Oaxaca, México / 2006
Hennig XXV
The Willi Hennig Society

MONDAY 14TH

SYMPOSIUM: CHARACTER SAMPLING

Geometric spaces for character sampling and quantitative methods for character state identity. *Efrain de Luna*[1] and Brent D. Mishler[2]. [1]Depto. Biodiversidad y Sistemática, Instituto de Ecología AC, Xalapa, Mexico. [2]University and Jepson Herbaria, Berkeley CA, USA.*

In assessment of morphological homology, character statements and conjectures of character states emerge from the similarity test. Character states among terminal units are classified either “same” or “not same”. We suggest that empirical judgment of similarity for character state identity should be quantitative, and that recognition of states is methodologically separated from the procedure of coding entries as primary homology in the data matrix. Under a morphometric perspective, such discovery consists of a vector space rotation for an appropriate character selection and statistical analyses for character state identity. Morphospace can be configured by distance measurements or "x, y" coordinates. Fixed or varying "morphs" constitute clouds of points in a multidimensional geometric space. Adjustment to an orthonormal space by rotation and extraction of a linear combination of multiple axes provides a suitable projection for character state recognition. Identification of the same phylogenetic state (taxic homology) or recognition of sufficiently different states (transformational homology) is a statistical question about structure of correlations and variance in such vector space. We use analyses of variance to test if there is a statistically significant association of the quantitative feature (a character state) with the a priori discrete groups (terminal units). Multiple comparison tests are used to discover which groups of means are significantly different from each other. We exemplify this approach with analyses of character variation in mosses, orchids, bromeliads, diatoms and bats. Conjectures of character states guided by quantitative procedures are still hypotheses of primary homology, which need to be tested for congruence.

Characters as Groups: Applying insights from cognitive psychology to improve morphological characters. *Bruce K. Kirchoff. Department of Biology, University of North Carolina, Greensboro, NC 27402-6170, USA*.

A new method of morphological character description uses direct comparison and sorting of images to produce hierarchical character-cladograms. A character-cladogram is a graphical representation of a single character that serves as a hypothesis of phylogeny based on that character. Each dichotomy in the character-cladogram represents a character state. Experiments with human participants were used to explore the conditions under which direct comparison produces reliable (consistent from investigator to investigator) and valid (in agreement with an independent estimate of phylogeny) characters. Participants were drawn from students taking a course in plant diversity at UNC Greensboro, and professional morphologists attending the Botany 2004 meetings. The students were randomly assigned to trained and untrained groups. Training was carried out using a method that has been shown to change a participant’s mode of visual processing from analytic (the mode used by visual novices) to holistic (an additional mode only employed by visual experts). Morphologists were included in the study to investigate the effects of disciplinary expertise on the ability to describe character-cladograms. They received no additional training beyond that available to them as disciplinary experts. The results suggest an improvement in both reliability and validity after the training regime. There was no support for the idea that the morphologists differed from untrained students in their ability to produce reliable or valid character-cladograms. Disciplinary expertise may not translate into the ability to make reliable and valid assessments of similarity without additional training. Based on these results, we suggest a new method for creating morphological characters and character states. This method is consistent with insights on plant growth and form originating with Goethe, and elaborated by Agnes Arber.

Barcoding, morphology, microsatellites and medicinal leeches. *Mark Siddall. Invertebrate Zoology, American Museum of Natural History, NY, USA.*

DNA barcoding, while useful in cases of species-identity questions, alone provides insufficient information regarding species delimitation except in cases of non-monophyly. Without broad geographic coverage to elucidate the within-species variation, false-postives and false-negatives cannot be evaluated. In situations wherein barcoding suggests sister species delimitation by some arbitrary molecular yardstick, other data must be brought to bear, such as those offered by microsatellite loci. Various examples from across leeches are examined including the ressurection of several named species of European medicinal leech and a determination that what is available commercially is not, in fact, *Hirudo medicinalis*.

Characters sampling at low taxonomic level - a phylogenetic analysis of species complex Poa sect. Dioicopoa. *Lone Aagesen*, Liliana M. Giussani, M. Amalia Scataglini, and Osvaldo Morrone. Instituto de Botánica Darwinion, Larbardén 200, San Isidro B1642HYD, Argentina.*

With the optimization of continuous characters now made possible within a cladistic context, phylogenetic studies can proceed to analyze groups that have previously been untreatable such as species complexes in which the species are only defined through the variation of continuous characters. We explore character sampling in a species complex of bluegrasses, *Poa* sect. *Dioicopoa*, in which sexual dimorphism and the lack of adequate qualitative characters complicate an analysis at species level. *Dioicopoa* has previously been analyzed through a multivariate analysis using 29 continuous and 14 qualitative characters. We use TNT to reanalyze this data set adding DNA sequence data. The analysis implies rescaling of the continuous characters in order to transform measurements such as culm length (mean 12-77 cm) and stomata length (mean 0.03-0.05 mm) into a comparable scale. Resampling methods suitable for detecting minor changes in branch support were used to evaluate the results.

The utility of Expressed Sequence Tags as phylogenetic characters. *Alfried P. Vogler. Department of Entomology, Natural History Museum, Cromwell Rd, London SW7 5BD, UK, and Division of Biology, Silwood Park Campus, Imperial College London, Ascot SL5 7PY, UK.*

Expressed Sequence Tags (ESTs) are a fast growing source of sequence information and potentially overcome the limitations of PCR based sequencing. However, the haphazard structure of EST data as available in public databases suffers from problems of insufficient taxonomic sampling, missing entries for target taxa, and unclear orthology. As PCR based data sets, they are also affected by genome-wide biases in nucleotide composition, differences in evolutionary rates and other confounding parameters which are not easily overcome by the larger number of genes used in EST based data sets. Here I will discuss these issues using examples from insects and metazoan animals. EST data provide a framework for phylogenetics and genomics, which require simultaneous analysis of diversification of genes and organismal lineages.

Contributions of characters with various qualities to phylogenetic studies of the grasses and monocots. *Jerrold I Davis. L.H. Bailey Hortorium and Department of Plant Biology, Cornell University, Ithaca, New York 14850, USA.*

Analyses of multigene data matrices for nested sets of taxa (monocots, grasses, and the grass subfamily Pooideae) demonstrate variation in evolutionary rates and other attributes among genes, gene regions, and lineages. Among the qualities that have been observed are relatively high evolutionary rates in grasses, alismatids, and related families; relatively low rates in palms; RNA editing (best documented in mitochondrial genes, but also occurring in plastid genes), which may influence the genome, and migration of portions of plastid-encoded genes into and out of the Inverted Repeat (IR) regions of the genome. The IR regions tend to evolve more slowly than other regions of the plastid genome, perhaps as a result of their duplicated nature, and there have been multiple migration events of this sort within the grass family. Examination of the contribution of different genes, genomic regions, and taxon subsets to the support of particular clades, in terms of the support for these clades in complete vs. partial data sets, reveals complex interactions among these factors, but does not indicate which of the underlying factors are contributing to or detracting from the accurate discovery of phylogenetic relationships. Moreover, the notion that the overall value of a particular character or character set for phylogenetic purposes can be measured quantitatively, except in trivial cases, is problematic. These considerations suggest that the variable contributions of different characters and taxa to the support of clades cannot be translated easily, if at all, into rules for the inclusion/exclusion or variable treatment of characters or taxa in cladistic analysis.

Phylogenetic utility of indels within ribosomal DNA and beta-tubulin sequences from fungi in the Rhizoctonia solani species complex. *Dolores González*[*1]*; Marc A. Cubeta*[2]*, and Rytas Vilgalys*[3]*.* [1]*Departamento de Biodiversidad y Sistemática, Instituto de Ecología, A.C., Apartado Postal 63, Xalapa, Veracruz 91000, México.* [2]*Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695-7567, USA.* [3]*Department of Biology, Duke University, Durham, NC 27708-0338, USA.*

In gene sequences each position corresponds to a hypothesis of transformational or taxic homology depending on nucleotide variation. Indels are difficult to code for phylogenetic analyses because they can be interpreted as an artifact from sequence alignment or as a phylogenetically informative character often associated with mutation. In this study, the effect of indels was examined on the stability of phylogenetic hypotheses. Parsimony analyses for a combined data set from three gene partitions (*ITS*, *LSU* rDNA and beta-tubulin) for fungi in the *Rhizoctonia solani* species complex were performed, where indels were either excluded or included as ambiguous characters. To explore whether indels were a source of phylogenetically informative characters, single-site indels were treated as a new state, while indels greater than one nucleotide were coded as: 1) multistate for different sequence, 2) multistate for different length and 3) different characters for each distinct sequence. The most well resolved cladograms and with higher support indices were obtained when indels were included in the analyses. Results suggest that indels in noncoding regions contain phylogenetic information and support that the *Rhizoctonia* species complex is not monophyletic. Six clades within *R. solani* (teleomorph = *Thanatephorus*) representing distinct anastomosis groups and five clades within binucleate *Rhizoctonia* (teleomorph = *Ceratobasidium*) were well supported in all analyses. The data suggest that clades with representatives of *Rhizoctonia* fungi belonging to anastomosis groups 1, 4, 6 and 8 be recognized as phylogenetic species.

Indel coding under parsimony. *Kai Müller. Nees Institute for Biodiversity of Plants, University of Bonn, Germany.*

It is widely accepted that length-mutational events during the evolution of nucleotide- and amino acid sequences can provide valuable phylogenetic information and that an attempt should be made to incorporate them into cladistic analysis. I describe the modified complex indel coding, a new method which is based on the earlier described complex indel coding and aims at maximizing the information retained from unambiguously aligned sequence regions (where the principal relative position of gaps to one another can be safely established). I discuss differences to previously published indel coding approaches as well as to the integration of ambiguously aligned regions into phylogenetic analysis. I conclude with introducing software that automates the new method as well as several previously published coding schemes, and also allows for an automated identification of taxon specific segments of questionable alignment quality and their exclusion from the indel coding process and subsequent phylogenetic analysis.

The Relative Performance of Indel-Coding Methods in Simulations. *Mark P. Simmons*[1] and Kai Müller[2]. [1]Department of Biology and Program in Plant Molecular Biology, Colorado State University, Fort Collins, CO 80523, USA. [2]Nees-Institut für Biodiversität der Pflanzen, Rheinische Friedrich-Wilhelms-Universität Bonn, Meckenheimer Allee 170, Bonn D-53115, Germany.*

We used simulations to compare the performance of ten approaches that have been applied for treating unambiguously-aligned gaps in phylogenetic analyses. These approaches were implemented in SeqState, which reads and outputs NEXUS-formatted data matrices. We examined how these approaches performed under the ideal conditions of correct alignments, as well as how robust they were to errors caused by the use of inferred alignments. Simulations were performed using different indel rates, lengths, and distributions. Performance was quantified using the averaged overall success of resolution of parsimony jackknife trees relative to the tree on which the characters were simulated. All of the approaches to incorporating phylogenetic signal from gap characters outperformed treating gaps as missing data or excluding gapped positions, using both correct and inferred alignments. Treating gaps as fifth states outperformed the other approaches, though further analyses in which weights were controlled indicated that this was an artifact caused by overweighting multi-position gaps. Simple indel coding and modified complex indel coding generally outperformed the remaining approaches examined.

CONTRIBUTING PAPERS: THEORY I

Complex Terminals and Forest Swapping. *Ward Wheeler*, Illya Bomash, and Andrés Varón. Division of Invertebrate Zoology, American Museum of Natural History, Central Park West at 79th Street, New York, NY 10024-5192,USA.*

The median problem is discussed for the optimization of complex (greater than one entity) terminals. The process of generating complex medians and the forest (multiple tree) structures inherent to the operation are discussed. Heuristic refinement techniques—forest swapping—are presented. Applications of this type of analysis extend to gene families, biogeography, and symbiotic systems.

POY Version 4.0. *Andrés Varón*[1], Ward Wheeler[2], Illya Bomash[3], and Le Sy Vinh[2]. [1]Division of Invertebrate Zoology, American Museum of Natural History and Computer Science Department, Graduate Center, The City University of New York. [2]Division of Invertebrate Zoology, American Museum of Natrual History. [3]American Museum of Natural History and Cornell University.*

The first public alpha release and demonstration of POY 4.0 will be presented. POY supports phylogenetic analyses using Maximum Parsimony as optimality criterion, under Static or Dynamic Homologies (SH and DH respectively). In the case of DH, insertions, deletions, and more complex rearrangement events such as moves, duplications, and inversions can be detected, making possible the analysis of complex molecular data sets. POY has been fully rewritten from scratch. Among the multiple new features we can highlight: Better performance. POY improves in several orders of magnitude its efficiency for SH characters, and in at least two orders of magnitude for DH characters. The computational power that POY 3.x achieved in a cluster can now be achieved in a PC. Extended sequence size support. POY allows for larger alphabet sizes in sequence data, making possible the analysis of annotated nucleotide, amino acid, and develop-mental sequences, using the same efficient algorithms and implementation that only nucleotide sequences supported before. Improved user interface. POY is no longer a command line oriented program. Version 4.0 supports a scripting language for more flexibility and increased readability of the analysis. In addition to this, an interactive console is also available, for users to experiment in an interactive manner with their data sets and the program. Parallel version. It is already available using MPI. The latest version will run efficiently with three processes (a master and two slaves), in a dual core processor. There is no difference between parallel and sequential scripts: POY will choose the best strategy to parallelize the search. In-tree parallelization. If a dataset is too complex, making the evaluation of a single tree a non-trivial task, POY 4.0 can parallelize a single tree evaluation, to achieve results faster. Libraries for researchers. All the internal libraries of POY 4.0 are publicly available and fully documented. The POY interactive console allows advanced researchers to fully program their own phylogenetic analysis scripts, output formats, or heuristics in Objective CAML, not being limited by what the regular user interface has already available for them. Every single function, from sequence alignment and median calculations, to table printing, can be used and modified to experiment with new strategies and explore data. As with previous versions, POY 4.0 is an open source software, available free of charge for Windows, Mac OS X, and Linux.

