

PLENARY ADDRESS

1 NABHAN, GARY P.

Center for Sustainable Environments, Northern Arizona University, Flagstaff, AZ 86011-5765

Bridging Western science and Indigenous science: ethnobiology and cross-cultural conservation collaborations in the binational Southwest

The demographics of graduate biology is changing to include more Native Americans, Latin Americans and indigenous peoples from other continents than ever before. Biology is not no longer Western science as much as it is cross-cultural science, with the capacity to integrate traditional ecological knowledge from diverse cultures to develop and test novel hypotheses. But with this opportunity comes the challenge of teaching biology less ethnocentrically, of developing multicultural field teams, and involving diverse communities as collaborators in interpreting and applying the results of field science. On incubation grounds for these experiments is the binational Southwest, where I have been involved in novel cross-cultural projects with indigenous peoples of the Colorado Plateau and Sonoran Desert. The Colorado Plateau is not only one of the most diverse ecoregions north of the tropics in terms of its species richness of plants, birds, butterflies and tiger beetles; it is also culturally diverse, with more speakers of Native American languages persisting in this region than all others in North America. It and the binational Sonoran Desert region are also rich in narrowly-distributed endemics for which local residents have considerably more information than scientists who have only sporadically visited their habitats. I will present as case studies two collaborations with indigenous communities which honor both Western and indigenous scientific knowledge, and which are leading to on-ground conservation benefits. Biologists can no longer ignore the vital links between biodiversity and cultural diversity; our future depends upon how well we link them.

ADDRESS OF THE BSA PRESIDENT-ELECT

2 JERNSTEDT, JUDY

Agronomy and Range Science, University of California, Davis, CA 95616

With apologies to Euell Gibbons: stalking the wild Welwitschia

One of the many professional attractions for me of a career in plant biology is the opportunity to meet and work with interesting colleagues, often in fascinating locations. A convergence of circumstances, beginning with my postdoctoral tenure at Manchester University and culminating with the XVI International Botanical Congress in St. Louis, took a colleague and me to southern Africa last year. One of the top two objectives of the trip was to see *Welwitschia mirabilis* in its native habitat. I wanted to add *Welwitschia* to my botanical “life list,” which already included the Rhynie chert, Linnaeus’ garden, *Sequoiadendron giganteum*, the Royal Botanic Gardens at Kew, and *Stigmara*, among other things. Through the wonders of e-mail, global positioning system (GPS) coordinates, and 4-wheel drive vehicles, our mission was accomplished, with the added bonus of finding and adding to the known populations of *Welwitschia* with extra foliage leaves.

PLENARY SYMPOSIUM

COMPARATIVE AND FUNCTIONAL GENOMICS: EVOLUTIONARY IMPLICATIONS

3 SOLTIS, DOUGLAS E.

Dept. of Botany and the Genetics Institute, University of Florida, Gainesville, FL 32611

Comparative and functional genomics: evolutionary implications

This symposium will explore the rapidly developing impact of genomics research on evolutionary biology. Functional genomics deals with what portions of the genome actually do; comparative genomics involves the comparison of genomes, including genome structure and evolution. Phylogeny has a major role to play in genomics research; phylogenomics exploits the use of evolutionary information to facilitate the assignment of gene function. The five speakers in this symposium will discuss evolutionary implications of their genomics-based research. Genomics research on maize has elucidated the major role that transposable elements play in accelerating the pace of allelic diversification. Allelic diversity is the “raw material” for natural selection; hence, mechanisms that modulate allelic diversity should play an important evolutionary role. Genomics research is playing a major role in crop improvement. Because crop improvement and evolution have been accompanied by dramatic morphological alterations, crops provide model systems for analyses of the evolutionary and developmental genetics underlying morphological innovation in nature. Concomitantly, because many important crops are polyploids, these crops provide models for analyzing the fate of duplicated genes and genomes following polyploidy, which is a major force in plant evolution. Genomic investigations reveal that polyploidy is associated with novel genomic interactions and molecular genetic mechanisms. Microarrays represent one of the most important experimental approaches for discovering the function of genes and have enormous evolutionary application. We may expect to have extensive data bases of gene expression information, which in turn will provide insights into the “ecology of the genome.”

4 OSBORN, T. C.*, M. E. SCHRANZ, P. A. QUIJADA, AND L. N. LUKENS

Dept. of Agronomy, University of Wisconsin, Madison, WI 53706

Polyploidy and genetic variation in Brassica species

Genome redundancy, generated by polyploidy, is a prominent feature of many plant species and may provide novel genetic variation for the evolution of phenotypic diversity. We have investigated the molecular basis of this phenomenon in the genus *Brassica* by analyzing both recent and ancient polyploid events. *Brassica rapa* and *B. oleracea* behave genetically as diploids, but they have replicated genomes probably due to ancient polyploid events. These species also contain genotypes with a wide range of flowering times, an important component of the vast morphological diversity within the species. Our results from comparative mapping suggest that much of the variation in flowering time within *B. rapa* is due to alleles at multiple copies of FLC, a key regulator of flowering time in *Arabidopsis thaliana*. Classical genetic and transgenic experiments in *A. thaliana* demonstrate that FLC inhibits flowering in a rheostat-like manner. In *B. rapa*, the effects of alleles within and between FLC loci are completely additive, suggesting that polyploidy has provided a mechanism for expanding the rheostat-like effects of FLC on flowering time. The *Brassica* genus also includes amphidiploid species that arose relatively recently through hybridization of the diploid species. These amphi-

diploids can be resynthesized by crossing diploids and treating with colchicine, and our molecular analyses of early generation progenies suggest that polyploid genomes can change rapidly after formation. Variation in flowering time also has evolved quickly among the progeny of resynthesized *B. napus* polyploids, and this variation is heritable in self- and out-cross progenies. Thus, polyploidy not only affects phenotypic diversity by providing additional loci for the accumulation and maintenance of allelic variation, but it also may trigger the generation of novel genetic variation. We are now studying the structure and function of genes in resynthesized polyploids to understand the molecular basis of new genetic variation.

5 SOMERVILLE, CHRIS

Carnegie Institution and Dept. of Biological Sciences, Stanford University, Stanford CA 94305

The evolution of chemical diversity

The evolution of higher plants has been accompanied by the evolution of enzymes that lead to the production of a wide range of chemical constituents. Chemical structures are known for more than 15,000 chemical constituents on plants and, by extrapolation, it has been estimated that higher plants collectively produce more than 100,000 chemical constituents. A relatively simple class of compounds that exhibit substantial chemical diversity is fatty acids that accumulate as major constituents of storage oils in many species. Many of the genes encoding the enzymes required for fatty acid desaturation were cloned by molecular genetic techniques in *Arabidopsis*. These genes were then used to identify variants of the genes from diverse plant species. These studies revealed that essentially all chemical diversity in plant fatty acids was due to the action of structural variants of a single enzyme. Mechanistic studies of this enzyme family showed that minor changes in the amino acid composition of the protein near the active site could change the outcome of the reaction catalyzed by this family of enzymes. In one instance we were able to show that as few as four amino acid changes in an enzyme could convert an enzyme that normally inserted a double bond into fatty acids into an enzyme that inserted a hydroxyl group. These studies provide an explanation for the mechanism by which chemical diversity in this class of compounds has evolved and provide a model for understanding the mechanisms underlying the evolution of other major families of compounds.

6 WALBOT, VIRGINIA

Dept. of Biological Sciences, Stanford University, Stanford, CA 94305

Accelerating the pace of allelic diversity: the role of transposable elements

Allelic diversity is the “raw material” for natural selection. Consequently mechanisms that modulate allelic diversity should play an important evolutionary role, and these mechanisms should themselves be subject to stringent natural selection. Maize alleles are remarkably polymorphic, and much of the diversity can be attributed to transposable element activity. Transposons remain resident in many alleles, proven to confer novel regulatory properties in some cases. Insertion-deletion mutations in allele comparisons are similar in size to the footprints created by transposon insertion-deletion events. Because transposons cause mutations, most of which are predicted to be deleterious, their activities are regulated at the cellular, organismal, and population levels. Retrotransposons comprise the majority of the maize genome; these elements can insert but never excise. Today, these retroelements are restricted mainly to intergenic regions; sporadic amplification of specific retroelements distinguish closely related grass genomes, but few retroelement are active today. In contrast, DNA transposons are active in a few individuals in every

population, and they show preferential insertion into transcription units. Such insertions often create null alleles in host genes, but a wide spectrum of functional alleles can be generated after transposon excision. Some transposons generate both somatic and germinal excision alleles (*Ac/Ds*, *Spm/dSpm* in maize), while others generate primarily somatic diversity (*MuDR/Mu* elements in maize). *MuDR/Mu* elements are the most aggressive known in terms of forward mutation, and these elements are under stringent developmental regulation. Somatic excisions are restricted to the terminal cell divisions of organ development, resulting in a fine mosaic of diverse revertant alleles. Germinal revertants are rare, although the *MuDR/Mu* elements proliferate during meiosis and in the gametophyte. Because plants have an alternation of generations in which genetic “quality” is tested in the gametophyte, individuals carrying deleterious or lethal mutations are eliminated in the haploid phase.

7 WENDEL, JONATHAN F.

Dept. of Botany, Iowa State University, Ames, IA 50011

Evolution of crop plants: models, mechanisms, and implications

Of approximately 300,000 species of flowering plants, humankind is fed and clothed by only several dozen major crops. These crops were largely developed by aboriginal domesticators in ancient times from often obscure origins. Interdisciplinary studies combining the tools of evolutionary and molecular biology have provided novel insights into the origins of modern crop species, including identification of wild progenitors and patterns of genetic diversity. Plant domestication has been characterized by sequential genetic bottlenecks, whereby relatively large gene pools were repeatedly winnowed during selection of modern cultivars and breeding populations. Crop improvement has been accompanied by dramatic morphological alterations, thereby providing model systems for analyses of the evolutionary and developmental genetics underlying morphological innovation in nature. These analyses are facilitated by genomic and proteomic approaches. Because many important crops, including wheat, maize, and cotton, are polyploids, these species provide model organismal frameworks for analyzing the fate of duplicated genes and genomes following polyploid formation. Polyploidy is associated with novel genomic interactions and molecular genetic mechanisms, and is suggested to have opened up new avenues for agronomic improvement.

BRYOLOGICAL AND LICHENOLOGICAL SECTION, BSA / ABLs

SYMPOSIUM: FORM AND FUNCTION IN BRYOPHYTES: DEVELOPMENT, CONSTRAINTS AND CONSEQUENCES

8 NEWTON, ANGELA E.

Botany Dept., Natural History Museum, Cromwell Road, London SW7 5BD, UK

Form and function in bryophytes: development, constraints and consequences

Observed form can be proposed to be the result of interacting constraints and demands. Historical factors (phylogenetic constraints) determine the range of structural features

from which novel forms can evolve, while developmental constraints influence which of all possible novel forms will be feasible in the genetic environment in which they are expressed. Environmental factors interact with morphology at different scales the relationship of growth form to life strategy and the physical and temporal exploitation of environmental resources, and the role of form in mediating the interaction between physiology and the environment through water & mineral capture, desiccation tolerance and gas exchange. In this symposium a selection of these interacting elements will be explored.

9 DURING, HEINJO J.

Dept. of Plant Ecology, Utrecht University, Went Building, P.O. Box 80084, NL-3508 TB Utrecht, The Netherlands

On the role of branching patterns in the density-dependent growth of pleurocarpous chalk grassland mosses

Density had both positive and negative effects on shoot growth of pleurocarpous chalk grassland mosses. In an attempt to understand the mechanisms involved, a simulation model of pleurocarp shoot growth was built that included interaction for light and water along an explicit vertical dimension. The model allowed coexistence of at least four 'species' differing in shoot angle and branch density. Density and mass/area ratio of side branches with determinate growth strongly affected biomass gain. From an experiment on the effects of light quantity and quality on branching patterns of *Ctenidium molluscum* and *Calliergonella cuspidata* we hope to derive rules to allow incorporation of plasticity in branching patterns into the model.

10 FISHER, KIRSTEN M.

Dept. of Integrative Biology and University Herbarium, University of California, Berkeley 94720

*Ontogenetic changes and their relationship to patterns of reproduction and diversification in a Paleotropical moss species complex, *Syrhropodon involutus**

Heterochronic changes in relative timing and/or rates of development in a descendant relative to its ancestor serve as a theoretical background for explaining morphological diversification. While some patterns of development may be comparable in plants and animals, the modularity and hierarchical organization of plants add another level of complexity that prohibits simple extrapolation from better known animal examples. Furthermore, the extent to which heterochronic changes are tied to changes in reproductive strategies remains unknown. Comparative developmental studies on plants are needed to improve our understanding of how heterochronic changes at the different levels of plant ontogeny interact with reproductive mode, and how these changes ultimately affect patterns of diversification. The study described here will focus on a group of Paleotropical mosses, the *Syrhropodon involutus* (Calymperaceae) complex. Members of this complex are united by an unusual leaf morphology, in which more than half of the leaf area is occupied by dead, empty cells. The general leaf morphology that unites the taxa of this complex appears in early stages of many moss ontogenies, suggesting pedomorphosis may be responsible for this unusual leaf form. This study uses the *S. involutus* complex and phylogenetic comparative methods to understand the relationship between heterochronic changes and morphological diversification in mosses. Specifically, I investigate the possibility that there is a trend towards increased neoteny within the *S. involutus* complex, and assess whether this trend is correlated with changing reproductive modes in an island (vs. continental) biogeographic context.

11 NEWTON, ANGELA E.

Botany Dept., Natural History Museum, Cromwell Road, London SW7 5BD, UK

Phylogenetic constraints on branching architecture in mosses

The range of possible morphologies for any given lineage of plant is constrained by its phylogenetic history. Mosses are relatively simple plants, with correspondingly few structural elements available to provide the units of different branching architectures. Consequently, phylogenetically diverse moss lineages may have superficially similar growth forms, such as dendroid, pendulous, or weft forming. For example, dendroid growth forms, with an upright "stipe" and spreading branches, appear to have developed independently in at least the Climaciaceae, Hypnodendraceae, Pilotrichaceae, Pterobryaceae and Thamnobryaceae. In this study, representatives of different lineages were dissected out, and the branching architecture analysed. Relatively few structural elements were found to interact in different combinations to result in the observed growth forms. In the case of dendroid mosses the growth form results from the interaction of characters relating to termination and origin of the primary module, "stipe" orientation (where a stipe may be a primary or secondary module), origin, density and plane of secondary modules, formation of a stolon, and reiteration. The distribution of the states of these characters was examined on a phylogenetic tree derived from molecular and morphological data. Although the states of some of these characters were found in several different lineages that are not closely related (based on this tree), others were restricted to monophyletic lineages. In the pleurocarpous mosses, release from morphological constraints through innovations in orientation, branching and modularity have permitted the development of a wide range of different growth forms.

12 RICE, STEVEN K.* AND SCOTT ROBINSON

Dept. of Biological Sciences, Union College, Schenectady, NY 12308

Canopy exchange and functional trade-offs in bryophytes

Governing the exchange between cellular physiological processes and the surrounding atmospheric environment, terrestrial bryophyte canopies control fluxes of energy (e.g., light, heat) and mass (most importantly H₂O, CO₂, CH₄). Measurements of mass transfer in wind-tunnels from small (10 cm diameter) cushions have demonstrated that unit increases in canopy roughness (i.e., average canopy depth) are related to exponential rates of mass transfer with a scaling factor $n > 1.5$. This suggests a potentially high physiological cost from water loss associated with increases in canopy depth, even though many species exhibit a rough-canopy growth form. We explored the magnitude of the scaling factor under field conditions using 14 cm diameter *in situ* cushions from forest floor bryophytes in mesic, temperate forests in New York state. By embedding the cushions within continuous carpets, exchange was influenced by length scales associated with substrate features in addition to intrinsic canopy properties. Mass transfer was determined gravimetrically in 1 hr sampling intervals. During sampling, wind velocity, humidity, and surface and air temperature were continuously monitored (10 s intervals) and recorded using a data logger. Under field conditions, scaling factors were much diminished ($n = 0.7$) and indicate a lower physiological cost than previously suggested in wind-tunnel studies where cushions experience high levels of through-flow initiated at cushion margins. Results from this study are used to parameterize a canopy exchange model for bryophytes that explores the physiological trade-offs associated with canopy structural variation and its influences on light penetration, heat loss, CO₂ uptake, and nutrient transport in evaporation streams.

SYMPOSIUM: LICHEN BIODETERIORATION: PROGRESS AND PROBLEMS

13 ST. CLAIR, LARRY L.^{1*} AND M.R.D. SEAWARD²

¹Dept. of Botany and Range Science, Brigham Young University, Provo, Utah 84602; ²Dept. of Environmental Science, University of Bradford, BD7 1DP, UK

Lichen biodeterioration: progress and problems

This symposium will examine the impact of lichens and other microflora on natural and human-manipulated rock substrates. Decomposition of rock is a natural phenomenon, with biological and non-biological factors interacting in a complex fashion, the effects of one accentuating the effects of the other, relentlessly breaking down rocks, large and small, to form the mineral component of soil. The process is inherently slow but constant. Biologically enhanced degradation of prehistoric and historic rock structures is receiving increasing attention from biologists, geologists, archaeologists, and cultural conservators. Papers in this session will address several aspects of this phenomenon from a variety of perspectives including the role of lichens in the biodeterioration process, the effects of other rock degrading microflora, changes in rock structure due to biodeterioration, issues related to the control of microflora on culturally significant substrates, and archaeological concerns relative to biodeterioration.

14 CHIARI, GIACOMO

Dipartimento di Scienze Mineralogiche e Petrologiche, Via Valperga Caluso 35, I-10125 Torino, Italy

Lichens on a sandstone: do they cause damage?

Seven samples of sandstone, covered with lichens and old petroglyphs were studied by optical microscopy, X-ray diffraction, ESEM, water absorption, mercury porosimetry, and a new porosimetry measurement based on color mode analysis of images, obtained from thin sections with impregnating resin colored with a blue dye. This technique measures the porosity gradient as well. The image is divided, on the computer, into parallel slices from the outside to the core, and porosity changes of each section are a function of depth. In our case, porosity was smaller toward the outside, since in the outer layer lichens occluded the pores. Counting them, the porosity was the same. The pure quartz sandstone has homogeneous grain size, which differ with rock type. ESEM imaging of lichens interaction with the sandstone (David Carson, GCI), showed a superficial layer (live lichens with smaller airborne particles) clearly distinguishable from the bulk (larger grains and pores). Consolidation tests were carried out using ethyl silicate [Wacker OH (with) and Monsanto Silbond (without catalyst)], on samples with the largest and smallest grains. Porosity decreased less for Silbond, which, without catalyst and an active surface, did not polymerize. For an ethyl silicate treatment it is advisable to use catalyzed products. Porosity depends on grain size: the larger the grains, the larger porosity, water absorption, fragility and de-cohesion of the rock. Lichens cannot etch quartz. The grains dislodgment seems not important from thin sections observations. Lichens fill the gaps between grains, which are large enough to accommodate them without them exercising a relevant pressure. This result may help to decide whether or not to eliminate the lichens from the surface. Of course surface appearance is important, but, at microscopic level, a serious damage due to the lichens can be ruled out.

15 DANIN, AVINOAM

Dept. of Evolution, Systematics, and Ecology, The Hebrew University of Jerusalem, Israel 91904

The impact of lithobionts on biodeterioration of desert rocks and the diversity of their microhabitat-dependant communities

In the desert areas of Israel there is hardly any place where rock surface is devoid of one or another kind of poikilohydric lithobiont. When dry, their thallus is dormant, but when wetted they rapidly resume physiological activity. Microscopic organisms such as cyanobacteria, lichens, and non-lichenized fungi, have constant specific impact on weathering of rocks. Typical kinds of rock surfaces are thus formed in association with each lithobiont community. In each climatic zones of Israel specific morphological types of weathered surfaces are confined to certain geomorphologic positions. Hard limestone rocks, with water holding capacity of 0.5-2.0%, at the Negev Highlands, subjected to 100-150 mm mean annual rainfall, are reported here. Epilithic crustose lichens cover most of the rocks at north-facing slopes. They protect the surface from direct deterioration by splashing raindrops. Efficient solar radiation over the south-facing slopes induces harsh microclimatic conditions. In the newly exposed surfaces the drought resistant fungi *Lichenothelia* species cause minute pits by dissolving the rock around their 0.1-0.2 mm globular body. Establishing in the micro-pits, cyanobacteria and cyanophilous lichens, which cause faster weathering in their close vicinity, lead to the formation of hemispheric depressions, 2-10 mm diameter, in the rock. More porous limestone, with 10-15% water holding capacity, looks like the previous, but supports cryptoendolithic filamentous cyanobacteria. Chasmoendolithic coccoid cyanobacteria cause or accelerate deterioration in mainly south-facing slopes. The specific morphology in these places is known as exfoliation. Detached stones in that area enjoy moisture of dew in addition to the rainfall water. They support euendolithic lichens, which cause jigsaw puzzle-like pattern on the stone surface. When rolled on slopes these stones display all their faces to the atmosphere and thus become weathered in a jigsaw pattern throughout. Pitting organisms on are common on man-made marble monuments in more mesic areas of Europe.

16 GINELL, WILLIAM S.^{1*} AND RAKESH KUMAR^{1,2}

¹Getty Conservation Institute, 1200 Getty Center Drive, Los Angeles CA 90049; ²OpronX Inc., 7450 Tilghman Street, Suite 105, Allentown, PA 18106

Limestone stabilization studies at a Maya site in Belize

Stone used in the construction of the 8th-11th century Maya structures at Xunantunich in Belize is a low strength, porous limestone that is nearly pure calcium carbonate. Degradation of archaeologically excavated stone structures in the humid, tropical environment of Belize is caused mainly by wind and water erosion and wide cyclic variations of humidity and temperature. However, damage to the limestone is accelerated to varying extents by the chemical and mechanical effects of lichens, mosses, algae, fungi, and bacteria that are endemic to the region. To evaluate the effectiveness of possible stabilization treatments, tests were conducted in which stone-penetrating consolidant solutions were applied to limestone samples, which were then exposed to both sunny and shaded environments over a period of about four years. The results of these treatments were evaluated by particle and water erosion resistance measurements on the aged samples. The effectiveness of several biocides in controlling the establishment and growth of microflora on the exposed samples and on in situ, ancient stone walls was also studied. Some tests were conducted to determine if the organic polymer consolidants would support, or even accelerate, the growth of microflora on the stone and how the

concurrent use of biocides would affect the results. Several consolidant solutions were found that could penetrate and stabilize the usually moist limestone and, in combination with biocides, would minimize the growth of the local microflora.

17 KNIGHT, KATHRYN B. *, LARRY L. ST. CLAIR, AND JOHN S. GARDNER

M.L. Bean Life Science Museum and Electron Optics Laboratory
Brigham Young University, Provo, UT 84602

Lichen-mediated degradation of historic and prehistoric panels at El Morro National Mounument, New Mexico

El Morro National Monument is located in Cibola County, New Mexico, about 200 km west of Albuquerque, New Mexico. The main attraction at the Monument is a large sandstone formation called Inscription Rock. The formation is a natural repository for more than 700 years of comments and notations recorded by travelers through the region. In excess of 2000 petroglyphs and inscriptions are preserved on the lower reaches of the rock. Recently, encroachment of lichens onto several, inscription panels has been documented. Because lichens are known to decompose rock surfaces physically and chemically, we are evaluating the impact of lichens on several panels. Species lists and relative abundance data for each panel have been compiled. Distribution of lichen species on each panel has been photographically documented in order to monitor growth/encroachment trends, exfoliation patterns, and changes in species composition. Samples of the major lichen species on the Inscription Rock panels were collected from a large boulder field north of Inscription Rock. These samples are being analyzed using Infrared spectroscopy, thin-layer chromatography, and SEM and light microscopy. These data will be used to evaluate the degree of lichen encroachment and substrate degradation. In addition, PIXE analysis is being performed on five samples of *Usnea hirta* from five locations in the Monument to determine if air pollution is influencing substrate degradation patterns. Since establishment of the Monument, protection of the local landscape from grazing and wood cutting/gathering has resulted in changes in the microenvironment in and around several of the panels. The effects of these changes are also being considered. Data from this study will be used to evaluate remedial procedures for the control and/or removal of lichens from some panels.

18 PIERVITTORI, ROSANNA

Dipartimento di Biologia Vegetale, Università di Torino, viale
Mattioli 25, 10125 Turin, Italy

Lichens and biodeterioration of stoneworks: the Italian experience

Lichens play an important role as biogeophysical and biogeochemical agents in the degradation of stone surfaces. Problems comes out where lichen-substratum relationships occurred on stoneworks of artistic value. In this case the process of alteration and disintegration of rocks is of primary interest because sometimes it can create serious problems for their recovery, restoration and conservation. This work presents an up to date review of the researches conducted till now in Italy specifically devoted to lichens and biodeterioration of stonework in archeological and monumental areas. This survey shows the main methodologies used in this field: systematic and ecological studies, lichen-substratum interface quali-quantitative analyses, chemical and physical mechanisms of deterioration by lichens, calcium oxalate films, prevention and control methods. Finally the lichens are investigated as a possible air-dispersed component. Sampling methods for the quantitative assessment of the presence of airborne lichen struc-

ture (i.e. spores, lichenized propagules) in areas of artistic and archeological interest are proposed.

19 ROSATO, VILMA GABRIELA

LEMIT, Calle 52 s/n, entre 121 y 122, (1900) La Plata, Argentina

Lichen species growing on mortar and concrete in the Buenos Aires Province, Argentina

Concrete was the principal building material since the beginning of the 20th. century, and the Buenos Aires Province as well as the rest of Argentina were no exceptions. For instance there are some "art-deco" buildings now appreciated and protected as a local heritage. Some of these buildings are colonized by lichens as well as other structures such as dams and road bridges, but were not studied until recently. Therefore, the aim of the present paper is to offer a list of lichens found up to now on mortar and concrete in the Buenos Aires Province that were collected and identified when these structures were inspected. The samples were collected mainly in the central and SW part of the province as well as the southern coast of the Rio de La Plata. These regions have important climatic differences but lichens don't seem to be influenced by them. Substrate porosity and water retention seem to be more important for lichen colonization. However, some species were collected only in the central part of the Province, but this can only be regarded as a trend. There are 22 species: 17 crustose (Acarosporaceae, Candellariaceae, Lecanoraceae, Teloschistaceae and Verrucariaceae) and 5 foliose (Physciaceae and Teloschistaceae). The most frequent and widespread is the crustose species *Caloplaca citrina* (Teloschistaceae). Crustose species are also known from Europe. On the other hand, foliose species are restricted to South America. Although no new species were found, the crustose species *Sarcogyne pruinoso* and *Staurothele catalepta* are recorded for the first time for Argentina. This list cannot be considered as conclusive. More extensive sampling of other regions of the Province, specially the coastal and the arid zone of the south is needed, as well as microhabitat studies to improve the knowledge about the ecology of these species.

20 SEAWARD, MARK R. D.

Dept. of Environmental Science, University of Bradford, Bradford
BD7 1DP, UK

Lichens as subversive agents of biodeterioration

Lichens play a major role in shaping the natural world, both physically and biologically. One such role, as biological agents in soil development, used to be considered only in a geological context, but recent research has shown that lichens are capable of biodeteriorating stone substrata within a relatively short time scale. Chemical alteration of the substratum is brought about by the disruptive action of many species, particularly those capable of producing oxalate(s) at the thallus-substratum interface. Raman microscopic analysis has proved invaluable in the interpretation and characterisation of the physical and chemical nature of this interface. The oxalate contributes significantly to the bulk and composition of the thallus itself and persists after the lichen.

21 SILVER, CONSTANCE S.

Preservar, Inc., 310 Riverside Dr., New York, NY 10025

Conservators confront lichens: a summary history of conservation's efforts to understand and control lichen-induced deterioration of cultural property

By the middle of the nineteenth century, deterioration of cultural property due to environmental agents was recognized and efforts at control initiated. Lichen-induced biodeterioration of exterior stone, such as architectural facades, sculpture,

tombstones, and even stained-glass windows, had been identified as one such agent. Conservation's uneasy relationship with lichen has continued; indeed, it has become increasingly more complex. For example, lichen's possible role in dating and as an indicator of environmental conditions militates for its preservation, while its deleterious effect on cultural materials prompts its eradication. Broader environmental concerns increasingly move conservators away from biocides, the standard method of lichen control. This paper will present an overview of control of lichen on cultural property through a summary review of historic and current literature. It will also explain data bases that address this issue. Lastly, a promising new avenue for control of lichen on cultural property will be described.

22 TRATEBAS, ALICE M.

Bureau of Land Management, P.O. Box 883, Newcastle, WY 82701

Biodeterioration of rock art and issues in site preservation

Lichens, algae, and mosses growing on rock surfaces that have prehistoric or historic rock art are a major problem for preserving these fragile remains of the past. Most rock art is superficial or shallowly pecked or incised into the rock surface. Breakdown of the rock by microflora can easily erase these images. The problem is worldwide. Archaeologists have several major issues for site preservation where biodeterioration is a factor. One issue is whether the rock surface is now so deteriorated that the lichen structures are holding it in place. Killing the lichens would release the undermined rock and leave the remaining rock art unprotected. If we kill the lichens, what method should we use? The recent development of dating techniques that analyze rock coatings, such as rock varnish, oxalate, and silica, means that we cannot contaminate the surface with chemicals that would prevent future dating. An associated issue is keeping any chemicals from getting into the environment, such as not contaminating archaeological deposits below the rock art. We cannot just spray on chemicals, but would need to carefully dab them on, time consuming work. A crucial issue is how fast the lichens are growing and whether they will deteriorate more of the panel. A slow growing lichen leaves plenty of time to investigate, conduct experiments, and make decisions. If removed, how fast will the lichen regrow? If removal leaves a fragile, exposed surface, should we use a rock consolidant to preserve the site? All known consolidants alter the rock porosity, which could negatively impact the rock art. Instead of major interventions, can we alter the microenvironment to discourage lichen growth? This ideal solution may be difficult in many settings. A final issue is the ethics of altering the natural environment. Whose sites are these and what is their view?

CONTRIBUTED PAPERS

23 BONINE, MARY L.* AND LLOYD R. STARK

University of Nevada-Las Vegas, 4505 S. Maryland Parkway, Box 454004, Las Vegas, NV 89154-4004

*Growth and gametangial maturation in the desert moss, *Syntrichia caninervis**

Populations of the desert moss, *Syntrichia caninervis*, were sampled approximately every four weeks, and/or immediately following significant hydration events at Red Rock National Conservation Area, Las Vegas, Nevada, USA. Samples were collected from 12 populations (4 exclusively female, 4 mixed sex, and 4 exclusively male) over a period of more than two years, from the fall of 1998 to the spring of 2001. Collections were made

using random coordinates on a grid to allow mapping of population structure. During dissection, the presence of distinct annual growth intervals permitted assessment of stem elongation, quantification of gametangial initiation and maturation, and determination of maturation indices for recent gametangia. Sporophytes were initiated, but not matured, in both the spring of 1999 and 2000, and hence, we will not report on sporophytic maturation. Stem elongation rates varied, apparently dependent on microsite differences. Stems within the main portion of the cushion elongated at approximately 0.3 mm per year, and stems on the edges of the cushion or in the open elongated at less than 0.2 mm annually. On average, growth intervals which contained gametangia consisted of either a perichaetium with 4-5 archegonia or a perigonium with 14 antheridia. Archegonia were initiated in the fall of 1998 and became receptive spring of 1999. Antheridia initiated at the same time matured to half their full size by the end of spring, were dormant during the summer of 1999, and did not disperse sperm until spring 2000. A few antheridia were completing maturation and dispersal of sperm into spring 2001. Based on previous studies of desert moss phenology, gametangial maturation, fertilization, and probably sporophyte maturation occur during the cooler, moister fall through spring months in the Mojave desert.

24 BRAGGINS, JOHN E.¹, JOHN J. ENGEL², MATTHEW J. VON KONRAT^{2*}, AND PETER J. DE LANGE³

¹Plant Science, School of Biological Sciences, The University of Auckland, Private Bag 92019, Auckland, New Zealand; ²The Field Museum, Chicago, IL 60605-2496; ³Science & Research Unit, Dept. of Conservation, Private Bag 68908, Auckland, New Zealand

Rare and threatened liverworts: an overlooked area of conservation in the New Zealand botanical region

New Zealand is an archipelago that is both geographically and climatically diverse. Recently, it has been stated that the decline in biological diversity is New Zealand's most pervasive environmental issue. The impact of potential pressures such as micro-habitat loss and fragmentation on the liverwort flora have not been previously investigated. This is alarming because it is estimated that New Zealand has c. 10% of the world's liverwort species, and more importantly, has 48 of the 73 liverwort families. Because of these factors together with the high level of endemism, the liverwort flora of New Zealand is considered to be of worldwide significance. First, this study identified potential threats to the New Zealand liverwort flora, and second, developed a preliminary checklist of threatened liverworts to be considered as candidates for the World Red List. Selection of species was based on field studies spanning three decades, extensive herbarium records, and bibliographic references. Case studies illustrating the different categories of threat occurring in New Zealand include examples from a monotypic family and a monotypic genus. We conclude that research relating to the conservation biology of the New Zealand hepatic flora requires great urgency and recommend areas of priority.

25 BRODO, IRWIN M.

Canadian Museum of Nature, P.O. Box 3443 Station 'D', Ottawa, Ontario, Canada, K1P 6P4

Patterns of distribution for North American lichens

North American lichens display recurring patterns of distribution that can be named, classified and analyzed. Past attempts at such classification systems have been used in various publications. A new system, expanding on previous works, was developed in the preparation of "Lichens of North America," a new reference work on the lichen flora of the continent scheduled to appear in the autumn of 2001. Interesting patterns and recurring

disjunctions seen in lichens are relevant in discussions of North American phytogeography.

26 BUNGARTZ, FRANK* AND THOMAS H. NASH III

Dept. of Plant Biology, Arizona State University, PO Box 87 1601, Tempe, AZ 85287-1601

Is Buellia subalbula (Nyl.) Müll. Arg. a "Diplotomma" with one-septate ascospores?

The lichen genus *Diplotomma* introduced in 1849 by Flotow has frequently been subject to taxonomic debate. Originally proposed as a segregate of *Lecidea* because of a double exciple, it soon became more widely accepted when Massalongo emphasized the pluriseptate ascospores as the main character of the genus. Modern checklists and floras are divided on whether to treat the group as part of *Buellia* which has been characterized in the strict sense by one-septate ascospores. Nordin criticized the classical concept and recently confined *Diplotomma* to a group of species with calcium oxalates in the thallus, moderately pruinose apothecia and a conspicuously thickened perispore. Material of *Buellia subalbula* from the Sonoran Desert Region was examined with the light microscope, and the scanning and transmission electron microscope. Calcium oxalate content of the thallus was studied with x-ray diffractometry and specimens were analyzed using thin layer chromatography. The species has not previously been reported from North America and was commonly misidentified as *B. retrovertens* Tuck., a taxon recently synonymized with *B. dispersa* A. Massal. *Buellia amabilis*, a taxon described by de Lesdain from Mexico is most likely a later synonym of *B. subalbula*. The species is characterized by a thickly crystalline-pruinose thallus with abundance of calcium oxalates, moderately pruinose apothecia and a thickened perispore. These characters are consistent with Nordin's concept of *Diplotomma* s. str. even though the perispore is only moderately thickened. However, *B. subalbula* has one-septate ascospores and only a proper, not a thalline exciple.

27 COX, CYMON J.*, A. JONATHAN SHAW, AND SANDRA B. BOLES

Dept. of Biology, Box 90338, Duke University, Durham, NC 27708

Toward a sub-familial classification of the recircumscribed Mniaceae (Bryopsida)

Molecular phylogenetic analyses of the family Mniaceae (including the Pohlioideae and *Roellia*) were conducted. Three data matrices were constructed: i) a 73-taxon data set of the chloroplast regions trnL-trnF, *rps4* and the atpB-rbcL intergenic spacer; ii) a 43-taxon data set representing a subset of data set 1 plus the addition of a further chloroplast region, namely *rpl16*; and iii) a 19-taxon data set of eight genes: two nuclear ribosomal regions (18S nrDNA and partial 26S nrDNA), one mitochondrial gene (*nad5*), and five chloroplast regions (trnL-trnF, *rps4*, *psbA*, atpB-rbcL, and *rpl16*). Each data set was analyzed using maximum parsimony, maximum likelihood, and Bayesian phylogenetic inference. The traditional taxa of the Mniaceae form a poorly supported monophyletic group. The genera *Mielichhoferia* and *Schizymerium* are derived from taxa in *Pohlia* sect. *Pohlia*. The propaguliferous sp. of *Pohlia* sects. *Cacodon* and *Nyhomia* form a well supported clade to the exclusion of non-propaguliferous species. In addition, *Epipterygium* is derived from a mniobryoid ancestor. Despite extensive data sampling among diverse taxa of the Mniaceae, a robust phylogenetic hypothesis of the family remains elusive; monophyly of the Pohlioideae cannot be statistically rejected by any dataset. Nevertheless, optimal trees under ML, MP, and Bayesian inferences indicate that the Pohlioideae is probably paraphyletic and that the traditional Mniaceous taxa are derived from a pohlioid ancestor. The lack of robust resolution (due to short internal branches)

among the major clades in all genomic partitions is interpreted as indicating a relatively rapid diversification of major lineages within the family. Morphological character reconstructions were performed to identify synapomorphies and provide diagnoses for the major clades. The novel relationships discovered by these analyses will provide a framework for a sub-familial classification of the Mniaceae.

28 DAVIS, CHRISTINE

Dept. of Biology, Duke University, Box 90338, Durham, NC 27708

Molecular identification of endophytic Xylariaceae (Ascomycota) from Jamaican species of Bazzania (Lepidoziaceae: Jungermanniopsida)

Abstract Fungi occurring in association with Jamaican specimens of *Bazzania* were identified. Using a light microscope, fungal hyphae were observed growing around and within the rhizoids of the liverworts. Fungal cultures were grown from the rhizoids following surface sterilization of the liverworts. The ITS region of nuclear ribosomal DNA was extracted, amplified and sequenced from pure cultures. BLAST searches revealed that the fungi are ascomycetes belonging to the family Xylariaceae. These samples, in conjunction with sequences obtained from GenBank, were phylogenetically analyzed to further resolve the identities of the fungi. This is the first report of endophytic Xylariaceae in liverworts, though species from the family occur as endophytes in a broad range of seed plants. Future avenues of research are discussed.

29 DE LUNA, EFRAIN* AND BEATRIZ BIASUSO²

¹Sistemática Vegetal, Instituto de Ecología, Xalapa, Ver, Mexico;

²Fundación M. Lillo, Fac. C. Naturales, UNT, San Miguel de Tucumán, Argentina

Morphometric variation and species delimitation in the Braunia exserta complex (Hedwigiaceae)

As a first step toward a phylogenetic analysis and classification of *Braunia exserta* species complex, character variation was studied in populations of *B. exserta*, *B. reflexifolia* and *B. tucumanensis* from Argentina, Bolivia, Chile and Peru. The goal of this study was to discover groups of populations that could be proposed as putative species. Specific questions addressed in this study were: 1) what is the extent of morphological variation in each of the three putative species in the complex?, 2) are there three phylogenetic distinct groups? Two approaches were employed to answer these questions. First, twelve populations (n=116) were studied for gametophyte and sporophyte quantitative characters. Multivariate analyses (ordination techniques and discriminant analyses) were used to describe morphologically homogeneous units. Second, character variation within and among twelve populations was evaluated with Analyses of Variance (ANOVA) followed by multiple comparison tests. Results of these tests were used to classify variation in character states, as basis for cladistic analyses. The morphological data matrix was complemented by additional qualitative characters from our examination of specimens and types. Cladistic analyses reconstructed three main lineages that correspond to the three morphometric groups detected in multivariate analyses. A taxonomic conclusion is that each of those groups should be given the rank of species: *Braunia exserta*, *B. reflexifolia* and *B. tucumanensis*.

30 FAHSELT, DIANNE

Dept. of Plant Sciences, University of Western Ontario, London, Ontario N6A 5B7 Canada

Detection of pigments in specimens of recent and subfossil Umbilicaria from north Greenland

Photosynthetic pigments were found in extant and Late Holocene subfossil lichens which had been buried beneath ice in north Greenland. Minor constituents present in nearby conspecific lichens were not observed in subfossils, but the major pigments of extant thalli were detectable. Thus, while concentrations were lower in subfossils, normal pigments survived glaciation for up to 1350 yr and could be detected in specimens that had been dry for as long as 4 yr. *Umbilicaria cylindrica*, *U. krascheninikovii* and *U. hyperborea* buried by glacier ice contained chlorophyll *a*, in some cases chlorophyll *b*, and up to seven carotenoids. High performance liquid chromatography of subfossil extracts revealed a preponderance of rapidly-eluted peaks, possibly degradation products, that were relatively inconspicuous in extracts of specimens from extant populations. Both glaciated and unglaciated samples of *U. hyperborea*, which had been stored longer than other species, yielded the lowest chlorophyll *a/b* ratios and Fv/Fm values, indicative of pigment deterioration in dry thalli. In all species chlorophyll *a*/chlorophyll *b* ratios and Fv/Fm readings were generally lower in subfossils than in comparable extant lichens which had escaped long-term ice burial.

31 FUSELIER, LINDA C.* AND D. NICHOLAS McLETTCHIE

University of Kentucky, Dept. of Biological Sciences, 101 Morgan Bldg., Lexington, KY 40506

Sex-specific and environment-dependent phenotypic selection on pre-adult traits in Marchantia inflexa

Sexual dimorphisms may evolve through sex-specific and/or environment-dependent selection that results in different phenotypic optima for the sexes. Sexual dimorphisms in clonal expansion traits have recently been documented in *Marchantia inflexa*, a dioecious thallose liverwort. To uncover possible mechanisms for the maintenance and evolution of these pre-adult sexually dimorphic characters we used selection analyses to measure the magnitude and direction of selection on traits associated with asexual fitness and tested for sex-specific and environment-dependent selection regimes. We planted replicate genotypes of male and female *M. inflexa* in two different light environments in a greenhouse and measured morphological and phenological characters associated with growth and asexual reproduction. Timing to cupule onset and plant size early in development were under sex-specific selection in a low light environment. Disruptive selection acted on timing to cupule onset in females in low light and on male size in high light. Females exhibited environment-dependent selection and a sex-specific cost of plasticity in cupule onset. Both females and males displayed maladaptive phenotypes in low light with respect to timing of cupule onset but males also displayed a maladaptive size phenotype in low light. The presence of sex-specific and environment-dependent selection acting on pre-adult traits in *M. inflexa* may drive different phenotypic optima in the sexes and maintain sexual dimorphisms in traits associated with asexual reproduction.

32 GOFFINET, BERNARD^{1*}, A. JONATHAN SHAW² AND SANDRA BOLES²

¹Dept. of Ecology and Evolutionary Biology, 75 North Eagleville road, University of Connecticut, Storrs, CT 06268-3043; ²Dept. of Biology, Duke University, Durham, NC 27708

Multigene phylogenetic reconstruction of the family Orthotrichaceae (Bryophyta)

The cosmopolitan family Orthotrichaceae comprise 27 genera arranged into to subfamilies. The Orthotrichoideae comprises primarily acrocarpous taxa distributed in temperate parts of the world, whereas the Macromitrioideae accommodates cladocarpous taxa centered in (sub-)tropical regions. Our taxon sampling encompasses much of the generic and subgeneric diversity within the family. Analyses of nucleotide sequences of the trnL-trnF region, the rps4 and rbcL genes supports this systematic concept. Chloroplast data also reveal a para- or polyphyletic nature of the large speciose genera *Orthotrichum*, *Zygodon* and *Macromitrium*. Broadening the character sampling to the mitochondrial (nad5 gene) and the nuclear genome (portion of the LEAFY gene) are currently underway to test these hypotheses. These data will also aid in addressing the hypothesis inferred from morphological and chloroplast suggesting that the genus *Bryomaltaea* (Orthotrichoideae, Zygodontaeae) is either of hybrid origin or represents the most basal lineage within the family.

33 HAX, NEVA P.* AND BERNARD GOFFINET

Dept. of Ecology and Evolutionary Biology, 75 North Eagleville Road, University of Connecticut, Storrs, CT, 06269-0343

Systematic inferences in Bryoxiphium based on morphological and molecular characters

The Bryoxiphaceae is a small family of mosses composed of one genus, *Bryoxiphium*, accommodating 2 to 5 taxa. The gametophyte of *Bryoxiphium* resembles somewhat that of *Fissidens*, and it is based on this similarity that the family has traditionally been placed within the haplolepidous mosses. A peristome, upon whose features the classification of mosses rests to a large extent, is, however, lacking. Recent phylogenetic reconstructions of mosses using nucleotide sequences of the nuclear and chloroplast genome, lead to *Bryoxiphium* being placed in a clade with *Drummondia* and *Scouleria*, at the base of either the haplolepidous mosses (Dicranidae) or diplolepidous opposite mosses (Funariidae). We have tested these relationships, as well as affinities to *Eustichia*, by sampling all species of *Bryoxiphium*; results of these analyses will be represented. Species of *Bryoxiphium* are morphologically distinct, and geographically allopatric. *Bryoxiphium norvegicum* is the most widely distributed species, extending from Eastern Greenland and Iceland to Western North America. *B. japonicum*, *B. mexicanum*, and *B. madeirense*, are endemic to Eastern Asia, Mexico and the island of Madeira, respectively. Whether these morphological species compose monophyletic lineages is not clear. The relationships among these taxa are examined using nucleotide sequences of the ITS region of the rDNA and the chloroplast regions trnL-trnF and rps4 gene based on an extensive sampling of populations.

34 KOBAYAMA, YUKI

Dept. of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509

Diversity of central strand structure in the Metzgeriidae

In spite of the common misconception of bryophytes as nonvascular plants, many detailed studies have demonstrated conducting strands in mosses and liverworts. The ultrastructure of the water-conducting cells in Metzgeriidae liverworts, such as

Symphogyna and *Pallavicinia*, have been well described by Smith (1966), Frey et al. (1996), and Ligrone and Duckett (1996). Central strands in different taxa of Metzgeriidean liverworts, in fact, show different levels of cell differentiation. The purpose of this investigation is to describe the structure of central strand cells in several simple thalloid liverworts, including *Jensenia*, *Hattorianthus*, *Cavicularia*, and *Calycularia*. Studies with optical and electron microscopy show that both the rhizome and the thallus midrib of *Jensenia* possess a central strand which is composed of thick walled, small diameter cells. SEM study shows that these cells possess numerous, oblong shaped pits on the inner surface of the wall and are connected by oblique end walls. These central strand cells of *Jensenia* are, in fact, structurally very similar to those in *Symphogyna*. The massive midrib of *Hattorianthus* possesses two central strands. The cells in the strand are smaller in diameter than surrounding cells and have brownish coloration. SEM study shows that end walls of some specialized parenchyma cells in *Hattorianthus* possess numerous small pits which seem to be of plasmodesmatal origin. The genus *Cavicularia* possesses three differentiated central strands in the midrib. The cells in the strand are smaller in diameter, but do not possess any wall thickenings. The cells of the thick, conspicuous midrib of *Calycularia* are filled with many starch grains, but there is no differentiated central strand. Continuing studies, using TEM and histochemistry, will focus on the internal structure and function of these cells.

35 KRAYESKY, DAVID M. AND BARBARA J. CRANDALL-STOTLER*

Dept. of Plant Biology, Southern Illinois University, Carbondale, IL 62901

An SEM photo atlas of spore terminology in the Fossombroniineae

Species delimitations and taxonomic groupings within the Fossombroniineae have traditionally relied on variations in spore wall architecture and consequently, many descriptors of spore wall morphology have been published. In most studies spores have been described on the basis of features resolved at the level of optical microscopy. With the increased resolution of SEM, many of the early descriptors are no longer applicable. For example, the epithet of *Fossombronia foveolata* Lindb. presumably described a foveolate distal spore wall surface, which in more recent times has been described by various other authors as reticulate, areolate, or even alveolate. To resolve the inconsistencies in spore wall terminology, we have compiled representative SEM micrographs of both distal and proximal spore wall architectures, prepared as part of a worldwide monograph of the Fossombroniineae. A variety of modern and classical treatments of pollen and spore morphology were consulted to identify the most appropriate descriptor for each of the major architectural patterns found in the group. These results are presented as a photo atlas, in which ten major distal face architectural designs are recognized. While there is less variation in proximal face designs, the systematically significant features of this face will also be presented.

36 LAWREY, JAMES D.^{1*}, PAUL DIEDERICH², AND PAULA T. DEPRIEST³

¹Dept. of Biology, George Mason University, Fairfax, VA 22030; ²National Natural History Museum, 25 rue Munster, L-2160 Luxembourg, Luxembourg; ³Dept. of Botany, NHB-166, National Museum of Natural History, Smithsonian Institution, Washington, DC 20560

Genetic differentiation among populations of the widespread lichenicolous fungus Marchandiomyces corallinus

The lichenicolous basidiomycete fungus *Marchandiomyces corallinus* is widely distributed in North America and Europe. Unlike most lichenicolous fungi, *M. corallinus* attacks numerous host lichens. Theoretically, either of these characteristics, a wide geographic range or generalized host ecology, could provide ample opportunities for genetic differentiation within this species. To determine how genetic variation is partitioned in *M. corallinus*, fungi were isolated from several locations in North America and Europe, and also from different lichen hosts in one of these locations; levels of genetic differentiation were then estimated among these samples. Samples were obtained from four sites in North America (Arkansas, Missouri, Maryland, Virginia) and two in Europe (Ireland and Scotland). At a single site (Scotland), samples were obtained from three different lichen hosts. All isolates were used in vegetative mycelial compatibility tests, which provide evidence of genetic identity. In addition, a variety of nucleotide sequences from both nuclear and mitochondrial ribosomal genes were obtained for each isolate. Mycelial compatibility groups were recognizable based on geography, not the choice of lichen host. Sequence data tended to confirm this result; sequence differences among populations, where they existed at all, were observed among geographically distant populations, not different lichen hosts from the same site. These results suggest that genetic differentiation among populations of *M. corallinus* have developed as a consequence of geographic isolation, not host-switching.

37 MCLETTCHIE, D. NICHOLAS*, GISELA GARCIA-RAMOS, AND PHILIP H. CROWLEY

Center for Ecology, Evolution and Behavior and T.H. Morgan School of Biological Sciences, University of Kentucky, Lexington, KY 40506-0225

A model of local sex-ratio dynamics and spore production in the dioecious liverwort Marchantia inflexa

In many dioecious bryophyte species, population sex ratios range from all female to all male. The focal species of the present study, the liverwort *Marchantia inflexa*, forms patches on rock surfaces, and these differ widely in sex ratio at a rainforest field site in Trinidad. This analysis addresses abundances of male and female *M. inflexa* through time within an individual patch. We represent the life-history of this species using seven different stages (non-reproductive, asexually reproductive, and sexually reproductive males, non-reproductive and asexually reproductive females, and unfertilized and fertilized sexual females) and express their dynamics using ordinary differential equations. Some of the stages grow by extending thalli over the substrate and may overgrow each other to capture space. Our simple representation of dynamics within the patch failed to stabilize the sex ratio: females gradually eliminated males at low disturbance frequency, and males eliminated females at high disturbance frequency. This pattern did not hinge on whether sexual propagules could germinate within the patch, but asexual reproduction (via gemmae dispersed within the patch) played an important role. This suggests that the maintenance of sex in these populations may hinge on metapopulation structure

and dynamics. Though sexual reproduction appears to be unimportant within patches, spores provide the primary means of recolonizing patches eliminated by large-scale disturbances. We found that shortly after the patch was fully occupied, the production of these wind-dispersed spores was maximized, but spore production declined thereafter as the sex ratio became increasingly biased toward one sex or the other. Much additional modeling and empirical work is needed to enable linkage of within-patch dynamics to represent the metapopulation.

38 O'BRIEN, TERRY J.

Dept. of Biological Sciences, Rowan University, Glassboro, NJ 08028

The dubious origins of pleurocarpous mosses: molecular evidence for the phylogenetic positions of Aulacomnium Schwägr. and Rhizogoniaceae

A maximum parsimony analysis of a four-gene cpDNA dataset including 55 exemplar taxa indicates that the Rhizogoniaceae plus *Aulacomnium* and *Calomnium* are the sister group or nearsister group to pleurocarpous mosses, which with 6600 species is the most diverse clade of extant mosses. The evidence suggests that the traditional genera of Rhizogoniaceae are a paraphyletic group, consisting of a minimum of 3 clades. *Aulacomnium* is a monophyletic group, and its sister lineage includes *Mesochaete*. The pleurocarps are comprised of a relatively small "racopilalean" clade and a large "hypnalean" clade (including Hookeriales, Hypnales and Leucodontales), a fundamental division that is consistent with the conclusions by DeLuna *et al.* and Newton and DeLuna. These results have implications for our understanding of diversification, adaptation, disparity, development, and genome evolution of the pleurocarps. The rhizogonean mosses –including *Aulacomnium* and *Calomnium* – have a Gondwanan distribution centered in Oceania, where most rhizogonean species have a substrate preference for tree ferns. Altogether this suggests an origin of pleurocarps within Oceania from an epiphytic ancestor during Cretaceous time. The rhizogonean mosses should be given high conservation priority because of their phylogenetic position and because they have low species richness compared to pleurocarps.

