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 multifaceted 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 binonal 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 “file list,” which already included the Rhynie chert, Linnaeus’ garden, Sequoiodendron giganteum, the Royal Botanic Gardens at Kew, and Stigmata, 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. Phylogenetics has a major role to play in genomics research; phylogenetics exploits the uses 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 accomplished 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 amph_
diploids can be resynthesized by crossing diploids and treating with colchicine, and our molecular analyses of early generation progeny suggest that polyploid genomes can change rapidly after formation. Variation in flowering time also has evolved quickly among the progeny of resynthesized B. rapus polyploids, and this variation is inheritable in self- and out-cross progeny. 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 and 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 retroelements 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 Cladina rangiferina and Calypogeia sp., 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, Syrhopododon involutus

Heterochronous 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 heterochronous changes are tied to changes in reproductive strategies remains unknown. Comparative developmental studies on plants are needed to improve our understanding of how heterochronous 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 Syrhopododon involutus (Calymeraceae) 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 paedomorphosis may be responsible for this unusual leaf form. This study uses the S. involutus complex and phylogenetic comparative methods to understand the relationship between heterochronous 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 it’s 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 Cetrariaeaceae, Hypnodendraceae, Pilotheridiaceae, 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 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.
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 decomposing microorganisms, 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?

Even 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 from the surface. Of course surface appearance is important, but, at microscopic level, a serious damage due to the lichens from the surface.}

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. Chasmendolithic cocoid 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. Fitting organisms on are common on man-made marble monuments in more mesic areas of Europe.

16 GINELL, WILLIAM S.1* AND RAKESH KUMAR1,2
1Getty Conservation Institute, 1200 Getty Center Drive, Los Angeles CA 90049; 2OptronX 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 Monument, 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 PIERVITTO, 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 occur when lichen-substratum relationships are disturbed or when lichens are present 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 research 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 quasi-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 structures (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 Calopla ca 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 Sarcogyn pruinosa and Stauropothele catalpata 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 subsersive 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 proven 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 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 conservators. It is imperative that while we are devoted to preserving these fragile remains of the past, we do not allow them to become further degraded. 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 KONRAT2*, AND PETER J. DE LANGE3
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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.

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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.

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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 perisepore. 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 perisepore. These characters are consistent with Nordin’s concept of Diplotomma s. str. even though the perisepore is only moderately thickened. However, B. subalbula has one-septate ascospores and only a proper, not a thalline exciple.

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

Molecular phylogenetic analyses of the family Mniaceae (including the Pohlioidae 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 Schizymenium are derived from taxa in Pohlia sect. Pohlia. The propaguliferous sp. of Pohlia sects. Cacodon and Nyhomiella form a well supported clade to the exclusion of non-propaguliferous species. In addition, Epipetrygium is derived from a mnioidyoid ancestor. Despite extensive data sampling among diverse taxa of the Mniaceae, a robust phylogenetic hypothesis of the family remains elusive; monophyly of the Pohlioidae cannot be statistically rejected by any dataset. Nevertheless, optimal trees under ML, MP, and Bayesian inferences indicate that the Pohlioidae is probably paraphyletic and that the traditional Mniaceae taxa are derived from a polyploid 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.

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

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.

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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.
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 glacion for up to 1350 yr and could be detected in specimens that had been dry for as long as 4 yr. Umbilicaria cylindrica, U. krasheninnikovii 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.

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.

Multigene phylogenetic reconstruction of the family Orthotrichaceae (Bryophyta)

The cosmopolitan family Orthotrichaceae comprise 27 genera arranged into subfamilies. The Orthotrichoidae comprises primarily acrocarpous taxa distributed in temperate parts of the world, whereas the Macromitrioidae 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 LEAF1 gene) are currently underway to test these hypotheses. These data will aid in addressing the hypothesis inferred from morphological and chloroplast suggesting that the genus Bryomaltaea (Orthotrichoideae, Zygodontae) is either of hybrid origin or represents the most basal lineage within the family.

Systematic inferences in Bryoxiphium based on morphological and molecular characters

The Bryoxiphioideae 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 haplolepideous 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 haplolepideous mosses (Dicranidaceae) or diplolepideous opposite mosses (Funariidaceae). 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. madeirensis, 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.

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 Metzgeridean liverworts, such as
Symphyogyna 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 Jensonia, Hattorianthus, Cavicularia, and Calycularia. Studies with optical and electron microscopy show that both the rhizome and the thallus midrib of Jensonia 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 Jensonia are, in fact, structurally very similar to those in Symphyogyna. 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.

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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.

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Genetic differentiation among populations of the widespread lichenicolous fungus Marchandiomycetes corallinus

The lichenicolous basidiomycete fungus Marchandiomycetes 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.

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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 thallus 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 unim-
portant within patches, spores provide the primary means of recol-
onizing 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 empir-
ical work is needed to enable linkage of within-patch dynamics to
represent the metapopulation.

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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 Rhizogoni-
aceae plus Aulacomnium and Calomnion are the sister
group or nearsister group to pleurocarpous mosses, which with
6600 species is the most diverse clade of extant mosses. The evi-
dence suggests that the traditional genera of Rhizogoniaceae are
a paraphyletic group, consisting of a minimum of 3 clades. Aulocom-
nium is a monophyletic group, and its sister lineage includes Mesos-
chaete. The pleurocarps are comprised of a relatively small "acopi-
lalean" clade and a large "hypnalean" clade (including Hookeriaria,
Hyponales and Leucodontales), a fundamental division that is con-
sistent 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 Calomnion - have a Gondwanan distribution
in Oceania, where most rhizogonean species have a sub-
strate preference for tree ferns. Altogether this suggests an origin of
pleurocarps within Oceania from an epiphytic ancestor during pre-
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.**, JOHN A. WHEELER, BRENT
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A bryophyte rehydrin trackable marker for the
evolution of desiccation tolerance
T he 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 analy-
ses 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
terns, 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 lev-
els in response to desiccation that are only used upon rehydration.
This gene has physical properties similar to the stress induced dehy-
drin 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 examplar species identified by Deep Green in their
synthesis of a phylogenetic tree for all land plants.

