*

An earlier attempt to identify characteristics of *Taxus* that fit into a phytogeographical species concept, as recognized by Pilger, Rehder and others, has not proved satisfactory for 8-12 species that have been generally recognized in the genus. An alternative approach has been to classify morphological features of *Taxus* without regard to their geographical parameters. Leaf anatomical data suggest a long evolutionary history for the genus, whereas morphological differences in reproductive structures are rarely evident. Generally, species are recognized in three groups with further subdivisions based on leaf anatomical features. These are the

*Wallichiana* Group that includes a *Chinensis* Subgroup, a *Sumatrana* Group, and a *Baccata* Group with *T. canadensis* and *T. cuspidata* species alliances or complexes. Currently, about 55 taxa are recognized, many of which are sympatric or allopatric in distribution, and many hybrids or intermediates are also evident. Examples of the key will be posted. It will also be placed online ([www.worldbotanical.com](http://www.worldbotanical.com)). The key includes more than 100 photographs and illustrations to show comparative examples of the same taxon from different geographic regions. Included are many type specimens. The similarity of taxa from distant geographic regions and their dissimilarity within a geographical area demonstrate that the taxonomic characters applied in the present study are more meaningful than the past arbitrary phytogeographic species concepts of the genus. Nomenclatural references, descriptions, and citations of specimens will be made available in a separate publication on a taxonomic revision of the genus.

**536** SUNDBERG, SCOTT D. Department of Botany and Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331—*The Oregon Flora Project*.

The goal of the Oregon Flora Project is to produce a checklist, a flora and an atlas of Oregon vascular plants in both paper and digital forms. The project is coordinated by Scott Sundberg and led by 21 professional and amateur botanists. Members of the Flora project are currently writing a vascular plant checklist, accumulating and entering plant distribution data, and preparing a Java applet (computer program) for the electronic atlas. The checklist of Oregon vascular plants includes accepted name, synonyms, common name, and origin (native or exotic). The Asteraceae portion of the checklist has been published and other portions are nearing completion. A prototype of the digital atlas has been prepared. It allows users to access data online and produce dot distribution maps on a variety of base maps (e.g., ecoregions, physiographic features, mean annual precipitation, vegetation zones). Additional information on each site record is available by clicking a mouse button on a locality dot. Data are derived from herbarium specimens and species lists from hundreds of sites throughout Oregon. The paper version of the flora will be an identification manual with dichotomous keys, descriptions and illustrations. The digital form will also include random access keys, photographs, a glossary and links to the atlas of Oregon plant localities.

**537** TAYLOR, ROBIN MARIE. Department of Biology, Northern Arizona University, Flagstaff, AZ 86011—*The phylogeny and adaptive radiation of Salvia pachyphylla (Lamiaceae)*.

*Salvia pachyphylla*, as currently recognized, has a disjunct distribution with one large division that occurs along the mountain ranges of southern California, Nevada, and the northern part of Baja California Norte, Mexico. The second, smaller division occurs in the eastern part of Arizona near Winslow. This curious distribution raises many questions as to the original distribution and adaptive radiation of this plant and the evolutionary processes that have taken place. To answer these questions, *Salvia pachyphylla* and a close relative of the *Salvia dorrii* complex have been examined to determine the relationship between *Salvia pachyphylla* and the other members of the complex using molecular techniques. The independent data set derived from nuclear ribosomal DNA (nrDNA) DNA sequences (ITS-1 and ITS-2) was then correlated with morphological characters. The results were used to determine where the most sequence diversity was and the adaptive radiation point of the original population.

**538** THOMPSON, JONATHAN E. AND SUSAN R. KEPHART.\* Department of Biology, Willamette University, Salem, OR 97301—*Varietal and species relationships of the Silene douglasii complex as delimited by pollen ultrastructure*.

Systematists use a broad range of evidence to construct classifications. Micromorphological characters such as pollen and seeds can be used to reevaluate phylogenetic and cladistic relationships based on macromorphology. However, among close relatives within a genus, micromorphological differences are often slight. We examined ultrastructural features of 15 species or varieties in the genus *Silene* L. (Caryophyllaceae), as a means of evaluating relationships within the proposed *S. douglasii* complex. Approximately 10% of the silenes known worldwide occur within North America, and are characterized by polyporate pollen. We detected significant differences among species for both quantitative and meristic characters of the pollen (e.g., grain and pore size, pore number), and used these for phenetic and cladistic analyses. Pollen grains ranged in size from  $35.25 \pm 0.98 \mu\text{m}$  for *S. parryi* to  $31.53 \pm 0.39 \mu\text{m}$  for *S. spaldingii*, which also had the largest number of pores. Surprisingly, we also detected differences in pollen surface ornamentation among varieties of *S. douglasii* Hook, which falls within the same clade as *S. parryi*, and whose position relative to *S. parryi* had previously been disputed.



