

A summit of cladistics: abstracts of the 27th Annual Meeting of the Willi Hennig Society and VIII Reunión Argentina de Cladística y Biogeografía

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The 27th meeting of the Willi Hennig Society was held at the Sierras de San Javier, Tucumán (27–31 October 2008), jointly with the VIII Reunión Argentina de Cladística y Biogeografía. This was the second Hennig meeting held in South America and the third in Latin America. The event was attended by 129 participants from 16 countries, with the strongest presence from Argentina, USA and Brazil. As pointed out in the minutes of previous meetings, student participation is a good measure of the health of a society, and by this measure, the Hennig society is doing very well. For this meeting, 64 of the participants (50%) were students, 40 of which had authored or co-authored a talk or poster. The schedule was intense, with 98 presentations (67 talks and 31 posters). The sessions consisted of contributed papers, and five symposia on diverse topics: Large Scale Analyses of Large Chunks of Life, Molecular Systematics, Latin American Biogeography in the 21st Century, Methodology, and Botanical Phylogenetics (each of the symposia, except the “green” one, had two or three student speakers). As is usual at these meetings, the atmosphere was informal and relaxed, with much discussion and debate (although the biogeographic symposium took first place for the heat of its exchanges). The Student Award Committee (Lone Aagesen, Dan Janies and Gitte Petersen) selected Santiago Catalano for the Hennig Award (‘The optimization of landmark data: a three-dimensional approach’), Prashant Sharma for the Brundin Award (‘Phylogenetic analysis of Sandokanidae (Arachnida, Opiliones, Laniatores): Evaluating the independence of associated gene regions’), and Sebastian Barrionuevo for the Rosen Award (‘Continuous characters in a phylogenetic analysis of the frog genus *Telmatobius*’). In addition to the logistics and funding provided by the Willi Hennig Society, the event was supported by the Consejo Nacional de Investigaciones Científicas y Técnicas, Fundación Miguel Lillo, Instituto Superior de Entomología ‘Dr Abraham Willink’, and the Agencia Nacional de Promoción Científica y Tecnológica.

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Molecular analysis of species of the subfamily Bryconinae based on mitochondrial and nuclear gene sequences. Kelly T. Abe*, C. Oliveira and F. Fausto Departamento de Morfología, Instituto de Biociências, Universidade Estadual Paulista, Botucatu, São Paulo, Brazil

Characidae is the most diverse group among Characiformes with about 65% of the species in the order. Among Characidae, the subfamily Bryconinae includes 42 valid species, of which 40 belong to *Brycon*, one to *Henochilus* and one *Chilobrycon*. In spite of the economic and ecological importance of the species of the subfamily Bryconinae, its phylogeny, classification and composition are not yet well solved. In the present study the DNA of 15 species of the subfamily (14 species of *Brycon* and *Henochilus wheatlandii*) and two species of *Salminus* (*S. hillarii* and *S. brasiliensis*) were analyzed. Two mitochondrial genes, 16S and cytochrome *b* and four nuclear genes, seven in absentia, the intron 5 of the α -tropomyosin, Rag1 and Rag2 were amplified and sequenced. Fishes are deposited in the collection of the Laboratório de Biologia e Genética de Peixes, Botucatu, São Paulo, Brazil. Additional sequences

were obtained from GenBank (*Brycon* sp., *Brycon hillarii*, *Chalceus macrolepidotus* and *Salminus brasiliensis*). The matrix included 4274 characters (737 of which were parsimony-informative). Maximum parsimony and minimum evolution trees were obtained with MEGA 4.1. *Chalceus macrolepidotus* was used as outgroup. The trans-Andean species *B. petrosus*, *B. chagrensis*, *B. henni* and *B. aff. atrocaudatus* are the sister group of all remaining cis-Andean species of *Brycon* analyzed (Brazilian, Colombian and Venezuelan). Our results also corroborate the previous placement for *Henochilus wheatlandii*, recovered among the species of *Brycon*, as the sister species of *B. insignis*, *B. opalinus* and *B. ferox*. However, we had an unexpected result: the species of the *Salminus* formed a sister group of *Brycon pesu*, but with low statistical support. These results reject the monophyly of *Brycon* and Bryconinae as currently defined. Complementary studies are being conducted to elaborate a more robust hypothesis for the relationship among the species of the Bryconinae and their relationships with other Characiformes.

Concordant geographic distribution and extensive hybridization within *Nothofagus* (subgenus *Nothofagus*) are reflected in the chloroplast genome. M. Cristina Acosta* and Andrea C. Premoli Centro Regio-

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Nothofagus is an important component in discussions of the biogeographical history of the Southern Hemisphere because of its disjunct distribution in Gondwana. The phylogeny of the genus has been investigated using morphology and sequences of chloroplast and nuclear DNA. Nevertheless, the interrelationships among their species remain poorly understood. The objective of this study is to analyze interspecific relationships within of the South American subgenus *Nothofagus*. We used a spatially explicit sampling design to analyze the extent of hybridization between their species. Leaf material was collected from 32 populations of *N. antarctica*, *N. betuloides*, *N. dombeyi*, *N. nitida* and *N. pumilio* (all in the subgenus *Nothofagus*). Hybrids among most of these species have been described at a local scale. Four populations of *N. obliqua* and *N. nervosa* (subgenus *Lophozonia*) were used as outgroups. The complete internal transcribed spacer (ITS) region, including the 5.8S rRNA gene, and three regions of the chloroplast genome (psbB–psbH, trnL–trnF, trnH–psbA) were amplified. Parsimony analysis was conducted using WINCLADA and NONA, and Bayesian inference was done in MrBayes, both on the separate nuclear and chloroplast datasets. A model of sequence evolution was selected using MrModeltest. Parsimony analyses of the aligned ITS data returned only one most parsimonious tree (MPT; L = 70, CI = 0.943, RI = 0.935) and the DNA chloroplast matrix generated 6 MPTs (L = 69, CI = 0.957, RI = 0.965). The nuclear and chloroplast DNA dataset contained 52 and 58 parsimony informative characters, respectively. The parsimony and Bayesian analyses yielded trees with the same topology. Incongruent nuclear and plastid DNA phylogenetic analyses were observed within the subgenus *Nothofagus*. ITS ribotypes showed relationships with the delimited species. Therefore, phylogenetic analysis of ITS sequences is assumed to show the true phylogeny. The monophyly of the subgenus *Nothofagus* is well supported. The evergreen species *N. dombeyi* and *N. betuloides* have been recently differentiated, which together with *N. nitida* are sister to the deciduous *N. antarctica*. *Nothofagus pumilio* had an early and distinct evolutionary history. In contrast, chloroplast haplotypes had no obvious relationship to species, but with geographic location instead. Not only do all species share several DNACp haplotypes, but most haplotypes occur in all species within the same area. This is probably due to hybridization, introgression, and chloroplast capture events throughout the evolutionary history of such ancient taxa. In order to avoid erroneous phylogenetic conclusions both nuclear and chloroplast DNA based studies and comprehensive sampling methods are needed.

Systematics of Tapinotaspidini (Hymenoptera, Apidae) and its implications to the biogeography of open areas of South America. Antonio Aguiar^{1*} and Antonio Melo². ¹Museo de Zoologia da Universidade de São Paulo, São Paulo, Brazil; ²Departamento de Zoologia da Universidade Federal do Paraná, Brazil

The historical relations of the open areas of South America were investigated through the phylogeny of the bee genera *Caenonomada* and *Tapinotaspoides*. These genera present endemic species in savanna and xeric areas of Cerrado, Chaco, Caatinga and Llano of South America. The biogeographic study was based on a morphological phylogenetic analysis of all species of these two genera. General area cladograms were reconstructed through Brooks Parsimony Analyses (BPA). The areas of endemism are referred to by the names of the biomes in which they are inserted—Chaco, Cerrado, Caatinga and Llanos. A primary BPA analysis resulted in one general area cladogram, (Llano (Caatinga (Cerrado, (Chaco, Pampa))). In order to remove two homoplasies in the primary BPA, involving Caatinga and Chaco, a secondary BPA was carried out in which Chaco was duplicated, considering species widespread in the Chaco (Chaco A) and species restricted to central and western portions of Chaco (Chaco B). The secondary BPA resulted in a

general area cladogram, (Llano ((Cerrado (Chaco A, Pampa) (ChacoB, Caatinga))). The hybrid nature of the Chaco is a replicated event observed in one clade of *Caenonomada* and in *Tapinotaspoides*. The phylogenetic patterns of these two genera of Tapinotaspidini indicate that the vicariance between the northern savanna (Llano) and the diagonal arid area (Chacoan subregion) represents an ancient event, while the cladogenesis between Chaco, Caatinga and Cerrado are more recent.

Cladistic analysis and considerations on the hypopygium of the genus *Coniceromyia* Borgmeier (Diptera: Phoridae). Danilo César Ament* and Dalton de Souza Amorim Depto. de Biologia, FFCLRP, Universidade de São Paulo, Av. Bandeirantes 3900, 14040-901 Ribeirão Preto SP, Brazil

Despite its diverse ecological role in ecosystems, the Phoridae are one of the less studied among the species-rich families of Diptera. This lack of knowledge is particularly severe in regards to the Neotropical fauna, in which the proportion of new species in relation to the known fauna is 1:9. Cladistic and biogeographical work on Neotropical genera of Phoridae are also almost absent in the literature. We performed a cladistic study of the fundamentally Neotropical Phorinae genus *Coniceromyia* Borgmeier. The genus has 40 Neotropical and two Nearctic described species. The inclusion of *Coniceromyia* in the Phorinae is justified mainly by distinctive clasping mechanisms of male terminalia, which are apomorphic in the family. There are considerable differences in this structure in the subfamily, but very few characters of the hypopygium have been used to separate the Phorinae species. The male terminalia of 19 described species and four new species of *Coniceromyia* are illustrated for the first time. A matrix with 26 characters and 23 species of *Coniceromyia*, one of *Chaetocnemistoptera* Borgmeier and one of *Plethysmochaeta* Schmitz (the latter two belonging also to Phorinae) was analyzed—12 of these species are from Atlantic Forest, of which four are new. Implicit weighting was used and a consensus of four most parsimonious trees with equal length was obtained. The monophyly of *Coniceromyia* was corroborated. There are three stable small clades in the genus—referred to as *affinis*-group, *epicantha*-group and *latimana*-group. The *epicantha*-group includes all species with maculate wings within the species sampled. These three clades form a larger clade, separate from other species of the genus. The homology of the sclerites of the asymmetric terminalia in the genus is discussed.

Areas of endemism along the Atlantic Forest in Brazil as shown by species of *Cluzobra* (Diptera: Mycetophilidae): Topographical units, parsimony, biogeographical layers, and secondary sympatry. Dalton de Souza Amorim* and Charles Morphy Dias dos Santos Depto. de Biologia, Faculdade de Filosofia, Ciências e Letras de Ribeirão Preto, Universidade de São Paulo, Av. Bandeirantes 3900, 14040-901, Ribeirão Preto-SP, Brazil

Areas of endemism are related to biogeography as species are to taxonomy: 150 years after the advent of the theory of evolution, both concepts are still hard to deal with. Areas of endemism are hypotheses about geographical units of evolution generated in the past with the origin of barriers that divided ancestral biotas. Detecting areas of endemism is more complex than merely finding congruence between plotted taxonomic occurrences. The idea that two congruent species distributions could indicate an area of endemism is a methodological simplification. PAE intends to delimit areas of endemism based on shared taxa under a parsimony assumption. Distortions are common, especially concerning the connection between areas of endemism. If the distribution of extant species includes more than one area of endemism, this is due to chance dispersal or expansion due to disappearance of barriers. Whatever the method, connections between areas of endemism based on species distribution reflect events of distribution changes, not historical connections between areas. Also, geographical coordinates are artificial geographical units that tend to join in the same term species that belong to different historical units

when borders of areas of endemism are sampled. This results in unnecessary input of noise in matrices. We try here to identify areas of endemism along the Atlantic Forest with some changes in the usual methodological approach: (1) units of analysis are topographically defined delimitations based especially on rivers and altitude; (2) Szumik–Goloboff protocol is used to run the matrix; (3) only taxa supposed to belong to the same biogeographical layer along the Atlantic Forest are used—i.e., species of typically tropical groups. Our database includes distribution of *Cluzobra* Edwards species (Diptera: Mycetophilidae) in eastern Brazil, Paraguay and northern Argentina. There is enough signal to recognize three areas of endemism: (1) from southern State of Bahia to the extreme north of the Atlantic Forest; (2) from southern Brazil, Paraguay, and northern Argentina to areas of higher altitude in the State of Minas Gerais; (3) from the west State of São Paulo to the States of Mato Grosso do Sul and Goiás. Another area of endemism may exist in the State of Espírito Santo, probably not recovered in our analysis due to taxonomic undersampling in that part of the country. The sympatry between species belonging to the same clade within some of the areas of endemism is discussed. Accumulation of data will refine the topographical units.