Phylogenetic analysis and alignment of behavioral sequences by direct optimization.
Tony Robillard[1,2], Frédéric Legendre[1], Laure Desutter-Grandcolas[1], and Philippe Grandcolas[1]. [1]UMR 5202, Département Systématique et Évolution, Muséum national d'Histoire naturelle, 45 rue Buffon, Paris 75005, France. [2]University of Missouri, Division of Biological Sciences, 215 Tucker Hall, Columbia, MO 65211, USA.*

The studies of behavior and phylogeny have a long common history. From the early times, comparative studies have shown that behavior can be remarkably informative regarding the relationships of taxa. In spite of recurrent arguments about misleading homoplastic evolution, behavioral characters can be defined as any other characters, either morphological or molecular following the classical rules of observation, definition and analysis. Some behavioral sequences (a succession of behavioral acts or events displayed by one individual or in dyadic interactions) are stereotyped, such as courting or construction behaviors. In this case, establishing primary homology before phylogenetic analysis seems quite easy and most studies assessed straightforwardly hypotheses of homology among acts based on the position and special similarity criteria. However, as for some DNA sequences, the situation is not as simple as equal length or similar sequences could let it to assume. In particular, the interspecific comparison of behavioral sequences of different lengths is obviously troublesome, involving the possibility of many insertions and/or deletions of acts. Such behavioral sequences can be analyzed using direct optimization, a method which does not require a priori alignment of sequences. A case study is provided with the phylogenetic analysis of a cricket clade, whose calling song rhythms are analyzed with DO. Empirically, this study shows that direct optimization of such sequences provides informative characters and that, once more, behavior can be used in the framework of phylogenetic analysis.

Phylogenetic analysis of non-stereotyped behavioral sequences: from successive event-pairing method to direct optimization. *Frédéric Legendre[1], Tony Robillard[1,2], Laure Desutter-Grandcolas[1], and Philippe Grandcolas*[1]. [1]UMR 5202, Département Systématique et Évolution, Muséum national d'Histoire naturelle, 45 rue Buffon, Paris 75005, France. [2]University of Missouri, Division of Biological Sciences, 215 Tucker Hall, Columbia, MO 65211, USA.*

The phylogenetic analysis of behavior is now recognized as a valid and heuristic procedure. Empirical studies have focused on behaviors which are stereotyped so that there is a one-to-one correspondence between behavioral sequences and taxa. Conversely, non-stereotyped behaviors have never been considered for phylogenetic studies because the sequences of acts can vary among individuals and contexts, preventing to propose hypotheses of homologies among sequences. Most displayed behaviors are non-stereotyped behavioral sequences and they can both contribute significantly to phylogenetic inference and be valuable subjects for evolutionary studies. Non-stereotyped sequences can be analyzed using different methodologies. A first possibility could be to adapt the procedure of event-pairing, considering only successive events with an emphasis on the transition between two behavioral acts. Species relationships can be therefore characterized by the occurrence of particular transitions and even by their frequencies. However, only pairs of acts are considered in this method, which is obviously an oversimplification of the real situation with whole sequences where the occurrence of one act can be characterized not only by the immediately preceding one but the whole succession. In this respect, a more accurate way to deal with such non-stereotyped sequences could be to use direct optimization analyses to classify behavioral sequences within species and then to derive characters for a phylogenetic analysis of these species. This problem is illustrated by the study of non-stereotyped social interactions between Neotropical cockroaches, combining behavioral, morphological and molecular data.

POSTER SESSION: THEORY

POY and the art of jackknife support justification. *Jan De Laet. Leuvenstraat 20, Veltem-Beisem B-3020, Belgium.*

In phylogenetic analyses of datasets of unaligned DNA sequences by means of tree alignment methods (available in programs such as POY), base-level correspondences among observed sequences are not hypothesized prior to the analysis but instead arise as part of the results. This poses a problem when trying to assess group support by means of character jackknifing: positional characters, which would be the units of prior resampling, are not available until after the analysis. POY's jackboot command patches this problem by using an exclusion mask, a mask that is fixed within a given pseudoreplicate and that consists of a (long enough) sequence of zeroes and ones in which zero stands for exclusion and one for inclusion. When calculating the cost of a tree alignment during analysis of the pseudreplicate, this mask is applied to the positional correspondences as they are reconstructed in that particular tree alignment, and steps in positions that are excluded are not counted. One of the problems with this approach is that positional correspondences may be different between different tree alignments. Therefore, different trees that are considered optimal for a given pseudoreplicate may in fact have been evaluated with respect to different sets of included residues; trees that are optimal for a given pseudoreplicate are only guaranteed to have their exclusion mask in common, not the included residues on which their evaluation was based. In a less used approach, sequences are resampled at the level of individual residues: a pseudoreplicate dataset is constructed by randomly turning a given fraction of the observed residues into "n", indicating the presence of a further unspecified residue. In this approach, readily applicable to aligned datasets and morphological datasets as well, the resulting support values can be understood in terms of independent pairwise similarity statements that can be explained as homology, an interpretation that is at a higher level of resolution than in the original parsimony jackknife procedure. Interestingly, this view allows for different support values for groups that are supported by the same number of characters but that differ in size, which raises the general question of calibration of jackknife support values.

Ancestral character-state reconstruction and its applications using BALANCE, an integrated software for calculating large phylogenies under the maximum parsimony criterion. *Nobuhiro Minaka*[1], Takashi Suemura[2], Kunihiro Okano[3], Norio Sugiura[3], Haruo Yamamoto[4], and Kouki Machii[2]. [1]Ecosystem Informatics Division, National Institute for Agro-Environmental Sciences, Tsukuba, Ibaraki 305-8604, Japan. [2]Turaltec Company Limited, Kasama, Ibaraki 309-1717, Japan. [3]Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki 305-8572, Japan. [4]Bogenpfeil Company Limited, Takanawa, Minato-ku, Tokyo 108-0074, Japan.*

BALANCE is an updated software of earlier versions of BOGEN / BLANCE for computing most parsimonious trees from large molecular sequence data. BALANCE gives an integrated computing environment for estimating phylogenies step by step: 1) manipulating and editing molecular sequence data; 2) building most parsimonious cladograms; 3) assigning hypothetical ancestral character-states to each internal node of a cladogram. Larger data matrices including tens of thousands OTUs can be analyzed using the current version of BALANCE which have some improved algorithms for tree search and ancestral reconstruction. A renewed graphical user-interface of BALANCE makes it possible easier manipulations of data and calculations of trees. As an example of using BALANCE for real data we conducted molecular phylogenetic analysis of a group including all known mycrocystin-degradating bacteria which degrade a strong liver toxin (mycrocystin) generated by cyanobacteria in polluted lakes in Japan, China, and other countries. *16S* rDNA sequence data were analyzed using BALANCE. We found several formerly unknown bacteria which have the gene for mycrocystin-degrading enzyme (mlrA). This result implies that highly reliable cladograms can be used to explore new useful biological resources. Further results on the evolution of mycrocystin-degrading function are given based on experimental analysis of hypothetical ancestral sequences of *mlrA*.

Relations in bioinformatic ontologies and "pattern cladistics": a philosophy of science-informed comment. *Francisco Vergara-Silva. Departamento de Biología Evolutiva, Instituto de Ecología, AC, Carretera Antigua a Coatepec 351 (Km 2.5), Congregación El Haya, Xalapa, Veracruz 91070, Mexico.*

A central feature in the elaboration of controlled vocabularies ("ontologies") in bioinformatics is the definition of "relations". Prominent developers of gene- and other molecular process-based ontologies state that a set of these relations (for example, PART_OF, LOCATED_IN and others) are not simply logical connectors, but a reflection of links that actually obtain between biological entities in nature. In this paper, I will consider a potential, subtle problem in the conception of the relation TRANSFORMED_OF, that presumably could arise if, in a departure from its current strict ontogenetic grounding, such relation is associated to evolutionary transformation notions, once abundant comparative data are available on the involvement of gene-centered processes in the specification of macroscopic biological organization -i. e. "morphology". These considerations will be informed by arguments entertained by systematists and philosophers of science during the controversy surrounding "pattern cladistics". In parallel, I will sketch an analysis of how the attainment of the goals of bioinformatic ontologies could play a positive role in the rational reconstruction of the theoretical foundations of a systematic practice that is independent of evolutionary process theory directives. This preliminary analysis will make reference, in a critical way, to the contemporary debate on the utility of refined conceptions of "natural kinds" in systematics.

TUESDAY 15TH

SYMPOSIUM: PHYLOGENY AND EVOLUTION OF SEED PLANTS

Phylogenetic relationships of the Mexican genus Dioon (Cycadales, Zamiaceae) based on nuclear and chloroplast DNA sequences data. *Dolores González, Andrew P. Vovides*, and Cristina Bárcenas. Instituto de Ecología, A.C., Apartado Postal 63, Xalapa, Veracruz 91070, México*

Previous hypotheses of relationships within *Dioon* indicated the presence of two large clades within the genus. However, relationships among species still remained unresolved. In this study, molecular phylogenetic analyses were performed with individual and combined data sets from the ITS region of the rDNA and the *trnL-F* of the chloroplast DNA. To explore whether indels were a source of phylogenetically informative characters indels were analyzed by including them as ambiguous data (Coding A); excluding them from the analyses (Coding B), and as multistate (Coding C). We found that the rate of mutation in the ITS region is appropriate to solve most relationships at the genus level in contrast with the *trnL-F* that showed almost no variation. Our results show that most clades obtained during analyses correspond with previously recognized species within *Dioon*. This phylogeny, groups the genus into two main clades that show clear biogeographic relationships between the species occurring along the Pacific Sierra Madre Occidental and the Atlantic Sierra Madre Oriental.

Data congruence and phylogeny of monophyletic genus Luzula, Juncaceae. *Lenka Drábková. Institute of Botany, Dept. of Taxonomy, Academy of Sciences, Zámek 1, 252 43 Průhonice, Czech Republic.*

Genus *Luzula* contains 115 species distributed throughout the world and divided into 3 subgenera (*Luzula*, *Marlenia* and *Pterodes*) and 7 sections of subg. *Luzula*. The relationships of the genus *Luzula* have been difficult to determine primarily due to its similar morphology even within geographically remote taxa. The evolution of characters in *Luzula* should be followed on the origin of various types of inflorescence and within subg. *Luzula* mostly via genome mutations (e.g., agmatoploidy). Molecular analyses based on chloroplast (*rbcL*, *trnL* intron and *trnL-F* intergenic spacer) regions revealed monophyly of *Luzula* within Juncaceae, however the situation within genus is more complicated. In addition to create hypotheses of relationships and testing classification within *Luzula*, we apply nuclear region (*ITS1-5.8S-ITS2*) that solved relationships within the genus in detail. Several phylogenetic analyses under the different criteria were performed for each data set (1) cpDNA data, (2) nrDNA data, (3) morphological data and also for (4) combined data. The parsimony analyses revealed well-supported monophyletic lineages (e.g., subg. *Pterodes*), but the classification of most of the section remains problematic. All phylogenetic trees of molecular data sets yielded a highly congruent hypothesis and partially differ from the trees based exclusively on morphology. This represents the first detailed summary of investigation about interspecific evolutionary relationships of the genus *Luzula*.

A molecular and morphological phylogenetic analysis of subtribe Bletiinae (Epidendreae, Orchidaceae). *Victoria Sosa. Instituto de Ecologia A.C., Biologia Evolutiva, Carretera antigua a Coatepec, Veracruz 9100, México.*

Subtribe Bletiinae is comprised of three neotropical, terrestrial, deciduous genera: Basiphyllaea, Bletia and Hexalectris. Morphological, molecular (ITS and trnL-F IGS DNA sequences) and combined phylogenetic analyses of subtribe Bletiinae (Epidendreae, Orchidaceae) were performed in order to estimate the relationships of the genera and species. Morphological analyses retrieved 84 trees poorly supported by homoplastic characters and resolved the seven species of Basiphyllaea in a clade sustained by four synapomorphic characters. Molecular and combined analyses retrieved almost identical trees in which the species of Bletia are in a clade with no support. Results indicate that in subtribe Bletiinae there is a trend from chlorophyllous plants with corms with small shoots to achlorophyllous plants lacking leaves.

Evolution of the flowering zones in Cactoideae-Cactaceae. *Teresa Terrazas[1,2]*, Monserrat Vázquez-Sánchez[2], and Salvador Arias[3]. [1]Departamento de Botánica, Instituto de Biología, UNAM, Apdo. Postal 70-233, México D.F. 04510, Mexico. [2]Programa de Botánica, Colegio de Postgraduados, Montecillo, Estado de México 56230, Mexico. [3]Jardín Botánico, Instituto de Biología, UNAM, Apdo. Postal 70-233, México D.F. 04510, Mexico.*

In the subfamily Cactoideae there are genera in which major differences in structure occur between juvenile and mature parts of the plant. Especially those differences are related to the specialized flower-bearing zones in stems or branches. The flowering zones known as cephalium or pseudocephalium have been designated differently by various authors. These flowering zones may develop in apical or lateral positions, which can be either permanent or periodic and are confined to one or several ribs below the apex. The presence of flowering zones has been considered a derived characteristic acquired independently in three tribes, although we do not know whether the pseudocephalium is an intermediate condition between a cephalium and the complete absence of this specialization. The evolution of the flowering areas in Cactoideae using parsimony analysis was investigated using *rpl16* and *trnL-F* sequences and 20 structural characters. One hundred and two species representing tribes of Cactoideae and *Calymmanthium substerile* as outgroup were included in the analysis. The consensus cladogram (length 1075, CI 0.67, RI 0.85) yielded a hypothesis that supports the cephalium independent origin. In two clades (Trichocereeae-Cereeae) and *Cephalocereus* (Pachycereeae) there is a transition from a cephalium to a pseudocephalium. Our results do not support the hypothesis that a pseudocephalium is an intermediate condition between a cephalium and the absence of specialization in all clades. We will discuss how the complex character “flowering zone” was coded in 18 morpho-anatomical characters that allowed us to recognized different combinations of character that gave origin to what we call cephalium or pseudocephalium.