- 539** TULIG, MELISSA\* AND CURTIS CLARK. Biological Sciences, California State Polytechnic University, Pomona, CA 91768—*Morphological Variation in Mimulus section Diplacus (Scrophulariaceae)*.

*Mimulus* section *Diplacus* consists of erect or prostrate shrubs found throughout California in many habitats. The group has a history of disagreement in taxonomic treatments, including its separation as a separate genus and the recognition of various species, subspecies, and varieties. Recent treatments describe as many as fourteen species or as few as two. Taxonomic boundaries between species and subspecies are obscured by hybridization, especially in southern California where there is overlap in the distributions of six taxa. Measurements of twenty-one floral and vegetative characters have been made from samples of all taxa throughout the range of the section to delineate morphological gaps. Principal components analysis shows a clear separation between species based on variation in the morphology of corolla, calyx, and pedicel features. Hybrid populations are variable in floral features and show an intermediacy between their putative parents. Although hybrids are problematic for the taxonomy of the group, they appear to be geographically limited and confined to disturbed areas.

- 540** URBATSCH, LOWELL E. Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803—*Phylogeny of the Rudbeckiinae (Heliantheae, Asteraceae) based on cpDNA restriction site data and ITS, ETS, and 5', 3' trnK sequence data*.

Subtribe Rudbeckiinae is a small North American monophyletic lineage of Heliantheae composed of approximately 35 species distributed among the genera *Dracopis*, *Ratibida*, and *Rudbeckia*. Four molecular data sets will be used individually and in combination with one another for the purpose of phylogenetic reconstruction. Chloroplast restriction site investigations provide strong support for certain species groups in Rudbeckiinae, but relationships among these clades are largely unresolved. ITS sequence data provide a highly resolved phylogeny that, in general, support traditional concepts for the group. The *Ratibida* clade has strong support, and in most analyses it is sister to *Rudbeckia*. *Rudbeckia*, is resolved as two sublineages corresponding to traditional circumscriptions of subg. *Macrocline* and subg. *Rudbeckia*. *Dracopis*, traditionally recognized as a distinct genus, is sister to *Rudbeckia* subg. *Macrocline*. Species relationships suggested by the two data sets are highly congruent, but some exceptions are evident. Examining additional sequence data from other nuclear and chloroplast markers seek explanations for such discrepancies. Preliminary analysis of external transcribed spacer (ETS) sequence data results in a phylogeny similar to that generated from ITS sequences. Additional chloroplast data are being sought from the 5' and 3' regions of the trnK intron. Efficacy of combining the data sets to generate a phylogeny based on total evidence is being examined.

- 541** VINCENT, MICHAEL A.\* AND KARA M. SHOCKEY. Department of Botany, Miami University, Oxford, OH 45056—*Is Trifolium polymorphum native to North America or introduced?*

*Trifolium polymorphum* has been used in a broad sense by Zohary and Heller in their 1984 monograph to include a wide range of both geographical and morphological variation. We have determined, in a morphometric study, that the broad circumscription encompasses several species, which have distinct morphological and geographical ranges. One species has an unusual disjunct distribution between northern Chile and south-central United States. The Chilean portion has traditionally been called *Trifolium polymorphum*, while the North American portion has been called *Trifolium amphianthum* by many authors. There is no morphological hiatus between these portions, and we believe that they represent a species in its native range and an introduction in the North American range. The correct name for this entity, as well as evidence that it is introduced into North America, are presented.

- 542** VON BALTHAZAR, MARIA\*, YIN-LONG QIU, AND PETER K. ENDRESS. University of Zurich, Zollikerstrasse 107, CH-8008 Zurich, Switzerland—*Phylogenetic relationships and character evolution in Buxaceae*.

Buxaceae are a small eudicot family of mostly monoecious evergreen shrubs and comprise up to five genera (*Buxus*, *Notobuxus*, *Sarcococca*, *Pachysandra*, *Styloceras*) and 120 species. Delimitation of the family and inter- and intrageneric relationships within the family have been controversial. Sequences of nuclear ITS and plastid *ndhF* from 25 representatives of Buxaceae were analyzed separately and in combination to resolve phylogenetic relationships among and within genera. Two major clades were identified: the clade of *Pachysandra*, *Sarcococca*, and *Styloceras* and the clade of *Buxus* and *Notobuxus*. *Pachysandra* and *Sarcococca* were two strongly supported monophyletic groups. The sister relationship of *Sarcococca* to the clade of *Pachysandra* and *Styloceras* is also strongly supported. American and Eurasian *Buxus* each form a strongly

supported clade. The controversial genus *Notobuxus* is embedded among African members of *Buxus*. Ongoing morphological studies will improve our understanding of the evolution of morphological characters and phylogenetic relationships of Buxaceae.