Biogeographical layers and circumantarctic distributions. Dalton de Souza Amorim* and Charles Morphy Dias dos Santos Depto. de Biologia, Faculdade de Filosofia, Ciências e Letras de Ribeirão Preto, Universidade de São Paulo, Av. Bandeirantes 3900, 14040-901, Ribeirão Preto-SP, Brazil

Strong emphasis in biogeographical evolution has been evidently placed on the origin of barriers: it is the cause of vicariance and diversity. Nevertheless, the loss of pre-existent barriers has an important role in biogeography. The disappearance of a barrier allows not only species, but in some cases entire biotas, to come into contact, overlapping their distributions. In other cases, however, there may have been long term, unidirectional invasion of biotas, so the diversity in an area is composed of both the original elements and those that secondarily occupied that area. The fact that the final composition of any area has elements of different chronological and biogeographical origins—called here biogeographical layers—has important implications. An outstanding example is that of groups with circumantarctic distributions. Molecular clock studies have supposedly shown that some groups are too young to have their circumantarctic distribution to be the result of Gondwanan origin, so their disjunction is assumed to be due to transoceanic dispersal. Classic vicariance interpretation states that the common biogeographical patterns shall be the result of common causes, so despite problems with the molecular clocks, circumantarctic disjunction is evidence of Gondwanan origin. The fact that the paleobotanical record reveals a major change in the southern Gondwanan flora only in the Cretaceous, with the modification of the ancient gymnosperm forests and the presence of different species of angiosperms, shows that a number of post-Gondwanan elements were added to the original truly Gondwanan elements. This means that, at least in principle, indeed not all elements with circumantarctic distribution would be Gondwanan in origin. Nevertheless, both Gondwanan and post-Gondwanan elements underwent the same sequence of tectonic-induced vicariations along the late Cretaceous and early Tertiary—there was connection between the Antarctica with a mild climate and South America and Australia at least until the Eocene. Hence, congruence is indeed evidence of vicariance, not dispersion, even in the cases of elements belonging to different biogeographical layers. This solves the conceptual problem of conflicting evidence concerning circumantarctic patterns, but not the problem of recognizing which are the truly Gondwanan and which are the post-Gondwanan elements. Phylogeny, paleontology and, in some cases, molecular information—i.e., non-biogeographical information—has to be used to recognize the layers in the circumantarctic flora and fauna. The recognition of the existence of biogeographical layers in different areas has implications on some details of biogeographical methods.

A comparison of NDM and PAE using real data. J. Salvador Arias¹, M. Dolores Casagrande^{1*} and Juan Manuel Díaz Gómez². ¹INSUE, CONICET, Instituto Miguel Lillo, Miguel Lillo 205, 4000 S.M. de Tucumán, Argentina; ²CONICET, Cátedra de Cordados, Facultad de Ciencias Naturales, Universidad Nacional de Salta, Argentina

Although identification of areas of endemism is an important step in a biogeographical analysis, explicit methods for searching this patterns (such as PAE or NDM), follow very different criteria for its definition, and its application might result in identification of different areas of endemism from the same data set. Whereas a few comparative analyses between methods for delimitation of areas of endemism have been done, up to now there are no numerical studies that formalize differences between those methods when real data are used. In order to do these comparisons we tested three methods for delimitation of areas of endemism: PAE (Morrone, 1994); PAE-PCE (García-Barros et al., 2002), and NDM as proposed by Szumik and Goloboff (2004), on 20 published distributional data sets, and compared the stability of results. Stability is measured by the number of areas of endemism found in jackknife resampled data that are also found in the complete matrix. Two kinds of jackknife were performed, a ‘taxon’ jackknife, which removes the distribution of a whole taxon from the data, and a ‘cell’ jackknife, which removes cells scored as ‘presence’ in the data matrix. The deletion probability is $1/e$ (the \log_n base, roughly 36%). We found that (1) NDM finds more areas than PAE or PAE-PCE; (2) PAE-PCE does not generally find more areas than those obtained with PAE; (3) NDM results were the most stable to taxon deletion, while stability in both PAE and PAE-PCE is poor; (4) Similarly, cell jackknife does not affect in a relevant way the number of stable areas obtained with NDM, but it greatly affects PAE and PAE-PCE performance. Our results highlight the limitations of parsimony, or its modifications, for the identification of areas of endemism, especially when the sampling of distributional data is ‘incomplete’, as happens in real distributional data.

Continuous characters in a phylogenetic analysis of the frog genus *Telmatobius*. J. Sebastián Barrionuevo Instituto de Herpetología, Fundación Miguel Lillo, Miguel Lillo 251, S.M. de Tucumán, 4000 Argentina

Frogs of the genus *Telmatobius* are aquatic dwellers of Andean streams and lakes, comprising 57 species from Ecuador to Argentina. So far the proposed phylogenies of *Telmatobius* include only species restricted to Peru and failed to resolve the internal relationships. The lack of clear external characters has led to a generalized use of morphometrics in the taxonomic studies of the genus. Amphibians are soft-bodied organisms whose body form is affected strongly by fixation making morphometric comparisons spurious. Additionally, the lack of external structures, especially evident in *Telmatobius*, precludes the establishment of precise measure limits, unlike other animal groups. For these reasons I explore the performance of this type of character in a phylogenetic analysis of *Telmatobius*. I generated a morphological matrix of 131 discrete characters of osteology (94), external morphology (24), larvae (9), chromosomes (2), and reproductive biology (2) for 23 species of the genus from Argentina, Bolivia and Peru, and for 11 outgroup species. I incorporated 15 continuous characters and analyzed the matrix with TNT, comparing the topologies from the analysis based on discrete characters with the combined analysis (discrete and continuous characters). The differences in group support between both analyses were also calculated. There are important differences in topologies between both analyses, but the group supports of the combined analysis are improved. These results suggest that the continuous characters, as shown in other groups, are phylogenetically informative and the incorporation of these data strengthens phylogenetic hypotheses.

A morphology based phylogenetic analysis of the *Xanthocephalum*-group (Asteraceae, Astereae). Adriana Bartoli¹, Gabriel H. Rua^{1*}, Liliana Katinas² and Roberto D. Tortosa¹. ¹Cátedra de Botánica Agrícola,

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The so-called ‘*Xanthocephalum*-group’ comprises six or seven genera (according to different authors) of the Astereae (Asteraceae), characterized by yellow ray florets (if present), corollas of disk florets abruptly amplified into the throat and basic chromosome number $x = 6$. It includes North and South American representatives. To test the monophyly of both the *Xanthocephalum*-group as a whole and each of its genera, a morphology-based phylogenetic analysis was conducted using parsimony under implied weights. Analyses were performed under 33 different k values and the resulting topologies were summarized as a majority rule consensus tree. All genera except *Grindelia* were monophyletic across the range of k values tried. *Olivaea* was nested within *Grindelia*. *Haplopappus* and *Grindelia* were sister groups, and some South American *Grindelias* were basal to the remainder of the genus. Nevertheless, other South American species were nested deeply within the genus. The monophyly of the *Xanthocephalum*-group as a whole was not confirmed, since the group included *Gutierrezia* in about 50% of the topologies. A more comprehensive taxon sampling comprising the whole tribe Astereae would be necessary to assess the phylogenetic relationships between the *Xanthocephalum*-group and the related species in the tribe.

Crafting a whole genome approach. Rebecca B. Budinoff Committee on Evolutionary Biology, The University of Chicago, Chicago, IL, USA

The increasing amount of whole genome data and computational power available today underscores the necessity for a comprehensive whole genome phylogenetic approach. The challenges, advantages, and theory behind such an approach are discussed in reference to a case study of the genus *Vibrio*. The genus *Vibrio* (Bacteria–Proteobacteria: Vibrionaceae) contains 76 species with diverse life histories, including human and marine pathogens and bioluminescent symbionts. Multiple species also exhibit the density dependent gene expression behaviour known as quorum sensing. A phylogenetic hypothesis is presented here for the 67 *Vibrio* species available on GenBank, based on five genes and analyzed under direct optimization as implemented in POY. The hypothesis to be presented is the most comprehensive analysis to date for this group. While a first hypothesis is important, the goal is to move toward using whole genome data. For eight species, the complete genome base-pair sequence is known and for each of these, two circular chromosomes have been detected. Different species, and even strains of the same species, vary greatly in the placement of genes both within and between chromosomes. Gene order data, without DNA base-pair information is considered first, along with a separate consideration of these data together. The history of gene rearrangement contains information not contained within the base-pair sequence and can clarify the mechanism for the emergence and maintenance of this two chromosome system and perhaps what role it has played in the development of diverse life histories and quorum sensing behaviour. Different levels of inquiry may produce different assessments of homology and the integration of these levels of data and homology is the challenge of a whole genome approach. How this approach then fits into the framework of total evidence, considering the complexity that duplication events, paralogy, and horizontal transfer introduce to the goal of including all data, is also considered.

Assembling the Tree of Life for Hymenoptera. James M. Carpenter American Museum of Natural History, Central Park West at 79th Street, New York, NY 10024, USA

The first comprehensive analysis of higher-level phylogeny of the order Hymenoptera is presented. The project has assembled more than 40 collaborators world-wide. The analysis included representatives of all extant superfamilies, scored for about 400 morphological characters, and sequenced for five genes (16S, 18S, 28S, COI and EF1alpha).

Including outgroups, about 140 terminals were analyzed. Relationships among symphytans (‘sawflies’) accord with work previously published in the pages of *Cladistics*. Relationships within Apocrita are resolved for the first time. Stephanoidea are supported as the sister-group of the remaining Apocrita. Aculeata are in a clade with Evanioidea, Trigonalioidea and Megalyroidea, not closely related to Ichneumonidea. Paraphyly of Proctotrupoidea is demonstrated, itself not a surprise, but here in terms of Chalcidoidea. Aside from this last, and failure to resolve the superfamilies within Aculeata, all the superfamilies are supported as monophyletic.

Systematics of the Bolivian and Peruvian species of the genus *Bothrops* (Serpentes: Viperidae: Crotalinae) based on morphology. Paola A. Carrasco^{1*}, Gerardo C. Leynaud¹ and Gustavo Scrocchi². ¹Laboratorio de Animales Venenosos y Herpetología, Centro de Zoología Aplicada, Universidad Nacional de Córdoba, Rondeau 798, CC122, CP5000, Córdoba, Argentina; ²CONICET-Instituto de Herpetología, Fundación Miguel Lillo, Tucumán, Argentina

Eleven species of the genus *Bothrops* occur in Bolivia and Peru: *B. jonathani*, *B. andianus*, *B. sanctaecrucis*, *B. mattogrossensis*, *B. pictus*, *B. roedingeri*, *B. barnetti*, *B. brazili*, *B. osbornei*, *B. atrox* and *B. moojeni*. The systematic relationships of some of these species remain unclear and some of them have never been included in any cladistic analysis. Internal and external morphological characters were recorded after the revision of specimens from Bolivian and Peruvian collections, and the relationships between species were analyzed through cladistic methods. The relative importance of some characters and the possibility that the phylogeny of this species group helps to understand the historical biogeography of the genus are discussed.

The optimization of landmark data: a three-dimensional approach. Santiago A. Catalano^{1*}, Pablo Goloboff² and Norberto Pedro Giannini³. ¹Facultad de Cs. Exactas y Naturales, UBA, CONICET, Argentina; ²INSUE, Instituto Miguel Lillo, CONICET, Argentina; ³CONICET, PIDBA, Facultad de Ciencias Naturales, Miguel Lillo 205, S.M. Tucumán, Argentina

Since the implementation of Farris optimization to analyze continuous characters in TNT, there has been a renewed interest in using such characters in phylogenetic analyses, and in trying to extend phylogenetic analysis to quantitative descriptions of shape. All previous approaches were based on the optimization of values from some sort of unidimensional shape descriptor from the terminals. We consider that a more natural method should be based on explicitly estimating optimal ancestral shapes. Particularly, in the case of landmark configurations, we propose a generalization of Farris optimization to more than one dimension. In this approach, each landmark in the ancestor can be placed on any position in a space that presents the same dimensionality as that on which the landmark data were defined. Under a 3D-optimization, the optimal landmark positions of ancestors are those which minimize the distances between homologous landmarks along branches. Our approach synthesizes well-known elements of phylogenetic analysis into a new perspective for the problem of phylogenetic analysis of shape.

Reconstructing patterns of gene rearrangements in mitogenomes. Megan E. Cevasco American Museum of Natural History New York, NY, USA

Analyses identifying gene rearrangements within a dataset of decapod complete mitochondrial sequences will be presented. A comparison will be made between the breakpoint/inversion and common interval algorithmic approaches to the rearrangement problem as implemented in GRAPPA and CREX respectively. Additionally, analyses that simultaneously optimize both nucleotide and gene rearrangement transformations will be contrasted to those reconstructing either sequence or rearrangement events separately.

Testing the role of sexual selection in the evolution of ponyfishes (Teleostei: Leiognathidae). Prosanta Chakrabarty^{1*}, William Leo Smith² and John S. Sparks³. ¹Louisiana State University, Museum of Natural Sciences, USA; ²Field Museum of Natural History, USA; ³American Museum of Natural History, USA

Sexual selection has long been assumed to have played a role in the diversification of ponyfishes. It has been proposed that sexual selection led to increased speciation rates in this family because of the presence of a sexually dimorphic light organ system (LOS) in most species of this clade. In this scenario we would expect evolution of body shape variation to be limited or outpaced by evolution of variation related to the LOS in sexually dimorphic leiognathids. We test this hypothesis using phylogenetic relationships of leiognathids that are reconstructed using molecular and morphological features and also by quantifying morphological shape diversity (disparity) among clades. We recover a single origin of sexual dimorphism in a pattern consistent with the hypothesis that sexual selection increased speciation rates in that clade. However, we also discover that leiognathids that are sexually dimorphic for the LOS are significantly more disparate in body shape than their non-dimorphic counterparts. Therefore, sexual selection on the LOS appears to have neutral effects on the external morphological diversification in the family and sexual selection on the LOS can not be the only mechanism influencing diversification in leiognathids.