40 PETERSON, ERIC B.
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Tour of a lichenological black-hole (Nevada)
N evada 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 staring 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!

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Lichen communities, pollution signals, and an issue of
scale
T he 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 con-
cern 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 qual-
ity. When we began analyzing the data, we had difficulty correlat-
ing 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.
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*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.

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*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 *Arecia 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 *Arecia catechu*, followed by *Corypha elata* and the least was seen in *Cocos nucifera*. The architecte 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.

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*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 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 truncations.

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, laciniate perichaetium. The pseudoperiant, which may be more aply 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 biserial 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.

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*The systematic status of Pellia X appalachiana*

The genus *Pellia* 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.

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Coniocybe gracilescens and Sphinctrinus 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 *Calcium pallidellum* had been transferred by Fink to the nonlichenized genus Calciella, 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 *Chaeotheca hispidula* with which it is growing in the type collection; *Calcium pallidellum* is not a Calcium or a Calciella, but a Sphinctrinus with 2-celled spores. Wondering how common Sphinctrinus 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.
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. capitillilium 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. mole, 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 Rigidgida, for example, are relatively distinct, as are the two species of Rigidgida (S. compactum and S. strictum). Molecular approaches to species delineation have not reached maturity yet, but appear very promising.

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 biomonitors of air quality. However, direct correlations between emission sources and pollutant 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 (R2=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 (R2=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 element ratios in accurately predicting elevated element concentrations in lichen thalli and making more effective decisions relative to possible sources of pollutant elements.

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. Laminar filaments tended to remain chlorophylline 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 refraction population cores; and (ii) the surface of the population is cleared of ramets and regrowth monitored.

Population structure and patterns of island radiation in the paleotropic 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 phylogenetics. 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.

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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 paroicous 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. ravenelli, P. acuminatum, P. subulatum, P. papillosum, P. longirostre, P. amollii, P. curvatum, P. costeisi, and P. pappeanum (9 species) while section Sclerastomonum includes P. nervosum, the designated type species of the section, P. robinsonii, P. sullivantii, P. mexicanum, P. laixete, P. subnervosum, P. andinum, P. venezuelanum, P. valetonii, P. dentlicatum, P. sinensis, and P. holldingi (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,* 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 eubryalene 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 rhizogonaceous 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 rhizogonaceous 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
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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 intraspecific 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. loveolata 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
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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°07'06" N, 159°02'37" 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, SHARON1*, CLIFFORD M. WETMORE2, KATHERINE GLEW3, AND JAMES P. BENNETT4

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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

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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) synonymsizes 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, exserted 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.

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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. BARHOLOMEW-BEGAN1, AND TATSUWO FURUKI2

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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 multilayered 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*
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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 on 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. Pseudovemia intensa (Nyl.) Hale and Vulpicipa pinastri (Scop.) I.-E. Mattsson & M.J. Lai. The lichens of the planted pine forests have are less diverse when compared to the naturally-occuring pine forests, but a few lichen species are currently known only from these man-made systems.

60 NOBLE, SARAH MARIE* AND DAVID K. SMITH
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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 bryoflora study. 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 bryoflora 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 phytoecographic 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.
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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 streamside 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
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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, Java Script, 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*, THOMAS H. NASH1, AND JACK A. ELIX*
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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 (ovic acid, 4-demethylnotatic acid, hydropunctaric acid, and eumitrin A1).

64 SMAW, SHERCODA*, LAFAYETTE FREDERICK, AND RAYMOND L. PETERSEN
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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., Oscillatoria sp., Phormidium sp., Hyrococlem homeotrichum, Anabaena sp. Anbeana cirinalis, Synecychocysitiss aquatilis, Shizothrix sp. Among the eukaryotic algae present are: Klebsomium sp. Ulothurx 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 MCLETCHIE
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Testing for sex-specific life history traits under field conditions in a dioecious liverwort

In the liverwort Marchantia inlexa, 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. inlexa 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. inlexa plants. Twenty plants of each sex were randomly planted per plot. Canopy photos (180 degrees) 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) 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 differences 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
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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
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Sieve-element plastids and evolution of monocotyledons with emphasis on Melanthiaceae sensu lato and Aristolochiaceae-Asaroidae, 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-Asaroidae) 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 Japonolinion osense (Nartheciaceae-Petrosavieae / Petrosaviaceae), Harpocalis illava, Plea tenuioliola, three Tofieldia species (all: Nartheciaceae-Tofieldioidae / Tofieldiaceae), and of Narthecium ossitragum. However, Aletris glabra and Lophiota americana (Nartheciaceae-Narthaceoidae) 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 Japanolirion) or ‘loose’ (in Harperocallis, Pleea, and Toliellia). 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, -P2cs 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.
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On the phylogenetic position of the New Caledonian endemic families Strasburgeriaceae, Oncocaphaceae, and Paracyphiaceae: 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, Oncocaphaceae, and Paracyphiaceae. They concluded that Strasburgeria, Oncocapha, and Paracyphia 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, phylogenes for eudicots based on multiple gene data sets firmly place Oncocaphaceae within Garryales, Paracyphiaceae within Dipsacales, and Strasburgeriaceae sister to berberidaceae 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.
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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.

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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, Connnaraceae, Cunoniaceae, Actinidiaceae, Clothraceae, Styracaceae, Aristolochiaceae, and smaller, less well-known families of tropical plants, such as the Bonnetiaceae, Phylleneaceae, Medusagnaceae, 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.
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Comparative anatomy and specialization of leaf structures in Arecaceae and Acoraceae

Leaf and petiole anatomy were investigated for nearly 400 samples representing 105 out of 106 genera of Arecaceae. The study included four duckweed genera (as Arecaceae) 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 Arecaceae. It varies from existing as peripheral bands in petioles and midribs in subfamilies Pothoideae and Pholidendroidae, to independent strands aligned with vascular bundles in the subfamily Aroidae. 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.
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 limbricate 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.