- 543** WALLICK, KYLE P\*, MIA MOLVRAJ, PAUL J. KORES, AND WAYNE J. ELISENS. Department of Botany and Microbiology, University of Oklahoma, Norman, OK 73019—*A phylogenetic analysis of Buddlejaceae s.s. inferred from the trnL region of cpDNA.*

The Buddlejaceae *sensu stricto* is a small group of plants which recent evidence has shown to consist of four genera. The genus *Buddleia* is the largest and most widely distributed genus, consisting of approximately 100 species distributed in Asia, Africa, and the Americas. *Emorya*, *Gomphostigma*, and *Nicodemia*, each mono- or ditypic genera, are more geographically restricted. Sequences from 28 ingroup and seven outgroup taxa were examined in a phylogenetic analysis of the *trnL* intron and *trnL*-F intergenic spacer region of the chloroplast DNA to test monophyly of the ingroup and to determine relationships among *Buddleia* and related genera. Parsimony analyses result in two major clades with modest support. One clade consists primarily of Asian species of *Buddleia* and the segregate genera. The sister clade is composed of New World and South African species of *Buddleia*. High bootstrap values support the close relationships among the four genera, but our data do not support recognition of *Emorya*, *Gomphostigma*, and *Nicodemia* as separate genera. Traditional sectional treatments of *Buddleia*, based primarily on floral morphological characters, are well supported. The two species of *Nicodemia*, often regarded as a section within *Buddleia* based upon its fleshy fruits, are shown to be closely related. Other interspecific relationships are poorly supported or unresolved.

- 544** WERNER, N. MISA\* AND ROBERT A. PRICE. Department of Botany, University of Georgia, Athens, GA 30602—*Phylogeny and morphological evolution of Marcgraviaceae: insights from three chloroplast genes.*

Marcgraviaceae comprises seven genera and approximately 130 species distributed from southern Mexico to northern Bolivia including the Caribbean islands. Distinctive morphological features include hemiepiphytic habit, hypophyllous glands, reversible heteroblasty, and highly modified bracts which are transformed into pitcher-like extrafloral nectaries. Phylogenetic analysis of *rbcL* sequence data strongly supports the monophyly of the family and an alliance with Tetrameristaceae, Pellicieraceae, and Balsaminaceae. A possible sister-group relationship of Marcgraviaceae with Tetrameristaceae + Pellicieraceae is weakly supported by this analysis. Marcgraviaceae exhibit an unusually low amount of sequence divergence in comparison to their close relatives. Relationships within the family are investigated using *trnL*-F and *ndhF* sequence comparisons. These data resolve two major lineages within Marcgraviaceae corresponding to subfamilies Marcgravioideae and Noranteoideae. The monogeneric Marcgravioideae are united by several morphological synapomorphies and a 4 bp indel in the *trnL* intron. In contrast, subfamily Noranteoideae appears to be delimited by plesiomorphic morphological characters, but it is supported by molecular data. Despite considerable morphological heterogeneity within Noranteoideae, our sequence data do not resolve currently recognized genera as monophyletic groups.

- 545** WETZEL, SABINE B., ALAN PATON, KONRAD BACHMANN, AND FRANK R. BLATTNER.\* Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Gatersleben, Germany, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, UK—*Phylogenetic studies within the genus Ocimum L. (Labiatae) based on ITS sequences of the nrDNA.*

*Ocimum* L. is a genus within the Labiatae, which contains several spices and medicinal herbs. The economically most important species are *O.basilicum*, *O.minimum*, *O.americanum* and the hybrid *O. x citriodorum*, which are used for essential oil production and as pot herbs. Species number is estimated between 30 and 160. A recent revision of the genus based on morphology and cytology described 65 species native in the tropical areas of America, Africa and Asia (Paton et al. 1999, in: Hiltunen and Holm *Basil: the genus Ocimum*.) Some species were placed into synonymy, and the genera *Erythroclamys*, *Becium* and *Orthosiphon* subgen. *Nautochilus* were incorporated into the genus *Ocimum*. Recently also the genus *Plectranthus* is suggested to be part of *Ocimum*. To assess phylogenetic relationships of *Ocimum* and related genera, the morphological hypothesis was tested with an analysis of nrDNA internal transcribed spacer sequences (ITS). Cladistic and phenetic analyses resulted in a paraphyletic genus *Ocimum* with *Plectranthus*, *Aeollanthus*, *Catoferia*, and *Pycnostachys* grouping within *Ocimum*. *Plectranthus* is a monophyletic sistergroup of subgen. *Nautochilus*, *Aeollanthus*, which morphologically resembles *Plectranthus*, is part of section *Gratissima*. Most morphologically defined sections of *Ocimum* could be confirmed by the molecular analysis. However,

*O. minimum*, often considered as a subspecies of *Ocimum basilicum*, is not conspecific with *O. basilicum* and even groups outside of section *Ocimum*.