An approach to the phylogeny of Chloraeinae (Orchidaceae). M. Amelia Chemisquy* and Osvaldo Morrone Instituto de Botánica Darwinion (IBODA)-CONICET, Labardén 200, B1642HYD San Isidro, Buenos Aires, Argentina

The systematic position and the relationships among some South American terrestrial orchids, *Bipinnula*, *Chloraea*, *Gavilea* and *Geoblata* is unclear. The four genera have been grouped in the subtribe Chloraeinae by several authors; also, Chloraeinae has been placed under the tribes Diurideae, Geoblasteae, Spirantheae and Cranichideae. Besides, some authors raised the subtribe Chloraeinae to the tribe level. Previous phylogenetic studies of the group have only included a few species of *Chloraea* and *Gavilea* (only one or two species) while *Bipinnula* and *Geoblata* have not been included in a phylogeny before. Therefore, the monophyly of Chloraeinae should be tested, and the monophyly of *Bipinnula*, *Chloraea*, *Geoblata* and *Gavilea* needs to be explored. For the molecular phylogenetic analysis three chloroplast markers were used: matK + trnK, atpB-rbcL spacer and rpoC1. The taxonomic sampling includes six species of *Gavilea*, 11 species of *Chloraea*, the only species of *Geoblata* and several species from tribes Diurideae, Spirantheae and Cranichideae as outgroups. *Bipinnula* was not included due to the lack of fresh material. Sequences were aligned using the program Dialign and then the alignment was edited manually, as conservatively as possible. The three matrices were analyzed separately and combined using TNT. All characters were equally weighted, and gaps were scored as missing data. Preliminary results show that *Chloraea*, *Gavilea* and *Geoblata* are in a clade with high support, with *Geoblata* and *Gavilea* nested inside *Chloraea*. Consequently, for the taxa sampled here, the subtribe is monophyletic, *Chloraea* is paraphyletic, and *Gavilea* turned out to be monophyletic with high values of support. As sister group of the Chloraeinae are the Cranichideae species, but a more exhaustive taxonomic sampling is needed to solve the taxonomic placement of the subtribe Chloraeinae.

Phylogenies from Morphometrics II. Missing values, females, character selection and scaling, support, and dependence optimization: Stylocellidae (Arachnida, Opiliones, Cyphophthalmi) as a challenging test. Ronald Clouse^{1*}, Benjamin de Bivort² and Gonzalo Giribet¹. ¹Department of Organismic & Evolutionary Biology, and Museum of Comparative Zoology, Department of Invertebrates, Harvard University, 26 Oxford St., Cambridge, MA 02139, USA; ²Rowland Institute at Harvard, 100 Edwin H. Land Blvd, Cambridge, MA 02142, USA

A comprehensive method for constructing phylogenetically informative data sets from raw measurements is described and discussed. Special consideration is given to the issues of handling missing data, including females in a group of species where most phylogenetically informative characters have been traditionally obtained from males, selecting and scaling characters to overcome known size and homoplasy influences, optimizing character independence, and measuring support. How to scale measured characters against body size had considerable impact on data quality, and proper scaling was best done locally and by parallel measures taken along body axes. The importance of avoiding suspected homoplastic characters and removing size information is shown in a test of the method with the large family of mite harvestmen Stylocellidae (Arachnida, Opiliones, Cyphophthalmi). This family includes extremely large, miniaturized and troglomorphic species, the relationships of which are already suspected from molecular studies. Only with proper character selection and scaling did we recover the known close relationship among the largest member of the suborder from Borneo, highly troglomorphic species from the Thai–Malay Peninsula and Borneo, and a miniaturized species from the forests of Sumatra, as suggested by unpublished molecular analyses. The methods for evaluating trees and the meaning of resampling measures in this context are discussed. Lastly, methods are explored to determine optimal methodological parameters in the absence of prior phylogenetic information about the taxa being studied.

Phylogenetic affinities of enigmatic African galliforms: the Stone Partridge *Ptilopachus petrosus* and Latham's and Nahan's 'Francolins' *Francolinus lathamii* and *F. nahani*. Tim Crowe DST/NRF Centre of Excellence at the Percy FitzPatrick Institute of African Ornithology, University of Cape Town, Private Bag X3, Rondebosch 7701, South Africa

Nahan's *Francolinus nahani* and Latham's 'Francolins' *F. lathamii* are threatened and poorly known phasianine galliforms endemic to forests of tropical Africa. They have traditionally been placed phylogenetically with the widespread Afro/Asian francolins (*Francolinus* spp. sensu lato). Nahan's Francolin has been linked to *F.* (now *Pternistis*) *squamatus*, *ahantensis* and *griseostriatus* which form the implicitly monophyletic 'Scaly Group' of francolins, and Latham's with *F.* (now *Peliperdix*) *coqui*, *schlegelli* and *albugularis* into the 'Red-tailed Group'. The monotypic Stone Partridge *Ptilopachus petrosus* is restricted to arid rocky areas of the Sahel savanna, north of the tropical African forests, and has been grouped tentatively with Asian, partridge-like, forest partridges (*Galloperdix* and *Bambusicola* spp.). Recent, DNA-based phylogenetic research suggests that Nahan's 'Francolin' is not related to francolins, but is most closely related to the Stone Partridge and places Latham's Francolin with 'true' francolins (*Francolinus*, *Peliperdix*, *Dendroperdix* and *Scleroptila* spp.). This study investigates these hypotheses in greater detail using additional DNA evidence and the behaviour and vocalizations of these enigmatic phasianine galliforms. We find overwhelming support for a sister relationship between *nahani* and *petrosus*. They, in turn, are the distantly related sister taxon of the New World quails (Odontophoridae), and to any other Old World galliform. Latham's Francolin is placed with quail-like francolins (*Peliperdix*, *Dendroperdix* and *Scleroptila* spp.) perhaps closest to *Peliperdix coqui*.

Phylogenetic relationships of the Arcoida (Bivalvia: Pteriomorphia): what morphology tells us. Louise Crowley^{1,2}. ¹American Museum of Natural History, New York, NY, USA; ²Graduate School and University Center, City University of New York, New York, NY, USA

The Arcoida is an extant order of bivalves, generally characterized on the basis of 'hard' shell characters: a duplivincular ligament; aragonitic shell microstructure; and an interlocking taxodont hinge. The relationships among this group have been greatly debated, and

many alternative classifications have been proposed. However, these changes have never been based on the evidence of a rigorous phylogenetic analysis. All previous analyses that included Arcoidea have suffered from poor taxon sampling. This study represents the largest phylogenetic analysis of any pteriomorphian group in terms of taxon sampling and characters included. This study seeks to remedy this by including representatives of all extant genera, as well as a large number of pteriomorphian outgroups. Moreover, the inclusion of original observations of both 'hard' and soft anatomical characters helps to elucidate the relationships of this group.

Areas of endemism of the Atlantic Rain Forest, Brazil: methods of delimitation using harvestmen distribution (Arachnida, Opiliones). Marcio B. Da Silva* and Ricardo Pinto-da-Rocha Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, Rua do Matão, t. 14, 321, Caixa Postal 11461, 05422-970, São Paulo, SP, Brazil

Areas of endemism are regions of common origin of many taxa due to their restricted long-time isolation. They harbour unique biotas and therefore are the units of historical biogeography and considered priorities for biodiversity conservation. Despite their importance, there is little discussion in the literature about their delimitation, both theoretically and methodologically. We used distributional information from 109 species of seven subfamilies of Gonyleptidae as a test for different methods. PAE (Parsimony Analysis of Endemicity) and NDM/VNDM 2.5 (Programs for identification of areas of endemism) were used as numerical methods to search for patterns of endemism. Alternatively, we developed and compiled from literature six Combined Criteria to delimit the areas: (1) congruence core (CC) with overlapping of at least two species ranges; (2) indicated CC, endemic species partially overlapping and widespread species; (3) separate general congruence from specific endemism; (4) areas that must be mutually exclusive; (5) species ranges outside of patterns of endemism that are evidence of another area of endemism; and (6) independent geographical evidence. Twelve areas of endemism were delimited using two methods and six criteria: Pernambuco, Bahia, Espírito Santo, Serra do Espinhaço, Serra da Mantiqueira, Serra dos Órgãos, Serra da Bocaina, coast of São Paulo/Rio de Janeiro border, Serra do Mar of São Paulo, south of São Paulo, Paraná and Santa Catarina. They are composed of a CC and maximum regions of endemism (MRE) indicating a source of falsifiability of the hypothesis of delimitation or transition zones as areas of recent range expansion. We also showed species status related with its degree of endemism, as in criterion 2. These 12 areas are the most detailed pattern of endemism ever found in the Atlantic Rain Forest. Five of the delimited areas were identified by PAE and seven by NDM/VNDM, mainly indicating CCs. These results indicate artefacts and ontological problems in numerical methods that support the Combined Criteria as an important analytical tool to complement them to find areas of endemism. Further analysis was also done in order to search for relationships of those areas of endemism. We used seven phylogenies of the same subfamilies and seven methods in cladistic biogeography and variations of them (Component, BPA, TASS and CADE). Results show different origins of fauna for most areas of endemism, despite the high congruence in specific endemic ranges. Those results may suggest other processes restricting species than a simple sequence of vicariant events.

Phylogenies from Morphometrics I. Method principles, independence analysis, character collapse, and alternative effective methods: Pettalidae (Arachnida, Opiliones, Cyphophthalmi) as proof of principle. Benjamin De Bivort¹*, Ronald Clouse² and Gonzalo Giribet². ¹Rowland Institute at Harvard, 100 Edwin H. Land Blvd, Cambridge, MA 02142, USA; ²Department of Organismic & Evolutionary Biology, and Museum of Comparative Zoology, Department of Invertebrates, Harvard University, 26 Oxford St., Cambridge, MA 02139, USA

A comprehensive method for constructing phylogenetically informative data sets from raw measurements is described and discussed.

Special consideration is given to mathematical techniques for analyzing character independence and handling dependent characters. Independence is recognized when a single taxon displays a combination of characters sufficiently different from the overall trend between those characters, and this level of sufficiency is treated as a parameter to be optimized. The sequence of steps required to recognize dependent characters and convert groups of them to single shape descriptors is described, including data formatting, scripting in MatLab, collapsing options available to the user, and creating input files for TNT. Dependent characters were collapsed using the alternative methods of principal components analysis and character weighting, and the relative benefits and caveats of these approaches are discussed. A test of this method is done using measurements from the Gondwanan family of mite harvestmen Pettalidae (Arachnida, Opiliones, Cyphophthalmi). In the optimal independence cutoff range, well corroborated or suspected clades were mostly recovered, including one containing a highly troglomorphic species from South Africa and all the other South African species.

Phylogenetic analysis of genus *Sacciolepis* (Poaceae: Panicoideae: Poaceae). Diego De Gennaro*, Raúl Pozner and Osvaldo Morrone IBODA (Instituto de Botánica Darwinion), San Isidro, Buenos Aires, Argentina

The genus *Sacciolepis* Nash (Poaceae: Panicoideae: Paniceae) comprises nearly 23 species widely distributed in southeastern and western Africa with a few species in America, Asia and Australia. This genus is characterized by spike-like inflorescences, lower glume gibbous and upper glume and lower lemma with conspicuous nerves. *Sacciolepis* was revised only in regional floras of Africa (e.g., Gibbs Russell et al., 1990), Asia (e.g., Bor, 1960) and Australia (e.g., Webster, 1987) or only studied for America (e.g., Judziewicz, 1990a,b; Wipff, 2003). These treatments reveal unresolved taxonomic problems and the existence of species with difficult circumscription. In addition, there is not a comprehensive study of the genus that provides information about interspecific phylogenetic relationships. The aims of this work are to test the monophyly of *Sacciolepis*, and to study the phylogenetic relationships among the species. Anatomical-morphological characters were included in the data matrix, with 30 continuous and 58 discrete characters. The heuristic searches were carried out using TNT under equal weights and implied weighting. Discrete and continuous characters were analyzed altogether and separated. The analysis revealed the monophyletic origin of the genus and the valuable contribution of continuous characters to elucidate interspecific relationships.

Historical biogeography of Liolaemidae: endemism and ancestral area analysis. Juan Manuel Díaz Gómez CONICET, Cátedra de Cordados, Facultad de Ciencias Naturales, Universidad Nacional de Salta, Argentina

Liolaemidae is a family of iguanian lizards that includes more than 200 species, distributed in arid South America. In recent years, the knowledge of this diverse clade has grown almost exponentially, with several species described every year, and new phylogenies (both morphological and molecular). However, there are few contributions to the historical biogeography of Liolaemidae, few based on explicit, quantitative methodology, or including significant samples of species. In this work, I studied the historical biogeography of Liolaemidae, using endemism and ancestral area analysis, in the first analysis using both explicit methods and representing most of the family. For the endemism analysis, the data were analyzed using Parsimony Analysis of Endemicity (PAE) and the analysis of endemism based on the optimality criterion of NDM. The NDM analysis identified 28 areas of endemism, with 45% of the species endemic to some area. The PAE analysis identified 32 areas, with almost 60% of the species being endemic to some area. However, most of the areas found by PAE are subsets of areas found by NDM, or have low scores of endemism. For ancestral area analysis I applied three different methods: Fitch

Optimization, Weighted Ancestral Area Analysis and Dispersal–Vicariance Analysis (DIVA). The areas used for this analysis were, for the first time, defined according to the distribution of the species, instead of using areas defined arbitrarily or based on distributions of other organisms. Fitch optimization found Prepuna, Chile Central and Payunia, and Desierto Intermedio in Perú as ancestral areas for Liolaemidae. Weighted ancestral area analysis found Chile Central, Payunia, Patagonia Austral and Desierto Intermedio as ancestral. DIVA found an ancestral area approximately equal to the actual distribution of the clade. These results are only partially congruent with previous proposals, mainly because of the differences on the definition of the areas.