Phylogeny of Rubiaceae: from the family to the genera. *Helga Ochotorena. Departamento de Botánica, Instituto de Biología, UNAM, Apdo. Postal 70-367, México DF 04510, México.*

In the past years a great amount of nucleotide sequences for Rubiaceae species has been produced and analyzed in the context of different frameworks. Nevertheless, the vast amount of available information has not yet been formally integrated into combined analyzes. The fact that these sequences were produced considering different goals, results in a major difficulty to combine the available sequences into a single matrix: the partial datasets are not completely parallel. The present work aims to propose a work strategy to critically analyze and integrate the spared knowledge that has been produced with DNA data. To do this, DNA sequences were downloaded from GenBank, including *rbcL*, *rps16* and *trnL*. The strategy to combine the data is fully discussed. The final matrix includes 456 taxa representing 279 out of the 662 genera (42.15%) accepted by Robbrecht, plus 12 controversial genera considered by him as synonyms. The matrix was analyzed using the parsimony criterion. A consensus of the most parsimonious trees was used as reference to map group membership variables following Robbrecht’s proposal, from the family level to tribes. This method allow for a direct identification of incongruence between the consensus and the cited classification. Most incongruence was already indicated by different authors, but it can be easily summarized by this method. Imminent changes in the classification based on this analysis are highlighted at all taxonomic ranks. Finally, problems with the method used here are addressed and strategies to critically analyze, integrate and further sample DNA data are suggested.

Current understanding of seed plant phylogeny. ***Kevin C. Nixon.*** *L.H. Bailey Hortorium and Department of Plant Biology, Cornell University, Ithaca, New York 14850, USA.*

Over the past 20 years, our understanding of seed plant phylogeny has improved dramatically, based largely on the availability of large sequence data sets, and faster algorithms that allow simultaneous cladistic analysis of hundreds (or even thousands) of terminals. This has resulted in different phases of our understanding of both angiosperm and seed plant phylogeny. These can be artificially classified as follows: 1) Paraphyletic gymnosperms-Magnoliidae sister phase; 2) Paraphyletic gymnosperms - *Ceratophylum* sister phase; 3) Paraphyletic gymnosperms - Nymphaeales or *Amborella* sister phase; 4) Paraphyletic gymnosperms - *Amborella* sister phase; and 5) Monophyletic gymnosperms - *Amborella* sister phase (where we currently flounder). Note that massive confusion exists in the literature about the implications of a sister taxon relationship, which in the case of *Ceratophyllum* or *Amborella* has often been referred to as "basal" within the angiosperms. Each of these phases has dramatically different implications for both seed plant ancestors (origins) and for ancestral form in angiosperms. Competing hypotheses regarding these questions will be discussed.

CONTRIBUTING PAPERS: BOTANY

Ganodermataceae (Fungi): How many genera are there? *Mabel Gisela Torres-Torres*[1], Laura Guzmán-Dávalos[2], and Aarón Rodríguez-Contreras[1]. Departamento de Botánica y Zoología, Universidad de Guadalajara, Apdo. Postal 1-139, Zapopan, Jalisco 45101, Mexico. [2]Universidad Tecnológica del Chocó, Ciudadela Medrano, Quibdó, Chocó, Colombia.*

The family Ganodermatacea has been divided into eight genera, but recently only three have been accepted (*Amauroderma*, *Ganoderma* and *Haddowia*). Similarly, *Ganoderma* has been arranged into two, three or four subgenera, according to the specialist. Modern phylogenetic analyses based on molecular data support two clades within *Ganoderma*, which correspond to the subgenera *Elfvingia* and *Ganoderma*. The molecular analysis did not include other genera of Ganodermataceae. Yet, analyses with morphological data have not been conducted. In this study, a phylogenetic analysis of 42 taxa and 38 morphological characters was performed using maximum parsimony in PAUP 4.0b10. The analysis included six genera: *Amauroderma*, *Ganoderma* (subgenus *Ganoderma* and subgenus *Elfvingia*), *Haddowia*, *Humphreya*, *Tomophagus* and *Trachyderma*. For rooting and character polarization, five outgroups were included: *Cryptoporus volvatus*, *Lentinus crinitus*, *Navisporus floccosus*, *Perenniporia ochroleuca* and *Perenniporia* sp. Heuristic searches were conducted with 1,000 replications and the support of the branches was calculated using bootstrap analysis. Thirty seven characters were phylogenetically informative. The most parsimonious tree was 158 steps long, CI = 0.36 and RI = 0.51. The consensus tree was not fully resolved and only one clade was supported with a bootstrap value of 55. This clade includes all members of Ganodermataceae. Even though there was not bootstrap support within Ganodermatacae, some clades were present. Roughly, they correspond to the subgenus *Elfvingia* and subgenus *Ganoderma*. Lastly, *Amauroderma*, *Haddowia*, *Humphreya* and *Trachyderma*, which have a distinctive pilear surface and basidiospores, appear at the base of the tree.

Homology in DNA sequences: ambiguous regions and informative characters in the rps4-trnaS intergenic spacer in Thuidiaceae (Bryopsida). *Deneb García-Avila* and Efraín de Luna. Departamento de Biodiversidad y Sistemática, Instituto de Ecologia AC, Km 2.5 carretera antigua a Coatepec, Congregación El Haya 351, Xalapa, Veracruz 91070, México.*

Homology in nucleotide characters has been approached under two methods: "static homology" compares sequences by similarity in order to define primary homology statements; whereas "dynamic homology" avoids a priori alignment by optimizing cladograms and alignments iteratively. We explored two implementations of static homology (manual and automatic alignment) as well as dynamic homology (via Direct Optimization) of the *rps4-trnaS* intergenic spacer in order to find variable characters to be used in a phylogenetic analysis of the moss family Thuidiaceae. Most parsimonious trees derived from each procedure were diagnosed with CI, RI, and ILD. Support was evaluated with Bremer and Jacknife. We found more informative characters and better Bremer and Jackknife support using the automatic alignment. Congruence of *rps4-trnaS* intergenic spacer with other molecular characters using both static homology approaches resulted in Thuidiaceae as monophyletic group; it did not happen under DO.

Phylogeny of Tillandsia infered from morphological characters; a preliminary approach. *Javier García-Cruz, Adolfo Espejo-Serna*, and Ana Rosa López-Ferrari. Departamento de Biología, Div. C. B. S., Universidad Autónoma Metropolitana Iztapalapa, Apdo. Postal 55-535, México DF 09340, Mexico.*

One of the most striking features of Mexican *Tillandsia* (sensu lato) is the extraordinary morphological variation, having plants from 2 or 3 cm high to giants from 3 to 4 m high. There are plants with tank, obconic or bulbous rosettes, with simple, pinnate, bipinnate or tripinnate inflorescences, nidular to scapous, erect to pendulous, etc. This variation is more notable in flowers, form and color of petals, stamens, anthers, etc. In spite of this, until now, no one has try to make a phylogenetic analysis using morphological characters. The results obtained from phylogenetic analysis using various genes, are not satisfying yet. The analysis here presented includes 87 taxa of which 85 correspond to ingroup taxa and 2 to outgroup taxa. All the traditionally groups and subgroups of *Tillandsia* (sensu lato) present in Mexico, were considered. We used 50 morphological characters. Fitch parsimony analysis was done using WINCLADA and NONA. Ratchet searches were made using 10,000 iterations, holding 10 trees at each iteration and saving all the trees from the all iterations. Bootstrap analysis was performed comprising 1,000 replicates. 11,799 trees were retrieved, with 470 steps length and with a RI = 0.59. Seven main clades were obtained: *Racinaea*, *Vriesea*, *Pseudalcantarea*, *Werauhia*, *Viridantha*, *Allardtia*, and *Tillandsia*. The last one is not completely resolved, however, we can distinguish at least 5 groups within: juncea group, utriculata group, imperialis group, recurvata group, and erubescens group. The ingroup is supported by two synapomorphies: the apical seed appendage and the perfect flowers, and is also supported by three non conflictive characters: the distichous inflorescences, the floral bracts equal or large than sepals, and the fusiform capsules. Is important to point out that we obtained characters that should had not been considered in the delimitation of groups in previous taxonomic works. The tribes previously recognized are here confirmed and some of the genera previously proposed are also ratified.

Phylogenetic analysis of Anulocaulis Standl. (Nyctaginaceae) based on morphologycal data. *Patricia Hernández-Ledesma*, Hilda Flores Olvera, and Helga Ochoterena. Departamento de Botánica, Instituto de Biología, UNAM, Apdo. Postal 70-367, México DF 04510, Mexico.*

Anulocaulis, with five species and four varieties of herbs, mostly perennial, is distributed in southwestern United States and northern Mexico. This genus has had a conflicting taxonomic rank either as a genus, or as a subgenus or section within the pantropical genus *Boerhavia*. A morphological phylogenetic analysis based on parsimony was conducted to test the monophyly of *Anulocaulis*, to evaluate its phylogenetic position with respect to other potentially related taxa, to postulate phylogenetic hypotheses for its species and to study the evolution of some morphological characters. The analysis included 25 terminals of tribe Nyctaginae. The ingroup included all currently recognized taxa within *Anulocaulis*. The outgroup consisted of 14 species of the three potentially closely related genera (*Boerhavia*, *Commicarpus* and *Cyphomeris*) plus *Okenia hypogaea* (subtribe Boerhaviinae) and *Nyctaginia capitata* and *Mirabilis glabrifolia* (subtribe Nyctagininae), the last one as the functional outgroup. A total of 41 potentially informative characters were coded, concerning vegetative and floral structures, fruits and seeds characters, plus chromosome numbers. The single tree obtained after the parsimony analyses corroborates *Anulocaulis*, *Commicarpus*, and *Cyphomeris* as monophyletic, with a paraphyletic *Boerhavia* and *N. capitata* as sister to *Anulocaulis*. Within the *Anulocaulis* clade, there are two groups; one includes *A. annulatus*, *A. eriosolenus* and *A. hintoniorum* and the other contains the four varieties of *A. leiosolenus* and *A. reflexus*. Due to the seeming paraphyly of *Boerhavia*, further cladistic analyses including a broader sampling of *Boerhavia* species and ideally also molecular data are necessary to decide whether the genus should be split into smaller monophyletic units or the generic status of *Anulocaulis*, *Commicarpus* and *Cyphomeris* should be reconsidered. Provisionally, we recognize these three genera as different from *Boerhavia* because they are supported by several synapomorphies. Characters traditionally used in the taxonomy of the group are re-evaluated and evolutionary hypotheses for some of them are thoroughly analyzed.

Phylogenetic Studies of Disterigma, an Andean Blueberry. *Paola Pedraza. New York Botanical Garden-City University of New York, Institute of Systematic Botany, Bronx, NY 10458-5126, USA.*

Molecular phylogenetic studies of neotropical Ericaceae are at an early state and problems are being identified as more collections and regions are incorporated into the analyses. Our understanding of the generic classification within the inferior-ovaried tribe Vaccinieae has been limited in one part by the collections (many taxa are under collected due to their natural scarcity and high endemism), and by the lack of morphological analyses testing those characters traditionally used. Within Vaccinieae, *Disterigma* has been considered one of those genera for which relationships are hard to assign and preliminary molecular studies indicated it is likely polyphyletic. To better understand the relationships of *Disterigma* within Andean blueberries and its generic circumscription, parsimony analyses combining morphological characters with molecular data from the nuclear nrITS and chloroplast *ndhF* regions are being conducted. The gene trees recovered are highly congruent and the combined molecular analysis shows one species of MesoAmerican/Caribbean origin while the rest of *Disterigma* clusters with taxa of Andean origin. Within the Andean group, it was recovered a “Core *Disterigma* clade” including more than two thirds of the species. These findings are also supported by the morphological and total evidence analyses. All data sets and the combined analyses support the segregation from the “Core *Disterigma* clade” of some short-pedicellate species from southern South America; however, their exact placement within Vaccinieae remains ambiguous. Phylogenetic analyses have allowed the identification of a monophyletic clade for the taxonomic revision, comprising about 35 species primarily found in cloud forest from southern Mexico to Bolivia. *Disterigma* s.s. is characterized by having a pair of opposite bracteoles well differentiated from the bracts, apical in position, and clasping the calyx; subsessile flowers, mostly 4-merous, with stamens all equal, and twice the number of floral parts. New characters not previously used in *Disterigma*, but which vary consistently enough to tell species apart, include: the proportion to which the bracteoles cover the calyx, sepal length and shape, sepal consistency and disposition at fruit maturity, corolla 3-dimensional shape, corolla lobe length and apex shape, staminal filament shape (front and lateral), and fruit color.

Phylogenetic analysis of the Tribe Plumerieae (Apocynaceae, Rauvolfioideae), based on molecular and morphological markers. *Leonardo O. Alvarado-Cárdenas* and Helga Ochotorena. Departamento de Botánica, Instituto de Biologia, UNAM, Apdo. Postal 70-367, Mexico DF 04510, Mexico.*

The tribe Plumerieae has had controversial circumscription, but the current classification includes 11 genera. Even though there are several phylogenetic analyses for the family, they have not focused on the tribe and therefore they have not included all the genera. The results of the partial analyses using different markers have shown controversy regarding the monophyly of the tribe. In this work, the monophyly of the tribe and the relationships of their taxa are re-evaluated using available molecular data and morphology. The sampled including 47 species, considering all the genera in the tribe; the outgroup includes members of 8 tribes from

Rauvolfioideae and Apocynoideae. The molecular markers were downloaded from NCBI; they include: rbcL, the partial sequence of the intron of *trnL*, the *trnL-F* intergenic spacer sequence, and *matK*. All the partitions were aligned by eye; gaps were coded as characters; the combined molecular data set includes 282 potentially informative characters. The morphological matrix was constructed from personal observations and literature; it includes 48 potentially informative characters. The matrices were created in Winclada and parsimony analyses were conducted with NONA. The results from each matrix gave contrasting resolutions. The combined analysis yielded 8 trees (L = 768, CI = 54, RI = 70). The consensus corroborates the monophyly of Plumerieae, supported by the homoplasic condition of presence of a wing in the seed. All trees support two clades within the tribe, but the relationships of *Cameraria*, *Mortoniella* and *Skytanthus* vary among them.

Systematics of Bernardia section Tyria (Euphorbiaceae) based on morphological data.