- 546** WHITLOCK, BARBARA A.\*, KENNETH G. KAROL, AND WILLIAM S. ALVERSON. Harvard University Herbaria, Cambridge, MA 02138; Cell Biology and Molecular Genetics, University of Maryland, College Park, MD 20742; Department of Botany, The Field Museum, Chicago, IL 60605—*Chloroplast DNA sequences confirm the placement of Oceanopapaver within the Grewioideae (Tiliaceae or Malvaceae s.l.).*

The monotypic genus *Oceanopapaver* is an endemic shrub found growing on serpentine soils in New Caledonia. Since its description in 1932, *O. neocaledonicum* Guillaumin has been placed in at least five families, including Capparaceae, Cistaceae, Oceanopapaveraceae, Papaveraceae and Tiliaceae. The chloroplast genes *rbcl* and *ndhF* were sequenced and phylogenetic analyses performed to clarify the taxonomic placement of this genus. The results strongly support the inclusion of *Oceanopapaver* in a clade of former Tiliaceae, the Grewioideae (Malvaceae s.l.). Within Grewioideae, *Oceanopapaver* forms a well-supported clade with representatives of the pantropical genus *Corchorus* and the endemic Malagasy genus *Pseudocorchorus*. This placement was anticipated by Trel et al. (1996) who, based on morphology, reduced *Oceanopapaver* to a synonym of *Corchorus*. Morphological characters consistent with this placement include stellate indumentum, mucilage canals, valvate sepals with stellate hairs on the adaxial surface, and pollen morphology.

- 547** WHITSON, MARY KATHRYN. Department of Botany, Box 90338, Duke University, Durham, NC 27708—*Does hybridization play a role in the morphological similarity between Physalis arenicola (Solanaceae) and a co-occurring, closely related species?*

Various workers have postulated that members of *Physalis* section *Lanceolatae* naturally hybridize. Successful artificial hybridizations have been accomplished, but documented cases of natural hybridization are rare. In areas of sympatry, different habitat preferences help keep species of the *Lanceolatae* separated. In north Florida, however, populations of *P. arenicola* and an undescribed species of the *Lanceolatae* co-occur along the bluffs of the Apalachicola river. This provides a unique opportunity to address the question of natural hybridization among species of the *Lanceolatae*. *Physalis arenicola* occurs throughout Florida, favoring sandy, open areas. The undescribed species grows on wooded river bluffs, and is apparently limited to a two county region. Vegetatively, these taxa are quite similar, though *P. arenicola* encompasses a broader range of morphological variation. The two taxa are best distinguished by differences in rhizome morphology. Is the vegetative similarity between these species due to the fact that they are closely related and still share plesiomorphic characters, or is there some gene flow between them? Leaf material was collected from multiple individuals in the mixed species populations, and from isolated populations of each taxon, including individuals of *P. arenicola* from southern Florida, where the river bluff taxon does not occur. Isozyme data was generated using the following 12 enzyme systems: ACO, ALD, GDH, G3PDH, IDH, MDH, ME, PGI, PGM, PRX, SKD, and TPI. Within *P. arenicola*, ACO, GDH, ME, PGI, PRX and TPI are polymorphic. IDH is variable within both species. IDH also shows species specific variation, as do MDH and SKD. Each species has a unique *ITS* sequence. Eight characters differentiate these sequences, including an 8 bp indel. The amount of *ITS* sequence variation between these species is similar to that between sequences of other closely related species within the *Lanceolatae*.

- 548** YOO, KI-OUNG\*, P. P. LOWRY, J. L. WALCK, AND JUN WEN. \*Department of Biology, Colorado State University, Fort Collins, CO 80523-1878, , \*\*Missouri Botanical Garden P.O. Box 299, St. Louis, Missouri 63166, \*\*\*Department of Biology, Middle Tennessee State University, P.O. Box 60, Murfreesboro, TN 37132—*A Phylogenetic and Biogeographic Analysis of Osmorhiza (Apiaceae) Based on ITS and ndhF Sequences.*