The Encyclopedia of Life & the Biodiversity Synthesis Center—accelerating the pace of scientific discovery. Torsten Dikow Field Museum of Natural History, Biodiversity Synthesis Center, 1400 South Lake Shore Drive, Chicago, IL 60605, USA

In this presentation the Encyclopedia of Life (EOL) and the Biodiversity Synthesis Center (BioSynC) will be introduced. The Encyclopedia of Life is an ambitious project to organize and make available via the Internet virtually all information about life present on Earth. At its heart lies a series of Web sites—one for each of the approximately 1.8 million known species. Each site is constantly evolving and features dynamically synthesized content ranging from historical literature and biological descriptions to stunning images, videos and distribution maps. The Biodiversity Synthesis Center helps to facilitate scientific discovery in biodiversity, evolution, and conservation biology by funding and hosting synthesis meetings. These meetings can bring together experts from around the world on a wide range of scientific and public issues to encourage progress towards specific goals proposed by the scientific community. They can focus on biodiversity informatics involving large data sets, the formulation of novel scientific ideas, building new bridges among disciplines, and in particular deal with issues in biodiversity or conservation research that have a direct relation to the Encyclopedia of Life. Of particular interest are megadiverse taxa such as many invertebrate lineages, novel research questions in biogeography, evolution, systematics, and taxonomy, visualization of large data sets, and study of biodiversity hotspots. In addition, the BioSynC synthesis meetings can help to highlight public benefits to informatics such as new educational materials and citizen science approaches or develop new ways of using the growing content of the EOL web-pages for scientific discovery. Meetings can take place at the BioSynC at the Field Museum of Natural History in Chicago, IL, USA or at other venues around the world. For more information see: www.eol.org and www.fieldmuseum.org/biosync.

Robber flies from the Cretaceous and Tertiary (Insecta: Diptera: Brachycera: Asilidae): phylogenetic placement, biogeography, and faunal comparison. Torsten Dikow^{1*} and David Grimaldi². ¹Field Museum of Natural History, Biodiversity Synthesis Center, 1400 South Lake Shore Drive, Chicago, IL 60605, USA; ²American Museum of Natural History, Division of Invertebrate Zoology, Central Park West at 79th Street, New York, NY 10024, USA

The study of extinct species has enormous potential for an examination of the early evolution of a taxon, its biogeography, and species diversity because fossilized specimens preserve in situ stages of the evolutionary history otherwise undetected. This presentation reviews the extinct Asilidae (robber flies, assassin flies) from the Cretaceous and Tertiary with particular reference to Dominican amber. The oldest fossils that can be unambiguously assigned to the Asilidae are Cretaceous in origin and can be placed on a comprehensive phylogenetic hypothesis providing not only a minimum age for Asilidae itself, but for a clade composed of Asilidae excluding Asilinae, Laphriinae, and Ommatiinae (110 Ma) as well as the Leptogastrinae (94 Ma). The comprehensive study of the 20 Ma specimens preserved in Dominican amber from Hispaniola Island offers an insight into the

faunal composition of the Caribbean Asilidae fauna in the Miocene. For this analysis, 26 amber specimens are available and the extinct diversity can be compared to recently published reviews of the extant robber-fly fauna of Central America and the Caribbean. The extant diversity is well represented by the extinct amber species particularly within Asilinae, Ommatiinae, and Stenopogoninae. A number of presently distributed Laphriinae and Trigonimiminae genera on Hispaniola have not been found in amber. On the other hand, four Neotropical genera (Laphriinae: *Lampria*, *Smeryngolaphria*; Leptogastrinae: *Leptopteromyia*, *Schildia*) have been preserved in amber, but do not presently occur on Hispaniola. An exceptionally surprising finding is the presence of the Old World Leptogastrinae genus *Lobus* in Dominican amber.

A cladistic and biogeographic analysis of the species of *Agathemera* Stål, 1875 (Phasmatodea, Agathemeridae). Cecilia Domínguez*, Germán San Blas, Federico Agrain and Guillermo Debandi Laboratorio de Entomología, CCT-Mendoza, CC: 507, CP: 5500, Mendoza, Argentina

Agathemera Stål, 1875 is a genus of the family Agathemeridae (suborder Agathemeroidea) that contains eight endemic species from Southern South America. Its species are distributed at both sides of the Andes Mountain range, approximately between parallels 23° and 50° (S). The monophyly of the genus has clearly been established (Camousseight 1995, 2005), however phylogenetic relationships among its species have never been treated in a cladistic analysis. The main objective of this study was to carry out a cladistic analysis based on adult and immature characters belonging to both sexes and a biogeographical analysis to reconstruct the history of the genus. A data matrix of 10 species and 26 morphological characters corresponding to the external morphology and genital structures of both sexes and egg morphology was analyzed. *Xeropsis crassicornis* and *Spicnema chilensis* (Phasmatodea: Pseudophasmatidae) were used as outgroups and all known species of the genus *Agathemera* were included. The data matrix was analyzed with the program TNT, using implicit enumeration; one tree of 51 steps was obtained. This tree supports the monophyly of the genus, with seven synapomorphies. The species *A. elegans* and *A. mesoauriculata* distributed in central Chile are in the base of the cladogram and they are the sister group to both the Argentinian (*A. claraziana*, *A. luteola*, *A. maculifulgens* and *A. millepunctata*) and the Chilean species (*A. grilloidea* and *A. crassa*). For the biogeographic analysis we used the program DIVA 1.1, TNT and Mesquite. DIVA found 276 equally optimal reconstructions. Two vicariance events were detected: the separation of Chilean Matorral from South Andean Steppe, Central Andean Steppe and Monte, and separation of the Patagonian Steppe from the Valdivian Forest and Chilean Matorral. The most frequent dispersions took place between the Chilean Matorral and the Valdivian Forest and between the Valdivian Forest and the Chilean Matorral in the opposite direction.

Backbone constraint trees in parsimony analyses: a possible remedy for missing characters? Torbjørn Ekrem Museum of Natural History and Archaeology, Norwegian University of Science and Technology NO-7491 Trondheim, Norway

Reliable zoogeographical and co-evolutionary analyses are dependent on well founded phylogenies that include all known species. This is difficult to obtain for many organism groups as the availability of both morphological and molecular data is limited and leave numerous entries in an otherwise comprehensive data matrix ambiguously scored. In this study, I investigated how a well founded molecular and morphological phylogeny as backbone constraint influenced the phylogenetic analyses of all known species in the genus *Stempellinella* (Diptera: Chironomidae). The results show that the analyses exclusively using morphological data produced results that were incompatible with the well supported backbone constraint. Thus, the use of backbone constraint trees might be a way to increase accuracy in

phylogenetic analyses of comprehensive data sets that contain a considerable number of missing characters. Some aspects on the use of backbone constraints in phylogenetic analyses are discussed, and several factors are expected to affect how well backbone constrained phylogenies perform with regard to the ‘true phylogeny’. Among the most important are the percentage of taxa and characters used to build the backbone compared to the full matrix, character type and the phylogenetic signal present in the available data. Future testing of the influence of backbone constraints in phylogenetic analyses on simulated data matrices might give indications on the usefulness of this technique.

Cladistic biogeography in Latin America: where are we? Tania Escalante* and Layla Michán Museo de Zoología ‘Alfonso L. Herrera’, Departamento de Biología Evolutiva, Facultad de Ciencias, Universidad Nacional Autónoma de México, Apartado Postal 70-399, México, D.F., 04510 México

Cladistic biogeography arose as a response to the necessity to find genealogical relationships between areas of endemism and determining the sequences of vicariance events. Cladistic biogeography assumes a correspondence between the phylogenetic relationships of the taxa and the relationships between the areas that they inhabit. Nowadays, there are several methods proposed to find those relationships represented in a general area cladogram: Component Analysis, Brooks Parsimony Analysis, Three Area Statement Analysis, Tree Reconciliation Analysis, Paralogy-free Subtree Analysis, Dispersal-vicariance Analysis, Area Cladistics, and Phylogenetic Analysis for Comparing Trees, among others. Given the high number of methods, some authors had even proposed different classifications of the methods, but there is no consensus about which is the best method. On other hand, the number of available phylogenetic and geographic data is increasing, and there are several databases of biological collections and bibliographic available on the web; and the distributional data have been improving through implementation of ecological niche modeling. What is the state of the art in Latin America? We performed a bibliometric analysis on some international and regional literature databases. A query on the Web of Science using as *topic* the words ‘cladistic biogeography’ retrieved 86 documents of 9 sources. The periodical publication with more records is the *Journal of Biogeography*. From the documents of the Web of Science, the most productive author was the Mexican Juan José Morrone with 12 papers. Argentina, Brazil and Mexico were within the top 13 countries. This is reflected in institutional affiliation of authors, because the Universidad Nacional Autónoma de México was the Latin American institution with the biggest number of records in the Web of Science, followed by the Museo de La Plata. There are few cladistic biogeographic analyses regarding Mexico. Mexico is biogeographically interesting because it is on the transition zone between the Nearctic and Neotropical regions. We have analyzed 40 phylogenies of taxa distributed in 14 biogeographic provinces and two regions, using a Paralogy-free Subtree Analysis. We found a general area cladogram, different from the traditional east-west pattern, possibly in response to an earlier process.

Patterns of endemism of the species of Nearctic mammals. Tania Escalante¹, Gerardo Rodríguez^{2*} and Juan J. Morrone¹. ¹Museo de Zoología ‘Alfonso L. Herrera’, Departamento de Biología Evolutiva, Facultad de Ciencias, Universidad Nacional Autónoma de México (UNAM), Apartado Postal 70-399, Mexico, D.F., Mexico 04510; ²Laboratorio de Macroecología, Departamento de Ecología de la Biodiversidad, Instituto de Ecología, Universidad Nacional Autónoma de México (UNAM), Apartado Postal 70-275, Mexico, D. F., 04510 Mexico

The Nearctic region, belonging to the Holarctic realm, was delimited since the 19th century by Sclater and Wallace, mainly based on bird and mammal species. For this region, 27 provinces from Canada to central Mexico and some systems of ecoregions have been proposed; however, there is no recent system of biotic provinces. The Nearctic region comprises North America (Alaska, Canada, and US to

central Mexico), although Nearctic elements can be found in the highlands of Chiapas (southern Mexico). We performed an analysis of endemism with NDM for 324 quadrats of 4° lat–long from Alaska and Canada to Panama, using a database of distributional data of 744 species of mammals, in order to identify the biogeographical patterns of the Nearctic mammals. We found 56 areas of endemism with a high score of endemism and obtained 43 consensus areas from them, using 50% of similarity in species composition. We can identify some major patterns, such as the Mexican Transition Zone and the northern Neotropical boundary (consensus area including central Mexico to Central America). The more southern consensus area of endemism (the five quadrats in Central America) had the higher score (55.25) with 71 endemic species. The Nearctic is not recovered as a whole by the analysis. There are two large patterns for eastern and western sections of the United States and Canada (similar to Bailey’s ecoregional domains), and another pattern on Canada and Alaska (similar to the Hudsonian province of Dice). Although the method used does not allow assigning a hierarchical scheme to these patterns, we suggest them as dominions.

Morphological phylogeny for the conifer genus *Araucaria*. Ignacio Escapa* and Rubén Cúneo CONICET-Museo Paleontológico Egidio Feruglio, Trelew, Argentina

The conifer family Araucariaceae is one of the most emblematic plant groups of the Southern Hemisphere, where its extant distribution is confined. The family originally included two genera, *Agathis* and *Araucaria*, and recently a third one was added: the monotypic *Wollemia*, which is represented by a remnant population of 100 trees in Australia. The genus *Araucaria*, with approximately twenty extant species, is generally divided into four sections: *Bunya*, *Intermedia*, *Araucaria* (= *Columbea*) and *Eutaeta*. The phylogenetic analyses of this family include only two studies based exclusively on sequences of the rbcL gene, whose validity for determining infra-familial relationships has been highly discussed. In terms of relationships between the *Araucaria* sections, however, both studies seem to agree on the presence of two main clades: one formed by the New Caledonian species (Section *Eutaeta*) and another with the remnant three sections. Araucariaceae, and particularly its type genus *Araucaria*, shows an extended fossil record with species recognized since the early Mesozoic in both hemispheres. Fossil species of *Araucaria*, especially those preserving seed cones, were often assigned to a particular section within the genus based on a few characters. In the present study we define and discuss near to forty morphological characters and build a matrix including all the extant species of *Araucaria*, some species of *Agathis*, and the monotypic *Wollemia*. The results are in agreement with molecular approaches in revealing two major clades within the genus as well as in the sections composing each clade. However, relationships inside the clade that includes sections *Bunya*, *Intermedia* and *Araucaria* show important differences. In a second instance we include fossil *Araucaria* species from the Mesozoic of both hemispheres. Unlike previous studies, our analysis does not support the placement of any fossil species within a particular section of the genus, showing that classical characters are insufficient in order to elucidate the past history of this family. Further investigations on this subject must include revisions of extant and fossil species in order to determine new morphological characters, the extension of the taxon sampling, and the combination with molecular data.