39 OLIVER, MELVIN J.^{1*}, JOHN A. WHEELER², BRENT D. MISHLER³, AND JEFF VELTEN¹

¹USDA-ARS Plant Stress and Water Conservation Laboratory, 3810 4th St., Lubbock, TX 79415; ²Dept. of Biology, University of Wisconsin-River Falls, 410 South Third St., River Falls, WI 54022-5001; ³University Herbarium, Jepson Herbarium, and Dept. of Integrative Biology, University of California, Berkeley, CA 94720

A bryophyte rehydrin trackable marker for the evolution of desiccation tolerance

The use of phylogenetic data to address the importance of individual genes in a complex phenotype or in the evolution of a particular trait, is an approach that has received little attention. In collaboration with The Green Plant Phylogeny Research Coordination Group ("Deep Green"), we have initiated a study of the evolution of desiccation tolerance. Phylogenetic analyses suggest that desiccation tolerance was primitively present in the bryophytes (basal-most living clades of land plants), but was lost early in the evolution of tracheophytes. Desiccation tolerance has re-evolved in seeds and pollen and vegetatively in Selaginella, the ferns, and at least eight independent evolutions in the angiosperms. In the moss *Tortula ruralis*, we have identified several genes that appear to be intimately involved in desiccation tolerance. One of these genes, a rehydrin Tr 288, accumulates transcript at high levels in response to desiccation that are only used upon rehydration. This gene has physical properties similar to the stress induced dehydrin proteins. Tr 288 however, has little sequence similarity with

dehydrins other than the presence of a rudimentary K-box sequence at its carboxy terminus. Our working hypothesis is that Tr288 is an ancestral dehydrin and as such may be a useful marker in a phylogenetic analysis of desiccation tolerance. We have devised a PCR based strategy, utilizing the highly repetitive nature of Tr288, to track the presence of Tr288 homologs in other species. Our studies indicate that we can find homologs within the *Tortula ruralis* complex and we are now expanding into other bryophyte groups and into the tracheophyte lineages. In particular we will be targeting the exemplar species identified by Deep Green in their synthesis of a phylogenetic tree for all land plants.

40 PETERSON, ERIC B.

Nevada Natural Heritage Program, 1550 E. College Pkwy #145, Carson City, NV 89706

Tour of a lichenological black-hole (Nevada)

Nevada has been largely ignored by lichenologists. Many other sciences have also neglected the state, considering it to be low in diversity... nothing more than a vast sagebrush monoculture. But if you leave the casinos and get off of interstate 80, you will discover something much different. The great basin ecoregion, which makes up most of Nevada, is ranked 4th in North America (north of Mexico) for richness of vascular plants. Nevada has more mountain ranges than any other state in the US, many of which rise from flat dry playas through forests to alpine peaks. As for lichens, very little is known about Nevada, but that is beginning to change. Several data sets are starting to illuminate the dark void of knowledge. Lichen diversity is greater than would be expected from the little attention the state has received. While Nevada may be a black-hole for lichen data, it is certainly not a black hole for the lichens themselves!

41 PETERSON, ERIC B.^{1*} AND PETER NEITLICH²

¹Nevada Natural Heritage Program, 1550 E. College Pkwy #145, Carson City, NV 89706; ²White Mountain Research Station, 3000 E. Line St., Bishop, CA 93514

Lichen communities, pollution signals, and an issue of scale

The Forest Health Monitoring project is a nationwide effort by the US to monitor several aspects of forest health. Lichen communities are included in the monitoring, mainly due to concerns over pollution. In Colorado, lichens were sampled through most of the 1990's leading to a statewide pollution gradient model. In developing the statewide model, a few places of particular concern were noted, including the Yampa Valley and Park Range. This area is downwind of two large coal-fired power plants that annually emit an estimated 20,000 metric tons of sulfur dioxide and 25,000 tons of nitrogen oxides. During the summer of 2000 we added 33 plots to the Park Range and an additional 2 plots to the Elkhead and Flat Top Ranges which flank the power plants. Our additional sampling was intended to (1) document lichen communities after 30 years of emissions, and (2) establish a baseline for following long term changes in lichen communities relative to changes in air quality. When we began analyzing the data, we had difficulty correlating the distance from the nearest power plant with the pollution index calculated from the statewide model. That model was based on the relative presence of pollution tolerant species. Many of these occur primarily on *Populus tremuloides*. We suspect that *Populus tremuloides* stands in the Park Range are naturally good habitats for these species independent of any pollution presence. What we did find correlating with distance from the nearest power plant was the absence of pollution tolerant species. These would be difficult to use in a statewide pollution gradient model because few lichen species occur in all forested areas of the state.

42 RISK, ALLEN C.

Dept. of Biol. and Env. Sc., Morehead State University, Morehead, KY 40351

On the distribution, abundance, biology, and habitat of Fissidens hyalinus Wils. & Hook

Fissidens hyalinus is often considered to be one of the rarest mosses in the eastern United States. The species, however, is much more abundant than has previously been assumed. Sixty-five new collections of *F. hyalinus*, in combination with previous collections, document the species from 28 counties, 7 states, and 5 major physiographic provinces. The species is most abundant on bare soil of streambanks in steep and deeply dissected landscapes with calcareous geology and mixed deciduous forests.

43 SAVILLO, ISIDRO

Assistant Professor III, Iloilo State College of Fisheries, Barotac Nuevo, Iloilo, Philippines 5000

Growth of lichens on palm trees

During ambient conditions, propagules of lichens were most likely observed to start appearing sporadically on the series of circular dents or scars carved around the trunk girth due to the sequential peeling of dead sheaths of the growing *Areca catechu*. After the rains, the 0.3 to 0.5 inch wide dents may hold substantial amount of water enough to sustain the moisture needs of the growing lichen. The dents or scars were observed to be hard, rough but chlorophyllous for some and not fibrously slippery thus allowing the propagules to attach and initiate growth by centrifugal spreading. The bases of the upwardly directed modified leaves of the palm trees serve as temporary reservoir of rain water that streams downward thus bathing particular portions of the trunk. Lichen growth and reproduction on palm trees may be continuously maintained in this manner. Palm trees have been observed to harbor crustose or powdery forms of lichens luxuriantly sometimes almost covering the whole trunk compared to other woody trees nearby. The most luxuriant growth was observed on the slim trunk of *Areca catechu*, followed by *Corypha elata* and the least was seen in *Cocos nucifera*. The architecture of the trunk of the *Cocos nucifera* having irregular dimensions may be responsible for the discontinuous pattern of lichen growth. *Cocos nucifera* about eighth to ten meters away from the sea's spray zone were not observed to harbor lichen growth. A *Terminalia catappa* in similar location was found to harbor lichen growth on its trunk facing away from the sea.

44 SCHUETTE, SCOTT W.

Dept. of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509

Morphology of the simple thalloid liverwort Jensenia Lindb. (Pallaviciniaceae)

Jensenia is a dioicous, dendroid liverwort which superficially resembles some species of *Pallavicinia*. In fact, *Jensenia* is sometimes regarded as but a subgenus of *Pallavicinia*. However, several morphological features viewed with SEM clearly distinguish *Jensenia* from all other genera of the Pallaviciniaceae. This study looks at representatives of the twelve species of *Jensenia*, focusing on those unique features that separate it from *Pallavicinia*. Preliminary investigations of *Jensenia erythropus*, from Venezuela, reveal that the thallus arises from a dark red to purplish, underground rhizome that is covered with unicellular rhizoids. The thallus wing margin is devoid of slime hairs and the apices are deeply incised in male and female plants. Optical microscopy shows there is a prominent midrib that is one-third to one-half the thallus width that dichotomously branches in correlation with thallus furcations.

The antheridia are reddish and wholly cover the midrib, unlike *Pallavicinia* where they are in parallel rows on both sides of the midrib. The archegonia are restricted to the dorsal surface at the basalmost furcation, which is different from the scattered arrangement seen in *Pallavicinia*, and are surrounded by a slightly elevated, lacinate perichaetium. The pseudoperianth, which may be more aptly called a caulocalyx, is long and cylindrical. The spores are approximately 25-40µm in diameter with a broadly pilate wall anastomosing at the pilae heads. The thick-banded elaters are bispiral and extremely long at ca. 300µm. At maturity the ellipsoid capsule appears to have a bistratose wall, becoming tri-to multi-stratose at the apex.

45 SELF, SHERRY L.* AND BARBARA J. CRANDALL-STOTLER

Plant Biology Dept. Southern Illinois University Carbondale, IL 62901-6505

The systematic status of Peltia X appalachiana

The genus *Peltia* comprises a group of simple thalloid liverworts, which are distributed throughout the north temperate region of the United States. One proposed species found in this area, *P. X appalachiana*, is postulated to be a hybrid between *P. neesiana* and *P. epiphylla* (Schuster, 1991). J. Hattori Bot. Lab. 70:143-150). In common garden experiments *P. X appalachiana* shows unreduced fertility. This does not support the hybrid hypothesis. Furthermore, isozyme studies suggest species-specific variation rather than intermediacy in the proposed hybrid. The systematic status of *P. X appalachiana* should be resolved through comparison of sequence data collected from the internal transcribe spacers (ITS) of nuclear ribosomal DNA from sympatric populations of *P. X appalachiana*, *P. epiphylla* and *P. neesiana*. ITS sequences taken from *P. X appalachiana* and *P. epiphylla* show homogeneity to be 73%. However, sequences of ITS regions obtained from several recombinant clones of *P. epiphylla* siblings suggest the possibility of genomic heterogeneity in the ITS region of this species. It is hypothesized that further ITS data will support the conclusions based on common garden experiments and isozyme gels, which identify *P. X appalachiana* as a phylogenetically distinct species.

46 SELVA, STEVEN B.

Division of Natural and Behavioral Sciences, University of Maine at Fort Kent, 25 Pleasant Street, Fort Kent, ME 04743

Coniocybe gracilescens and Sphinctrinas with 2-celled spores

When it became clear that the two calicioid lichens described by Henry Willey in his 1892 "Enumeration of the Lichens found in New Bedford, Massachusetts" hadn't been heard from since, an investigation was launched to try and come up with some answers. While *Calicium pallidellum* had been transferred by Fink to the nonlichenized genus *Caliciella*, thereby precluding its listing on the North American lichen checklist, *Coniocybe gracilescens* remains on the checklist as the only species in the world still assigned to that genus. As one thing led to another, including a review of the type specimens, the following results are being reported: *Coniocybe gracilescens* is, in fact an "albino" form of the *Chaenotheca hispidula* with which it is growing in the type collection; *Calicium pallidellum* is not a *Calicium* or a *Caliciella*, but a *Sphinctrina* with 2-celled spores. Wondering how common *Sphinctrinas* with 2-celled spores actually were, the ongoing investigation has uncovered three others—two apparently known only from their type localities in India and Finland, respectively, the other currently being described by the author.

47 SHAW, JON

Dept. of Biology, Duke University, Durham, NC 27708

What can molecular data tell us about species delineation in the peatmosses (Sphagnum)?

Sphagnum is arguably the most controversial genus of mosses with regard to species delineation. The four large sections of *Sphagnum* are readily distinguishable, but within sections there are complexes of closely related taxa that some bryologists recognize as a single polymorphic species while others distinguish multiple, more narrowly defined species within these complexes. Phylogenetic architecture within sections of *Sphagnum* was investigated using DNA sequences from the chloroplast and nuclear genomes. Although it is still too early to make taxonomic decisions on the basis of molecular data, evidence available to date suggests that such groups as the *S. capillifolium* complex represent monophyletic groups but that the "little" species within such complexes are often para- or polyphyletic. These observations suggest that either the "little" species within complexes are unnatural and are based on convergent morphological features, or that these species are so recently derived that gene coalescence predates speciation. On the other hand, some *Sphagnum* species, including *S. molle*, *S. fuscum*, and *S. tenerum*, are clearly distinct in terms of DNA sequences. Across the genus, phylogenetic structure at the population and species level is very heterogeneous. Populations in the section *Rigida*, for example, are relatively distinct, as are the two species of *Rigida* (*S. compactum* and *S. strictum*). Molecular approaches to species delineation have not reached maturity yet, but appear very promising.

48 ST. CLAIR, SAMUEL B.^{1*}, LARRY L. ST. CLAIR², NOLAN F. MANGELSON³, DARRELL J. WEBER², AND ALAN WHALON⁴

¹Dept. of Plant Physiology, The Pennsylvania State University, State College, PA 16803; ²Dept. of Botany and Range Science, Brigham Young University, Provo, UT 84602; ³Dept. of Chemistry, Brigham Young University, Provo, UT 84602; ⁴Chiricahua National Monument, Willcox, AZ 85643

Using Cu/Zn ratios in lichens to determine anthropomorphic sources of copper pollution

Accumulation of airborne pollutants by lichens is, in part, the basis for their use as bioindicators of air quality. However, direct correlations between emission sources and pollutant element accumulation by lichens are often difficult to document. In this study copper accumulation patterns by lichens, along a copper pollution gradient, were examined. Data from four locations, along a 1500-km, north-south transect, with increasing distance from copper smelting activity (southeastern Arizona, southwestern New Mexico, and adjacent parts of Mexico), were collected. Lichens, representing two growth forms (foliose and fruticose), were collected from each study site. Copper and zinc concentrations were determined for all samples using PIXE analysis. In addition, ambient air concentrations of copper and zinc for all sites were obtained from the AQG web site (<http://improved.cnl.ucdavis.edu/>). Correlation of copper concentrations in lichen samples and ambient air along the transect showed a highly significant positive linear relationship ($R^2=0.97$). Data also showed that foliose lichens accumulated approximately twice as much copper as fruticose species. Cu/Zn ratios from lichen samples and ambient air were correlated along the transect and also showed a highly significant positive linear relationship ($R^2=0.98$). Background Cu/Zn ratios are < 0.5 . Values from the two sites nearest the copper smelting operations ranged between 0.6 and 1.45, while the "clean" sites had values between 0.1 and 0.35. Substrate Cu/Zn ratios from the Arizona location were all below 0.5. These patterns support the use of ele-

ment ratios in accurately predicting elevated element concentrations in lichen thalli and making more effective decisions relative to possible sources of pollutant elements.

49 STARK, LLOYD R.* AND CLAUDIO DELGADILLO M.

Dept. of Biological Sciences, University of Nevada, Las Vegas, NV 89154-4004; Instituto de Biología, UNAM, Apartado Postal 70-233, Delagacion Coyoacan, 04510 Mexico, D.F.

Is Crossidium really an annual? Initial observations from the Mojave Desert

Species of *Crossidium* have long been considered plants of annual habit. This attribute probably derives from their short stature and frequent sexual reproduction. Populations of *Crossidium crassinerve* represent the dominant species of bryophyte in some of the hottest and driest regions known from the North American continent: along the north-facing slopes of low elevation washes in the Mojave Desert. Annual precipitation, all rain, averages approximately 100 mm/year in these areas, with growth and reproduction in the mosses restricted to the cooler, wetter months of winter and early spring. The annual nature predicts that such populations should appear in early winter and senesce by spring or summer. Cores of populations were removed, placed in 20 mL scintillation vials, and vigorously shaken in water for several minutes to remove soil particles while not severing organic connections of individuals. The upper few mm of stem was dissected to reveal innate growth interval distinctions based upon color changes of leaves and stems. Allocation was assessed to stems and leaves based on number, length, and dry biomass. Yearly growth intervals were approximately 0.10-0.20 mm long, with yearly leaf allocation consisting of about 12 leaves. Laminal filaments tended to remain chlorophyllose longer than the blade. Individual ramets routinely extended 10 mm below the substrate surface. Conservative calculations indicate that many ramets in a well established population are on the order of 50 years old. Longer term experiments are underway in which (i) individual ramets are marked and periodically photographed in retractable population cores; and (ii) the surface of the population is cleared of ramets and regrowth monitored.

50 WALL, DENNIS P.

University of California, Berkeley

Population structure and patterns of island radiation in the paleotropical endemic moss, Mitthyridium: insights from a rapidly evolving nuclear gene, glyceraldehyde 3-phosphate dehydrogenase (gpd)

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. In the present analysis I optimize biogeographic data and data on reproductive strategy to a large phylogeny of *Mitthyridium*, consisting of 140 population exemplars, in order to comprehend causal factors driving its relatively recent radiation. To reconstruct adequately this shallow level of phylogenetic divergence, I employ a single copy nuclear gene Glyceraldehyde-3 phosphate dehydrogenase (gpd). The gene's utility for plant systematics is poorly known, and this represents the first study to use gpd for moss phylogeography. Using gpd, I reconstruct the relationships among 140 populations distributed across the known geographic range *Mitthyridium*. I optimized to this phylogeny the variation in reproductive strategy (*Mitthyridium* has a range of reproductive expression from fully sexual to vegetative) to test the influence of island isolation on reproductive mode and the consequent influence of reproductive strategy on diversification rate shifts. Results show a trend towards increased loss of sexual repro-

duction among island populations. These island groups were found sister to mainland populations that show significantly higher frequencies of sexual reproduction. This finding suggests a general evolutionary trend towards loss of sex on islands. Furthermore, the shift in reproductive mode is correlated with a shift in diversification rate. This correlation suggests a plausible cause of the rapid lineage radiation among island members of *Mitthyridium*.

51 YIP, KWOK LEUNG

University of Cincinnati Herbarium (CINC), Dept. of Biological Sciences, Cincinnati, OH 45221-0006; Current address: University Herbarium (UC), 1001 VLSB, University of California, Berkeley, CA 94720-2465

A revision of the genus Pleuridium (Ditrichaceae, Musci)

The genus *Pleuridium* (Ditrichaceae) is revised on a worldwide basis. *Pleuridium* species feature immersed, cleistocarpous, basally stomatose capsules, cucullate calyptrae, and a parocous or autoicous sexual condition. Mostly ephemerals or annuals, the species are widespread in the temperate regions and at higher elevations in the tropics. Twenty-one species are classified in two sections: Section *Pleuridium* includes *P. ravenelii*, *P. acuminatum*, *P. subulatum*, *P. papillosum*, *P. longirostre*, *P. arnoldii*, *P. curvisetum*, *P. costesii*, and *P. pappeanum* (9 species) while section *Sclerastomum* includes *P. nervosum*, the designated type species of the section, *P. robinsonii*, *P. sullivantii*, *P. mexicanum*, *P. laxirete*, *P. subnervosum*, *P. andinum*, *P. venezuelanum*, *P. valetonii*, *P. denticulatum*, *P. sinensis*, and *P. holdridgei* (12 species). Two widespread, polymorphic, and morphologically similar species, *P. subulatum* and *P. acuminatum*, have caused much confusion since their inception. Correlations of sexual condition and leaf lamina thickness with chromosome numbers show that the two species are distinct.

CONTRIBUTED POSTERS

52 BELL, NEIL E.^{1,2*} AND ANGELA E. NEWTON¹

¹Dept. of Botany, Natural History Museum, Cromwell Road, London, SW7 5ED, UK; ²The Centre for Plant Diversity and Systematics, School of Plant Sciences, The University of Reading, Whiteknights, Reading, RG6 6AS, UK

Phylogenetic studies of the Rhizogoniaceae (Bryales): unravelling the origins of pleurocarpy

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 character states associated with acrocarpy and pleurocarpy, the normally closely associated suite of secondary pleurocarpous traits being variably present in conjunction with more typically acrocarpous features. Such observations are consistent with recent cladistic analyses which place rhizogoniaceous exemplars in a critical phylogenetic position at the base of the other pleurocarpous groups. In the initial stages of a combined morphological and molecular phylogenetic study of the Rhizogoniaceae, an examination of morphological characters was undertaken within the context of recent redefinitions of pleurocarpy. Observations confirm that the family contains both unambiguously acrocarpous and pleurocarpous taxa according to currently accepted definitions. Preliminary molecular analyses resolve several novel clades, many of which can be supported by morphological synapomorphies, and suggest that the family may represent part of a diverse grade immediately basal to the other pleurocarps. Lack of well supported

resolution in the basal nodes of this grade compared with the apical rhizogoniaceous and "true" pleurocarp nodes can be interpreted as evidence for a relatively ancient origin of the former, a differential rate of either molecular evolution or of cladogenesis, or a combination of such factors. Further sampling of both characters and taxa will be required if this level of the phylogeny is to be convincingly resolved.

53 BRAY, JR., JAMES R., ABEL J. KINSER*, AND BARBARA J. CRANDALL-STOTLER

Dept. of Plant Biology, Southern Illinois University, Carbondale, IL 62901

Community structure and spore bank dynamics in the Fossombroniineae of South-central Texas

Many species of the Fossombroniineae are adventives, occurring most abundantly in either disturbed or seasonally dry habitats. Their distribution within communities is generally patchy, with the patches isolated from each other by denuded soil or more often by other vegetation. Frequently, all patches of the community are comprised of but a single species, but in some localities several species may coexist. To investigate the spatial relationships among species as well as infraspecific patch dynamics and establishment potential, field studies were undertaken at Bastrop State Park near Austin, TX. In year one of the study, patch distributions of *Fossombronia* and *Petalophyllum* were mapped in eight randomly selected sites within the park in the early spring growing season. To evaluate microhabitat variation among these sites, soil pH, temperature at patch surface, and intensity of red, far-red and blue radiation were measured. Soil samples were systematically removed from each site for subsequent spore bank analysis to assess the re-establishment potential of each species. The eight sites were revisited and sampled for spore bank analysis in midsummer of the following year to evaluate the impact of seasonal changes on community structure. These studies suggest that patches of the four taxa found within the sites are clustered by species rather than being randomly mixed, with typically no more than three species at any one site. In year one, only *F. foveolata* and a few patches of *Petalophyllum* germinated from the spore bank soil samples, while in year two, a single patch of *F. porphyrorhiza* also developed. Such germination events modify patch distributions but species composition of each site seems to be consistent from year to year.

54 DILLMAN, KAREN L.^{1*}, LINDA H. GEISER², JIM RILEY², AND GARY LAURSEN³

¹Arizona State University, Tempe, AZ; ²USFS Siuslaw National Forest, Corvallis, OR; ³University of Alaska-Fairbanks, Fairbanks, AK

Lichens of the Great Kobuk Sand Dunes of Northwestern Alaska

The Great Kobuk Sand Dunes of the Kobuk Valley National Park in northwestern Alaska (67° 07.636' N, 159° 02.371' W) were surveyed for lichens in August of 1999 and 2000. These 62 sq.km sand dunes are located in the Kobuk River valley about 160 km east of the town of Kotzebue, Alaska and the Chukchi Sea. Annual precipitation and frost-free days at the sand dunes, nearby sub-arctic forests and tundra average 203mm and 70 days, respectively. The sand dunes were created during the late Pleistocene and consist of calcareous sands eroded from the Brooks Range by glaciers and transported to their present location by the Kobuk River and wind. Much of the material has been stabilized by vegetation and the remaining active dunes are now separated from the Kobuk River by coniferous forest. At the perimeter and within the active dunes area, vegetation islands in various stages of succession and soil stabilization can be found. To exam-

ine lichen communities characteristic of the various successional stages, monitoring plots were located on a gradient of weakly stabilized sand to fully forested habitats. Lichens identified from the sand dunes and surrounding habitats comprise 63 genera and 160 species, many with circumpolar arctic-alpine and Amphi-Beringian distributions. Results from this research will assist the US National Park Service in the development of dune conservation strategies and visitor-use regulations, and contribute to the knowledge of the cryptogamic flora of the Beringian region.

55 EVERSMAN, SHARON^{1*}, CLIFFORD M. WETMORE², KATHERINE GLEW³, AND JAMES P. BENNETT⁴

¹Ecology Dept., Montana State University, Bozeman, MT 59717; ²Dept. of Plant Biology, University of Minnesota, St. Paul, MN 55108; ³Biology Dept., University of Puget Sound, Tacoma, WA; ⁴Institute for Environmental Studies, University of Wisconsin and Biological Resources Division, U.S. Geological Survey, Madison, WI 53705

Lichen ecology in Yellowstone National Park

Three hundred sixty-one species are currently reported from Yellowstone National Park. We found 72% of the total number of species in Engelmann spruce forests and 57.1% of the total number in Douglas fir forests, compared to 41.8% in lodgepole pine sites, including two talus slopes, and 36.3% in lodgepole/whitebark pine sites; 29.1% of the species were restricted to the old moist Douglas fir and spruce forests that have not burned for at least 300 years. Since about 80% of the forests in Yellowstone National Park are seral and climax lodgepole pine forests, and 8% are considered moist forests, the lichen distributions illustrate the importance of the old Douglas fir and spruce forest sites for lichen diversity in the park. Species with thalli large enough to identify are beginning to recolonize substrate burned in the 1988 fires.

56 HASTINGS, ROXANNE I.* AND DONNA M. CHERNIAWSKY

Provincial Museum of Alberta, 12845-102 Avenue, Edmonton, Alberta, Canada, T5N 0M6

*Species separation in the *Grimmia longirostris*-*G. pilifera* (*Grimmiaceae*) complex in North America*

Largely due to the use of relative differences, the separation of species in the *Grimmia longirostris*-*G. pilifera* complex has often proven problematic. Using character combinations of stem anatomy, seta/capsule lengths, and sexuality we recognize four species in the complex in North America and demonstrate that *G. arizonae* and *G. catalinensis*, both lost in synonymy, are good species. *Grimmia pilifera* typically has long, acuminate apices with a short ovate base, short awns, and lacks a central strand (Cao and Vitt 1986, Crum 1994, Greven 1999). *Grimmia arizonae* has broader, ovate-lanceolate leaves, long awns, and a central strand. However, Munoz (1999) synonymizes *G. arizonae* with *G. pilifera*, dismissing their differences as a result of locality variation and sexual development. He reports that in eastern North America, and in shade, *G. pilifera* has its typical form. However, in the west, and in sun, leaves are ovate-lanceolate without distinct bases. To him, the absence of a central strand, is "too variable to be reliable;" fertile stems have a distinct strand, sterile stems have none. By contrast, we found no correlation between sexual maturity and strand development; sterile or fertile *G. pilifera* lack a central strand. Further, its stem epidermis is consistently 2x thicker than *G. arizonae*. In the west there are specimens without a central strand, long, acuminate apices and ovate bases (*G. pilifera*) and others with a central strand, and broadly ovate-lanceolate leaves (*G. arizonae*). Both Munoz and Greven classify *G. catalinensis* as *G. longirostris* with immersed capsules. However, specimens with long setae (*G. longirostris*) are cladautoicous, while specimens with short setae (*G. catalinensis*)

are gonioautoicous. Thus we recognize four species. *Grimmia longirostris*: cladautoicous, exerted capsules, with a central strand. *Grimmia catalinensis*: gonioautoicous, immersed capsules, with a central strand. *Grimmia arizonae*: dioicous, immersed capsules, with a central strand. Finally, *G. pilifera*: dioicous, immersed capsules, and no central strand.

57 INDOE, KEVIN E.

The New York Botanical Garden, 200th Street & Southern Blvd., Bronx, NY, 10548-5126

The New York Botanical Garden's American Bryophyte Catalog

The NYBG American Bryophyte Catalog consists of approximately 200,000 specimens of bryophytes from Canada, Greenland, and the United States. In addition to transcribing specimen label data into NYBG's electronic database, the work of this project has included editing and correcting data, extracting data for publication on the World Wide Web, updating the web interface, and imaging type specimens. The NYBG American Bryophyte Catalog web site (<http://www.nybg.org/bsci/hcol/bryo/>) provides public access to the data captured in this project. The site provides checklists to the taxa of bryophytes that occur in Canada, Greenland, and the United States, with links to the full bibliographic citation for the name (provided by Missouri Botanical Garden's MOST project (<http://mobot.mobot.org/Pick/Search/most.html>)). Clicking on a taxon name in the checklist initiates a search for all catalog records with that name. Records can also be selected through a search screen that permits the user to specify different criteria (e.g., geography, collector, date of collection). The results of a search, whether specified through the checklist or other criteria, are displayed first in abbreviated, tabular form. Each abbreviated record links to the full record. Specimen images, where available, are accessed through the full record display.

58 JONES, NICOLE L.*¹, SHARON E. BARTHOLOMEW-BEGAN¹, AND TATSUWO FURUKI²

¹Dept. of Biology, West Chester University, West Chester, PA 19383; ²Natural History Museum and Institute, Chiba 955-2 Aoba-cho, Chou-ku, Chiba-shi, Chiba 260-8682, Japan

*A preliminary overview of gemmae morphologies in *Cavicularia densa* Steph*

The simple thalloid liverworts use several forms of asexual reproduction with gemmae often serving as significant taxonomic characters. *Cavicularia densa* Steph. (Blasiales, Marchantiophyta), a Japanese endemic, bears multicellular stalked gemmae within specialized receptacles. Two kinds of gemmae have been described: a lenticular, discoid form with serrulate margins and two opposite marginal notches, and a smaller, spherical form. Conversely, this small, spherical form has been considered a transitional stage to the serrulate form. Alternately, the presence of only one type of gemma has been used as an identifying character for the taxon. In this investigation, comparative light and scanning electron microscopy was performed on field collected materials to clarify the locations and morphological variations of *C. densa* gemmae. Sectioned thalli revealed the gemmae receptacles to be semi-enclosed, pillared chambers that contain numerous stalked gemmae at various stages of maturity. One gemma form is characteristically elliptical in surface view, fusiform in section with conoidal external cell surfaces. Another form, of similar structure, is more ovoid, lacks conoidal relief and is smaller at germination. Also present in the chamber are massive gemma-like structures whose potential for germination is questionable as no germinating structures were observed. Described for the first time are ventral gemmae, which occur in tightly arranged linear rows along the midline

of the plant interspersed with the rhizoids. These gemmae are ellipsoidal with trapezoidal attenuation toward the apices and bases. The delineation of gemmae morphologies in *C. densa*, specifically the unique occurrence of ventral gemmae along with contained dorsal forms, provides a platform for the necessary ontogenetic studies required to ascertain phylogenetic relationships.

59 MORGAN, SARA M. AND ROBERT S. EGAN*

Dept. of Biology, University of Nebraska at Omaha, Omaha, NE 68182-0040

Lichens of the ponderosa pine forests of Nebraska

Although thought of as a prairie state, Nebraska retains sizeable areas of both eastern deciduous and western pine forests. The state has five main western pine forest regions dominated by *Pinus ponderosa*. Three of these forests are naturally occurring the northern Niobrara River Valley area of Brown and Cherry counties, the northwestern Pine Ridge region in Dawes County, and the Wildcat Hills area of Scotts Bluff County. Samuel R. McKelvie National Forest in Cherry County and the Halsey Unit of the Nebraska National Forest in Thomas County were both planted in the early 1900's. Our lichen collections from these pine forest areas have revealed numerous new county records as well as additions to the state's lichen flora, e.g. *Pseudevernia intensa* (Nyl.) Hale and *Vulpicida pinastri* (Scop.) J.-E. Mattsson & M.J. Lai. The lichens of the planted pine forests have are less diverse when compared to the naturally-occurring pine forests, but a few lichen species are currently known only from these man-made systems.

60 NOBLE, SARAH MARIE* AND DAVID K. SMITH

University of Tennessee, Dept. of Botany, 437 Hesler, Knoxville, TN 37920

Floristic and ecological studies of bryophytes in a Southern Appalachian gorge

The Southern Appalachian Mountains contain many protected gorges, which support a very diverse bryoflora, including many endemic, rare and disjunct species. A small, pristine and protected tributary of the Little Tennessee River, Falls Branch Falls was chosen as the focus of this bryophyte flora and study. Falls Branch Falls is located in the Cherokee National Forest, Tennessee at an elevation of 1131m (3710 ft.). Inventory methods consist of ecological niche observation and field collections. The tributary landscape was sampled along ecological gradients and subunits from which specimens of bryophyte associations were collected. Each sample was treated by laboratory identification of all associated taxa and each taxon was scored for dominant, co-dominant, consociated, or incidental occurrence. The inventory and descriptive ecology of the bryophyte flora of this small area will add to our knowledge of flora within the Southern Appalachian Mountains, and stand as the beginning survey of bryophytes for Cherokee National Forest. A number of phytogeographic elements have been discovered in Falls Branch Falls: Endemics, notably *Megaceros aenigmaticus*; and a number of Tennessee-North Carolina state-listed rare; and disjunct bryophyte species. To date 125 bryophyte taxa have been identified. Collections and identification are planned to continue through December 2001.

61 PUTERBAUGH, MARY N.

Allegheny Institute of Natural History, University of Pittsburgh at Bradford, Bradford, PA 16701

*Preliminary investigation of the interaction between the liverwort *Frullania eborascensis* and *Bdelloid rotifers**

Bryophyte and invertebrate interactions abound, but they are poorly understood. I examined the frequency of *Bdelloid* rotifers within lobular-shaped leaves of an epiphytic liverwort (*Frullania eborascensis*) in northwestern Pennsylvania. Liverworts were randomly sampled from the bark of three neighboring stream-side trees from July through September, 2000. Between 13-68% of the lobules on any given plant were occupied by rotifers (mean=30%; N = 34 samples; 5054 lobules). Of occupied lobules, 71% contained one rotifer, 20% two, and 9% three or more. This distribution is significantly different from that expected at random (*Chi-square* test using Poisson distribution for expected values, *P*.

62 SCHOENINGER, ROBIN*, CORINNA GRIES, AND THOMAS H. NASH

Lichen Herbarium, Dept. of Plant Biology, Arizona State University, P.O. Box 871601, Tempe, AZ 85287-1601

Herbarium databases: creation, maintenance and access via the Internet

The use of databases in herbarium management has become a vital tool in the organization and analysis of large collections. With a well thought-out structure, a database can yield a wealth of uses, ranging from basic management tasks, e.g., generating specimen labels, maintaining an annotation history, the management of specimen loans and exchanges, to a more advanced analysis of label data, e.g., creating distribution maps or analyzing community relationships. The Microsoft Access 2000 lichen herbarium database, developed at the Arizona State University Lichen Herbarium uses state-of-the-art programming options to facilitate uniformity in data entry, reduction of spelling errors and data updates according to taxonomic name changes. A barcode system for herbarium specimens is used as a relatively inexpensive method of accurately retrieving digital label data. Likewise, the World Wide Web holds vast possibilities for querying herbarium collections databases. Researchers around the world can quickly and accurately view herbarium holdings to select specimens for future loans or retrieve a list of the species collected in a region. A web-searchable interface, created in collaboration with the Center for Environmental Studies at Arizona State University, uses JSP, JavaScript, and Java Beans technologies to conduct queries on the ASU lichen herbarium database as well as other ASU collections databases available over the Internet.

63 SCHOENINGER, ROBIN*¹, THOMAS H. NASH¹, AND JACK A. ELIX²

¹Lichen Herbarium, Dept. of Plant Biology, Arizona State University, P.O. Box 871601, Tempe, AZ, 85287-1601; ²Australian National University, Chemistry Dept., Canberra, A.C.T. 0200, Australia

*The chemistry of *Acarospora* subgenus *Xanthothallia* (Lichenized Ascomycete, Lecanorales) in Southwestern North America*

Acarospora is a poorly known crustose lichen genus commonly found in the southwestern United States and Mexico. The genus is commonly divided into two subgenera: *A. subgen. Xanthothallia* and *A. subgen. Phaeothallia* (or *A. subgen. Acarospora*). These subgenera are generally distinguished by chemistry. Members of the subgen. *Xanthothallia* contain the intense yellow pigment rhizocarpic acid, thus exhibiting a yellow color,

whereas members of the subgenus *Phaeothallia* lack rhizocarpic acid and are usually brown. The use of secondary products as taxonomic characters in Lichenology has gained popularity over the last 30 years. As the initial stage of a thorough study of this subgenus in the greater Sonoran Desert, the secondary products of over 800 specimens were analyzed using thin layer chromatography (TLC). One new secondary product was found (xanthothallic acid), and four secondary products were recognized for the first time in this subgenus (ovoic acid, 4-O-demethylnotatic acid, hyprotocetraric acid, and eumitrin A1).

64 SMAW, SHERCODA*, LAFAYETTE FREDERICK, AND RAYMOND L. PETERSEN

Biology Dept., Howard University, Washington, DC 20059

The urban moss Bryum capillare Hedw.: cyanobacterial and algal associates as biogenic crusts

Bryum capillare Hedw. is a cosmopolitan moss ubiquitous in cities, where it occurs as a dense-green velvet growths between the cracks in sidewalks. We report on the cyanobacterial and algal associates of *B. capillare* and the role they have in building biogenic crusts. Individual plantlets of *B. capillare* are cultured on 1/5 strength Hoagland's 1% agar medium. After five days a variety of cyanobacteria and algae are observed growing out from *B. capillare* implants. Some of the more abundant cyanobacterial taxa observed are: *Lyngbya* sp., *Calothrix* sp., *Osillatoria* sp. *Phormidium* sp., *Hyrocoleum homeotrichum*, *Anabaena* sp. *Anabeana circinalis*, *Synechocystis aquatilis*, *Shizothrix* sp. Among the eukaryotic algae present are: *Klebsomium* sp. *Ulothrix* sp. and an unidentified diatom. Most of these cyanobacteria and algae are filamentous. This morphology probably adds a textile-like resiliency to the biogenic crust. Based on these observations it is hypothesized that the laying down of a cyanobacterial/algal mat is a prerequisite for *B. capillare* colony growth. This suggestion is supported by the field observation of a biogenic crust of cyanobacteria and algae subtending *B. capillare* colonies. This study is ongoing and should have applications to moss ecology and processes of primary succession.

65 CAREY, SYDNEY* AND D. NICHOLAS MCLETHIE

Dept. of Biological Sciences, 101 Morgan Building, University of Kentucky, Lexington, KY 40506

Testing for sex-specific life history traits under field conditions in a dioecious liverwort

In the liverwort *Marchantia inflexa*, sex-specific differences in life histories were documented in greenhouse-grown plants. Such sex-specific life history patterns can lead to biased population sex ratios as seen in the field. Greenhouse and field conditions are likely to differ and sex-specific differences might be dependent on environmental conditions. Therefore, we undertook a study to test for sex specific differences in life histories of *M. inflexa* in the field across relevant environmental variation. Along a river in a tropical rain forest in Trinidad, plants likely to be male and plants likely to be female were collected and planted on ten plots (40 cm x 60 cm) cleared of other *M. inflexa* plants. Twenty plants of each sex were randomly planted per plot. Canopy photos (180 degree) were taken above each plot. Analysis of these photos allowed us to categorize each plot as a low, medium or high light plot. Data were taken on initial plant size, and after six months we recorded final size, number of cups (structures that produce asexual propagules) and number of growing tips (analogous to shoots) of each plant. Females and males did not differ in any of the three response variables. However, there was a strong light effect where plants had greater growth, produced more cups and produced more growing tips in high light compared to low light. The lack of sex-specific dif-

ferences in life history traits might be due to the slower growth rates in the field compared to the greenhouse. Plants grew approximately three times faster in the greenhouse than in the field, and sex-specific differences became evident after three months of greenhouse growth.

DEVELOPMENTAL AND STRUCTURAL SECTION, BSA

SYMPOSIUM: STRUCTURAL BOTANY IN SYSTEMATICS: A SYMPOSIUM IN MEMORY OF WILLIAM C. DICKISON

66 STEVENSON, DENNIS WM.* AND KENNETH M. CAMERON

New York Botanical Garden, Bronx, NY 10458

Structural botany in systematics: A symposium in memory of William C. Dickison

This symposium is being organized to celebrate the life and influence of the late William C. Dickison, whose early death was felt by family, former students, and countless colleagues throughout the botanical community. Bill authored or co-authored more than 100 scientific papers, abstracts, and books during his career. Most notable is the posthumous publication last year of *Integrative Plant Anatomy*, a textbook that represents the culmination of his lifelong work in systematic, ecological, and structural botany. This text is certain to influence generations of scientists and students well into the future. In keeping with the integrative theme of his book, this symposium will cover the broad subject of using structural data in contemporary plant systematics. From monocots to dicots and floral morphology to molecules, the topics being presented by the participants emphasize the diversity of subjects and plant groups that Bill's closest collaborators and former students study today.

67 BEHNKE, H. DIETMAR

Zellenlehre, University of Heidelberg, Im Neuenheimer Feld 230, D-69120 Heidelberg, Germany

Sieve-element plastids and evolution of monocotyledons with emphasis on Melanthiaceae sensu lato and Aristolochiaceae-Asaroideae, a putative dicotyledon sister group

Monocotyledons are distinct from dicotyledons by their sub-type-P2 sieve-element plastids containing cuneate protein crystals, a synapomorphic character uniformly present from basal Acorales and Alismatales through Lilioids to Commelinoids. The dicotyledon genera *Asarum* and *Saruma* (Aristolochiaceae-Asaroideae) are the only other taxa with cuneate crystals, but their sieve-element plastids include an additional large polygonal crystal, as typical of many paleoherbs. New investigations in the Melanthiaceae *sensu lato* revealed the same pattern (polygonal plus cuneate crystals) in the sieve-element plastids of *Japonolirion osense* (Nartheciaceae-Petrosavieae / Petrosaviaceae), *Harperocallis flava*, *Pleea tenuifolia*, three *Tofieldia* species (all: Nartheciaceae-Tofieldioideae / Tofieldiaceae), and of *Narthecium ossifragum*. However, *Aletris glabra* and *Lophiola americana* (Nartheciaceae-Narthecioideae) and all of the 15 species studied and belonging to the Melanthiaceae *sensu stricto* contain cuneate crystals only. High resolution TEM pictures reveal a crystal substructure which in cuneate forms is always densely-packed, but in

polygonal ones is either 'dense' (in *Asarum*, *Saruma*, and *Japonolirion*) or 'loose' (in *Harperocallis*, *Pleea*, and *Tofieldia*). In *Narthecium* 'loose' polygonal crystals often break up into many small pieces, a process that is also recorded within the Velloziaceae. Moreover, small 'loose' crystals in addition to 'dense' cuneate ones are found in a few Lilioids and many taxa of the Poales (Commelinoids). These results suggest (1) that form-P2c sieve-element plastids evolved through the breakup of a single large polygonal into many cuneate crystals, (2) that this partition was incomplete, i. e. left over a smaller polygonal crystal which through steps of (3) loosening and (4) further breakup (5) eventually dissolved, whereas (6) form-P2cs, -P2cfs and -P2cf subsequently developed by the addition of starch and/or protein filaments. This hypothesis is tested against the distribution of the different subtype-P2 sieve-element plastids and phylogenetic trees derived from molecular data.

68 CAMERON, KENNETH M.

The Lewis B. & Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458

On the phylogenetic position of the New Caledonian endemic families Strasburgeriaceae, Oncothecaceae, and Paracryphiaceae: a comparison of molecules and morphology

Following a collecting trip to New Caledonia in the early 1970s, Bill Dickison and collaborators published a series of papers focused on the anatomy, morphology, and systematic relationships of the endemic families Strasburgeriaceae, Oncothecaceae, and Paracryphiaceae. They concluded that *Strasburgeria*, *Oncotheca*, and *Paracryphia* should each be treated as distinct families positioned near Ochnaceae, Theaceae, and Sphenostemonaceae, respectively. These anatomical data proved to be a valuable source of systematic characters, but the precise phylogenetic positions of these enigmatic families was still left in doubt. In fact, even the ordinal classification of flowering plants published by the Angiosperm Phylogeny Group (1998) left uncertain the position of two of these three families. More recently, however, phylogenies for eudicots based on multiple gene data sets firmly place Oncothecaceae within Garryales, Paracryphiaceae within Dipsacales, and Strasburgeriaceae sister to Ixerbaceae near Crossosomatales. A comparison of anatomy and morphology for these groups is presented in the context of these new phylogenetic hypotheses.

69 ENDRESS, PETER K.

Institute of Systematic Botany, University of Zurich, 8008 Zurich, Switzerland

Morphology and angiosperm systematics in the molecular era

The great progress in phylogenetic understanding of angiosperms in the past decade is primarily due to comparative work on nucleotide sequences. Still, a combination of molecular and morphological analyses may give better support, and structural studies on fossil plants place the results in temporal perspective. In turn, the better phylogenetic relationships are resolved, the more it will be possible to study the evolution of structural and other biological traits. At present, it seems that many of the earlier assumptions of evolutionary change of structure in angiosperms are supported by the phylogenetic topologies and by paleobotanical evidence, but some almost dogmatic assumptions appear to be wrong. Whereas phylogenetic reconstruction by molecular studies proceeds rapidly, the contributions to the elucidation of evolution by comparative morphology and by molecular developmental genetics are slower. The slower pace is in part due

to the greater complexity of the features studied in structural research. But this investment is more than compensated for by the amount of biological information it yields.

70 GENSEL, PATRICIA G.

Dept. of Biology, University of North Carolina, Chapel Hill, NC 27599

William C. Dickison's contributions to botanical science

William C. Dickison's PhD thesis entitled *Comparative Morphological Studies on Dilleniaceae*, resulted in seven papers each dealing with a different plant organ or structure - e.g. wood, carpels, pollen, leaves, etc. This essentially set the stage for his life's work, which involved careful and thorough anatomical investigations of several angiosperm families, with the intent of using the information to solve systematic problems. Some of these taxa fell in or near the Dilleniidae or Rosidae *sensu* Cronquist but are more scattered now (core eudicots, rosids, asterids in current phylogenies). His seminal paper in 1975 in the *Bases of Angiosperm Phylogeny* volume on the contributions of vegetative anatomy to understanding angiosperm phylogeny still is pertinent to current morphological based phylogenetic analyses. During his 30 year career, Bill collected, studied and provided basic documentation of wood, floral, leaf or pollen morphology/anatomy on, for example, Connaraceae, Cunoniaceae, Actinidiaceae, Clethraceae, Styracaceae, Aristolochiaceae, and smaller, less well-known families of tropical plants, such as the Bonnetiaceae, Physenaceae, Medusagynaceae, Caryocaraceae, Alseuosmiaceae, and Strasburgeriaceae. This information was used to address questions of relationships and, frequently, ecological adaptations. His posthumously published book, *Integrative Plant Anatomy*, both introduces the study of plant anatomy and illustrates how anatomy is used in various aspects of society and other areas of botany. Numerous undergraduate and graduate students recall him as positively influencing their view and knowledge of botany. Thus his legacy is multifaceted: precise and excellent data applicable to phylogenetic assessments of relationships for many angiosperm families, an excellent slide and preserved specimen collection housed at the UNC Herbarium, an overview of the nature and value of plant anatomical research, and numerous students well trained in plant morphology/ anatomy/diversity.

71 KEATING, RICHARD C.

Missouri Botanical Garden

Comparative anatomy and specialization of leaf structures in Araceae and Acoraceae

Leaf and petiole anatomy were investigated for nearly 400 samples representing 105 out of 106 genera of Araceae. The study included four duckweed genera (as Araceae) and two species of *Acorus* (as Acoraceae). The questions posed involved the identification of anatomical characters most useful in microscopic diagnosis, as well as in elucidating evolutionary trends of specialization. The tissue patterns best relating to these aims include mechanical tissues (sclerenchyma and collenchyma and their relationship to each other), laticifers and other secretory tissues, and raphide crystals and their cell structure. Mesophyll structure and ground tissue patterns of the petiole also exhibit unexpected systematic value. Collenchyma patterns, considered as uninteresting in most families, is very informative in Araceae. It varies from existing as peripheral bands in petioles and midribs in subfamilies Pothoideae and Philodendroideae, to independent strands aligned with vascular bundles in the subfamily Aroideae. Various transitions exist. The anatomical data correlate well with results of the previous cpDNA study of the family by French, Chung and Hur and are the basis for a modified arrangement of genera.

72 MUSSELMAN, LYTTON JOHN

Dept. of Biological Sciences, Old Dominion University, Norfolk, VA 23529-0266

Surface features of Quillwort (Isoetes, Isoetaceae, Lycophyta) microspores

Traditionally, the surface features of *Isoetes* megaspores have provided the foundation for determining species. Microspores, on the other hand, have been largely neglected in taxonomic schemes and no descriptors for ornamentation have been widely used other than spinulose, papillate, tuberculate, and smooth. Using species from Africa, Asia, Australia, Europe, and North and South America, I examined microspore ornamentation with the scanning electron microscope. Ornamentation and sculpturing of microspores are more diverse than previously reported. Aculate, cristate, echinate, rugulate, and verrucate macro-ornamentation were found in different taxa. Bacillate and fimbriate micro-ornamentation characterize a diversity of species. Surface features vary on the three faces of the microspore (two proximal, one distal surface, and the single ridge). Based on this limited sampling, species with higher ploidy level have larger microspores but no clear relationship between microspore ornamentation and ploidy level was established nor were any geographical or ecological trends clear. Species with unornamented or psilate microspores are few and reports of this trait could be due to examination of immature spores. Like megaspores, microspores of hybrids are polymorphic, varying both in size and sculpturing.

73 RUDALL, PAULA J.

Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AB, UK

Floral morphology of Asparagales: unique structures and iterative evolutionary themes

Although relationships between the lilioid and commelinoid monocot orders are still unresolved, there is emerging consensus regarding family relationships within these orders, prompting a reevaluation of character evolution in these groups. In particular, relationships are now fairly well established between the basal clades of the large monocot order Asparagales (the asparagoid lilies), based mainly on molecular data. Asparagales comprise a 'higher asparagoid' clade and a 'lower asparagoid' grade, which includes some small families such as Tecophilaeaceae, the monogeneric Eurasian family Ixioliriaceae, and the monotypic South African genus *Lanaria* (Lanariaceae), plus some large, cosmopolitan families such as Iridaceae and Orchidaceae, the latter putatively sister to all other Asparagales. A revised morphological cladistic analysis of Asparagales was undertaken to evaluate character support for these hypotheses of relationships and assess character evolution in Asparagales. Synapomorphies for the order include the presence of simultaneous microsporogenesis, epigynous ovaries, and phytomelan in the seed coat, but there are some reversals in these characters, especially in the higher asparagoids. A major reversal to hypogyny in the higher asparagoids and their sister clade is concomitant with the presence of infralocular septal nectaries in the latter. Recurrent evolutionary themes in floral structure of lower asparagoids include loss or reduction of either one stamen whorl (in actinomorphic taxa) or selected stamens (in zygomorphic taxa), and various other androecial and gynoecial modifications, such as centrifixed anthers, presence of a gynostemium (primarily an orchid character), and unilocular ovaries.

74 TERRAZAS, TERESA

Programa de Botanica, Colegio de Postgraduados. Montecillo, Estado de Mexico 56230

Comparative stem anatomy in the subfamily Cactoideae-Cactaceae

Since the XVI century basic anatomical features of Cactaceae have been studied. Mostly this anatomical research has focused on selected features related to different external forms or to stem photosynthesis Crassulacean acid metabolism. However anatomical stem features have rarely been taken into consideration in systematic studies. Recent work has focused in the subfamily Cactoideae because it is the largest and highly diverse subfamily in Cactaceae. Moreover, molecular phylogenies have supported Cactoideae monophyly, but tribal and generic relationships are mostly unresolved. It is thought that Cactoideae originated in the Caribbean and Northern South America and then diverged in two main evolutionary groups, one in South America and the other in Mexico and North America. Anatomical stem characters useful for considering phylogenetic questions in North American Cactoideae members specially tribes Cacteeae, Echinocereae and Pachycereae, were generated. Analysis revealed that most dermal characters like uni-multiseriate epidermis and dermal cell contents (silica grains, various crystal types) prove to be valuable at the species and genus level, but when analyzing the whole subfamily most of them have originated independently several times. Cortex and pith are more variable, however occurrence of fibers in cortical bundles and distribution of mucilage cells were features shared by many North and South American members that were also originated independently. Wood in North American members is more homogeneous than in members of South America and is not informative at the genus level. The combination of anatomical and morphological features with molecular data will be useful to better understand phylogenetic relationships among Cactoideae members.

75 WHEELER, ELISABETH A.^{1*} AND PIETER BAAS²

¹North Carolina State University, Dept. of Wood and Paper Science, P.O. Box 8005, Raleigh, NC 27695-8005; ²Nationaal Herbarium Nederland, Universiteit Leiden Branch, P.O. Box 9514, 2300 RA Leiden, The Netherlands

Dicotyledonous woods: the fossil record

Recent experimental studies on the hydraulic functioning of a range of extant woody plants have demonstrated trade-offs between vessel diameter, vessel density and total vessel length. Hydraulic architecture can be classified into five extreme types: 1) long, wide diameter vessels in high density (prevalent in modern lianas); 2) long, wide diameter vessels in low density (prevalent in modern lowland tropical rainforest trees); 3) short, narrow diameter vessels in high density (prevalent in modern temperate diffuse-porous woods, especially in desert shrubs); 4) a combination of long, wide earlywood vessels and numerous, narrow and short latewood vessels (in modern ring-porous woods of temperate and subtropical regions); 5) a combination of long, relatively wide vessels and narrow, short vessels mixed throughout the wood (in a number modern lianas and xeric woody species). The first appearance of these 5 wood types in the fossil record (1500+ records reviewed) and their incidence over time will be briefly reviewed and related to environmental changes, as will the wood anatomy of selected families, e.g., Fagaceae, Juglandaceae, Lauraceae, Ulmaceae.