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Bernardia is a neotropical genus of ca. 72 species distributed from southern United States to Argentina, with some species in the West Indies. Although molecular phylogenies have suggested the monophyly of *Bernardia*, there are no studies establishing hypotheses for the phylogenetic relationships at species and sectional levels. Among the seven sections proposed by Pax & Hoffmann, *Bernardia* secc. *Tyria* contains the higher number of species and it is the better known taxonomically. The main objective of this study was to test the monophyly of this section, although our sampling allows us to preliminary test the monophyly of *Bernardia* as well as the Pax & Hoffmann's infrageneric classification. A cladistic analysis based on parsimony was conducted including 70 potentially informative morphological characters from vegetative and reproductive structures. 40 species were considered in the analysis, representing all sections of *Bernardia* (23 species from sect. *Tyria*), three other genera out of six of Bernardieae (*Adenophaedra*, *Discocleidion* and *Necepsia*), and one genus out of five of Adelieae (*Adelia*). *Discocleidion* was used as the functional outgroup. The consensus of the 60 obtained trees revealed that *Bernardia* section *Tyria* is paraphyletic, as the most recent common ancestor also includes *B. crassifolia* (the single species of sect. *Crassifoliae*). On the other hand, *Bernardia* section *Alevia* is supported as a monophyletic group, and the monotypic sections *Passaea* and *Traganthus*, which some authors have suggested that they could deserve a generic status, are nested within a clade that includes the sampled species of sections *Polyboea* and *Phyllopassaea* (not retrieved as monophyletic). Thus, the cladistic analysis supports the monophyly of *Bernardia*, but not the classification scheme of Pax & Hoffmann. To recognize *Bernardia* sect. *Tyria* as a monophyletic group, *B. crassifolia* is included within it, so a re-circumscription of section *Tyria* is proposed.

Conflicts between molecular and morphological data in the phylogeny of Adelia (Euphorbiaceae s.s.).

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Among flowering plants, Euphorbiaceae is one of the families that show an impressive morphological variation in both vegetative and floral structures. In previous phylogenetic studies of the tribe Adeliae (Euphorbiaceae), topological conflicts between morphological and molecular phylogenies have been detected. In this study, taxa from the Acalyphoid clade and tribe Adelieae were included to investigate the conflict between morphological and molecular (chloroplast and nuclear DNA sequences) data. The level of phylogenetic signal in both partitions was determined based on the ILD test to explore the cause of incongruence. Three indices were calculated to evaluate phylogenetic signal: the skewness index (g1), the data decisiveness index (DD), and the density distribution of the retention index (RI). A significant incongruence was detected between the morphological and molecular data according to the ILD test. Values of DD showed that the molecular and morphological data analyzed here are similarly decisive. Estimates of g1 and RI density detected a considerable proportion of homplasy present in both data sets. However the phylogenetic signal increases when the two data matrices are combined. Therefore, the combined topology was used as the preferred phylogenetic hypothesis in this group of Euphorbiaceae.

POSTER SESSION: BOTANY

Molecular phylogeny of Laurencia complex (Rhodophyta) in the Mexican Caribbean based on rbcL region. *Jhoana Díaz L.*[1], Abel Sentíes G.[1], Mutue Fujii T.[2], and Francisco F. Pedroche[1]. [1]Departamento de Hidrobiología, UAM-Iztapalapa, Apdo. Postal 55-535, México DF 09340, México. [2]Instituto de Botánica, Sao Paulo 01051, Brasil.*

The classic taxonomy of *Laurencia* complex does not show a necessary character differentiation and delimitation, because of this the group classification is unstable. The objectives of the present work was studied the molecular biological diversity of the complex based on nucleotides sequences analysis of *rbcL* gene, and to elaborate phylogenetic hypothesis that reflect a more robust classification scheme of the species located on the Mexican-Caribbean coasts. The genetic divergence was estimated in percentage among 25 taxa, and phylogenetics analysis was carried out using parsimony and maximum likelihood. In both analyses the *Laurencia* complex assemblage contained three distinct clades, corresponding to the genera *Chondrophycus*, *Laurencia sensu stricto* and *Osmundea*. The basal clade of *Osmundea* includes the species: *O. pinnatifida* and *O. spectabilis* var *spectabilis*. In all phylogenetic trees the genus *Chondrophycus* is sister to the genus *Laurencia*. The clade of *Laurencia* includes *L. brongniartii*, *L. intricata*, *L. filiformis*, *L. obtusa*, *L. venusta*, *L. "tulunesa*", and *L. "amarilla"*. The clade of *Chondrophycus* includes two clades. One clade includes only two species: *C. gemmiferus* and *C. poiteaui* and the other clade includes *C. flagelliferus*, *C. papillosus* and *C. corallopsis*.

The Order Corallinales (Rhodophyta): A phylogenetic proposal. *Dalila Fragoso* and Dení Rodríguez. Laboratorio de Ficología, Facultad de Ciencias, UNAM, Apdo. Postal 70-592, Ciudad Universitaria, Coyoacán, México DF 04510, Mexico.*

Previous analysis of morphological traits prompted the recognition of informal subdivisions in the order Corallinales as several suprageneric groups. Recently, based on morphological evidence, other authors suggested modifications for the recognitions of groups within Corallinales. Molecular phylogenetic studies of the whole order have been performed predominantly with data from the small subunit (SSU) *18s* rRNA. Most phylogenetic studies to date have consistently identified seven to eight major lineages within Corallinales. Some relationships among these lineages match well the classical taxonomical proposals, but others do not. In this paper we use the cladistic methodology to combine the available molecular information in GenBank, with morphological information that has been used in different taxonomical schemes. We explore the congruence between morphological and molecular cladograms to assess the phylogenetic utility of the different character sets, and suggest a preferred estimate for the phylogeny of the order Corallinales. Our results show seven different lineages but only one of them corroborates previous proposals, the rest imply the paraphyly or polophyly of the currently recognized groups. The translation of these lineages to a proposal of classification permits the re-circumscription of some groups, while others have to be abandoned. The synapomorphies supporting each clade are discussed.

Exploratory analysis of the quantitative characters usefulness in phylogenetic analysis: an example in the genus Codium (Chlorophyta) in Veracruz, Mexico. *R. C. Tufiño Velázquez*[1]; J. Díaz Larrea[1], and F. F. Pedroche[1,2]. [1]Departamento de Hidrobiología, UAM-Iztapalapa, Apdo Postal 55-535, México DF 09340, Mexico. [2]University Herbarium, University of California 1001 VLSB # 2465, Berkeley, CA 94720-2465, USA.*

The current controversy about the usefulness of the quantitative characters in phylogenetic analyses has an influence on opinions and postures displayed in many papers; at present there is a whole conceptual gradient that consider, in one way, that the meristic characters do not contribute to any phylogenetic information and, on the other hand, there has been a pronunciation that they can only be used in a coding way. To recognize character states is a fundamental stage in phylogenetic analyses. In this sense, the development of different quantitative methodologies to detect or delimit character states is very interesting. In order to define "gap coding", in this paper we show a statistical methodology applied on 7 anatomical characters for 13 exemplars of the genus *Codium* recollected in the state of Veracruz, Mexico. Six average morphospecies registered in the literature were added in the data matrix. The resolved clades in the topology of the web of the specimens recollected do not correspond with the established morphospecies. A coherent position is that, a priori, we can use any kind of characters (i.e. quantitative) in the phylogenetic analysis; so, when they do not resolve the topologies, we have two options: there was a failure in the codification or, they do not have phylogenetic information. This last position has been almost the only one choosing to let the molecular characters to provide the exploration for the taxa. It will be very interesting to explore other quantitative methods of codification.

Gymnosperms and cladistic biogeography of the Mexican Transition Zone. *Raúl Contreras-Medina*, Isolda Luna Vega, and Juan J. Morrone. Departamento de Biología Evolutiva, Facultad de Ciencias, UNAM, Apdo. Postal 70-399, Mexico DF 04510, Mexico.*

Distributional patterns of 81 species of three genera of Mexican gymnosperms (*Ceratozamia*, *Dioon*, and *Pinus*) were analyzed in order to evaluate their contribution to the cladistic biogeography of the Mexican Transition Zone, applying Brooks Parsimony Analysis (BPA) and parsimony analysis of paralogy-free subtrees. BPA showed three main groups of areas: clade A is composed by Baja California, Great Basin and Mojavean provinces; clade B includes Valle de Tehuacán-Cuicatlán, Balsas Basin, Planicie Costera del Noreste, Planicie Costera del Noroeste, Costa del Golfo de México and Costa Pacífica, provinces located at both coasts and central lowlands of Mexico; and clade C includes the Appalachian, Atlantic and Gulf Coastal, Yucatán Peninsula, Caribbean, Californian, Vancouverian, Eastern Central America, Soconusco, Serranías Transístmicas, Serranías Meridionales, Sierra Madre Occidental, Altiplano and Sierra Madre Oriental, provinces that correspond to the Mexican montane areas of the Mexican Transition Zone, Central America and some areas of the United States of America. The parsimony analysis of the paralogy-free subtrees showed three groups of areas: clade D includes Vancouverian, Appalachian and Atlantic and Gulf Coastal provinces; clade E includes Balsas Basin, Planicie Costera del Noreste and Planicie Costera del Noroeste; and clade F includes Serranías Transístmicas, Soconusco, Serranías Meridionales, Sierra Madre Occidental, Altiplano, Sierra Madre Oriental, Baja California, Californian, Great Basin and Mojavean provinces. Comparing both analyses, three common area relationships emerge: 1) Appalachian and Atlantic and Gulf Coastal, 2) Great Basin, Mojavean and Baja California, and 3) Altiplano, Sierra Madre Oriental and Sierra Madre Occidental. The general area cladograms obtained support some area relationships not explained in previous works, and may complement the historical distributional patterns of the biota of the Mexican Transition Zone.

Phylogeographic analysis of Pinus leiophylla in Mexico. *Abril Rodríguez-Banderas*[1], Carlos F. Vargas[1], and G. G. Vendramin[2]. [1]Prolongacion de Carpio y Plan de Ayala s/n Col. Casco de Santo Tomas, Mexico 11340, Mexico. [2]Istituto di Genetica Vegetale, CNR, Via Madonna del Piano, Sesto Fiorentino (Firenze) I-50019, Italy.*

We used six chloroplast microsatellite loci to assess the phylogeographic structure across the natural range of *Pinus leiophylla* in Mexico (including its two varieties: *P. leiophylla* var. *leiophylla* and *P. leiophylla* var. *chihuahuana*). We found 92 haplotypes in 22 populations of which each variety showed a distinctive group. The average values of genetic diversity were He=0.7604 and D2sh=0.9313. Interestingly, populations of *P. leiophylla* var. *chihuahuana* exhibited diverse values below the average (opposite to those of *P. leiophylla* var. *leiophylla* populations). All the different approaches used (haplotype frequency map, PCA, SAMOVA, Nst vs. Nst permutated) detected the presence of a phylogeographic pattern in tree groups that correspond well to the geographic positions of the populations, but there was no isolation by distance. The first group is constituted by *P. leiophylla* var. *chihuahuana* populations and two *P. leiophylla* var. *leiophylla* populations from the north that share haplotypes with *P. leiophylla* var. *chihuahuana*; the second group by *P. leiophylla* var. *leiophylla* populations from the center (south of Sierra Madre Occidental and Trans-Mexican Volcanic Belt), and the third group by populations from the south. According to a haplotype network, those haplotypes found predominantly in *P. leiophylla* var. *chihuahuana* or in the northern populations of *P. leiophylla* var. *leiophylla* clustered together to form a little star-like shape network, separated in several points and by several hypothetical ancestors from a reticulate pattern conformed by the distinct haplotypes of *P. leiophylla* var. *leiophylla*. We conclude that the ancestral area of *P. leiophylla* var. *leiophylla* is in central Mexico (with the Trans-Mexican Volcanic Belt as reference) and that its differentiation and its dispersion have been to the south and to the north. For the case of *P. leiophylla* var. *chihuahuana*, it seems that its ancestral area is in the north and that its populations are in recent expansion. Our results also suggest that *P. leiophylla* var. *leiophylla* and *P. leiophylla* var. *chihuahuana* are very different from each other and we could consider them as different species.

A phylogenetic morphological analysis of Puya subgenus Puya (Bromeliaceae). *Claudia T. Hornung-Leoni* and Victoria Sosa. Departamento de Biología Evolutiva, Instituto de Ecologia, AC, Xalapa, Veracruz, México.*

Traditionally, *Puya* has been included in subfamily Pitcairnioideae; however, molecular analyses have shown that its position is problematic, and that it probably belongs to subfamily Bromelioideae. *Puya* is a genus distributed mainly in the Andes and it has been taxonomically divided into two subgenera: *Puya* and *Puyopsis*, based on a single character, the presence of sterile apices in the apex of branches of the inflorescence. Subgenus *Puyopsis* comprises the majority of the species. Subgenus *Puya* includes eight species distributed mainly in Chile, Argentina, Bolivia and Peru. In this work, phylogenetic analyses are conducted with morphological characters to determine if the diagnostic character is a synapomorphic character state. The single-most parsimonious tree retrieved in parsimony analysis indicates that subgenus *Puyopsis* is paraphyletic and subgenus *Puya* is monophyletic. The eight species of subgenus *Puya* are supported by several synapomorphies, including the diagnostic character.

Phylogeny of an American bamboo, Otatea (Poaceae: Bambusoideae), based on rpl16 intron sequence data. *Eduardo Ruiz-Sánchez*, Victoria Sosa, Ma. Teresa Mejia-Saulés, and Flor Rodríguez-Gómez. Apdo. Postal 63, 91000, Xalapa, Veracruz, Mexico.*

Otatea, whose relationships are unknown, has been classified together with other two genera (*Guadua* and *Glaziophyton*) within Guaduinae, an American subtribe of neotropical woody bamboos. A parsimony analysis was performed in order to determine the position of *Otatea* within this subtribe. All three species of *Otatea* were considered in addition to representative species of the other genera in the subtribe. As outgroups, 16 representative taxa of subtribes

Arthrostylidiinae, Chusqueinae and Bambusinae were selected. A total of 19 species were included. The data set consisted of DNA sequences of a non-coding chloroplast region, the intron rpl16. From the 88 variable sites only 18 were phylogenetically informative. Seven most parsimonious trees were recovered, in which *Otatea* was sister to a clade formed by *Aulonemia fulgor- Olmeca recta-Olmeca reflexa*. Tribe Guaduinae formed a clade including *Aulonemia fulgor*, which is classified in another subtribe, Arthrostylidiinae. In previous analysis based on chloroplast restriction sites, rpl16 and ndhF, *Otatea* was sister to *Guadua paniculata*, or *Glaziophyton mirabile*. The first taxon has been classified in Guaduinae and the second in Arthrostylidiinae. Both taxa are distributed from Mexico to Argentina and Brazil respectively. However in this work, *Otatea* resulted closely related to species endemic to Mexico such as *Aulonemia fulgor*, *Olmeca recta*, and *O. reflexa*. This work confirms the close relationships between the two subtribes Athrostylidiinae and Guaduinae, sister to subtribe Chusqueinae, the three with a Neotropical distribution.