Tests and Metabasis. James S. Farris Molekylärsystematiska laboratoriet, Naturhistoriska riksmuseet, Box 5007 SE-104 05 Stockholm, Sweden

A good many published arguments concerning statistical or quantitative procedures tests do not actually involve statistical—or even systematic—principles but instead amount to changing the subject. This paper summarizes some particularly egregious examples, the purpose of this being to clear up a few long-standing confusions.

Turnover patterns in bats related to areas of endemism in northwestern Argentina. L. Ignacio Ferro^{1,2*}, M. Leonor Sandoval^{1,2}, Marcos I. Mollerach¹ and Rubén M. Barquez^{1,2}. ¹Programa de Investigaciones de Biodiversidad Argentina (PIDBA), Universidad Nacional de Tucumán, Argentina; ²Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Argentina.

Bats are used to characterize areas of endemism in the Yungas forest of Northwestern Argentina. An area of endemism (AE) is defined by the congruent distribution of two or more species spatially restricted to that area. Then, an AE should exhibit high homogeneity of the distributional ranges of its biotic elements, with respect to neighbouring areas. Thus, high rates of species turnover and/or pronounced gradients of richness are expected in transitional zones between AEs, as a consequence of abrupt changes in the patterns of species distribution. We analyze here the geographical distribution of 42 species of bats from northwestern Argentina. We used more than 1000 georeferenced records and square grids with cells of 0.5 and 0.25°. To measure the species turnover we used Whittaker's index (WI) and the density of distributional range edges per cell (DDR). The correspondence between edges of AEs obtained by an optimality criterion and the patterns of species' turnover were evaluated by superimposing maps. Both WI and DDR showed high values on the margins of the AE of the northern Yungas. In particular, DDR reached the highest values all along the western margin of the AE of the northern and southern Yungas. There is a sharp elevation gradient in these areas that probably limits the distribution of the majority of the species. In the eastern border, however, the DDR was lower and the gradient of richness was less pronounced. In the eastern border the value of WI was high in both AEs of the northern and southern Yungas. The western edge of the AE of the Yungas is then characterized by an abrupt gradient of species richness, while the eastern edge is dominated by the high species turnover rates.

Implications of continuous characters on Polistinae phylogeny. Zioneth García^{1*}, Luiz F.F. Gelin² and Fernando B. Noll². ¹University of São Paulo, Ribeirão Preto, Brazil; ²State University of São Paulo, São José do Rio Preto, Brazil

Social wasps of the subfamily Polistinae (Hymenoptera: Vespidae) have been important in studies of the evolution of sociality, kin selection, and within-colony conflicts of interest. Polistinae includes two major behavioural groups, differing in their mode of colony founding and mechanism of reproductive dominance. In independent founding the colony begins by a single queen or few queens, without the assistance of workers. It is represented by four genera: *Polistes* (Polistini), *Mischocyttarus* (Mischocyttarini), *Belanogaster* and *Parapolybia* (Ropalidini). By contrast, swarm founding species have large colonies initiated by swarms consisting of multiple queens and a large number of workers, represented by two tribes, Epiponini (with nineteen Neotropical genera) and Ropalidini (with *Ropalidia* and *Polybioides*). Moreover, phylogenetic studies in Polistine have been conducted since the 1990s. In these studies, morphological, behavioural and molecular data have been analyzed on their own and together in order to find a more robust tree. In this work, we carried out an analysis using a matrix with morphological/behavioural data and we added twenty more morphometric characters. We used 67 species of Polistinae, excluding the Ropalidini. The morphometric characters are measures from body parts and measurement ratios. The data were analyzed under TNT (WHS edition). We also analyzed the data on ratios alone (ten continuous characters). In the second analysis we added to the first matrix with ten more continuous characters (the measures). A morphological data matrix (Carpenter, unpublished) was combined with the morphometric one. The first and second analyses produced trees based on size, with larger individuals as plesiomorphic. Such results are incongruent with the actual history of Polistinae, which includes several reversions on shape and size. Fortunately, we could see a separation into two main clades based on the size (with large wasps as plesiomorphic). When the combined analysis is done,

the topology is similar to the current phylogeny of Polistinae. In summary, the analysis showed that these continuous characters can be useful for studies of evolution of Polistinae shape.

Phylogenetic analysis of the Neotropical social wasps of the genus *Polybia* Lepeletier, 1836 (Hymenoptera, Vespidae, Epiponini). Luiz F.F. Gelin* and Fernando B. Noll State University of São Paulo (UNESP)—Campus São Jose do Rio Preto, Brazil

Polybia is a large genus of tropical swarm-founding wasps that contains 57 described species, 19 subspecies and it was divided into 11 subgenera by Richards. These species are widely distributed, extending from Mexico to Argentina, and widespread in the Amazon. '*Phragmocyttarus*' nests of *Polybia* consist of several combs hanging from a leaf or branch. These nests have an envelope made of paper or mud. Colonies typically contain a few hundred of individuals but some can reach thousands of individuals. Also, caste differences in this genus are highly variable. The taxonomic history of *Polybia* is tortuously complex. We summarize previous cladistic treatments, and present a phylogenetic analysis of the species of *Polybia* based on morphological characters of the adult females. Fifty-three species were used in this analysis and *Protonectarina*, *Chartergus*, *Brachygastra*, *Epipona* e *Protopolybia* were used as outgroups. The matrix includes 59 adult characters, and 54 larval and nest-architecture characters. The analysis was carried out with TNT (WHS edition). The analysis under implied weighing resulted in two cladograms. *Polybia* is supported as monophyletic as well as its subgenera, with the following relationships: (*Pedothoea* + (*Cylindroeca* + (*Trichinothorax* + ((*Furnariana* + *Platypolybia*) + (*Formicicola* + (*Apopolybia* + (*Synoeccoides* + (*Polybia* + *Alpha*)))))) + (*Myrapetra*)). This topology agrees with previous hypotheses, but resolves the basal dichotomy, with *Pedothoea* as the most basal subgenus.

Resolving the correlation of a phylogenetic character and a non-evolving variable. Norberto Pedro Giannini^{1*} and Pablo A. Goloboff². ¹CONICET, PIDBA, Facultad de Ciencias Naturales, Miguel Lillo 205, S.M. Tucumán; ²INSUE, Instituto Miguel Lillo, CONICET, Miguel Lillo 205, S.M. Tucumán, Argentina

Species are related by phylogeny and this poses a statistical problem of non-independence in data gathered from terminals. A diverse family of phylogenetic comparative methods deal with various aspects of the problem, chiefly in the context of correlation/regression of two characters on a tree. This is a commonly encountered problem across all biology. One instance would be the response of basal metabolic rate to changes in body size. In this case, both characters clearly evolve in any lineage of interest. However, other biologically interesting cases involve a variable that cannot be transferred to descendants via genomic transmission. Some demographic parameters and geographic location (e.g., latitude) are examples of variables that do not evolve. We argue that when two such variables are measured in terminals, then a randomized version of correlation/regression is a valid analytical option. Here we deal with a more complicated situation, the correlation of one evolving character (e.g., body size) with one non-evolving variable. For the evolving character, phylogenetic dependence among terminals is rampant. Therefore the tree structure should be taken into account, and by this we mean a very specific concept: both the branching pattern and the total amount of evolution should be taken into account. By contrast, for the non-evolving character, the tree structure is irrelevant, so considering this difference is crucial to develop a test. We propose a rather simple solution. We calculate an observed correlation coefficient r between the two variables, x and y , the first being an evolving character and the second a non-evolving variable, conserving the original pairing of data. Then we optimize x on the tree and collect the changes between nodes (whose sum equals total steps on the tree), sampling a reasonable number of reconstructions. Next we randomly assign the changes (not the ancestral assignments) of a given reconstruction in the nodes of the tree, and recalculate each

terminal's value by summing the changes from root to tip. Thus, terminals acquire new values while preserving the exact same amount of evolution on the tree. The new set of x -values is correlated with the original y -values. In this way, a distribution of random r is generated (e.g., 5000 times) and the observed r is compared with that distribution, obtaining a randomized significance test for r . We discuss unexpected properties of this procedure, called here dual phylogenetic correlation.

A glimpse into the mammal branch of the 'large' eukaryote tree. Norberto Pedro Giannini^{1*}, Pablo A. Goloboff², Santiago A. Catalano³, J. Marcos Miranda⁴, Claudia Szumik², J. Salvador Arias², Mari Källersjö⁵ and James S. Farris⁵. ¹CONICET, PIDBA, Facultad de Ciencias Naturales, Miguel Lillo 205, S.M. Tucumán; ²INSUE, Instituto Miguel Lillo, CONICET, Argentina; ³Facultad de Cs. Exactas y Naturales, UBA, CONICET, Argentina; ⁴Fundación Miguel Lillo, CONICET, Argentina; ⁵Molekylarsystematiska laboratoriet, Naturhistoriska riksmuseet, Stockholm, Sweden

In a very recent development, Goloboff et al. (in prep.) analyzed the largest phylogenetic dataset so far assembled in terms of taxonomic diversity and character representation for eukaryotes. Remarkably, most major eukaryotic clades were recovered. Mammals represent one prominent example. This group is important in this context because, rather unsurprisingly, it was best represented among all recovered clades in terms of both ingroup taxonomic diversity and sequence completeness. This study looks into the structure of the mammalian subtree and compares its branching pattern with hypotheses of mammal phylogeny at several hierarchical levels. As with other major clades, but more strikingly so, the majority of currently recognized ordinal and familial relationships are accurately represented in the mammal subtree. The main structure of the mammal subtree, with a *ca.* 50-fold increase in taxonomic representation as compared with the most comprehensive previous molecular analysis, closely corresponds with many aspects of the current mammalian classification. But significantly, the dataset does not include a single gene used in recent higher-level phylogenetic studies of mammals. Group recovery is surprisingly accurate not only among major groups but at all taxonomic levels, including an exceedingly long list of monophyletic genera. We use the subtree to examine selected patterns of mammal evolution and discuss its implications.

Reconstructing the Protostome Tree of Life—the past, the present and the future. Gonzalo Giribet*, Casey Dunn, Greg Edgecombe, Andreas Hejnol, Reinhardt Kristensen, Mark Martindale, Matthias Obst, Greg Rouse, Elaine Seaver, Martin Sørensen, Ward Wheeler and Katrine Worsaae Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology, Harvard University, 26 Oxford Street, Cambridge, MA 02138, USA

One of the most vexing questions in animal systematics is to understand the composition and relationships of protostome animals—which include more than 20 animal phyla and the most diverse ones. Through the NSF AToL initiative we assembled a multidisciplinary team of researchers to focus on the anatomy, molecules and developmental biology of the major protostome lineages. Through the application of novel techniques and approaches in phylogenomics we have been able to establish a well-supported skeleton for protostome diversity and have explored important issues such as the composition of annelids, or the relationships among the major arthropod and molluscan lineages. However, new developments in DNA sequencing technologies make our study—the largest data set ever assembled to study metazoan relationships—look obsolete in many respects. Here we explore some of the possibilities of the new technologies for improving taxon and character sampling in phylogenomic studies.

A new dimension in combining data? The use of morphology and phylogenomic data in metazoan systematics. Gonzalo Giribet*, Greg Edgecombe, Reinhardt Kristensen, Fredrik Pleijel, Greg Rouse,

Martin Sørensen and Katrine Worsaae Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology, Harvard University, 26 Oxford St., Cambridge, MA 02138, USA

After almost two decades of combining morphology and molecular data in phylogenetics, it is now widely accepted that both sources of evidence have their role in modern systematics. However, recent developments in the scalability of generating molecular data have made some authors doubt about the future contribution of morphology to phylogenetic hypotheses. Here we present evidence that morphology still plays an important role in modern systematics, even when combined with large amounts of genetic data, among other things, for their ability to include fossils and their key information into phylogenetic testing. Our results are based on the combined analysis of morphological and genomic (primarily EST-based) data for a large array of metazoan taxa representing almost the totality of known animal phyla.

A multilocus mtDNA and nrDNA phylogeny of thick-headed flies (Conopidae). Joel F. Gibson^{1,2*} and Jeffrey H. Skevington^{1,2}. ¹Agriculture and Agri-Food Canada, Canadian National Collection of Insects, Arachnids, and Nematodes, K.W. Neatby Building, 960 Carling Avenue, Ottawa, ON, K1A0C6, Canada; ²Department of Biology, Carleton University, Ottawa, ON, K1S5B6, Canada

The Conopidae are a fascinating family of parasitic flies. The larvae of most species in the family are parasitoids of bees and wasps. The adults usually feed on flowers and can serve as important pollinators. Many species are mimics of bees and wasps, sometimes even of the same species that serve as hosts to their young. While the family has been classified into four extant subfamilies (Conopinae, Dalmanniinae, Myopinae and Stylogasterinae), no tests of the monophyly of these clades has been performed. Also, no phylogeny for the Conopidae has been attempted. We have reconstructed the first higher-level phylogenetic tree for the family using molecular characters. DNA was extracted from 60 specimens representing 21 genera, all four extant subfamilies, and numerous, suitable outgroups. Mitochondrial and nuclear DNA was amplified with PCR and sequenced. Large segments of the 12S ribosomal RNA gene, the cytochrome oxidase I (COI) gene, the 28S ribosomal RNA gene, and the wingless gene were included in the analysis. The 12S, COI, and wingless genes provided phylogenetically useful characters. The subfamilies Conopinae and Dalmanniinae are found to be monophyletic, while the Myopinae are monophyletic only when the genus *Zodion* is excluded. The Stylogasterinae are found to be monophyletic but placed outside of the Conopidae, in agreement with its proposed, but largely unaccepted, status as a separate family. The Dalmanniinae are found to be the sister group to the rest of the Conopidae (excluding the Stylogasterinae). The topologies of trees generated using each of the three informative genes are compared with the total-evidence tree. The informative qualities of mitochondrial versus nuclear genes and ribosomal versus protein-coding genes are investigated. We intend to extend the current dataset to include representatives of most valid genera. Additional sequence data from other genes and a morphological matrix will also be added in the future.