CONTRIBUTED PAPERS

76 ALBERT, VICTOR A.^{1*} AND RICHARD W. JOBSON^{1,2}

¹Biodiversity and Systematics, Dept. of Biological Sciences, The University of Alabama, Tuscaloosa, AL 35487-0345; ²Dept. of Botany, The University of Queensland, Brisbane, QLD 4072, Australia

Relaxed structural constraints in Utricularia (Lentibulariaceae): a possible basis in one or few genes regulating polar auxin transport

Lloyd (1942) documented the unusual embryogeny of *Utricularia*, a morphologically and ecologically diverse genus of carnivorous plants in the Lentibulariaceae (Lamiales). Specifically, the traits of apparent rootlessness (or retention of an aborted primary root), asymmetrical phyllotaxis, and production of pin-like, anisophyllous stems are suggestive of systemically altered regulation of polar auxin transport. For example, mutants of the *MONOPTEROS* gene in *Arabidopsis* are impaired in polar auxin transport, lack a primary root, may have profound phyllotactic asymmetry, and may produce inflorescence stems devoid of appendicular structures. Mutations in other auxin-involved *Arabidopsis* genes are known to produce pin-like inflorescences, and blockage of leaf organogenesis in tomato through chemical inhibition of polar auxin transport can be reversed by microapplication of auxin to the shoot tip. The embryonic developmental problems of *MONOPTEROS* and similar mutants have been ascribed to inhibition of an apical-basal auxin signal, whereas the later effects on phyllotaxis (which include pin production) have been attributed to disrupted radial auxin regulation. *Utricularia* plants may represent naturally occurring polar auxin transport mutants, and the resulting pleiotropic alterations of the typical angiosperm body plan may have provided reduced selection pressure for individuals with diverse morphologies to establish founder populations and diverge. The possibility of a narrow genetic basis for *Utricularia* vegetative diversity impacts the interpretation of significantly higher molecular rates observed for *Utricularia* plus *Genlisea* versus their sister clade, *Pinguicula*, among seven loci spanning all three genomic compartments (see abstract by Jobson and Albert, Botany 2001).

77 BAKER, DAVID M.

c/o Donald Kaplan, Dept. of Plant Biology, 111 Koshland Hall, University of California, Berkeley, CA 94720-3102

Stipules and shoot development of Exbucklandia populnea

Leaves of *Exbucklandia populnea* (Hamamelidaceae) bear a large, leathery, persistent structure at the base of their stipules which encloses the next youngest leaves produced by its shoot. By means of electron micrographs and serial sections, it was determined that the structure is formed by the appression of two lateral stipules. Such stipular morphology, but in a less elaborated form, also occurs in the inflorescence region. During a vegetative flush, between one and four branches expand out from between the stipules. The origin of these branch buds within the stipular bud was studied to determine whether they arise as either collateral axillary buds or from a condensed branching system. The phyllotaxis and plastochron of leaves borne on these shoots was determined; rates of growth of these shoots during their subsequent expansion was studied and compared in relative and absolute terms. The significance of these observations for an understanding of tree architecture will be discussed.

78 COOPER, RANESSA L.^{*}, SENNAIT A. YOHANNES, AND DAVID D. CASS

Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada, T6G 2E9

A structural study of the rare willow, Salix planifolia ssp. tyrrellii, from the Athabasca sand dunes of northern Alberta

Salix planifolia ssp. *tyrrellii*, from the Athabasca sand dunes, has been considered to be a recent derivative of the widespread *S. planifolia* ssp. *planifolia*. It is endemic to the Athabasca sand dunes of northern Saskatchewan and was documented recently from the Maybelle River and Richardson dunes in Alberta. *Salix planifolia* ssp. *tyrrellii* and its putative progenitor are similar in appearance and can be difficult to distinguish. A diagnostic feature of *S. planifolia* ssp. *tyrrellii* is the presence of adaxial stomata. In specimens of *S. planifolia* ssp. *tyrrellii* from each of the Athabasca sand dunes in northern Alberta, adaxial and abaxial stomatal frequencies were examined. In addition, vessel element (VE) characters were evaluated, including VE density, VE lumen diameter, VE length, and VE clustering. Stomatal frequencies were similar in specimens from each Alberta dune, but some VE characters were variable. These structural data were compared to those of *S. planifolia* ssp. *tyrrellii* from the Athabasca sand dunes in Saskatchewan. Similarities among values of adaxial stomatal frequency between specimens from Alberta and Saskatchewan suggest adaptation to this high light intensity environment. Overall, structural similarities described in this study provide additional support for the close taxonomic relationship of this endemic-progenitor *Salix* pair.

79 DAYANANDAN, P.^{1*} AND J. PONSAMUEL²

¹Dept. of Botany, Madras Christian College, Tambaram, India 600059; ²Plant Transformation and Gene Expression, Dow AgroSciences, 9330 Zionsville Road, Indianapolis, IN 46268-1054

Electron microscopy of terpenoid secreting cells of neem (Azadirachta indica A. Juss.)

The neem plant is known to accumulate about 25 diterpenoids and 100 different triterpenoids, including the biologically most active azadirachtins. Azadirachtins possess a wide spectrum of therapeutic and powerful pesticidal properties. The terpenoids are synthesized and accumulate within idioblasts known as secretory cells. The cotyledons of neem are the richest source of terpenoids, up to 3% of seed weight. Cotyledons also store considerable quantity of neem oil. The secretory cells differentiate about 40 days after pollination in cotyledons that are 4-6 mm long. Development of a secretory cell commences with cell enlargement, increase in the size the nucleus and vacuole. The cell walls of secretory cells are strengthened by the addition of wall material by the adjacent cells. Small vesicles containing terpenoids accumulate in the cytoplasm. The terpenoid vesicles appear to originate by the enlargement of endoplasmic reticulum (ER). A string of terpenoid vesicles interconnected by narrow regions gives a beaded appearance. The mature vesicles do not possess a boundary membrane. Each vesicle consists of many small droplets, in the range of 50-100 nm in diameter. The vesicles grow by the addition of terpenoids synthesized by ER in the vicinity of the terpenoid vesicles. As the vesicles develop the vacuole fragments into two or more bodies. The cytoplasm contains numerous ribosomes and ER. Plastids, mitochondria and microbodies, and a few dictyosomes also occur. Lipid bodies accumulate at later stages of development. The plastids are likely to provide the isoprenoids that may be further elaborated by other organelles. In addition, the vacuoles, cytoplasm and ER may all provide the enzymes and compartments necessary for the synthesis of a large variety of terpenoids. In vitro extraction of terpenoids is possible only if the cultured neem tissues are induced to differentiate secretory cells.

80 DOUST, ANDREW N* AND ELIZABETH A KELLOGG

University of Missouri-St Louis, Missouri

Integrating phylogeny, developmental morphology and genetics: a case study of inflorescence evolution in the 'bristle grass' clade (Panicoideae; Poaceae)

Our studies in the grass family Poaceae have concentrated on understanding diversity in inflorescence morphology. We have focused on the analysis of inflorescence evolution in the panicoid 'bristle grass' clade (including *Setaria*, *Pennisetum* and *Cenchrus*), as an example of the way in which molecular phylogenetic hypotheses can be combined with developmental and genetic data to understand morphological evolution. Analysis of developmental morphology with phylogenies derived from molecular data sets has enabled us to identify a small number of parameters that can control morphological diversification. These include numbers of orders of branching, numbers of primordia produced on each branch, and timing and amount of branch axis elongation. Changes in these characters occur numerous times throughout the phylogeny, suggesting that only minor changes in a few genes are required to change inflorescence morphologies. We are testing this hypothesis by a quantitative trait loci (QTL) analysis of a *Setaria italica* by *S. viridis* cross. Preliminary results indicate that numbers of primary branches and length of the inflorescence are controlled by only a few genes, as predicted.

81 DUVAL, MELVIN R.

Dept. of Biological Sciences, Northern Illinois University, DeKalb, IL 60115-2861

Screening a spurious synapomorphy: an ultrastructural study of "monocot" type anther wall development in Acorus L. (Acoraceae)

Critical morphological synapomorphies have not been found in support of the Acoran hypothesis, the molecular phylogenetic discovery that Acoranae are the basal monocots. The previously undetermined pattern of anther wall development in *Acorus* has been suggested to be one such character. Two main types of anther wall development have been recognized: 1) the "monocotyledonous" type which, variously characterizes both monocots and dicots, and 2) the "dicotyledonous" type, which is almost exclusive to dicots. An anatomical study of anther wall development in *Acorus* was here undertaken using electron microscopy. Development of the anther wall in *Acorus* was found to be somewhat irregular or perhaps even intermediate between the two types, although largely consistent with the "monocotyledonous" type. The apparent homoplasy of this character among species of paleoherbs and the phylogenetic uncertainty of monocot/dicot relationships undermines the presumed significance of anther wall development and other morphological characters to the Acoran hypothesis.

82 FREUDENSTEIN, JOHN V. AND ELIZABETH M. HARRIS*

Herbarium and Dept. of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, OH 43212

Re-evaluating critical anther characters in Orchidaceae: a developmental anatomy approach

The anther is the source of several of the principal characters traditionally used for classification in Orchidaceae, particularly in Epidendroideae, where the greatest amount of variation is present. We examined the diversity of pollinium arrangement and anther orientation in Epidendroideae as well as in representatives of the other subfamilies using serial sections of succes-

sive ontogenetic stages of columns. An important question is whether the incumbent anther in Vanilloideae is distinguishable from that in Epidendroideae, as the shared possession of an incumbent anther is the key feature that unites the two groups, in disagreement with molecular patterns that suggest that they are not closely related. Anatomical study reveals that the principal difference in anther bending between the two subfamilies is the enormous expansion in the connective in the Vanilloideae, which is not seen in Epidendroideae. This connective expansion contributes substantially to positioning of the thecae near the rostellum. The anther in the vandoid subset of Epidendroideae is shown to be truly incumbent, with the bending achieved by a redirection of growth in very early ontogenetic stages, as opposed to the inflexing of a nearly fully-formed anther, as in the remainder of Epidendroideae. This heterochronic change is largely correlated with cellular pollinium stalks, and may facilitate the development of the complex pollinarium. It can also result in unusual pollinium shapes among the vandoids. Superposed pollinia result from a reorientation of developing thecae, and may be fully or only partially superposed. These results allow us to further refine character states that are crucial to our understanding of orchid relationships.

83 GHOSH, NABARUN^{1*}, A. CHATTERJEE², AND DON W. SMITH³

¹Dept. of Life Earth and Environmental Sciences, West Texas A&M University, Canyon, TX 79016-0001; ²CAS, Dept. of Botany, University of Calcutta, Calcutta-19, India; ³Dept. of Biological Sciences, University of North Texas, Denton, TX 76203

Albizia lebeck Benth.: in vitro regeneration via embryogenesis, karyotypic analysis and SEM studies

Albizia lebeck Benth. is known as the East Indian Walnut in Europe. *A. lebeck* plantations are found in Hawaii and different parts of Florida in the United States. It is an erect deciduous tree of Mimosaceae with umbrella shaped crown and is preferred as a timber yielding ornamental tree. Large-scale plantation forestry and afforestation of degraded forestlands are the solution to ensure future sufficiency in biomass. Tissue culture is a very useful and reproducible technique for mass clonal propagation. We used leaf explants on modified MS (Murashige and Skoog 1962) medium to establish *in vitro* culture. On MS medium modified with 6, BAP (0.4 mg/l), Kinetin (0.25 mg/l) and coconut milk 12% (v/v) the leaflet explants produced callus from the cut end of the explants. We used 0.5% PVP to reduce and dissolve the polyphenol exudation from the explant. The calli could be classified into 4 major types: friable white callus, friable white and green mixed callus, compact green callus and very compact green callus. We found friable white and green mixed callus as the most suitable one for establishing the suspension culture in the liquid medium. We tried different concentrations and combinations of growth regulators (6, BAP, Kinetin, 2,4-D, IAA, NAA) and growth supplements (coconut milk, casein hydrolysate) to induce morphogenesis in the suspension culture. MS medium with 6, BAP (8 mg/l), IAA (0.25 mg/l) and coconut milk 8% (v/v) produced embryoids. The embryos followed rhizogenesis and caulogenesis on agarified medium. We fixed the tissue in 4% Glutaraldehyde and observe the regeneration with SEM after Critical Point Drying and gold plating. Karyotyping was done from well scattered metaphase plate from root tip squash. A pre exposure of the plantlets to the Knop's medium increased the survival efficiency. 66% of the transferred plantlets survived in the greenhouse. The regenerated plants showed normal fast growth and reach the roof of the greenhouse (20 ft.) within 6 months.

84 GROOT, E. P.^{1*}, S. A. NICHOL¹, J. A. DOYLE², AND T. L. ROST¹¹Section of Plant Biology, University of California, Davis, CA 95616; ²Section of Evolution and Ecology, University of California, Davis, CA 95616*Phylogenetic relationships and root apical meristem organization in the dicots*

There are two basic types of root apical meristem (RAM) organization in dicotyledonous angiosperms: open and closed. In taxa with closed organization, longitudinal cell files terminate apically into distinct tiers of initials sometimes called histogens. In RAMs with open organization, the cell files terminate in a zone of initials with uncertain cell lineage. An intermediate type of open organization has specific initials for the epidermis and peripheral root cap cell lineages, but the other histogens do not appear to be clonally distinct. In a survey of one-week-old seedlings grown in sand, about half of the dicot families represented had closed organization. One-third of the families had the intermediate type of open organization, and about 10% of the families were mixed. Only Cucurbitaceae and Fabaceae had the true open type. Mapping RAM organization on recent phylogenies based on DNA sequences of several genes indicated that the ancestral state in angiosperms was the intermediate type of open organization, and the closed type originated in the eudicots, above Ranunculales. Several clades in the eudicots showed reversals to the more primitive, intermediate open type, resulting in some taxa containing a mix of closed and intermediate open members. What particular ecological adaptations these RAM organizations represent remains to be investigated.

85 GROOT, E. P., K. CHAPMAN*, AND T. L. ROST

Section of Plant Biology, University of California, Davis, CA 95616

Root apical meristem organization is a dynamic character in dicot roots

The root apical meristem (RAM) is the source of the cells making up the root cap and body. Initial cells in the RAM divide, producing derivative cells that elongate, mature and differentiate into specific cell types. In closed RAM organization these initials are arranged in specific tiers (histogen layers); in open organization cell files terminate in a zone of initials lacking apparent organization. Despite this obvious difference, both open and closed roots form protoderm and peripheral root cap through a periclinal T-division of a root cap protoderm initial. It has been commonly assumed that RAM organization remains constant over the developmental life of the root. The primary roots of *Arabidopsis* (a closed species) became determinate in 3-4 weeks, this process was correlated with a loss of closed RAM organization. In addition, the RAM of *Pisum*, an open species, changed in shape and size during the lifetime of the root. Studies of other dicot species reinforced these findings. T-divisions appeared to be a constant feature among dicots because it was present regardless of root age and organization. We will propose that RAM organization in dicot roots undergoes certain changes through ontogeny. 1. All the radicles of early embryos have closed organization. 2. The organization changes by the time germination occurs in open species, but remains the same in closed species. 3. By the time a root has reached its determinate stage, all RAMs have open organization. The RAM of dicots is a dynamic structure; therefore, it is important to consider the developmental state of the root when classifying apical organization types.

86 HISER, KENNETH M.* , ANDREW N. DOUST, AND ELIZABETH A. KELLOGG

Dept. of Biology, University of Missouri-St. Louis, 8001 Natural Bridge Rd., St. Louis, MO 63121

*Inflorescence development and phylogenetic relationships of the genus *Ixophorus**

The genus *Ixophorus* (Paniceae: Poaceae) has a set of morphological characters that suggest relationships to disparate genera in the grass tribe Paniceae. The bristles in the inflorescence imply a connection to *Setaria*, whereas the mucronate lemma and unilateral primary inflorescence branches imply a connection to *Urochloa*, and the enlarged lower palea suggests a relationship with some species of *Panicum*. We have undertaken studies of molecular phylogeny and developmental morphology to investigate the placement of *Ixophorus* and the developmental basis of its distinctive combination of characters. Sequence data from the chloroplast genes *ndhF* and *trnL* strongly support the placement of *Ixophorus* within a monophyletic 'bristle clade', and specifically, closely allied to *Setaria*. We have documented the development of inflorescences, from the vegetative stage through fully developed spikelets, using Scanning Electron Microscopy (SEM). Variations on themes of branching pattern and primordium differentiation are compared and contrasted to those in *Setaria*. This enables us to characterize precisely at which stages *Ixophorus* is developing in a way typical of *Setaria*, and at what points it is displaying unique developmental patterns. Integrating molecular phylogenetics with SEM data enables us to make more precise statements regarding the morphological variation we use in taxonomy. In this case, our taxonomic product will be a monograph of *Ixophorus*, which will include this particularly rigorous assessment of its morphology.

87 HORNER, HARRY T.^{1*}, TERESA CERVANTES MARTINEZ¹, TED HYMOWITZ², A.H.D. BROWN³, AND REID G. PALMER⁴¹Dept. of Botany, Iowa State University, Ames, IA 5001; ²University of Illinois, Champaign-Urbana, IL; ³CSIRO Plant Industry, Canberra, Australia; ⁴USDA ARS CICGR, Ames, IA 50011*A survey of calcium oxalate crystal patterns in leaves of the genus *Glycine* and related taxa*

Calcium oxalate crystals have been identified in the majority of flowering plants, including soybean. The relationship between calcium oxalate and soluble oxalate is not known. A search for natural or induced variation in crystal numbers and patterns included mutagenized seedlings of a soybean line, transposon-tagged plants, plant introductions (accessions) of the cultivated, wild annual and wild perennial soybean, and accessions of related taxa to *Glycine*. Leaf samples (circular leaf punches) were taken from herbarium specimens and greenhouse and field-grown plants. The samples were chemically cleared, mounted on slides and viewed with a compound light microscope between crossed polarizers. The number and arrangement of leaf prismatic crystals (calcium oxalate, monohydrate) in an individual plant were similar but varied among accessions and species. The crystals were typically associated with the veins and lamina. The utility of leaf crystals as an aid in classification of these taxa will be presented. No accessions devoid of calcium oxalate crystals were found even though one taxon from Japan had the smallest and fewest numbers of crystals of any specimen observed.

88 JANSEN, STEVEN¹*, PIETER BAAS², AND ERIK SMETS¹

¹Laboratory of Plant Systematics, Institute of Botany and Microbiology, K.U.Leuven, Kasteelpark Arenberg 31, B-3001 Leuven, Belgium; ²Nationaal Herbarium Nederland, Universiteit Leiden branch, P.O. Box 9514, 2300 RA Leiden, The Netherlands

Vestured pits: a wood anatomical character with strong phylogenetic signals at high taxonomic levels

Based on original observations and a critical literature survey, vestured pits are found in approximately 48 families according to the APG-system, including 14 families in which vestures were not recorded previously. Constancy in the presence or absence of vestured pits throughout the secondary xylem of a given specimen is generally supported. However, in some taxa that frequently show vestigial vestures, the occurrence is restricted to particular areas within the limits of a single wood sample. Phylogenetic hypotheses based on DNA sequences are frequently supported by the presence or absence of vestured pits in eudicots. The character is found to be relatively widespread at the base of the eurosids I (Zygophyllaceae, Fabales, very few Rosales, Malpighiales), eurosids II (Myrtales, Malvales, Brassicales), and euasterids I (Gentianales, Lamiales, Solanales), but the feature probably has been lost or originated independently in several more derived branches of these clades. Representatives from euasterids II always show nonvestured pits. Vestured pits characterise the orders Myrtales and Gentianales sensu APG. Other taxa that consistently show vestured pits include Malpighiaceae, Polygonaceae, Brassicaceae, and most Fabaceae. While numerous parallel origins undoubtedly underlie the occurrence of vestured pits, there are at least few instances where vestured pits most likely have been lost during evolution. Our results put major doubt on the earlier suggested homology of vestures and warts. Possible functions of both structures remain speculative or unclear.

89 KIM, INSUN

Biology Dept., Keimyung University, Taegu 704-701, Korea

Greatly reduced duckweed morphology with highly effective structural organization

Morphologically, duckweeds are poorly differentiated hydrophytes that only produce connected fronds with a single or multiple root system on each frond. Such morphological reduction in small, free-floating plants of *Lemna* and *Spirodela* has led to the speculation of their simple anatomy. In the current study, complex structural organization, in respect to the cellular differentiation, is revealed within each organ of the *Lemna* and *Spirodela* plant body. In particular, laterally connected translucent stalk cells, commonly with polymorphic mitochondria, fibrillar supporting structures and unevenly thickened walls are the most noticeable features. A distinct boundary layer filled with fibrillar materials at the root-root cap junction, chloroplasts having grana with 3-9 stacked thylakoids and starch grains distributed throughout the plant are other interesting structural attributes drawing attention in the study. In summary, characteristics such as an entirely chlorenchymatous plant body, poorly developed vesicular tissue, well-established plasmodesmatal connection, rapid vegetative reproduction, offspring protection, aerenchyma formation, effective abscission in the connective stalk and a well-organized root proper having a prominent root cap are clearly demonstrated in these greatly reduced species. Such reduction and differentiation of the plant body effectively contribute to the better adaptation of smaller plants to superficial aquatic environments, while enabling rapid growth.

90 KIM, INSUN

Biology Dept., Keimyung University, Taegu 704-701, Korea

*Ultrastructure and immunolocalization of the C-4 photosynthetic enzyme in cotyledons and leaves of two *Salsola* species*

Some deviation in the type of photosynthesis and Kranz structure are found in cotyledons and leaves of the same plant among the C-4 *Salsola* species. The current study attempted to reveal the pattern of Kranz and cell-type-specific C-4 enzyme accumulation in cotyledons and leaves of *Salsola collina* and *S. komarovii*. Structural aspects of the bundle sheath and mesophyll cell differentiation, as well as immunolocalization of the bundle sheath cell-specific enzyme, RuBPCase, and the mesophyll cell-specific enzyme, PEPCase, were used particularly in *S. komarovii* to follow the development of the C-4 pattern. The study revealed the Salsoloid Kranz type having either continuous or discontinuous concentric chlorenchyma in all leaves and cotyledons. The Kranz pattern and ultrastructure of the bundle sheath and mesophyll cell in the cotyledons were almost identical to those of mature leaves in *S. komarovii*, where cellular differentiation into the bundle sheath cell and mesophyll cell occurred simultaneously with development of the secondary plasmodesmata. Accumulation of RuBPCase appeared early in the bundle sheath precursor cell stage. Strong RuBPCase reaction was shown at the time of bundle sheath tissue-delimitation and further on in developing stages. PEPCase was restricted to the mesophyll cells and detected only in later stages at low levels. The leaf/cotyledon structure in these species was C4-S/C4-S, according to Pyankov et al. (2001), with a characteristic bundle sheath- and mesophyll cell-specific C-4 enzyme accumulation pattern.

91 KONG, HONGZHI*, ANMING LU, AND ZHIDUAN CHEN

Laboratory of Systematic and Evolutionary Botany, Institute of Botany, The Chinese Academy of Sciences, Beijing 100093, China

*Floral organogenesis of *Chloranthus sessilifolius* K. F. Wu (Chloranthaceae) with special emphasis on the morphological nature of the androecium of *Chloranthus* Sw*

Whether the androecial structure of *Chloranthus* represents a single stamen with four pairs of sporangia or three independent stamens that have undergone fusion with one another towards their base, has remained a major controversial issue. In literature, it has been described as "a single stamen", "three stamens", "three anthers", "a single tripartite anther", or "a three-lobed filament". Two classes of hypotheses were also proposed to interpret its evolutionary process, but no accordance has reached yet. In this study, we observed the floral organogenesis of *C. sessilifolius* K. F. Wu, a perennial herb with androecial lobes cohered only at the base. Inflorescence primordium, produced at the end of leafy shoots, is dome-like at the beginning and then elongates upwards, from which bract primordia initiate almost decussately. Floral primordium, arising from the axil of the bract, soon becomes a scale-like structure, with androecial primordium originating from its adaxial margin, and gynoecial primordium in its abaxial position. As three primordia of androecial lobes become visible in the adaxial margin of the floral primordium, four thecae are already in differentiation, and the gynoecial primordium appears as a shallow disc. The androecial lobes do not extend its length until the thecae approach maturity, and the elongation of the androecial lobes is simultaneous with the differentiation of the stigma. Ontogenetically, *C. sessilifolius* shares many character states with *Sarcandra* species, and more with *C. spicatus* (Thunb.) Makino.

Based on these results and those of Endress, combined with evidence from neobotany, palaeobotany and molecular systematics, the morphological nature of the androecium of *Chloranthus* is further discussed. The second hypothesis of Endress, that the androecial structure of *Chloranthus* might have arisen by splitting of a single stamen with 2 marginal thecae, seems to be the most plausible interpretation.

92 KORN, ROBERT W.

Biology Dept., Bellarmine University, 2001 Newburg Rd., Louisville, KY 40205

The origin of stomatal clusters in Begonia bracteosa

The number of stomata in clusters of *Begonia bracteosa* ranges from one to ten with an average of 3.78 and its distribution follows a Poisson process as analyzed by the chi square test with a P value greater than 25%. Each stomatal cluster comes from a single cell with the number of stomata in a cluster directly related to the size of the cell at the time of specialization. The probability distribution frequencies of epidermal cells can be given as a complex equation that can be simplified into a binomial distribution which, in turn, can be restated as a Poisson distribution. This set of mathematical transformations parallels the changes in developmental features from epidermal cells to stomatal clusters.

93 LARSON, TROY AND PHILIP J. VILLANI*

Augustana College, 639 38th Street, Rock Island, IL 61201

The effects of thidiazuron on the release of foliar embryos in Bryophyllum calycinum

Leaves on the plant of *Bryophyllum calycinum* produce foliar embryos in the notches of the leaf margin. These embryos remain dormant while the leaf is attached to the plant. However, detaching a leaf will cause many of these foliar embryos to be released from dormancy and develop into plantlets. The effects of thidiazuron (TDZ), a hormone with cytokinin activity, on the release of foliar embryos and root formation was investigated. Two centimeter explants of the leaf margin including the notch region were removed from the leaves and grown in tissue culture on Murashige and Skoog media supplement with B5 vitamins and various hormones. Overall, TDZ causes significantly more embryos to be released from dormancy compared to the control or some concentrations of 6-Benzyl-aminopurine (BAP). At concentrations of 10^{-8} and 10^{-10} TDZ, greater than 92% of the foliar embryos placed in culture were released from dormancy compared to 84% or 82% on 10^{-6} or 10^{-8} BAP, respectively, or 73% on the control media. In addition, a trend was observed that higher concentrations of TDZ causes the release of fewer embryos than lower concentrations. TDZ at various concentrations had little affect on the number of roots per explant unlike BAP or 2,4-D compared to the control.

94 LITT, AMY* AND VIVIAN IRISH MCDB

Yale University, New Haven, CT 06520

The A of the ABC model: phylogeny of the AP1-like gene family

The ABC model of floral development postulates that three classes of genes are responsible for determining the identity of the four types of floral organs. The genes overlap in function in adjacent organ whorls, thus A-gene function alone determines sepal identity, A+B determine petal, B+C determine stamen, and C alone determines carpel identity. *APETALA1* (*AP1*) of *Arabidopsis thaliana* has been identified as an A-function gene, but it is also involved in the determination of floral meristem identity. The phenotype of the mutant has features that can be interpreted

as a failure of either function, thus there is no clear evidence that *AP1* is involved in specifying floral organ identity as a separate function. *AP1* homologs from other species have not been shown to affect floral organ identity, thus there is little documentation of the A component of the ABC model. *AP1* belongs to a large and complex subfamily of the MADS-box gene family, and it is not clear that homologs have been correctly identified in other species. This is a requirement for comparative studies, therefore we are studying the phylogeny of *AP1*-like genes to be able to identify homologs for further expression and function studies and to determine where significant evolutionary events have occurred. Preliminary results suggest that during angiosperm evolution there was a duplication that produced the paralogous *AP1* and *FRUITFULL* lineages present in higher eudicots. There is some evidence that this duplication may have occurred within the basal eudicots, and may coincide with a similar duplication in the *AP3* (B-function gene) lineage. These duplication events may be related to the fixation of basic floral structure that is seen in the higher eudicots.

95 MCDILL, JOSHUA R.^{1*}, ROBERT W. PATTERSON¹, AND J. MARK PORTER²

¹Dept. of Biology, San Francisco State University, 1600 Holloway Avenue, San Francisco, CA 94132; ²Rancho Santa Ana Botanic Garden, 1500 North College Avenue, Claremont, CA 91711

A comparative anatomical study of Linanthus and related genera (Polemoniaceae), with implications for their relationships and evolution

Phlocideae is a newly recognized tribe of Polemoniaceae that reflects generic relationships revealed by recent molecular phylogenetic work. This tribe features several closely related annual and perennial lineages and includes the genera *Phlox*, *Microsteris*, *Gymnosteris*, *Leptosiphon*, and *Linthus*. While the Polemoniaceae has been intensively studied using macromorphological and molecular methods, it has received little attention from anatomists. The nature and degree of anatomical variation in the family is thus largely unknown. The primary goal of this project has been to document the anatomical characteristics of leaves, stems, and flowers in the lineages of Phlocideae, with emphasis on *Linthus* and *Leptosiphon*, and to examine the evolution of those characters using the phylogenetic model provided by molecular data. With few exceptions, species in Phlocideae exhibit bifacially distributed stomata, leaf bundle sheaths composed of large, non-photosynthetic cells, and some degree of stem secondary growth. Less conserved characters, informative intergenerally, include the presence of an abaxial mass of fibers in the central leaf vein (characteristic of *Linthus* and some *Leptosiphon*), the formation of bundle sheath extensions from the central vein to either leaf surface (in *Microsteris* and *Phlox*), and the extension of the lignified cells of the central vein into a spine-like leaf tip (*Linthus*). Within genera, lineages differ in trichome structure and distribution, degree of leaf mesophyll differentiation into palisade and spongy layers, and cuticular features. Anatomical data support the inclusion in *Linthus* of four species previously assigned to *Gilia* but transferred to *Linthus* based on molecular data.

96 MIKESSELL, JAN E.

Dept. of Biology, Gettysburg College, Gettysburg, PA 17325

Comparison of gametophyte and sporophyte development in ragweed species

Variation in sex expression in ragweed taxa occurs to the extent that ordinarily monoecious species can exhibit dioecy. Gametophyte and sporophyte development was analyzed in two annual ragweed species, *Ambrosia artemisiifolia* (common) and *Ambrosia trifida* (giant). Seed analysis was used to

obtain indirect recognition of female gametophyte and sporophyte characters. Whorls of axillary branches differentiated along the main stem axes of both species, with staminate racemes forming terminally on main and axillary branches. Pistillate heads formed in leaf axils. Pollen grains and seeds were analyzed from the base to the terminus of axillary and main stems. All characters were significantly larger in giant ragweed such as: seed mass, pollen diameter, axillary branch length, number of staminate heads per axillary branch, number of staminate flowers per head, and pollen grain number. The percent increase in giant ragweed characters compared to common ragweed ranged from 483% (seed size) to 10% (pollen diameter). Seed size revealed a greater variation than pollen size in giant, but a smaller variation in common ragweed. The size of pollen grains or seeds exhibited no recognizable trends from older to younger axillaries. The size of grains and seeds manifested no correlation at each of the different branch levels. The largest seeds differentiated at basal branches in common, and at middle branches in giant ragweed. Heaviest seeds compared to lightest exhibited 18% and 33% more mass in common and giant ragweed, respectively. However, little difference in pollen grain size was discernable in either taxon from the base to the terminus of axillary or main stems. For example, the largest grains differed in diameter from the smallest grains in common ragweed by 1% and in giant ragweed by 4%. Assemblages of pennate diatom species were associated with staminate flowers of both species.

97 NGUYEN, HONG*, ROY C. BROWN, AND BETTY E. LEMMON

Dept. of Biology, University of Louisiana @ Lafayette, Lafayette, LA 70504

Cytoskeletal patterns in endosperm development of Coronopus didymus (Brassicaceae)

Study of microtubules and F-actin during endosperm development revealed distinct developmental domains in the micropylar chamber (MC) containing the embryo, the large curved central chamber (CC), and the small chalazal chamber (ChC). As is characteristic of nuclear endosperm development, the common cytoplasm is organized into nuclear cytoplasmic domains defined by nuclear-based radial microtubule systems which determine placement of walls at the cellularization stage. Both microtubules and F-actin are reorganized in preparation of the syncytium for simultaneous cytokinesis. New findings are 1) the interrelationships between microtubules and F-actin during development in all three chambers, 2) an early stage of syncytial endosperm characterized by unusual fusiform to multangular nuclei sheathed by parallel arrays of microtubules, and 3) organization of a multinucleate cyst of cytoplasm in the ChC that never cellularizes. Comparison of *Arabidopsis thaliana* and *Coronopus didymus* shows endosperm development to be a conservative process in mustard seeds. Supported in part by NSF MCB-9726968 to R.C.B and B.E.L. and Louisiana Board of Regents Fellowship LEQSF-1998-03-GF-28 to H.N.

98 NIKLAS, K. J.*¹, F. MOLINA-FREANER², C. TINOCO-OJANGUREN², AND D. J. PAOLLILO, JR.¹

¹Dept. of Plant Biology, Cornell University, Ithaca, NY 14853;

²Instituto de Ecología UNAM, Hermosillo, Sonora CP83000, Mexico

Biomechanics and anatomy of Pachycereus pringlei root systems.

We report the morphology, anatomy, and biomechanics of *Pachycereus pringlei* root systems and explore the hypothesis that anchorage and nutrient absorption/storage are functionally specialized and spatially partitioned in response to

selection in windy and arid habitats. The root systems of 18 plants were excavated, and root samples were anatomically and biomechanically examined. Our analyses indicate that anchorage is provided by a large bayonet-like root that typically emerges from the stem base in conjunction with the woody proximal elements of a horizontally extensive, shallow lateral root system that absorbs and stores water. Wood stiffness and strength correlated with the volume fraction of axial tissues, which dramatically increased toward the base of lateral roots. Calculations indicate that the ability to resist wind-throw decreases with increasing plant size, due to a disproportionate increase in stem size with respect to the depth of burial and size of the bayonet-like root. In contrast, the capacity of more distal lateral root elements to provide for nutrient absorption/storage increases. These and other lines of evidence support our hypothesis that the root system of this species is highly compartmentalized with respect to anchorage and nutrient absorption/storage.

99 OSBORN, JEFFREY M.^{1*}, GAMAL EL-GHAZALY², AND RANESSA L. COOPER³

¹Division of Science, Truman State University, Kirksville, MO 63501;

²Palynological Laboratory, Swedish Museum of Natural History, SE-

104 05 Stockholm, Sweden; ³Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Development of the exineless pollen wall in Callitrichaceae and the evolution of underwater pollination

The Callitrichaceae are a monogeneric family of aquatic angiosperms comprising approximately 50 terrestrial, amphibious, and obligately submersed species. *Callitriche* is unique in being the only known genus with co-occurring aerial and underwater pollination systems. Mature pollen structure is correlated with growth habit, pollination biology, and phylogeny within the genus. In the present study, development of exineless pollen in the obligately submersed species *Callitriche truncata* was examined, with particular emphasis on the tetrad stage. Pollen ontogeny occurred rapidly and non-synchronously; tetrads, free microspores, and two-celled pollen grains were identified within the same anthers. Formation of the intine also occurred relatively early, during the tetrad stage. Tetrads were surrounded by a structurally distinct envelope, and its ultrastructure and histochemistry indicate that this callose-like envelope is in a transitional state. Reduction or complete loss of the exine has evolved at least twice in Callitrichaceae, and the new ontogenetic data indicate that exine loss evolves more quickly than the loss of callose. In addition, developmental information on exineless pollen in *C. truncata* coupled with other palynological data for the exine-bearing terrestrial and amphibious growth forms provide support for the hypothesis that underwater pollination has had a relatively recent origin in the family.

100 PIZZOLATO, THOMPSON D.¹ AND MARSHALL D. SUNDBERG^{2*}

¹Dept. of Plant and Soil Sciences, University of Delaware, Newark,

DE 19717-1303; ²Dept. of Biological Sciences, Emporia State University, Emporia, KS 66801-5087

Initiation of the vascular system in the shoot of Zea mays L (Poaceae). 1) The procambial nodal plexus

All procambial strands in six contiguous nodes below the tassel primordium of a young maize plant were traced from serial transections to reveal the pattern of vascular development. Each node consists of a disk of insertion and its subtended leaf primordium. Within each disk of insertion, concentric, successive waves of isolated procambial strands are generated by a

peripheral primary thickening meristem. These discrete traces become linked into sympodial leaf traces by merging with procambial traces from the subtended leaf primordia and with procambial traces of adjacent waves of their own and of adjacent disks of insertion. Median leaf traces, major lateral leaf traces, bud traces and intermediate leaf traces penetrate the disks of insertion to respectively decreasing depths. In addition, some procambial in the successive waves within a disk of insertion persist with blind ends. The nodal plexus arises as ground parenchyma adjacent to these blind endings dedifferentiates and forms horizontal procambial strands.

101 RENTZ, ERIN D.* AND ROBERT W. PATTERSON

Dept. of Biology, San Francisco State University, 1600 Holloway Ave., San Francisco, CA 94132

Effects of burning on the anatomical structure of Corylus cornuta and Xerophyllum tenax, plants commonly used in California aboriginal basketry

For centuries, Native Americans in northwestern California have utilized fire as a tool to manage important plant resources. Regular burning is performed to clear excess brush and increase the quality and quantity of plant species used by tribes in this region as a food source or to weave baskets. *Xerophyllum tenax* (bear grass) and *Corylus cornuta* (hazelnut) are two plant species which require regular burning to produce materials suitable for basket weaving. Leaves and stems produced after fire are straighter, more flexible and more even from base to tip than those produced on unburned plants. The goal of this project was to determine how fire affects anatomical structure of *Xerophyllum tenax* and *Corylus cornuta* and to determine the structural characteristics important to weaving. We collected leaf and stem samples from plants in unburned populations as well as from burned populations, one year after a fire and used light microscopy to compare anatomical structure. In *Xerophyllum tenax*, post-fire leaf growth exhibited a reduction of support fibers along the adaxial and abaxial surfaces as well as a reduction in secondary wall thickness in fibers. This is consistent with morphological characteristics weavers recognize as good quality.

102 ROTHWELL, GAR W.^{1*} AND RUTH STOCKEY²

¹Dept. of Environmental and Plant Biology, Ohio University, Athens, OH 45701; ²Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada

Pollen tubes, contractile tissue, and pollination biology in Cycadeoidales/Bennettitales

Anatomically preserved specimens of *Cycadeoidea/Bennettites* and *Williamsonia* have provided a wealth of information about a the reproductive biology in a group of Mesozoic seed plants that may be more closely related to flowering plants than is any living clade. Newly discovered seed cones from Upper Cretaceous (Santonian-Campanian) deposits of west coast British Columbia, Canada are permineralized with calcite, and show histological details of the pollen receiving mechanism, megagametophytes and dicotyledonary embryos, as well as new information about post-pollination ovule biology and even pollen tubes. A new species of *Cycadeoidea* displays spiral contortion of the vascular tissue for several mm below the seed/seed stalk juncture. This tissue is separated from the straight cortical tissues, and does not occur at more proximal levels of the seed stalks. This feature is diagnostic of the contractile roots of living flowering plants, and indicates that some species had cones that retracted their elongated ovules following pollination. Several seeds of one *Williamsonia* cone show large, branched tubular structures within tissues of the nucellus that are structurally equivalent to the siphonogamous pollen tubes of *Agathis australis* and other living

araucarian conifers. Like the living species, the tubular structures are concentrated in the distal region of the *Williamsonia* seeds, but some extend to the chalaza. Together with previously documented facets of reproductive ontogeny, these new specimens demonstrate that cycadeoid/bennettite reproductive biology shared numerous derived characters with living conifers, gnetophytes and flowering plants.

103 SCHNEIDER, HARALD^{1*}, KATHLEEN M. PRYER¹, AND RICHARD LUPIA²

¹Dept. of Biology, Duke University, Durham, NC 27708; ²Sam Noble Oklahoma Museum of Natural History and School of Geology and Geophysics, University of Oklahoma, 2401 Chataqua Avenue, Norman, OK 73072

A comparative analysis of structure and function of spores in extant heterosporous ferns (Salviniales)

Heterosporous ferns are a monophyletic lineage comprising five extant genera that fall into two clades: Marsileaceae, including *Marsilea*, *Pilularia* and *Regnellidium*; and Salviniaceae, including *Azolla* and *Salvinia*. The Marsileaceae have an amphibious habit, whereas the Salviniaceae are exclusively floating aquatics. Observations from light and scanning electron microscopy indicate that the megaspores of each of the heterosporous fern genera have a uniquely modified outer spore wall (perine) above the aperture, which is referred to as an acrolamella, and they also differ substantially in the details of their perine ultrastructure. The megaspores of Marsileaceae are dispersed freely into water and possess an ephemeral gelatinous outer perine that acts as a flexible floating apparatus. In Salviniaceae, the megaspores are retained in the sporangium wall and have either a completely (*Salvinia*) or partly (*Azolla*) alveolate outer perine, which also functions in providing buoyancy. In *Azolla*, parts of the indusium and the sporangium wall form, together with the megaspore body, an extraordinary megaspore apparatus, making these spores the most complex among living land plants. As with the megaspores, the microspores of Marsileaceae are freely released in water and possess a gelatinous perine layer, whereas, the microspores of Salviniaceae are retained in massulae (*Azolla*), or within the microsporangium (*Salvinia*). The evolution of mega- and microspore characters is inferred using a phylogeny obtained from an independent analysis of nucleotide sequence data. Because extant genera in both clades each exhibit multiple unique perine structures, it is not possible to definitively reconstruct spore wall ultrastructure characters in the common ancestor of heterosporous ferns. To help resolve this dilemma, approaches using comparative developmental data and the integration of fossil heterosporous ferns will be outlined.

104 SEAGO, JAMES L.

Dept. of Biology, SUNY at Oswego, Oswego, NY, 13126

Root cortex development in Cyperus alternifolius

This study is a continuation of my analyses of the development and structure of the root cortex in wetland plants. The root cortex in *Cyperus alternifolius* is very large. It has an endodermis with Casparian bands, suberin lamellae, and secondarily lignified walls. The inner cortex is 5-8 cells thick with slightly thickened cellulosic walls. The bulk of the cortex is lysigenous-originated arenchyma; the circumferential lysigenous cells are held in place by radial strands of cells. The hypodermis is multi-layered with a uniseriate exodermis. The exodermis contains Casparian bands and suberin lamellae.

105 SHOCKEY, KARA M.*, HARRY T. HORNER, AND JONATHAN F. WENDEL

Dept. of Botany, Iowa State University, Ames, IA 50011

Calcium oxalate crystals in the tribe Gossypieae and the genus Gossypium (cotton)

Calcium oxalate crystals are common in leaves and other tissues throughout the angiosperms. The morphology and distribution of crystals vary widely among genera and often between closely related species. These traits have been shown to be systematically relevant in some cases. Phylogenetic relationships among members of the cotton genus and tribe are reasonably well understood, providing a context for evaluating evolution of leaf crystal patterns in the group. An anatomical study was undertaken, using leaf clearings, to characterize the type, morphology and patterns of the crystals. Patterns of crystal distribution and morphology are compared among taxa and are evaluated with respect to phylogeny and biogeography.

106 TIAN, HUI-QIAO^{1,2}, TONG YUAN¹, AND SCOTT D. RUSSELL^{1*}

¹Dept. of Botany and Microbiology, University of Oklahoma, Norman, OK 73019; ²School of Life Science, Xiamen University, Xiamen 361005, Fujian, P.R. China

Relationship between double fertilization and the cell cycle in male and female gametes of tobacco

Cell cycle changes in the nuclear concentration of DNA were measured in male and female gametes of tobacco (*Nicotiana tabacum* L.) using 4',6-diamidino-2-phenylindole (DAPI) labeling and microfluorimetry. Mitotic generative nuclei were used as a reference for 2C DNA concentrations. After division of the generative nucleus, the two sperm cells remained at a 1C DNA concentration in pollen tubes growing in the style. Sperm cells deposited within the synergid, however, had DNA concentrations approaching 2C. Egg nuclei are formed at a 1C state and approach 2C at 48 h after pollination, approximately 4 h before expected karyogamy. If pollination was withheld, the onset of DNA synthesis in the egg nucleus was delayed by 12 to 24 h. Sperm appear to be retained within the synergid until they reach cell cycle synchrony with the female nuclei at 2C. Zygote nuclei display a 4C concentration of DNA soon after fusion and up to 84 h after fertilization. These data provide evidence for gamete fusion at 2C in dicotyledons with bicellular pollen. This differs from some modern studies on monocotyledons and is consistent in the fusion condition with *Arabidopsis thaliana*.

107 TOMLINSON, P. BARRY

Harvard Forest, Harvard University, Petersham, MA 01366; National Tropical Botanical Garden, 3530 Papalina Rd., Kalaheo, Kauai, HI 96741

Does Gnetum show reaction tissue?

Many woody plants have a secondary capacity to re-orient axes, or sustain the existing orientation of axes, by producing modified cells, i.e., form reaction tissue. Usually this is eccentric secondary xylem ("reaction wood"). "Compression wood" is formed in conifers on the lower side of branches and leaning trunks, exerting a compressive force ("push"); "tension wood" in flowering plants is formed on the upper side and exerts a tensile force ("pull"). Which of these types might be shown by *Gnetum*, a gymnosperm with vessels in its wood? Experiments on *G. gnemon* demonstrate the existence of reaction tissues which are extra-xylary, i.e., differing from both conifers and flowering plants. *Gnetum gnemon* provides a precise example of Roux's model in the Halle-Oldeman system of tree architecture, with clearly differ-

entiated orthotropic and plagiotropic axes. Both kinds of axis produce the reaction tissues and there is a cortical but not xylary eccentricity clearly associated with the secondary growth response. Furthermore, reaction fibers (which resemble "gelatinous fibers") are of both primary and secondary (from the phloem) origin; the primary fibers originate in a very unusual way.

108 VON BALTHAZAR, MARIA* AND PETER K. ENDRESS

Institute of Systematic Botany, University of Zurich, Zollikerstrasse 107, CH-8008 Zurich, Switzerland

Floral structure and phylogeny of Buxaceae

Buxaceae is a small family of basal eudicots comprising up to five genera (*Buxus*, *Notobuxus*, *Pachysandra*, *Sarcococca*, *Styloceras*) and about 120 species. The delimitation of the family and the systematic relationships within the family have been problematic in the past. Our previous molecular study revealed two major clades: the clade of *Buxus* and *Notobuxus*, and the clade of *Pachysandra*, *Styloceras*, and *Sarcococca*. *Pachysandra* and *Styloceras* form a strongly supported sister group to *Sarcococca*. The African genus *Notobuxus* is embedded among African members of *Buxus*. The basic structure of inflorescences and flowers, in particular the development and trimery of the gynoecium, of *Notobuxus* is very similar to that of *Buxus*. The other major clade is also supported by identical basic floral structures as the dimery of the gynoecium or the very similar male flowers in *Pachysandra* and *Sarcococca*. Floral structure and development of representatives of all genera have been studied in detail and will be discussed in connection with the molecular results.

109 WHEAT, BRIAN P.* AND JAMES L. SEAGO

Dept. of Biology, SUNY at Oswego, Oswego, NY, 13126

Selected aspects of root development in a cotton variety and its genetically modified forms

We examined root development in a variety of cotton and three of its genetically modified derivatives, RR, Bt, and RRbt. The cortex in all was essentially the same; Casparian bands developed in the endodermis at 5-10 mm behind the root tip. There was then rapid development of suberin lamellae opposite the protophloem; passage cells remained opposite protoxylem. Further development resulted in an endodermis with Casparian bands, suberin lamellae, and some secondary wall thickening. The cortex in the genetically modified forms was slightly smaller than the control; none had an exodermis. The stele in the control had fewer cells with lignified walls than the GMO's; secondary growth quickly followed.

110 WILLIAMS, JOSEPH H. JR.* AND W. E. FRIEDMAN

Dept. of EPO Biology, University of Colorado, Boulder, CO 80309

Double fertilization and diploid endosperm in basal angiosperms?

Although the process of double fertilization is a defining feature of angiosperms, it has only been carefully documented in relatively few, mostly derived, angiosperm species. Recent phylogenetic analyses have placed Nymphaeaceae as either the first or second diverging lineage from the base of the angiosperm tree. We studied the fertilization biology of *Nuphar polysepalum* (Nymphaeaceae). Here we confirm for the first time, using modern tools, the presence of double fertilization in an angiosperm basal to the monocot and eudicot clades. Another important and presumed synapomorphy of angiosperms, virtually unstudied in early angiosperms, is the highly reduced, monosporic eight-nucleate female gametophyte (embryo sac). The second fertilization in such

an embryo sac is expected to produce a triploid primary endosperm nucleus, via the fusion of two female polar nuclei and one male sperm nucleus. Interestingly, the mature *Nuphar* embryo sac consists of only four nuclei: two synergids, an egg, and one polar, or central cell, nucleus. We confirmed the haploid nature of the central cell nucleus using DNA quantitation of individual nuclei. The central cell nucleus has the same DNA content as known haploid nuclei, such as the egg. We further show that, in cross-pollinated flowers, the products of double fertilization, the zygote nucleus and the primary endosperm nucleus, have equal initial DNA quantities, instead of the 2:3 ratio. Thus, contrary to expectation, the endosperm in one of the earliest angiosperm lineages is biparental and diploid, not triploid. The lack of information regarding basic reproductive biology in basal angiosperms represents a huge gap in our knowledge that may hold further surprises.

111 ZANIS, MICHAEL J.^{1*}, DOUGLAS E. SOLTIS², AND PAMELA S. SOLTIS³

¹School of Biological Sciences, Washington State University, Pullman, WA 99164; ²Dept. of Botany and the Genetics Institute, University of Florida, Gainesville, FL 32611; ³Florida Museum of Natural History and the Genetics Institute, University of Florida, Gainesville, FL 32611

Isolation and characterization of floral MADS Box genes from Nuphar and Illicium

The ABC model of floral organ development proposes combinatorial interaction of A, B, and C class genes whereby these three classes of genes specifies the four floral organs, sepals, petals, stamens, and carpels. A class genes specify sepal identity, A plus B class genes specify petal identity, B plus C class genes specify stamen identity, and C class genes specify carpel identity. Many of the genes involved in the ABC model are members of the MADS box gene family. The ABC model has been primarily characterized in *Arabidopsis* and *Antirrhinum*. Significantly, the B and C functions of this model also extend to maize (*Zea*), although functional conservation of the A function remains to be demonstrated. Nevertheless, the strong genetic and molecular evidence for the conservation of at least portions of the ABC model suggests that this is an ancient regulatory network, perhaps applicable to most angiosperms. However, various modifications of the specific components of the ABC model may have occurred in different lineages of angiosperms. We have developed a protocol that permits the extraction of quality RNA from small amounts of tissue from a wide range of angiosperms. Using this approach, we have extracted RNA from young flowers, as well as floral organs at various stages of development from the basal angiosperms *Nuphar* (Nymphaeaceae) and *Illicium* (Illiciaceae). We have isolated MADS-box genes from *Nuphar* and *Illicium* and present phylogenetic analyses as well as preliminary expression analyses of these genes.

112 ZARINKAMAR, FATEMEH

Laboratory of Plant Anatomy, Research Institute of Forests and Rangelands, P.O.Box. 13185-116, Tehran, Iran

Anatomical/ecological studies of rare species in Arasbaran's protected area in Iran

Arasbaran, a protected region of Iran contains a large variety of bio diversity, some of them on the endangered lost. This paper introduces an anatomical-structural study and its relation with ecological, systematic characters of some 400 rare species in a very valuable protected area, named Arasbaran. This mountainous region was designated as a protected area in 1971. It is about 72465 hectares, and encompasses a variety of natural features, such as high mountains, deep valleys, sharp slopes, dense

forests and vast rangeland, indicating a very rich environmental diversity. The altitude variations are between 450 to 2841 meters. The average temperature in February and August are 1.8 and 25C respectively. The annual precipitation is around 450-500 mm. (semi-humid zone). In the Arasbaran protected area, some 785 plant species have been recognized so far. Research on adaptive characters has been directed mainly towards leaves. Given the importance of foliar anatomy on ecological development in environment, systematic efforts are required for research and investigation of the maximum number of species possible. Some 400 samples from various ecological situations and different altitudes have been collected representing some 60 families, including: Compositae, Caryophyllaceae, Papilionaceae, Chenopodiaceae, Labiateae, Liliaceae, Rosaceae, Boraginaceae, Rhamnaceae, Anacardiaceae, Cruciferae, Malvaceae, Umbelliferae, Zygophyllaceae. Structural and anatomical studies were conducted to compare anatomical characters of similar families in different ecological conditions and observe the impact of ecological factors on the structure of the plant. From the systematics point of view, this work led to recognition of certain unknown or incorrectly known species in some cases. From the ecological and protection point of view, this study has contributed to the recognition of some elements, which have impact on rare and endangered species. This paper presents proposals for future analysis and plans for the management of the ecosystem.