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 Illes), based mainly on molecular data. Asparagales comprise a ‘higher asparagoid’ clade and a ‘lower asparagoid’ grade, which includes some small families such as Tecomataceae, the monogenic Eurasian family Isotetaceae, 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 hypogynous 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.

Since the XVI century basic anatomical features of Cactoideae 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 Cactaeae, Echinocereeae and Pachycereeae, were generated. Analysis revealed that most dermal characters like uni-multiserate 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.

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.
RELAXED STRUCTURAL CONSTRAINTS IN UTRICULARIA (LENTIBULARIACEAE): A POSSIBLE BASIS IN ONE OR FEW GENES REGULATING POLAR AXIN TRANSPORT

Loyd (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 systematically 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 inflated, anisophyllous stems with 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 disruption of the 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 Gentiana versus their sister clade, Pingucula, among seven loci spanning all three genomic compartments (see abstract by Jobson and Albert, Botany 2001).

STIPULES AND SHOOT DEVELOPMENT OF EXBUCKLANDIA POPULNEA

Leaves of Exbucklandia populnea (Hamamelidaceae) bear a large, leathery, persistent structure at the base of their petioles 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.
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 panicooid '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.

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 Acoraneae 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 and other morphological characters to cot/dicot relationships undermines the presumed significance of species of paleoherbs and the phylogenetic uncertainty of monodons.

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 successive ontogenetic stages of columns. An important question is whether the incumbent anther in Vanillioideae 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 Vanillioideae, 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.

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

Albizia lebbeck Benth. is known as the East Indian Walnut in Europe. A. lebbeck 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 the 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.*+, S. A. NICHOL1, J. A. DOYLE1, AND T. L. ROST1
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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.

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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.

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Inflorescence development and phylogenetic relationships of the genus Ixophorus

The genus Ixophorus (Poaceae: Alloatherae) 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.

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

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As originally observed and a critical literature survey, vestured pits are found in approximately 48 families according to the APG-system, including 14 families in which vessels 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 vessels, 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 euasterids I (Zygocephylaceae, Fabales, very few Rosales, Malpighiales), euasterids 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 Malpighiales, Polygonaceae, Brassicaeae, 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.

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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 vascular 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.

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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.

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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 primordium 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 gyroecial 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 gyroecial 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.
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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*
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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 supplemented 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-Benzylaminopurine (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
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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.

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

Polemoniaceae 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 Linanthus. 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 Polemoniaceae, with emphasis on Linanthus and Leptosiphon, and to examine the evolution of those characters using the phylogenetic model provided by molecular data. With few exceptions, species in Polemoniaceae exhibit bifacially distributed stomata, leaf bundle sheaths composed of large, non-photosynthetic cells, and some degree of stem secondary growth. Less conserved characters, informative intergenerically, include the presence of an abaxial mass of fibers in the central leaf vein (characteristic of Linanthus 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 (Linanthus). 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 Linanthus of four species previously assigned to Gillia but transferred to Linanthus based on molecular data.

96 MIKESSELL, JAN E.
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Comparison of gametophyte and sporophyte development in ragweed species

Variation in sex expression in ragweed taxa occurs to the extent that ordinarily monoeccious species can exhibit dioecy. Gametophyte and sporophyte development was analyzed in two annual ragweed species, Ambrosia artenmisifolia (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 discernible 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
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Cytoskeletal patterns in endosperm development of Coronopus didymus (Brassicaceae)

Study of microtubules and F-actin during endosperm development revealed distinct developmental domains in the microsporal 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.*, F. MOLINA-FREANER*, C. TINOCO-OJANGUREN*, AND D. J. PAOLILIO, JR.*
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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.*, GAMAL EL-GHAZALY, AND RANESSA L. COOPER 1
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 monogenic family of aquatic angiosperms comprising approximately 50 terrestrial, amphibious, and obligately submerged species. Callitrichaceae 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 submerged species Callitrichaceae 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, development, informational data 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.

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

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 it’s subtended leaf primordium. Within each disk of insertion, concentric, successive waves of isolated procambial strands are generated by a
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. Corylus cornuta (hazelnut) and Xerophyllum tenax (bear grass) 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.

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

Anatomically preserved specimens of Cycadeoidae/ 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, from Upper Cretaceous (Santonian-Campanian) deposits of west coast British Columbia, Canada are permineralized with calcite, and indicate 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.

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

Heterosporous ferns are a morphologically lineage comprising five extant genera that fall into two clades: Marsileaceae, including Marsilea, Pilularia and Regnellidium; and Salviniaeaceae, including Azolla and Salvinia. The Marsileaceae have an amphibious habit, whereas the Salviniaeaceae 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 Salviniaeaceae, 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 megasporangia, an extraordinary megasporangium 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 Salviniaeaceae 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 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.

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

calum 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.

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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 nuclei display a 4C DNA concentration after division and up to 84 h after fertilization. These data provide evidence for gamete fusion at 2C in flowering plants is formed on the upper side and exerts a tensile compression opposite. 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.

107 TOMLINSON, P. BARRY
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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 extraxylary, 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-

108 VON BALTHAZAR, MARIA* and PETER K. ENDRESS
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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 dimers 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
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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
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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 gametocyte (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.

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he ABC model of floral organ development proposes combinatorial interaction of A, B, and C class genes whereby these three classes of genes specify 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.
to chlorophyllide 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*
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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 germination 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 surfaces; 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 nigosin 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 alcan 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
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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*, NABARUN GHOSH, A. CHATTERJEE, AND DON W. SMITH*
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Effect of Arsenic 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⁻ and 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 defoliants 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 10⁻⁰²⁰⁰⁰⁰) 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.