Phylogeny of *Miconia* (Melastomataceae): patterns of stamen diversification in a megadiverse Neotropical genus. Renato Goldenberg^{1*}, Darin S. Penneys², Frank Almeda², Walter S. Judd³ and Fabián A. Michelangeli⁴. ¹Universidade Federal do Paraná, CNPq, Brazil; ²California Academy of Sciences, Botany, USA; ³Department of Botany, University of Florida; USA; ⁴New York Botanical Garden, USA

Phylogenetic relationships within *Miconia* and other genera in the Neotropical tribe Miconieae were investigated using a maximum parsimony analysis of nuclear internal transcribed spacer and *ndhF* nucleotide sequences. Included were all sections in *Miconia* (212 species; about 20% of the genus) and 12 of the 15 remaining genera assigned to the tribe (an additional 239 species). Given the tribe's reputation for problematic generic distinctions, it was not surprising

that most traditionally recognized taxonomic groups—both genera and sections—were shown to be polyphyletic or paraphyletic. Nevertheless, *Miconia* is composed of several distinct monophyletic groups, with a large majority of the species belonging to only four clades. Some of these groups represent parts of sections proposed in the last revision of the genus, but most of the diversification seems to have occurred in geographical areas that are more restricted than would have been predicted by the distribution of these sections. Moreover, parallel evolutionary trends are seen in anther form, i.e., shifts from elongate to shorter anthers and from minute-pored to large-pored or slit-like dehiscent anthers. These changes may relate to pollinator shifts, especially from buzz pollination to nonvibrational pollination. Thus, the major evolutionary diversifications within the tribe have been obscured by convergence in stamen morphology, leading to many arbitrary generic and sectional circumscriptions.

Re-defining 'large'. Pablo A. Goloboff¹, Santiago A. Catalano^{2*}, J. Marcos Mirande^{3*}, Claudia Szumik¹, J. Salvador Arias¹, Mari Källersjö⁴ and James S. Farris⁴ ¹INSUE, Instituto Miguel Lillo, CONICET, Argentina; ²Facultad de Cs. Exactas y Naturales, UBA, CONICET, Argentina; ³Fundación Miguel Lillo, CONICET, Argentina; ⁴Molekylarsystematiska laboratoriet, Naturhistoriska riksmuseet, Stockholm, Sweden

This paper will present an analysis based on the largest phylogenetic dataset ever assembled, consisting of 13 genes and morphology for numerous eukaryotic taxa. The results for the combined dataset recover the existing taxonomy with high accuracy. For the molecule-only dataset, the results present more differences with major taxonomic groupings, but the agreement is still very highly significant. A few misplaced species aside, the molecule-only trees display the bulk of the metazoans, green plants, fungi, red algae, stramenopiles, alveolates, and euglenozoans, in discrete groups. This shows that tree-calculation algorithms can effectively retrieve phylogenetic history for very large datasets, and provides at the same time strong corroboration for the major eukaryotic lineages long recognized by taxonomists on the basis of morphology alone.

On weighting characters differently in different parts of the cladogram. Pablo A. Goloboff^{1*}, J. Marcos Mirande² and J. Salvador Arias¹. ¹INSUE, Instituto Miguel Lillo, CONICET, Argentina; ²Fundación Miguel Lillo, CONICET, Argentina

One commonly heard criticism of weighting methods such as successive or implied weighting is that they assume uniformity of weights throughout the cladogram. A variant of the same criticism is that current weighting methods rely on the dubious assumption that instances of homoplasy in distant clades are as relevant as instances of homoplasy in more closely related clades. While the assumption of uniformity can hardly be part of a relevant criticism of weighting (since equal weighting also assumes it), developing a method which does not assume it may be desirable. Although it is of course possible to run separate analyses, compartmentalizing the data and using different weights for each part of the tree, the ideal method should consider all the evidence simultaneously and provide a globally optimal solution to the problem. This paper describes a modification of the method of auto-weighted optimization (Goloboff, 1997) to downweight the cost of each character-state transformation according to the number and distance of other transformations between the same states. The method was experimentally implemented, and tested with simulations to confirm that it performs as expected. However, hypothetical examples show that such type of weighting cannot be considered to be a form of parsimony—that is, a form of the criterion that compares trees based on the degree to which similarities can be explained as resulting from common ancestry. If perhaps realistic, the variable-weights criterion necessarily implies that other additional considerations—possibly in conflict with parsimony—come into play. Apparently such undesirable consequences would be a necessary part of any method which weights characters differentially in different parts

of the tree. Therefore, uniformity of weights throughout the cladogram seems to be a *sine qua non* requirement of the parsimony criterion, and parsimony-based weighting methods cannot be criticized for assuming uniformity of weights.

Phylogenetic analysis of the ostracod family Cypridinidae and the evolution of bioluminescence. Vanessa Liz Gonzalez^{1*} and Elizabeth Torres². ¹Department of Organismic and Evolutionary Biology, Harvard University, 26 Oxford St., Cambridge, MA 02138, USA; ²Department of Biological Sciences, California State University, Los Angeles, 5151 State University Drive, Los Angeles, CA 90032, USA

Sequence information from the 12s rRNA mitochondrial gene and cytochrome oxidase one (CO1) sequences were used to reconstruct the evolutionary relationships within the family Cypridinidae (Ostracoda: Myodocopida) in order to study the evolution of bioluminescence within this group. Bioluminescence is described as the production of light by any living organism and is proposed to have developed first as an anti-predatory behavior in cypridinid ostracods and, second as a courtship ritual performed by males of some Caribbean species of the family Cypridinidae. This project combined the 12s rRNA and CO1 mitochondrial gene sequences from Caribbean Cypridinidae species with information from the 16s rRNA gene from a previous study. A more robust molecular phylogeny was generated and evolutionary relationships were resolved within the Cypridinidae, than with previous molecular data. Cohen and Morin (2003) hypothesized that bioluminescence evolved once in this group, and luminescent signalling used in courtship, evolved later and only once, based on morphological data. Molecular information from this project supports the previous hypothesis of the evolution of bioluminescence and the luminescent signalling, through the monophyly of both taxa.

Phylogenetic reconstruction using secondary structures of Internal Transcribed Spacer 2 (ITS2, rDNA): Finding the molecular and morphological gap in Caribbean gorgonian corals. Alejandro Grajales*, Catalina Aguilar and Juan Armando Sanchez Departamento de Ciencias Biológicas-Facultad de Ciencias, Laboratorio Biología Molecular Marina (BIOMMAR), Universidad de Los Andes, Bogotá, Colombia

Most phylogenetic studies focus on primary DNA sequence information. However, RNA secondary structures are particularly useful in systematics because they include characteristics not found in the primary sequence that give 'morphological' information. Despite the number of recent molecular studies on octocorals, there is no consensus opinion about a region that carries enough phylogenetic resolution to solve infrageneric or close species relationships. Moreover, infrageneric morphological information by itself does not always produce accurate phylogenies; intraspecific comparisons can reveal greater differences than infrageneric ones. The search for new phylogenetic approaches, such as by RNA secondary structure analysis, is therefore a priority in octocoral research. Initially, twelve predicted RNA secondary structures were reconstructed to provide the basic information for phylogenetic analyses; they accorded with the six helicoidal ring model, also present in other groups of corals and eukaryotes. We obtained three similar topologies for nine species of the Caribbean gorgonian genus *Eunicea* (candelabrum corals) with two sister taxa as outgroups (genera *Plexaura* and *Pseudoplexaura*) on the basis of molecular morphometrics of ITS2 RNA secondary structures only, traditional primary sequence analyses and maximum likelihood and a Bayesian analysis of the combined data. The latter approach allowed us to include both primary sequence and RNA molecular morphometrics; each data partition was allowed to have its own rate. In addition, each helix was partitioned as if it had evolved at a distinct rate. *Plexaura flexuosa* was found to group within *Eunicea*; this was best supported by both the molecular morphometrics and combined analyses. We suggest that *Plexaura flexuosa* should be transferred to *Eunicea* and present the description of a new species. *Eunicea flexuosa*, *E. pallida*, *E. laxispica* and *E. mammosa* formed a separate clade in the

molecular phylogenies, and were reciprocally monophyletic with respect to other *Eunicea* (subgenus *Euniceopsis*, e.g., *E. tourneforti* and *E. laciniata*) in the molecular morphometrics tree, with the exception of *E. fusca*. Moreover, we suggest a new diagnostic character for *Eunicea*, also present in *E. flexuosa*: middle layer sclerites > 1 mm in length. ITS2 was a reliable sequence for infrageneric studies in gorgonian octocorals because of the amount of phylogenetic signal, and was corroborated against morphological characters separating *Eunicea* from *Plexaura*. The ITS2 RNA secondary structure approach to phylogeny presented here did not rely on alignment methods, but provided clearly homologous characters for partition analysis and RNA molecular morphometrics. These approaches support the divergence of *Eunicea flexuosa* comb. nov. from the outgroup *Plexaura*, although it has been considered part of this outgroup for nearly two centuries because of morphological resemblance.

Cladistic biogeography of islands: A variety of ad hoc hypotheses. Philippe Grandcolas*, Tony Robillard, Romain Nattier and L. Desutter-Grandcolas UMR 5202 CNRS, Département Systematique et Evolution, case 50, Muséum national d'Histoire naturelle, 45, rue Buffon, 75005 Paris, France

After a period of methodological advance and sophistication, phylogenetic biogeography often comes back to the old ad hoc and usual proposals to justify the preferred scenarios of the authors. We illustrate this trend using some recent studies in cladistic biogeography of islands. After a period where vicariance biogeography succeeded in evacuating unjustified and constant use of ad hoc hypotheses of dispersal, different kind of studies all call for their preferred scenarios without inferring hypotheses with data. On one side, dispersalism has become again in fashion and the supposed influence of dispersal is studied without first eliminating other possible explanations for distributional patterns. On the other side, to evacuate the horrific inference of possible specific cases of dispersal, ad hoc calls for survival of taxa on previously existing and drowned islands is made repeatedly. We will look at this second side to understand what is implied by these ad hoc scenarios and whether there is a means to make them more scientific and testable.

Indicators of endemism. Peter Hovenkamp* and N. Raes Nationaal Herbarium Nederland, Leiden Branch, The Netherlands

In the field of ecological community analysis, various methods are in use to distinguish patterns of co-occurrence between taxa. Endemism analysis as implemented in NDM/VNDM, although developed for use in historical biogeography, conceptually has close parallels to these methods—as the authors note: ‘it could be seen as an “ecological” method as much as a “historical” one’. We compared the performance of NDM/VNDM with two of the methods for analysis of ecological communities: TwinSpan analysis (implemented in WinTwins), which is mostly used in analysis of vegetation data; and Indicator species analysis (Dufréne and Legendre 1997) which is used more generally in community analysis. Both methods apply a hierarchical analysis to specimen/location data. As a basis for comparison, we investigated the capacity of each of the three methods to recognize patterns that are diagnosable by the presence of two or more characteristic (‘endemic’) taxa. The dataset we used consisted of distribution data for 1439 species, compiled for 289 grid of ½° for the island of Borneo, based on Raes et al. (2009). Our results show that the hierarchical methods found results similar to those found by the non-hierarchical one at best at low levels of splitting. NDM retrieves some patterns that are missed by the hierarchical methods, while hierarchical methods retrieve few patterns that are missed by NDM and are not obviously artefacts resulting from the hierarchical approach to classification. We conclude that ecological community analysis can potentially benefit from incorporating non-hierarchical methods, in particular NDM, in at least two ways: (1) to obtain patterns that are invisible in a hierarchical clustering analysis, due to the absence in NDM/VNDM of restrictions inherent to hierarchical clustering, and (2) to allow a role for spatial

distribution of taxa in the retrieval of patterns, due to the application of the evenness rule in NDM/VNDM.

Tracking the geographic spread of avian influenza (H5N1) with multiple phylogenetic trees. Rasmus Hovmøller^{1,2*}, Boyan Alexandrov² and Daniel Janies². ¹Mathematical Biosciences Institute, The Ohio State University, USA; ²Department of Biomedical Informatics, The Ohio State University, USA

In this study we apply phylogenetic tree search and character optimization under the parsimony criterion to track the spread of avian influenza (H5N1) across time and space. We performed a reanalysis of the hemagglutinin (HA) sequence dataset representing 481 viral isolates used by Wallace and Fitch (2008) as well as a new analysis of 1646 isolates representing all of the high-quality HA data in the public domain as of June 2008. The parallel version of TNT was used to find the most parsimonious trees. The TNT command ‘xmult’ was used to perform heuristic searches to find a presumed minimum tree length. Next we performed tree fusing to find a large pool of trees at the presumed minimum length. Character analyses were performed on tens of thousands of most parsimonious trees. For the 481 HA sequence dataset 74 393 trees were used. For the 1646 HA sequence dataset 50 950 trees were used. In contrast Wallace and Fitch used a single tree to study the spread of H5N1. We coded major geographic and political regions as states of a multistate character, limited to 31 regions at a time. We use the TNT command ‘change’ to perform character state optimization to find the minimum and maximum number of state changes over the pools of most parsimonious trees. We evaluated possible pathways for viral traffic by investigating state changes for many important geographic state pairs (e.g., China to Japan). Large number of state changes indicates repeated viral traffic between geographic regions. A minimum number of state changes at 0 and a maximum number of state changes > 0 indicates possible viral traffic. Results of the reanalysis of Wallace and Fitch’s dataset comprised of 481 HA sequences show that using a single tree misestimates the frequency of transmission events and in some cases fails to detect possible transmission events among regions. The analysis of 1646 HA sequences reveals transmission routes that have not been reported previously. For example we find many possible transmission routes to African nations and Vietnam compared to the results found by single tree analyses from other authors. We also present a workflow for management of sequence data, metadata, tree search results, character optimization results and generation keyhole markup files suitable for visualizing summaries of multiple tree analyses in a geographic information system such as Google Earth.