Variation, development an evolution in the column of the Pleurothallidinae subtribe (Orchidaceae). *Rodolfo Solano Gómez. Centro Interdisciplinario de Investigación para el Desarrollo Integral Regional Unidad Oaxaca, Instituto Politécnico Nacional. Hornos 1003, Santa Cruz Xoxocotlan, Oaxaca 71230, Mexico.*

The taxonomy of Pleurothallidinae, the largest orchid subtribe, had traditionaly been based on floral characters, but these are homoplasic traits which are product of plant-pollinator interactions and they do not reflect the phylogenetic relationships within the group. Up to now the orchidologists have not analyzed the variation and evolution of Pleurothallidinae floral traits in a comparative way, specially those characters that have been employed for its taxonomy. The column is one of such structures; its evolution seems to be the consequence of selection pressures imposed by the pollination syndromes, so it is important to know if there are some basic types which can define lineages within the subtribe. In this study morphological variation in the column was analyzed to define the basic types, the changes that occur during the development of these types were studied and the column evolution was optimized onto a Pleurothallidinae cladogram. The column variation fits to five basic types: I. column with dorsal anther and entire apical stigma; II. column with dorsal anther and bilobed apical stigma; III. column with dorsal anther and ventral stigma; IV. column with apical anther and stigma, V. column with ventral anther and stigma. In types I, II, and III the anther always occupy a dorsal position through the column develop. In type IV the anther start in a dorsal position but in final stage it ends in an apical position. The anther from type V is dorsal in early stages, in intermediate stages it turns apical, and at the end it acquires a ventral position. The development of type III column shows a recapitulation of the mature stages from types I and IV, while the type III column recapitulate the mature stage from type I. The type III column is primitive condition among Pleurothallidinae, within the subtribe every type evolved from the ancestral type III column. The type II column evolved independently in several subtribe lineages, which include two of the largest genera, *Pleurothallis* and *Stelis*.

Phylogenetic analysis of the Patagonian Calceolaria polyrhiza complex based on ITS DNA sequences. *Andrea Cosacov[1], Victoria Sosa*[2], Alicia Sérsic[1], and Arturo de Nova[2]. [1]Biología Floral, Instituto Multidisciplinario de Biología Vegetal, CC 492, Córdoba 5000, Argentina. [2]Biología Evolutiva. Insituto de Ecologia, AC, Apdo. Postal 63, Xalapa, Veracruz 91000, Mexico.*

Calceolaria is a South and Central American plant genus of 270 species, traditionally classified into 24 sections. Four taxa are in the southern limit of distribution, in Patagonia: *C. polyrhiza*, *C. lanceolata*, *C. prichardii* and *C. mendocina*. Relationships among these species have not been studied in detail and furthermore, the position of *C. mendocina* is problematic. It has been placed either in Section *Bellidifoliae* or as part of the *C. polyrhiza* complex, which includes *C. polyrhiza*, *C. lanceolata* and *C. prichardii*, species traditionally placed in Section *Kremastocheilos*. To determine the position of *C. mendocina* and understand relationships of these taxa, a parsimony analysis of nuclear DNA ITS sequences that considered 87 taxa representative of almost all sections of *Calceolaria* was performed. Even though that the position of the studied taxa was not resolved, results show that *C. mendocina* is nested together with *C. polyrhiza*, *C. prichardii* and *C. lanceolata*. Consensus revealed a clade comprising *C. prichardii*, *C. lanceolata* and an Argentinean sample of *C. polyrhiza* while *C. mendocina* and the Chilean *C. polyrhiza* form a polytomy together in this clade. More characters are needed to resolve the position of this group of species, but undoubtedly *C. mendocina* should be placed as part of the *Calceolaria polyrhiza* complex.

Rhus s.str. (Anacardiacee) phylogenetic analysis and the evolution of leaf. *Agustina Rosa Andrés-Hernández*[*1], Teresa Terrazas[1,2], and Helga Ochotorena[2]. [1]Programa de Botánica, Colegio de Postgraduados, Montecillo, Estado de México 56230, Mexico. [2]Departamento de Botánica, Instituto de Biología, UNAM, Apdo. Postal 70-233, México DF 04510, Mexico.*

The genus *Rhus* has a long taxonomic history and its limits had been controversial, however several molecular phylogenies support *Rhus s.str.* monophyly including nearly 35 species grouped in two subgenera. Ten species are grouped into the subgenus *Rhus* and are distributed in eastern Asia, North America, southeastern Europe, and Hawaii. The subgenus *Lobadium* contains 25 species, mainly distributed in southwestern United States and Mexico. The infrageneric relationships of *Rhus s. str.* are unresolved and it is unknown if there are structural characters that support the existing infrageneric classification. The phylogenetic relationships using parsimony analysis of *Rhus s. str.* were investigated using ITS, *ndh*F and *trn*L-F sequences and 40 structural characters. Thirty one species of *Rhus s. str.* representing both subgenera plus seven species that are members of *Rhus s. l.* and *Schinus molle* as the functional outgroup were included in the analysis. Analysis resulted in more than 100 trees (length 806, CI 0.69, RI 0.78). The consensus cladogram yielded a hypothesis that supports the traditional classification of *Rhus s. str.* The occurrence of glandular trichomes in the inflorescence, fruit and leaves and ciliate sepals are the characters that support *Rhus s. str.* monophyly. Percurrent tertiary veins and seven resin canals in the vascular bundle of the petiole are the evolutionary novelties of subgenus *Rhus*, while 14 species grouped in a clade recognized as the subgenus *Lobadium* have shorter pedicels and bractlets. The tendency in the species of section *Styphonia* of having simple or compound evergreen leaves with mostly eucamptodromous and cladodromous venation with sclerified bundle sheath cells towards fifth order veins and well-developed terminal idioblasts are undoubtedly related to the radiation events that *Rhus s. str.* had in Mexico.

On the phylogenetic relationships of Stenocereus (Cactaceae): a combined molecular and morphological approach. *Hilda J. Arreola-Nava[1], Salvador Arias*[*2], and Teresa Terrazas[2]. [1]Universidad de Guadalajara, CUCBA, Zapopan, Jalisco, Mexico. [2]Instituto de Biologia, UNAM, Mexico DF 04510, Mexico.*

Stenocereus (A. Berger) Britton & Rose is a relatively extensive genus of Cactaceae, consisting of approximately 22 species in the subfamily Cactoideae, tribe Pachycereeae. Species of *Stenocereus* are generally characterized as tree-like, low shrubs growing erect, semirect or prostrate. *Stenocereus* species are found from the SW United States to Venezuela, but most of them are Mexican in distribution. The phylogenetic relationships of *Stenocereus* species were studied using parsimony analyses of DNA sequence and structural data. The plastid *rpl16* and *trnL-F* regions were sequenced and 43 morphological and anatomical characters were codified for 29 taxa including all species of *Stenocereus*, and representatives from all genera of subtribe Stenocereinae plus *Echinocereus pensilis*. *Stenocereus* is recovered as monophyletic with 22 species, and *Echinocereus pensilis* is revealed basal to all the species of *Stenocereus*. The synapomorphies that support the genus are a long floral tube, dehiscent fruit, mucilage and silica bodies presence. Three clades within *Stenocereus* are recovered. The first group is integrated by the species with clear areoles where *S. dumortieri* is the basal species. In this clade five species are distinguished by their shrubby habit and their flower pollinated by sphingids and hummingbirds. The second group is defined by species with brown areoles and includes seven species. A third group is recovered with three species, as basal the clade.

Phylogenetic relationships of Cephalocereus species (Cactaceae). *María Luisa Bárcenas-Aguello*[1], Teresa Terrazas[2], and Salvador Arias[3]. [1]Programa de Botánica, Colegio de Postgraduados, Montecillo, Estado de México 56230, Mexico. [2]Departamento de Botánica, [3]Jardín Botánico, Instituto de Biología, UNAM, Apdo. Postal 70-233, México DF 04510, Mexico.*

Cephalocereus Pfeiff. is an endemic genus from Mexico and its species are distinctive by their monopodic stems with basitonic branching and flowering regions. Recent classifications recognized that five species belong to *Cephalocereus* and this delimitation was supported by molecular phylogenies, however it is not known if those diagnostic features that allow to recognizing the genus and its species are apomorphic characters. The phylogenetic relationships, using parsimony analysis, of *Cephalocereus* species were evaluated using 68 structural characters. The five species of *Cephalocereus*, *Neobuxbaumia mezcalaensis*, its sister species, and *Pseudomitrocereus fulviceps*, the outgroup species, were included in the analysis. Analysis resolved one most-parsimonious tree (length 102, CI 0.75, RI 0.68). The monophyly of *Cephalocereus* is supported by several synapomorphies among them occurrence of apical pseudocephalium, ausence of spines in the flowers, presence of crystals in trichomes and of terpenoids in stem tissues. Two clades were recovered with high support values and are in agreement with those recognized by molecular data. The two clades correspond to the infrageneric classification proposed by Bravo-Hollis, thus the subgenus *Cephalocereus* and the subgenus *Neodawsonia* should be recognized. The subgenus *Cephalocereus* groups the sister species *C. columna-trajani* and *C. senilis*, defined by the occurrence of lateral cephalium, which is one of their evolutionary novelties as well the striate surface of the external perianth and various seed features. The subgenus *Neodawsonia* groups the sister species *C. apicicephalium* and *C. nizandensis* sister to *C. totolapensis*. Morphological characters previously considered important for defining species and subgeneric groups are not recovered as novelties; however new characters especially micromorphological floral ones will be discussed

Systematics of genus Acanthocereus (Engelmann ex A. Berger) Britton & Rose (Cactaceae). *Carlos Gómez-Hinostrosa* and Héctor M. Hernández. Departamento de Botánica, Instituto de Biología, UNAM, Apdo. Postal 70-233, México DF 04510, Mexico.*

Acanthocereus (Cactaceae) is currently understood as a group of 6-7 shrubby species distributed from southeastern United States (Florida and Texas) and northwestern Mexico (Sonora) to Venezuela and Colombia. It is primarily found in tropical dry and semi-evergreen forest, along the Pacific and Atlantic slopes, at altitudes ranging from sea level to 1500 m. The vegetative and reproductive morphology of all members of genus *Acanthocereus* was studied on the basis of herbarium material and extensive fieldwork in Mexico and Guatemala. The morphological study, along with anatomic observations of the stem, allowed us to determine that the genus comprises only one species with a great morphological variability: *A. tetragonus* (L.) Hummelinck. In addition, we have transferred of *A. chiapensis* to *Peniocereus*. A phylogenetic analysis based upon morphological characters was carried out. *Acanthocereus tetragonus* and some species belonging to genera in tribes Cereeae, Pachycereeae and Hylocereeae (*Cereus*, *Dendrocereus*, *Pachycereus*, *Peniocereus*, *Pseudoacanthocereus* and *Selenicereus*) were included in the analysis. The resulting cladogram reflected that: 1) *Peniocereus* sensu lato is a poliphyletic group, 2) *Peniocereus* subg. *Peniocereus* should be elevated to generic rank, 3) *A. tetragonus* is sister to *Peniocereus* subgen. *Pseudoacanthocereus*, suggesting the possibility to transfer that subgenus to *Acanthocereus*.

Phylogenetic analysis of Axiniphyllum Benth. (Asteraceae: Heliantheae). *Alberto González-Zamora* and Isolda Luna Vega. Departamento de Biología Evolutiva, Facultad de Ciencias, UNAM. Av. Universidad 3000, Circuito exterior, Ciudad Universitaria, México DF 04510, Mexico.*

A cladistic analysis based on morphological characters was undertaken to determine the phylogenetic relationships among the species of *Axiniphyllum* Benth. (Asteraceae: Heliantheae). This genus is endemic to the montage regions of western Mexico; it distributes from Durango and Nayarit in the Sierra Madre Occidental to Guerrero and Oaxaca in the Sierra Madre del Sur. For this study we included 19 terminals, five of them representing the recognized species of *Axiniphyllum* sensu Turner (1978). The external groups used in our work were one species of *Milleria*, five species of *Rumfordia*, three species of *Sigesbeckia*, two species of *Smallanthus* and two species of *Trigonospermum*. *Zaluzania augusta* var. *augusta* was also included as the functional external group. All these genera (except *Zaluzania*) were considered within the subtribe Milleriineae by Robinson (1981). Revision of the original descriptions of this genus and its species, as well as the detailed revision of the morphology in herborized specimens and fresh material, let us recognize morphological variation on its species. This task let us redescribe *A. sagittalobum*, species only known from the type specimen. Phylogenetic analysis of 28 morphological characters threw a single cladogram, where the relationships among the taxa involved are shown, suggesting that *Axiniphyllum* is a monophyletic group.

WEDNESDAY 16TH

CONTRIBUTING PAPERS

Re-emergence of Seasonal Influenza Viruses and Comparative Visualization of the Geographic Spread of Influenza. *Daniel Janies[1]*, Diego Pol[1,2], Farhat Habib[1], Rob Guralnick[3], Andrew Hill[3], Susan Perkins[4], Eric Waltari[4], Ward Wheeler[4], David Spiro[5], and Elodie Ghedin[5,6]. [1]Department of Biomedical Informatics, The Ohio State University, Columbus, OH, USA. [2]Museo Paleontologico Egidio Feruglio, Consejo Nacional de Investigaciones Cientificas y Téchnicas, Argentina. [3]University of Colorado Museum, CO, USA. [4]Division of Invertebrates, American Museum of Natural History, New York, USA. [5]Viral Genomics, The Institute for Genomic Research, Rockville, MD, USA. [6]Division of Infectious Diseases, University of Pittsburgh, PA, USA.*

Most influenza infections of humans since 1968 have been attributed H3N2 or H1N1 antigenic subtypes. However due to recent novel infections of humans with an avian strain of influenza (H5N1), a great deal of attention has been focused on the types of birds carrying H5N1 and any mutations of H5N1 associated with host shifts. We have created an interactive genomic and geographic map using Google ™ Earth to reconstruct evolution and spread of H5N1 influenza lineages over the past decade. Our map provides insight on competing hypotheses as to whether H5N1 is spread via migratory or domestic bird hosts or both. The answer to these questions depends on the temporal and geographic context in which the question is asked. Several lineages of H5N1 spreading from southern China in the past decade have exploited distinct pathways in terms of types of avian hosts and geography. Also, we compare and contrast the results of the study of 291 H5N1 genomes with analyses of 546 to 1343 genomes of seasonal influenza isolated over several decades and sequenced by the Influenza Genome Project. The analyses of seasonal influenza include mutational, recombination, host, and geographic studies of isolates of subtypes: H1N1, H1N2, H3N2, H3N3, H3N1, H3N4, H3N5, H3N8, and H2N2 in avian, human, and swine hosts. It is apparent that H5N1 has thus far spread gradually across Eurasia and South East Asia using various forms of avian hosts. In contrast, seasonal influenza moves rapidly across the globe and jumps readily among human and swine hosts. Seasonal influenza infrequently infects avian hosts however these events have not lead to recent novel epidemics among humans. However we observe complex patterns of host shifts, mutations, and genomic reassortment events in the evolution of seasonal influenza. Notable among these patterns are several key mutations associated with the re-emergence of a lineage of H3N2 in New York State and New Zealand in 2003-05. This H3N2 lineage was apparently extinct in New York and New Zealand after 1999-2000. The re-emergence of 2003-05 H3N2 was seeded by H3N2 viruses that circulated among swine in South China and humans in Asia and Europe between 1999 and 2003 rather than by locally persistent strains in New York and New Zealand.