113 ZAVALETA-MANCERA, HILDA A.^{1,2*}, IAN SCOTT², AND THOMAS HOWARD³

¹Universidad Autonoma del Estado de Mexico, UAEMex, Facultad de Ciencias, Unidad Academica del Cerrillo, 50200 Edo. Mex. Mexico; ²University of Wales, Institute of Biological Sciences, Aberystwyth Dyfed, SY23 3DA, UK.; ³Institute of Grassland and Environmental Research IGER, Aberystwyth Dyfed, SY23 3EB, UK

Re-differentiation of senescent Nicotiana rustica chloroplasts by cytokinins treatment

Leaf senescence represents a genetically programmed sequence of events highly coordinated at the cell and tissue levels that happens at the final stage of development. The main symptom of leaf senescence is the yellowing of the blade, due to the loss in the chloroplasts of chlorophylls and membrane structure. It is a common observation that greening and senescence occur at opposite ends of the life span of plant tissues. Greening generally implies differentiation of etioplasts or proplastids into chloroplasts in the presence of light, characterized by the formation of thylakoids. In contrast, during chloroplast senescence, the structure changes markedly: the chloroplast polyribosome population decreases, the organized granal stacks are lost, the plastoglobuli appear larger and more abundant, and finally the plastid envelope ruptures. The present work gives evidence for re-differentiation of senescent chloroplasts (gerontoplasts) in cytokinin-induced regreening of senescent *Nicotiana* leaves. During regreening the chlorophyll content, chloroplast structure and photosynthetic activity recovered. Ultrathin sections of leaf tissue were examined at several times during senescence and regreening. It was apparent that granal stacks were rebuilding in the senescent chloroplasts, which were still recognizable by the presence of some plastoglobuli. No ultrastructural evidence of proplastids or chloroplast division was observed at any of the developmental stages examined. Trends in plastid numbers per cell also supported the gerontoplast-re-differentiation route. Plastid numbers did not increase during regreening, and when many plastids were lost during advanced senescence, regreening capacity deteriorated. Re-differentiation of gerontoplasts was associated with increased levels of light-harvesting chlorophyll a/b-binding protein (LHCP-2), cytochrome f, small and large subunits of Rubisco, and the appearance of NADP-pro-

tochlorophyllide oxidoreductase (POR) detected by Western blotting. Differentiation, de-differentiation, and re-differentiation concepts are discussed.

CONTRIBUTED POSTERS

114 HEALY, R.A., C.R. BRONSON, AND H.T. HORNER*

Depts. of Botany and Plant Pathology, Iowa State University, Ames, IA 50011-1020

Visualization of the extracellular matrix of the pathogenic fungus Cochliobolus heterostrophus

Many plant pathogenic fungi produce an extracellular matrix (ECM). The ECM is known to play a role in pathogenesis through adhesion of the conidiospore and/or germling to its host. The ECM may contribute to pathogenesis in other ways once the fungus has entered the host tissues. We suspect this is true for the maize pathogen *Cochliobolus heterostrophus* because a mutant that lacks the full ECM is unable to form normal lesions after it enters the leaf. Otherwise, it behaves normally in culture and on the leaf surface. The ECM of the wild type consists of two layers: an inner layer that binds to a wide variety of stains; and an outer layer that appears in negative relief with India ink. The mutant lacks the outer layer and this provides a good control for testing the hypothesis that the outer layer plays a role in pathogenesis within host tissues. Study of the outer ECM layer within host tissues has been unsuccessful due to the difficulty of visualizing it. Our research has focused on further characterizing the entire ECM and rendering the outer layer visible using a variety of staining techniques on germlings incubated on cellophane membranes, and on hyphae within maize leaf lesions produced after conidiospore inoculation. Both were studied in the fresh state, as well as after conventional fixation and cryofixation followed by freeze substitution. Visualization with light microscopy included nigrosin and India ink, silver-enhanced, gold-labeled antibody and colloidal gold staining, and differential interference contrast. Localization techniques with the electron microscope included enbloc staining using tannic acid and/or uranyl acetate, enbloc staining with ruthenium red or alcian blue followed by ruthenium red and osmium tetroxide; colloidal gold staining, Thiery technique, and antibody labeling. Our results are presented pictorially.

115 HOU, GUI-CHUAN*, JEFFREY P. HILL, LAURENS H. JR. SMITH, AND BECKY A. NIELD

Dept. of Biological Sciences, Idaho State University, Pocatello, ID 83209-8007

*Molecular genetic studies of root development in fern *Ceratopteris richardii**

Root heteroblastic development during early sporophyte ontogeny and the developmental anatomy of the fifth root were characterized in previous investigations of the homosporous fern *Ceratopteris richardii*. Here we report preliminary results of a molecular genetic study of root development in *C. richardii*. Total mRNA was extracted from gametophytes, sporophylls, and roots of the species. Reverse transcription-polymerase chain reaction (RT-PCR) was employed to copy cDNAs from the original RNA populations. The differential display-polymerase chain reaction (DD-PCR) technique was used to identify putative root specific cDNAs. Six root specific subclones were recovered from a display of 6 primer combinations. Northern analysis of the first subclone (designated as *RSG1*) has confirmed that it is specifically expressed in roots of *C. richardii*. Efforts are in progress to characterize the full-length sequence of *RSG1* and determine its expression pattern in situ.

116 JANA, BALARAM^{1*}, NABARUN GHOSH², A. CHATTERJEE¹, AND DON W. SMITH³

¹CAS, Dept. of Botany, University of Calcutta, Calcutta-19, India; ²Dept. of Life, Earth and Environmental Sciences, West Texas A&M University, Canyon, TX 79016; ³Dept. of Biological Sciences, University of North Texas, Denton, TX 76203

*Effect of Arsenicum Album (Arsenious Oxide, AS₂O₃), a homeopathic drug as a potential mutagen on *Corchorus olitorius* L. (Jute)*

Arsenic is a deadly poisonous metalloid. The main sources of arsenic in soils are the parent materials from which they are derived. Arsenic exists in water always in ionic forms (H₂ASO₄ H₂ASO₃) and the water is used for the cultivation of various crop plants (rice, soybean, tomato, cotton, tobacco etc.). The Arsenic ions (H₂ASO₄) absorbed by the plants might have effects on physiological, biochemical as well as cytogenetical system of the plant. The various forms of arsenic compounds applied in the cultivation field as fungicides, pesticides, herbicides as well as plant defoliant having impact on the crop plants as well as on the whole ecosystem. The homeopathic drug Arsenicum album, prepared from the deadly poisonous Arsenious Oxide (ASO₃) was applied in dilutions of different potencies (10-3 to 10-200000) on seeds of the commercially jute yielding plant *Corchorus olitorius* Linn var. JR0 632. Viable seeds were soaked in a solution prepared by adding 10 drops (one drop=0.06 ml) of the drug of specific dilutions to 50 ml of distilled water for 12 hours. The treated seeds were washed thoroughly and allowed to germinate. The growth and behavior of the plants were noted from seedling stage up to maturity. Inheritance studies were done through progeny trial in the successive generations. These include tall plants, dwarf plants, bifurcated stem, bushy head, branched stem, broad leaves, dark green and yellowish green leaves, early and late flowering plant, fruit mutants, suppressed leaf mutant (leaf gap) and coppery red plant with notched petals. Although majorities of these mutants are reported to be available after treatment with ionizing radiation, at least a few were considered to be new and these were not reported earlier. This investigation reveals that the homeopathic drug prepared from Arsenious-Oxide in ultra-diluted potencies is capable of inducing mutation in plant system like jute.

117 KIRCHOFF, BRUCE*, TAM LE, ALLYSON PREVETTE, SONJA CAUBLE, ELIZABETH SHELTON, AND KIMBERLY HAMLET

Dept. of Biology, P.O. Box 26174, University of North Carolina at Greensboro, Greensboro, NC 27402-6174

*Early floral development in *Musa velutina* (Musaceae)*

The genus *Musa* is monocious, with flowers arranged in hands. 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. The flowers consist of three sepals, three petals, two outer whorl stamen, two inner whorl stamen, and a tri-locular, inferior ovary. The adaxial petal is not opposed by an inner whorl stamen, resulting in only two stamen in this whorl. Flower organogenesis begins with the flattening of the flower primordium, the production of two bulges (the presumptive sepal primordia) in adaxial-lateral positions, and the growth of the periphery of the apex to produce the beginning of a floral cup. Growth of the periphery of the primordium, which deepens the floral cup, is accompanied by the differentiation of the adaxial side to produce three distinct primordia, two sepal and one petal. At about this stage, or slightly before, the abaxial sepal begins to be visible as a primordium that is partially distinct from the lower rim of the floral cup. Continued differentia-

tion around the periphery of the flower begins the formation of the outer stamen whorl on the adaxial side of the flower, and produces two common petal/stamen primordia on the abaxial side. Growth of the common primordia produces distinct abaxial petal and inner stamen primordia. The adaxial petal continues to develop without the production of an associated stamen, though the inner flank of this primordium (the portion that forms a wall of the floral cup) does develop a slight swelling. Growth of the floral cup, below the insertion of the floral members, produces the cavity that forms the gynoecial primordia.

118 POSLUSZNY, USHER¹* AND JEAN, M. GERRATH²

¹Dept. of Botany, University of Guelph, Guelph ON N1G 2W1, Canada; ²Dept. of Biology, University of Northern Iowa, Cedar Falls, IA 50614-0421

Floral morphology and development in Rhoicissus digitata (Vitaceae)

As part of a continuing comparative study of floral development in the Vitaceae, this paper describes the floral morphology and development of *Rhoicissus digitata* (L.f.) Gilg & Brandt. Inflorescences in this southern African species are small and cymose and arise in either a terminal or leaf-opposed position. The five sepals are initiated individually, but by maturity they appear as small teeth, as a result of growth of a basal ring primordium. The five petals arise individually in a position alternate to the sepals, and are thick, green, valvate, and cucullate at maturity, with forked brown hairs on their abaxial surface. The five petal-opposed stamens are initiated more or less simultaneously, separate from the petals. The gynoecium forms two chambers, each with two ovules. The pinkish, five-lobed nectariferous disc arises from the base of the gynoecium. Fruits are blue-black with purple juice at maturity, containing two or three seeds with equal frequency. Floral developmental characters resemble those found in *Ampelopsis* and *Cissus* most closely, and appear less derived than those of *Vitis*.

119 SKALSKY, JEANNIE* AND MANOJ MISTRY

Dept. of Biology, Butler Hall, MS 3258, Texas A&M University, College Station, TX 77843

Fractal analysis of leaf edges

The genus *Silphium* (Asteraceae) is comprised of roughly 15 species, which are limited to eastern and central United States. Naturally occurring hybrids have not been documented, though they have been produced artificially. Two species, *S. laciniatum*, which is wide spread, and *S. albiiflorum*, endemic to Texas, were utilized for this study. *S. laciniatum* has large leaves, some over two feet long each, which are very lacinate and lobed. *S. albiiflorum*, which is theorized to have evolved from *S. laciniatum*, is smaller and also has lacinate leaves. The larger leaves overlap when they are folded to fit inside a plant press so analysis of entire leaves from typical herbarium specimens is impossible. This also prevents accurate measurements of leaf area, etc. and limits the amount of data gathered from an individual plant. Fractals are traditionally used to analyze geographic structures, such as coastlines. Defined as irregular fragmented shapes that exhibit intricate structure at all sizes so that details are reminiscent of the entire object, fractal measurements utilize different box sizes to measure a perimeter. A smaller box size provides a larger value for the perimeter. When fractals were used to measure small portions of leaves from *S. laciniatum*, *S. albiiflorum* and putative hybrid populations, PCA analysis revealed delineation between the two species with the putative hybrid intermediate.

120 STRITTMATTER, LARA* AND VIVIAN NEGRON-ORTIZ

Botany Dept., Miami University, Oxford, OH

Consolea corallicola (Cactaceae): a sexually dimorphic species with only one morph remaining?

Consolea Lem., subfamily Opuntioideae, comprises nine species endemic to the Caribbean region. Within this genus, *C. corallicola* Small. is a species with a single remaining wild population of only 12 individuals on Little Torch Key, FL. Floral morphology indicates that this species is hermaphroditic. The flowers produce viable pollen grains, but rarely set viable seeds. When seeds do initiate they do so by agamospermy. Embryological studies show that although the flowers begin as hermaphrodites, at anthesis the ovules are aborted and papery. During sex differentiation, the megagametophytes are characterized by an excessive presence of starch grains, indicating abortion. The anthers have a normal developmental process, resulting in viable pollen grains. The study suggests that these superficially hermaphroditic flowers are functionally staminate, and that all surviving individuals are males. Therefore, we hypothesize that *C. corallicola* had a cryptically dioecious system, which we have also found in other *Consolea* species. The female sexual morph is, apparently, extinct.

121 VOLSKEY, ALLENA R.* AND TIMOTHY P. HOLTSFORD

Division of Biological Sciences, University of Missouri, Columbia, MO 65211-7400

Morphogenesis of key floral traits in Nicotiana Section Alatae

Nicotiana section *Alatae* contains species with a surprising variety of mating systems and interactions with pollinators, associated with variation in floral morphology. We are exploring the development of those different floral shapes and sizes, with a general look at perianth growth in seven species and more detailed analyses of developmental switches in two pairs of sister species. *N. alata* has a longer corolla tube than *N. forgetiana*, which is important in determining which pollinators visit the flowers. Another difference between these two is that the stamens are adnate to the corolla for a much smaller percentage of their length in *N. forgetiana* than *N. alata*, which may be due at least partly to differences in cell expansion basal to the point of filament insertion. *N. longiflora* and *N. plumbaginifolia* flowers differ in size and anther-stigma relationships. As the buds of *N. longiflora* grow and the flowers open, the stigma remains distal to the anthers. In *N. plumbaginifolia* the pistil growth slows down in relation to the corolla and attached stamens, and just before the flower opens the anthers pass-and deposit pollen on-the stigma. We have compared calyx and corolla growth curves among all seven species. For the two species pairs we are measuring cell division and expansion in the corolla tube by mitotic index, cell length measurements, and cell counts, and measuring growth of different locations within the corolla and pistil by marking growing floral organs and recording the movement of those marks. Because these traits are important to the mating systems of these species, this research will contribute directly or indirectly to our knowledge of floral morphogenesis, plant-pollinator interactions, floral evolution and plant speciation.

ECOLOGICAL SECTION, BSA

SYMPOSIUM: PLASTICITY IN INTEGRATED PHENOTYPES

122 PRESTON, KATHERINE A.^{1*} AND THEODORE G. WONG^{1,2}

¹Dept. of Biological Sciences, Stanford University, Stanford, CA 94305; ²Dept. of Biological Science, Florida State Univ., Tallahassee, FL 32306

Plasticity in integrated phenotypes

Plants are not collections of independent traits. Rather, they are integrated wholes whose components are interlinked biochemically, functionally, and developmentally. A trait's response (or lack thereof) to an environmental stimulus influences, or even constrains, concurrent responses in other traits, through common control pathways, compensatory plasticity, or other mechanisms of phenotypic integration. This symposium explores the tension between single-trait reaction-norm evolution, and whole-plant trait integration. The papers describe a range of integrating processes and discuss consequences for the evolution of integrated responses to the environment.

123 BONSER, STEPHEN P.* AND MONICA A. GEBER

Dept. of Ecology and Evolutionary Biology, Corson Hall, Cornell University, Ithaca, NY 14853

Growth form controls developmental and morphological responses to light quality in two annual plant species

Environmental conditions can influence a plant's rate of development and induce morphological responses that may affect fitness. Plant growth form can also constrain or promote developmental and morphological responses, since plants of different growth form differ in the placement and timing of production of vegetative and reproductive modules. In this study, we examine how growth form controls developmental and morphological responses, and fitness across light environments in *Brassica rapa* and *Arabidopsis thaliana*. Erect (wild type) and rosette (mutant) genotypes of *Brassica* and rosette form genotypes (mutants differing in traits related to rosette size) of *Arabidopsis* were grown in high light (control) and green light filtered (spectral shade) environments. Spectral shading reduced fitness and altered patterns of development in genotypes of both species. Spectral shading induced a shade avoidance response of increased vertical extension, although the strength of this response was not consistent across all genotypes. For example, hypocotyl extension was relatively greater in the rosette form and internode extension was relatively greater in the erect form of *Brassica*. Rosette genotypes (*Brassica*) and genotypes with high rosette allocation (*Arabidopsis*) suffered relatively high fitness reduction in spectral shade treatments. The results of this study demonstrate that growth form can influence morphological and developmental responses that may have important fitness consequences across a range of environments.

124 PRESTON, KATHERINE A.

Dept. of Biological Sciences, Stanford University, Stanford, CA 94305

Plasticity in integrated phenotypes: a conceptual overview

In most ecological and comparative studies, phenotypic integration is inferred from phenotypic correlations. Four main elements characterize phenotypic correlation: 1. strength (correlation coefficient), which is the most common measure of integration; the form of the relationship between trait pairs, including 2. the intercept and 3. the slope (scaling coefficient); and 4. the pattern of correlation across environments (plasticity integration). These elements may vary somewhat independently. For example, it is not necessary for traits to show correlated plasticity in order to remain strongly correlated in different environments. If there is correlated plasticity and two traits respond proportionally, then there will be no change in either the strength of the correlation or the form of the relationship between them. By contrast, if traits change in a coordinated fashion but disproportionately relative to one another, then the scaling relationship between them will change, reflecting a change in their functional relationship. Thus traits may show a consistent pattern of integration in various environments, while the forms of the pairwise relationships and the degree of plasticity integration varies. Although plasticity integration is not necessary to maintain phenotypic integration across environments, plasticity integration makes consistent patterns of integration more likely. Analyzing the combination of changes in correlation strength and form across environments, and the degree of plasticity integration, may provide insight into mechanisms underlying phenotypic integration and the potential for integration to constrain the evolution of adaptive plasticity in integrated traits.

125 SANDQUIST, DARREN

Dept. of Biological Science, California State University, Fullerton, CA 92834

Integrated physiological, morphological and phenological responses to drought associated with "adaptive" leaf pubescence in a desert perennial shrub

Putative phylogenetic constraint of plasticity for physiological and morphological traits in the genus *Encelia* (Asteraceae) appears to have resulted in strong selection for plasticity of leaf pubescence within at least one species, *Encelia farinosa*. Leaf pubescence is a crucial component of the energy balance, water relations and photosynthetic physiology of this drought-deciduous desert shrub, but pubescence development is also irreversible and thus prevents adaptive responses under certain conditions such as mid-drought rainfall. Carbon-gain and water-use tradeoffs associated with these developmental responses play a complex role in adaptation of this species across a broad environmental matrix. I will discuss how a combination of population genetic and eco-physiological studies has been used to elucidate these complex relationships and relate them to the environmental heterogeneity of this species' range. Of these analyses, one (carbon isotope ratio) provides an integrated measurement of multiple physiological responses (photosynthesis and water-use). Due to the unique but fairly well understood interplay of phenotypic limitations and plasticity in this species, *Encelia farinosa* provides a model system for the study of phenotypic integration and adaptation in plants.

126 WEINIG, CYNTHIA* AND JOHANNA SCHMITT

Dept. of Ecology and Evolutionary Biology, Box G-W, Brown University, Providence, RI 02912

Constraints on the evolution of plasticity: insights from molecular marker-based linkage mapping

Molecular genetic approaches, such as marker-based linkage mapping, can help identify whether multiple traits possess common or independent genetic pathways. Such analyses are important to studies of plasticity because they can suggest across-environment genetic correlations that may constrain the evolution of plasticity. In a recent field experiment, recombinant inbred lines of *Arabidopsis thaliana* (Ler x Col) experienced variable herbivory levels. Herbivorized plants exhibited the classic increase in basal branching that occurs after removal of the apical meristem. This increase in basal branches was associated with enhanced fitness in the herbivorized plants, whereas basal branches had no effect on fitness of non-herbivorized plants. In contrast, fitness of the non-herbivorized plants was strongly influenced by the number of branches on the primary flowering inflorescence. This variable selection across herbivory environments suggests that the observed plasticity is adaptive. Preliminary QTL (quantitative trait loci) and quantitative-genetic analyses show that basal branch number is determined by a different genetic mechanism in herbivorized and non-herbivorized plants; the QTLs for branch number were located on different chromosomes. Although these independent genetic bases are somewhat surprising, the result indicates that plasticity of branch number can evolve freely in response to ambient herbivory conditions. In the non-herbivorized plants, we detected two QTL in common for inflorescence and basal branch number. Thus, these two traits may have a common genetic basis such that selection on inflorescence branches results in a correlated response in basal branch number. These results taken together illustrate that different traits may or may not be correlated in a manner that constrains the evolution of adaptive plasticity.

127 WINN, A. A.* AND K.S. MORIUCHI

Dept. of Biological Science, Florida State University, Tallahassee, FL

Integration of plastic responses of leaves and flowers to seasonal environmental variation in a perennial violet

Theoretical treatments of the evolution of adaptive phenotypic plasticity commonly invoke a cost of plasticity as the force that limits further evolution of a particular plastic response. To date, there is little empirical support for the existence of such costs. One way in which a particular plastic response could be costly is if it disrupts the expression of another trait or the plasticity of another trait. We are examining the possibility that compromises between plasticity in leaf morphology and in flower morphology in a single species limit the evolution of adaptive plasticity in both traits. The perennial violet, *Viola septemloba* exhibits seasonal leaf and flower dimorphism in response to day length. Individuals produce primarily entire leaves during the fall and winter and switch to the production of deeply lobed leaves during the spring and summer. Lobed leaves are able to maintain average mesophyll temperatures nearly 3 degrees C lower than entire leaves during the hot summer. Thus heterophylly appears to be adaptive plasticity in response to seasonal environmental variation. Individuals of this species also exhibit seasonal variation in flower morphology. The production of open (chasmogamous) flowers occurs simultaneously with increasing production of lobed leaves during the late winter, and the production of closed (cleistogamous), obligately selfed flowers during the mid-summer and fall corresponds to increasing production of entire leaves. We have raised replicates of inbred lines of *V. septemloba* under long and

short days and demonstrated heritable variation in response of leaf and flower morphology to day length. Preliminary results also suggest a genetic covariance between the plastic responses of the two traits, which could underlie a cost of plasticity. We will illustrate how simultaneous consideration of adaptive plasticity in multiple traits can contribute to understanding the existence and mechanistic basis of costs that limit the evolution of adaptive plasticity.

128 WONG, THEODORE G.

Dept. of Biological Science, Florida State Univ., Tallahassee, FL 32306

Architectural integration of traits and plasticity in simulated plants

A plant's program of architectural development can be a powerful driver of phenotypic integration, and architectural plasticity an important mechanism behind integrated trait responses. In order to assess architecture's contribution to overall trait integration, I simulated architectural growth computationally using several realistic models consisting of combinations of branching, elongation, and meristem-identity rules. Architectural plasticity was embodied in the rules themselves and was expressed as the architectural response to simple simulated environmental variables. In contrast to many plant-growth simulations, mine was based exclusively on individual metamer behavior: architectures, trait correlations, and trait responses all emerged from the iterated application of rules to each metamer of the simulated plant in each time-step of the simulation. The architectural program's contribution to trait and plasticity integration was assessed by changing rule parameters and observing changes in traits, their correlations, their plastic responses, and the correlations among the responses. Architecture was responsible for strong correlations among many architectural and life-history traits, correlations which persisted across environmental conditions but which differed when rule parameters or the rules themselves were changed. The rules with the greatest integrating effect were those that defined the control of flowering. Rules that defined branching frequency or the duration of meristem viability had relatively little integrating effect. That architecture should play a large role in trait and plasticity integration is unsurprising given the importance of other types of developmental linkage. That architectural rules differ in their effect suggests that the dissection of architecture is an important early step in the study of architecture's evolutionary and ecological consequences. Given how straightforwardly the architectural program can be described computationally, simulation should prove to be a useful tool both in the definition of architectural models and in the elucidation of their importance.

CONTRIBUTED PAPERS**129 ADAMS, CHRISTOPHER A.^{1*}, JERRY M. BASKIN¹, AND CAROL C. BASKIN^{1,2}**

¹School of Biological Sciences, University of Kentucky, Lexington, KY 40506; ²Dept. of Agronomy, University of Kentucky, Lexington, KY 40506

Comparative seed dormancy in three Aristolochia species: a test of two hypotheses on changes in ecological requirements in plant lineages

The overall purpose of this research is to examine two opposing views on changes in physiology of closely-related plant taxa that evolved in response to changes in climatic and other environmental factors following geographical breakup of the "Arcto-Tertiary" forest. The first view, advocated by Daniel I.

Axelrod, suggests that although modern taxa may have slight to moderate morphological differences compared to Tertiary ancestors, their ecological tolerances and physiological requirements essentially have remained unchanged. The contrasting view, put forth by Jack A. Wolfe, is that taxa diverged in physiological and ecological requirements as lineages were exposed to climatic changes through geologic time. These two hypotheses are being evaluated via a comparative study of seed dormancy and germination characteristics of three closely-related *Aristolochia* species: the California endemic *A. californica*, the Appalachian endemic *A. macrophylla*, and the southeastern U.S. species *A. tomentosa*. The three species are the North American members of a monophyletic group (subg. *Siphisia*) that became geographically separated and diverged, presumably in the late Tertiary. Seeds of all three species have linear underdeveloped- and physiologically dormant embryos, thus morphophysiological dormancy (MPD). Seeds of *A. californica* require warm (e.g., 30/15C) stratification for dormancy-break and a low (e.g., 15/6C) temperature regime for nondormant seeds to germinate. In contrast, seeds of *A. tomentosa* and *A. macrophylla* require cold (5C) stratification for dormancy-break, but nondormant seeds will germinate over a wide range of temperature regimes (i.e., 15/6-35/20C). These preliminary results seem to indicate that seeds of *A. tomentosa* and *A. macrophylla* have nondeep simple MPD and those of *A. californica* nondeep complex MPD. In any case, seed dormancy-breaking and germination requirements of the Mediterranean-climate species, *A. californica*, differ considerably from those of the temperate rainy-climate species, *A. tomentosa* and *A. macrophylla*, thus supporting Wolfe's view on physiological changes in a lineage.

130 ANDERSON, GREGORY J.* AND JAMES D. HILL

Dept. of Ecology and Evolutionary Biology, University of Connecticut, U-43 Storrs, CT 06269-3043

Many to flower, few to fruit: the reproductive biology of Hamamelis virginiana (Hamamelidaceae)

Hamamelis virginiana flowers late September to late November. In 1977, we began studying the reproductive biology of this eastern USA tree, including: floral phenology and rewards, pollen-ovule ratios, breeding system, pollination, pollinator and resource limitation, and seed dispersal. The homonymous, self-incompatible flowers emit a faint odor, bear nectar with sucrose ratios typical of bee and fly flowers, and produce abundant sticky pollen. Flowers were visited infrequently by insects representing six orders. Flies were the most common floral visitors, specifically members of the genus *Bradysia*, whereas small bees carried high percentages of *Hamamelis* pollen. Despite high P/O ratios (11 445 grains/ovule), bees and flies are likely pollinators as experiments indicate wind pollination is much less likely. Pollen quantity and resource availability did not appear to limit reproductive output, but pollen quality did. Tests of > 40 000 flowers showed natural fruit set to be < 1%. The flowering time, breeding system, and clumped dispersion of plants due to limited seed dispersal combine to yield this remarkably low fruit set. Because all other *Hamamelis* flower from late winter to early summer, it may be that *H. virginiana* evolved a fall flowering phenology to avoid competition for pollinators with the closely related *H. vernalis*.

131 ARMSTRONG, JOSEPH E.

Behavior, Ecology, Evolution, and Systematics Section, Biological Sciences, Illinois State University, Normal, IL 61790-4120

Competition among floral brooding insects and reproductive success in Anaxagorea crassipetala (Annonaceae)

Anaxagorea crassipetala is a small understory tree of Central American lowland rainforests. As the specific epithet suggests, petals of the outer whorl are thick and fleshy having the general appearance and texture of little bananas. Floral brooding is commonly associated with obligate mutualism and with beetle pollination, but while a brood substrate is a large reward, competition for this reward may affect the reproductive success of all parties. In this case beetle mutualists compete for this limited and ephemeral brood substrate with non-pollinating fruit flies and beetles. While beetle pollinators only visit during anthesis, non-pollinating insects who oviposit prior to anthesis win the competition both with the mutualists and non-pollinating, floral-brooding insects who visit during anthesis. By experimentally denying access to pre-anthesis flowers, the reproductive success, as measured by fruit set, of the tree was significantly increased over open access controls. No mutualist beetle reproduction was recorded. This may be the result of a high rate of competition from fruit flies, whose feeding larvae may reduce the attractiveness of the petals as a brood substrate. Even among the fruit flies, oviposition prior to anthesis resulted in significantly higher reproductive success than ovipositions on the day of anthesis. Flowers were visited at a rate significantly higher than pre-anthesis buds suggesting that while ovipositing in buds increased fruit fly reproductive success, non-attractive buds were difficult to find in comparison to scent-producing flowers.

132 ASHLEY, NATALIE* AND GARY K. GREER

Dept. of Biology, West Virginia State College, Institute, WV 25112

Effects of above-ground injury on the ability of Ailanthus altissima to effect neighbors via soil properties

Ailanthus altissima (Tree-of-Heaven, TOH) is a widespread invasive common to disturbed habitats and an increasing component of near urban forests in eastern North America. An allelopathic compound (ailanthone) has been previously isolated from TOH, however, production is greatest in seedlings. We investigated the effects of above-ground injury on the ability of reproductively mature TOH to effect neighbors via soil properties. Five small TOH trees at the edge of each of three populations received the following injury treatments: 0% (control) 10%, 20% 40%, and 100% removal of above-ground biomass, based on height. Moderate injury treatments were designed to simulate those that may occur naturally, whereas more severe injury simulated frequently used roadside management. Soil from the top 20 cm was collected each week, 0.5 meters from each TOH, dried, and an extract made by pouring 5.0 L water through the soil suspended in a cheesecloth. The extract was used to water seeds of *Fagopyrum esculentum* (buckwheat) for germination and radicle growth studies and to water seedlings for studies of growth and reproduction. Seed germination rates were reduced in the 40% and 100% injury treatments, relative to control, only during the second of three weeks. Patterns of radicle growth across treatments were complex and changed in sign (increased vs. decreased growth) between weeks, however, most treatments were associated with increases in radicle growth. In the seedling experiment, no differences in total dry weight biomass (DWB) were detected. In contrast, root: shoot DWB ratio was reduced, whereas height and reproductive effort (reproductive DWB ÷ total DWB) were ele-

vated in the more severe (30%, 40% and 100%) injury treatments. In general, a trend of increasing release from TOH effects with increasing injury was observed. Loss of leaf tissue, which has been previously associated with aianthone production, may be responsible for these trends.

133 BAACK, ERIC J.

Center for Population Biology, University of California-Davis, One Shields Ave, Davis, CA 95616

Barriers to reproductive success of tetraploid snow buttercups (Ranunculus adoneus) due to interference from diploid plants

Polyploid speciation has played a significant role in the production of flowering plant diversity. Despite its importance, several aspects of the ecology of the speciation process remain poorly understood. Reproductive interference from surrounding diploid plants is thought to be a major factor limiting the establishment of novel tetraploid populations of outcrossing plants. In this study I examined barriers reproduction in snow buttercups (*Ranunculus adoneus*: Ranunculaceae). I conducted hand pollinations in the field using plants from diploid or tetraploid buttercup populations. I compared seed mass and number among cross-ploidy, within-ploidy, and mixed ploidy pollinations to assess the potential barriers to tetraploid reproduction when in a diploid population, and scored the ploidy of the resulting seeds by flow cytometry. Cross-ploidy crosses resulted in fewer, lighter seeds than within-ploidy crosses, indicating an incomplete barrier to the formation of triploids. Mixed ploidy pollinations using both tetraploid and diploid plants as pollen donors produced fewer seeds but of the same mass as the within-ploidy crosses, indicating that cross-cytotype pollen interfered with fertility when within-cytotype pollen was present. Flow cytometry revealed that the seeds resulting from mixed-ploidy crosses were largely diploid (for diploid dams) or tetraploid (for tetraploid dams), not triploid. This confirms that interference from cross-ploidy pollinations could decrease the fitness of tetraploid plants in mixed populations.

134 BAGGS, JOANNE E.* AND JOYCE MASCHINSKI

The Arboretum at Flagstaff, 4001 S. Woody Mountain Rd., Flagstaff, AZ 86001

Detecting morphological and growth rate differences of a confusing Purshia complex using a common garden study

P*urshia subintegra* (Kearney) Henrickson is a rare soil endemic found in 4 populations across central Arizona. In the Verde Valley, the range of *P. subintegra* overlaps with the more common cliffrose, *Purshia stansburiana* (Torr.) Henrickson, and introgression or hybridization occurs. Because *P. subintegra* was federally listed as an endangered species in 1984, understanding the dynamics of the hybrid complex is critical to the management of *P. subintegra* as well as understanding the factors that limit the distribution of *P. subintegra*. In a common garden study, we examined the morphological and growth differences of *P. subintegra*, *P. stansburiana*, and the introgressed form across a soil gradient. The soil gradient consisted of soil from 3 habitats: undisturbed limestone outcrops where *P. subintegra* grows, disturbed limestone roadsides where the introgressed forms grow, and a wash where *P. stansburiana* grows. In a greenhouse, we established plants from stem cuttings in 1 gallon pots using amended soils from the 3 habitats and measured morphological characteristics after 80 weeks. Using discriminant function analysis, we could distinguish *P. subintegra* and *P. stansburiana* but introgressed forms showed more phenotypic variability. Genetic individuals of the introgressed forms also showed more variability across the soil gradient than individu-

als of *P. subintegra* and *P. stansburiana*. Using the same experiment, we measured aboveground biomass after 84 weeks. Using analysis of variance, the aboveground biomass was significantly different between species and soil types. *P. stansburiana* grew the largest compared to *P. subintegra* and the introgressed forms which had similar aboveground biomass. Each species grew best in the soil from its habitat. *P. subintegra* and the introgressed form grew best in both undisturbed and disturbed limestone soils while *P. stansburiana* grew best in soil from the wash.

135 BASKIN, CAROL C.^{1,2*}, OLLE ZACKRISSON³, AND JERRY M. BASKIN³

¹School of Biological Sciences, University of Kentucky, Lexington, KY 40506-0225; ²Dept. of Agronomy, University of Kentucky, Lexington, KY 40546-0091; ³Dept. of Forest Vegetation Ecology, Swedish University of Agricultural Sciences, S-901 83 Umea, Sweden

Role of warm plus cold stratification in promoting germination of seeds with stony endocarps: Empetrum hermaphroditum

Seed (true seed + endocarp, hereafter seeds) of *Empetrum hermaphroditum* are dormant at maturity in September and October, and fresh seeds collected at various sites in Sweden germinated to only 2-5% in light at daily alternating temperature regimes of 15/6, 20/10, and 25/15C. Dormancy was not due to impermeability of the stony endocarp surrounding each seed, and embryos did not grow prior to radicle emergence. Thus, seeds did not have physical dormancy or morphological dormancy. Long periods of cold stratification (32 wk) and of warm stratification (16 wk) given separately resulted in a maximum of only 25 and 10% germination, respectively, in light at 25/15C. After 12 wk warm stratification plus 20 wk cold stratification, however, seeds germinated to 83-93% in light at the three temperature regimes. When length of the cold stratification period was constant (e.g. 20 wk), germination increased with increase in length of the warm stratification treatment preceding cold stratification. Gibberellic acid promoted germination in a high percentage of the seeds. Based on dormancy-breaking requirements and response to gibberellic acid, seeds have intermediate physiological dormancy. In regions where summers are relatively short and cool (or if seeds become buried in soils that are cool during summer), the requirement for warm plus cold stratification to break dormancy may cause germination of a cohort of seeds to be spread over time, thus helping explain the occurrence of persistent soil seed banks in this species.

136 BELL, TIMOTHY J.^{1*}, MARLIN BOWLES², JENNY MCBRIDE², KARYI HAVENS³, AND PATI VITT³

¹Chicago State University, Chicago, IL; ²Morton Arboretum, Lisle, IL; ³Chicago Botanic Garden, Glencoe, IL

Viability analysis of a restored Illinois population of the federal threatened pitcher's Thistle (Cirsium pitcheri)

There are few population viability analyses of restored endangered species populations. This analysis was used to determine optimal strategies for establishing restored populations of the federal threatened Pitcher's thistle (*Cirsium pitcheri*). This herbaceous perennial of western Great Lakes shoreline dune habitats went extinct from its Illinois habitat before 1920. It is self-compatible, with little allozyme variation across its range. As part of federal and state recovery planning, suitable restoration habitat was identified at Illinois Beach Nature Preserve and population restoration began in 1991 using Wisconsin, Indiana and Michigan seed sources. Because this species is monocarpic, annual translocation of greenhouse-propagated plants was used to build up large cohort

numbers. 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 growth rate (λ) is > 1 . Stage structured demographic analysis indicates that extinction risk is lowest when populations are initiated by transplanting juveniles rather than seedlings or flowering plants or by sowing seeds. Relatively high variation in transition frequencies for non-fecundity stages indicates that, due to environmental stochasticity, a relatively high minimum population size is required to reduce extinction probability to $< 5\%$ for 100 years. Elasticity analysis indicates that *Cirsium pitcheri* matrices with $\lambda > 1$ have greater proportional contribution of growth and reproduction elasticities to population growth rate.

137 BHASKAR, RADIK* AND DAVID ACKERLY

Dept. of Biological Sciences, Stanford University, Stanford, CA 94305

Responses of hydraulic traits to light and water availability in a California chaparral shrub

Water transport to the leaves is influenced in part by leaf-specific hydraulic conductance (LSC). Studies have found that LSC may be sensitive to environmental factors such as the supply of water in the soil or the evaporative demand. Among individuals LSC can vary due to changes in biomass allocation such as differences in the ratio of leaf area/sapwood area (A_L/A_S). Increased sapwood specific hydraulic conductivity (K_S) also affects LSC but leads to increased xylem vulnerability to embolism. These two aspects of LSC were examined separately in seedlings of *Heteromeles arbutifolia*, a native California chaparral species. *H. arbutifolia* is present in shade as well as full sun, where summer drought conditions resulting in water stress are intensified by the combination of incoming radiation and high air temperatures. In order to examine the effects of light and water on hydraulic architecture, *H. arbutifolia* seedlings were grown in a common outdoor garden under a factorial design with sun and shade conditions and high and low soil water availability. Physiological measurements made on the seedlings at the end of the growing season, including stomatal conductance and maximum transpiration rates, indicated significant differences in water use in the four treatments. Aspects of canopy architecture were also measured before seedlings were harvested to quantify biomass allocation patterns. Hydraulic conductance was determined using a bench-top conductance set-up in order to examine variation in LSC. In particular plasticity in different aspects of LSC was examined to determine whether A_L/A_S varied in response to higher transpiration rates while K_S responded to variation in soil water supply.

138 BLOOM, THOMAS C.¹, JERRY M. BASKIN^{2*}, AND CAROL C. BASKIN^{2,3}

11209 Glade Street, College Station, TX 77840; ²School of Biological Sciences, University of Kentucky, Lexington, KY 40506; ³Dept. of Agronomy, University of Kentucky, Lexington, KY 40546

Ecological life history of the facultative biennial Arabis laevigata var. laevigata (Brassicaceae)

The ecological life history of *Arabis laevigata*, a facultative biennial native to e. North America, was studied in a rocky deciduous woodland in nc. Kentucky from 1985-1994. Its woodland rock outcrop habitat is stable and thus differs from the ruderal habitat of many other facultative biennials. Seeds of *A. laevigata* mature in June and dispersal lasts > 1 yr; most fall within 0.5m of parents. Seeds have nondeep physiological dormancy, which is broken during winter. Germination occurs in March and April, and seeds that fail to germinate become part of a persistent seed bank.

Plants form a rosette the first year and flower in their second or a later year. There was no consistent pattern of transition between size intervals. Vernalization is required for bolting/flowering, but plants are day-neutral. Bolting occurs in March, and anthesis peaks in mid-April. *Arabis laevigata* is capable of both self- and cross-fertilization and is not agamosperous. Probability of survival and of bolting increased with rosette size, which was highly correlated with number of seeds produced. Low leaf litter cover, low herbivory, and a rock/moss substrate were associated with increased bolting. Flower stalk herbivory was the primary reason many plants that bolted did not produce seeds. Less than 5% of 3,083 plants marked in the seedling stage survived 1 yr, and *A. laevigata* exhibits a stress-tolerant ruderal (SR) strategy (*sensu* J.P. Grime's triangular model).

139 CARDON, ZOE G*, LOUISE A LEWIS, AND DEBORAH TYSER

Dept. of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269

Evolutionary physiology of photosynthesis in desert-dwelling green algae

Green algal species live as components of microbiotic crusts in many deserts of the world, enduring extremes of temperature, water availability, and, perhaps, light. Using a phylogenetic approach, we are investigating components of the photosynthetic physiology of Southwestern US desert green algae and aquatic sister species from three classes of green algae: the Chlorophyceae, Trebouxiophyceae, and Charophyceae. Because these desert algae are similar morphologically, sequence data from the 18S ribosomal RNA gene is required for identification of related pairs of aquatic and desert species. We hypothesize that the desert-living habit, which has evolved at least six times in the green algae, is associated with enhanced photoprotective mechanisms compared to photosynthetic physiology found in the aquatic habit. To date, analysis of chlorophyll fluorescence quenching in desert and aquatic sister species reveals that at least within the Chlorophyceae and Trebouxiophyceae, desert algae exhibit altered patterns of non-photochemical quenching (qNP) in response to light relative to their aquatic relatives. Such changes in qNP are indicative of altered energy dissipation mechanisms associated with the photosynthetic apparatus, and may prove to be a physiological feature common to desert algal lineages.

140 CHOESIN, DEVI N.^{1*}, SRI AMNAH S.², AND H. TAUFIKURAHMAN¹

¹Dept. of Biology, Institut Teknologi Bandung, Bandung 40132, Indonesia; ²Haluoleo University, Kendari 93232, Indonesia

Ecological aspects of Vaccinium varingiaefolium growing in a stressed volcanic environment

V*vaccinium varingiaefolium* (Ericaceae) is a dominant species found in many subalpine forests (above 1800-2000 meters) on the mountains of Java, Indonesia. As a species with high plasticity, it can grow as a tree of up to 20 meters tall under favorable conditions, or as a shrub in open, dry, or nutrient-poor substrate. It is also a pioneer species on ashy or volcanic soil of crater ridges. We compared several morphological and ecophysiological aspects of *V. varingiaefolium* growing at 0, 100, and 200 meters away from the main crater of Mount Tangkubanparahu volcano in Western Java. Measurements indicate that ambient concentrations of volcanic sulphur dioxide decreased as we move away from the crater. Chlorophyll content, leaf proline content, mean leaf area, plant height and stem diameter of *V. varingiaefolium* increased with greater distances from the crater, while mean leaf thickness decreased. However, there were no significant differences among

locations in terms of plant transpiration rate, total sulphuric compounds in leaves, number of stomates, and number of fruits. This last finding suggests that reproductive allocation by *V. varingiaefolium* may not be affected by stress. We are currently conducting further studies to understand allocation and life history patterns in this species.

141 COLOSI, JOSEPH C.^{1*}, JAMES J REILLY², AND WILLIAM S CURRAN³

¹Biology Dept., DeSales University, 2755 Station Ave., Center Valley, PA 18034; ²Dept. of Anatomy, Pathology, and Cell Biology, Thomas Jefferson University, 1020 Locust Street, Philadelphia, PA 19107; ³116 ASI, Dept. of Agronomy, Pennsylvania State University, University Park, PA 16802

The spread of herbicide resistance in Chenopodium album

Chenopodium album, a widespread dicot weed of corn and other crops was first reported to have atrazine resistance in 1975 in Canada. In most weed species including *Chenopodium album*, atrazine resistance is conferred by a point mutation in the chloroplast photosystem II psbA gene, resulting in a substitution of glycine for serine at position 264. This mutation is a dominant character conferred by the maternal parent. The mutation rate in *Chenopodium album* is much higher (10^{-3} to 10^{-4}) than expected from random mutations of a chloroplast gene (10^{-9} to 10^{-12}) and may be influenced by a mutator nuclear gene. French and Canadian studies of *Chenopodium album* with protein electrophoresis suggest that atrazine resistance has evolved frequently through mutation. Both studies found different protein patterns in resistant populations from well-separated areas. The resistant populations had low levels of within population genetic variability compared to nearby susceptible populations. We wanted to determine if the spread of atrazine resistant *Chenopodium album* within and between adjacent farm fields was primarily caused by frequent mutation or by rare mutations followed by migration. We collected seed from five individuals in each of 11 fields on 5 Farms in central and southeastern Pennsylvania. We measured atrazine resistance by spraying 2.7 kg/ha on three reps of seedlings at the 4 to 8 leaf stage, assessing the plants visually, and measuring dry mass. We assessed genetic relationships of individuals by RAPD's (Random Amplified Polymorphic DNA). In some fields, atrazine resistant and susceptible individuals had identical genotypes suggesting recent mutation within the field. In other fields, resistant genotypes had distinctly different genotypes from those of susceptible neighbors, suggesting immigration of the resistant biotype from elsewhere. The spread of atrazine-resistant *Chenopodium album* in Pennsylvania appears to be a mixture of frequent local mutation and dispersal of resistant biotypes by seed.

142 CULLEY, THERESA M.

Dept. of Ecology & Evolutionary Biology, University of California-Irvine, Irvine CA 92697

Genetic effects of forest fragmentation in woodlot populations of an understory herb, Viola pubescens (Violaceae)

Habitat fragmentation has become an important concern in the midwestern United States due to conversion of temperate deciduous forests to agricultural land during the past two centuries. The genetic effect of forest fragmentation in these areas was examined in a common understory herb, *Viola pubescens*, a species that produces self-pollinated cleistogamous (CL) flowers and potentially outcrossing chasmogamous (CH) flowers. Using allozymes, genetic variation was measured in populations inhabiting woodlots of differing sizes (0.540.5 ha) and distances

from one another (0.311.4 km) within the agricultural landscape of central Ohio. Woodlot size was significantly and positively correlated with all measures of genetic variation (A , P , H_O , and H_E), with variation highest in the larger woodlot populations (e.g., $P = 0.88$, $H_O = 0.39$) and lowest in the smaller woodlots ($P = 0.25$, $H_O = 0.03$). Overall, populations were genetically differentiated from one another ($q = 0.34$), but there was no relationship between genetic and geographic distance. More likely, limited gene flow in this species may reflect a reduction in pollinators in the fragmented woodlots, leading to an increase in selfing rates through automatic selfing in CL flowers and delayed selfing in CH flowers. Despite the commonality of *V. pubescens* and the reproductive advantage it has through the CH/CL system, fragmented populations still experience genetic erosion. This study highlights the need for conserving the remaining populations of this species, along with other less common taxa in the temperate deciduous forest.

143 DAVIES, STUART J.¹, SHAWN K.Y. LUM^{2*}, RAYMUND CHAN³, AND LUAN KENG WANG⁴

¹Harvard University Herbaria, Dept of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA; ²Natural Sciences Academic Group, National Institute of Education, Singapore; ³Jepson Herbarium and Dept of Integrative Biology, University of California, Berkeley, CA; ⁴Burke Museum, Dept of Zoology, University of Washington, Seattle, WA

Evolution of myrmecophytism in west Malesian species of Macaranga (Euphorbiaceae)

Plants inhabited by ants (myrmecophytes) have evolved in a diversity of tropical plant lineages. The Paleotropical tree genus *Macaranga* (Euphorbiaceae) includes ~300 species. Twenty-six west Malesian species of *Macaranga* are myrmecophytic, and they vary in their morphological specializations for ant association. In order to ascertain the origins and diversification of myrmecophytism in *Macaranga*, phylogenetic analyses of selected Malesian species were conducted using morphological and nrITS DNA characters, followed by the mapping of ant-plant associations and allied traits onto the resulting phylogenetic trees. Combined analysis of morphological and ITS data resulted in a well-supported hypothesis of relationships. Mapping 'myrmecophytism' on all most parsimonious trees resulting from the combined analysis indicated that myrmecophytism evolved independently in *Macaranga* between two and four times and was lost between one and three times (five changes). Mapping morphological traits on the phylogeny suggested that myrmecophytism was not homologous among lineages, and that each independent origin involved a suite of different specializations for the ant-plant association. A number of different morphological, ecological and biogeographic factors appear to have facilitated and constrained this radiation of ant-plants.

144 DEVAL, MARGARET^{1*}, NATHAN SCHIFF¹, AND DOUGLAS BOYETTE²

¹Center for Bottomland Hardwoods Research, P.O. Box 227, Stoneville, MS 38776; ²Agricultural Research Service, Stoneville, MS 38776

Ecology and reproductive biology of pondberry (Lindera melissifolia [Walt.] Blume, Lauraceae), an endangered species

Lindera melissifolia [Walt.] Blume (pondberry) is an endangered plant that occurs in seasonally flooded wetlands and on the edges of sinks and ponds. It is a stoloniferous, clonal shrub that grows to a maximum of two meters in height and is dioecious, with small yellow flowers that bloom in spring. Pondberry occurs in six southern states of the USA, but it has always been rare,

and knowledge of its ecology and reproductive biology is sparse. The species has been affected by habitat destruction and alteration, especially timber cutting, clearing of land, and drainage or flooding of wetlands. Female clones are smaller than male clones, and are sometimes absent from stands. Hand-pollinated flowers did not set more fruit than open-pollinated flowers, and flowers covered with mesh bags produced no fruit. Seed production is erratic, and as in many other clonal species, few seedlings occur even when seed production is high. In addition, stem dieback is widespread, but monitored populations do not appear to be declining. Three fungal pathogens were isolated from stems. Six insect species were found in association with pondberry but none appear to be limiting to the plant. Individual stems can be easily transplanted and multiply rapidly. Opportunities for dispersal are very limited now due to land use of areas surrounding pondberry populations and to changes in hydrology. Introduction of plants to new areas will be necessary if the species is to recover.

145 DOLAN, REBECCA W.^{1*}, ERIC S. MENGES², AND REBECCA YAHR³

¹Friesner Herbarium, Butler University, Indianapolis, IN, 46208;

²Archbold Biological Station, PO Box 2057, Lake Placid, FL, 33862;

³Dept. of Botany, Box 90338, Duke University, Durham, NC, 27708

*Genetic variation in *Nolina brittoniana*, an endemic of the central ridges of Florida*

N*olina brittoniana* is a perennial agave endemic to the central ridges of the Florida peninsula. Its upland scrub and sand-hill habitats have suffered extensive destruction and fragmentation, and indirect alteration through fire suppression. We examined genetic variation in 48 populations from throughout its range using isozymes. Features of the life history and ecology of the species led us to predict that this federally listed plant would not be genetically impoverished, in spite of its narrow range. However, we found lower values for percentage of polymorphic loci, average numbers of alleles per locus and expected heterozygosity than those generally reported for endemic plants. Populations were fairly well differentiated (mean $F_{ST} = 0.363$). Inbreeding rates were low and allele number and frequency did not indicate recent bottlenecks. Significant clines in allele frequency were detected along the north-south axis of distribution. Spatial structure of genetic variation and high population differentiation reflect the patchy distribution of scrub habitats and support the need to preserve populations from throughout *N. brittoniana*'s range.

146 ENDRESS, BRYAN A. AND DAVID L. GORCHOV*

Dept. of Botany, Miami University, Oxford, OH 45056

*Effects of leaf harvesting and browsing on the demography of *Chamaedorea radicalis* Mart. (Arecaceae) palms in the El Cielo Biosphere Reserve*

Extracting Non-timber Forest Products is sustainable only if the harvest does not cause negative population growth. Leaves of *Chamaedorea* palms are harvested from Mexican forests and exported for floral greenery. We examined the effect of alternative harvest schedules, and livestock browsing, on demography of *Chamaedorea radicalis* Mart., a dioecious understory palm, in El Cielo Biosphere Reserve (23_08'N, 99_09'W), Tamaulipas, Mexico. In Jan. 1999 we assigned 100 adult palms to each of 5 treatments: Control (no leaf removal), 1X/year (marketable leaves removed each Aug.), 2X/year (Aug., Feb.), 4X/year (Feb., May, Aug., Nov.), and Modified 4X/year (max. 1 leaf per palm removed, and no palms defoliated). We calculated stage transition probabilities and fecundities of adults over 1 year (Aug. 1999-Aug. 2000). We parameterized a stage transition matrix for each treatment using these values and transition probabilities for seeds, seedlings,

and juveniles obtained from the same site. Eigenanalysis of each matrices yielded λ (finite rate of increase) for each treatment. To quantify effects of browsing by free-range livestock, we randomly assigned 2 100m² plots to each of 3 treatments; No browse, 1X browsed (Feb. 2000) by 1 burro for 15 min., and 2X browsed (Aug. 1999, Feb. 2000). The 4X harvest treatment reduced adult survival and reproduction, and caused some adults to regress to "younger" stages, resulting in $\lambda=1.00$, while the control was projected to grow with $\lambda=1.06$. Browsing elevated mortality of most stages. Incorporating this mortality into the control's matrix, λ declined to 0.96 for 1X browse and 0.82 for 2X browse. Furthermore, adults that survived defoliation by harvest or browse showed a developmental response; their next leaf was frequently smaller than previous leaves. In Jan. 2001 the youngest fully-expanded leaf on the 4X treatment averaged 34 cm long vs. 45 cm on controls ($T=5.99$, $df=136$, $P < 0.05$), so defoliated palms have a respite from harvest. Treatments are continuing, allowing assessment of their impact beyond the first year. Present results suggest occasional browsing more negatively effects populations than periodic leaf harvest.