RAUP*: Recombination Analysis Using Parsimony*. Leandro R. Jones Estación de Fotobiología Playa Unión-CONICET, CC 15, Playa Unión (9103), Chubut, Argentina

*And no other method.

Recombination appears to be an important evolutionary mechanism in the AIDS virus, for some recombinant forms (the so called Circulating Recombinant Forms or just CRFs) have spread in human populations. The methods used for inferring recombination are based on detecting conflicting signals along sequence alignments. Among virologists, *bootscanning* is one of the most popular methods. This technique uses a sliding window approach, comparing the phylogenetic signal from each window, and discovering recombination when these signals are unevenly distributed. Recently, a method based on the jumping-alignment approach, namely *jpHMM* (for ‘jumping profile Hidden Markov Model’), has received much attention. This second approach aligns the query sequence against the groups, which are represented by ‘match states’, present in a reference dataset. The approach described here, *cladoscanning*, was implemented through a series of TNT and R scripts. It uses both the phylogeny and distribution of character patterns to infer recombination based on detecting changes in character fit along the sequence alignment. The low cost of computation of the algorithms underlying *cladoscanning*

makes the method suitable for the analysis of large datasets. *Cladoscanning* was compared to *bootscanning*, *jpHMM* and *DSS* (a distance method suitable for large datasets) using two empirical datasets and two simulated sequence alignments as benchmarks. In terms of mosaic identification, the results obtained with *cladoscanning* were similar to those obtained by *bootscanning* and *jpHMM*, though *cladoscanning* was faster and much more conservative than *bootscanning*, especially when small window sizes were used.

Syringal, osteological, nest and molecular characters used in assessing the phylogenetic relationships of Furnariidae (Aves, Passeriformes). Cecilia Kopuchian*, Pablo L. Calderón and Pablo L. Tubaro División Ornitología, Museo Argentino de Ciencias Naturales 'B. Rivadavia' Ángel Gallardo 470, C1405DJR, Ciudad Autónoma de Buenos Aires, Argentina

Furnariidae is a Neotropical group of birds with dull coloration and adapted to all biomes. The systematic position of furnariid species, genera and subfamilies is very controversial. The general objective of this research was to study the variation of morphological, behavioural and molecular characters of furnariids, in order to obtain a phylogeny which synthesizes the relationships between the main taxa that compose this family. For this purpose, we have made a detailed anatomical comparative description of their osteology (74 characters) and syringal morphology (26 characters), and we have also added molecular (7760 sites) and nest (22 characters) data for the main genera. In this way, this study comprises one of the largest sets of characters of a very diverse Neotropical family of birds. These data were analyzed cladistically under equal weights and under several parameters of implied weights, applying a different rate of relative implied weights to molecular characters. Results were compared in sensitivity analyses. Cladistic analysis showed that dendrocolaptids should be considered together with furnariids in a monophyletic group. Dendrocolaptidae appeared as paraphyletic because of the position of the genus *Sittasomus* (Dendrocolaptidae) which was placed as the sister group of the monophyletic group Furnariidae. On the other hand, *Geositta* (Furnariidae) was not placed as an outgroup of Dendrocolaptidae, as had been suggested by previous studies. None of the subfamilies traditionally recognized (Furnariinae, Synallaxinae and Phylidorinae) were recovered. *Synallaxis*, *Asthenes*, *Phacellodomus*, *Geositta* and *Cinclodes* were monophyletic in the analyses, but *Upucerthia*, *Automolus* and *Phylidor* appeared as polyphyletic or paraphyletic groups. Moreover, each pair of monotypic genera *Phleocryptes-Spartonoica*, *Anumbius-Coryphistera*, and *Pygarrhichas-Xenops* were placed as sister groups. Regarding the evolution of characters, in general, in this study the plesiomorphic state of the scored morphological characters were the ones we have found in dendrocolaptids, in contrast with what would have happened if those characters were mapped over previous molecular phylogenies.

Weevils of the *Pantomorus*–*Naupactus* complex: cladistics and generic classification. Analía Lanteri¹*, M. Guadalupe del Río¹, Marcela Rodríguez² and Viviana Confalonieri². ¹División Entomología, Museo de La Plata, 1900 La Plata, Argentina; ²Departamento de Ecología, Genética y Evolución, Facultad de Ciencias Exactas y Naturales, UBA, 1428 Buenos Aires, Argentina

The *Pantomorus*–*Naupactus* (*P-N*) complex is a group of broad nosed weevils, ranging from USA to Argentina, that includes about 250 species. Some of them, showing parthenogenetic reproduction, have colonized several countries around the world becoming pests of agriculture. In a preliminary phylogenetic analysis (*Cladistics* 21, 131–142) we compiled a data matrix of 17 species and 30 morphological characters, plus sequences of the COI mitochondrial gene. The main goal of that contribution was to test independent origins of the parthenogenesis within the group. Now, we have enlarged the taxon sampling to 70 species representative of the morphological diversity present in the *P-N* complex, to test the monophyly of the 15 generic

names associated to it. The new data matrix includes 813 characters, 86 morphological (65 external and 21 from the genitalia) and 726 COI sequences, the latter corresponding to 30 South American species. The trees were rooted with *Teratopactus gibbicollis* and the support of the clades was evaluated with jackknife. The combined parsimony analysis performed with TNT under equal weights, resulted in four similar MP trees of 2093 steps. In the strict consensus the following genera are recovered as monophyletic, with supports above 60%: *Teratopactus* (mainly distributed in subtropical forests and Chaco–Cerrado savannas of Brazil), *Aramigus* and *Eurymetopus* (prairies of Southern Brazil to Central Argentina), and *Athetetes* plus *Phacepholis* (Central America, Western Mexico and Great-Plains of North America). Most species of *Naupactus*, ranging in South America, gather in three main groups forming a paraphyletic sequence from the root of the tree: *N. rivulosus* group (with the type species), *N. leucoloma* group, and *N. xanthographus* group, the latter close to the monotypic genus *Alceis*. The type species of *Pantomorus*, *P. albosignatus*, endemic to Mexico, forms a weakly supported clade with other Mexican *Pantomorus* (e.g., *P. picipes* and *P. horridus*) and with some South American species of the *P-N* complex previously assigned to *Pantomorus*, *Naupactus*, *Parapantomorus*, *Symmalthetes* and *Asynonychus* (e.g., *P. bondari*, *N. ambiguus*, *S. kollari*). We conclude that *Pantomorus* as previously circumscribed is a polyphyletic group based on convergent characters, such as the small body size, the reduced to absent humeri and the lack of hind wings. To redefine *Pantomorus* and to advance towards a natural classification of the *P-N* complex, it is essential to complete the molecular matrix with sequences of the Mexican–Central American species. This is our next goal.

Preliminary results towards a molecular phylogeny of the Racomitriodeae (Bryophyta: Grimmiaceae). Juan Larraín¹*, Dietmar Quandt² and Jesús Muñoz³. ¹Departamento de Botánica, Universidad de Concepción, Casilla 160-C, Concepción, Chile; ²Nees-Institut für Biodiversität der Pflanzen, Rheinische Friedrich-Wilhelms-Universität, Meckenheimer Allee 170, D-53115 Bonn, Germany; ³Real Jardín Botánico (CSIC), Plaza de Murillo 2, E-28014 Madrid, Spain

The traditional genus *Racomitrium* has been recently divided into four genera based on morphological characters such as the shape and distribution of papillae over the leaf lamina, the presence, shape and papilosity of the hyaline hair-points of the leaves, the papilosity of the seta and calyptrae and some peristomial traits. In this contribution we report results from molecular data from the chloroplast *rps4-trnL* region for 40 specimens corresponding to 37 species of the Racomitriodeae complex (i.e., *Racomitrium s.str.*, *Bucklandiella*, *Codriophorus* and *Niphotrichum*), using as outgroups several specimens of related genera (*Dryptodon*, *Grimmia*, *Schistidium*, *Campylosetium* and *Ptychomitrium*). Our data include part of the *rps4* gene, the spacer between *rps4* and *trnT*, the *trnT* gene, the spacer between *trnT* and the *trnL* 5'Exon, and the *trnL* 5'Exon gene. Our results suggest a strongly supported and well defined clade containing the *Racomitrium s.str.* species, and another monophyletic clade including the *Niphotrichum* species. *Bucklandiella* appears as a polyphyletic clade, with a big clade containing most of the circum-subantarctic species, a second clade containing species from sections *Subsecunda*, *Marginata*, and *Sudetica*, and a third clade grouping the North American endemic *Bucklandiella lawtonae* and the Asian *B. laeta* (the only two members of section *Lawtonia*). *Codriophorus* is paraphyletic: species belonging to Section *Codriophorus* form a strongly supported monophyletic clade, while the members of section *Fascicularia* appear nested in the base of the *Niphotrichum* clade. The latter results are congruent with some morphological traits such as the very long peristome teeth and large capsules, but would make leaf papilla shape and the papilosity of the calyptrae homoplastic. Further studies are in progress to compare the present results with data from the *matK/trnK* chloroplast region and the nuclear ITS region, as well as a morphological matrix.

Phylogeny and wing morphometrics in *Haemagogus* Williston (Diptera: Culicidae) of Venezuela. Jonathan Liria^{1*} and Juan C. Navarro². ¹Departamento de Biología, FACYT, Universidad de Carabobo, Venezuela; ²Laboratorio de Biología de Vectores, Instituto de Zoología Tropical, Universidad Central de Venezuela, Venezuela

The species of *Haemagogus* are the main vectors of Yellow Fever, a re-emergent arbovirus in South America. This genus comprises 22 species restricted to the Neotropics, and eight reported to Venezuela. This work seeks to use the morphometry of wings in Venezuelan species as possible evidence for phylogenetic relationships. Photographs from 200 specimens (of eleven species) were obtained: *Albomaculatus* Section *Hg. equinus*, *Hg. anastasionis* and *Hg. janthinomys*, from *Splendens* Section: *Hg. celeste* and *Hg. lucifer*, and from *Conopostegus* subgenus, *Hg. clarki* and *Hg. leucocelaenus*. The species *Heizmannia scintillans*, *Johnbelkinia ulopus*, *Anopheles aquasalis* and *An. pseudopunctipennis* were included as outgroups. Seven landmarks were digitized for each wing, as well as Euclidean Distance Matrix Analysis (EDMA), procrustes + EDMA, partial warps (PW) + centroid size (CS), and relative warps (RW) + CS, with 95% confidence intervals and analyzed with TNT by implicit enumeration. Simultaneously, a discrete matrix was built for these taxa, based on previous analyses with re-interpretation of states, adding taxa and characters. The topology of the consensus of the discrete matrix was compared with the results of the continuous data by mean of SPR distances. The solutions for the discrete matrix show monophyly of *Haemagogus*, including *Conopostegus* species as sister group of the *Lucifer* + *celeste* clade (with one MPT show the *Albomaculatus* section monophyletic). The addition of morphometric data increased the support of *Haemagogus* and *Albomaculatus*, but the monophyly of *Conopostegus* + *Splendens* was supported only by EDMA and RW + CS. As for the strict consensus of the trees for the continuous data, EDMA and PW + CS were more similar (SPR = 0.875) than those for procrustes + EDMA and RW + CS (SPR = 0.750). These results reveal the importance of the morphometric characters in phylogenetic studies of *Haemagogus*, allowing the comparison of landmark analyses such as EDMA, PW and RW, and using a matrix with confidence intervals for the first time. Funded by CDCH-UC.