CONTRIBUTING PAPERS: ZOOLOGY

Multigene analysis to resolve the phylogenetic status of sponges. *Romain Derelle* and Michaël Manuel. Université Pierre et Marie Curie, UMR7138 SAE, bat. A, 4eme étage, 7 quai Saint Bernard, Paris 75005, France.*

Sponges (phylum Porifera) are traditionally divided into three classes: Calcispongia, Hexactinellida and Demospongiae. Recent phylogenetic studies suggest the paraphyly of sponges, with Calcispongia branching of Calcispongia as sister group of Eumetazoa. Moreover, it was shown that a particular subclass of Demospongiae, Homoscleromorpha, which are the only sponges to possess basal lamina (with collagen IV and laminin), seem to cluster apart from the demosponges. But the relationships between the main sponge's lineages are not well supported in published molecular phylogenies, which are mostly from ribosomal RNA sequences. Beyond taxonomic implications, this question is crucial to understand the origin and early evolution of animals, in particular because sponge paraphyly would favor a sponge-like organism as the last common ancestor of Metazoa. In order to obtain sufficient phylogenetic signal, we developed a phylogenomic approach by sequencing 2000 ESTs from four species belonging to each one of these four evolutionary lineages of sponges: Oopsacas minuta (Hexactinellida), Ephydatia muelleri (Demospongiae), Oscarella lobularis (Homoscleromorpha) and Sycon raphanus (Calcispongia). The presentation will highlight some methodological issues for analyzing such large sequence data sets. The main results will be commented, with particular focus on the phylogenetic status of sponges and the position of homoscleromorphs and calcisponges.

Molecular phylogeny of the Leptothecata (Hydrozoa, Cnidaria): implications for the evolution of life cycle and colony architecture. *Lucas Leclère*[1], Peter Schuchert[2], and Michael Manuel[1]. [1]UMR 7138 CNRS UPMC MNHN IRD ENS, Case 05, Université Pierre et Marie Curie, Paris, France. [2]Muséum d'histoire naturelle, CP 6434, CH-1211 Genève 6, Switzerland.*

The *Leptothecata* (= *Leptomedusae*) are a highly diversified monophyletic group of Hydrozoa (Medusozoa, Cnidaria). Their main synapomorphy is the presence of a theca, a skeletal structure surrounding each polyp. This group includes in particular the cosmopolite families Plumulariidae, Aglaopheniidae, Sertulariidae, Haleciidae, and Campanulariidae. There is a diversity of life cycles in this group. In many species there are alternating generations, the asexual, benthic polyp and the sexual and pelagic medusa. However, in some species the medusa has been reduced to medusoids or - in the majority of species - it is lost altogether. In this latter case, the polyp generation reproduces sexually. Polyps are always colonial in *Leptothecata*, and these colonies exhibit a great diversity of organizations. We performed a detailed phylogenetic analysis of this group using mitochondrial (*16S*) and nuclear (*18S* and *28S*) ribosomal DNA sequences for about a hundred species. Our molecular trees are sufficiently resolved to set up a framework for a phylogenetic classification of the leptothecates, and to explore the evolution of various morphological characters. These results support new and sometimes provocative hypotheses about the evolution of life cycle and colonial organization.

Towards dynamic homology of morphological characters? A first step with the simple case of chaetotaxy in the family Odontellidae (Poduromorpha, Collembola, Hexapoda). *Mikaël Agolin. Laboratoire "Origine, Structure et Evolution de la Biodiversité", UMR CNRS 5202 / USM MNHN 0601, Département Systématique et Evolution, Muséum National d'Histoire Naturelle de Paris, Bâtiment Entomologie, CP 50,45 rue Buffon, Paris 75005, France.*

In the traditional phylogenetic routine, one of the most delicate steps is character definition. This sensitive process consists in defining homology classes, hence forbidding a number of attribute comparisons and constraining phylogenetic inferences. In most cases, the considered attributes are so integrated that the matter is obvious and quite trivial. Contrastingly, some morphological datasets are prone to bring the biologist to make difficult (and unnecessary) decisions. An instance of those difficult cases is provided here, with chaetotaxic datasets of the collembolan family Odontellidae. Chaetotaxy is the use of setae as taxonomic characters. Theoretically, setae have definite positions and are organized in specific patterns. Consequently, with the exception of extreme plurichetotic cases, many setae can be recognized through entire families, and sometimes orders. Named setae are defined by their relative positions, nature and shape, each seta being a putative character. Chaetotaxic datasets have proved to be very informative during the past 20 years. Unfortunately, most setae are alike, and when a loss or gain occurs, the distances between the setae are readjusted, making the correspondences fuzzy. Consequently, the produced phylogenetic inferences vary with the interpretations of characters. In order to avoid loss of information without either making unreasonable or arbitrary decisions, I chose to consider setae as attributes, and define them only by relative connections. On the body tergites, each half-segment bears one to three rows of up to six setae each. Considering this linear organization to be the only objective connection between them, several homology hypotheses can be explored between the setae of homologous rows in the different species. The rows are therefore defined by their setae sequences, and the homologies can be decided by alignment. Each type of row is considered a separate dataset. In order to optimize overall coherence while inferring homologies and phylogenetic trees, the sequences are analyzed using an unweighed parsimony direct optimization algorithm implemented in POY. Some preliminary results on the phylogeny of Odontellidae and homology hypotheses between the setae, rows and segments are given, as well as some methodological perspectives.

Phylogeny of Collembola: Were the first springtails semi-aquatic? *Cyrille A. D'Haese. UMR 5202 CNRS, Département Systématique et Evolution, Muséum National d'Histoire Naturelle, Paris, France*.

Colonization of land from an aquatic environment is one of the major evolutionary transitions within the arthropods. More specifically, it is often considered that first Collembola were semi-aquatic and secondarily conquered fully terrestrial habitats. Recently, it was proposed that Collembola were not closely related to the remaining hexapods but rather embedded into crustaceans. That result would also point to an aquatic origin. To understand Collembola ecological origin and evolution, a phylogenetic framework is proposed. Multiple molecular loci and morphology for a broad taxonomic sampling are analyzed through Direct Optimization to address the placement of the four orders Neelipleona, Symphypleona, Entomobryomorpha and Poduromorpha, along with the familial relationships within the orders. The question of interest is answered by mapping the ecological attributes onto the obtained phylogeny.

Systematics of Cyrtacanthacridinae (Orthoptera: Acrididae) and the evolution of locust phase polyphenism. *Hojun Song and John W. Wenzel*. Department of Entomology, The Ohio State University, Columbus, Ohio 43210, USA*.

Phase polyphenism is a dramatic and important phenomenon by which fairly harmless, solitary, sedentary grasshoppers become a destructive swarm of insects (called locusts in this phase) that move together, crossing continents. This has evolved several times in different lineages, and most study focuses on the separate species of locusts. Phase polyphenism is complex, consisting of numerous density-dependent phenotypically plastic traits. A phylogenetic study shows that different components evolved independently, and that certain of these are actually rather ancient, phylogenetically conserved traits.

On false click-beetles and whether different data partitions click as well – the molecular phylogeny of Eucnemidae (Coleoptera, Polyphaga: Elateriformia). *Marianna Teräväinen*[1,2] and Jyrki Muona[1]. [1]Finnish Museum of Natural History, Department of Entomology, P.O. Box 26, University of Helsinki FI-00014, Finland. [2]American Museum of Natural History, Division of Invertebrate Zoology, Central Park West at 79th Street, NY 10024, USA.*

The Eucnemidae are part of the triad of clicking beetles with the closely-related families Elateridae and Throscidae. They are often described as an elusive group in field guides due to the difficulties in capturing them. However, findings of an abundance of eucnemids in tropical lowland forests and what little is known about their life-history suggest they play an important role in forest regeneration. The most comprehensive molecular study of the family to-date is presented. The data set is based on 200 dried specimens from which nuclear *28S* (2400 bp), *18S* (1900 bp), *H3* (330 bp), and mitochondrial *COI* (800 bp), *16S* (550 bp), and *12S* (400 bp) were sequenced with varying success. The influence of missing data is revisited through comparisons of the total evidence approach with different ways of partitioning the data. Morphological characters used to make delineations within the family are discussed in the light of the tree.

The evolutionary history of the thylacosternid-beetles (Coleoptera: Elateridae: Thylacosterninae); mission impossible? *Varpu Vahtera* and Jyrki Muona. Department of Entomology, Zoological Museum/Finnish Museum of Natural History PO Box 26, University of Helsinki FI-00014, Finland.*

Thylacosterninae is a characteristic clade of beetles belongingto the superfamily Elateroidea. The group is pantropical in distribution with species in Africa, Asia, South America and northeast Australia. The known fifty species have been placed in four genera; Balgus, Thylacosternus, Cussolenis and Pterotarsus. The thylacosternid-clade has several apomorphic characters, of which some connect it with the family Eucnemidae, some with Elateridae and some with Throscidae. However, all the old attempts to classify these beetles have been based on “sensible” reasoning, not analyses. In order to resolve the phylogeny of the group, we sampled specimens from all known genera, re-studied altogether 125 morphological characters and analyzed this new data set simultaneously with the *16S* and *28S* genes. Our results show that thylacosternid-beetles belong to the family Elateridae but the relationships within the genera are far from unambiguous.

Molecular phylogenetics of Syrphinae (Diptera: Syrphidae) based on mitochondrial COI and nuclear 28S rRNA genes. *Ximo Mengual*[1], Gunilla Ståhls[2], and Santos Rojo[1]. [1]CIBIO (Centro Iberoamericano de la Biodiversidad), University of Alicante, Spain. [2]Entomology Dept., Finnish Museum of Natural History, University of Helsinki. Finland.*

The family Syrphidae (Diptera: Cyclorrapha) is traditionally divided into three subfamilies: Eristalinae, Microdontinae and Syrphinae. The subfamily Syrphinae includes the majority of predatory syrphids. The current classification basically follows Vockeroth (1969; Mem. Ent. Soc. Can. 62: 1-176) and, on the basis of adult characters, four tribes are typically recognized: Bacchini, Paragini, Syrphini and Toxomerini. Using larval characters, Rotheray & Gilbert (1989; Zool. J. Linn. Soc. 95: 29-70) recognized five tribes including Pipizini in Syrphinae. The aim of the present study is to use molecular data for exploring phylogenetic relationships of Syrphinae. The results of the present study were obtained using a large fragment of the mitochondrial *COI* gene and the *D2-3* region of nuclear *28S* rRNA gene, sequenced for 100 ingroup species of 40 genera; *Volucella pellucens* (Eristalinae) was used as outgroup. Direct optimization, a parsimony algorithm as implemented in the computer program POY, was used for analyses using parallel computing. Eight equally parsimonious trees were obtained, and the strict consensus supports the monophyly of multiple clades, some of which are congruent with the present classification. *Pipizini* are resolved as sister to all other ingroup taxa. *Baccha* and *Pyrophaena* are not supported as members of Melanostomini. A major part of the Syrphini was resolved in one clade, excluding *Allograpta*, *Asarkina*, *Episyrphus*, and *Sphaerophoria* that were resolved in another lineage. *Ocyptamus* Macquart, 1834 appears as a non-monophyletic genus and some of its species appear more closely related to the monophyletic genus *Toxomerus* Macquart, 1855, the single member of Toxomerini. *Paragus* + *Allobaccha* were resolved as sister to a clade with taxa confined to the Neotropical region (*Ocyptamus*, *Salpingogaster* and *Toxomerus*).

Towards the phylogeny of robber flies (Insecta: Diptera: Asilidae) - evidence from morphology of the imagines. *Torsten Dikow. Cornell University, Department of Entomology, Comstock Hall, Ithaca, NY 14853, USA and American Museum of Natural History, Division of Invertebrate Zoology, Central Park West at 79th Sreet, NY 10024, USA.*

Robber flies form a distinct part of the global insect fauna with approximately 7000 described species that have attracted researchers attention for centuries. Despite ongoing interest in species-level revisionary studies, phylogenetic relationships within Asilidae are poorly understood and have never been addressed in a comprehensive morphological analysis nor in a combined morphological and molecular total-evidence analysis. In the present study, morphological features of the imagines used in classifications by past authors are combined with previously unreported character complexes to resolve relationships among 158 species sampled from 139 genera from all over the world. Of particular interest to this project is the position of Leptogastrinae within Asilidae, a taxon comprising robber flies of rather unusual morphology and which has been ranked as a distinct family sister to Asilidae by previous authors. This adelphotaxa relationship was supported by a recently published molecular phylogenetic study involving 26 Asilidae species of which 2 were representatives of Leptogastrinae. In this analysis Asilidae is supported as monophyletic based on a number of autapomorphies with respect to the 14 Asiloidea included as outgroups. The analysis supports monophyly of six Asilidae subfamily taxa and non-monophyly of five. Leptogastrinae is monophyletic and nested deep within Asilidae, contradicting its previous placement as adelphotaxon to all other Asilidae. *Acronyches maya*, a morphologically distinct Stenopogoninae from Mexico, is supported as the sister-taxon of Leptogastrinae; sharing with it a number of autapomorphic features. Comments on a tentative higher-level classification of Asilidae are made based on the morphological synapomorphies resulting from this hypothesis. To further augment the morphological hypothesis and to resolve some of the relationships among higher-level taxa not supported by the morphological characters, a preliminary molecular data-set including a subset of 40 species and approximately 4.7 kbp of nucleotide-sequence data of three nuclear genes (*28S* rDNA, *EF-1alpha*, & *CAD*), is concatenated to the morphological matrix, analysed simultaneously with parsimony, and compared to the morphological hypothesis. Although the taxon-sampling is much smaller, the total-evidence hypothesis enhances the resolution at the higher level and highlights interesting relationships not recovered by morphology alone.