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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 stamens 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 primordium.

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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.

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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. lacinatum, which is wide spread, and S.albilorum, endemic to Texas, were utilized for this study. S. lacinatum has large leaves, some over two feet long each, which are very laciniate and lobed. S.albilorum, which is theorized to have evolved from S. lacinatum, is smaller and also has laciniate 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. lacinatum, S. albilorum and putative hybrid populations, PCA analysis revealed delineation between the two species with the putative hybrid intermediate.

120 STRITTmatter, LARA* and Vivian Negron-Ortiz
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Cnosa coralllicola (Cactaceae): a sexually dimorphic species with only one morph remaining?

Cnosa Lem., subfamily Opuntioideae, comprises nine species endemic to the Caribbean region. Within this genus, C. coralllicola 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. coralllicola had a cryptically dioecious system, which we have also found in other Cnosa species. The female sexual morph is, apparently, extinct.

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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. plumaginifolia 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. plumaginifolia 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.
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.

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.

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.
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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
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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 heterophily 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.

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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

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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., 30/15°C) stratification for dormancy-break and a low (e.g., 15/6°C) temperature regime for nondormant seeds to germinate. In contrast, seeds of A. tomentosa and A. macrophylla require cold (5°C) stratification for dormancy-break, but nondormant seeds will germinate over a wide range of temperature regimes (i.e., 15/6-35/20°C). 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 rainforest-climate species, A. tomentosa and A. macrophylla, thus supporting Wolfe’s view on physiological changes in a lineage.

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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 homogamous, 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.

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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 oviposition 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
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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-
mediated 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 ailanthone production, may be responsible for these trends.

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

Polyplody 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.

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

Purshia 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 individuals 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.

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

Seeds (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 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.

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 (l) 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 l > 1 have greater proportional contribution of growth and reproduction elasticities to population growth rate.

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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.v, JERRY M. BASKINv*, AND CAROL C. BASKINv*
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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).

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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, Trebouxioiphyceae, 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 Trebouxioiphyceae, 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.

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Ecological aspects of Vaccinium varingiaeolium growing in a stressed volcanic environment

Vaccinium varingiaeolium (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 substrates. It is also a pioneer species on ash or volcanic soil of crater ridges. We compared several morphological and ecophysiological aspects of V. varingiaeolium 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. varingiaeolium 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. variegata-folium may not be affected by stress. We are currently conducting further studies to understand allocation and life history patterns in this species.

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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.
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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_E, and H_O), with variation highest in the larger woodlot populations (e.g., P = 0.88, H_E = 0.39) and lowest in the smallest woodlots (P = 0.25, H_E = 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., SHAWN K.Y. LUM2*, RAYMUND CHAN3, AND LUAN KENG WANG4
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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 antplant 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.

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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 ponderbbery 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 ponderbbery populations and to changes in hydrology. Introduction of plants to new areas will be necessary if the species is to recover.

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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 sandhill 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.

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

**E**xtracting 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 effects of alternative harvest schedules, and livestock browsing, on demography of Chamaedorea radicallis 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 λ=1.00, while the control was projected to grow with λ=1.066. 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 40 cm long, 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.

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

**V**irginia 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 outlets 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.

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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.

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Functional physiology of Amborella and ‘ITA’ plants

Recent phylogenetic studies have placed the extant lineages Amborella, Nymphaeales, and a clade including, Illiciales, Trimeniaceae, and Austrobaileyaceae (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.

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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.

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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 grains 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.

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

P. 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-
Ecological life cycle and phenology of biomass allocation in Cryptotaenia canadensis

Cryptotaenia 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.

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 clearcutting 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.

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

Field-collected individuals of Jacquemontia curtisii (Convolvulaceae), a perennial herb, were cultivated in a greenhouse to control conditions for hand-pollinations and floral measurements. This work was a 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.

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

Rumex 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+XY+YY 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.

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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 suggest 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 sibships inside the ovary. The lack of incompatibility among sibships and backcrosses, as well as the complete lack of selling 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 Goodvillie (1997) found sporophytic SI with linear dominance in Linanthus parviflorus. The SI system for Polemoniaceae appears to be more complex than previously thought.

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Evolution of floral specificity in a group of andrenid bees

Callandrena 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.

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

S tudying 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 s.n. 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.

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. Chatahoo, 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.

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.

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.
Viola 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 (BL). 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 BL 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(1,314) = 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.
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 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. aegyptii* larvae when reared in pitcher-plant liquid in the presence and absence of the larvae of the pitcher-plant midge, *Metriocnemus knabii* (Coq.) and found that the percent survivorship for *W. smithii* was high (90%) whether *M. knabii* larvae were present or absent. We also found that *Ae. aegyptii* larval survivorship was 82% when *M. knabii* larvae were absent and less than 2% when present in the culture plates. Based on these findings, we suggest that *M. knabii* 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. knabii* attacking and devouring *Aedes* and *Anopheles* larvae, while at the same time leaving *W. smithii* unharmed. Possibly the long setae of the *W. smithii* larva may prevent access to its body wall by the mandibles of the *M. knabii* larva. Application of these findings to other mosquito-plant associations is suggested.

**170** **PIGLIucci, Massimo*** and **Johanna Schmitt**

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**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.*** and **Scott J. Meiners**

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**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.***+, **Erica Corbett**, **Dianna L. Bannister**, **Jennifer Marble**,**†**, **Ian B. Maness**, and **Jonathan V. Edelson**

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**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.
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 519 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 maiden cane (Panicum hemitomon) and beakrush (Rhyynchospora 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.

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 quantified 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 (Wilks' Lambda=0.1 F=1.3 p<0.05) and sex (Wilks' 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 sex and time (Wilks' Lambda=0.9 F=1.6 p<0.01), genotype (Wilks' Lambda=0.2 F=1.3 p<0.0001) and the combination of light and sex (Wilks' 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).