147 ENZ, JOHN

Dept. of Biological Sciences, University of Louisville, Louisville, KY 40292

*Nectar robbers and non-nectar robbers: their visitation rates and their effects on seed set in Virginia Bluebells, *Mertensia virginica* (L.) Pers*

Virginia Bluebells, *Mertensia virginica*, (L) Pers. is a herbaceous perennial that grows along streams and moist hillsides within the deciduous forests of the Northeastern United States. *M. virginica* produces a maximum of four nutlets per flower and is visited by a variety of insect species, some of which exhibit nectar robbing behavior. Nectar robbing is a behavior by which insects obtain nectar from flowers without contacting the reproductive parts of the flowers and has been extensively reported in the literature. In 1997, 13 patches (four contained one plant, three contained five plants, three contained ten plants, and three contained 20 plants) were chosen within the Horner Wildlife Sanctuary in Oldham County, Kentucky USA where *M. virginica* blooms for approximately four weeks during the month of April. The flowers in each patch were monitored and visitation rates of nectar robbing insects and non-nectar robbing insects were calculated. The effects on seed set of nectar robbed vs. non-nectar robbed flowers in the different patch sizes were compared as well. Comparisons were carried out using ANOVA statistical procedures in SAS. Twelve insect species were found to visit *M. virginica*, although *Bombus bimaculatus* (non-nectar robber) and *B. affinis* (nectar robber) together accounted for over 70% of all visits regardless of patch size. *B. bimaculatus* spent an average of 6.09 seconds per flower. *B. affinis* spent an average of 9.7 seconds per flower on their initial visit and 4.8 seconds on their visit to a previously robbed flower. In contrast to most studies of other flower species in the literature, nectar robbery in *M. virginica* was found to significantly increase seed set across all patch sizes.

148 EULISS, KATY W.* AND JEFFREY S. CARMICHAEL

Biology Dept., University of North Dakota, Grand Forks, ND, 58202

*The effects of selenium accumulation in canola (*Brassica napus*)*

Trace amounts of selenium are considered essential for proper growth and development in most organisms. However, high levels of selenium can cause adverse effects in animals as well as most plants. Canola (*Brassica napus*) has been studied for its potential use in phytoremediation of seleniferous soil because of

its ability to accumulate relatively high levels of this potentially toxic element. While much is known about the role of selenium in higher plants and the use of plants for phytoremediation, relatively little is known about the effects of selenium on developmental events and the impacts of selenium on reproductive success (e.g., seed set). Studies presented here reveal intriguing and unexpected results. We found that canola plants grown hydroponically in 2 ppm selenium displayed significantly reduced flowering and seed set. In particular, we found that compared to controls, selenium treatment resulted in fewer plants flowering and an overall lower seed yield. Comparable numbers of seeds per pod were produced in selenium-treated and control plants, but seed viability was reduced in selenium-treated plants. Plant height and leaf production were also negatively impacted by selenium. The effects of selenium on vegetative anatomy along with herbivore and pathogen defense will be discussed.

149 FEILD, TAYLOR* AND N. MICHELE HOLBROOK

Havard University, 16 Divinity Ave., BioLabs, Cambridge, MA 02138

Functional physiology of Amborella and 'ITA' plants

Recent phylogenetic studies have placed the extant lineages *Amborella*, Nymphaeales, and a clade including, Illiciales, *Trimenia*, and *Austrobaileya* (the 'ITA clade') near the base of the angiosperm tree. *Amborella* and ITA members share a suite of ecophysiological and morphological traits related to their occurrence in wet forest understory habitats. In particular, *Amborella* and ITA members exhibit a variety of growth forms ranging from shrubs to woody vines and a number of physiological traits associated with adaptation to shade. This suggests that angiosperms arose in shady, wet forest understory habitats. In contrast, Nymphaeales possess a suite of ecophysiological features generally associated with sunny to shady aquatic environments. Because these specialized ecophysiological features are closely linked with the aquatic habit, Nymphaeales may represent a separate ecological experiment and thus have little bearing on the ecological circumstances surrounding the origin of the angiosperms. A view of the earliest flowering plants as understory shrubs and vines growing in wet environments differs from previous suggestions that the first angiosperms arose in disturbed, exposed, and semi-arid environments. However, further work on the ecophysiology, phylogenetic relationships, and fossil history of these lineages is necessary to clarify how faithfully the modern representatives of the *Amborella* and ITA lineages reflect the ecological roles and environmental conditions surrounding the origin of the angiosperms.

150 FRAZIER, CHRISTOPHER K.1* AND TIMOTHY K. LOWREY2

¹New Mexico Natural Heritage Program, Dept. of Biology, University of New Mexico, Albuquerque, NM 87131; ²Dept. of Biology, University of New Mexico, Albuquerque, NM 87131

Pollination and reproductive ecology of three lowland tropical pitcher plants (Nepenthes)

Tropical pitcher plants, *Nepenthes*, have been the subject of substantial scientific scrutiny for their prey digestion, but other aspects of their biology, particularly their reproductive ecology have garnered much less attention. I studied the three species of *Nepenthes* present in Johore, Malaysia and Singapore, *N. gracilis*, *N. ampullaria* and *N. rafflesiana*, to determine if there are significant differences among species in phenology, floral and nectar characteristics and pollinators. Differences in flowering period represents at best a partial barrier to cross-pollination among species. Each species has three flowering periods between January and July, but the timing of these episodes is offset among species such that at any given time one, two or all three species are in

flower. Floral presentation differs among species in such characters as the number of flowers per inflorescence, flower size and color and sepal shape. *N. ampullaria* flowers present pollen during the day, while the other two species open their flowers in the evening. Nectar is produced nocturnally in all three species, but they differ in sugar composition and quantity of nectar produced. These differences suggest the species are adapted to attract different suites of pollinators. All species are pollinated by moths and small Diptera, but to differing degrees. *N. rafflesiana* is pollinated almost entirely by moths and all of its pollination is nocturnal. *N. gracilis* is pollinated almost equally by moths and small Diptera at night and also by wasps during the night and day. By day, *N. ampullaria* flowers have a foul odor and are pollinated by large flies, wasps and butterflies. The flowers produce a sweet odor at night and are then visited by moths. These differences are significant between species, but are still not sufficient to constitute a complete barrier to cross-pollination.

151 GEIGER, JOHN H.

Florida International University, University Park, Dept. of Biological Sciences, Miami, FL 33199

Pollination and reproduction of Ruellia succulenta Small in pine rockland fragments

The purpose of this research was to study the effects of habitat fragmentation on pollination and reproduction of *Ruellia succulenta* Small (Acanthaceae). Many studies have documented reduced seed set in plants occurring in fragments relative to plants in continuous habitat. The mechanisms explaining this reduction in reproduction have generally been resource limitation, pollinator limitation, and genetic erosion/inbreeding depression. My study focused on resource and pollinator limitation. I chose three sites in each of the following four size classes of habitat: small (< 3 ha), medium (3-9 ha), large (> 10 ha), and intact (in Everglades National Park). At each site, 20 randomly chosen plants were tagged. All plants were surveyed weekly for a year and data were collected on # of open flowers, # of mature fruit, # of seeds/fruit, and seed predators/fruit. If present, stigmas from untagged plants were mounted in Fuchsin gel on microscope slides. These were analyzed for number of conspecific and heterospecific pollen grains. If open flowers were present, timed pollinator watches were performed. Number and identification of floral insect visitors were recorded. The results of the ANOVA test on area of site and the three reproductive variables all were highly significant but the trend of reduced reproduction in smaller size classes was not shown. All three reproductive variables had highly significant negative Spearman rank correlations with the factor time since last fire. There appeared to be no correlation between conspecific/heterospecific pollen on stigmas (indirect measure of pollination) and either area of site or time since last fire. There were highly significant differences in the proportion of the orders of flower visiting insects by site. In conclusion, reduced seed set appeared to be the result of resource limitation (light and nutrients) rather than pollinator limitation. Fragmentation did, however, affect the composition and abundance of the pollinator guild.

152 HANNAN, GARY L.

Dept. of Biology, Eastern Michigan University, Ypsilanti, MI 48197

Size-related changes in biomass allocation to male and female function in a wind-pollinated annual plant

Platystemon californicus is a self-compatible, perfect-flowered, wind-pollinated annual plant exhibiting strict modular architecture (solitary flower per node) and extreme variability in numbers of stamens and carpels within flowers. Theory predicts that wind-pollinated species should allocate an increasing propor-

tion of resources to male function as plants become larger. I found that larger plants produced more massive flowers (300-400% increase) and invested proportionally more resources (estimated as biomass) in stamens than in carpels than did flowers of smaller plants. Carpels represented less than 20% of the biomass contained in stamens at anthesis. Total flower biomass at anthesis and allocation to stamens vs. carpels also change at successively formed nodes. The first flower on a plant (the only flower produced by the smallest plants) produced fewer stamens and carpels and had a lower ratio of stamens to carpels than did subsequently produced flowers. Allocation shifts without a change in architecture suggest that changes in resource availability occur at successive nodes as plants grow larger. If resource availability influences allocation patterns within flowers and if carbon is a limiting resource, then carbon distribution patterns among nodes or carbon fixation rates at independent nodes must change during plant development. Such changes have been found in crop plants, but many models of resource allocation ignore demand-driven changes in carbon transport or photosynthetic rate and assume a constant resource pool.

153 HAWKINS, TRACY S.^{1,2*}, JERRY M. BASKIN¹, AND CAROL C. BASKIN^{1,3}

¹School of Biological Sciences, University of Kentucky, Lexington, KY 40506; ²Hazard Community College, Jackson, KY 41339; ³Dept. of Agronomy, University of Kentucky, Lexington, KY 40546

*Ecological life cycle and phenology of biomass allocation in *Cryptotaenia canadensis**

C*ryptotaenia canadensis* is an herbaceous plant species of mesic to wet-mesic deciduous forests of eastern North America. The ecological life cycle and biomass allocation is being studied for plants of this species growing in a second-growth mixed mesophytic forest on the Cumberland Plateau in eastern Kentucky. *Cryptotaenia canadensis* reproduces sexually, flowering and fruiting during early to mid-summer, with concurrent asexual reproduction via monocarpic ramets produced at the base of the stem. Plants produced from seeds have a biennial life cycle, thus requiring two growing seasons to reproduce (sexually and asexually). Ramets behave as annuals and reproduce (sexually and asexually) after one growing season. Throughout the active growth stages of the sexual and asexual phases of the life cycle, relative percent biomass allocated to above-ground parts increased until death of the (entire) parent plant following reproduction. Twenty-five to 28% of the total biomass was allocated to reproduction, 80% of which went to sexual reproduction (entire umbel). A graphical model of the ecological life cycle and the phenology of biomass allocation in *C. canadensis* will be presented, and biomass allocated to reproduction in this species will be compared to that of other life cycle types in the Apiaceae.

154 HUEBNER, CYNTHIA D.

USDA Forest Service, Northeastern Research Station, 180 Canfield St., Morgantown, WV 26505-3180

Distribution of invasive plant species in eastern oak-hickory forests of West Virginia

Are invasive plant species a threat to oak-hickory forests of West Virginia? Invasive plant species are often characterized by early successional traits, including small seeds that are wind and animal dispersed, vegetative growth, and shade-intolerance, all of which enable the plants to take advantage of disturbed areas and spread rapidly. One may conclude that these traits do not lend themselves to easy invasion of a forest and the apparent low impact of invasive plant species on forests, compared to riparian and rangeland sites, may support this. However, oak-hickory

forests are unique because their canopies are relatively open compared to other hardwood forests, and the native species respond well to openings caused by various disturbance types. In fact, management regimes to maintain oak-dominated forests include clear-cutting and fire, both of which may promote exotic invasion. Moreover, eastern forests may be described as patches within an urban and agricultural matrix; i.e., the sink of invasion is embedded in its source. While there are over 180 potential oak-hickory forest invaders, we found the following species of most concern: *Alliaria petiolata*, *Microstegium vimineum*, *Lonicera japonica*, *Celastrus orbiculatus*, *Rosa multiflora*, *L. maackii*, *L. tatarica*, *L. morrowii*, and *Ailanthus altissima*. I compared each species' traits (physical, reproductive, and physiological), competitive ability, control measures, and known impacts on succession and ecosystem processes (based on the literature). I then related the distribution of these species (using herbarium records) to patterns of forest fragmentation and land use (using digital images). I used this information to predict future impacts of invasive plant species on oak-hickory forests.

155 KACZOROWSKI, RAINEE* AND TIM HOLTSFORD

105 Tucker Hall, UMC, Columbia, MO 65211

*Are nectar traits associated with pollination syndrome in wild tobaccos (*Nicotiana*, Solanaceae)?*

N*icotiana*, section *Alatae* is a monophyletic group which contains seven species with at least three pollination syndromes. The pollinators that visit these plants have been documented. Hawkmoths are the primary pollinators of the long-tubed, white flowers, small perching moths are the primary pollinators of the short-tubed, white flowers, and hummingbirds are the primary pollinators of the short-tubed, colored flowers. Nectar is the primary floral reward supplied by plants to attract pollinators. Previous research has found correlations between pollinator type and nectar characteristics. My poster presents preliminary data on nectar volume and sugar concentration at different flower ages for all seven species. These data are correlated to the different pollination syndromes exhibited by these *Nicotiana*. Preliminary results show that hummingbird-pollinated flowers have a lower nectar volume with higher sugar concentration than the hawkmoth-pollinated flowers. The small moth-pollinated flowers have only trace amounts of nectar, which leads us to believe that there may be other rewards associated with these flowers. These results are currently being validated. Analysis of sugar constituents, amino acid constituents and amino acid concentration is ongoing.

156 KOPTUR, SUZANNE

Dept. of Biological Sciences, Florida International University, Miami, FL 33199

*The floral biology and breeding system of *Jacquemontia curtissii*, an endemic morning glory of south Florida pine rocklands*

Field-collected individuals of *Jacquemontia curtissii* (Convolvulaceae), a perennial herb, were cultivated in a greenhouse to control conditions for hand-pollinations and floral measurements. This work was companion to field studies on the effects of habitat fragmentation on pollination of this species, after attempts to determine compatibility were complicated by field conditions. Flowers last one day, open from dawn through mid-morning, and produce nectar as reward for pollinators. Each flower contains from .25 - 1 microliter of nectar, from 22-50% sugar on a wt/wt basis; larger nectar volumes usually correspond to lower sugar concentrations. Flowers on each individual were subjected to one of four treatments: not manipulated (autogamy), anthers removed (apomixis), selfed, or crossed. Five flowers on each plant

received each treatment, except for crosses, where ten flowers were used, crossed with different individuals. Results show the species to be highly self-incompatible, and the lack of pollen tube growth in all treatments except compatible crosses demonstrates sporophytic self-incompatibility. Fruit set observed in the field can therefore be interpreted as evidence of pollinator activity, and successful transfer of pollen from another compatible individual.

157 KORPELAINEN, HELENA

Dept. of Biosciences, Division of Genetics, P.O. Box 56, FIN-00014 University of Helsinki, Finland

A genetic method to resolve gender before sexual maturity complements investigations on sex ratios in dioecious Rumex acetosa

R*umex acetosa* (Polygonaceae) is a perennial dioecious weed and one of the few plant species which possess well-differentiated sex chromosomes ($2n=12+XX$ in females and $2n=12+XY1Y2$ in males). Such a chromosomal sex determination system constrains the average primary sex ratios to a 1:1 ratio. Yet, the operational sex ratios (the number of males per female at sexual maturity) may become biased due to differential mortality, longevity or vegetative vigor between the sexes. Although time-consuming cytological analyses would allow studies on sex ratios among seedlings in dioecious species that have distinguishable sex chromosomes, investigations on sex ratios have mostly relied on information obtained at sexual maturity. A genetic method has now been applied to resolve gender among nonflowering plants of *R. acetosa*. The method involves amplification of a Y chromosome specific DNA sequence by PCR. To detect the mechanisms responsible for the observed sex ratio variation, a combination of methods is used to examine the patterns of seasonal sex ratio variation observed in populations of *R. acetosa* living in different habitats.

158 LADOUX, TASHA* AND ELIZABETH A. FRIAR

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

Self-incompatibility in Ipomopsis tenuifolia (Polemoniaceae)

Results from reciprocal diallele crossing experiments among a parental generation, as well as a full-sib family of 34 sibs suggests a novel, complex system of self-incompatibility (SI) in *Ipomopsis tenuifolia* (Polemoniaceae). Thirteen individuals from a population in Baja California, Mexico, were randomly chosen as parental plants. All crosses among parental and F1 individuals were successful, including backcrosses to parents, with the exception of three non-reciprocal crosses in the parental generation. All selfs were incompatible. Pollen tube growth was observed within selfs inside the ovary. The lack of incompatibility among sibships and backcrosses, as well as the complete lack of selfing success may suggest either a multi-locus gametophytic SI system or late-acting SI. Pollen tube growth within the ovary is more consistent with late-acting SI. Thus far, this study does not clarify the discrepancy between previous results of crossing studies in Polemoniaceae. Levin's (1993) results suggested single-locus gametophytic SI in *Phlox drummondii*, whereas Goodwillie (1997) found sporophytic SI with linear dominance in *Linanthus parviflorus*. The SI system for Polemoniaceae appears to be more complex than previously thought.

159 LARKIN, LEAH L.*; JOHN L. NEFF², AND BERYL B. SIMPSON¹

¹Section of Integrative Biology, University of Texas at Austin, Austin, TX 78712; ²Central Texas Melittological Institute, 7307 Running Rope, Austin, TX 78731

Evolution of floral specificity in a group of andrenid bees

C*allandrena* is a subgenus of 80 described species in the bee genus *Andrena* (Hymenoptera: Andrenidae). The group is delimited mainly by branched scopal (pollen-carrying) hairs and shortened mouthparts. All are specialists to varying degrees on pollen of the Asteraceae, with females collecting pollen from plants in at least five composite tribes. Some species are narrow specialists, using pollen from one genus or a few related genera; others collect pollen from plants in more than one tribe. Why bees should specialize on flowers that are easily manipulable and morphologically similar is unknown. We generate an hypothesis of phylogenetic relationships based on both mitochondrial and nuclear DNA markers for 55 species of *Callandrena* (eight of which are undescribed) and 40 additional *Andrena* species, representing 23 subgenera, to investigate the evolution of floral host choice in these bees. Host preference was ascertained by analysis of pollen loads on museum specimens. Both molecular data sets dispute the monophyly of *Callandrena*; there are at least three distinct and strongly supported clades. They have independently evolved a preference for pollen of the Asteraceae and have also evolved convergent morphological traits to accompany this preference. Within monophyletic groups, host shifts are generally among plants within a tribe, however, shifts to other tribes have occurred and may lead to adaptive radiation.

160 LARSON, KATHERINE C.

Dept. of Biology, Univ. of Central Arkansas, Conway, AR 72035

Lack of pollinators limits fruit set in the exotic Lonicera japonica

The non-indigenous invasive, *Lonicera japonica*, is a woody vine with a well-documented capacity for vegetative spread. Few data exist on its potential for establishment by seed, but anecdotal reports span the range from abundant seed reproduction to little seed reproduction. Atypical for an invasive alien, *L. japonica* is biotically-pollinated and xenogamous, requiring pollen from a genetically distinct individual for fruit set. I addressed the question of whether the services provided by the locally-available pollinator community were adequate for fruit set of *L. japonica* within its naturalized range. Hand-pollinations indicated that fruit set of *L. japonica* in Arkansas was pollinator limited. Naturally-pollinated control shoots produced fruit from 17.4% of their flowers, but the hand-pollinated flowers had a fruit set of 78.7%, an increase of over 4.5 times. As expected for a plant reported to be biotically pollinated and xenogamous, the shoots with pollinators excluded set fruit on only 2.1% of the flowers. In a survey of seven different sites along the western edge of the naturalized range of *L. japonica*, we found an average fruit set on primary shoots of 11.5±1.4% (mean±SE), while the secondary shoots averaged 20.1±2.8%. These results indicate that sexual reproduction by *L. japonica* is limited along the western edge of its naturalized range, and that the invasive character of *L. japonica* in this area is largely due to its prolific vegetative spread. Because this is one of the few empirical data sets on sexual reproduction by this important plant within its naturalized range, we do not extend our conclusions to other areas of the US, but instead emphasize the importance of documenting geographic differences in the reproductive potential of *L. japonica*.

161 LINDER, C. RANDAL^{1*}, BRIAN VANDEN HEUVEL¹, AND ROBERT B. JACKSON²

¹Section of Integrative Biology, University of Texas, Austin, TX 78712; ²Dept. of Biology, Duke University, Durham, NC 27708

Making the connection: using DNA fingerprinting to link above- and below-ground plant parts in ecological studies

Studying below-ground ecological processes of plants in natural systems can be very difficult. It can be even more difficult to connect individual roots and shoots in population level and ecophysiological studies. To overcome this problem, we demonstrate that rapid and simple polymerase chain reaction (PCR), DNA sequencing, and DNA fingerprinting techniques can be used to reliably link above- and below-ground parts of plants in ecological studies of natural systems. We used PCR and DNA sequencing of the internal transcribed spacer (ITS) region of the ribosomal DNA repeat to determine the species to which roots belong. Then, amplified fragment length polymorphisms (AFLPs) and inter-simple sequence repeats (ISSRs) were used to link individual roots with individual shoots. Using *Bumelia lanuginosa* syn. *Sideroxylon lanuginosum* (Sapotaceae) as a test case, we showed, at two different sites, that both ISSR and AFLP approaches to fingerprinting roots and leaves are excellent means of establishing above- and below-ground connections in natural systems. Individuals were readily distinguished and the methods also revealed when stems were ramets from a single genet. We will discuss the strengths and weaknesses of each fingerprinting method for use in ecological studies.

162 MEEKER, RALPH B.^{1*} AND KATHERINE C. LARSON²

¹University of Central Arkansas, Dept. of Biology, Conway, AR 72035; ²University of Central Arkansas, Dept. of Biology, Conway, AR 72035

Fragmentation in a Southern oak-hickory forest: impacts on species richness and invasibility

Habitat fragmentation results in the isolation of habitats from one another, increases the ratio of edge area to interior area, and reduces the total area of habitat. Smaller habitats often exhibit more dramatic microclimatic characteristics (higher light levels, higher soil temperatures, and lower soil moisture), are more susceptible to invasion from both non-indigenous and indigenous invasive plant species, and exhibit lower species richness than larger habitats. Smaller fragments are also more likely to display "edge" effects. I measured the impact of fragment size (5 ha and 20 ha) and distance from the edge of the fragment (0, 5m, 20m, and 50m) on (1) tree densities for eastern red cedar, *Juniperus virginiana*, and hardwood species collectively, (2) tree/shrub species richness, and (3) frequency of the invasive vine *Lonicera japonica*. The fragments were anthropogenically created, and all edges were cut more than 30 years ago. The fragments were formed from a southern oak-hickory forest at Ft. Chaffee, an Army National Guard base in northwestern Arkansas. The invasive, non-indigenous *L. japonica* and the invasive indigenous *J. virginiana* are more abundant along edges. Preliminary analysis indicates these species are also more abundant in smaller fragments and that species richness is greater in large fragments.

163 MILLER, JILL S.

University of Colorado, Dept. of Environmental, Population, & Organismic Biology, Campus Box #334, Boulder, CO 80309

*Floral morphometrics and the evolution of sexual dimorphism in *Lycium* (Solanaceae)*

Gender dimorphism has evolved at least twice in the genus *Lycium* (Solanaceae) and occurs in three species that are present in southwestern North America. Plants of *L. californicum*, *L. exsertum*, and *L. fremontii* are either male-sterile (i.e., female) or perfect-flowered (i.e., hermaphroditic) and populations are morphologically gynodioecious. Eleven floral characters were measured on female and hermaphroditic plants for the three North American dimorphic species to characterize sexual dimorphism between flowers on female and hermaphroditic plants. Despite notable shifts in floral size and shape among the dimorphic species, the general pattern of floral dimorphism between females and hermaphrodites was similar for all three species and consistent with the single origin of gender dimorphism in North America. Specifically, flowers on female plants are smaller than on conspecific hermaphrodites and have a long style equal to or slightly exerted from the corolla tube and reduced stamens with abortive anthers. Flowers on hermaphrodites are more flaring than on females, have a style of variable length and long stamens with fertile anthers that are typically exerted from the mouth of the corolla tube. However, the degree of sexual dimorphism between females and hermaphrodites varied among the dimorphic species, suggesting that flowers on females and hermaphrodites of the three species may be specialized for gender function to different degrees. In addition, morphometric measurements for the dimorphic species were compared to five species of cosexual (i.e., hermaphroditic) *Lycium*. These data, along with the presence of a phylogenetic hypothesis, allowed historical reconstruction of the shifts in floral size and shape across the transition from cosexuality to gender dimorphism.

164 MILLER, JILL S.* AND PAMELA K. DIGGLE

Dept. of Environmental, Population, and Organismic Biology, University of Colorado, Boulder, CO 80309

*Evolutionary diversification of plastic sex expression in andromonoecious *Solanum* section *Lasiocarpa**

The genus *Solanum* is predominately hermaphroditic in sexual expression, but andromonoecy has evolved numerous times within the genus. Andromonoecy shows a single origin in the subgenus *Leptostemonum*, and within section *Lasiocarpa* there has apparently been diversification in the expression of andromonoecy; the number and proportion of staminate flowers per inflorescence varies among species. Experimental analysis of sexual expression in one species of *Lasiocarpa*, shows that the production of staminate flowers is phenotypically plastic. Therefore, the observed variation in the expression of andromonoecy among species may be the result of plasticity. We assessed both plasticity and andromonoecy for four species in section *Lasiocarpa*: *Solanum candidum*, *S. hirtum*, *S. pseudolulo*, and *S. quitoense*. Replicates of eight genotypes of each species were grown under two treatments: high fruit set and no fruit set. When andromonoecy is defined as the mean proportion of staminate flowers produced by fruit-bearing plants, then andromonoecy varies from 25% staminate flowers in *S. hirtum* to nearly 65% staminate flowers in *S. quitoense*. The species also differ in plasticity, measured as the difference between the mean proportion of staminate flowers per inflorescence on fruit bearing and fruit-less plants. *S. hirtum*, *S. candidum*, and *S. pseudolulo* are all plastic, that is, more staminate flowers are produced by fruit bearing plants, but the degree of staminate flower production in the absence of fruit, as well as the magnitude of change in sexual expression between treatments, differ among the species.

Solanum quitoense, the species with the “strongest” andromonoecy is not plastic; a large proportion of flowers are staminate regardless of fruiting status. Analysis of these characters within the phylogeny of Bruneau et al. 1995, shows that plasticity of sex expression is likely ancestral within *Lasiocarpa* and that the fixed production of large numbers of staminate flowers by *S. quitoense* is derived.

165 MOREHOUSE, SARAH AND STEVEN B. CARROLL*

Division of Science, Truman State University, Kirksville, MO 63501

Effect on pollinator behavior of a flower-color polymorphism in Viola pedata

V*iola pedata* (bird’s-foot violet) is an eastern spring wildflower common in open woodlands and savannas. Populations generally include two flower-color morphs, one in which the color of all five petals is light lavender (LT) and one in which the upper two petals are dark violet and the lower three petals are lavender (BI). We followed dusky-wing butterflies (*Erynnis*), which are the primary pollinators in northern Missouri, to determine (1) if time spent on the two flower types differed, and (2) if time spent on an individual flower was affected by the color of the flower most recently visited. All four possible transition types were included in the second analysis. Pollinators spent an average of 12.1 s (se: 1.77) on LT flowers and 14.7 s (0.61) on BI flowers ($t = 1.71$, $df = 357$, $p = 0.09$). Time spent by pollinators on individual flowers was not significantly affected by the color of the previously-visited flower ($F_{3,314} = 0.47$, $p = 0.70$). Previous work has shown that pollinators visit the two flower-color morphs in proportion to their numerical representation. These visitation patterns, in combination with factors such as pollen load size and the compatibility of within- and between-morph crosses, are likely to have important consequences for the population genetic structure in this species.

166 MORRIS, LORNA L.* AND JEFFREY L. WALCK

Dept. of Biology, Middle Tennessee State University, Murfreesboro, TN 37132

Growth and reproduction of the nonnative Ligustrum sinense and native Forestiera ligustrina (Oleaceae): implications for invasibility of exotic shrubs

L*igustrum sinense* Lour. is a shrub native primarily to China, and has been introduced into several areas of the world. In southeastern United States, it grows with the native shrub *Forestiera ligustrina* (Michx.) Pour. The present study compared the branch architecture, leaf characteristics, reproduction, and phenology of the two species to identify aspects that might influence the invasiveness of *L. sinense*. Both species were sampled along the woodland edges of cedar (limestone) glades (1362 ± 79 mmol m⁻² s⁻¹, clear day at noon in August) and in the (mostly) redcedar forest (112 ± 13 mmol m⁻² s⁻¹) in middle Tennessee between March 2000 and February 2001. Multivariate analyses of variances (MANOVAs, $P \leq 0.05$) indicated significant differences between the species. Regardless of the habitat, *L. sinense* had higher stem elongation rate, leaf weight ratio, leaf area ratio, and number of fruits per branch, had lower leaf abscission rate and percentage of insect-damaged leaves, and a more tree-like growth form than *F. ligustrina*. Leaf area expansion rate, leaf area, and height of *L. sinense* growing in the woods were greater than those of *L. sinense* growing along the glade and greater than those of *F. ligustrina* in both habitats. Branch architecture based on branch length and orientation and on bifurcation ratio was similar between the species. However, leaves of *L. sinense* in both habitats and those of *F. ligustrina* in the woods were oriented at 98-107° from vertical but those of *F. ligustrina* along the glade were at 132°. The results suggest that *L. sinense* has a competitive advantage over *F. ligustrina* due to its

greater ability to spatially and temporally capture light, particularly in response to the light environment, and its higher fruit production.

167 MORROW, PATRICE A.¹ AND JOEL P. OLFELT^{2*}

¹Dept. of Ecology, Evolution and Behavior, 1987 Upper Buford Circle, University of Minnesota, Twin Cities, St. Paul, MN 55108;

²Dept. of Biology, St. Olaf College, 1520 St. Olaf Avenue, Northfield, MN 55057-1098

Defoliation elicits long term disappearance of clones

A large fraction of plant species in temperate, boreal and alpine floras can propagate clonally allowing genets (genetic individuals) to tolerate periods of reproductive failure, and often to obtain great size and age. However, genets are vulnerable to herbivores, pathogens and other localized disturbance. We monitored the status of 140 putative *Solidago missouriensis* clones in central Minnesota before, during and after intense defoliation by insects. Five of the putative clones, though apparently killed, reappeared 1 to >13 years they disappeared, largely or completely recovering their original territories within a single season. We tested the hypothesis that territories were recovered by seedling establishment using 38 RAPD markers obtained from 162 ramets collected from the recovered territories. We detected a single genotype in each of three territories, two genotypes in one territory, and eleven genotypes in the fifth territory. The probability of detecting the identical genotypes by chance is small ($< 1 \times 10^{-14}$). Since the reoccupied territories are large relative to the area that could be colonized by a single ramet in a single season, we conclude that pre-and post-recovery clones are the same.

168 NIKLAS, KARL J.* AND BRIAN J. ENQUIST²

¹Dept. of Plant Biology, Cornell University, Ithaca, NY 14853;

²Dept. of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721

An axiomatic tree biomass allocation pattern: derivation and verification

A quantitative framework describing how biomass allocation varies across plant species, communities, and ecosystems is lacking despite its fundamental importance to basic plant biology, global change studies, and evolutionary and ecological theory. Here we derive a model for biomass allocation using an allometric and engineering approach. This model predicts that foliage biomass will scale as the 3/4-power of stem (and root) biomass and as the 2-power of trunk diameter. These scaling relationships are predicted to be invariant with respect to species phyletic affiliation as well as community latitude or elevation (which may be used as crude surrogate measures of community diversity). A world-wide compendium for tree biomass is used to test these predictions in terms of empirically determined scaling exponents. The data in this compendium are shown to comply with the predictions of our model in every critical respect. The implications of our axiomatic tree biomass allocation pattern are discussed in the broader context of ecological and evolutionary theory.

169 PETERSEN, RAYMOND L.* AND ANDREA FAUST, JACQUELINE NAGAWA, CHANDI THOMAS, AND ANNICK VILMENAY

Biology Dept., Howard University, Washington, DC 20059

Foreign mosquito survivorship in the pitcher plant Sarracenia purpurea the role of the pitcher-plant midge Metriocnemus knabi

There are few reports of mosquito larvae other than those of the species-specific mosquito *Wyeomyia smithii* (Coq.) in leaves of *Sarracenia purpurea* L. We investigate why this

might be so in two sets of experiments. In the first set, we compare the percent survivorship of *W. smithii*, *Aedes aegypti* (L.), and *Anopheles stephensi* Liston larvae when reared in intact pitcher plant leaves to *in vitro* rearings and we found that the survivorship of the *Aedes* and *Anopheles* larvae was close to zero when reared in intact pitcher plant leaves compared to 37% and 64%, respectively, when reared in fish-food medium and 78% and 82%, respectively, when reared in pitcher-plant liquid. *Wyeomyia smithii* larvae had high percent survivorship under all three rearing conditions. In the second set of *in vitro* experiments, we compared the percent survivorship of *W. smithii* and *Ae. aegypti* larvae when reared in pitcher-plant liquid in the presence and absence of the larvae of the pitcher-plant midge, *Metricnemus knabi* (Coq.) and found that the percent survivorship for *W. smithii* was high (90%) whether *M. knabi* larvae were present or absent. We also found that *Ae. aegypti* larval survivorship was 82% when *M. knabi* larvae were absent and less than 2% when present in the culture plates. Based on these findings, we suggest that *M. knabi* larvae prevent non-*Wyeomyia* mosquito taxa from exploiting the resources of *S. purpurea* leaves, thereby maintaining it as an exclusive mosquito niche for *W. smithii*. This is confirmed by visual observation of *M. knabi* attacking and devouring *Aedes* and *Anopheles* larvae, while at the same time leaving *W. smithii* larvae unharmed. Possibly the long setae of the *W. smithii* larva may prevent access to its body wall by the mandibles of the *M. knabi* larva. Application of these findings to other mosquito-plant associations is suggested.

170 PIGLIUCCI, MASSIMO^{1*} AND JOHANNA SCHMITT²

¹Dept. of Botany, University of Tennessee, Knoxville, TN 37996-1100; ²Dept. Ecology & Evolutionary Biology, Brown University, Providence, RI 02917

Phenotypic plasticity to foliar and neutral shade in gibberellin mutants of Arabidopsis thaliana

To examine the role of gibberellins in plasticity to foliage shade, we characterized the reaction norms of gibberellin-insensitive and deficient mutants of *Arabidopsis thaliana* to variation in photosynthetically active radiation (PAR) and in the ratio of red : far red light (R:FR). We asked: (1) Do mutations in the gibberellin (GA) signaling system alter the phenotypic plasticity of *A. thaliana* to foliage shade? (2) Do GA-deficient mutants at distinct loci differ in their effects on reaction norms when compared to a GA-insensitive mutant? (3) If a mutation in GA signaling affects plasticity to foliage shade, does it affect resource-mediated plasticity to reduced PAR, or phytochrome-mediated plasticity to the R:FR cue? Mutations at GA signaling loci altered the reaction norms of *A. thaliana*, but mostly in their height, not in the degree of plasticity. There were clear quantitative differences in reaction norms among GA loci, but the gibberellin-insensitive mutant was not phenotypically distinguishable from the gibberellin-deficient ones. The only effect of mutations on the shape of reaction norm was detected for fruits production, implying the existence of other traits affected by GA that we did not measure and which mediate the role of these hormones in response to light quantity but not quality. Certain GA mutants dramatically increased reproductive fitness relative to the wild type under the favorable conditions and unlimited growing season encountered in the greenhouse. While this fitness advantage might not occur under the stricter selective regime imposed by field conditions, it does demonstrate that mutations at major regulatory loci can dramatically and positively affect fitness, depending on the environmental circumstances.

171 QUINN, JAMES A.^{1*} AND SCOTT J. MEINERS²

¹Dept. of Ecology, Evolution, and Natural Resources, Rutgers University, New Brunswick, NJ 08901-1582; ²Dept. of Biological Sciences, Eastern Illinois University, Charleston, IL 61920-3099

Sex ratios, growth rates, and survivorship of red cedar (Juniperus virginiana) on the New Jersey Piedmont from 1963-2000

The objective of this research was to investigate sex ratios, growth rates, and survivorship among cohort groups of *Juniperus virginiana* L. in successional fields on the New Jersey Piedmont. Males and females in six old-fields of different ages were analyzed, starting with the initial data on height and sex expression collected by John Small on labeled recruits from 1963 through 1976. These plants were relocated and censused during the summer and fall of 2000. No changes in sex expression were recorded between 1976 and 2000. The overall sex ratio was exactly 1:1 (332 M, 332 F); only one of the fields showed a significant departure from 1:1. When young, males grew slightly, but significantly, faster in height than females, but relative growth rates dropped by approximately 50% for both males and females once they became reproductive. Female trees were on average 23 cm taller than males at first reproduction. Heights in those males and females surviving to 2000 were not significantly different. There was no effect of an individual's sex on its likelihood of dying, but the plants that became established later, were shorter, and were non-reproductive had an increased risk of mortality. These long-term results strongly support genetically-determined sex ratios and a lack of major differences between males and females in growth rates and survival, which had been suggested by short-term studies elsewhere in the species range.

172 RICE, STANLEY A.^{1*}, ERICA CORBETT¹, DIANA L. BANNISTER¹, JENNIFER MARBLE^{1,2}, IAN B. MANESS¹, AND JONATHAN V. EDELSON²

¹Dept. of Biological Sciences, Southeastern Oklahoma State University, Durant OK 74701-0609; ²Wes Watkins Agricultural Research and Extension Center, Box 128, Lane, OK 74555

Seasonal changes in herbivore defense in oak leaves: results from bioassays

Tobacco hornworms (*Manduca sexta*) and brine shrimp (*Artemia salina*) were used as bioassays of the toxicity of leaves of post oak (*Quercus stellata*). Leaves from three post oak trees in the cross timbers of southern Oklahoma were ground in liquid nitrogen and stored at -70 C until the bioassays. Oak leaf material was incorporated into commercial hornworm chow at 1% and 3% concentrations. Ethanol extracts were used for brine shrimp LC₅₀ analyses. Control hornworms grew much faster and larger than worms that ate chow containing oak leaf material. A significant decrease in toxicity of oak leaves occurred over the season from April to October. Leaves gathered in early, rainy months had a greater effect on bioassay organisms than did leaves gathered in later months during a prolonged drought. These results agree with the optimal defense theory, which says that younger leaves should be defended more than older leaves. However, leaf toughness (as measured with a penetrometer) increased over the season as chemical defense decreased. Therefore young leaves had more chemical, and older leaves more physical, defense from herbivory.

173 RICHARDS, J.H.^{1*}, Q.J. STOBER², R.D. JONES³, AND S.L. RATHBUN⁴

¹Dept. of Biological Sciences, Florida International University, Miami, FL 33199; ²EPA Region 4 Science and Ecosystem Support Division, 980 College Station Road, Athens, GA 30605; ³Southeast Environmental Research Center, Florida International University, Miami, FL 33199; ⁴Dept. of Statistics, University of Georgia, Athens, GA 30602

A quantitative analysis of wetland plant communities in south Florida Everglades

South Florida's Everglades, which are the focus of an \$8 billion, 30-year restoration plan, have diverse subtropical wetland plant communities. In May and October, 1999, we censused 240 sites in the Everglades for plant species presence and relative abundance, then used UPGMA to cluster these sites into groups based on this data. Sites were chosen in a stratified-random sampling design, and 1 or 2 10-m transects were sampled at each site for a total of 418 transects. Soil and water nutrients were also analyzed for each site. The species present were determined for 5 1-m² quadrats per transect. Each quadrat was subdivided into 4 0.25-m² units. We found 161 taxa, but 91% of these occurred in fewer than 10% of the transects. Transects had a mean of 5 species (range = 0 - 30). When the transects were aggregated into 8 clusters, we had 4 small clusters with 1-3 transects each and 4 larger clusters. The larger clusters were a sawgrass (*Cladium jamaicense*) cluster, a spikerush (*Eleocharis cellulosa*) cluster, a water lily (*Nymphaea odorata*) - bladderwort (*Utricularia purpurea*) cluster, and a cattail (*Typha domingensis*) cluster. Some commonly recognized Everglades plant associations, such as maidencane (*Panicum hemitomon*) and beakrush (*Rhynchospora tracyi*) flats, did not form distinct clusters in our analysis. The absence of large clusters defined by these species could represent differences among studies in scale or type of analysis, or it could reflect historical changes in the Everglades ecosystem. Logistic regression of species occurrence against soil phosphorus (P) or ash-free dry weight (AFDW) showed that sawgrass occurs across a broad range of P levels and soil types, while cattails increase in abundance with increasing soil P. Beakrush, bladderwort and spikerush are found at relatively low soil P, and water lilies are found in soils with intermediate P and high AFDW.

174 RICHARDSON, CHARLES R.* , D. NICHOLAS MC LETCHIE, AND PHILIP H. CROWLEY

Center for Ecology, Evolution and Behavior and the T.H. Morgan School of Biological Sciences, University of Kentucky, Lexington KY, 40506-0225

*Life-history tradeoffs and genotypic variation in the dioecious liverwort *Marchantia inflexa**

Tradeoffs among growth, asexual and sexual reproduction have not been extensively documented despite the vast number of organisms that can reproduce through asexual and sexual methods. This experiment characterizes life-history variation among genotypes and tests for tradeoffs among life-history traits in the dioecious bryophyte *Marchantia inflexa*. *Marchantia inflexa* can reproduce asexually from gemmae produced in cupules or sexually through spores. Genotypes were collected from populations in Trinidad that were classified as either Sex Expressing (SE) or Non Sex-Expressing (NSE) based upon the presence or absence of sex expression in the population at the time of collection. Sixty-four genotypes, sixteen males and sixteen females from both SE and NSE populations were grown in a greenhouse in either high or low light conditions. The plants were censused thrice weekly and the dates of first asexual and sexual reproduction were recorded. Plant size and the number of cupules and sex structures were quan-

tified bi-weekly. MANOVA's were used to assess the variation for two growth, asexual and sexual characters (i.e. 6 parameters) and repeated measure analysis was used to compare the amount and pattern of cupule and sexual production. Genotype identity was nested within sex for all analyses. The MANOVA detected a significant genotype (Wilk's Lambda=0.1 F=1.3 p < 0.05) and sex (Wilk's Lambda=0.32 F=3.6 p < 0.0001) effect on *M. inflexa* life-histories. Genotypes displayed clonal heritability estimates between 0.74 and 0.017. The repeated measures analysis detected significant interactions between time and sex (Wilk's Lambda=0.9 F=1.6 p < 0.01), genotype (Wilk's Lambda=0.2 F=1.3 p < 0.0001) and the combination of light and sex (Wilk's Lambda=0.9 F=1.3 p < 0.05) on cupule production. Pearson's correlations did not find evidence of negative tradeoffs as early cup production was positively correlated with early sex expression (r = 0.21 p < 0.01) and high growth rates (r = 0.17 p < 0.01).

175 SAMSON, N.P. AND P. DAYANANDAN*

Botany, Madras Christian College, Tambaram, India 60059

Photosynthetic pathways and ecology of Indian grasses

The occurrence of C₃ and three different subtypes of C₄ photosynthetic pathways in the 1,263 Indian grasses was surveyed using a combination of taxonomic and anatomical criteria. All species of the subfamilies Pooideae, Bambusoideae and Oryzoideae are C₃. Some arundinoid and panicoid species are C₃ while others are C₄. All members of Chloridoideae are C₄. The C₃, NADP-ME, NAD-ME and PEP-CK pathways occur in 536, 504, 132 and 59 species. The all-India C₃: C₄ ratio is 3:4. In the high altitude Himalayan region this ratio is 4:1 while it is 1:4 in the rest of India. Two grass Domains are recognized: the Temperate Himalayan Domain is dominated by C₃ species, mostly pooids, while the Peninsular Domain has mostly C₄ grasses. A transitional region occurs in north-east India. Within the C₄ species NADP-ME, NAD-ME and PEP-CK subtypes occur in 8:2:1 ratio. This ratio is characteristic of Indian C₄ grasses in a wide variety of habitats including the ten Botanical Regions, and also among the endemic species. Cold temperature favors growth of C₃ species; aridity and salinity promote NAD-ME species, and PEP-CK species are common in wetlands. These findings are analyzed in relation to the origin of Indian grass flora, phytogeography and seasonal availability of fodder for grazing animals.

176 SHANER, MARIEKEN G.M.* AND DIANE L. MARSHALL

University of New Mexico-Biology Albuquerque, NM 87131

*Under how wide a set of conditions will nonrandom mating occur in *Raphanus sativus*?*

Sexual selection has been shown to be a powerful evolutionary force in animals, however in plants it has been more controversial. Research with the weedy annual *Raphanus sativus* has demonstrated that nonrandom mating can occur in greenhouse plants. We asked whether this nonrandom mating can occur under a wide range of conditions, including conditions that might occur in the field. To answer this question we constructed a continuum of treatments including variation in both maternal condition and pollen load size. Maternal condition was varied by altering the watering regime. Pollen load size was varied from 30 to 400 pollen grains per stigma. Seed siring success was influenced by the pollen donor and the maternal family. Additionally, maternal condition and pollen load size had an effect on seed siring success. The results suggest that there is a threshold below which nonrandom mating does not occur.

177 SKAGGS, DALE^{1*}, HEATHER SWEET², AND JOHANNE BRUNET²

¹Dept. of Horticulture, Oregon State University, Corvallis, OR 97331; ²Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331

The impact of plant architecture on selfing rate in Aquilegia coerulea (Ranunculaceae)

The number of flowers open on a plant can influence the level of among flower selfing or geitonogamy. We compared selfing rate, estimated with allozyme data from progeny array, between two populations of *Aquilegia coerulea* in southwest Utah. In the Archery population 55 % of the plants had a single flower, in contrast to 21 % of the plants in the Cedar Breaks population. As no geitonogamous selfing can occur in single-flowered plants, we hypothesized that selfing rate would be lower at the Archery population. This assumes that geitonogamous selfing contributes to selfing rate in these populations. To control for other variables that could potentially influence selfing rate between these two populations, we measured the level of protandry, recorded pollinator abundance, flower size and plant density. We also bagged plants in each of these two populations to determine the potential for autogamous selfing in these populations. There was no difference in the multilocus estimate of selfing rate, using PGM and MPI, for Cedar Breaks (selfing rate = 0.22 +/- 0.08, 41 families and 549 progenies) and Archery (selfing rate = 0.20 +/- 0.8, 38 families and 284 progenies). At both sites, bees did the majority of pollination. Our results suggest that plant architecture and geitonogamy do not strongly influence selfing rate in these two populations of *A. coerulea*.

178 ST. OMER, LUCY

Dept. of Biological Sciences, San Jose State University, San Jose, CA 95192

Parasitic choice of host individuals in a seemingly homogeneous environment

It has been postulated that differences in environmental conditions among hosts species existing at microsites influence spatial patterning of plant parasites. Distribution pattern among halophytic host species for the parasite, *Cuscuta salina*, is patchy at the Palo Alto saltmarsh in Northern California. The preferred host, among several halophytic host species, is *Salicornia virginica*. To test this hypothesis studies of the biotic and abiotic environments of host plant species were examined. Marked spatial heterogeneity was present within the biotic and abiotic environments of the three infested host species examined. Significantly different among the three host species were succulence of shoot tissues, salt accumulations on shoot surfaces as well as water contents of associated soils. Ionic accumulations in plant tissues also indicated spatial differences for specific ions. However, examinations of soil nutrients in soils associated with parasitic infestations as compared with soils of non-infested areas failed to indicate any spatial differences between the two soil types. The data presented here in this study suggest that parasitic host preference may indeed be influenced by spatial heterogeneity among host plant species and their associated soil environments.

179 SUDLER, K. NICOLE

School of Biological Sciences, University of Kentucky, 101 T.H. Morgan Bldg., Lexington, KY 40506

Phenotypic selection on sexual reproduction vs. clonal expansion in five populations of Viola blanda

Viola blanda is a common forest understory plant that produces new individuals both sexually and vegetatively, via stolons. The goal of this research was to evaluate the relative

importance of plant size on sexual reproduction and clonal expansion in five different populations. Plant size was estimated using leaf number and leaf size. Number of fruit capsules and number of stolons were employed as sexual and clonal fitness measures, respectively. Phenotypic selection on leaf number and leaf size was found to differ in both magnitude and direction on several levels: 1) within fitness measures, among populations, and 2) within populations, between sexual and clonal fitness. There is some suggestion that different growth strategies are being utilized in different populations. The interaction between leaf traits and population (site) were significant for two of the five populations in relation to sexual fitness and four out of five populations relative to clonal fitness. The five populations are known to differ in their distribution of light, soil type and understory density. Selection differences on leaf number and leaf size may be in response to local environmental conditions. No clear tradeoffs were found between sexual reproduction and clonal expansion. However, within some populations, selection on a given leaf characteristic was found to be in opposite directions when assessing sexual vs. clonal fitness.

180 TODD, BRENT L.^{1*}, HENRY R. OWEN¹, JANICE M. COONS², AND CHRISTINA J. HEISLER¹

¹Dept. of Biological Sciences, Eastern Illinois University, Charleston, IL 61920; ²Dept. of Natural Resources and Environmental Sciences, University of Illinois, Urbana, IL 61801

Seed germination and seedling development of Stylisma pickeringii (Patterson bindweed), an Illinois-endangered sand prairie species

Management and reintroduction efforts of *Stylisma pickeringii* (Torr.) Gray (Patterson bindweed) are limited by a lack of knowledge about its reproductive biology, including information about its seed germination and seedling development. The purpose of this study was to investigate its requirements for seed germination and its seedling development. To investigate seed requirements, seeds were harvested from Mason County over three growing seasons (1998, 1999 and 2000). For all three years, seeds of different colors (yellow, tan, maroon) were counted and germinated in petri dishes at 25 C with or without scarification. In 1999 and 2000, flowers were tagged and seeds were collected to determine how seed age and harvest date affect seed color. To investigate seedling development, seedlings were counted in the field and component parts (shoot, root, and underground shoot branching) were measured. Seed germination was different depending on seed color with yellow being the highest (55-96%) and maroon being the lowest (0%). Also, the seed coat inhibited germination as scarification increased germination. Effects of seed age and harvest date on seed color were inconclusive. The highest seedling density recorded was 1.8 plants/m². For seedling development, *S. pickeringii* develops an extensive taproot before developing its shoots. Its shoot branches originate 7.2 cm beneath the soil surface. This research has provided knowledge about the seed and seedling biology of *S. pickeringii*, which will be useful in the management of this species.

181 TYLER, ANNA P.* AND DIANE L. MARSHALL

Biology, University of New Mexico, Albuquerque, NM, 87131

Effects of elevated CO₂ on male fitness in wild radish, Raphanus sativus

It is widely predicted that atmospheric CO₂ concentrations will double from 350 ppm to 700 ppm within the next one hundred years. The impact of elevated CO₂ on biological systems is of considerable interest. As the amount of fixed carbon available to a plant increases, both growth and reproduction may increase. If increases in reproduction, and hence fitness occur and they

increase differentially among species populations or genotypes, the increases in [CO₂] may affect community structure, and/or selection within populations. While changes in reproductive output as a result of increased levels of CO₂ have been shown in various species, generally these studies have focused on developing seeds and ovaries the female half of plant reproduction; considerably less information exists about these effects on developing pollen grains the male half of plant reproduction. Wild radish, *Raphanus sativus*, was used as a model organism to study the effects of elevated ambient CO₂ on male reproductive success. Sibling pairs of pollen donors were grown in growth chambers in one of two CO₂ levels, ambient (~360ppm) or elevated (~700ppm). Pollen collected from these plants was used to pollinate a set of unrelated plants. In addition to the pollinations, flowers and pollen were collected from the donors in order to measure pollen quality and quantity. Results will be discussed in terms of siring success, offspring seed weight, amount of pollen produced, and pollen germination ability.