*Osmorhiza* Raf. (Apiaceae) consists of ten species disjunctly distributed in temperate Asia (1 sp.) and the Americas (9 spp.). *Osmorhiza berteroi* DC. and *O. depauperata* Philippi are disjunct between North and South America. Within North America, these two species are disjunctly distributed in eastern and western North America and the Great Lakes regions. Phylogenetic analysis was conducted to clarify the interspecific and intraspecific relationships of based on sequences of the ITS regions of nrDNA and *ndhF* chloroplast gene. With *Myrrhis* as the outgroup, the monophyly of *Osmorhiza* is strongly supported. The ITS phylogeny suggests the basal position of the Asiatic *O. aristata* and the monophyly of the nine New World species. *Osmorhiza aristata* is relatively divergent from other species even though it is morphologically similar to the eastern North American *O. claytonii* and *O. longistylis*. *Osmorhiza claytonii* and *O. longistylis* form a clade. *Osmorhiza brachypoda*, *O. depauperata*, *O. occidentalis* and *O. purpurea* constitute a monophyletic

group. The seven populations of the widespread *O. berteroii* form a clade, which showed no or little sequence divergence, suggesting recent colonization of these widely separated regions by this species. Disjunct populations of *O. depauperata* from the Rocky Mountains and eastern North American have similar ITS profile and form a clade. *Osmorhiza occidentalis*, however shows a high level of infraspecific sequence divergence. The sequence divergence of *ndhF* gene within *Osmorhiza* is low. Congruent with the ITS data set, the *ndhF* phylogeny suggests that *O. aristata* from Asia is basal within the genus. The remaining nine from the New World form a monophyletic group. *Osmorhiza glabrata* and *O. depauperata* form a subclade, whereas the ITS phylogeny places *O. glabrata* basal to the New World clade. The ITS and *ndhF* phylogenies suggest rapid diversifications of *Osmorhiza* in western North America.

## XV. Teaching Section

### Symposium: Using educational technology to foster learning centered pedagogies

- 549** BUCKLEY, DONALD\* AND DAVID KRAMER. Department of Biological Sciences, Quinnipiac University, Hamden, CT 06410 and Department of Evolution, Ecology, and Organismal Biology, Ohio State University at Mansfield, Mansfield, OH 44906-1547—*Symposium Abstract: Using Educational Technology to Foster Learning Centered Pedagogies.*

During the past decade, concerns about low levels of science literacy have led to serious soul-searching about the effectiveness of science education in American colleges and universities. In its recent “Shaping the Future” call to arms, the National Science Foundation has emphasized the need to strengthen the quality of science education by fostering learning-centered and inquiry-orientated approaches to teaching. Educational technology has been touted as a tool that can improve the quality of teaching, but it could be argued that this claim is paradigm-dependent. For example, some technologies may improve presentations, but they do not necessarily increase the likelihood that a student has been moved from passive to active learning. This symposium will explore uses of educational technology that are intended to support learning-centered and inquiry-oriented pedagogies, especially those applications that encourage student experience in the process of science.

- 550** BUCKLEY, DONALD. Department of Biological Sciences, Quinnipiac University, Hamden, CT, 06518—*The “Coverage Dilemma”: Can we make room for learning-centered and inquiry-oriented pedagogies with educational technology?*

Many faculty believe that they cannot compromise content coverage by committing precious class time to the incorporation of powerful teaching styles and inquiry-oriented content. However, we may be able to use web-based instructional technology to transfer the authority of learning foundational information to our students. These tools will serve as “smart” home work assignments before class. They will be smart in the sense that the web server can monitor student engagement and notify the students and instructor automatically about non-participation. These environments can provide interactivity to foster active learning styles and powerful assessment tools to provide real-time feedback, incentive systems to facilitate competency-based learning standards, and diagnostic clues about individual learning experiences and needs. This learning-centered technology will allow us to move important lower-level learning processes out of the class time and into the student’s study time, making more room in the classroom for powerful pedagogies and more inquiry orientation.

- 551** DONOVAN, SAM. Biology Department, Beloit College, Beloit, WI, 53511—*The Biology Student Workbench: Resources for Bioinformatics in the Classroom.*

Interested in developing curricular materials that support the use of molecular data to frame and address biological questions in your courses? Resources including problem sets, laboratory investigations, and other teaching materials submitted by faculty who are currently using bioinformatics in their classrooms <bioquest/bioinformatics/intro.html> with the Biology Workbench <biology.ncsa.uiuc.edu> will be introduced. This web-based suite of tools for finding, analyzing and visualizing molecular data is a publicly available, full-featured bioinformatics research interface developed at the National Center for Supercomputing Applications (NCSA).