Photosynthetic pathways and ecology of Indian grasses

The occurrence of C4 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 PEPC-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 poosids, 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 PEPC-CK subtypes occur in 2:1:1 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 PEPC-CK species are common in wetlands. These findings are analyzed in relation to the origin of Indian grass flora, phyogeography and seasonal availability of fodder for grazing animals.
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 auto- nous selfing in these populations. There was no difference in the multifocus estimate of selfing rate, using PCM 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.

Parasitic choice of host individuals in a seemingly homogeneous environment

It has been postulated that differences in environmental conditions among host 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 tissue 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.

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.

Management and reintroduction efforts of Stylosma pickeringii (Torr.) Gray (Patterson bindweed), an Illinois-endangered sand prairie species

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

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

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 sire success, offspring seed weight, amount of pollen produced, and pollen germination ability.

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

H. parviflora Bartr. var. parviflora occurs primarily in southeastern North America and H. cylindrica Doug. 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 phenotype. 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 15/6-25/10°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.

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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.

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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 none 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 fragans (48.4%) and Liatris ohiangerae (47.3%), are intermediate resprouters; four species (Asclepias curtissii, Carateria heterophylla, Helianthemum nashi and Sisyrinchium xerophyllum) are weak resprouters (>10% but Paronychia chartacea ssp. chartacea, Polygonella myriophylla, P. robusta and Schizachyrium nivenum) 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 deckerti, Cnidacolus stimulosus, Stipulicida secta and Stylosma abidita). 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.
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 – upper produced ten times more seed than the South Bowl, and sixty times more seed than the North Bowl – lower. 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 – 3240 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.

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 U.S. 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.

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. TWINSPLAN 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.

Population ecology of the endangered Buxus vahlii Ballon (Buxaceae)

Buxus vahlii Ballon 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.
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.

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

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.

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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.

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

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.

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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.
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 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 genotypes could be either infected or not infected. It is important to note that isozymes often do not display adequate levels of variation to resolve genetic identities in clonal populations (Cruzan 1998, Escaravage 1998, and Waycott 1998). Whereas isozyme 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.

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 northwest 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.

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.

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). Theses 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.
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.

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.

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

Spatial-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 foliar chemistry may influence preference-performance in moths of the genus Phyllonorycter (Lepidoptera: Gracillariidae), a *Q. gambelii* associated leaf-mining herbivore. Larval performance is currently being investigated.

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.
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205 **DA SILVA, JAIME A.T.**  
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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 also 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 saito, the tea ceremony and in the funeral ceremony, representing a symbol of peace. Certain chrysanthemums are edible garbage/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/litorti’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**  
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Agrobiodiversity of Armenia  

Human life is absolutely impossible without plants. 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, lenses, 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- and berry plants. According to 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.

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

Phoenix 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. pendunculata, 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**  
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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 rather intensive way. In the past few years the population intensively harvests and sells 28 species of edible plants, various farms 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**

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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**

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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 neyrautii. In order to analyze early molecular changes affecting natural hybrid and allopolyploid species, and their role in adaptation and stabilization of a new species, molecular 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 bottlenecks at the time of the species formation, and structural stasis of the homeologue subgenomes.

**211**

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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 adaptations, 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.

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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-atpB) 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 transspecific 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.

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Genetic differentiation and adaptation in the mangrove Avicennia germinans L.

The mangrove Avicennia germinans L. is found along tropical and subtropical 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.

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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 alloploids 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 nuclear dominance is well-documented from model alloploids. Ribosomal genes are differentially expressed in at least some Glycine alloploids, both in cases where there are great differences in copy number between homoeologous repeats and where homoeologous copy number is approximately equal. The chloroplast-encoded 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 alloploids 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 alloploids.

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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 multi-
ple base deletions relative to tobacco) were noted in the variable 
regions V2, V6, V12, V15, and V16. These deletions varied in size, 
and of lesser magnitude retained sequences that were 
alignable with tobacco. Relatively few mutations were seen in the 
peptidyl transferase loop, thus suggesting retention of function.

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
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Potential multiple origins for Helianthus deserticola, a 
diploid hybrid species

Homoploid hybrid speciation has traditionally been consid-
ered a rare event, dependent on the establishment of both 
a novel, balanced genotype and reproductive isolating bar-
riers 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 geo-
graphical range were assayed based on four PCR amplified frag-
ments of chloroplast DNA, digested with a total of seven restriction 
enzymes. The cpDNA haplotypes for H. deserticola were com-
pared 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 character-
istic 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 cyttoplasmic introg-
ression or by multiple diploid hybrid speciation events. Microsatellite 
markers were used to further investigate these two possibilities.

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

Camissonia 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 popu-
lations). 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 loca-
tions where they are found. In addition, they share other charac-
teristics affecting patterns of genetic variation such as an annual 
habit, a primarily selling mating system, and passive seed dispersal. 
All populations of the two taxa on San Clemente Island were sur-
veyed 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 He = 0.088 vs. 0.003) and population levels (P = 8.8 vs. 
3.5, A = 1.09 vs. 1.03, and Hc = 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 (GST = 0.810) than among populations of Cryptantha 
(GST = 0.042). Clear differences exist in patterns of genetic varia-
tion in the two taxa despite their shared habitat, distribution, recent 
history, and species characteristics.