Tiny Dancers: A Preliminary Phylogeny of North American Argia (Odonata: Coenagrionidae). *Ryan Caesar* and John Wenzel. Department of Entomology, Museum of Biological Diversity, Ohio State University, Columbus, Ohio, USA.*

The new world odonate genus *Argia* (Odonata: Zygoptera: Coenagrionidae) contains 110 nominal species, making it the second largest genus in the order. The nearctic species are essentially common and can be abundant in and near aquatic habitats, where they are important as both predator and prey in trophic interactions. The prevalence of *Argia*, together with the unique reproductive biology of odonates, makes it an excellent taxon for studying the interaction between reproductive character evolution and speciation. To date no phylogenetic hypothesis for this genus has been proposed. A preliminary phylogeny of the North American species, based on mitochondrial 16s RNA, will be presented. Patterns of diversity and character evolution, as well as future work, will be discussed.

The phylogeny of termites (Dictyoptera: Isoptera) based on mitochondrial and nuclear genes and the evolution of worker caste and foraging behavior*. F. Legendre*[1], M. Whiting[2], C. Bordereau[3], E. Cancello[4], T. Evans[5], and P. Grandcolas[1]. [1]UMR 5202, Département Systématique et Évolution, Muséum national d'Histoire naturelle, 45 rue Buffon, Paris 75005, France. [2]Department of Integrative Biology, 693 Widtsoe Building BYU, Provo, Utah 84602, USA. [3]UMR 5548, Développement - Communication chimique, Université de Bourgogne, 6, Bd Gabriel, Dijon 21000, France. [4]Muzeu de Zoologia da Universidade de São Paulo, Avenida Nazaré 481, São Paulo 04263-000, Brazil. [5]CSIRO Entomology, Ecosystem Management: functional biodiversity, Canberra, Australia.*

Termites are certainly the most poorly known of eusocial insects having differentiated castes and complex behaviors of nest construction and foraging. Very few and very limited phylogenetic hypotheses have been proposed until now, a dearth which hinders the study of their evolution. All termite species (more than 2700) are known to be eusocial with castes but many modalities of their social behavior vary within a continuum. A historical and phylogenetic framework is needed to study the origin of this behavioral diversity, and especially with respect to the so-called "lower termites" which are supposed to show the first steps of this evolution. We sequenced the following genes: 12S, 16S, 18S, 28S, COI, COII and Cytb for a total amount of about 7000 bp in 40 termite species belonging to the seven families currently recognized. The taxon sampling was complemented with 10 cockroaches, 3 mantids and Locusta migratoria. Phylogenetic analyses under direct optimization as implemented in Poy 3.0.11a were carried out in parallel on a supercomputer. A sensitivity analysis, including ten sets of parameters, was conducted in order to test the sensitivity of the phylogenetic results to different costs of insertion-deletion, transversion and transition events. Phylogenetic analyses were also performed under the likelihood criterion using Phyml v2.4.4 and in a Bayesian framework with Mrbayes v3.0b4.Termites were found monophyletic with Mastotermes darwiniensis as sister-group to the remainder of termites. Unexpectedly, the family Kalotermitidae was sister-group to other families in this remainder, consistently with only few and old hypotheses. The families Kalotermitidae, Hodotermitidae and Termitidae were retrieved monophyletic whereas the Termopsidae and Rhinotermitidae appeared paraphyletic. All these results were very stable and supported with high resampling statistics values. The evolution of worker caste and foraging behavior are discussed according to the phylogenetic hypothesis. It suggests that true workers appear 3 times and thus are polyphyletic whereas pseudergates ("false workers") have a single origin.

A phylogenetic test of the ecological paradigm of "escape and radiation" in Depressaria moths. *Sibyl Bucheli and John Wenzel*. Department of Entomology, The Ohio State University, Columbus, Ohio 43210, USA.*

Host-plant use is commonly studied in the small moth *Depressaria* Haworth (Elachistidae: Depressariinae) because of physiological and behavioral reactions exhibited by *Depressaria pastinacella* in response to toxic furanocoumarins produced by its host plants. This model system is often cited as the basis for an ecological concept of "escape and radiation" by which herbivores successively colonize increasingly toxic host plants. Although this concept is implicitly phylogenetic in principle, no species level phylogeny has been available. Here, a phylogeny of Depressariinae, with a focus on the species of the genus *Depressaria*, is constructed using morphological data analyzed under the parsimony criterion. This study is the only modern phylogeny, and the largest to date, including virtually all New World species and about half the Old World species. Our results suggest that feeding on plants bearing toxic furanocoumarins is the ancestral condition for genera in the subfamily Depressariinae, and that ecological "escape and radiation" is not supported in this model system.

Homology and character evolution in megachiropteran bats. *Norberto Giannini*[1], Nancy Simmons[1], and Francisca Alemida[2]. [1]Division of Vertebrate Zoology (Mammalogy), [2]Division of Invertebrate Zoology (Molecular Systematics Laboratory), American Museum of Natural History, Central Park West at 79th Street, NY 10024-5192, USA.*

Megachiropteran bats (Mammalia: Chiroptera: Pteropodidae) are a group of ca. 180 species in 43 genera. Megabats show a number of morphological traits that can be considered closer to non-flying mammals than to typical bats, including character states of their flying apparatus. We used results from the latest iteration of our combined (morphology + DNA) data matrix to study the evolution of selected characters, including some of the traditional morphological features used in megabat classification such as dentition, and characters of ecological and physiological significance such as body size. We applied Direct Optimization to 248 morphological characters and 8 genes both mitochondrial (the *cytb*, *12S* rDNA, tRNA-valine, *16S* rDNA) and nuclear (*c-mos*, *RAG-1*, *RAG-2*, and *vWF*). All currently recognized genera were included in the analysis. Sequence representation varied across the 76 terminals used (7.3 kbp in complete species). Representatives of just 2 genera lacked DNA data. Our search strategy consisted of 200 replications followed by refinements (including tree fusing and the parsimony ratchet). Resulting optimal trees made the basis for the subsequent character analysis. For discrete characters of the dentition, we examined parsimonious reconstructions and based our interpretation of changes on dental field theory, which postulates the existence of incisivization, caninization, and molarization fields that determine the presence or absence of each dental element. The (hypothetical) genetic field signal would exhibit peaks that coincide with the realization of a tooth in one particular spot of the primordial alveolar surface. In the frame of this theory, the reversals observed on the tree representing reappearances of ancestrally lost teeth do not require dismissal of primary homology of the dental element and allow invoking regulatory mechanisms instead. In turn, optimization of body size, a continuous character not included in tree search, allowed testing a recent hypothesis of size evolution of these bats, which postulated a small-to-medium body size of the megabat ancestor.

POSTER SESSION: ZOOLOGY

Phylogeny of Sphaeriodesmus Peter, 1864 (Diplopoda: Polydesmida: Sphaeriodesmidae). Cladistic analysis based on morphological data. *Julian Bueno-Villegas*[1], Petra Sierwald[2], and Alejanro Espinosa[3]. [1]Programa de Doctorado en Ciencias (Sistemática), [3]Departamento de Biología Evolutiva, Instituto de Ecología, A. C., Km. 2.5 carretera antigua a Coatepec No. 351, Congregacion el Haya, A.P. 63, Xalapa, Veracruz 91070,* Mexico*. [2]Field Museum of Natural History, Zoology, Insects, 1400 S Lake Shore Drive, Chicago, IL 60605, USA.*

The use of cladistic methodology to analyze millipede relationships across all taxonomic levels using both morphology and molecules has been minimal. Moreover, millipede taxonomy, in general, has been based primarily on male genitalic morphology. Recently, diplopodologists have been exploring the use of other types of morphological structures in an attempt to more exhaustively investigate millipede morphology for taxonomic and systematic purposes. In this poster we define and delineate the genus *Sphaeriodesmus* using a comprehensive suite of 95 morphological characters. Based on these data we discuss the monophyly of the genus and species level relationships.

Phylogeny of Coenagrionidae (Insecta: Odonata). *Rasmus Hovmöller. Dept. Entomology, Swedish Museum of Natural History, PO Box 500 07, SE 10405, Sweden.*

Coenagrionidae is a group of damselflies with a worldwide distribution. The current classification is based on quantitative wing venation characters, and borders between families and subfamilies are only vaguely defined. I here present a preliminary phylogeny from the mitochondrial *16S* rDNA and *COII* genes. Implications on classification from trees obtained with parsimony, direct optimization and Bayesian inference will be discussed, as well as new quick-and-dirty method for finding better alignments without need for parallel computing.

Systematics of subtribe Agriotina Laporte (Coleoptera: Elateridae: Elaterinae). *Martín Leonel Zurita-García*[1], Santiago Z. Caballero[1], Helga Ochoterena[1], and Juan J. M. Lupi[2]. [1]Instituto de Biología, UNAM, Mexico DF 04510, Mexico. [2]Museo de Zoología, Facultad de Ciencias, UNAM, Mexico DF 04510, Mexico.*

The elaterids correspond to a family of Coleoptera with more than 10,000 species around the world and are characterized by the possession of a prosternal process that gives them the skill to “jump”. The subtribe Agriotina has many species that are known in larval state as “wireworms”, which have great economic importance in Agriculture, such as the species from the genus *Agriotes*. In spite of the great importance of the subtribe, phylogenetic analysis had previously not been carried out. This study aims to test the monophyly of subtribe Agriotina using parsimony analysis on a total of 78 potentially informative morphological characters. Twenty-nine species of Agriotina were chosen to represent the 10 genera that have traditionally been considered within this group: *Agriotes*, *Cardiorhinus*, *Chatanayus*, *Chiagosnius*, *Dalopius*, *Ectinus*, *Hypodesis*, *Insuliectinus*, *Pittonotus*, and *Pomachiloides*. Outgroup taxa included nine species belonging to six genera from different tribes and subfamily: *Diplostethus*, *Horistonotus*, *Leptoschema*, *Psiloniscus*, *Sericus*, and *Smilicerus*. The parsimony analysis of the matrix yielded 56 trees; ambiguously supported nodes were collapsed and duplicated trees were eliminated prior to the consensus calculation. The consensus hypothesis conflicts with traditional classifications for Agriotina. The monophyly of the subtribe was not supported and the group was retrieved instead as paraphyletic. The genera *Psiloniscus* and *Smilicerus* were not grouped within the clade containing most Agriotina. The characters that have traditionally been considered for the circumscription of subtribe Agriotina were interpreted as homoplasies. The new characters that support the subtribe principally correspond to mouthparts and the grove mesocoxal. A taxonomic synopsis for the re-circumscribed subtribe and their included genera is provided. Our results suggest the need for taxonomic revision of the genera in this subtribe as well as phylogenetic studies to test the monophyly of the genera.

Phylogeny and historical biogeography og the genus Humboldtiana (Pulmonata: Humboldtnianidae). *Omar Mejía* and Gerardo Zúñiga. Laboratorio de Variación Biológica y Evolución, Departamento de Zoología, Escuela Nacional de Ciencias Biológicas-IPN, Carpio esq. Plan de Ayala s/n Col. Casco de Santo Tomás, México DF 11340, Mexico*.

The three brown banded land snail genus *Humboldtiana* (Pulmonata: Humboldtianidae) comprises 46 recognized species of insular distribution from South Texas to Central México; its low vagility and dispersal potential are reflected in high levels of endemism and highly restricted distributions. As in other Helicoids, there is a controversy relative to monophyly of the genus and its relationships with other members of the Superfamily Helicoidea. Current scheme of classification recognizes three subgenera: Polyomphala, Oreades and Humboldtiana (the last one with three groups). In the present work mitochondrial *16S* rDNA and ribosomal large subunit (*5.8S* + *ITS*-2 + *28S*) partial sequences from 26 recognized species and 2 populations from unknown identity were studied to assess the phylogenetic relationships of *Humboldtiana* through parsimony and bayesian analysis. Biogeographic history was constructed through Dispersal-Vicariance (DIVA) and Weighted Ancestral Area Analysis (WAAA). Results showed that *Humboldtiana* is a monophyletic group with a complex biogeographical history.

Evolutionary tendencies of some reproductive aspects, habitat type and feeding habits within snakes of the genus Thamnophis (Reptilia: Sauria). *Angélica Lizarraga* and Gustavo Casas. Departamento de Zoología, División de Herpetología, Instituto de Biología, UNAM, México DF 04510, México.*

The genus *Thamnophis* comprises 30 species, and is one of the most diverse among colubrid snakes in North America. Several kinds of relationships within these snakes of highly aquatic habits have been recognized, but the phylogenetic relationships of the genus have been very poorly studied. Our objectives are to determine if the type of prey consumed by these snakes depends on the habitat and if the exploitation of such habitat depends on the phylogenetic relationship within the genus; if the species show changes in both (feeding and habitat) we explore whether they can occur within the same linage and finally we explore the relationship between female length and size of the litter. An exhaustive bibliographical revision about the natural history of the species, its ecology and biology was performed, as well as checking specimens in scientific collections and museums to get additional information on the different species. The obtained data were analyzed elaborating a presence-absence matrix (feeding an habitat) using MacClade, and the data were mapped using the purposed phylogeny of Thamnophis by De Queiroz et al. (2002). In this way, we were able to denote possible tendencies between species; we also correlated length of female to number of juveniles to denote patterns. We found that the food type is strongly related to the habitat of the species, however it appears that there are slight changes in some species because they feed on certain kind of prey despite the fact that they occupy different habitats. We also found that related species exploit the same type of habitat. The most uniform clade in which more marked tendencies are observed is the one of wide distribution, where sister species share the same kind of habitat, keeping most of them their aquatic habits. A third part of species show changes in feeding habits as well as in habitat. Within the genus, the clutch size is correlated to female size. The genus *Thamnophis* occupies a wide variety of habitats, perhaps in relation to a grade in which the food is available in the habitat. Thus evolution in garter snakes in its aquatic and terrestrial habits may be deduced in several degrees or scales.