- 552** MICKLE, JAMES E. Department of Botany, North Carolina State University, Raleigh, NC 27695-7612—*LeafLab: A research simulation to foster the students' experience in the process of science.*

LeafLab is a newly developed on-line simulation program for the study of photosynthesis. The program simulates use of an infrared gas analyzer that measures rate of net CO<sub>2</sub> absorption. Plant variables include C3 vs. C4 photosynthesis, shade vs. direct sunlight, and ploidy level under parameters including light intensity, light quality, temperature, gas flow, and carbon dioxide concentration. Data collected from these virtual experiments are calculated to determine photosynthetic rates. The simulation is based on published data and permits students to run a variety of experiments under various conditions. The program also has graphing capacity so that students can compare and interpret multiple experiments. An advantage to this system is that physiological principles can be taught without purchase of expensive, single-use equipment. Students observed using this program have gained insight into both the scientific method and environmental parameters that affect photosynthesis.

- 553** NIESENBAUM, RICAHRD A. Biology Department, Muhlenberg College, Allentown, PA, 18104-5586—*Using technology to broaden the scientific experience through project based learning.*

Full engagement in science includes the development of a hypothesis, designing and conducting an appropriate experiment to test that hypothesis, and appropriate analysis and dissemination of results. Here I report on an NSF-ILI funded project to enhance the data acquisition, analysis, and presentation components of a project-based curriculum focusing on an advanced undergraduate plant ecology course. The course is taught almost exclusively in the field and is focused on articulating scientific questions. Students conduct semester-long experimental research projects and present their results at a public poster session on campus. Using NSF funded computers, peripherals, and software, the quality of the student research was enhanced, and student pride and ownership over the work increased. Students exhibited a greater understanding of science and quantitative analysis. One student project was published in a peer-reviewed journal, and another was presented at a regional meeting. The number of students taking elective courses in related areas, continuing research and senior honors projects, and applying and accepted to graduate programs in ecological and plant sciences significantly increased. Student poster sessions served to create a campus-wide culture of science.

- 554** RUSSELL, SCOTT D. Department of Botany and Microbiology, University of Oklahoma, Norman, OK 73019-0245—*Interactivity on the Internet and interactive learning environments.*

The challenge of incorporating interactivity into the sciences and particularly botany seem increasingly to require technically-gifted coalitions of educators, illustrators, computer graphic artists and programmers. Methods for incorporating interactivity are numerous, ranging from Internet delivery (Java, various movie formats, virtual reality, ray-tracing reconstructions, Shockwave, Chime, etc.) to offline proprietary solutions (DVDs, CD-ROMs, restrictive individual use licenses). Economic models to develop and purchase sophisticated technologically advanced products run counter to diminishing resource and budget availability. Problems also exist in making the message and not the medium memorable. The problem now is how to develop a contextually rich interactive environment that scales between significant ranges of intellectual ability. Despite an increase in the means of interactive delivery, why has development seemed to languish?

- 555** WATERMAN, MARGARET A\* AND ETHEL STANLEY. Department of Biology, Southeast Missouri State University, Cape Girardeau, MO, 63701., BioQUEST, Beloit College, Beloit, WI, 53511—*Investigative Case-Based Learning.*

We would like to invite undergraduate biology faculty to discuss teaching strategies for using case-based materials in their courses. We will look specifically at a prototype LifeLines OnLine (BSA version) configured for plant biology at <http://bioquest.org/bsalife>. LifeLines OnLine is a web based resource of highly contextualized learning materials that uses the accessible, familiar format of a newspaper to support investigative, case-based learning strategies. Students access these materials by reading items of interest, such as headlines, articles, classifieds, editorials, comic strips and obituaries that link to case-based extensions, e.g., interviews, reports, emails, press releases, bibliographies and internet sites. Students decide on questions to investigate, develop portfolios of tools, methodologies and knowledge, and practice coming to defensible resolutions of their questions. It is our goal to support the building of information management skills needed not only for the biology course, but also for lifelong learning.

## Contributed Papers

- 556** GIBSON, J. PHIL. Department of Biology, Agnes Scott College, Decatur, GA 30030—*Why is that cell red? A microtechnique based approach for teaching a plant anatomy lab.*

Many introductory biology laboratories include a session devoted to plant anatomy. Students often view these laboratory sessions as tedious, laborious, and requiring little more than memorization of slides. Thus, students do not sufficiently learn the fundamentals of plant anatomy, nor do they develop an appreciation of histological techniques and comparative approaches that can be used in biology. I propose the use of plant anatomy laboratory exercises in which students not only view prepared slides, but they also prepare their own slides. In the laboratory exercise I will describe, students use histological techniques for the staining of biological tissues to identify slides containing unknown plants. Through this approach, students not only make a more detailed study of plant anatomy, but they also learn fundamentals of histological techniques, concepts related to cell wall biochemistry, and how to conduct comparative analyses. It has been my experience that students develop a greater understanding of plant anatomy and key anatomical concepts through the use of this approach.