218 HELENURM, KAIUS
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High levels of genetic polymorphism in the insular 
endemic herb Jepsonia malvifolia (Saxifragaceae)

Jepsonia malvifolia is a long-lived perennial herb 
endemic to the Channel Islands of southern California and 
Guadalupe Island, Mexico. Twelve populations of J. malvifolia 
San Clemente Island were surveyed for their genotypes at 21 
allozyme loci, revealing high levels of genetic polymorphism. For all 
individuals across San Clemente Island, 95.2% of loci are polymor-
phic with Ap = 2.90 and Hc = 0.179. Populations averaged 60.2% 
polymorphic loci with Ap = 2.42 and Hc = 0.158. Most variation is 
found within rather than among populations (GST = 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 dis-
tance. Gene flow among populations is Nm = 9.5 based on private 
alleles and Nm = 2.2 based on RST. Outcrossing rates based on fix-
ation indices average t = 0.733, indicating a primarily outcrossed 
mating system. The genetic variation observed is unusually high for 
insular endemic herb and indicates that J. malvifolia is unlikely to 
be endangered by genetic factors.

219 HERMAN, SALLIE J.* AND LINDA A. RAUBESON
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Genetic diversity of a rare buttercup

Ranunculus tritematusoccurs as a few isolated populations in 
Washington, Oregon, Idaho, and Nevada. We have used 
RAPD (randomly amplified polymorphic DNA) polymor-
phisms 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 
glomeratus. 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. 
tritematusand 17 were unique to R. glaberninus. The rare species, R. 
tritematus, has a higher number of variable loci (62% polymor-
phism versus 22% for R. glaberninus), a higher proportion of genet-
ically distinct individuals (100% for R. tritematus vs. 88% for R. glabe-
minus), and a greater average genetic distance among individuals 
(0.19 for R.tritematusand 0.06 for R. glaberninus). Thus, this rare 
species, considered a species of concern in Washington State, does 
not seem to be suffering from reduced genetic diversity as com-
pared 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 con-
tention will need to be further investigated by examining samples
from additional populations of each species. This further sampling is currently underway.

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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. HAMRICK1, AND THEODORE H. FLEMING2**

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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 griesei 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. griesei and C. repandus were predominantly outcrossing at the population (tm = 0.926 – 1.00) and individual (mean tm = 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 (tm = 0.764) and individual (mean tm = 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 correlated outcrossing among progeny within a maternal plant (rp = 0.050 – 0.158), but correlated paternity increased significantly within fruits, with substantial differences between S. griesei (rp = 0.852) and C. repandus (rp = 0.228). For M. curvispinus, correlated paternity among fruits within a family was low (rp = 0.059) and increased moderately within fruits (rp = 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.

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

Poa bulbosa 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.

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

Lepidium 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 autopolyploid 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.
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 Jewellflower, 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 "Serpenthanth Complex" of genera (Serpentanthus, Caulanthus, Guillenia) were examined using nuclear ribosomal internal transcribed spacer (ITS) and chloroplast trnL intron sequences. Phylogenetic hypotheses supported monophyly of subgenus Eulesia — which includes the bulk of the serpentine endemics in the Serpenthanth 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.

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

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 10 cM in size, and the QTL of largest effect for each trait occur in 21 genomic regions. 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 (gynoecomyoecy to monoecy). We measured four vegetative and 12 reproductive trait differences in an F2 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 (R² 53%), ray floret number (R² 65%), and ray to disk floret ratio (R² 83%). Although reproductive features exhibit dominance in the F1, 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.

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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

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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 Grecum 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
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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, gladin 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.

CONTRIBUTED POSTERS

231 GARDNER, KEITH A.*, STUART J.E. BAIRD*, SHANNA E. CARNEY, and LOREN H. RIESEBERG
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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 $F_{st}$ 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.

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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.

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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 Hansenkamp 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 zygote 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±89.97 μm) was comparable to the average obtained in the 1985 study (1246±160.3 μm). 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 commelina- ceous species.

234 KHAILENKO, NINA ALEXANDROVNA AND VLADIMIR ALEKSEEVICH KHAILENKO*
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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. (AAABDD), 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 Saratovksaya-29 and species: *T.araraticum* v.araxianum thumanianis (AbAbGC) , *T. mil- itinae* Zhuk. et Migusch.(AbAbGC) , (T.turgidum v. nigrorbatbum AuAuBB) , *T.compactum* Host. (AuAuBBDD) , *T.mopheevii* Zhuk. (AuAuGG) . Emasculation and pollination were carry out on classic methods (Udolskaya, 1961; Khaileenko,1998). The cultivar Saratovksaya-29 was farther always. Percent of impregnative ovaries reached to 80%, but percent of setting grains was hestitated 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 Saratovksaya-29. This anomalies can be caused both as incom-patible of genomic composition by crossed species (Dorofeev at all., 1978; Gandilyan, Shakaryan,1992) and as various breaches in function of female gametophyte (Khaileenko,1999). The questions of origin of wheat species and practical using biodiversity of interspecific hybrids of wheat will be discussed.

235 KHAILENKO, NINA ALEXANDROVNA
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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* ô Ulianovka, Ulianovka ô Ô.kiharae, Mironovskaya 808 ô T.dicoccum was investigated. Since F1, in all combinations of crossing, annually were sowing a grain under the following scheme: ear with grains of 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 ô Ulianovka, Ulianovka ô Ô.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 steril-
ity (CMS). The majority of plants were sterile in F2 and F3, but ob-
served 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 & T. dicoccum in F1 all plants were half-fertile,
and in F2 and F3 were segregated on sterile, half-sterile, fertile and
half-sterile 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
Ö. 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 steri-
ility at wheat, arising at carrying out of works on the remote
hybridization of cereal plants are discussed.

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Towards understanding the role of transgressive
segregation in adaptation

Transgressive segregation provides a simple and plausible
explanation for the niche divergence and phenotypic novel-
ity 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 adapta-
tion in nature. We are currently conducting field experiments using
synthetic hybrid lineages between Helianthus annuus and H. petio-
laris, 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 nat-
ural "hybrid habitat". Preliminary results of these selection experi-
ments will be presented and discussed.

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Cloning and Characterization of Guanylate Kinase
from Sunflower (Helianthus annuus L.)