182 WALCK, JEFFREY L.* AND SITI N. HIDAYATI

Dept. of Biology, Middle Tennessee State University, Murfreesboro, TN 37132

Seed germination ecology of North American Heuchera species (Saxifragaceae): the eastern H. parviflora and western H. cylindrica

Heuchera *parviflora* Bartl. var. *parviflora* occurs primarily in southeastern North America and *H. cylindrica* Dougl. var. *cylindrica* in northwestern North America. Both species are herbaceous perennials that grow in rocky habitats. Seeds of *H. parviflora*, collected in eastern Kentucky in November 1995 and 1996, and those of *H. cylindrica*, collected in western Washington in August 1996, were used to test temperature and light requirements for dormancy-break and germination and to determine germination phenology. Fresh seeds of *H. parviflora* germinated to 2-64% during 2 wk of incubation in light at alternating temperature regimes of 15/6, 20/10, 25/15, 30/15, and 35/20°C, with highest germination at 25/15°C; none of them germinated in darkness. Dry storage under laboratory conditions for up to 52 wk was not effective in overcoming dormancy. However, seeds given a 12-wk cold stratification period at 5°C in light germinated to 76-96% in light over the range of thermoperiods but those given cold stratification in darkness germinated to only 0-1% in darkness. Peak germination of *H. parviflora* seeds sown in November 1996 in a nonheated greenhouse occurred in early March 1997, when mean weekly maximum and minimum temperatures were 14.8 and 8.7°C, respectively. On the other hand, fresh seeds of *H. cylindrica* germinated to 0-37% during 2 wk of incubation in light at 15/6-35/20°C, with highest germination at 15/6 and 20/10°C, and none germinated in darkness. Seeds continued germinating to ≥76% at 15/6-20/10°C during 4-12 wk of incubation in light. Neither dry storage for up to 52 wk nor cold stratification at 5°C for 9 wk was effective in overcoming dormancy. Peak germination of seeds sown in the greenhouse in September 1996 occurred in late October 1996, when mean weekly maximum and minimum temperatures were 20.7 and 11.9°C, respectively.

183 WALKER, JASON C.1* AND KATHERINE C. LARSON2

¹University of Central Arkansas, Dept. of Biology, Conway, AR 72035; ²University of Central Arkansas, Dept. of Biology, Conway, AR 72035

Morphological plasticity in two types of Lonicera in response to light availability

Japanese honeysuckle (*Lonicera japonica*) is an invasive vine that is currently outcompeting its native congener coral honeysuckle (*Lonicera sempervirens*). Some studies have demonstrated that in response to herbivory and CO₂ enhancement, *L. japonica* was more plastic than its native congener. *L. japonica* has also been shown to be more morphologically plastic than *L. sempervirens* in response to climbing supports. The goal of this study was to compare morphological plasticity of *L. japonica* and *L. sempervirens* in response to light. My hypothesis was that *L. japonica* would show greater plasticity than would the *L. sempervirens*. The study included seventy-two honeysuckle plants that were grown in three separate light treatments-30% neutral shade, 70% neutral shade, and 70% green film. The two neutral shade treatments were used to measure the effect of light intensity; and the two 70% shade cloths, neutral and green, were used to measure the effects of light wavelength. Four different morphological variables were measured on each plant: internode length (cm) on the primary shoot, internode length (cm) of the lateral shoots, branching index, and the lateral angles (angle of the first lateral in relation to primary shoot). I predict, based on past evidence, that *L. japonica* will show stronger phenotypic plasticity in conjunction with all four morphological variables.

184 WEEKLEY, CARL W.* AND ERIC S. MENGES

Archbold Biological Station, PO Box 2057, Lake Placid, FL 33862

Fire and Florida scrub: responses of 13 endemics and postburn community shifts

We investigated the effects of prescribed fire on a long-unburned sand pine scrub on central Florida's Lake Wales Ridge. We quantified the postburn survival of 13 endemic plant species by censusing tagged individuals before and after prescribed fire and by comparing survival of burned vs. unburned individuals. Ten of our study species were herbs, two were woody shrubs, and one was a woody prostrate subshrub. We assessed changes in the species composition and community structure of the scrub ecosystem through pre- and postburn sampling of 12 100m² plots. We also investigated the effect of changes in community structure on overall herb abundance. We found that nine of 13 species had postburn resprouting rates varying from 15% to 98%. Three species (*Bonamia grandiflora*, *Nolina brittoniana* and *Prunus geniculata*) are strong resprouters (well over 50% of burned plants resprouting); two species, *Clitoria fragrans* (48.4%) and *Liatris ohlingerae* (47.3%), are intermediate resprouters; four species (*Asclepias curtissii*, *Garberia heterophylla*, *Helianthemum nashii* and *Sisyrinchium xerophyllum*) are weak resprouters (>10% but *Paronychia chartacea* ssp. *chartacea*, *Polygonella myriophylla*, *P. robusta* and *Schizachyrium niveum*) are killed by fire. Postburn reductions in subcanopy, shrub, litter, lichen and *P. myriophylla* cover were paralleled by increases in the frequency and abundance of scrub herbs (including *Lechea deckertii*, *Cnidocolus stimulosus*, *Stipulicida sectacea* and *Stylisma abdita*). While overall species richness decreased postburn, herb species richness increased. Although some scrub herbs resprout, most postburn increases in herb abundance were due to seedling recruitment.

CONTRIBUTED POSTERS

185 BEACH, SHANNON E.^{1*}, JANICE M. COONS¹, HENRY R. OWEN², BRENT L. TODD², AND MARY ANN L. SMITH¹

¹Dept. of Natural Resources and Environmental Sciences, University of Illinois, Urbana, IL 61801; ²Dept. of Biological Sciences, Eastern Illinois University, Charleston, IL 61920

Comparison of seed production and germination in three distinct colonies of Lesquerella ludoviciana

Lesquerella ludoviciana (Nutt.) S. Wats. (silvery bladderpod) is an endangered, sand prairie plant in Illinois, where its only known habitat is the Henry Allen Gleason Nature Preserve. Three colonies are found within the preserve: North Bowl – upper, North Bowl – lower, and South Bowl. Objectives were to compare seed production and germination in these colonies. Stages of plant development (seedlings, vegetative, and reproductive), flower stalks, flowers, and fruits were counted in each colony on May 4, June 1, June 16, and July 16, 2000. Seed was collected from each colony on June 1 and 16, 2000. On June 1, seed was divided into early (lower portion of the flower stalk) and late (upper portion of the flower stalk) flowering groups. On June 16, only seed of the late flowering group remained on plants. Thus, three seed lots of differing maturity were tested. Seeds were germinated in petri dishes at 25°C in continuous light, and counted every two to three days. Seed production was estimated using reproductive plant density, fruit numbers, and seeds per fruit. The three colonies varied greatly in seed production. The North Bowl – lower produced ten times more seed than the South Bowl, and sixty times more seed than the North Bowl – upper. Differences in seed production in each colony are due to many factors including: area (South Bowl – 270 m², North Bowl, upper – 1025 m², North Bowl, lower – 3248 m²), density of reproductive plants (South Bowl – 1.4 plants/m², North Bowl, upper – 0.1 plants/m², North Bowl, lower – 1.1 plants/m²), and presence of other plant species. Overall, germination percentages ranged from 20% to 66%. No colony differences in germination were observed. For each seed lot, a different colony exhibited better germination. Thus, no differences in germination were found due to colony but the seed production differed greatly between the colonies.

186 BINGHAM, ROBIN A.* AND NANCY D. COHEN

Dept. of Natural and Environmental Sciences, Western State College, Gunnison, CO 81231

Flowering, reproduction, and kleptoparasitism in an extreme southern disjunct population of Drosera rotundifolia

Drosera rotundifolia is a carnivorous plant found in wetland habitats throughout Canada and the northern US. Two extreme southern disjunct populations are found in Colorado, one in Gunnison county, and the second in Jackson county. Due to their unusual disjunct distribution, both populations are listed as sensitive by the USFS. Little is known about flowering and reproduction in these Colorado populations, but historical reports suggest that the Gunnison county population may be primarily cleistogamous. The objective of this study was to collect data on phenology and reproduction to shed light on the mating system of this unusual population. In the summer of 2000 flowering phenology was closely monitored. The population was visited 2-3 times per week throughout the flowering season and visits were made at different times of day. We also collected data on the types of insects captured and the rate of capture. At the end of the season seed capsules were collected and examined. On average,

plants in this population capture one insect per week. The insects captured are primarily small dipterans. Larger prey may be robbed from *D. rotundifolia* by ants. Though floral buds were prolifically produced, only one open flower was observed. However, the majority of capsules collected produced seed. We hypothesize that this population is primarily cleistogamous, possibly as a result of a historical population bottleneck.

187 CALLAHAN, PRISCILLA H.^{1,2*}, BRUCE HOAGLAND^{1,3}, AND PHILLIP T. CRAWFORD²

¹Dept. of Geography, University of Oklahoma, Norman, OK 73019; ²Dept. of Botany and Microbiology, University of Oklahoma, Norman, OK 73019; ³Oklahoma Biological Survey, University of Oklahoma, Norman, OK 73019

The effects of mesquite (Prosopis glandulosa) encroachment on species diversity and composition of a mixed grass prairie

Honey mesquite (*Prosopis glandulosa*) has been shown to modify grasslands in the southwestern United States by altering soil characteristics, modifying microclimate, and facilitating the migration of understory shrubs. However, there has been little investigation of mesquite at the northern edge of its range. We investigated a mesquite savanna within native mixed grass prairie in southwestern Oklahoma. The vegetation at the site included dense, closed canopy mesquite patches, scattered mesquite individuals, and open grassland. Vegetation and environmental data was collected from 15 m transects that were located: within a mesquite patch, in the open grassland, and across grassland-mesquite patch transition. TWINSpan identified six vegetation types along the grassland-mesquite patch transition. A runs test determined that the distribution of the vegetation types was non-random. Results from detrended correspondence analysis (DCA) illustrate the overlapping nature of the six vegetation types in ordination space, but distinct changes in plant community composition were indicated. Species richness and diversity decreased with increased mesquite cover. Mesquite canopy cover was positively correlated to exotic species cover and cactus cover. Mesquite may be facilitating these changes, but the mechanisms at this site are yet to be determined.

188 CARRERO, GLORYVEE^{1*} AND DUANE KOLTERMAN²

¹PO Box 3210, Lajas, PR 00667; ²University of PR, Mayaguez Campus, Dept. of Biology, PO Box 5000, Mayaguez, PR 00681

Population ecology of the endangered Buxus vahlii Baillon (Buxaceae)

Buxus vahlii Baillon is an endangered plant species endemic to Puerto Rico and St. Croix (USVI). There are five known populations, three in Puerto Rico (Rincón, Isabela and Bayamón) and two in St. Croix (Frederiksted and Christiansted). The populations status was studied in order to provide information on the ecology of the species. Data regarding associated vegetation and habitat was obtained at all populations. Height, diameter and reproductive status were only measured in Puerto Rico. The species showed the ability to adapt to different environmental conditions. Such adaptations include shrub-like growth in dry areas where it forms part of the understory (Rincón, Frederiksted and Christiansted), but can also grow in a tree-like form in high precipitation areas (Isabela and Bayamón). Identified human impacts on the studied populations were: development (Frederiksted), illegal immigrants and fires (Rincón), and rock climbing and introduced species (Bayamón). The Isabela and Christiansted populations were not human impacted since both populations are located in places with poor accessibility. Hurricanes impact was minimal for *B. vahlii*

in the two studied populations (Rincón and Isabela); therefore, this event should not be considered as an imminent threat for the species. An actualization of the management plan is suggested for reversing the decline of this species and restore the populations to a stable, secure, and self-sustaining status.

189 COOPER, CLIFTON E.^{1*}, SEAN C. THOMAS², AND WILLIAM E. WINNER¹

¹Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331; ²Faculty of Forestry, University of Toronto, Ontario, Canada M5S 3B3

Gas exchange behavior of old-growth conifer foliage in the Pacific Northwest

The Wind River Canopy Crane Research Facility near Carson, Washington provides access to canopy foliage of a 450-year old forest. We use the crane facility to measure gas exchange parameters of foliage of the dominant tree species, which include *Pseudotsuga menziesii*, *Tsuga heterophylla* and *Thuja plicata*. We have done so since 1996, quarterly, on multiple trees of each species, at upper and lower canopy positions. We use an LI-6400 Portable Photosynthesis System to maintain controlled environments around small, intact branchlets of foliage, and to measure foliar rates of exchange of CO₂ and H₂O gases with the atmosphere. We expose foliage samples to saturating, ambient and zero light levels, and thus determine rates of maximum and *in situ* photosynthesis, and dark respiration. We also record stomatal conductances and transpiration rates. We then harvest all samples, and by two techniques measure areas of the foliage exposed to controlled environments: projected silhouette areas of the intact branchlets, and aggregate one-sided areas of the disarticulated leaves. We then dry and weigh the samples. We may thus express gas exchange rates on the basis of branchlet silhouette area, total leaf area and leaf mass. Results to date show that *Pseudotsuga menziesii* maintains the highest photosynthetic capacity year-round, followed by *Tsuga heterophylla* and *Thuja plicata*. All respiration rates are depressed in winter, as, to a lesser extent, are photosynthetic capacities. However, climate is mild enough for the three dominant species to remain photosynthetically active year-round. Year-to-year variation is substantial, and may be influenced by climate. We have separately measured total stand leaf area, and partitioned it according to species and canopy height. We plan to combine these measurements with our branchlet-level gas exchange values to produce stand-level estimates of foliar carbon exchange.

190 ECCLES, CHRIS* AND DARREN R. SANDQUIST

Dept. of Biological Science, California State University, Fullerton, CA 92834

Temperature acclimation of photosynthesis in four populations of the desert shrub Encelia farinosa

Perennial desert plants experience a broad range of temperatures over the course of their active growing season. Changing the optimal temperature for photosynthesis (thermal acclimation) is one adaptive mechanism for tolerating such fluctuations, but not all species are known to have this capability. Previous studies found that thermal acclimation is absent in the genus *Encelia*, although comparisons among species in this genus indicate that the capacity for evolutionary change in thermal optimum exists. We investigated thermal-acclimation potential in four populations of *Encelia farinosa* which span a broad temperature gradient. In each population there was some evidence of thermal acclimation, but the degree of acclimation was small in comparison to the temperature range in which the plants were grown. The thermal optimum for all populations was fairly consistent for plants raised in high temperature, but thermal optimum for plants raised

at lower temperatures was correlated with average minimum spring temperatures of the population's habitat. These results suggest that some local adaptation for optimal photosynthetic temperature exists in this species, but that thermal acclimation may be limited as a mechanism for tolerating large seasonal temperature changes.

191 JOHNSON, MONICA L.* , DAVID A. TAIT, AND LOREEN ALLPHIN

Dept. of Botany and Range Science, Brigham Young University, Provo, UT 84602

Ecological and genetic diversity in Draba burkei sp. nov. (Brassicaceae), a critically imperilled taxon

Draba burkei sp. nov. (Brassicaceae) is a newly discovered species from a narrow geographic range in Northern Utah, USA. The species is known from only a few localities in the Wellsville and Wasatch Mountains. The largest population of this extremely rare, alpine species was compromised in order to make a safe ski run for the 2002 Winter Olympics, Men's Down-hill Event. Concern for the species preservation has elucidated the need for more biological information, as a foundation for development of management plans for this new, rare mustard. Therefore, five long-term monitoring plots were established representing the largest populations of the species and its entire geographic range. One hundred individuals were randomly selected and tagged in each population. Vegetative and reproductive data were collected for tagged individuals at these sites including clump diameter, number of inflorescences per plant, number of flowers per inflorescence, etc. Soil characteristics and associated species were also determined for each monitoring site. For reproductive studies, fruits were collected from tagged individuals, and seed to ovule ratios were calculated. Enzyme electrophoresis was performed to assess genetic diversity within and among populations. Genetic variation at 15 allozyme loci was compared with morphological and reproductive variation within and among populations. *Draba burkei* exhibited much genetic variation, both within and among populations. All populations showed unique alleles at several of the loci, likely due to their geologic and elevational variation and their large geographic separations. Populations also differed significantly for several vegetative and reproductive traits. These differences once again are likely due to elevation and geographic distribution. Because there is a high degree of genetic differentiation and geographic isolation between populations, they appear to be genetically drifting apart.

192 LEVERICH, W. J.* , JESÚS M. DESANTIAGO, AND PHUONG JULIE NGUYEN

Saint Louis University, Dept. of Biology, 3507 Laclede Ave., St. Louis, MO 63103

Inequality in individual plant reproductive performance

Individual variation in total plant reproduction was studied in experimental populations of *Phlox drummondii* and *Brassica rapa*. Variation was studied with respect to differences in area available to each plant for growth, distance to nearest neighbor, average plant density, and emergence date. The results showed significant inequality in reproductive performance between individuals. Date of emergence was clearly a significant factor when this was variable. Among even-aged plants, available area and distance to nearest neighbor accounted for some differences. In establishing a reproductive hierarchy, earlier germination has a very large influence.

193 MORRIS, ASHLEY B.

Dept. of Botany, University of Florida, Gainesville, FL 32611

Assessing the potential for genetic resistance to beech bark disease in Fagus grandifolia Ehrh. (Fagaceae)

In recent years populations of *Fagus grandifolia* (American Beech) have been decimated across the species' range due to an insect mediated fungal pathogen complex known as beech bark disease (BBD). As this disease spreads throughout the range of *F. grandifolia*, average mortality within a population is estimated to be as much as 85% (Houston 1979). Houston and Houston (1994) observed resistance in less than 1% of 325 *F. grandifolia* trees that they sampled, but they note that resistant stems often occurred in discrete clumps or groups, suggesting the possibility of resistance clonal genotypes. Houston and Houston (1994, 2000) used isozymes in an attempt to identify resistant genotypes in *F. grandifolia* and found that individual stems sharing the same genotype could be either infected or not infected. It is important to note that allozymes often do not display adequate levels of variation to resolve genetic identities in clonal populations (Cruzan 1998, Escaravage 1998, and Waycott 1998). Whereas allozyme studies are commonly limited to less than 10 polymorphic loci, studies using markers based on DNA variation can include many times that number of loci for the resolution of individual genotypes. I used inter-simple sequence repeats (ISSRs) to investigate the potential of genetic resistance to beech bark disease in *Fagus grandifolia* in Great Smoky Mountains National Park. Clonemates exhibited all possible levels of infection, ranging from none to greater than 75%, suggesting that genetic resistance is not a factor in the sites studied.

194 NORTH, GRETCHEN B.^{1*}, PIERRE MARTRE², EDWARD G. BOBICH², AND PARK S. NOBEL²

¹Dept. of Biology, Occidental College, Los Angeles, CA 90041;

²Dept. of OBEE, University of California, Los Angeles, CA 90095

Roots and rocks: how soil rockiness affects shoot and root growth, root distribution, and other root properties for two desert species, Agave deserti (Agavaceae) and Pleuraphis rigida (Poaceae)

The effects of subterranean rocks on shoot productivity and several root properties were investigated for the sympatric CAM succulent *Agave deserti* and C₄ bunchgrass *Pleuraphis rigida*. Plants of both species were examined at a site in the north-western Sonoran Desert along a gradient of soil rockiness, with rocks composing 5% to 60% of the total soil mass. Ten and 50 d after August rainfalls totaling 67 mm, *A. deserti* had 1.7-fold more newly unfolded leaves in sandy than in rocky soils. The greatest leaf productivity for *P. rigida* also occurred in the sandiest soils. Fifty d after the summer rain pulse, leaf number for *P. rigida* had decreased by 66% and 31% in sandy and rocky soils, respectively, but leaf number was still 2.5-fold higher in sandy than in rocky soils. *Agave deserti* had more than 2-fold greater root surface area and mean rooting depth in sandy than in rocky soils, whereas the root surface area per plant and mean rooting depth for *P. rigida* were not affected by soil rockiness. Moreover, the hydraulic conductance for root segments of *P. rigida* collected under rocks and in rock-free soil did not differ. For both species, new root surface area represented 1% to 3% of the total root surface area per plant in both sandy and rocky soils. The distribution of the thick main roots of *A. deserti* was significantly affected by the presence of rocks, perhaps contributing to the higher productivity of *A. deserti* in sandy soils. The distribution of the finer main roots of *P. rigida* was not affected by the presence of rocks, and its greater productivity in sandy soil may reflect both the deeper penetration of water and its greater ability to extract water from a drying soil compared to the succulent *A. deserti*.

195 SMITH-HUERTA, NANCY L.* AND M. BARBARA NEMETH

Dept. of Botany, Miami University, Oxford, OH 45056

Pollen grain deposition, pollen competition, and progeny vigor in a natural population of Clarkia unguiculata (Onagraceae)

When the number of pollen grains deposited on a stigma exceeds ovule numbers, the potential for competition between individual pollen grains exists. In natural plant populations, pollen grain deposition patterns can vary greatly, thus affecting the intensity of pollen competition for ovules. Intensity of pollen competition can in turn affect progeny vigor. We examined pollen deposition patterns, the relationship of pollen deposition to seed set, and the relationship of pollen competition intensity to seedling vigor in a natural population of *Clarkia unguiculata*. Within 6 hours of receptivity, an average of 61 pollen grains were deposited on stigmas, by 48 hours this number rose to an average of 148 pollen grains. These numbers were sufficient for full seed set in this population which averages 49 seeds/capsule. However, flowers exposed to pollinators for only 6 hours set significantly fewer seeds (23 seeds/capsule) than flowers exposed for 48 hours (35 seeds/capsule), and both treatments set significantly fewer seeds than the average of 49 seeds/capsule for this population. All measures of progeny vigor (percent germination, cotyledon width, and first foliar leaf width) showed no significant differences between the 6 hour and the 48 hour treatments. Our data suggest that the intensity of pollen competition in *Clarkia unguiculata* affects seed set but does not affect progeny vigor.

196 STOVER, DANIEL B.* AND KEITH GARBUTT

West Virginia University, Dept. of Biology, Morgantown, WV 26506

Fitness of clonal genotypes of Juncus effusus L. in differing nutrient regimes

It has been hypothesized that there is a genetic tradeoff between resource use efficiency (RUE) and resource acquisition rate (RAR) in that it is not possible for selection to maximize both these traits. In low resource environments RUE is expected to be favored while in high resource environments RAR will be maximized. In this study we examine this hypothesis using *Juncus effusus* L. clones from sites with high and low nitrogen availability. Ten genotypes of *J. effusus* were removed from each of four field sites differing in nitrogen availability (two high and two low). These were hydroponically cloned and then were reciprocally transplanted back into the field sites. Tiller number, length, time of reproduction and death was measured biweekly. Plant growth was assessed by determining the relative (tiller/tiller/day) and absolute growth rates (tillers/day). Preliminary results show a direct correlation between site nutrient level and growth rates. Genotypes from high nitrogen sites had the lowest efficiencies when transplanted into low nitrogen field sites. In low nitrogen environments, native genotypes consistently had higher growth rates than high nitrogen genotypes. Conversely, the highest growth rate for high nitrogen clones was observed within their home field sites. This inverse interaction between genotypes and nitrogen status implies that a home site advantage has been developed. Clones from high nutrient sites appear to exhibit higher RAR to adapt to the higher relative abundance of nitrogen. In conclusion, our preliminary trends show an inherent divergence in the growth responses of *J. effusus* to site nitrogen availability. This divergence may represent genetic tradeoffs between RAR and RUE and overall inability to maximize both these traits in opposing nitrogen environments.

197 TIDWELL, LEITH* AND MARK BRUNSON

Dept. of Forest Resources, Utah State University, Logan, UT 84321

Community-based management of invasive plants: applying social research and education to an ecological problem

The Southwest Rangeland Invasive Plants Initiative, or SRIPI, is a multi-part outreach and research project that will promote and evaluate low-cost, community-based approaches to the management of invasive plants. SRIPI will use a "wildfire" model of invasive species management focusing on prevention, early detection, and eradication. As part of SRIPI survey research will be conducted to assess citizens' knowledge, attitudes, and willingness to participate in weed management. This research will help to identify the specific information needs of extension audiences. Concurrent studies will examine the organizational dynamics of community-based weed management and analyze economic costs and benefits of the community approach. Research will use a social-psychological approach to identifying factors that will facilitate or constrain efforts to control invasive plants. A self-administered mail-back survey is to be completed by residents in eight non-metropolitan counties in the desert southwest. The survey will measure personal and land ownership characteristics, plant ecology knowledge, impacts and effectiveness of control efforts, and effectiveness of citizen-based stewardship. It will also ascertain attitudes towards management practices, assessment of peers' attitudes, willingness to support or take part in control efforts, and preferences towards and use of alternative education methods.

198 VOLIS, S.*, S. MENDLINGER, AND D. WARD

Mitrani Dept. for Desert Ecology, The Blaustein Institute for Desert Research, Ben Gurion University, Beer Sheva, 84100, Israel

*Tests for adaptive RAPD and allozyme variation in population genetic structure of wild barley, *Hordeum spontaneum* Koch*

We tested the adaptive importance of allozyme and RAPD variation in population genetic structure of wild barley, *Hordeum spontaneum*. The test involved: 1) a nested sampling design with four population groups representing a definite environment each; and 2) a comparison of observed variation in molecular markers with that expected as a result of natural selection. An analysis of selection done previously on fitness-related traits by reciprocal introductions served as guidelines for expected pattern of RAPD and allozyme variation. We found no concordance between the observed pattern of population genetic structure and that expected under the null hypothesis of environment-specific natural selection. Limited gene flow and genetic drift could explain the pattern of variation over all loci as well as in each locus studied. Our results oppose repeatedly suggested adaptive importance of molecular marker variation in wild barley. The fact that environmentally-induced adaptation, detected by fitness-related traits, was not reflected in inter-population genetic structure assessed by RAPD and allozyme markers: 1) strongly enhances the neutralists' point of view in a neutralist-selectionist debate; and 2) doubts the methodology that regards significant correlation between some environmental parameter and allozyme frequencies in one or more loci as evidence of selection on the latter.

199 WEINIG, CYNTHIA* AND JOHANNA SCHMITT

Dept. of Ecology and Evolutionary Biology Box G-W, Brown University, Providence, RI 02912

Antagonistic selection in complex environments: adaptive plasticity to UV vs. competition

Plasticity is commonly viewed as an adaptive mechanism enabling organisms to express a phenotype suited to local conditions. However, the physical environment is complex, and adaptive plasticity to one selective agent may counter responses to a second selective agent. In a recent study with *Impatiens capensis*, we tested whether plasticity of stem elongation to ultra-violet radiation was adaptive and whether this response affected plasticity to competitive cues. Plants possess photoreceptors that enable them to detect many aspects of the ambient light environment, such as levels of ultra-violet, red, and blue light. In some cases, shifts in light quality are reliably associated with changes in the physical environment. For instance, the ratio of red:far-red light is reliably correlated with neighbor proximity, because chlorophyll selectively absorbs red light while transmitting far-red. The phytochrome photoreceptors, which switch photoreversibly between red- and far-red-absorbing forms, enable plants to detect R:FR cues of neighbor proximity. Perception of low R:FR stimulates increases in stem elongation, which enables plants to overtop their neighbors and achieve higher fitness. This response also increases exposure to ultra-violet radiation, which is known to decrease elongation in other species. We found that selection favored decreased elongation in high UV environments, but increased elongation in non-UV environments, demonstrating that plasticity of stem elongation is explicitly adaptive. The physiological basis for this selection is unclear, however, elongation responses in the natural environment may reflect a compromise between selection imposed by UV and competition.

200 WIGGAM-HARPER, SHELLY D.* AND CAROLYN J. FERGUSON

Biology Division, Kansas State University, Manhattan, KS 66506

*Pollination biology of *Phlox divaricata* L. (Polemoniaceae): visitation, pollen threshold, and mating system in a Central Plains population*

Phlox divaricata is a widespread and variable species within a group of taxa noteworthy for geographic variation and hybridization. Pollination biology of this species is intriguing, and has not been adequately investigated. Because observed flower visitors are not necessarily sufficient pollinators, quantification of pollinator effectiveness has become an integral part of pollination biology studies, allowing a more accurate interpretation of the effects of pollinators on plant floral and reproductive traits, the distribution of individuals, population dynamics, and phylogeography. *Phlox divaricata* has a wide geographical distribution, with the Central Plains representing the westernmost portion of its range, where *P. divaricata* occurs in scattered populations on rich slopes and creek bottoms. This study focused on the tallgrass prairie of the Central Plains. Visitors to *P. divaricata* were identified using caging and observation to determine diurnal, crepuscular, and nocturnal visitors and their effects on seed set. Additional studies were conducted to document the breeding system of *P. divaricata* and its pollen threshold. To look for shifts in pollinator types across geographic regions, surveys of *P. divaricata* populations along latitudinal and longitudinal transects were compared. These results lay the foundation for experimental studies on the effectiveness of individual visitors to *P. divaricata*.

201 YARNES, CHRISTOPHER T.* AND WILLIAM J. BOECKLEN

New Mexico State University, Dept. of Biology MSC 3AF, P.O. Box 30001, Las Cruces, NM 88003

Foliar chemistry variation in Quercus gambelii Nutt.: bottom-up cascade within a trophic system

Spatio-temporal changes in *Quercus gambelii* Nutt. foliar chemistry were measured along an elevation gradient. The carbon-nutrient balance hypothesis predicts nutrient use and carbon allocation is determined through balancing effects of competition and herbivory. Accordingly, when nutrients are in ample supply, it is predicted competition should favor carbon use primarily in growth. Conversely, within nutrient stressed environments, change in carbohydrate status is expected to increase carbon amounts allocated for defense. Competition pressure varies with edaphic and ambient quality. Changes in topography represent sharp local gradients of environmental heterogeneity that can affect plant and insect populations and communities. Foliar carbon/nitrogen ratios were measured across several elevations on Mount Withington in the Cibola National Forest of west-central New Mexico, U.S.A. Preliminary analyses indicate variation in leaf chemistry with elevation. This variation produces a cascade of bottom-up effects through which *Q. gambelii* foliar chemistry may influence preference-performance in moths of the genus *Phyllonorycter* (Lepidoptera: Gracilariidae), a *Q. gambelii* associated leaf-mining herbivore. Larval performance is currently being investigated.

ECONOMIC BOTANY SECTION, BSA

CONTRIBUTED PAPERS

202 ESTRADA-FLORES, JULIETA G.¹ AND HEIKE VIBRANS^{2*}

¹Facultad de Ciencias, Universidad Autonoma del Estado de Mexico, Instituto Literario 100, Toluca, Estado de Mexico, Mexico; ²Laboratorio de Etnobotanica, Especialidad de Botanica, Colegio de Postgraduados en Ciencias Agricolas, km 35.5 carretera Mexico- Texcoco, 56230 Montecillo, Estado de Mexico, Mexico

Reconstructing the spread of Toluca teosinte (Zea mays subsp. mexicana)

Zea mays subsp. *mexicana*, the Chalco teosinte, was recently shown to be widespread in the Valley of Toluca. It is distributed in a larger area than the Chalco populations themselves. Also, it grows at higher altitudes. Its presence is supposed to be the result of introduction. Several surveys of teosinte and weeds by competent biologists in the 1960's failed to find the populations. Herbarium specimens only exist for the last 10 years. In 1995, we systematically interviewed farmers about their recollections of the time of the introduction. The results show that teosinte has been present for at least 40 years, so they were missed in the 60s. Perhaps the populations were still small, and restricted to a not very accessible area on the former lake bottom in the southeast of the Valley. Teosinte is still in expansion. Comparison of the interviews with population density data show that the likely area of early introduction coincides with the highest population densities today. It is probable that teosinte was introduced inadvertently, as numerous folk names are applied to the plant in the Valley, many of which appear to be newly minted. The widespread common name of "acece" in the Valley of Chalco was not found, nor the names

derived from the roadrunner bird, huiscatote, which are associated with the Balsas teosinte growing a few kilometers further south and west.

203 VERHOEK, SUSAN

Dept. of Biology, Lebanon Valley College, Annville, PA 17003

Botany in European fairy tales

Ethnobotanists have found that information about uses of plants is frequently passed through generations. In the Euro-American culture, sets of oral traditions have been repeated and subsequently transcribed, and are now categorized as "folk tales", "fairy tales", "nursery tales", or "Märchen". These tales were originally told for adults. As stories for children, they are recognized by psychologists as contributing to developmental understanding, and by other researchers as being useful societal teaching tools. A survey was made of fairy tales available in English to assess the extent of botanical knowledge that could be taught by the tales to contemporary Americans. The predominant botanical information transmitted is eco-geographical. Fairy tales teach that Europe is a land of woods and forests and some heathlands. They cite particular trees such as oak, ash, rowan, and walnut. Certain specific foods and ornamentals are mentioned, including oat, apple, orange, parsley, rose, and lily. There are isolated references to medicinal cures and some information about plants used for fibers and construction. Plants that are said to attract or to protect from fairies are sometimes listed. However, the botanical lore is secondary to the stories and is used only to further the verisimilitude of the tale. Fewer than half of the stories mention plants. European fairy tales, while giving a vegetational picture of their homelands, rarely transmit much information concerning instructions or detailed uses of botanical materials.

204 VIEYRA-ODILON, LETICIA¹ AND HEIKE VIBRANS^{2*}

¹Facultad de Ciencias, Universidad Autonoma del Estado de Mexico, Instituto Literario 100, 50000 Toluca, Estado de Mexico, Mexico; ²Laboratorio de Etnobotanica, Especialidad de Botanica, Colegio de Postgraduados en Ciencias Agricolas, km 35.5 carretera Mexico- Texcoco, 56230 Montecillo, Estado de Mexico, Mexico

Contribution of maize field weeds to a rural economy in the Valley of Toluca, Mexico

Observations show that maize field weeds are an important resource in rural areas of Mexico, especially in the high valleys of the south-central part of the country. They are used as quelites (spinach-like vegetables), fodder, ornamentals and a nectar source for bees. We attempted to quantify and evaluate these uses in economic terms for an area that is neither very traditional, nor very modernized. San Bartolo del Llano is a village in the northwest of the Valley of Toluca, with a relatively productive, irrigation-supported, maize-based agriculture, with fertilizer, herbicide and some mechanization inputs, but traditional maize varieties. Also, smallscale, double-purpose cattle breeding is widespread. We interviewed 24 families weekly during a whole growing season on their use of weeds for food and fodder (the other uses were minor) and calibrated quantity measures. In one family, all weeds used were measured. Also, we obtained data on prices and costs. The results show that fodder is the dominant use in economic terms, and that it elevates the economic value of the useful biomass of the maize field by an average of 50%, with a potential that is even higher. The fodder is harvested between July and October, when the critical period of competition between maize and weeds is over.

CONTRIBUTED POSTERS

205 DA SILVA, JAIME A.T.

Ereganto Haitsu 206, Hiragi 353-4, Miki-cho, Kita-gun, Kagawa-ken, 761-0702, Japan

Chrysanthemums: balancing revenue and culture through novel biotechnology

There are few flowering plant species that have been as embraced by the economic and cultural sectors as chrysanthemum. In Japan chrysanthemum is the imperial flower and is only transcended in spiritual and religious (Buddhist) value by the lotus flower. The Japanese culture also exquisitely utilizes chrysanthemums in the flower arranging ceremony, *ikebana*, harmoniously intertwined with *sado*, the tea ceremony and in the funeral ceremony, representing a symbol of peace. Certain chrysanthemums are edible garland/*shungiku*/*Chrysanthemum coronarium*), while others produce valuable secondary metabolites such as pyrethrin (*C. coccineum* or *C. cinerariaefolium*) or sesquiterpene lactones (*C. indicum* or *C. morifolium*). At present chrysanthemums are globally the third most important cut flower crop, after rose and carnation, with over 2 billion cut flower stems annually being used in Japan alone. In many cut flower-producing countries (primarily Colombia, Italy, Japan, the Netherlands) they are firmly rooted, and are stable income bringers in other countries. The global floricultural sector is under constant dynamic change, always seeking new varieties with enhanced characteristics to satisfy ever-increasing individualized consumer demands. Since advances in the improvement of certain chrysanthemum qualities (flower color; longer shelf-life; secondary metabolite production; stress tolerance; virus, viroid and pest resistance, *inter alia*) are time-consuming through conventional breeding practices, we are presently improving and dynamizing select Japanese standard and spray-type chrysanthemum (*Dendranthema grandiflora*/florist's daisy) through novel *in vitro* culture and micropropagation methods, as well as the establishment of efficient genetic transformation protocols (model and applied) with the objective of further strengthening the value of this already wealthy cultural floral asset.

206 FAYVUSH, GEORGE

Institute of Botany, Yerevan 375063, Armenia

Agrobiodiversity of Armenia

Human life is absolutely impossible without plants. However, in most cases, are completely independent from human activity. Nevertheless, in some cases because of human activity or inactivity, many species of plants are threatened with extinction. Whereas, among them there are species with huge significance for human life, and in the first place representatives of agrobiodiversity. Armenia is a small mountainous country located in the Caucasus region. Its territory covers less than 30,000 km² and presents a complex terrain with a high diversity of vegetation and ecosystems. The country combines different habitats like deserts and semi-deserts, alpine meadows, forests, feather grass steppes, and others. The diversity of natural and climatic conditions, the location of the country at the crossroads of different floristic regions, and an active geological record has resulted in the presence of 3,500 species of vascular plants. Armenia is a center of species diversity for many genera such as *Centaurea*, *Pyrus*, *Astragalus*, etc. The local endemic flora comprises more than 120 species. N. I. Vavilov identified Armenia as one of the centers of biodiversity for wild relatives of cultivated plants and as one of the centers of origin of cultivated plants (wheat, pea, lentils, grape, etc.). Also there is a significant diversity of other wild relatives of cultivated plants. A total of 543 species has been recorded here.

The list comprises of 4 genera (22 species) of wild relatives of grain cultures, 3 genera (6) of grain-bean plants, 21 genera (366) of fodder, 6 genera (65) of vegetable crops, and 22 genera (62) of fruit-berry plants. According our investigations about half of them are endangered. We have elaborated a project for the conservation and sustainable use of agrobiodiversity of Armenia. We would like to ask for your assistance in its implementation.

207 JOHNSON, SUSANNAH B.

Dept. Animal & Range Sci., MSC Box 3-I, New Mexico State University, Las Cruces, NM 88003

An ethnobotanical study in Tamil Nadu, India, of Phoenix humilis and Borassus flabellifer (Arecaceae), focusing on their combined use in the construction of brooms

P*hoenix humilis*, commonly known as the Dwarf Date Palm or the Hill Date Palm, is native to India and is found throughout the country in hilly regions. The variety studied in this report, *Phoenix humilis* var. *pedunculata*, grows at about 2,000 m in the Western Ghats Mountain Range. The fruits are sweet and edible and the pith of the stem can be eaten and juiced. The leaves are used in the construction of mats, baskets, handbags, brooms, and cordage. *Borassus flabellifer*, which is thought to have originated from Africa, is commonly known as the Palmyra Palm. The edible fruit contains 3 nut-like portions, each of which encloses a seed. The sweet sap of the palm is fermented to make toddy, a popular alcoholic beverage. The sap is also used medicinally and can be made into a granulated sugar. The leaves and petioles are used for thatching, matting, making baskets, hats, boxes, and rope. The leaves of *P. humilis* and *B. flabellifer* are used in the construction of brooms in Chavidi Pudur, a village in the western part of Tamil Nadu, India. The leaves of *P. humilis* are gathered and dried in the mountains near the village and the petioles of *B. flabellifer* are purchased from men who climb the palms to collect. The brooms are constructed in Chavidi Pudur and are then sold in nearby villages and in the city, Coimbatore.

208 TAMANYAN, KAMILLA

Institute of Botany, Yerevan 375063, Armenia

Sustainable use and conservation of useful plants in Armenia

Armenians have a long tradition of making good use of plant biodiversity for economic purposes. It is estimated that local populations have used in past about 2,000 species of plant (60% of the flora) for a variety of purposes such as medicine, food, coloring, etc. The tradition still persists although circumscribed to a limited assortment of plants that are used in a rather intensive way. In the past few years the population intensively harvests and sells 28 species of edible plants, various firms process 52 species of medicinal plants. These data are confirmed by the a survey of a major market in Yerevan, in which 15 species of edible plants totaling 18.5 tons and 14 species of wild fruit and berry totaling 9.5 tons were commercialized in 1995. Unfortunately, neither past research programs, nor current research activities provide information on sustainable harvesting rates. An important missing indicator is the volume of their natural reserves. This determines the level of harvesting that can be done without threatening their long-term survival. Cultivation the over-harvested species of useful plants on small scale in house backyards, small farms etc., will go a long way to preserving the original populations in the protected areas. There were research studies on the development of planting methods for some species of edible and medicinal plants, for example, *falcaria* (*Falcaria vulgaris*), horse-fennel (*Hippomarathrum microcarpum*), *eremurus* (*Eremurus spectabilis*), and *valerian* (*Valeriana officinalis*).

These indicate that there is a potential to protect the Agrobiodiversity of the Useful and Medicinal plants, by encouraging propagation of the same at the individual consumer level. And there is possibility to restore the elderly assortment of useful plants.

GENETICS SECTION, BSA

CONTRIBUTED PAPERS

209 AFZAL-RAFII, ZARA¹ AND RICHARD S. DODD^{2*}

¹CNRS UMR 6100, Université d'Aix-Marseille III, Marseille, France; ²Dept. Environmental Science Policy and Management, University of California, Berkeley, CA 94720

Population genetic structure in Pinus nigra subspecies salzmannii from southern France

European black pine (*Pinus nigra* Arnold) is widespread from North Africa through southern Europe, the Balkans and eastwards to Turkey and the northeastern shores of the Black Sea. Throughout this wide range, fragmentation of populations has undoubtedly led to differentiation through isolation and through differential selection pressure. Our population analyses of the western range of this species using foliar terpenes had indicated the existence of three main groups: ssp. *nigra* from Bulgaria, Greece, Italy and Austria, ssp. *laricio* from Corsica and ssp. *salzmannii* from southern France and northern Spain. Chloroplast microsatellite data confirm genetic differentiation of Corsican, Austrian/Italian and French populations with Corsican populations the most distinct. Populations from southern France are likely to have been seriously modified by replanting, after exploitation, with preferred provenances from Corsica and Austria. The degree to which native stands of this species in the French Cevennes are genetically polluted by imported provenances is unknown. We have identified stands of *salzmannii* that appear to be more or less pure. These are growing on very harsh sites, suggesting lack of competition from the exotic provenances. We have also detected the presence of *nigra* and *laricio* genotypes on adjacent, more fertile sites.

210 AINOUCHE, LILY M.^{1*}, ALEX BAUMEL¹, RANDALL J. BAYER², RUSLAN KALENDAR³, AND ALAN SCHULMAN³

¹UMR CNRS 6553 University of Rennes1, Campus Scientifique de Beaulieu, 35042 Rennes Cedex France; ²CSIRO Plant Industry, Australian National Herbarium, GPO Box 1600, Canberra, ACT, 2601, Australia; ³Institute of Biotechnology, University of Helsinki, Plant Genomics Laboratory, Viikki Biocenter, PO Box 56, FIN-0014, Helsinki, Finland

Hybridization, speciation and genome evolution in European Spartines (Poaceae)

Most *Spartina* species originate from the New World, and among the four species which are native to the Old world, three are of hybrid origin, being the result of the introduction of the East American *Spartina alterniflora* in western-Europe, and its subsequent hybridization with the indigenous *Spartina maritima*. In England, hybridization resulted in a sterile hybrid, *S. x townsendii*, which gave rise around 1890, to the new fertile allopolyploid *Spartina anglica*. This species has since spread into several continents, causing dramatic ecological changes. Another sterile hybrid between *S. alterniflora* and *S. maritima* has been reported at the end of the 19th century in southwest France, which has been named *S. x neyraudii*. In order to analyze early molecular changes affecting natural hybrid and allopolyploid species, and their role in adaptation and stabilization of a new species, molecu-

lar investigations have been undertaken on populations of European spartines. All the species involved in the speciation process are analyzed: the parents *S. alterniflora* and *S. maritima*, the F1 sterile hybrids, and the allopolyploid *S. anglica*. The latter species has been analyzed in both its native range and in more recently colonized areas (Australia). Different portions of the genome have been investigated using sequencing, RFLPs, and retrotransposon based fingerprinting methods, and genetic divergence between the parental species has been estimated. Our results show that the parental species display consistent genetic differentiation, and that both genomes remain unchanged when reunited and duplicated in the same nucleus. Most populations of *Spartina anglica* contain the same major genotype, which has been colonizing different continents. This young species then represents a system where genetic diversity is restricted to the intra-individual (intergenomic) level, as a result of both genetic bottleneck at the time of the species formation, and structural stasis of the homeologue subgenomes.

211 CALIE, P. J.^{1*}, N. SELTSAM¹, A. T. DENHAM¹, AND B. A. FORD²

¹Dept. of Biological Sciences, Eastern Kentucky University, Richmond, KY; ²Dept. of Botany, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2

Genetic diversity present in the restricted endemic Solidago shortii (Asteraceae)

Short's goldenrod (*Solidago shortii*) is known from a single locality in northern Kentucky, and at present consists of 12 separate populations scattered over a 2.2 km² area. At present the species is listed as Rare and Endangered in the Federal Register. The species is an outcrossing clonal perennial, inhabiting a variety of habitats (e.g. cedar glades, rock outcrops, fallow pastures) and exhibiting a wide range of morphological variation, as determined by previous morphometric analysis. Several populations have been either recently extirpated or are experiencing significant declines in numbers of individuals. To assess variability at the genetic level, a total of 85 individuals from 9 populations were sampled for the following allozymes: ADH-1, ADH-2, MDH-1, EST-1, EST-2, IDH-1, SOD-1, and ME-1. All loci surveyed exhibited varying levels of polymorphism. The least variable locus was malic enzyme (only 2 alleles); the most polymorphic was ADH-2. Varying levels of heterozygosity are observed within different populations for different loci. *Solidago shortii* is known to be self-incompatible. Therefore, our findings indicate that populations are highly differentiated suggesting restricted gene flow between populations. The genetic uniqueness of each population underscores the need to conserve all populations of this species.

212 CANNON, CHARLES H.^{1,2*} AND PAUL S. MANOS¹

¹Dept. of Biology, Duke University, Box 90339, Durham, NC 27708; ²IBEC, University of Malaysia, Sarawak, Kota Samarahan 94300 Malaysia

The molecular phylogeography of Lithocarpus (Fagaceae): limited migration and ancient persistence

The stone oaks (*Lithocarpus*) form the largest genus (300 spp.) in the insect-pollinated chestnut subfamily in the Fagaceae and produce fruit with similar ecological characteristics as *Quercus* acorns. These trees are largely restricted to mesic habitats throughout much of Southeast Asia and have two centers of diversity: Indochina and the island of Borneo. To investigate whether current landscape level genetic variation might indicate historical migration routes and refugia, we sequenced an intergenic region (rbcL-atpBE) on the chloroplast genome from 166 individuals in eight different locations. Our taxonomic sampling included 49 species in at least eight sections to address the question of inter-

specific introgression. We found 66 unique genotypes, which exhibited strong phylogenetic and geographic structure. Two major lineages, one shared between Indochina and Borneo ("continental") and one found only on Borneo ("Bornean"), contained roughly equal numbers of individuals. Numerous transpecific polymorphisms were observed and only one species was fixed on a type, which was shared with other species. In general, individuals from a single location were more closely related than expected, indicating limited seed migration. Populations found in the northwest part of the island possessed the highest degree of overall diversity and appeared to lie nearest the center of origin of the group. The presence of a shared ancestral genotype between China and Borneo suggests limited genetic drift and persistence of a neutral transpecific polymorphism through a time span perhaps exceeding ten million years. A number of macroevolutionary processes, acting simultaneously and at different times in the past, are responsible for the observed patterns, including incomplete lineage sorting, introgressive hybridization, local population dynamics, and isolation by distance. Further sampling of the other Southeast Asian landmasses will be necessary to pinpoint migration routes and refugia and to calibrate the timing of these events.

213 DODD, RICHARD S.^{1*} AND ZARA AFZAL-RAFII²

¹Dept. Environmental Science Policy and Management, University of California, Berkeley, CA 94720; ²CNRS UMR 6100, Université d'Aix-Marseille III, Marseille, France

*Genetic differentiation and adaptation in the mangrove *Avicennia germinans* L.*

The mangrove *Avicennia germinans* L. is found along tropical and sub-tropical coastlines of the Atlantic coasts of Africa and America, the Caribbean and the Pacific coast of America from Mexico to Peru. It has been assumed that mangrove species are dispersal specialists, long distance migration being relatively facile by ocean currents. However, our recent biochemical data (foliar cuticular hydrocarbons) have indicated population structure suggesting that even between relatively geographically close populations, migration may be infrequent. We have compared the biochemical population structure with genetic structure using AFLP molecular analyses of genomic DNA. A total of 349 polymorphic bands from 4 primer sets were scored. Estimated population differentiation ranged from $F_{ST} = 0.379$ assuming a panmictic model for these dominant markers to $G_{ST} = 0.285$ assuming complete inbreeding. The Central American Isthmus accounted for the greatest genetic differentiation among populations that included 4 from West Africa, 3 from French Guiana, 2 from Guadeloupe, 1 from Florida and one from the Pacific coast of Mexico. Two populations from French Guiana were anomalous, clustering closely with African populations, which raises the question of possible transport of propagules by French shipping. Mantel correlations for the biochemical and molecular databases were significant and the biochemical data were also correlated with climatic variables. Partial Mantel correlations indicated a significant climate effect after removal of the phylogenetic effect. This supports our earlier work suggesting genetic adaptation of cuticular chemistry to environmental stress.

214 DOYLE, JEFF J.^{1*}, RAYMOND H. MAK¹, JASON T. RAUSCHER¹, AND JULIE M. VOGEL²

¹L. H. Bailey Hortorium, Dept. of Plant Biology, 462 Mann Library Building, Cornell University, Ithaca, NY 14853; ²DuPont Agricultural Biotechnology, Genome Sciences, Del Tech Park, Suite 200, PO Box 6104, Newark, DE 19714-6104

The evolution of gene expression in a wild soybean polyploid complex: conventional and genomics approaches

There is relatively little published information on the evolution of gene expression in polyploids, particularly outside of model groups such as maize, wheat, *Brassica*, and *Arabidopsis*. Our work on the systematics of allopolyploids in the wild perennial relatives of soybean (*Glycine* subgenus *Glycine*) provides us with the knowledge of genome origins that is required for testing hypotheses of gene and genome evolution. We have sought evidence of gene silencing in these recently formed polyploids. Initially we adopted a gene-by-gene approach, choosing classes of genes we felt were candidates for silencing. The 18S-26S nuclear ribosomal gene family was chosen because nucleolar dominance is well-documented from model allopolyploids. Ribosomal genes are differentially expressed in at least some *Glycine* allopolyploids, both in cases where there are great differences in copy number between homoeologous repeats and where homoeologous copy number is approximately equal. The chloroplast-expressed nuclear-encoded isozyme of glutamine synthetase was chosen as an example of a nuclear gene functioning in the maternally-inherited chloroplast. However, we found no evidence of silencing. This led us to adopt a genomics approach to searching for silenced genes. We isolated a potentially methylated DNA fraction from allopolyploids and their diploid progenitors, and used this fraction to probe filters containing 2,300 unique *Glycine* max cDNA clones. Hybridization patterns were very similar both among diploids from different genome groups and from polyploids, suggesting that few, if any, homoeologous copies of genes are methylated in *Glycine* allopolyploids.

215 GARCIA, MIGUEL A.^{*}, ERICA H. NICHOLSON, AND DANIEL L. NICKRENT

Dept. of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509

*Intra-individual variation in plastid rDNA sequences from the holoparasite *Cynomorium* (Cynomoriaceae)*

It is now generally recognized that intraspecific variation in cpDNA is relatively common; however, less is known about plastid genome variation within individuals. cpDNA chimeras (plants with different cpDNA genotypes) are well-known from variegated cultivars and may result from biparental inheritance or somatic mutations. We document here an example of intra-individual variation in plastid rDNA in a wild species, *Cynomorium coccineum*, a nonphotosynthetic holoparasite. PCR amplifications of all portions of the ribosomal DNA cistron (16S, 23S, 4.5S, 5S and intervening spacers) were made. The PCR products were cloned and the inserts sequenced from 19 colonies. Sequence variation has been observed for all portions of the cistron, however, we will here focus on variation in the large-subunit (LSU, 23S) rDNA which is 2.7 kb in length. Of the 19 clones, five distinct types were identified. Fifteen of the sequences were nearly identical (11 differences or less) and these were designated Type I. The remaining types (II-V) were each represented by a single clone and differed from Type I by 90-235 changes. Of the five types, Type I sequences were the most derived when compared with a tobacco outgroup sequence (range across Types 250-370 differences). Higher-order structures were constructed for representatives of the five Types to address

questions of functionality. Major structural changes (mainly multiple base deletions relative to tobacco) were noted in the variable regions V2, V6, V12, V15, and V16. These deletions varied in size, and those of lesser magnitude retained sequences that were alignable with tobacco. Relatively few mutations were seen in the peptidyl transferase loop, thus suggesting retention of functionality. Given that the PCR products were obtained from total genomic DNA, it is not presently known whether heteroplasmy in *Cynomorium* derives from variation among cpDNAs of different plastids, cells or tissues within the individual plant.