- 557** MITRA, MADHUMI. Department of Natural Sciences, University of Maryland Eastern Shore, Princess Anne, MD 21853—*Richer pedagogic outcomes in Marine Botany course through integration of service learning.*

Service learning combines academic instruction with service that addresses the needs of the community. This active learning was integrated in Marine Botany course in Fall'99 at the University of Maryland Eastern Shore. The community needs were identified following partnerships with Eastern Shore parks. The service learning project involved preparing brochures for Assateague Island National Park and Pocomoke State Park (Maryland) respectively. These brochures were designed to focus on the lists of both identified and unidentified floras found in different marine and estuarine environments of the parks. Through planning, action and reflection, the students were able to hone some of their academic and life skills. At the end of the project, a survey was conducted for evaluating this experience. Survey results show that more than 90 percent of the students had a better appreciation of plant science and its social impact.

- 558** MUELLER, RICHARD J. Department of Biology, Utah State University, Logan, UT 84322—*Using the plastochron index to improve student's understanding of exponential plant growth and the use of logarithms.*

The plastochron and leaf plastochron indices are methods created by R.O. Erickson and F.J. Michelini in 1957 to measure the age of whole plants and individual leaves based on their morphology rather than chronological age. They have been particularly useful for detailed studies of whole shoot and leaf development. Since the indices are based on measurements of exponential plant growth, they provide an opportunity to demonstrate the value of applying mathematics to a biological problem. I will describe a laboratory exercise from a upper-division Plant Structure course in which students are presented with the theoretical basis of the indices and then calculate them for *Xanthium strumarium* (cocklebur) plants of various ages (4-6 weeks). The exercise demonstrates both the potential variability in plant growth and the results of an exponential growth rate. Pre- and post-tests showed a significant increase in the student's understanding of exponential growth and their ability of work with logarithms. This exercise was created as part of the BioMathLab project at USU supported by Department of Education FIPSE grant P116B 71688.

- 559** REINSVOLD, ROBERT J.\* AND DAVID W. KRAMER. Department of Biological Sciences, University of Northern Colorado, Greeley, CO 80639 and Department of Biology, Ohio State University at Mansfield, Mansfield, OH 44906—*Educational outreach activities of the Botanical Society of America.*

In 1995, the Botanical Society of America identified major educational goals for the future of plant science in their report *Botany for the Next Millennium*. One of the primary "calls to action" was to "promote effective botanical education of K-12". In response to this call, the Education Committee and the Teaching Section of BSA has led a national effort to help K-12 teachers learn how to use plants to teach general biology principles. In addition, BSA is collaborating with other organizations to advance botanical education at both the precollege and undergraduate levels. These organizations include American Society of Plant Physiologists, Project Kaleidoscope, American Phytopathological Society, American Society of Agronomy, Coalition for Education in the Life Sciences, BioQUEST, American Institute of Biological Sciences, National

Association of Biology Teachers, and National Association of Science Teachers. This presentation will report on the success of past workshops and outreach activities that BSA has sponsored. A discussion will follow to generate additional ideas and suggestions for additional improvement in outreach opportunities and effectiveness.

- 560** RICE, STANLEY A. Department of Biological Sciences, Southeastern Oklahoma State University, Durant OK 74701-0609—*Teaching principles of fluid dynamics using xylem and transpiration measurements.*

The Hagen-Poiseuille principle (which relates water flux rate to the fourth power of the radius of a pipe) has cross-disciplinary applications (in engineering and human and plant physiology) and is thus useful for teaching general laboratories in which we want the students to see connections between scientific disciplines. Students in a general botany measured frequency distributions of xylem diameters in bean stems. They then calculated total xylem conductance based upon these models: the sum; the sum of squares; the sum of cubes; and the sum of fourth powers, of measured diameters. They compared conductance calculations with actual transpiration rates, determined earlier by the instructor, using linear regression. The expected result was that transpiration would be most closely related to the sum of the fourth powers. However, all of the models were equally good at predicting transpiration, except the sum of diameters. This contradictory result led to an interesting consideration of the differences between a simple physical law and the complexity of biological processes.

- 561** VERHEY, STEVEN D.\* AND STEVEN STEFANIDES. Department of Biology, Central Washington University, Ellensburg, WA 98926 (SDV); and Wenatchee Valley College, Wenatchee, WA 98801 (SS)—*The plastid genome project: integrated cell biology/molecular biology/genomics teaching laboratory.*

It can be difficult to present courses in molecular techniques without having the techniques seem prescribed, “cookbook,” and disembodied from the realities of the practice of science. It can also be difficult to give students the sense of being part of a larger research community, and of collecting data that will have value once the course is finished and the student has moved on. In this series of laboratory exercises, which lasts approximately one academic quarter, students are introduced to numerous cellular and molecular techniques as they isolate plastids, prepare plastid DNA, construct a plastid DNA library, and sequence clones from the library. Using their data and data from their classmates, students can carry out a variety of self-designed analyses including ones based on genomics and taxonomy. By connecting courses carrying out these exercises at numerous institutions, it will be possible to sequence entire genomes and build a literature of sequence, functional, genomic, taxonomic, and proteomic data.