Guanylate kinase is a sensitive enzyme in the biosynthesis of
nucleotides. It catalyzes the reaction (dGMP + ATP ⇌
dGDP + 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 fun-
damental 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 dis-
play 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 concentra-
tions. This implies that the expression of SGK may be specifically
related to signaling the onset and/or effect of water deficit through-
out the plant. Further characterization of SGK (e.g., promoter stud-
ies and protein expression) will be very helpful in understanding the
function of guanylate kinase in plant cell stress-response.

238 SCHWARZBACH, ANDREA E.*, LISA A. DONOVAN, DAVID M. ROSENTHAL, AND LOREN H. RIESEBERG1
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The role of transgressive segregation in hybrid
speciation: an example from sunflowers

Helianthus annuus 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 gener-
ates novel characteristics directly through hybridization is trans-
gressive segregation, which QTL studies explain through comple-
mentary 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 deter-
mine whether characters that are unique to the natural hybrid
species are present in artificial hybrids.

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Comparative allozyme and RAPD genetic studies on the
demic Borderea chouardi 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 con-
ducted using allozyme and RAPD markers. Sampling
included individuals from the only known population of the criti-
cally endangered B. chouardi and from 6 populations within the
distribution range of its congener B. pyrenaica. Both codominant
and dominant alleles have provided markers that genetically sepa-
rate 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 RAPD bands
are observed in both populations but not in the allozyme
polymorphic taxa, suggesting that the allozyme loci do not
answer to evolutionary changes. The allozyme data show the
existence of a "natural hybrid zone" between the two species
with intermediate characters, whereas RAPD data support the
existence of independent populations within the same areas.
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 reintroductory 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.

Ancient genome duplications in the angiosperms: lessons from Arabidopsis

Polyplody 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.
PALEOBOTANICAL SECTION, BSA
CONTRIBUTED PAPERS

247 BOYCE, C. KEVIN
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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 ranging in age from Middle Devonian through the end of the Permian. Paleobotanists have long wondered why this was so. One key event is the radiation of Spermopteris and Phasmatocycas floras, which are among the best-preserved and most complete fossil records of any in the world. These floras 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.

A B S T R A C T S

244 ARENS, N. C.*, A. THOMPSON, L. CHENG, A. FRUMES, J. HSU, J. LEE, AND S. NOSRATINIA
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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 and compared leaf dimensions from the Upper Carboniferous (Virgilian) Lawrence Nee, from the Lower Permian and from the Late Triassic. We then assembled leaves from vouchered herbarium specimens from the abaxial lamina surface of the specimens to species. This analysis shows that (1) a quantitative morphometric analysis can be useful in delimiting leaf paraspaces 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.

246 BOUCHER, LISA D.
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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.

245 AXSMITH, BRIAN J.*, RUDOLPH SERBET2, MICHAEL KRINGS2, THOMAS N TAYLOR2, AND EDITH L TAYLOR2
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New interpretations of the enigmatic Paleozoic plants Spermopteris and Phasmatocycas

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 Phasmatocycas, 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 Phasmatocycas. This putative transformation entailed the phylogenetic shift of the ovules from the abaxial lamina surface of Spermopteris to the megasporophyll midrib in Phasmatocycas and extant Cycas. We have initiated a restudy of these fossils based on the original Spermopteris conicea specimens from the Upper Carboniferous (Virgilian) Lawrence Shale described by Cridland and Norris, which are more complete and informative than previously realized, and newly collected specimens of Phasmatocycas 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 Phasmatocycas 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 Phasmatocycas 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 Phasmatocycas will be discussed.
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.** and **GEORGE W. ARGUS**

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*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. Nanophylic and leptophylltic 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**

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*Sporuses 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 lycopsods, these are all large, with central woody axis, showing an arboreous 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 Permount. 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.** and **KEVIN C. NIXON, AND MARIA A. GANDOLFO**

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*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 Plain localities including Martha’s Vineyard. Flowers are five-merous with superior ovaries and have 5 stamens alternating with 5 seemingly staminal nectaries. The disparate taxa share a common floral plan, abaxial sepal glands, clawed petals, axile/intruded parietal placenta, lobed spheroidal stigmas, dorsifixed anthers, tricolporate pollen and distinctive triarchenes. 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 character 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.** and **KATHLEEN B. PIGG** and **STEPHEN J. MOUTON**

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*Permineralized fruit with malvaceous 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 locale. 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
Tilaceae). Of these families, the Almont fruit compares most
closely with Tilaceae, in particular because of the presence of sin-
gle-seeded locules. The malvanean fruit from Almont is of particular
significance because of its similarity with Carpolithus bowerbanki
by Reid & Chandler, an anatomically preserved form based on a single
specimen from the Lower Eocene London Clay flora. Carpolithes
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 Carpolithes bowerbanki strongly suggest that
there were also shared floristic elements.

252 DILLHOFF, RICHARD M.1,2*, ESTELLA B. LEOPOLD2, and STEVEN R. MANCHESTER3
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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 pub-
lications 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.
Megasfossils 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 confir-
mation of Fagus, also recognized from Princeton and Republic, pro-
vides 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 ther-
mophic 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.

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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 dif-
fferences 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 con-
straints, 277 MA with minimum constraints, and 215 MA with max-
imum 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.

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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 mor-
phogenus Rhynchogenium. Described from four specimens from
the upper Chesterian Fayetteville Formation of Arkansas,
Rhynchosperma is radially symmetrical with a two layered integu-
ment. The apical portion of the integument is ribbed and non-vas-
cularized; the nucellus is fused to the integument and apically dif-
ferentiated into a dome shaped pollen receiving structure. The vas-
cular 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.
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 florae 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.

Fossil flowers with possible nymphaeal affinities

The aim of this report is to describe a suite of fossil flowers with possible nymphaeal 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 perigonous/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.

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 240 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.