216 GROSS, BRIANA L.^{1*}, ANDREA E. SCHWARZBACH², AND LOREN H. RIESEBERG³

¹Biology Dept., Willamette University, Salem, OR 97301; ²Dept. of Biological Sciences, Kent State University, Kent, OH 44242; ³Dept. of Biology, Indiana University, Bloomington, IN 47405

Potential multiple origins for Helianthus deserticola, a diploid hybrid species

Homoploid hybrid speciation has traditionally been considered a rare event, dependent on the establishment of both a novel, balanced genotype and reproductive isolating barriers between the new species and its progenitors. However, more recent studies have shown that synthetic hybrids converge to match the chromosomal structure of natural hybrids after only a few generations, suggesting that this phenomenon may be more frequent than previously assumed. Here the possibility that the diploid hybrid species *Helianthus deserticola* has arisen from more than one hybrid speciation event was investigated using chloroplast DNA PCR-RFLPs. The haplotypes present in eight different populations of *H. deserticola* from locations spanning its known geographical range were assayed based on four PCR amplified fragments of chloroplast DNA, digested with a total of seven restriction enzymes. The cpDNA haplotypes for *H. deserticola* were compared to the haplotypes found in seven populations of the parental species *H. annuus* and six populations of the parental species *H. petiolaris* with the same geographic distribution. A total of eleven different haplotypes were detected in the three different species; seven of the *H. deserticola* populations had haplotypes characteristic of *H. petiolaris*, while one had a haplotype characteristic of *H. annuus*. This variation in cpDNA haplotype may be explained by a single origin for *H. deserticola* followed by cytoplasmic introgression or by multiple diploid hybrid speciation events. Microsatellite markers were used to further investigate these two possibilities.

217 HALL, SUZANNE S.^{1*} AND KAIUS HELENURM²

¹Dept. of Biology, San Diego State University, San Diego, CA 92182; ²Dept. of Biology, University of South Dakota, Vermillion, SD 57069

Dissimilar patterns of genetic variation in two insular endemics with similar habitat, distribution, recent history, and species characteristics

C*amissonia guadalupensis* ssp. *clementina* (Onagraceae) and *Cryptantha traskiae* (Boraginaceae) are insular endemics identified as Species of Concern (USFWS). *Camissonia g. clementina* is known only from San Clemente Island, California (10 populations), while *Cryptantha traskiae* is known from both San Clemente Island (9 populations) and San Nicolas Island (~ 3 populations). Both taxa show strong habitat specificity, occurring only on sandy coastal flats and partially stabilized sand dunes. Although not closely related phylogenetically, they share recent history by virtue of being endemic taxa that co-occur at nearly all of the locations where they are found. In addition, they share other characteristics affecting patterns of genetic variation such as an annual habit, a primarily selfing mating system, and passive seed dispersal.

All populations of the two taxa on San Clemente Island were surveyed for genotypes at 16 allozyme loci, revealing generally low levels of genetic variation. *Camissonia* has higher levels of variation than *Cryptantha* at both the taxon ($P = 37.5$ vs. 18.8, $A = 1.69$ vs. 1.31, and $H_E = 0.088$ vs. 0.003) and population levels ($P = 8.8$ vs. 3.5, $A = 1.09$ vs. 1.03, and $H_E = 0.017$ vs. 0.003), although some populations of each taxon are monomorphic at all loci. Locations of the more variable populations of each species do not coincide. A greater proportion of variation is found among populations of *Camissonia* ($G_{ST} = 0.810$) than among populations of *Cryptantha* ($G_{ST} = 0.042$). Clear differences exist in patterns of genetic variation in the two taxa despite their shared habitat, distribution, recent history, and species characteristics.

218 HELENURM, KAIUS

Dept. of Biology, University of South Dakota, Vermillion, SD 57069

High levels of genetic polymorphism in the insular endemic herb Jepsonia malvifolia (Saxifragaceae)

J*epsonia malvifolia* (Saxifragaceae) is a long-lived perennial herb endemic to the Channel Islands of southern California and Guadalupe Island, Mexico. Twelve populations of *J. malvifolia* on San Clemente Island were surveyed for their genotype at 21 allozyme loci, revealing high levels of genetic polymorphism. For all individuals across San Clemente Island, 95.2% of loci are polymorphic with $A_P = 2.90$ and $H_E = 0.179$. Populations averaged 60.2% polymorphic loci with $A_P = 2.42$ and $H_E = 0.158$. Most variation is found within rather than among populations ($G_{ST} = 0.101$) although differentiation among populations is significant. Genetic identities range from 0.936 to 0.999 with mean $I = 0.975$. There is no significant relationship between genetic and geographic distance. Gene flow among populations is $N_m = 9.5$ based on private alleles and $N_m = 2.2$ based on FST. Outcrossing rates based on fixation indices average $t = 0.753$, indicating a primarily outcrossed mating system. The genetic variation observed is unusually high for an insular endemic herb and indicates that *J. malvifolia* is unlikely to be endangered by genetic factors.

219 HERMAN, SALLIE J.* AND LINDA A. RAUBESON

Central Washington University, Dept. of Biological Sciences, Ellensburg, WA 98926

Genetic diversity of a rare buttercup

R*anunculus triternatus* occurs as a few isolated populations in Washington, Oregon, Idaho, and Nevada. We have used RAPD (randomly amplified polymorphic DNA) polymorphisms to measure genetic diversity among 25 individuals from one population from Columbia Hills Preserve near Goldendale, WA. For comparison, we have also examined 25 individuals from a population of the widespread sagebrush buttercup, *Ranunculus glaberrimus*. Using ten different 10-mer primers with the 50 DNAs, we generated a total of 87 different RAPD bands. Thirty-two bands were common to the two species; whereas 37 were unique to *R. triternatus* and 17 were unique to *R. glaberrimus*. The rare species, *R. triternatus*, has a higher number of variable loci (62% polymorphism versus 22% for *R. glaberrimus*), a higher proportion of genetically distinct individuals (100% *R. triternatus* vs. 88% for *R. glaberrimus*), and a greater average genetic distance among individuals (0.19 for *R. triternatus* vs. 0.06 for *R. glaberrimus*). Thus, this rare species, considered a species of concern in Washington State, does not seem to be suffering from reduced genetic diversity as compared to the widespread species. In addition to showing a higher level of genetic diversity among members of the rare species, the RAPD data also support the separateness of the two species. As only one population of each species has been tested, this last contention will need to be further investigated by examining samples

from additional populations of each species. This further sampling is currently underway.

220 LEE, JUNGHO^{1,2,3*} AND J. R. MANHART¹

¹Biology Dept., Texas A&M University, College Station, TX 77843, USA; ²Institute of Systematic Botany, University of Zurich, 8008 Zurich, Switzerland; ³Biology Dept., University of Massachusetts, Amherst, MA 01003

Transition from aquatic algae to land plants phylogenomic evidence

We have characterised the chloroplast genomes of green plants (an ulvophyte, a prasinophyte, charophyte lineages, and embryophyte lineages), and we found that known embryophyte unique operons and introns originated not from early embryophytes but from a charophyte ancestor (The chloroplast genomic maps of *Coleochaete* and *Spirogyra* will be presented). In a phylogeny produced from the evolution of operons, genes, and introns, basal charophytes do not contain introns found in the more derived charophytes, and the most derived charophytes and all embryophytes are defined by the presence of *clpP* and 3' *rps12* operons containing trans-splicing *rps12*. We discuss here the likely charophyte sister to embryophytes and the Antithetic hypothesis of embryophyte origin.

221 NASSAR, JAFET M.^{1,2*}, J. L. HAMRICK³, AND THEODORE H. FLEMING²

¹Instituto Venezolano de Investigaciones Científicas, Centro de Ecología, Apdo. Postal 21827, Caracas, 1020-A, Venezuela; ²University of Miami, Biology Dept., P.O. Box 249118, Coral Gables, FL 33124; ³University of Georgia, Depts. of Botany and Genetics, 2502 Plant Sciences, Athens, GA 30602

Outcrossing rates and correlated paternity in Venezuelan cacti with contrasting reproductive strategies

Outcrossing rates and levels of correlated outcrossing within and between fruits were estimated for Venezuelan cacti with contrasting mating and pollination systems: (a) Two columnar cacti, *Stenocereus griseus* and *Cereus repandus*, both self-incompatible and predominantly bat-pollinated; and (b) one globose cactus, *Melocactus curvispinus*, self-compatible and predominantly hummingbird-pollinated. Estimations were conducted on a single population of each species in Central Venezuela using five allozyme loci. *S. griseus* and *C. repandus* were predominantly outcrossing at the population ($t_m = 0.926 - 1.00$) and individual (mean $t_m = 0.930 - 0.960$) levels and had negligible levels of biparental inbreeding (*M. curvispinus* behaved as a facultatively xenogamous species with significant selfing at both population ($t_m = 0.764$) and individual (mean $t_m = 0.18 - 1.00$) levels. No biparental inbreeding was detected for the population studied. Overall, outcrossing rates for the three cacti were consistent with their mating systems. Our results indicate that bats and hummingbirds promote outcrossing on these plants; however, animal-mediated outcrossing of *Melocactus* flowers is not guaranteed. The two columnar cacti had relatively low correlations of outcrossed progeny among fruits within a maternal plant ($r_p = 0.050 - 0.158$), but correlated paternity increased significantly within fruits, with substantial differences between *S. griseus* ($r_p = 0.852$) and *C. repandus* ($r_p = 0.228$). For *M. curvispinus*, correlated paternity among fruits within a family was low ($r_p = 0.059$) and increased moderately within fruits ($r_p = 0.198$). These results suggest that, for the three cacti, outcrossed progeny was primarily the product of multiple pollen donors. This pattern is consistent with the foraging strategies of the pollinators associated with these plants; however, at the flower level, correlated paternity can become an important factor increasing genetic relatedness within families.

222 NOVAK, STEPHEN J.* AND ANGELA Y. WELFLEY

Dept. of Biology, Boise State University, Boise, ID 83725-1515

*Allozyme variation within and among populations of the introduced plant *Poa bulbosa* (Poaceae)*

P*oa bulbosa* L. is a small perennial bunchgrass that possesses a wide distribution throughout Western Europe and the Mediterranean. This grass has been introduced into North America and now occurs throughout much of the western United States, particularly in the Intermountain West. In its native range, *P. bulbosa* reproduces through both sexual and asexual means; however, in its introduced range in the Intermountain West it primarily reproduces clonally through the production of bulbils. Also, high chromosome numbers are frequently reported, suggesting that this grass is a polyploid. Using enzyme electrophoresis, we analyzed 10 populations of *P. bulbosa* from Idaho, Oregon and Washington by staining for 14 enzymes that were coded for by 19 putative loci. Our results indicate that *P. bulbosa* contains higher levels of genetic variation than would be expected for an introduced clonal plant species: 27.9% of loci are polymorphic per population, with an average of 1.54 alleles per locus, and a mean observed heterozygosity of 0.202. The high levels of heterozygosity observed for this grass are consistent with previous reports for autopolyploid plant species. Finally, the complex distribution of multilocus genotypes exhibited by *P. bulbosa* suggests the possibility of multiple introductions of this species into its new range.

223 NOVAK, STEPHEN J.^{1,2*}, JOHN K. SCOTT², AND PAUL C. QUIMBY³

¹Dept. of Biology, Boise State University, Boise, ID 83725; ²CSIRO European Laboratory, Campus International de Baillarguet, Montferrier-sur-Lez, France; ³USDA European Biological Control Laboratory, Campus International de Baillarguet, Montferrier-sur-Lez, France

*Genetic diversity is low in naturalized populations of *Lepidium latifolium* (Brassicaceae) from southern France*

L*epidium latifolium* L. is a polyploid, perennial herbaceous plant with semi-woody stems, and creeping rhizomes, that is native or naturalized throughout much of Eurasia. This species was accidentally introduced into the USA, and has become a noxious weed in coastal New England and wetlands, meadows, pastures, and riparian areas of many western States, especially California and Nevada. The work reported here represents our initial attempt to determine the genetic diversity of *L. latifolium* in Eurasia. We assessed genetic diversity in six populations (380 individuals) of this species from the Mediterranean coast of southern France by staining for 14 enzymes that were coded for by 29 loci. Genetic diversity in *L. latifolium* is extremely low: we detected only two multilocus genotypes across all six populations. Five populations (280 individuals) were fixed for a single multilocus genotype, whereas all 100 individuals in the sixth (and easternmost) population were fixed for the other genotype. Enzyme banding patterns are consistent with allopolyploid gene expression, and chromosome counts reveal that all populations possess tetraploid chromosome numbers ($2n = 24$). The low levels of genetic diversity we report for *L. latifolium* may result from two factors: 1) these populations may have experienced a genetic bottleneck associated with their relatively recent naturalization in this region of southern France, and 2) these populations appear to reproduce almost exclusively through clonal means by rhizome expansion and fragmentation. Our results clearly indicate that further sampling and analysis of *L. latifolium* across larger portions of Eurasia is required before a better picture of genetic diversity in this species in its native range can be obtained.

224 PEPPER, ALAN E*, HEATHER HERRICK, AND LAURA E. NORWOOD

Dept. of Biology, Texas A&M University, TAMUS 3258, College Station, TX 77843

Evolution and population structure of Caulanthus amplexicaulis var. barbarae (Brassicaceae), a rare serpentine endemic plant

Serpentine soils are characterized by low levels of the essential plant nutrients nitrogen, phosphorus, potassium, and calcium, as well as high levels of iron, magnesium, and manganese, and toxic levels of chromium, cobalt, and nickel. Serpentine-derived soils have been found to be a significant impetus for plant speciation and endemism worldwide. The Santa Barbara Jewelflower, *Caulanthus amplexicaulis* var. *barbarae* (J. Howell) Munz (Brassicaceae), is a rare herbaceous annual plant restricted to an archipelago of serpentine exposures in the San Rafael mountains of central California, USA. Its sister taxon, *C. amplexicaulis* var. *amplexicaulis* S. Watson, has a more widespread distribution in southern California. *C. amplexicaulis* var. *amplexicaulis* is largely restricted to granitic soils. Intra- and interspecific phylogenetic relationships *Caulanthus amplexicaulis* var. *barbarae* and related taxa in the "Streptanthoid Complex" of genera (*Streptanthus*, *Caulanthus*, *Guillenia*) were examined using nuclear ribosomal internal transcribed spacer (ITS) and chloroplast trnL intron sequences. Phylogenetic hypotheses supported monophyly of subgenus *Euclesia* – which includes the bulk of the serpentine endemics in the Streptanthoid Complex – but showed that as a group, the serpentine tolerant taxa were nonmonophyletic, occurring in at least three distinct clades. Extant population structure and recent population dynamics in *C. amplexicaulis* var. *barbarae* were examined using a combination of microsatellite loci and nuclear ITS sequence variation. These studies suggest a role for fire in the long-term maintenance gene flow among isolated populations on serpentine outcrops. Although ecologically and geographically isolated, *C. amplexicaulis* var. *barbarae* and *C. amplexicaulis* var. *amplexicaulis* remain fully interfertile in artificial crosses. The existence of genetically compatible taxa with such distinct edaphic requirements presents a unique opportunity for intensive study of the genetic basis of tolerance to serpentine soils.

225 PIKE, LEE M.1*, SEAN A. WHITCOMB², AND DANIEL L. NICKRENT²

¹Dept. of Biological Sciences, East Tennessee State University, Johnson City, TN 37614; ²Dept. of Plant Biology and Center for Systematic Biology, Southern Illinois University, Carbondale, IL 62901

A survey of linkage between nuclear 5S and 26S rDNA in land plants

A recent publication demonstrated linkage between the 5S and 26S rDNA genes in a liverwort (*Marchantia*) and a moss (*Funaria*). No linkage was detected in a green alga (*Chlamydomonas*), a gymnosperm (*Pinus*) and an angiosperm (*Oryza*), hence it was suggested that the colocalization of the 5S and 45S rDNA repeat occurred via an insertion event (transposon-mediated?) within bryophytes. Using primers specific to the 26S and 5S rDNA genes, we conducted a PCR survey of greater than 60 species representing all major land plant lineages. Given that longer amplicons may not always be recovered with standard PCR methods, lack of a PCR product is not definitive evidence for lack of linkage. Despite this, PCR products of varying sizes were obtained from approximately 20 species. These products were cloned and to date some have been sequenced and their identity as IGS (intergenic spacer) confirmed by noting the presence of the 26S rDNA (ca. 200 bp, 3' end) and 5S rDNA (ca. 30 bp, 5' end).

To date, the following are confirmed to possess a linked 26S and 5S rDNA: a charophyte (*Nitella*), a hornwort (*Megaceros*), liverworts (*Conocephalum*, *Monoclea*), a moss (*Sphagnum*), and a fern (*Botrychium*). The presence of linkage in a charophyte and a fern thus indicate that colocalization is not a feature unique to bryophytes but occurs more widely among land plants than previously reported.

226 RIESEBERG, LOREN H.* AND JOHN BURKE

Biology Dept., Indiana University, Bloomington, IN 47405

The biological reality of species: gene flow, selection, and collective evolution

Some authors have claimed that species are passive end products of evolution and thus not substantially different than higher taxa. This claim is based on reports that (1) levels of intraspecific gene flow may be too low to account for species' integration, and (2) populations are likely to diverge rather than evolve in parallel when exposed to uniform selection pressures. These conclusions are premature. A review of the plant literature reveals that there is sufficient gene flow to enable the efficient spread of strongly favorable alleles (s greater than 0.05), the most likely agents of collective evolution. Moreover, estimates of s for major quantitative trait loci (QTLs) are sufficiently large to enable their spread across the range of a species, although minor QTLs seem more likely to evolve locally. In addition, evidence that intraspecific variation in genetic background affects the response of alleles to selection is rare, but examples of parallel genotypic evolution are becoming increasingly common. We conclude that, as traditionally believed, species are the most inclusive entities that directly participate in evolutionary processes. However, we also note that the traditional role of gene flow as a force that constrains differentiation due to genetic drift or local adaptation has been over-emphasized relative to its creative role as a mechanism for the spread of advantageous mutations.

227 WHITKUS, RICHARD^{1*}, HAHN DOAN², VINCENT WENG³, AND TIMOTHY LOWREY⁴

¹Sonoma State University, Rohnert Park, CA 94928; ²University of California, Los Angeles, CA 90024; ³University of California, Riverside, CA 92521; ⁴University of New Mexico, Albuquerque, NM 87131

A QTL analysis of intersectional differences in Hawaiian Tetramolopium (Asteraceae)

Adaptive radiation in Hawaiian *Tetramolopium* has resulted in three separate sections distinguished by a host of morphological and ecological traits. *Tetramolopium humile* (section *Alpinum*) and *T. rockii* (section *Tetramolopium*) are representative of their sections. The main vegetative differences between these sections are plant height, leaf size, and leaf thickness. A suite of reproductive features characterizes section *Tetramolopium*, and are associated with a switch in breeding system (gynomonoecy to monoecy). We measured four vegetative and 12 reproductive trait differences in an F_2 population from a cross between these species, and used a genetic linkage map of 66 molecular markers (RFLP and RAPD) to conduct a QTL analysis. The aim was to gain an understanding of the genetic changes associated with the early stages of divergence in the adaptive radiation. Forty-six putative QTL were obtained over all traits with 76% explaining less than 20% of the phenotypic variance for a trait. QTL of very large effect were found for leaf width (R^2 53%), ray floret number (R^2 65%), and ray to disk floret ratio (R^2 83%). Although reproductive features exhibit dominance in the F_1 , only ray floret number and the ray to disk floret ratio had D/A ratios over 1. All QTL occur in 21 genomic regions of 10 cM in size, and the QTL of largest effect for each trait occur

on 7 of the 9 linkage groups. The location of the QTL explaining the greatest amount of phenotypic variation for each trait results in a minimum of 11 genomic regions necessary to account for the majority of the variation exhibited by the 16 traits measured. The results from this study suggest that morphological evolution associated with adaptive radiation in Hawaiian *Tetramolopium* does not have a simple genetic basis.

228 WOLF, PAUL G.^{1*}, BERNARD DOCHE², LUDOVIC GIELLY², AND PIERRE TABERLET²

¹Dept. of Biology, Utah State University, Logan, UT 84322;

²Laboratoire de Biologie des Populations d'Altitude, Université Joseph Fourier, Grenoble, France

Genetic structure of alpine Rhododendron across a wide range of spatial scales

Rhododendron ferrugineum L. (Ericaceae) is a subalpine shrub found throughout the Pyrenees and Alps, usually at elevations of 1600 – 2200 m. We used 115 dominant AFLP markers to assess genetic structure over wide spatial scales, to gain insights into the relationships between genetic and geographic distance. Leaf tissue was sampled from 10 plants from each of 17 sites across the species' range, with the maximum distance between sites of over 1000km. In addition, at two of the sites we used transects to sample at distances ranging from 10m to 3000m. We found no distinct patterns in terms of the distribution of polymorphic loci, so that it is not yet possible to distinguish recently-colonized sites based on the effects of genetic drift. We observed a positive relationship between genetic distance and spatial distance at the small scales (10 – 1000m), but this breaks down at greater geographic distances. However, there is considerable variation among loci: at some loci, the dominant allele has a restricted geographic range, whereas alleles at other loci are distributed more continuously over the range. Overall patterns of genetic variation are consistent with rapid postglacial colonization as well as high levels of gene flow among sites.

CONTRIBUTED POSTERS

229 BOGDANOVA, ELIZAVETA DMITRIEVNA*, KIRILL L'VOVICH GOSTENKO, AND KARINA KHAMIDOVNA MAKHMUDOVA

Institute of Plant Physiology, Genetics and Bioengineering, 45 Timiryazev Str., 480090 Almaty, Kazakhstan

Breeding of varieties free from gene of hybrid necrosis

Hybrid necrosis determined by two dominant genes Ne1 and Ne2. The wheat varieties may be divided into non-carriers and carriers either one, or other necrosis gene. Obviously, that the frequent use of certain carriers-varieties as parents in crosses has promoted the distribution of the necrosis genes. This became an important problem for practical plant breeding. The investigation of the authors showed that any variety of winter and spring wheat of Kazakhstan, which have been extensively used in crosses are heterogenic carriers of Ne2 gene. Using heterogeneity, it is possible from variety-carriers of dominant genes to secure lines deprived of these genes and to frame varieties free from them. The forced method was used for crosses 10-30 ears marked by labels of plants every of heterogenic variety to the Greicum 476 donor Ne1 gene. Among F1 hybrids were a perfect vitality, sublethal and full lethal. The lines of variety in F1 which absent a necrosis were selected. The breeding of this lines are utilized for developing non-carrier of the variety.

230 BOGDANOVA, ELIZAVETA DMITRIEVNA* AND KARINA KH. MAKHMUDOVA

Institute of Plant Physiology, Genetics and Bioengineering, 45 Timiryazev Str., 480090 Almaty, Kazakhstan

Mutations with non standard spike in wheat (Triticum aestivum L.)

One of the possible ways to increase productivity of spike can be the use of gene resources with non-standard spike morphology in wheat. The objectives of this study were large genotroph type of Kazakhstanskaya 126 with non-standard of spike morphological structure, induced by nicotinic acid from plant source. Plant variation (genotroph) has shown differences from original plants in a number of parameters such as stem height and diameter, leaf surface area, spike length and grain productivity, weight of thousand grains, gliadin and amilase composition and other genetic variabilities caused by gene mutations. Spike of Kazakhstanskaya 126 has normal structure. Spike of genotroph has vertical sessile spikelets or spike branching caused by short day. Lines obtained from hybrids with genotroph (F2-F6) based on the spike morphology were classified into several groups: A. normal spike structure (NS), a single spikelet is situated in one node of spike rachis. B. vertical sessile spikelets (VSS), when two or three spikelets grow up vertically in spike rachis node. The VSS expression were controlled dominantly or recessively. C. tetrastichon (TSS-tetrastichon sessile spikelets) when three or mostly spikelets were sessile closed to each other in a horizontal position in a spike rachis node. The TSS expression was controlled recessively. D. spike branching (TFS-transitional forms spikelets). The TFS expression was controlled recessively. Spike branching were usually less stable in the phenotype in various environments. Haploid plants obtained from anther culture of genotroph have branching spike.

231 GARDNER, KEITH A.^{1*}, STUART J.E. BAIRD², SHANNA E. CARNEY³, AND LOREN H. RIESEBERG¹

¹Dept. of Biology, Indiana University, Bloomington, IN 47405;

²University of Queensland, Brisbane, Australia; ³Dept. of Biology, Colorado State University, Fort Collins, CO 80523

A comparison of different molecular and morphological markers for hybrid index estimation in a natural hybrid zone

Areas of hybridization between related species have become fertile ground for studying the evolutionary process at the genetic level. To fully exploit the opportunities offered by hybrid zones, we need a reliable index of the hybridity of individual organisms. We have developed maximum likelihood methods for the analysis of molecular and morphological marker data, both for codominant and dominant markers and for qualitative and quantitative morphological traits. In simulation studies, we looked at the effects of marker number, marker diagnosticity, linkage and allelic dominance relations on these estimates and their support limits (confidence levels). In addition, for dominant markers, we examined the degree to which violation of Hardy-Weinberg equilibrium in the parental populations biases estimates. We tested the predictions of the simulation study by analysis of a large data set (304 hybrid individuals) from a natural hybrid zone between *Helianthus annuus* and *Helianthus bolanderi*, for which we screened microsatellite (codominant molecular), AFLP (dominant molecular) and morphological marker traits. Comparisons of hybrid indices based on these three kinds of markers generally confirm our earlier simulation conclusions. Over most of the range of possible hybrid index values, a given number of codominant markers give significantly, but not dramatically, better confidence intervals than dominant markers. For most hybrid zone studies, about 50 dominant or 30-40 codominant markers would produce accept-

able confidence intervals, assuming that they are non-diagnostic but do show significant differences in frequency between the parental populations. The hybrid index estimates are also very robust to deviations of F_{IS} from 0. The codominant microsatellite-based hybrid index scores were significantly better predictors of morphology-based hybrid index scores ($R^2=0.65$) than were the AFLP hybrid index scores ($R^2=0.34$). Surprisingly, the codominant index was a poorer predictor of the AFLP index than it was of the morphology based index. We are currently investigating whether these discrepancies have a methodological or biological explanation.

232 HARTER, A.V.*, ALLEN HWANG, AND LOREN H. RIESEBERG

Dept. of Biology, Indiana University, Bloomington, IN 47405

A microsatellite investigation into the origin(s) of cultivated sunflowers

Although the *Helianthus* species most closely related to the cultivated sunflower is known to be the widespread *Helianthus annuus*, the geographic origin(s) of the cultivated sunflower is still unresolved. We have used nine microsatellite loci to investigate the relationships among 12 geographically diverse populations of *H. annuus* and 11 strains of cultivated sunflowers including both commercial lines and Native American-developed strains from Mexico and the United States. Our analyses of wild populations of *H. annuus* have revealed high levels of gene flow among populations throughout its geographic range and high levels of genetic diversity in all populations. In contrast, the cultivars exhibit a range of genetic diversity from almost monotypic at all loci examined to diversity indices nearly comparable to wild populations. A global Analysis of Molecular Variance (AMOVA) of all wild and cultivated populations revealed 72% of the variance was accounted for by differences within populations. Conversely, only 10% of the variance was explained by the differences between cultivated and wild *H. annuus*. There was considerably greater variance among individual cultivated populations than between cultivated and wild populations. This observation suggests multiple origins for the cultivated sunflower. Among the cultivars, only three strains showed strong genetic relatedness to each other: two Native American strains and the Mammoth commercial line. The latter of these was re-introduced to the United States from Russia in the late 19th century. Thus, it appears to have originated from cultivars developed by Native Americans in the east-central United States. Although some relationships were observed between cultivated strains and geographic regions, the exact genetic relationships between specific wild populations and specific cultivated strains were difficult to determine due to the high level of gene flow and genetic diversity in the wild populations.

233 HAUBER, DONALD P.

Dept. of Biological Sciences, Loyola University, New Orleans, LA 70118

Synaptonemal complex formation in diploid Tradescantia ohiensis

The synaptonemal complex (SC) is the linear, tripartite structure that is believed to play a critical role in the orientation of homologous chromosomes during synapsis in prophase I. Over the past 25 years, a whole-mount spreading procedure has been used that allows for detailed examination of intact SCs. A follow-up to a study performed by Hansenkampf and colleagues (1984a,b, 1985) on *Tradescantia ohiensis* was recently performed using a modified SC spreading technique. The modified technique, which calls for desalted sulfatase enzyme in the bursting medium to break down the pollen mother cell walls, produced several

nearly completely synapsed, whole pachytene spreads. The earlier studies had little success in obtaining pachytene SC spreads and mainly focused on spreads in zygotene in which synapsis was never complete. This current study demonstrates that synapsis in *Tradescantia* does progress nearly to completion. It agrees with the previous reports in that synapsis appears to initiate at the telomeres. Also, the average total SC length from the present study ($1092\pm 89.97 \mu\text{m}$) was comparable to the average obtained in the 1985 study ($1246\pm 160.3 \mu\text{m}$). The current study also revealed for the first time, the "bouquet" arrangement of the pachytene SCs, which is often observed in cases where synapsis initiates at the telomeres, and has been reported for *Rhoeo*, another commelinaceous species.

234 KHAILENKO, NINA ALEXANDROVNA AND VLADIMIR ALEKSEEVICH KHAILENKO*

Institute of Plant Physiology, Genetics and Bioengineering, 45 Timiryazev Str., 480090 Almaty, Kazakhstan

Interspecific crossings in genetics investigations of common wheat

The use of wild-growing cereals in genetics investigation on wheat allows to decide fundamental problems of botany and genetics, and received hybrid forms can be using in practical breeding for raising of new cultivars. The purpose of investigation was creation and study of hybrid plants, received by crossing of species *Triticum aestivum* L. (AABBDD), with wild-growing species of cereals, for study the questions of species's origin and creation of hybrid wheat on the basis of cytoplasmic male sterility. As a material for researches have served the cultivar Saratovskaya-29 and species: *T.araraticum* v. *araxianu thumanianis* (AbAbGG), *T. militinae* Zhuk. et Migusch. (AbAbCG), (*T.turgidum* v. *nigrobarbatum* AuAuBB), *T.compactum* Host. (AuAuBBDD), *T.timopheevii* Zhuk. (AuAuGG). Emasculation and pollination were carry out on classic methods (Udolskaya, 1961; Khailenko, 1998). The cultivar Saratovskaya-29 was farther always. Percent of impregnative ovaries reached to 80%, but percent of setting grains was hesitated from 13,79% to 54,90%. About half of obtained grains were good filled, in the main, visually its had good developed embryos and endosperms, but other half of hybrid grains had wrinkled small embryos and wrinkled endosperms. Te development these hybrid grains was corresponded to 4-7 days by grains of control the cultivar Sara-tovskaya-29. This anomalies can be caused both as incompatible of genomic composition by crossed species (Dorofeev at all., 1978; Gandilyan, Shakaryan, 1992) and as various breaches in function of female gametophyte (Khailenko, 1999). The questions of origin of wheat species and practical using biodiversity of interspecific hybrids of wheat will be discussed.

235 KHAILENKO, NINA ALEXANDROVNA

Institute of Plant Physiology, Genetics and Bioengineering, 45 Timiryazev Str., 480090 Almaty, Kazakhstan

Male sterility at interspecific hybrids winter soft wheat at crossing it with species Triticum kiharae Dorof. et Migush. and Triticum dicoccum Shuebl

The display of trait of male sterility at interspecific hybrids F1-F3, BC1 BC2 of combinations *T. kiharae* \bar{o} Ulianovka, Ulianovka \bar{o} \bar{O} . *kiharae*, Mironovskaya 808 \bar{o} *T.dicoccum* was investigated. Since F1, in all combinations of crossing, annually were sowing a grain under the following scheme: ear with grains from free pollination, ear with grains from compulsory self-pollination and ear with grains from synthetic pollination under by individual parchment isolator. The plants of all families of combinations *Triticum kiharae* \bar{o} Ulianovka, Ulianovka \bar{o} \bar{O} . *kiharae*, since F1, were sterile, had structure of anthers such as « a tail of swallow » and high

sterility of pollen, characteristic for trait of cytoplasmic male sterility (CMS). The majority of plants were sterile in F2 and F3, but observed and half-fertile plants. The ears of all plants blossomed was open within 10-17 days, but grains from free pollination the insignificant quantity was setting, as a rule. In combination Mironovskaya 808 \times *T.dicoccum* in F1 all plants were half-fertile, and in F2 and F3 were segregated on sterile, half-sterile, fertile and half-fertile forms. The sterile plants blossomed are open during 15 - 20 days, anthers had both filamentous form, and form « a tail of swallow ». Pollen grains in both types of anthers were sterile. According to our researches (Khailenko, 1995), the species *O.kiharae* has trait CMC, but the species *T.aestivum* (the cultivars Ulianovka and Mironovskaya 808) and *T.dicoccum* don't have of such trait. Probably, in the investigated combinations of crossing there is a display both trait CMC, and dominant trait of gene male sterility (GMS). The problems of cytoplasmic and gene male sterility at wheat, arising at carrying out of works on the remote hybridization of cereal plants are discussed.

236 LEXER, CHRISTIAN*, MARK WELCH, OLIVIER RAYMOND, AND LOREN H. RIESEBERG
Biology Dept., Indiana University, Bloomington, IN 47405

Towards understanding the role of transgressive segregation in adaptation

Transgressive segregation provides a simple and plausible explanation for the niche divergence and phenotypic novelty often associated with plant hybrid lineages. QTL studies in numerous plant species indicate that transgressive segregation is frequent in plants, and that it is an expected consequence of the genetic architecture of differentiated populations or species. However, existing QTL studies of transgressive traits in plants have not attempted to validate the fitness effects of transgressive traits in natural habitats, nor have they measured the effects of individual QTL alleles on hybrid fitness. Studies like this may bridge the gap between transgressive segregation and the origin of novel adaptation in nature. We are currently conducting field experiments using synthetic hybrid lineages between *Helianthus annuus* and *H. petiolaris*, the two sunflower species that gave rise to *H. paradoxus*, the Pecos puzzle sunflower. Our goal is to study the relationships between hybrid fitness and transgressive traits associated with niche divergence (salt tolerance in this model system). Ultimately, we plan to study the fitness effects of individual QTL alleles in natural "hybrid habitat". Preliminary results of these selection experiments will be presented and discussed.

237 LIU, XIANAN^{1*}, EL-SAYED HASSANEIN², AHMED BALHEIDIN², MOHAMED EL-DOMYATI², SHERIF EDRIS², AND WM. VANCE BAIRD¹

¹Clemson University, Dept. of Horticulture, Clemson, SC 29634-0375; ²Dept. of Genetics, Faculty of Agriculture, Ain Shams University, Cairo, Egypt

Cloning and Characterization of Guanylate Kinase from Sunflower (Helianthus annuus L.)

Guanylate kinase is a critical enzyme in the biosynthesis of nucleotides. It catalyzes the reaction (d)GMP + ATP \Rightarrow (d)GDP + ADP. This step is very important in the recovery of cyclic-GMP, and the balance of ATP and GTP concentration within the cell. Therefore, guanylate kinase is thought to be a fundamental enzyme that is important in second-messenger signal transduction pathways. A fragment of a presumptive guanylate kinase gene (designated Cap1-1U) was isolated by differential display RT-PCR during investigations into the effects of drought and osmotic stress on gene expression in sunflower. The full-length cDNA of 1547 bp, which encodes 382 amino acids (predicted 42

kDa), was cloned by Rapid Amplification of cDNA Ends (RACE). Searching electronic databases showed that the deduced amino acid sequence shared a high degree of homology with guanylate kinases. Sunflower guanylate kinase (designated SGK) contains the six highly conserved active-site domains (i.e., three "kinase" domains and three nucleotide-binding domains) known from all other guanylate kinases studied to date. Using quantitative RT-PCR, the expression of SGK was confirmed to be up-regulated in drought-treated leaves, seedling roots and shoots, but not in these same organs when plants were exposed to high salt concentrations. This implies that the expression of SGK may be specifically related to signaling the onset and/or effect of water deficit throughout the plant. Further characterization of SGK (e.g., promoter studies and protein expression) will be very helpful in understanding the function of guanylate kinase in plant cell stress-response.

238 SCHWARZBACH, ANDREA E.^{1*}, LISA A. DONOVAN², DAVID M. ROSENTHAL², AND LOREN H. RIESEBERG³

¹Dept. of Biological Sciences, Kent State University, Kent, OH 44242; ²Dept. of Botany, University of Georgia, Athens, GA 30602; ³Dept. of Biology, Indiana University, Bloomington, IN 47405

The role of transgressive segregation in hybrid speciation: an example from sunflowers

H*elianthus 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. We are interested in the genetic bases of adaptations that allow the hybrid to occupy habitats that are not suitable to the parental species. Novel characteristics can slowly evolve through mutational divergence or might be an immediate byproduct of hybridization. One possible mechanism that generates novel characteristics directly through hybridization is transgressive segregation, which QTL studies explain through complementary gene action. We have identified several morphological and ecophysiological characters that are unique to the hybrid species. We have compared artificial and natural hybrids to determine whether characters that are unique to the natural hybrid species are present in artificial hybrids.

239 SEGARRA, JOSE GABRIEL* AND PILAR CATALAN

Dept. Agricultura, University of Zaragoza, Miguel Servet 177, 50013 Zaragoza (Spain)

Comparative allozyme and RAPD genetic studies on the endemic Borderea chouardii and on its congener B. pyrenaica (Dioscoreaceae) from the Pyrenees (North-eastern Spain)

Comparative genetic studies on the two taxa of the Pyrenean relict genus *Borderea* (Dioscoreaceae) have been conducted using allozyme and RAPD markers. Sampling included individuals from the only known population of the critically endangered *B. chouardii* and from 6 populations within the distribution range of its congener *B. pyrenaica*. Both codominant and dominant alleles have provided markers that genetically separate these two species. Whereas allozymes have failed to detect significant levels of genetic diversity within and among populations, the RAPD alleles have shown to be useful to discern the genetic structure of those populations. Fixed heterozygous patterns found for two allozyme loci might indicate a shared gene duplication event, a hybrid origin of this genus or a different selection rate depending on the genotype.

240 THORNTON, HANNAH E. B.^{1,2*}, CYNTHIA LANE², AND JAVIER FRANCISCO-ORTEGA^{1,2}

¹Dept. of Biological Sciences, Florida International University, Miami, FL 33199; ²Fairchild Tropical Garden, 11935 Old Cutler Rd., Miami, FL 33156

Genetic variation in fragmented populations of an endangered dune plant: implications for its conservation

The preservation of genetic diversity in populations of endangered plants has become an important part of many conservation programs. A knowledge of genetic diversity can help researchers assess the ability of rare plant populations to adapt to changes in their natural environment, to respond to reintroduction programs, and to respond to natural selection. *Jacquemontia reclinata* (Convolvulaceae) is a federally listed endangered species, endemic to the coastal dune system of southeastern Florida. Fewer than 700 individuals of *J. reclinata* remain today, persisting in seven populations, on scattered and fragmented parcels of habitat. As part of a larger program aimed at the preservation of this species, we used allozymes to assess the genetic diversity both within and among the seven *J. reclinata* populations. Results of this work will be presented and applications to the conservation of *J. reclinata* will be discussed. Implications for a study of the quantitative genetic variation within *J. reclinata* will also be discussed.

241 VISION, TODD J.^{1*}, DANIEL G. BROWN², AND STEVEN D. TANKSLEY³

¹USDA-ARS Center for Agricultural Bioinformatics; ²Dept. of Computer Science, University of Waterloo; ³Depts. of Plant Breeding and Plant Biology, Cornell University

Ancient genome duplications in the angiosperms: lessons from Arabidopsis

Polyploidy has been a major force in the evolution of plants, but our ability to detect ancient polyploidy events has limited. Extensive DNA sequence, such as we now have for a number of model plants, allows us to detect common ancestry between protein coding genes that diverged hundreds of millions of years ago. Provided that gene order rearrangements are not too extensive, one can use this to detect common ancestry between chromosomal regions. Applying this principle to the recently completed *Arabidopsis thaliana* genome sequence, we have identified extensive regions of putative common ancestry among all chromosomes. The extent of sequence divergence suggests that there have been at least four major duplication events, possibly genome-wide in scale, and that they occurred roughly 100-200 million years ago. Thus, these duplications are likely to have shaped the ancestral genome(s) of many plant taxa.

HISTORICAL SECTION, BSA

CONTRIBUTED PAPERS

242 MCCOURT, RICHARD M.* , EARLE E. SPAMER, AND ALFRED E. SCHUYLER

Academy of Natural Sciences, 19th and the Parkway, Philadelphia, PA 19103

The Herbarium of the Lewis and Clark Expedition: saving an American treasure

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, the Institute for Museum and Library Services, and private donors.

243 TOUWAIDE, ALAIN

OU-History of Science Dept., 601 Elm, Norman, OK 73019

From Phylo-code vs. Linnaeus, back to Dioscorides vs. Theophrastus. A study in the transformation of systems of plant classification

The system of natural classification created by Linnaeus (1707-1778), exposed in the *Systema naturae* and universally adopted, is currently being challenged by the so-called Phylo-code. This transformation of taxonomy deeply modifies not only the system of classification, but also, if not above all, the concept of classification itself. Such a radical mutation is not unprecedented, however. Not to speak of Linnaeus' system, a true revolution happened well before, in antiquity. In the 1st cent. AD, indeed, Dioscorides renounced to classify plants according to the four types system created by Theophrastus (ca. 371-ca 287 BC), but adopted a new order, based on a first evolutionist concept of nature. On the basis of a full analysis of ancient treatises in their original language, the paper will present this radical mutation. To this end, it will first briefly present Theophrastus' system and then reconstruct the new one adopted by Dioscorides. It will identify its theoretical fundament, and follow its diffusion and reception in ancient science, focusing then on its persistence and adaptations over time, until the dawn of Pre-Modern Botany.

PALEOBOTANICAL SECTION, BSA

CONTRIBUTED PAPERS

244 ARENS, N. C.*, A. THOMPSON, L. CHENG, A. FRUMES, J. HSU, J. LEE, AND S. NOSRATINIA

Dept. of Integrative Biology, 3060, Berkeley, CA 94720-3140

A morphometric method for parataxa delimitation in Quercus of the Neogene

Delimiting meaningful parataxa in dispersed dicot leaf floras is among paleobotany's greatest methodological challenges. Neogene oaks present a particularly thorny problem because of their morphological variation. Nonetheless, biologically meaningful assessments of taxonomic richness are essential to a variety of studies including those focusing on diversification of clades and paleoclimate reconstruction. To develop a repeatable method for delimiting taxa from a mixed collection like those in the fossil record, we assembled leaves from vouchered herbarium specimens from three co-occurring and morphologically similar California oaks: *Quercus agrifolia* Nee, *Q. chrysolepis* Liebm., and *Q. wislizenii* A.DC. For each leaf, we took digital images, measured 11 quantitative variables, and calculated five derived variables. These variables have been used to diagnose parataxa in Neogene oaks. ANOVA also showed that length, width, length/width, and average secondary vein distance showed statistically significant difference among species. However, no single variable distinguished all three species. Discriminant analysis correctly assigned 82% of the specimens to species. This analysis shows that (1) a quantitative morphometric analysis can be useful in delimiting leaf parataxa within oaks, and (2) that some portion of any fossil collection is likely to remain in the morphological overlap between parataxa. A morphometric approach will help refine diagnoses of fossil leaf parataxa to include quantitative and empirical ranges of variation. To demonstrate this approach, we performed the reverse analysis on a large sample of Middle Miocene oaks from the Mint Canyon Formation of southern California. Multivariate ordination suggests extensive overlap in morphology among the oaks in this collection. Only two taxa, rather than the three originally described, can be conservatively recognized from this collection.

245 AXSMITH, BRIAN J^{1*}, RUDOLPH SERBET², MICHAEL KRINGS², THOMAS N TAYLOR², AND EDITH L TAYLOR²¹Dept. of Biological Sciences (LSCB 124), University of South Alabama, Mobile, AL 36688; ²Dept. of Ecology and Evolutionary Biology and Natural History Museum and Biodiversity Research Center, University of Kansas, Lawrence, KS 66045*New interpretations of the enigmatic Paleozoic plants Spermopteris and Phasmatoxycas*

Despite being somewhat overshadowed by relatively recent reports of indisputable cycad remains from the Permian of China, the North American Upper Carboniferous and Lower Permian taxa *Spermopteris* and *Phasmatoxycas*, respectively, have been of considerable interest, due primarily to their suggested status as basal cycads with links to the "pteridosperms." According to an influential theory, cycad megasporophylls were derived from those of a *Spermopteris*-like ancestor via *Phasmatoxycas*. This putative transformation entailed the phylogenetic shift of the ovules from the abaxial lamina surface of *Spermopteris* to the megasporophyll midrib in *Phasmatoxycas* and extant *Cycas*. We have initiated a restudy of these fossils based on the original *Spermopteris coriacea* specimens from the Upper Carboniferous (Virgilian) Lawrence Shale described by Cridland and Morris, which are more complete

and informative than previously realized, and newly collected specimens of *Phasmatoxycas kansana* from the Lower Permian (Leonardian) Wellington Formation. We have found that the ovules of *Spermopteris* are attached to the midrib rather than the leaf lamina. Based on this and other characters, we propose that *Spermopteris* and *Phasmatoxycas* megasporophylls are nearly identical, differing only in venation density and the height of the lamina attachment on the midrib. We also provide evidence that the apical cleft of the ovules of both forms is an original feature rather than a preservational artifact as previously suggested. Comparisons with *Spermopteris* reveal that the abaxial "flange" of *Phasmatoxycas* is an artifact produced by compression of an originally inflated midrib. The implications of these new interpretations for the supposed cycadalean affinity of *Spermopteris* and *Phasmatoxycas* will be discussed.

246 BOUCHER, LISA D.

Dept. of Biology, University of Nebraska-Omaha, 6001 Dodge St., Omaha, NE 68182

Cuticular features in Late Cretaceous floras from northwestern New Mexico

The Fruitland-Kirtland Formations in the San Juan Basin contain an excellent record of Late Campanian-early Maastrichtian macrofloras deposited in a floodplain setting. The fossil material consists primarily of leaf compressions, and cuticle is well-preserved at some sites that are high in clay content. Although pteridophytes, gymnosperms, monocots and dicots comprise the macroflora as a whole, at these sites only dicot cuticle was preserved. In this study, cuticle was removed from more than 15 specimens representing at least five different leaf morphotypes from four sites, and prepared using standard techniques. Epidermal cells and stomata generally have random orientations except over major veins. Stomatal types include paracytic and cyclocytic with some variation on individual specimens. Trichome bases are present on most specimens, and some have distinct secretory glands. Papillae were present to varying degrees on the upper and lower surfaces of all specimens. In a few specimens, surface papillae overhang the stomatal pore. Cuticle striations over some of the subsidiary cells were perpendicular to the long axis of the guard cells. Most of these features are consistent with families belonging to the Magnoliidae and comparisons with leaf architecture and extant families will be discussed. This represents the first description of cuticle from this flora, and with other information from entire leaves, permineralized wood, and palynology, provides a more complete vegetative record of this Late Cretaceous floodplain environment.

247 BOYCE, C. KEVIN

Harvard Botanical Museum, 26 Oxford St., Cambridge MA 02138

The evolution of leaves and leaf development in the Paleozoic

Four vascular plant lineages, the ferns, sphenopsids, progymnosperms, and seed plants, each independently evolved laminated leaves in the Paleozoic. A principal coordinates analysis of 634 leaf species from North American and European floras ranging in age from Middle Devonian through the end of the Permian shows that the clades followed parallel trajectories of evolution: each clade exhibits rapid radiation of leaf morphologies from simple (and similar) forms in the Late Devonian/Early Carboniferous to diverse, differentiated leaf forms, with strong constraint on further diversification beginning in the Mid Carboniferous. Similar morphospace trajectories have been documented in studies of morphological evolution in animals; however, plant fossils present unique opportunities for understanding the

developmental processes that underlie such patterns. Comparison of the details of venation of Paleozoic leaves with modern leaves for which developmental mechanisms are known suggests developmental interpretations for the origination and early evolution of leaves. The parallel evolution of a marginal meristem by modification of the only developmental mechanisms available in the common ancestor of all the groups resulted in the pattern of early evolution repeated by each clade. The early steps of leaf evolution are followed by constraint on further diversification after the exhaustion of the possible elaborations of marginal growth. Hypotheses of the development of Paleozoic leaves can be tested by the study of living plants with analogous leaf morphologies.

248 BUECHLER, WALTER K.^{1*} AND GEORGE W. ARGUS²

¹1408 Shoshone Street, Boise, ID 83705; ²R.R.3-310 Haskins Rd., Merrickville, Ontario, Canada K0G 1N0

Is this a willow leaf? A review of diagnostic traits in modern Salix (Salicaceae) for use in fossil identification

The purpose of this project is to compile morphological, ecological and taxonomic information on worldwide, contemporary *Salix* to better recognize and interpret fossil remains of that genus. Leaves from 52 species of all four subgenera and from 36 sections were cleared, stained and scanned on a high-resolution flatbed scanner. These specimens, together with extensive herbarium material, were examined, and classified by overall shape, form of leaf base and apex, venation patterns, and epidermal and marginal traits. The modern genus includes a much broader spectrum of leaf forms than is widely recognized as "typical". Some broad-leaved species occur in riparian habitats, together with narrow willow-like forms. Nanophyllic and leptophyllic taxa grow in high mountain habitats and are usually only found in Quaternary deposits. Venation is pinnate camptodromous (eucamptodromous with a varying tendency towards brochidodromous loops) in the vast majority of species. Several members of subgenus *Chamaetia* show a more scale-like venation with three or more strong secondaries emerging from the petiole. "Willow-like" leaves are found in numerous families from tropical to alpine or arctic habitats; for extra-generic demarcation, leaf shape, venation pattern, leaf base, characteristics of the margin (salicoid teeth, presence or absence of a fimbrial vein) and epidermal traits are the most important criteria. For infra-generic classification, leaf shape, secondary vein patterns, and margin characteristics are used. Marginal teeth and glands vary considerably in size, shape, and frequency within the genus and are therefore important tools in paleobotanical taxonomy. This study is part of a larger project which will include 1) an examination of fossil and modern pollen, and modern stipules, inflorescences, and infructescences, and 2) a worldwide classification of the contemporary genus (*G. Argus*).

249 CHITALEY, SHYA* AND WILMER STOWE

Cleveland Museum of Natural History, 1 Wade Oval, University Circle, Cleveland, OH 44106-1767

Spores from within the late Devonian Lycopsid cones of Ohio, U.S.A. and from the matrix around the cones

Studies of the 363 million-year-old Cleveland Shale of Ohio have revealed many lycopsid cones. Unlike the tiny cones of modern lycopods, these are all large, with central woody axis, showing an arborescent habit. While no permineralized cones have been found, the preserved compressions of these coaly films are being investigated. The sporophylls of a few cones and some pieces of the shale matrix around these cones were selected for study. Samples were chemically macerated using published paleontological techniques. Microslides were prepared using glycerine

jelly or Permian. Many spores were found both inside the cones and from the shaly matrix around the cones. Algal cysts Tasmanites were found only in the samples of matrix around the cones. The sporophylls of the cones showed clusters of spores attached to sporangia. Spores from the sporangia were round with triradiate marks and sculpturing on the wall. Spores from the matrix were round, triangular, and boat shaped with triradiate marks. However, with some exceptions, they have little affinity with the spores from the cones. It is likely that the cones had not opened to release the spores. The spores found in the matrix might have traveled from distant forests either by wind or water and deposited in the Cleveland Shale which also provided abode for the cones.

250 CREPET, WILLIAM L.* , KEVIN C. NIXON, AND MARIA A. GANDOLFO

Dept. of Plant Biology and L. H. Bailey Hortorium, Cornell University, Ithaca, NY 14853

A Cretaceous Atlantic Coastal Plain "ericoid" complex

An apparently ericoid complex of taxa represented by over 1000 flowers, inflorescence fragments, fruits and leaves is a dominant element of the Upper Cretaceous (Turonian) New Jersey fossil flora, but is also represented in other Upper Cretaceous Atlantic Coastal Plant localities including Martha's Vineyard. Flowers are five-merous with superior ovaries and have 5 stamens alternating with 5 presumably staminodal nectaries. The disparate taxa share a common floral plan, abaxial sepal glands, clawed petals, axile/intruded parietal placentation, lobed spherical stigmas, dorsifixed anthers, tricolporate pollen and distinctive trichomes. They are linked by a subset of these attributes. Fruits are capsules and leaves are folded and have distinctive glands. Different taxa are distinguished by sometimes dramatically contrasting characters including: sepal gland distribution, stamen height vs. style length, anthers with or without spurs, trichome type and distribution, and pollen in monads vs. loose polyads. These taxa share many characters with modern Ericales and related families including Diapensiaceae, but other possibilities must be considered including families of Sapindales. These species are interesting from the perspective of pollination biology because they have characters consistent with highly derived forms of insect pollination.