- 562** WANDERSEE, JAMES H.\* AND ELISABETH E. SCHUSSLER. Louisiana State University, 15° Laboratory, 223-F Peabody Hall, Baton Rouge, LA 70803—*National Survey on the Public's Perception of Plants.*

In February 2000, the authors conducted a national study of the public's perception of plants. The investigation involved 502 participants from 26 states. It was designed in conjunction with BSA's “Botany for the Next Millennium” document and the authors' own Theory of Plant Blindness (ABT,1999). This survey probed participants' perception level for plants in their environment, their past plant-related activities, the relative importance they ascribe to plants in their life, their plant identification skills, the influence of others on their perceptions and understandings of plants, their knowledge of plant experts, their ranked importance of various uses of plants, and their perceived knowledge of plant organs. The study focused on “Generation Y” youth—which includes the age of students now in high school and undergraduate college classrooms (n=302), and on women with children (n=200), who are currently involved in raising our nation's youth. Chi-square analysis and cross-tabulation, as well as analysis of agreement using Cohen's kappa, Pearson's r correlation coefficient, and Krippendorff's content analysis, were used to interpret the survey item responses. Model response patterns for today's teenagers and for today's active mothers were constructed—with similarities and differences between groups highlighted. Finally, implications for botanical education were drawn, centering upon the study's finding that prior informal educational experiences with plants appear to be a key instructional variable, and on the finding that the mother's plant-related experiences signal the plant-related experiences that she will provide for her children.

## Contributed Posters

- 563** HANUS<sup>1</sup>, FRANK JOSEPH\*, KEN FERSCHWEILER<sup>2</sup>, AND SHERRY KAY PITTAM<sup>3</sup>.  
<sup>1,3</sup>Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, USA <sup>2</sup>Northwest Alliance for Computational Science and Engineering, 218 Alumni Center, Oregon State University, Corvallis, OR 97331, USA—*Present your data on the Web.*

Funding agencies are insisting that scientific research data be published on the web. They are requiring that funded projects make the data available on the web to the public and to other researchers. Of course, issues of privacy, security and sensitivity must be addressed. In making this data easily available on the Web we have developed methods and software designed with the research scientist, typically a person not trained in computer science, in mind. The software is implemented to minimize the use of restrictive and arcane database and programming languages utilized in conventional Web-to-database sites. We will present a demonstration of the power of this approach to web accessible database development. We will also present several biological research projects and teaching tools implemented using the methods and software designed by our research team and often maintained by the scientists themselves. Each project was publically funded, had data in a spreadsheet or PC/MAC database and held information that was of interest to other scientists. That data is now available on the Web from interfaces that allows the user to query for results and should the database owner decide, to download the data. This data is being used by school students, teachers, other researchers, government agencies and the general public.

- 564** HIRREL, MARC C. AND JOHN S. CHOINSKI.\* Department of Biology, University of Central Arkansas, Conway, AR 72035—*The use of investigative biology exercises in freshman labs improves the retention of biology majors in advanced courses.*

Traditional introductory courses in sciences provide students with a “cookbook” laboratory experience that absolves them of taking responsibility for their education. Such courses fail to engage them in science as a dynamic process. To address this problem, we, in Fall 1997, adopted the approach, “less is more!” Rather than having to learn new methodologies each week, students work through a directed investigation on an important principle, and then, explore that principle in more depth with an experiment of their own design the following week. The use of computer workstations integrated with Vernier science hardware and software allows investigative labs to be performed in a 2.5-3 hr lab period. Three important advantages to this approach for students are: 1) gaining hands-on experience with the scientific method while investigating fundamental principles, 2) learning to take responsibility for lab preparedness and, ultimately, for their education, and 3) greater success in upper division courses. The limitations to this approach include: 1) not covering the breadth of introductory topics, 2) time constraints sometimes limit discussion of data and the principles investigated, and 3) poor K-12 science backgrounds cause problems in mastering the curriculum. Student success rates have followed a traditional learning curve. They were low at first, but have begun to rise primarily as a result of continual curriculum modification. We have found that the effort spent teaching freshmen students about the process of science pays off later with greater retention of biology majors in advanced courses. Preliminary assessment of students by faculty teaching upper division courses suggests that they are better prepared and more engaged. Through the “less is more” approach, students learn the foundations of biology by studying a few, well connected principles, rather than by memorizing a series of disconnected facts.



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