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 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 Aphanoalyx, which includes ca. 15 species primarily in western and central tropical Africa today. Fossil leaves of another caesalpinioioid taxon are similar to leaves of the extant genera Cynometra, Julbernardia, and Guibourita, but precise relationships remain to be determined. The Mimosoideae are 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.

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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 Caesalpinioidae. 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, Deviacera, Metasequoia, Corylites, Platanus raynoldsi, and Macginitia 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, Diplotropis, Sakoanal, 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.

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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 axial 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 borne 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.

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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. Stamata 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 sporae dispersae genus Potonieispites Bharadwaj. They are monosaccate, with a proximal, bent monolete 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.

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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
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 fremouvensis, 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.

An upper Paleozoic floras of New Mexico

With the exception of the Virginian 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-swap 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 neotropiloid fern reconstructed from specimens from Carizzo 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, Carizzo Arroyo as a mixed conifer, Cordatales, medullosan flora, and Placitas as a streamside peltasperm flora.
(ascending order): Eoginkgoites, Dinophyton and Sanmiguelia zones. This biostratigraphy can be evaluated by stratigraphically ordering Chinle plant localities using litostratigraphic 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.

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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 charcoalified 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 much detail. The megaspore floras and fern mesofossils that have been recovered from these localities are described. Cumulatively, at least ten genera and thirteen species of megasporas are recognized from Northeast Plaza (Aptian, 115Ma, Maryland), Mauldin Mountain (Cenomanian, 99Ma, Maryland) and Upatoi Creek (Santonian, 84Ma, Georgia) localities. Megasporas identified so far have affinities either to heterosporous lycophytes—Bohemisporites, Erlensonisporites, Minensisporites, Pavittiletes, and three additional “genera”—or to heterosporous ferns—Arcellites, Arindicesporites, and Molaspora. On the basis of recently described sporocarp remains, Molaspora is a dispersed megasporangium belonging to the extant genus Regnellidium (Marsileaceae). At both sites in Maryland, lycopsid megasporas are more diverse and abundant than fern megasporas. At Upatoi Creek, lycopsid megasporas are more diverse, but approximately equivalent in abundance to fern megasporas. 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.

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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, pinnatifid venation, numerous pectinal veins, closely spaced perradiate terminal teeth, 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 septa but do not form an axial strand. The fossil fruits are only about half the size of the fruits of living Davidia involucrata, 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.

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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 cirratum. Acer section Palmata can be divided into three series: Palmata, Sinensis, and Penninervia. The latter contains species with entire margins, 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 Sinensis. Species in the series Sinensis have 3-7 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 Sinensis 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.

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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 sub-fossil 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.

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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, Flacourtiaeflora, Juglandaceae (Pterocarya), Macclintockia, Myrtaceae, Nelumbo(?), Phytocere sordida, Rhus, Rhizophoraceae(?), Temstromites, 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.

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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 treacleate epiphyllous bisexual flowers along with similar flow ers 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.

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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 Dithodeales, are also present. The thyrhothecia of Phragmothyrites were found mainly on Persea, Lithocarpus, Betula, and Magnolia, and are uniquely characterized by concentric cell divisions. Stomiopeltites perithea are non-radiate and ostiolate, and were found on Betula, Smilax and Zeaiphiones. Entopeltacites hyphae were found on leaves of Persea. Other fungi present include non-radiate, non-ostiolate cleistotheca and hyphae similar to Thielavia on almost all plant genera, and plentichomatous 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.

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Fagaceous infructescences from the Oligocene Catahoula Formation of Texas

Spiny, husk-like infructescences (“frilly fruits”) are described from the Oligocene Catahoula Formation 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 Castanopsis and Bernophyllum 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.

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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 intersemmal 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 gilsonianus Carruthers, Bennettites monerei (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 Cycadeoidea/Bennettitales lack a cupule, have radical scales, have nucellar vascular tissue (but no integumentary trachedeal), and that no pollen chamber is present. 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 Cycadeoidea.  

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Secondary phloem of the Late Devonian progynosperm tree Archaeopteris

Well preserved secondary phloem was found in a trunk-sized axis (Callixylon trifilievii/zenkii-type) and a small branch (C. trifilievii/zenkii-type) of Archaeopteris from Late Devonian beds of Morocco and New York (early Famennian marine beds near Jebel El Maktib, Morocco, and basal Frasnian Oneonta Fm. from Ashland, NY). Previous reports of bark in Callixylon (Arnold 1929, 1930; Lemoigne, Junia, 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 aneurhypoxy 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 aneurhypoxy, differing only by fibers occurring mostly in concentric tangential bands in older external phloem. Bifacial VC of Archaeopteris is also organized like that of aneurhypoxy. Despite differences of vegetative and reproductive morphology, the similar secondary tissues and VC of Archaeopteris and aneurhypoxy support interpreting them as closely related basal lignophyte groups.

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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 cellu-lose 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 episp- tase 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 sagittiloba (Rodsky.) 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.
Systematic analysis of fossil fruits placed in the eurosid II clade

Several orders and families of the angiosperm clade eurosid 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 eurosid II. Relevant fossil taxa include Dressiantha (Capparales), Florissantia (Malvales), Sterculiocarpus coloradensis (Sterculiaceae), Peteleacarpum (Tiliaceae, Craiga), Daberenocarp (Malvaceae), Landeenia (Sapindales), Sapindaceacarpum and Wehrwollea (Sapindaceae), and Turpinia (Staphyleaceae).

Development and architecture of a gondwanan representative of the late Devonian genus Pietzschia (Cladoxyllopsida)

Cladoxyllopsida, 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 cladoxylalean 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 cladoxylloid occurrence in Africa. It provides a basis for reconstructing a younger member than those that bears tightly packed intersegmental 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.

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 columbiaun Dawson. The integument of these seeds consists of a thick sarcotesta that surrounds a spongy zone of the integment 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 corona, 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.

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 Asteroscyx 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 unitunicate asci. Ascospores may be uni-multicelled, elongate, and demonstrate ger-