251 DEVORE, MELANIE L.^{1*}, KATHLEEN B. PIGG², AND STEPHEN J. MOUTON¹

¹Dept. of Biological & Environmental Sciences, Georgia College & State University, Milledgeville, GA 31062; ²Dept. of Plant Biology, Arizona State University, Box 871601, Tempe, AZ 85287

Permineralized fruit with malvalean affinities from the Late Paleocene Almont Flora, North Dakota

The Almont flora of southwestern North Dakota occurs in silicified shale that preserves morphological and anatomical details of fruits and seeds. Among these remains we find a small multiloculate fruit containing around 15-20 seeds, with a single seed per locule. Fruits are 10.5 mm wide and 4.5-5 mm high in transverse section and up to around 13 mm long. Seeds are borne with their long axes parallel to one another, and are separated by a distinctive honeycomb-like pattern of septa. Septa are formed by two adjacent layers of prominent palisade cells. Seeds are flattened, ovoid, and triangular in section with a rounded end and pointed apex. They have an outer layer of somewhat elongate cells that parallel the surface of the seed, and tend to change orientation toward the inside of the seed. This portion of the seed coat is usually only partly preserved. An inner seed layer forms a reticulate pattern on the surface of the silicified seed casts. Based on comparisons of extant taxa, it appears that this fruit type is most closely allied to the

core Malvales (Bombacaceae, Malvaceae, Sterculiaceae, and Tiliaceae). Of these families, the Almont fruit compares most closely with Tiliaceae, in particular because of the presence of single-seeded locules. The malvean fruit from Almont is of particular significance because of its similarity with *Carpolithus bowerbanki* Reid & Chandler, an anatomically preserved form based on a single specimen from the Lower Eocene London Clay flora. *Carpolithus bowerbanki* is similar to the Almont fruit in many features, but somewhat larger. The Paleocene-Eocene was an interval of major faunal exchange across the North Atlantic. The similarities between the Almont fruit and *Carpolithus bowerbanki* strongly suggest that there were also shared floristic elements.

252 DILLHOFF, RICHARD M.^{1,2*}, ESTELLA B. LEOPOLD², AND STEVEN R. MANCHESTER³

¹Evolving Earth Foundation, 1217 212th Ave NE, Sammamish, WA 98074; ²University of Washington, Dept. of Botany, Box 351330 Room 241 Johnson Hall, Seattle, WA 98195; ³Florida Museum of Natural History, Dickinson Hall PO Box 117800, University of Florida, Gainesville, FL 32611

The McAbee Flora and its relation to the proposed Middle Eocene "Okanogan Highlands" flora of the Pacific Northwest

The concept of an "Okanogan Highlands" flora has come into common usage to describe as many as six roughly co-eval Middle Eocene lacustrine floras extending from Northern Central Washington into Central British Columbia. While early publications exist for the Eocene localities of British Columbia, only Republic and Princeton have recent, detailed floral descriptions on which to base comparisons. We have begun a comprehensive investigation of the McAbee site, near Kamloops, British Columbia. Megafossils and pollen are used to infer climate and compare the flora found at the McAbee site to that at Republic and Princeton as well as approximately co-eval lowland assemblages in the Puget Group and Chuckanut formations. Conifers are common and diverse at McAbee, with at least twelve separate taxa present. There are also at least twenty two angiosperm genera with many yet to be described. The dominant dicot leaf taxon at McAbee is *Fagus* which is also represented by nuts and cupules. The confirmation of *Fagus*, also recognized from Princeton and Republic, provides the oldest well documented occurrence of the genus, pre-dating the early Oligocene records of *Fagus* previously reported for North America, Asia and Europe. McAbee apparently lacks thermophilic elements such as *Sabal*, found at Princeton or *Ensete* and *Dioon* found at Republic. It also appears to lack the diversity seen at Republic, although this may be an artifact of the intensive public collecting done there in recent years. In summary, the McAbee site appears to be a good fit overall for the Okanogan Highlands floral construct but also has unique elements that expand our knowledge of the Middle Eocene flora of the Pacific Northwest.

253 DOYLE, JAMES A.* , MICHAEL J. SANDERSON, AND SUSANA MAGALLON

Section of Evolution and Ecology, University of California, Davis, CA 95616

Integrating fossil and molecular data on the age of angiosperms: effects of fossil age constraints and rate smoothing methods

Most molecular estimates of the age of angiosperms, based on the assumption of a molecular clock, have predated the oldest fossil records of crown-group angiosperms in the Early Cretaceous (135 MA). Previous experiments with *rbcl* showed marked variation in evolutionary rates among lineages and suggested that ages based on this gene had been overestimated

due to reliance on high-rate herbaceous taxa and failure to consider rate variation across sites, and they revealed large, unexplained differences between ages based on different codon positions. Proposed solutions include use of more fossil age constraints on nodes and new methods that allow deviation from a clock. Using all positions of *rbcl* and assuming a clock, addition of 18 minimum ages within angiosperms and outgroups, which pushes back the ages of some ancient clades (e.g., Proteales) before their inferred molecular ages, increases the estimated age of angiosperms from 141 to 201 MA. Assuming a maximum age of 125 MA for eudicots lowers this only slightly, to 184 MA. Nonparametric rate smoothing (NPRS), which assumes that rates vary gradually, results in ages that conflict more with the fossil record, not less: 207 MA with no constraints, 277 MA with minimum constraints, and 215 MA with maximum and minimum constraints. A new penalized likelihood method designed to overcome possible shortcomings of NPRS gives ages similar to those based on NPRS. These results may mean either that angiosperms are much older than their known fossil record, or that rates of molecular evolution did not change smoothly but rather accelerated during the radiation of angiosperms and slowed in "living fossils" such as *Platanus*, *Nelumbo*, and *Winteraceae*. Plastid photosystem genes show less conflict between dates based on different codon partitions, suggesting that *rbcl* may not be a good choice for molecular age estimates.

254 DUNN, MICHAEL T.* , GAR W. ROTHWELL, AND GENE MAPES

Dept. of Environmental & Plant Biology, Ohio University, Athens, OH

Upper Mississippian ovules with characteristics of two unique morphogenera: Stephanospermum and Rhynchosperma

Two new ovules from the Fayetteville Formation blur the generic boundaries of *Rhynchosperma* and *Stephanospermum* and provide a possible link with *Medullosa*. The genus *Rhynchosperma* Taylor and Eggert was erected for permineralized seeds that are externally indistinguishable from the seed cast morphogenus *Rhynchogonium*. Described from four specimens from the upper Chesterian Fayetteville Formation of Arkansas, *Rhynchosperma* is radially symmetrical with a two layered integument. The apical portion of the integument is ribbed and non-vascularized; the nucellus is fused to the integument and apically differentiated into a dome shaped pollen receiving structure. The vascular system is poorly preserved and apparently restricted to the integument. Nothing is known about the plant that produced those ovules. In contrast, the trigonocarpalean genus *Stephanospermum* is widely regarded as belonging to medullosan seed ferns. As in all other trigonocarps, *Stephanospermum* is radially symmetrical, with a stalked nucellus attached to the integument only at the base, and has a three parted integument. Seven species ranging from the Westphalian D to the Stephanian A-B boundary are placed in *Stephanospermum*, typically characterized by the presence of a sheath of tracheids in the nucellus and usually, a micropylar crown. The new Fayetteville specimens are similar to *Rhynchosperma* in external shape, two layered integument, number of ribs, and the presence of a dome shaped pollen receiving structure. However, they are more like *Stephanospermum* in vascular architecture and nucellar attachment in that the nucellus is vascularized by a sheath of tracheids, the integument is vascularized by discrete bundles, and the nucellus is attached to the integument at the base. A stalked nucellus has not been observed. The discovery of the Fayetteville specimens with characters of two unique Carboniferous ovules provides exciting insights into the evolution and phylogeny of upper Paleozoic seed plants.

255 FIELDS, PATRICK F.

Dept. of Botany and Plant Pathology, Michigan State University, East Lansing, MI 48824-1312, fieldspa@msu.edu

A review of the middle Miocene Mahonias of western North America and a key to their species

Although *Berberis* (*sensu stricto*) is virtually unknown in the Miocene megafossil record of western North America, the compound leaved barberries (*Mahonia sensu stricto*) have an interesting fossil history. About 15 years ago, Axelrod devoted much effort to taxonomically sorting out these leaflet impressions based on their morphology. Recent work by the present author has added overlooked material, newly discovered occurrences, and the renaming of an invalid taxon. Regardless of how many biologic entities the currently-recognized paleotaxa may actually represent, they do serve as a useful set of identifiable morphotypes. To that end, a simple dichotomous key to the Miocene megafossil *Mahonia* taxa of the western United States is presented. Application of this revision to the floras of western North America reveals the Neogene paleobiogeographic history of this group. There appears to be one primary center of *Mahonia* diversity, near the southwestern end of the Snake River Plain (centered on the region of the Succor Creek, ID/OR and Trout Creek, OR floras). One of two secondary centers is located about 280 km (180 mi) east on the southern edge of the central Snake River Plain (Trapper Creek, ID flora) and the other, about 400 km (250 mi) south in west-central Nevada. Later fossil occurrences appear to be restricted to the Columbia Plateau and intermountain regions east of the coastal ranges and are far less diverse taxonomically.

256 GANDOLFO, MARIA A.*, KEVIN C. NIXON, AND WILLIAM L. CREPET

L. H. Bailey Hortorium, Dept. of Plant Biology, Cornell University, Ithaca, NY 14853

Fossil flowers with possible nymphaealean affinities

The aim of this report is to describe a suite of fossil flowers with possible nymphaealean affinities. The fossil remains were collected from the Old Crossman Pit locality near Sayreville, New Jersey, in outcrops of the Raritan Formation, estimated as Turonian (~90 MYBP, Upper Cretaceous). The fossil remains, exhibiting exceptional preservation, are three-dimensional and preserved as charcoal. Flowers are bisexual, actinomorphic with a cup-shaped "receptacle" and perigynous/hypogynous. The perianth is formed by numerous spirally arranged tepals. The androecium is composed of numerous stamens and staminodes also spirally arranged. Stamens and staminodes are laminar with an acute tip and free from one another. Pollen grains unknown. What appears to be a central sterile column is surrounded by a whorl of more or less free carpels. Additional appendages, probably sterile, surround the gynoecium. Between the cup-shaped receptacle and the androecium there is an elongated zone which does not bear any appendages. The sum of features of this fossil suggests Nymphaeales but other magnoliid groups cannot yet be ruled out. The results of a cladistic analysis to determine more exactly the relationships of these fossils will be presented. Nymphaealean fossils are of great interest because of recent molecular analyses placing this small relic group as a sister group of all, or most, of the remainder of angiosperms.

257 GROTE, PAUL J.*¹, CHONGPAN CHONGLAKMANI², AND PRAMOOK BENYASUTA¹

¹School of Biology, Institute of Science, Suranaree University of Technology, Nakhon Ratchasima 30000, Thailand; ²School of Geotechnology, Institute of Engineering, Suranaree University of Technology, Nakhon Ratchasima 30000, Thailand

Tertiary floras of Northern Thailand: charcoalified conifer wood

Investigations have been made of charcoalified wood fragments from the remains of a presumed ancient forest fire at Li Basin, Lamphun Province, Northern Thailand, and thought to be of Late Oligocene or Miocene age. The wood fragments are situated on a thick layer of lignite in the Ban Pu Subbasin of the Li Basin, one of many Tertiary basins extending from Northern Thailand, along the Malay Peninsula, to Java and Sumatra. All wood fragments observed are from conifers. The wood occurs as thin, tangentially compressed fragments, up to approximately 3 cm long. Tracheids are long and slender (>1.7 mm length by 21- 58 micrometers width). Bordered pits are arranged in a single row or rarely in 2 opposite rows on radial and tangential walls of the tracheids. Axial parenchyma and resin canals were not observed. Rays are uniseriate, homocellular, reach a height of >40 cells, consist of parenchyma cells, and lack ray tracheids. Crossfields show one bordered pit in the tracheid wall, bordered pits not occurring in the ray cells. Presence or absence of annual rings could not be determined. The wood is assigned to the form genus *Podocarpoxylon*, with possible affinity to Podocarpaceae. The presence of these charcoalified remains may indicate a period in which the lignite-forming swamp dried, at least locally, and supported a grove of conifers subject to forest fire.

258 HERENDEEN, PATRICK S.*¹ AND BONNIE FINE JACOBS²

¹Dept. of Biological Sciences, George Washington University, Washington, DC 20052; ²Environmental Science Program, Southern Methodist University, P.O. Box 750395, Dallas, TX 75275-0395

Fossil legumes from the Eocene of Tanzania

The Leguminosae has a diverse and abundant fossil record, which has been well documented from numerous Tertiary age localities, primarily in North America, Europe, and Asia. The record from these areas shows a sudden appearance of diversity in the middle Eocene. The available fossil data have been useful in providing minimum ages of clades within the family and in providing historical context for modern biogeographic patterns. However, several holes exist in the known record, one of the most significant being a lack of fossils from low paleolatitudes. The fossils described in this paper are significant therefore because they are from the Eocene of Tanzania. The fossils were recovered from lacustrine sediments from the Mahenge site (Singida District) in central Tanzania. The deposit represents a small paleolake that formed in a kimberlite eruption crater. The fossil plant assemblage is strongly dominated in taxonomic diversity and abundance by members of the legume family, which is represented by fossil leaves and fruits. The Caesalpinioideae is documented by leaves of several taxa, including the extant genus *Aphanocalyx*, which includes ca. 15 species primarily in western and central tropical Africa today. Fossil leaves of another caesalpinoid taxon are similar to leaves of the extant genera *Cynometra*, *Julbernardia*, and *Guibourtia*, but precise relationships remain to be determined. The Mimosoideae is represented by at least two taxa, one of which is the genus *Acacia*. There are no confirmed papilionoids in the assemblage. Also present are two types of legume fruits, one of which is moniliform and most specimens show evidence of seed predation, possibly by bruchid beetles. Thus the Mahenge site is a valuable addition to our under-

standing of the fossil history of the Leguminosae by providing much needed insight on legume diversity at low latitudes during the early Tertiary.

259 HERENDEEN, PATRICK S.^{1*} AND SCOTT WING²

¹Dept. of Biological Sciences, George Washington University, Washington DC 20052; ²Dept. of Paleobiology, National Museum of Natural History, Smithsonian Institution, Washington DC 20560

Papilionoid legume fruits and leaves from the Paleocene of northwestern Wyoming

The fossil record of the Leguminosae is abundant and diverse in Eocene and younger sediments. Caesalpinioideae, Mimosoideae, and Papilionoideae were all diverse by the middle Eocene, and many fossils are referable to extant genera. By contrast, the Paleocene record is not diverse and the several taxa that have been reported are all referable to the Caesalpinioideae. The fossils we describe here are significant because they are Paleocene in age and are clearly referable to the subfamily Papilionoideae. The fossil locality is a fine-grained, abandoned channel fill deposit in the lower part of the Willwood Formation in the northwestern Bighorn Basin of Wyoming. Mammalian fossils from above and below the plant site indicate a latest Paleocene age, probably not more than 100 ky prior to the carbon isotope excursion that marks the Paleocene/Eocene boundary. Other fossil plants from the site are consistent with a late Paleocene age, including, *Acer silberlingii*, *Deviacer*, *Metasequoia*, *Corylites*, *Platanus raynoldsii*, and *Macginitiea gracilis*. The legume fossils at this site consist of a single type of fruit and a single type of leaf, which are inferred to represent the same plant species. The fossil fruits are stipitate, membranous, and narrowly winged on the placental suture. The fruits are ca. 10 cm long and contain numerous ovules. The seeds are transversely oriented and have a prominent radicular lobe, below which is the funiculus attachment. The co-occurring leaves are imparipinnate and leaflet position varies from opposite to alternate on a single leaf. This fossil taxon is not referable to an extant genus, but it is most comparable to several genera in the tribe Sophoreae, including *Acosmium*, *Bowdichia*, *Diploptropis*, *Sakoana*, and *Maackia*. A precise understanding of relationships of this extinct taxon will require a phylogenetic analysis that includes these and other basal woody papilionoid legumes.

260 HERNANDEZ-CASTILLO, GENARO* AND RUTH A. STOCKEY

Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada

Taxodiaceous pollen cones from the Eocene of British Columbia, Canada

The North American record of fossil conifers from the Upper Cretaceous and Early Tertiary is extensive. Most of these conifers have been assigned to the Cupressaceae/Taxodiaceae. However, the internal anatomy of cones is only known for a few of these taxa. Two fossil pollen cones have been collected at the Late Eocene Appian Way Locality, just south of Shelter Point on the east coast of Vancouver Island, British Columbia. Fossils are permineralized, and studied using the cellulose acetate peel technique and scanning electron microscopy. Cones are attached to stems that bear oppositely arranged leaves with a single vascular bundle and an adaxial resin canal. The cone axis bears decussate scale-like leaves that subtend and enclose the microsporophylls. Microsporophylls are peltate with upturned distal tips and a central resin canal. Three abaxial pollen sacs are born on each sporophyll, and contain abundant non-saccate, papillate pollen grains that are 13-20 µm in diameter. The walls of pollen sacs are composed of thick-walled rectangular cells. These cones

show closest similarities to those in the Cupressaceae/Taxodiaceae. Curved papillae on pollen grains, the opposite arrangement of scale leaves, and the number of pollen sacs per microsporophyll suggest affinities with the genus *Metasequoia*. These cones are associated with numerous taxodiaceous leaf and twig remains at the locality that show similar anatomical characters to those of pollen cones, and will be the subject of further study in the attempt to reconstruct this conifer as a whole plant.

261 HERNANDEZ-CASTILLO, GENARO^{1*}, GAR ROTHWELL², AND GENE MAPES²

¹Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada; ²Dept. of Environmental and Plant Biology, Ohio University, Athens, OH, 45701

Evidence for compound pollen cones in Paleozoic conifers

A rich fossil biota from the Upper Pennsylvanian 7-11 mine of eastern Ohio contains numerous vegetative and fertile compression/impression specimens that conform to a single species of primitive walchian conifers. Among these specimens is a compound pollen cone that is superficially similar to an ultimate vegetative shoot. However, chemical maceration with HF reveals that the specimen has small appendages and pollen sacs in the axil of each bract. The cone is cylindrical, 8.2 cm long, and 0.9 mm in maximum width. Bracts are simple, linear, 3-5 mm long, and 1-2 mm wide. Stomata are distributed across the entire adaxial surface. Bracts subtend a single axillary dwarf shoot with five to eight sterile scales, and 3-4 sporophylls with terminal pollen sacs. Sterile scales are borne on the side of the dwarf shoot axis that faces the bract, and laterally. They overlap each other as if borne in a helical arrangement. Sterile scales are simple, linear with adaxial stomata. Pollen sacs are upright, ellipsoidal with a rounded tip. The pollen sacs occur only on the side of the dwarf shoot that faces the cone axis. Grains correspond to the spore dispersal genus *Potoniaisporites* Bharadwaj. They are monosaccate, with a proximal, bent monolet suture, and a maximum diameter of 6-130 µm in polar views. This specimen provides the first unequivocal evidence that some Paleozoic conifers produced compound pollen cones that are morphologically equivalent to the ovulate cones of ancient conifers, and to the pollen cones of Paleozoic cordaitaleans and modern gnetophytes.

262 JACOBS, BONNIE F.^{1*} AND PATRICK S. HERENDEEN²

¹Environmental Science Program, Southern Methodist University, P.O. Box 750395, Dallas, TX 75275-0395; ²Dept. of Biological Sciences, The George Washington University, 2023 G Street NW, Washington, D.C. 20052

Evidence for dry climate at the Eocene Mahenge site, north-central Tanzania

The Mahenge site consists of crater lake deposits formed subsequent to a kimberlite eruption dated at approximately 46 Ma. The sediments contain plant fossils dominated by leaf remains, with a smaller number of seeds and fruits, as well as abundant fish remains, and other vertebrates including a bat and frog. This locality provides a unique opportunity to evaluate an environment at a tropical low latitude in the Middle Eocene, a time of warmth at high latitudes and unresolved global circulation patterns. A minimum of 20 species (based on leaf morphotypes) is present among the approximately 200 plant specimens, which include at least 7 species in the Leguminosae family. Among these is the genus *Acacia*, which today is limited to hot or warm, seasonally dry environments. A preliminary analysis of leaf area, which is positively correlated with mean annual and wet season precipitation, indicates that rainfall at Mahenge was approximately 700 mm/year, or

about 400mm/yr less than what would be required to support tropical forest vegetation today. The Mahenge flora provides a first data point for paleoclimate in the Eocene of tropical Africa and the paleovegetation reconstruction fits well within the larger framework established by a limited number of palynological and fossil wood records from North and West Africa. These have been interpreted as indicating relatively low diversity communities in the Early to Middle Eocene, followed by the initial development of lowland forest represented by increasing diversity in the Late Eocene and Oligocene. Our interpretation of the Mahenge paleocommunity is concordant with the hypothesis that forest vegetation was not yet established within the tropical belt of Africa 46 million years ago.

263 KLAUVINS, SHARON D.*, EDITH L. TAYLOR, AND THOMAS N. TAYLOR

Dept. of Ecology and Evolutionary Biology and Natural History Museum and Biodiversity Research Center, University of Kansas, Lawrence, KS 66045

Anatomy of the ovulate cupules of Umkomasia (Corystospermales) from the Triassic of Antarctica

Umkomasia is a cupulate ovule-bearing organ belonging to the Corystospermales, a small group of pteridosperms known from the Triassic. Since their initial description, these reproductive structures have been known only from compressions. Although many species of *Umkomasia* have been described, important details of morphology have remained ambiguous due to the lack of anatomical information. Conflicting interpretations of morphology, as well as missing information on key characters, have resulted in poor resolution of the position of the corystosperms in seed plant phylogeny. Anatomically preserved *Umkomasia* has recently been identified for the first time in permineralized peat from the early Middle Triassic of Antarctica. These specimens provide the opportunity to correlate the morphological details of *Umkomasia* with anatomical information. *Umkomasia* is a determinate cupulate branch with helically arranged, recurved, pedicellate cupules, each of which bears one to two abaxially-attached unitegmic ovules. Cupules are ovoid and either bilobed with elongate ventral and dorsal apertures or unlobed with an elongate ventral aperture. The cupule cortex is two-zoned and includes sclerified cells and abundant secretory cavities. Ovules are small, orthotropous, broadly attached basally, and also possess secretory cavities in the thin integument. The bifid apex of the integument extends past the cupule lobes. The cupulate branch is ovoid and displays stem-like anatomy, producing paired traces into each cupule stalk. We speculate that the cupules can be related to other corystosperm organs from Antarctica, particularly the pollen-organ *Pteruchus fremouwensis*, based on similar secretory cavities. These specimens further support the interpretation of corystosperm reproductive structures as branching systems. In addition to aiding in the assessment of homologies among the Mesozoic pteridosperms, these new specimens may provide critical information on the placement of the corystosperms in seed plant evolution.

264 KNAUS, M. JANE^{1*} AND SPENCER G. LUCAS²

¹Dept. of Biology, Southwest Texas State University, San Marcos, TX 78666; ²New Mexico Museum of Natural History and Science, 1801 Mountain Road NW, Albuquerque, NM 87104

Upper Paleozoic floras of New Mexico

With the exception of the Virgilian Kinney Brick Quarry, information available on Upper Paleozoic floras of New Mexico consists primarily of sporadic preliminary reports. Sites currently under study include El Cobre Canyon (Missourian?), Carrizo Arroyo (3 quarries uppermost Pennsylvanian or Permian), and Placitas (Lower Permian); with focus on providing time-ordered

documentation of the "great drying" of the Late Carboniferous. Historically, these "transition" floras were viewed as admixtures of relictual coal swamp elements and newly-evolved "upland" plants. In the absence of reliable taxonomic age indicators, tentative age estimates have been proposed based on relative abundances of swampy to dry-climate taxa. If such estimated ratios are to serve as a proxy for age, it is required that draining through lowered eustatic sea level was a continuous process and accompanied by regional shifts toward dryer climatic patterns without localized backsliding into temporary coal-swamp conditions. Resurgences of humid-indicator floras into the Permian indicates that global drying was not strictly progressive. In addition, the picture of depositional environments in New Mexico is complicated by elevational relief associated with tectonics of the Ancestral Rockies and progradation within fragmented north-south trending intermontane basins. Idiosyncratic depositional characteristic may possibly obscure a regional signal. A new neuropterid frond reconstructed from specimens from Carrizo Arroyo site L-3431 indicates that "typical" coal swamp elements were also simultaneously evolving into dryer climate forms. As an alternative interpretation, DiMichele has proposed that "transition" floras are more accurately viewed as having been mixed by transport within fragmented habitats characterized by localized topographic highs and lows, a condition typified by the depositional characteristics of New Mexico. Analyses in progress show El Cobre Canyon as a Appalachian equivalent coal-measures flora, Carrizo Arroyo as a mixed conifer, Cordaites, medullosan flora, and Placitas as a streamside peltasperm flora.

265 LITTLE, STEFAN A.^{1*}, RUTH A. STOCKEY¹, AND GRAHAM BEARD²

¹CW 405, Dept. of Biological Sciences, University of Alberta, Canada T6G 2E9; ²Vancouver Island Paleontology Museum, Qualicum Beach, British Columbia

Angiosperm fruits and seeds from the Eocene of Vancouver Island

Large numbers of permineralized angiosperm fruits and seeds and one flower have been recovered from the Appian Way Locality (Late Eocene) of Vancouver Island, British Columbia. The plant remains were water washed and preserved in calcareous concretions containing gastropods that have been used to date the sediments. Plant remains at the locality include conifer and angiosperm leaves and stems, toredo bored wood, monocot roots, at least three types of ferns, and associated fungi. Some of the most prominent recognizable fruits and seeds include those of Juglandaceae, Annonaceae, Cornaceae (Mastixioideae) and Magnoliaceae. These remains are closely comparable to those of the London Clay Flora of southern England and the Clarno Nut Beds Flora of western North America. At least 14 other kinds of unidentified fruits and seeds have been recovered from Appian Way. Despite obvious transport and abrasion, there is much promise for future study at this locality due to the numbers of specimens available and their excellent preservation.

266 LUCAS, SPENCER G.

New Mexico Museum of Natural History, 1801 Mountain Road NW, Albuquerque, NM 87104

Upper Triassic megafossil plant biostratigraphy, Chinle Group, western United States

Chinle Group strata are siliclastic red beds that record fluvial, lacustrine and minor eolian deposition in a Late Triassic basin that extended from West Texas-Oklahoma to eastern Nevada, southeastern Idaho and Wyoming. Megafossil plants have been known from the Chinle Group since 1850, and they have been used to construct a biostratigraphy of three floral zones

(ascending order): *Eoginkgoites*, *Dinophyton* and *Sanmiguelia* zones. This biostratigraphy can be evaluated by stratigraphically ordering Chinle plant localities using lithostratigraphic and vertebrate-fossil-based correlations, which are independent of the plant biostratigraphy. This reveals that the three zones are stratigraphically successive, and that the bulk of the Chinle paleoflora (more than 50% of the taxa) is from the *Dinophyton* zone. *Eoginkgoites* is confined to basal Chinle strata, but co-occurring genera restricted to these strata are rare and/or known from a single locality. The *Sanmiguelia* zone is represented by scattered localities in the middle-upper Chinle and cannot be characterized except by the presence of *Sanmiguelia*, which is known from less than 10 localities and endemic to Chinle strata. Correlation of Chinle Group plant zones with Newark Supergroup plant sites is consistent with vertebrate-fossil-based correlations. However, Chinle plants only provide a useful biostratigraphy of upper Carnian strata (*Eoginkgoites* and *Dinophyton* zones). The Norian-Rhaetian paleoflora of the upper Chinle (*Sanmiguelia* zone) needs further collecting and study before it can be of much biostratigraphic utility.

267 LUPIA, RICHARD

Sam Noble Oklahoma Museum of Natural History and School of Geology and Geophysics, University of Oklahoma, 2401 Chautauqua Avenue, Norman, OK 73072

Megaspore and fern mesofossil floras from the Aptian-Santonian (Cretaceous) of the Atlantic and Gulf Coastal Plains

Numerous mesofossil floras, deposited approximately 80-115 million years ago (Ma), containing charcoaled and lignitized flower, fruits, seeds and leaves, have been found along the Atlantic and Gulf Coastal Plains of the United States. Although angiosperms from these localities have been intensively studied, other plant remains have not been examined in as much detail. The megaspore floras and fern mesofossils that have been recovered from three localities are described. Cumulatively, at least ten genera and thirteen species of megaspores are recognized from Northeast Plaza (Aptian, 115Ma, Maryland), Mauldin Mountain (Cenomanian, 99Ma, Maryland) and Upatoi Creek (Santonian, 84Ma, Georgia) localities. Megaspores identified so far have affinities either to heterosporous lycophytes—*Bohemisporites*, *Erlansonisporites*, *Minerisporites*, *Paxillitrites*, and three additional “genera”—or to heterosporous ferns—*Arcellites*, *Ariadnaesporites*, and *Molaspora*. On the basis of recently described sporocarp remains, *Molaspora* is a dispersed megaspore belonging to the extant genus *Regnellidium* (Marsileaceae). At both sites in Maryland, lycopsid megaspores are more diverse and abundant than fern megaspores. At Upatoi Creek, lycopsid megaspores are more diverse, but approximately equivalent in abundance to fern megaspores. Fern mesofossils—pinnules with and without sporangia, and rachis fragments—are present at all sites. At Mauldin Mountain, isolated pinnules enclosing sporangial clusters are among the most common fossils. At Mauldin Mountain and Upatoi Creek, fertile pinnules assignable to *Onychiopsis*, a fern with affinities to Dicksoniaceae and previously known only from sediments of Cenomanian age and older, have been identified.

268 MANCHESTER, STEVEN R.

Florida Museum of Natural History, Gainesville, FL 32611-7800

Leaves and fruits of Davidia (Cornales) from the Paleocene of North America

Although now endemic to China, the genus *Davidia* (Nyssaceae) is well represented in the Paleocene of mid-latitude North America. The leaves, for more than a century called *Viburnum antiquum* (Newberry) Hollick, conform to extant

Davidia in the long petioles and laminae with cordate base, pinnipalmate venation, numerous pectinal veins, closely spaced percurrent secondaries, and large, simple, marginal teeth with medial vein insertion. Ovoid, longitudinally ribbed, woody fruits co-occur with the leaves at six localities in the Fort Union Formation of North Dakota, Montana, Wyoming, and Colorado. Although usually preserved as impressions without anatomical detail, silicified fruits from the Almont flora, North Dakota, reveal internal structure diagnostic of *Davidia*. The endocarps have six to eight single-seeded locules, each with an elongate dorsal germination valve; vascular bundles pass through the septae but do not form an axial strand. The fossil fruits are only about half the size of the fruits of living *Davidia involucreta*, but they are otherwise indistinguishable in the morphological and anatomical characters studied. The confirmation of *Davidia* as a common element of North American Paleocene floras, along with the recently described extinct genus *Amersinia*, adds to growing evidence that Cornales occupied a prominent position in the Paleocene vegetation of North America accompanied by Platanaceae, Cercidiphyllaceae, Betulaceae and Juglandaceae.

269 MCCLAIN, AMY M.

Dept. of Botany, University of Florida, Gainesville, FL 32611-7800

Acer section Palmata in the leaf fossil record

Acer section *Palmata*, the group of maple trees that includes the horticulturally important Japanese maple, *Acer palmatum*, has usually been considered to be among the most primitive sections of *Acer*. Species in this section have few bud scales and terminal inflorescences, which place it close to *Dipteronia*, the presumed sister group of the genus. Recent molecular studies using a limited number of taxa also seem to support the basal placement of section *Palmata* in *Acer*. However, the stratigraphic record does not fully support this hypothesis. All modern species in the section *Palmata* occur in eastern Asia, except the single western North American species *Acer circinatum*. *Acer* section *Palmata* can be divided into three series: *Palmata*, *Sinensia*, and *Penninervia*. The latter contains species with entire margined, unlobed leaves, which are not known from the fossil record. Series *Palmata* has distinctive many-lobed leaves with serrate margins. Leaves of this type are apparently lacking in the fossil records of North America and Europe, but are found in Asia beginning in the Miocene. *Acer* series *Palmata* has been suggested to be a derived subset of the paraphyletic series *Sinensia*. Species in the series *Sinensia* have 3- to 7-lobed leaves with serrate or entire margins. However, no fossils of this series have been reported. It is possible that leaves of species in series *Sinensia* may have been misidentified, since they are similar to the leaves of species in many other *Acer* sections. There are species in other sections of *Acer* that date back to the Eocene and perhaps the Paleocene in both North America and Asia. Therefore, the fossil record suggests that the section *Palmata* may be a relatively recent, derived group rather than one of the basal *Acer* sections, and that the dispersal of the section between North America and Asia occurred in the late Tertiary.

270 MCELWAIN, JENNIFER C.

Dept. of Geology, The Field Museum, 1400 S Lake Shore Drive, Chicago, IL 60605

A novel climate-independent method for estimating paleo-elevation from fossil plants

Currently the majority of methods used to estimate paleo-elevation are based on the relationship of temperature with altitude, and for this reason, are inherently climate-sensitive. It remains difficult therefore to decipher the effects of changing elevation and broad scale global climatic change on these paleo-

altimeters, which critically hampers our ability to evaluate or constrain theories relating to tectonic and climatic evolution. The reduction in CO₂ partial pressure with altitude exerts a physiological limitation on plant photosynthesis, which is compensated for, in many species, by an increase in stomatal frequency (density and index) and altered stomatal distribution. This strong inverse relationship between stomatal frequency and atmospheric CO₂ concentration, which has been repeatedly demonstrated experimentally and historically over the past 200 years of anthropogenic CO₂ rise, has been successfully utilized to reconstruct paleo-CO₂ concentrations on timescales of centuries to millennia. The accuracy with which paleo-CO₂ concentrations can be estimated from subfossil and fossil stomata, and the observation that stomatal density and index increase with decreasing CO₂ partial pressure with altitude, now offers the exciting potential of utilizing this relationship as a novel paleo-altimeter. A model for estimating paleo-elevation from fossil stomatal frequency will be presented and the implications of this new method discussed.

271 MYERS, JEFFREY

Dept. of Earth and Physical Sciences, Western Oregon University, Monmouth, OR 97361 myersj@wou.edu

Coastal vegetation from the Middle Eocene of San Diego, California

Impression macrofloras recovered from two localities in the ~43-44 Ma Friars and lower Mission Valley Formations, San Diego County California, were deposited in a fresh or brackish water coastal lagoon during the middle Eocene sea level maximum. The newly recovered assemblages further constrain the timing and magnitude of vegetational and climatic change established from previously known middle Eocene macro and microfloras of the San Diego region. Preliminary identifications of taxa in the newly discovered floras include *Acrostichum*, Polypodiaceae?, *Sabalites*, Flacourtiaceae(?), Juglandaceae (*Pterocarya*?), *Macclintockia*, Myrtaceae, *Nelumbo*(?), *Phytocrene sordida*, *Rhus*, Rhizophoraceae(?), *Ternstroemites*, and numerous unidentified forms. Nearest living relatives and leaf physiognomy of plants in the assemblages suggest dense evergreen broadleaved forest growing under humid paratropical climatic conditions, similar to conditions interpreted from previously described floras of the 45.5 Ma Torrey Sandstone, San Diego. Overlying ~ 42-43 Ma pollen and macroflora assemblages from floodplain and fluvial facies of the Mission Valley Formation are interpreted to record open woodland vegetation growing under seasonally dry climatic conditions. The timing of the development of seasonally dry climate and corresponding vegetational change in the San Diego sequence correlates with comparable events recognized in the Clarno Formation, Central Oregon, and the Gulf Coast sequence of the southeastern US. Because middle Eocene floras from the San Diego sequence co-occur with terrestrial vertebrate faunas and are interbedded with marine macro and microfossil-bearing strata, they provide a precise benchmark for the timing and magnitude of continent-wide climatic and vegetational trends.

272 NIXON, KEVIN C.*, MARIA A. GANDOLFO, AND WILLIAM L. CREPET

L. H. Bailey Hortorium, Dept. of Plant Biology, Cornell University, Ithaca, NY 14853

Origins of Fagaceae: a review of relevant Turonia fossil material from New Jersey

Turonian sediments from New Jersey have produced a wide array of angiosperm floral and fruit remains. These sediments are ca. 90 million years old, and constitute the oldest records for several important angiosperm clades, some very specific (e.g.,

Clusiaceae) and others much more generalized (e.g., a broad array of ericalean taxa). Within this assemblage are several examples of what can be considered to be proto-fagaceous remains, consisting of tricarpellate epigynous bisexual flowers along with similar flowers that appear to lack ovaries and are functionally male. These flowers are found isolated but also sometimes attached to axes with complexes of bracts that are probably homologous to cupules found in modern Fagaceae. However, these cupule-like structures are much more highly branched, and probably less regular in pattern, than are modern fagaceous cupules. In combination, these fossils provide a view of early fagaceous diversity that would not be predicted directly from analysis of extant taxa alone, and reiterate the value of fossil and morphological studies in combination with both morphological and molecular analyses of modern taxa.

273 PHIPPS, CARLIE J.^{1*}, THOMAS N. TAYLOR¹, EDITH L. TAYLOR¹, AND WILLIAM C. REMBER²

¹Dept. of Ecology and Evolutionary Biology and Natural History Museum/Biodiversity Research Center, University of Kansas, Lawrence, KS 66045; ²Dept. of Geology, University of Idaho, Moscow, ID 83844

Fossil fungi from the Miocene of Idaho

The excellent preservation of the Miocene *Clarkia* locality in north central Idaho has provided for many investigations of the floral components, including their chemical and ultrastructural constituents, and reconstructions of the paleoecosystem. Although fungi and fungal spores were noted in several early studies, a concerted examination of the plant fossils suggested that epiphyllous fungi were rare, partially contradicting other evidence of a warm and humid environment. Recent collections suggest that epiphyllous fungi are in fact abundant at the locality. *Phragmothyrites* has been previously noted in the literature; *Stomiopeltites*, *Entopeltacites*, and a number of other fungi, predominantly from the Dothideales, are also present. The thyrothecia of *Phragmothyrites* were found mainly on *Persea*, *Lithocarpus*, *Betula*, and *Magnolia*, and are uniquely characterized by concentric cell divisions. *Stomiopeltites* perithecia are non-radiate and ostiolate, and were found on *Betula*, *Smilax* and *Zeusiphoides*. *Entopeltacites* hyphae were found on leaves of *Persea*. Other fungi present include non-radiate, non-ostiolate cleistothecia and hyphae similar to *Thielavia* on almost all plant genera, and plectenchymatous stromata with similarities to the Capnodiaceae on legume pods. These findings support the warmer interpretations of the environment and indicate that a thriving epiphyllous fungal community was present in this paleoecosystem.

274 PIGG, K. B.^{1*}, M. L. DEVORE², D. L. DILCHER³, AND D. FREILE⁴

¹Dept. of Plant Biology, Arizona State University, Box 871601, Tempe, AZ 85287-1601; ²Dept. of Biological and Environmental Sciences, Georgia College & State University, Milledgeville, GA 31062-0001; ³Florida Museum of Natural History, University of Florida, Gainesville, FL 32611-7800; ⁴Geology, Berry College, Mt. Berry, GA 30149

Fagaceous infructescences from the Oligocene Catahoula Formation of Texas

Sipiny, husk-like infructescences ("frilly fruits") are described from the Oligocene Catahoula Formation from near Huntsville, Texas, and the middle Eocene Claiborne Formation of Tennessee, USA. The fruits are 5.5- 8 mm long and 8 mm wide and have a peduncle up to 10 mm long. They have a central body surrounded by a fibrous flange that becomes thin and paper-like and covered with "fringe" and trichomes toward its periphery. The peduncle also has trichomes of two sizes.

Specimens lack seeds and are fractured to show internal carpel walls, which sometimes have vertical stripes similar to those seen in extant *Fagus*. The general organization of these fruits suggests possible affinities with Fagaceae, particularly *Fagus* or perhaps *Castanea*. Associated with these fruits are leaves of the *Castenophyllum* and *Berryophyllum* types, some of which may represent the same fagaceous plant. The occurrence of these infructescences in both the western Tennessee Claiborne Formation and the eastern Texas Catahoula Formation floras is significant because it suggests that elements of the middle Eocene Claiborne flora may have migrated westward along the Gulf coastal plain. These infructescences have not been reported from Eocene floras of Texas. The Catahoula Formation represents a very different depositional environment than the fine clays deposited in the oxbow lakes of the Claiborne. The Catahoula, which contains large amounts of volcanic ash, was most likely deposited in a tidal flat-paralic marginal marine environment.

275 ROTHWELL, GAR W.^{1*} AND RUTH STOCKEY²

¹Dept. of Environmental and Plant Biology, Ohio University, Athens, OH, 45701; ²Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada

Systematic characters of ovulate Cycadeoidea/Bennettites cones from the Cretaceous of Vancouver and Hornby Islands, British Columbia, Canada

Four fragments of anatomically preserved ovulate cycadeoid cones have been recovered from Upper Cretaceous (Santonian-Campanian) sediments of Vancouver and Hornby Islands, British Columbia, Canada. All of the specimens consist of tightly packed interseminal scales and ovulate sporophylls with terminal ovules. One specimen also preserves remains of a small receptacle. Interseminal scales and ovulate sporophylls are oriented more-or-less parallel to one another. Ovules are distinctly stellate proximal to the tubular micropyle, and the sarcotesta consists of longitudinally oriented tubular cells that are attached to the sclerotesta only at the apex. The vascular strand below the base of each ovule is highly contorted in a pattern characteristic of contractile tissue in some living plants, and this provides evidence for some post-pollination facets of reproductive biology. These cones are quite similar to *Bennettites gibsonianus* Carruthers, *Bennettites morierei* (Saporta and Marion) Lignier, *Bennettites albianus* Stopes, and several species of ovulate *Cycadeoidea* as described by Wieland. The superb preservation of these and other cones from Vancouver Island demonstrates that Cycadeoidales/Bennettitales lack a cupule, have radial seeds, have nucellar vascular tissue (but no integumentary tracheids), and that no pollen chamber is produced. Together with a *Williamsonia* preserved in the same deposits, these specimens also provide a clear set of contrasting systematic characters for differentiating between isolated cones of the Williamsoniaceae and Cycadeoidaceae.

276 SCHECKLER, STEPHEN E.^{1*}, BRIGITTE MEYER-BERTHAUD², AND JEAN GALTIER²

¹Dept. of Biology, Virginia Polytechnic Institute & State University, Blacksburg, VA 24061-0406; ²Laboratoire de Paleobotanique, Universite Montpellier 2, Place Bataillon, 34095 Montpellier cedex 5, France

Secondary phloem of the Late Devonian progymnosperm tree Archaeopteris

Well preserved secondary phloem was found in a trunk-sized axis (*Callixylon trifilievii/henkei*-type) and a small branch (*C. trifilievii/zalesskyi*-type) of *Archaeopteris* from Late Devonian beds of Morocco and New York (early Famennian marine beds near Jebel El Mrakib, Morocco, and basal Frasnian

Oneonta Fm. from Ashland, NY). Previous reports of bark in *Callixylon* (Arnold 1929, 1930; Lemoigne, Lurina, and Snigirevskaya 1983) did not clearly identify secondary phloem so that the existence of this tissue in *Archaeopteris* was uncertain, but described as simple. Our new material shows unequivocally that *Archaeopteris* has complex secondary phloem and bifacial vascular cambium (VC) similar to those of aneurophytes where these tissues are better known. The small (1.5 cm diam) branch has intact VC and a thin layer of secondary phloem. The large (11 cm diam) branch or trunk lacks preserved VC but has a thick zone (7 mm) of secondary phloem with conspicuous rays and concentric tangential bands of fibers and parenchymatous cells. Short radial files of fibers are abundant in the innermost (0.5 mm) youngest phloem. Both axes show that phloem rays have similar widths and heights as xylem rays, have similar but larger procumbent cells, and lack ray tracheids. Clusters of sclereid-like (tanniniferous?) cells and elongate sieve cell-like elements occur amongst the axial parenchyma. Expansion adjustment of older tissues is by enlargement of axial parenchyma cells, preferentially in the radial direction, so that concentric fiber bands are spaced farther apart. Secondary phloem of *Archaeopteris* is thus histologically similar to that of aneurophytes, differing only by fibers occurring mostly in concentric tangential bands in older external phloem. Bifacial VC of *Archaeopteris* is also organized like that of aneurophytes. Despite differences of vegetative and reproductive morphology, the similar secondary tissues and VC of *Archaeopteris* and aneurophytes support interpreting them as closely related basal lignophyte groups.

277 SMITH, SELENA Y.* AND RUTH A. STOCKEY

Dept. of Biological Sciences, University of Alberta, Edmonton Alberta, T6G 2E9 Canada

Further investigations of Keratosperma allenbyensis (Araceae) from the Middle Eocene Princeton chert (Allenby Formation) of British Columbia

Keratosperma allenbyensis seeds from the Middle Eocene Allenby Formation near Princeton, British Columbia were reexamined from over 200 new specimens. Anatomical characters have shown their affinities to seeds of Araceae, Subfamily Lasioidae. The seeds were reexamined using the cellulose acetate peel technique modified for hydrofluoric acid. Seeds are campylotropous with three rows of spiny ridges on the integument. Idioblasts that contained raphides are found scattered in the outer integument. The micropylar end of the seed shows an epistase and a thin micropylar cover that was easily displaced at the time of germination. At the chalazal end of the seed a prominent hypostase and podium are present. Endosperm tissue and monocotyledonary embryos are present in some but in most specimens these tissues have been invaded by fungi. Anatomical comparisons with the extant lasioids *Cyrtosperma ferox* Linden et N. E. Br. and *Urospatha sagittifolia* (Rods.) Schott were made using paraffin and cryo embedding and sectioning techniques. A reconstruction of the fossil seed was made from serial sections allowing the fossils to be compared to extant taxa based on external morphology. Affinities of *Keratosperma* were originally believed to be with *Cyrtosperma* from tropical southeast Asia. While shape is most similar to seeds of *Urospatha* from Central and South America, integumentary zones are distinctly different making these seeds unique. *Keratosperma allenbyensis* are the oldest known lasioid seeds in the fossil record and represent an extinct araceous lasioid taxon.

278 SMITH, UNA R.

Los Alamos National Laboratory, MS K710, Los Alamos, NM 8754

Systematic analysis of fossil fruits placed in the eurousid II clade

Several orders and families of the angiosperm clade eurousid II include well-documented fossil fruits. Published descriptions of these fossil fruits are analyzed to test whether the fruits do in fact belong where they have been placed; and, if so, examine how selected characters of these fruits compare with those which would have been inferred from current phylogenies of eurousid II. Relevant fossil taxa include *Dressiantha* (Capparales), *Florissantia* (Malvales), *Sterculiocarpus coloradensis* (Sterculiaceae), *Pteleaearpum* (Tiliaceae, *Craigia*), *Daberocarpon* (Malvaceae), *Landeenia* (Sapindales), *Sapindaceacarpum* and *Wehrwolfia* (Sapindaceae), and *Turpinia* (Staphyleaceae).

279 SORIA, AUDE^{1*}, BRIGITTE MEYER-BERTHAUD¹, AND STEPHEN E. SCHECKLER²

¹Paleobotanique, Universite Montpellier 2, Place Bataillon, 34095 Montpellier cedex 5, France; ²Virginia Polytechnic Institute and State University, Blacksburg, VA 24061

Development and architecture of a gondwanan representative of the late Devonian genus Pietzschia (Cladoxylopsida)

Cladoxylopsida, the most ancient group of ferns s. l. (late Early Devonian Early Carboniferous) exhibited a variety of growth habit from small forms to trees and possibly lianas. Distinctive characters of these plants include a complex cauline anatomy and the possession of helically arranged leaf-like organs. Architectural traits and growth habit of a new cladoxylolean plant affiliated to the enigmatic genus *Pietzschia* are reconstructed. Analysis is based on a 40 cm long preserved proximal portion of stem from the Late Devonian (Famennian) of south-eastern Morocco. Anatomically, the axis is characterized by a primary vascular system comprising numerous xylem plates surrounding a large aerenchymatous pith, sclerenchymatous plates alternating with the xylem plates, a sclerenchymatous outer cortex and no secondary tissue. Large, bilaterally symmetrical decurrent bases of lateral organs ensheath the stem. They are supplied by 8-12 vascular traces. Adventitious roots occur at the stem base. The plant is reconstructed as a small, erect, possibly monocaulous form. Lateral organs are arranged according to a near-Fibonacci type of organotaxis and separated by alternating short and long internodes. This specimen represents the first cladoxylopid occurrence in Africa. It provides a basis for reconstructing a younger member than those reported previously. It will help to better circumscribe vegetative characters of cladoxylopsids used in analysis of fern phylogeny.

280 STOCKEY, RUTH^{1*} AND GAR W. ROTHWELL²

¹Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada; ²Dept. of Environmental and Plant Biology, Ohio University, Athens, OH 45701

An ovulate Williamsonia cone from the Upper Cretaceous of western North America

One anatomically preserved ovulate cone similar to those of the cycadeoidalean/bennettitalean genus *Williamsonia* has been recovered from the Upper Cretaceous (Santonian) sediments of Vancouver Island, British Columbia, Canada. This well preserved and nearly complete specimen consists of a receptacle that bears tightly packed interseminal scales and ovulate sporophylls with terminal ovules. Sporophylls and interseminal scales extend from the receptacle around an arch of more than 300 degrees. Interseminal scales do not show an epidermis except at

the apex, and the boundaries between adjacent interseminal scales are not discernible. In cross sections the ovules are round to elliptical at all levels, and the sarcotesta consists of small radial projections. There is no cupule. The vascularized nucellus is attached to the integument only at the chalaza, and it terminates apically in a cellular projection that fits tightly into the micropylar canal. No pollen chamber is produced. Several ovules show highly branched structures that are comparable to the pollen tubes of living araucarian conifers. Cellular megagametophytes and immature embryos demonstrate that archegonia are positioned laterally, in the apical region of the seed cavity. The superb preservation of these specimens allows for clarification of several systematic characters, and for the interpretation of pollination biology.

281 STOCKEY, RUTH^{1*} AND GAR W. ROTHWELL²

¹Dept. of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada; ²Dept. of Environmental and Plant Biology, Ohio University, Athens, OH 45701

Permineralized cycad seeds from the Jurassic of British Columbia, Canada

Thirty three large seeds have been studied from cycad remains from Jurassic sediments of South Balch Island (Queen Charlotte Islands) on the west coast of Canada. Seventeen of the specimens range up to 6 cm long and 5 cm in diameter, and conform to *Cycadeocarpus columbianus* Dawson. The integument of these seeds consists of a thick sarcotesta that surrounds a spongy zone of the integument that is similar to the specialized flotation anatomy associated with water dispersal in some living species of *Cycas*. However, radial symmetry of these specimens is unlike the bilateral seeds produced by living species of *Cycas*. These specimens also display a ring of small teeth and associated oval channels surrounding the micropyle. These form a structure that is similar to the coronula, a germination mechanism common to many living cycad species. Five additional seed specimens compare more favorably with living species of *Cycas*. These seeds range to 5 cm long and 4 cm wide and are more-or-less flattened in cross sections. A thick sarcotesta surrounds the stony sclerotesta, with two longitudinally disposed sclerotestal ribs that extend from near the micropyle to the chalaza. The nucellus is confluent with the integument below the level of the pollen chamber. These specimens display unique combinations of characters, demonstrating both modern dispersal and germination mechanisms and previously unknown diversity among Mesozoic cycads of North America.

282 TAYLOR, THOMAS^{1*}, HAGEN HASS², HANS KERP², AND MICHAEL KRINGS²

¹Dept. of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66045; ²Geologische-Paläontologische Institut und Museum, Westfälische Wilhelms-Universität, Münster, Germany

Ascomycetes in the Rhynie chert

In recent years studies of the Rhynie chert have contributed appreciably to our understanding of the fungi that existed during the Lower Devonian. One of the recently documented groups is the ascomycetes, the largest group of true fungi with nearly two thousand genera. The principal morphological feature of ascomycetes is the sac-like ascus in which sexual ascospores are produced. Sections of *Asteroxylon* aerial stems and rhizomes have been discovered that contain numerous perithecia that appear just below the epidermis, often associated with a stomatal complex. In a few specimens perithecia occur at the base of enations. Perithecia are globose-spherical and possess a slightly elongate neck. The ostiole is lined with periphyses. Extending from a two-layered hymenium are elongate paraphyses and uniloculate asci. Ascospores may be uni-multicelled, elongate, and demonstrate ger-