Nested Clade Analysis indicates population fragmentation and range expansion in Pteronotus davyi (Chiroptera:Mormoopidae) in Mexico. *L. M. Guevara-Chumacero*[1], R. López-Wilchis[1], F. Flores-Pedroche[2], and I. D. L. A. Barriga-Sosa[2]. [1]Departamento de Biología. [2]Departamento de Hidrobiología, Universidad Autónoma Metropolitana Unidad Iztapalapa. San Rafael Atlixco 186, Col. Vicentina, Delegación Iztapalapa, Mexico DF, Mexico*.

Phylogeographic studies allow us to investigate the recent history of species, particularly the origin and the dispersal processes involved in their actual geographic distribution. *Pteronotus davyi*, is a Mormoopidae bat for which their evolutionary processes have not been studied. Thus the present study is devoted to investigate the phylogeographic patterns of the species based on the analysis of their mitochondrial control region. Tissue samples of *P. davyi* from 18 localities including the Pacific and Gulf of Mexico ranges. Five hundred and fifty five nucleotides were analysed from 105 organisms. Their genetic structure was analysed via an AMOVA. A Mantel test was carried to determine isolation by distance and a Nested Clade analysis was conducted to determined possible phylogeographic patterns. The AMOVA results suggest a significant population structuring, FST = 0.301 ($P<0.05$), with higher values of variation within (69.9%) than between populations (30.1%). The Mantel test results indicate a positive correlation between the genetic and geographic distances (0.5027, $P<0.05$), and the Nested Clade results suggest a significant association between the putative genetic structure and the geographic distribution of the species. The geographic patterns allow us to suggest two different trends: a) a contiguous range expansion interval of two groups of populations, Southeast region, and Central-North region, and b) a past fragmentation between the same population groups. Results also indicate that the most ancestral populations are those from the North region of Mexico, whereas the most recent populations are those from the Southeast, this allows us to propose that P. davyi possible had a North-South diversification.

THURSDAY 17TH

CONTRIBUTING PAPERS: THEORY II

Is repatriation of entomological data really that useful? *Jyrki Muona* and Diane Alaruikka. Entomology department, Finnish Museum of Natural History, PL 26, University of Helsinki 00014, Finland.*

Repatriation is becoming a more and more important issue between states. Much of the entomological type material is kept in European and North American museums and the information this material represents should be freely available to the scientific community of the country the specimens came from. It appears clear, however, that the importance of these data is frequently overestimated. When limited resources are available, funding should perhaps be in better use if directed to other activities.

Sociological aspects of taxonomy and determinants of alpha diversity. *Joseph Raczkowski[1] and John W. Wenzel*[2]. [1]Department of Evolution, Ecology, and Organismal Biology, [2]Department of Entomology, Ohio State University, Columbus, Ohio 43210, USA.*

Accurately assessing biodiversity remains a difficult task critical to conservation efforts and useful in evolutionary contexts (e.g. areas of endemism, modes of speciation). Historically, species richness has been attributed to abiotic and biotic factors, however it has been widely suspected that species counts in an area are correlated with the number of researchers working in that area. We present a regression analysis to develop a model that predicts the number of ant species (from a total of more than 11,000) described from an area. Total land area, average precipitation, average temperature, and the number of taxonomic authors are used as predictors for about 100 areas with more than 25 species described. We find that the number of taxonomists is the best predictor of the number of ant species described, accounting for about 60% of the variance. The relative contribution of the different factors is discussed, with attention to the importance of personal philosophy regarding species definitions. Relevance to such modern agendas as DNA barcoding is specified.

Philosophical arguments and phylogenetic methods. *James S. Farris. Molekyläsystematiska laboratoriet, Naturhistoriska rikmuseet, Box 50007, Stockholm SE 104 05, Sweden.*

Seemingly philosophical arguments intended to do away with issues in phylogenetic systematics often depend on misattributions or inaccuracies, but some of them go further, achieving a level at which they would be irrelevant even if accurate. This kind of creativity is well known in the writings of anticladists and antiPopperians, but even some cladists do much the same, as some surprising examples will reveal.

Popper, systematics and the combined corroboration metric. *E. Kurt Lienau. AMNH Invertebrate Zoology, 79th Street at Central Park West, New York 10024, USA.*

The discussion of how Popper's empirical method is best applied (or not) to the study of evolution has waxed and waned over the last half century. There remains no consensus in the literature. This conversation has focused mainly on the applicability of Popper's severity of test to particular methods of tree reconstruction. I share the view that the mp tree accounts for the most severe test of the data at hand. I also agree with the view that the use of total evidence provides for the most severe test possible. Within this framework, the construction of homology hypotheses, or "basic statements" becomes of particular interest. I assert that from the total evidence perspective that the background knowledge for a particular taxa range is zero each time new data is included in an analysis. From this I further assert the most well resolved strict consensus tree is the boldest hypothesis possible, and thus the most testable. The most highly corroborated data set, then, is that arrangement of homology hypotheses that maximizes both the resolution of the tree (boldness of the hypothesis), and the consistency of the homology hypotheses I suggest a metric called the Combined Corroboration Metric (CCM), which is the product of a consistency index and a measure of the resolution of strict consensus trees, is a measure of corroboration. I show the previously published results of the use of this method in the construction of tree of life data sets.

On Objective Support. *Taran Grant[1] and Arnold G. Kluge*[2]. [1]American Museum of Natural History, Central Park West at 79th Street, NY 10024, USA. [2]3140 Dolph Drive, Ann Arbor, MI 48103, USA.*

Empirical knowledge claims are either objective or subjective. Repeatability is necessary to achieve objectivity, but it is not sufficient. Rather, objective knowledge is based on the ability of competing hypotheses to explain the critical evidence, and any empirical knowledge claim that does not derive from this is subjective. We define objective support conceptually as the degree to which competing hypotheses are refuted by the critical evidence. Stated more simply, the objective support for a hypothesized group is its explanatory power relative to that of competing groups. According to this concept of support, groups are ranked in relation to their power to explain the total, unpartitioned evidence, which necessarily takes into account the relative amounts of evidence contradictory and favorable to each group. Resampling measures of support (the jackknife and nonparametric bootstrap) do not rank groups according to their relative explanatory power and therefore do not measure objective support. Instead, they rank groups according to the proportion of the evidence that favors each competing hypotheses. The relative fit difference (RFD; relative Bremer support) also fails to measure objective support, and its application has illogical results. Bremer support measures objective support as the difference between the explanatory power of competing hypotheses and correctly ranks groups according to their relative explanatory power. The ratio of explanatory power (REP support) is also a measure of objective support that provides the same ranking of groups within a dataset, but it varies between 0 and 1 and allows meaningful comparison of support across datasets.

An optimization-based method to estimate and test character correlation for continuous characters. *Pablo Goloboff*[1] and Norberto Giannini[2]. [1]CONICET, Instituto Miguel Lillo, Miguel Lillo 205, 4000 S.M. de Tucuman, Argentina. [2]Mammalogy, The American Museum of Natural History, Central Park West at 79th Street, New York, NY 10024, and PIDBA/CONICET, Instituto Miguel Lillo, Miguel Lillo 205, 4000 S. M. de Tucumán, Argentina.*

A common problem in evolutionary and ecological studies is whether one character responds to change in another. Using species as sampling units introduces dependence because of common ancestry; so called "phylogenetic comparative methods" attempt to address this problem, but none of the techniques proposed is based on optimization, except for Maddison's (1991) "concentrated changes" method for binary characters. Here, we explore the problem of regressing two continuous characters x and y, with y dependent on x, as optimized on a given phylogeny. A method to estimate the slope (or correlation coefficient) of such relationship, and its statistical significance, is proposed. The need to consider that a response in the dependent variable may be delayed, relative to change in the independent variable, is demonstrated. We propose a way to take this delay into account when forming the data pairs for the regression analysis. For a given set of most parsimonious reconstructions for both characters, the procedure tracks character changes in an upward pass (i.e. considering the sequence with which the characters are hypothesized to have evolved). For the significance of the regression slope, we used permutation, considering ambiguities in optimizations so as to make the test as conservative as possible. For the observed data, a range of slopes can be obtained (by comparing every possible reconstruction of one character with every possible reconstruction of the other, or at least a sample of reconstructions). For each of the permuted data sets, a similar range of slopes can be obtained. Significance is calculated as the proportion of permuted slope ranges that overlap with the observed slope range. Given our procedure for taking into account delays, it is possible to have cases where changes on a character, y, significantly depend on changes on another character, x, while changes in character x show no significant dependence from changes in character y. This procedure is implemented with a TNT script. Examples are analyzed, and general implications discussed.

GLOCSA: a GLObal Criterion for Sequence Alignment. *Helga Ochoterena*[1], Edgar Arenas[2], Esteban Ricalde[2], Cristian Segura[2], and Katya Rodríguez-Vázquez[2]. [1] Instituto de Biología, UNAM, Apdo. Postal 70-367, México DF 04510, Mexico. [2] Instituto de Investigaciones en Matemáticas Aplicadas y en Sistemas, UNAM, Apdo. Postal 7-221, México DF 04510, Mexico.*

For many systematists, alignment of multiple DNA sequences is a necessary step before conducting phylogenetic analyses. In recent years, several alignment programs have been improved or newly released. Also, visual alignments have become more common and accepted than in the past. In spite of the variety of alignment tools, few criteria assessing the comparative quality of alignments have been proposed. In general, these are based on average pair wise comparisons, in most cases only considering average matches in aligned pairs of sequences, while global parsimony based criteria are lacking. We propose a new criterion to globally assess the quality of sequence alignments: GLOCSA. In general terms, GLOCSA uses a function that globally evaluates alignments considering different parameters that can be associated with parsimony: 1) the average proportional identity of nucleotides on each column, including a weighted function for internal gaps (not leading or trailing), which is inversely related to the information content of the column (considering gaps as weighted matches/mismatches); 2) a ratio that indicates the proportional increase in the number of columns (positions) with respect to the longest original sequence, which is related to the size and number of inferred gaps; 3) the size of gaps and the proportion of positions with gaps and nucleotides, calculated from all sequences. GLOCSA can be applied to pairs of sequences as well as to complete matrices, which do not need to have the same size (specially, they can have different number of characters). Our criterion can be used to compare the results of alternative alignments, including those produced by different algorithms (or visual alignments), or different parameters used for the alignment. This represents a tool to objectively asses the relative quality of alternative alignments prior to the phylogenetic analyses. Also, it is possible to identify the general causes of the differences among alignments (e.g., some parameters, algorithms or algorithm versions are more prompt for the insertion of small gaps than others). Potentially, GLOCSA will be implemented in alignment algorithms to use heuristic methods that can improve the results.

Incorporation of Gap Characters and Lineage-Specific Regions into Phylogenetic Analyses of Gene Families from Divergent Clades: An Example from the Kinesin Superfamily across Eukaryotes. *Mark P. Simmons*, Dale Richardson, and Anireddy S.N. Reddy. Department of Biology and Program in Molecular Plant Biology, Colorado State University, Fort Collins, CO 80523, USA.*

The kinesin superfamily across eukaryotes was used to examine how incorporation of gap characters scored from conserved regions shared by all members of a gene family (the motor domain in kinesins) and incorporation of amino acid and gap characters scored from lineage-specific regions affect gene-tree inference of the gene family as a whole. We addressed these two questions in the context of two different densities of sequence sampling (100 vs. 525 sequences), alignment programs (ClustalX vs. DIALIGN-T vs. MAFFT vs. MUSCLE), and methods of tree construction (Bayesian vs. parsimony). Our results are useful for developing guidelines as to which alignment program should be used, whether gap characters should be incorporated, and whether lineage-specific regions should be included in gene-tree inference for gene families sampled from divergent taxa. Taken together, our findings suggest the following.

First, gap characters should be incorporated into gene-tree inference. However, the most appropriate way of treating these characters in parametric gene-tree inference methods remains unclear. Second, gene regions that are not conserved among all or most sequences sampled should not be automatically discarded without evaluation of potential phylogenetic signal that may be contained in gap and/or sequence characters. Third, among the four alignment programs evaluated using their default alignment parameters, ClustalX may be expected to output alignments that result in the greatest gene-tree resolution and support. Yet, this high resolution and support should be regarded as optimistic, rather than conservative, estimates. Fourth, this same conclusion regarding resolution and support holds for Bayesian gene-tree analyses relative to parsimony-jackknife gene-tree analyses. We suggest that a more conservative approach, such as aligning the sequences using DIALIGN-T or MAFFT, analyzing the appropriate characters using maximum likelihood and/or parsimony, and assessing branch support using the bootstrap or the jackknife, is most appropriate for inferring gene trees of divergent gene families.

A comparison of algorithms for identification of specimens using DNA barcodes: examples from gymnosperms. *Damon P. Little* and Dennis Wm. Stevenson. Lewis B. and Dorothy Cullman. Program for Molecular Systematic Studies, The New York Botanical Garden, Bronx, New York 10458-5126, USA.*

In order to use DNA sequences for specimen identification (e.g., barcoding, fingerprinting) an algorithm to compare query sequences to a reference database is needed. Precision and accuracy of query sequence identification was estimated for hierarchical clustering (parsimony and neighbour joining), similarity methods (BLAST, BLAT, and megaBLAST), combined clustering/similarity methods (BLAST/parsimony and BLAST/neighbor joining), diagnostic methods (DNA-BAR and DOME ID), and a new method (ATIM). We offer two novel alignment-free algorithmic solutions (DOME ID and ATIM) to identify query sequences for the purposes of DNA barcoding. Publicly available gymnosperm nrITS 2 and plastid matK sequences were used as test data sets. On the test datasets, almost all of the methods were able to accurately identify sequences to genus, however no method was able to accurately identify query sequences to species at a frequency that would be considered useful for routine specimen identification. Clustering methods performed the worst (perhaps due to alignment issues). Similarity methods, ATIM, DNA-BAR, and DOME ID all performed at approximately the same level. Given the relative precision of the algorithms (median = 67% unambiguous), the low accuracy of species level identification observed could be ascribed to the lack of correspondence between patterns of allelic similarity and species delimitations. Application of DNA barcoding to sequences of CITES listed cycads (Cycadaceae) provides an example of the potential application of DNA barcoding to enforcement of conservation laws.