Culicidae phylogeny, implied weighting and K selection. Jonathan Liria^{1*}, Adriana Zorrilla² and Juan C. Navarro². ¹Departamento de Biología, FACYT, Universidad de Carabobo, Venezuela; ²Laboratorio de Biología de Vectores, Instituto de Zoología Tropical, Universidad Central de Venezuela, Venezuela

Recently, several morphology-based cladistics analyses in Culicidae have used implied weighting with low values of the concavity constant (from $K = 1$, the minimum in Piwe, to $K = 3$, the default), which weights very strongly against characters with homoplasy. Empirical studies demonstrate that variations of K between 1 and 6, obtain in some cases resolved trees, but they often differ from the trees obtained with equal weights. Also, the program TNT allows exploring a wider range of concavities (from near 0 to 1000). For these reasons, we re-analyzed five published matrices of Culicidae with the aim of finding the best value of K , and comparing different weighting strengths. The C2P software was used to generate 500 replications of character elimination (Jackknifing $P = 36$). Then, TNT was used and op/p_cj macros to search trees with 500 replications and 50 iterations of Wagner-Ratchet (or 500 replications and 100 iterations in the Aedini data set) for $K1$ – 15 in unperturbed and perturbed data. Subsequently in SF2 software, common nodes (CN) and other topological measures were compared among trees obtained in the pseudoreplicates and the trees for the unperturbed data. The number of contradictory groups and SPR distances among trees with/without weighting were also calculated. The K values which produced the highest CN were different from the ones that had been used, and some clades contradicted those found in the previous analyses. In three matrices previously analyzed under $K = 1$ (Culicidae, Culicidae + *Onirion*, and subgenera of *Anopheles*), the values of CN and SPR distances under $K = 1$ were

0.82–0.97 (respectively), while $K = 14$ produced better values of CN and SPR moves (CN = 10.15, 10.01 and 18.41, with an average SPR distance of 1 move in every matrix). In those matrices previously analyzed under $K = 3$ (Aedini and Anophelinae), SPR distances of 0.72–0.75 were obtained under $K = 3$, while $K = 9$ (CN = 40.40; SPR = 0.90) and $K = 8$ (CN = 22.98; SPR = 1.00) maximized congruence for each of those matrices. Although recent work demonstrates that weighting against homoplastic characters improves the results of phylogenetic analyses, our comparisons show that very low values of concavity (like $K = 1$) easily obtain groups unlikely to be monophyletic, as *Orthopodomyia* (*Culiseta* + *Toxorhynchites*), Aedini, *Heizmannia* + *Zeugomyia*. We conclude that future phylogenetic analyses should more carefully select a range of K values in order to recover ‘true’ natural groups.

Cladistic analysis of the subgenus *Australosymmerus* (Melosymmerus) Munroe and a proposal of a new status. Rafaela Lopes Falaschi* and Dalton de Souza Amorim Faculdade de Filosofia, Universidade de São Paulo, Ciências e Letras de Ribeirão Preto, Departamento de Biologia, Av. Bandeirantes 3900, 14040-901 Ribeirão Preto, São Paulo, Brazil

Ditomyiidae, included by some authors in the family Mycetophilidae s.l. as a subfamily, is a small clade of the infraorder Bibionomorpha, placed within the Mycetophiliformia. Mycetophiliformia is relatively well represented in the fossil record of the Jurassic (144 Ma), while the oldest record of ditomyids is from the Eocene (52 Ma). According to recent topologies, the Ditomyiidae form a monophyletic group with Bolitophilidae, Diadocidiidae and Keroplatidae. Fifteen genera are now accepted for the Ditomyiidae, with about 107 species described for the world, except for Afrotropical region. The clade composed by the Neotropical subgenera of *Australosymmerus*, *Melosymmerus* and *Calosymmerus* is closely related to the subgenus *Australosymmerus*, with circum-antarctic distribution. At a higher level, the Holarctic genus *Symmerus* is the sister-group of the whole *Australosymmerus* clade. The pattern in *Australosymmerus* is quite characteristic of the fragmentation by tectonics in southern Gondwanaland. There are ten described species for *Melosymmerus*—seven from Brazil, one from Ecuador and two from Mexico. Eight new species of *Melosymmerus* collected with Malaise traps along the Atlantic Forest are described in this work and the known Brazilian species are re-described. A key for the species of the genus is presented. The distribution of *A. (Melosymmerus) bororo* and *A. (Melosymmerus) bisetosus* is expanded to include southern of Minas Gerais state. A generic status is suggested for *Melosymmerus*. A phylogenetic analysis of the relationships among the species of the genus was performed, corroborating the monophyly of *Melosymmerus*. The relationships for the species were as follows: (*M. lenkoi* (*M. minutus*, *M. sp.n. 5*, *M. sp.n. 1*, *M. acutus*, *M. truncatus* (*M. guayanasi*, *M. sp.n. 2* (*M. sp.n. 3*, *M. sp.n. 4*) (*M. tupi* (*M. sp.n. 7* (*M. sp.n. 6*, *M. sp.n. 8*)) (*M. pediferus* (*M. bororo* (*M. guarani*, *M. bisetosus*)))))). The description of the species of *Calosymmerus* in the literature makes clear that it would fit as the sister clade of *M. lenkoi*, suggesting that *Melosymmerus* is paraphyletic in relation to *Calosymmerus*. A synonymy is proposed for both genera.

Conserving Amazonian biodiversity: a phylogenetic approach. Federico López Osorio* and Daniel Rafael Miranda Esquivel Laboratorio de Sistemática & Biogeografía, Escuela de Biología, Universidad Industrial de Santander, AA 678 Bucaramanga, Colombia

Amazonia is a heavily threatened rainforest that encompasses a major proportion of Earth's biological diversity; therefore, conservation of Amazonia demands immediate study, ideally from a multiplicity of viewpoints. In this study, our main goal was to establish conservation priorities for Amazonia's areas of endemism based on measures of evolutionary distinctiveness. We considered two previously suggested approaches to areas of endemism in Amazonia. The first approach consisted of eight large areas traditionally used in

biogeographical studies: Belem, Tapajós (= Pará 1), Xingu (= Pará 2), Guiana, Rondônia, Imeri, Inambari and Napo. The second approach comprised sixteen smaller areas congruent with the larger areas. We assembled a dataset of fifty phylogenies representing various taxonomic groups and 1715 distributional records. We identified priorities for the aforementioned areas of endemism according to node-based metrics and contrasted these results with priorities based on raw species richness and species endemism. In the first analysis, we identified Guiana as the most important area for conservation, immediately followed by Inambari. The remaining areas in this first ranking decreased by a half (e.g., Napo) or less for all indices. In the second analysis, a subdivision of Guiana corresponding to Guyana, and the east and north-east of the Brazilian states of Roraima and Amazonas respectively, was at the top of the ranking; followed by a subdivision of Inambari corresponding to the north-west of the Brazilian state of Amazonas, at the left bank of Rio Jurua; the third position was occupied by yet another subdivision of Guiana corresponding to Suriname, French Guiana, and the Brazilian state of Amapá. The distinctiveness-based rankings were directly correlated with those based on species richness and species endemism. Current conservation strategies in Amazonia, although relying on many other criteria apart from phylogeny, do agree on the most important areas for conservation identified in this study.

Weevils in the Beetle Tree of Life: Exploring the phylogeny of Curculionoidea using morphology and molecules. Adriana E. Marvaldi^{1*}, Duane D. McKenna² and Brian D. Farrell². ¹IADIZA, CONICET, CC 507, 5500 Mendoza, Argentina; ²Department of Organismic & Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA

Exploration of meaningful markers of genealogy is fundamental for making progress in the phylogenetic systematics of weevils, and this approach is essential towards having a better understanding of their evolution. Results of recent phylogenetic studies based on evidence from DNA sequences are presented along with an updated phylogenetic hypothesis for Curculionoidea based on morphology. Approximately 130 morphological characters (35% and 65% from larvae and adults, respectively) are so far described and coded for weevil species representative of all families and subfamilies. A cladogram resulting from analysis of these data recovers seven major lineages or families and the relationships among them, with the relevant nodes defined by both larval and adult synapomorphies. This study sets the stage for ongoing exploration of subfamily relationships. Results from a recent higher level molecular phylogenetic study including rDNA sequences from more than 100 species of weevils and several closely related outgroups (in Cucujiformia) are also presented. This study incorporates an annotated alignment based on secondary structural information, which in turn, provides improved rRNA structure models useful for phylogenetic reconstruction in beetles. The resulting cladogram indicates that Chrysomeloidea are the closest relatives of weevils. Interestingly, the curculionoid phylogeny recovered from the aligned 18S and 28S segments, which is independent of morphological data, is in agreement with recent hypotheses based on morphological evidence, particularly with respect to families. The next step is to perform a combined analysis using the morphological and molecular data sets. The value of incorporating structure information in the process of alignment is highlighted. Results from these studies indicate two data sets as informative phylogenetic markers for weevils: larval morphology and nuclear rDNA sequences.

Extended consensus outperforms strict consensus for large tree sets. Anton Mates¹ and John Wenzel^{2*}. ¹Department of Mathematics, Ohio State University, Columbus, OH 43210, USA; ²Department of Entomology, Ohio State University, Columbus, OH 43210, USA

Competing phylogenetic trees are usually combined and summarized through methods of topological consensus. These range from majority rule (where any topology found among 51% of the solutions

is plotted as the preferred solution), through Adams consensus (preserving topology found in all trees except for ambiguous taxa, which are plotted ambiguously) to strict consensus (illustrating only clades found in all trees). While clades represented in a strict consensus are the most solid empirically (they are found in all solution trees), the strict consensus is often poorly resolved, with large and numerous polytomies that obscure the structural relationships between their component taxa. It is well known that we can determine 'maximum' and 'maximal' solutions that are found in all competing trees by pruning problematic taxa. These solutions sacrifice taxon completeness for superior resolution to the strict consensus. Whereas the original tree search requires simultaneous solutions to all the polytomies later considered in consensus, we suggest solving polytomies one at a time during the consensus procedure to preserve local decisions among competing solutions. Examining consensus polytomies one-by-one makes the problem of summary statements much more tractable. We present a method for constructing summary trees that contain more taxa than maximal subtrees, but have greater resolution than the strict consensus. From these we assemble a multi-tree extended consensus, which displays compactly all the structure common to our competing topologies. We provide a metric for the mobility of a taxon within those topologies. We present a method for rapid generation of maximum and maximal subtrees.

Phylogeography of the subgenus *Nothofagus* from Patagonia. Paula Mathiasen*, M. Cristina Acosta and Andrea C. Premoli Centro Regional Universitario Bariloche (CRUB), Universidad Nacional del Comahue, Bariloche, Argentina

Geological forces have affected the geography of the austral continents as well as the distribution of plant populations and their genetic patterns. Patagonia has suffered the impact of ancient events such as plate tectonics, sea-level changes, and even more recent Pleistocene glaciations and volcanic eruptions. We hypothesize that these historical factors will be reflected in the phylogeographic structure of plant populations of old angiosperm lineages inhabiting austral latitudes. The aim of this study is to examine the levels and distribution of chloroplast DNA variation in populations of widespread *Nothofagus* in relation to past events that occurred in Patagonia. We sampled 190 populations of *N. antarctica*, *N. betuloides*, *N. dombeyi*, *N. nitida* and *N. pumilio* along their entire range of distribution, and 10 populations of *N. nervosa* and *N. obliqua* that were used as outgroup. Non-coding regions of chloroplast DNA were amplified by polymerase chain reaction (PCR) using three universal primer pairs: psbB-psbH, trnL-trnF and trnH-psbA. Relationships among haplotypes were analyzed by means of phylogenetic analyses of maximum parsimony using WINCLADA and NONA and Bayesian inference with MrBayes. Finally, the haplotype median-joining network was constructed using Network. The matrix of aligned sequences of *Nothofagus* species contained 65 parsimony informative characters and yielded 20 different haplotypes. Parsimony analyses generated 68 most parsimonious trees (L = 121, CI = 71, RI = 80), the consensus of which showed the same topology as the tree obtained by Bayesian inference. Two major clades separated latitudinally were identified. The north clade (35°35' to 42°31'S) includes one well defined subclade containing populations located south of 39°35'S, and the rest of the terminals are located to the north of this latitude. The south clade includes populations located between 42°39'S and 55°3'S. Greatest haplotype and nucleotide diversity was found towards the north of the distribution range. Our results suggest that populations of *Nothofagus* suffered significant latitudinal disjunctions due to repeated glaciations, as it was widely discussed in previous studies, and also to other processes such as vulcanism and tectonism that occurred in Patagonia.

Towards an all-species phylogeny of the scorpion family Bothriuriidae. Camilo Mattoni^{1*}, José Ochoa², Andrés Ojanguren-Affilastro³

and Lorenzo Prendini². ¹Cátedra de Diversidad Animal I, Facultad de Ciencias Exactas, Físicas y Naturales, Universidad Nacional de Córdoba, Av. Vélez Sársfield 299, 5000 Córdoba, Argentina; ²American Museum of Natural History, Division of Invertebrate Zoology, 79th Street at Central Park West, New York, NY 10024-5192, USA; ³División Aracnología, Museo Argentino de Ciencias Naturales 'Bernardino Rivadavia', Av. Angel Gallardo 470, 1405 DJR Buenos Aires, Argentina

The scorpion family Bothriuridae comprises 127 described species in 13 genera, with a Gondwanan distribution in South America, southern Africa and Australia. Phylogenetic relationships among the bothriurid genera were previously studied, but lacked resolution for internal nodes. Recent fieldwork provided sufficient samples to obtain DNA sequences from most species in the family, for combination with new and existing morphological characters. The goals of the study were to (1) test the monophyly of Bothriuridae and determine its phylogenetic position with respect to other scorpion families; (2) resolve the phylogenetic relationships among and test the monophyly of the bothriurid genera; (3) evaluate the effect of increased taxon sampling on phylogenetic relationships in the family. The dataset comprised 141 bothriurid terminals (80% of the described species plus 36 undescribed species, including a new genus) and 16 outgroups. A comprehensive revision of external morphology and internal anatomy was undertaken, resulting in more than 250 characters, to which DNA sequences from five loci (ca. 4.2 kb) were added after aligning with Mafft and Prank + f. Phylogenetic analyses, under equal and implied weights, were conducted and support for each group calculated using TNT. The addition of DNA sequences slightly changed results of the separate morphological analysis, increasing support for most internal branches. A denser taxon sample increased stability and yielded stronger support for most branches. The monophyly of Bothriuridae was supported, but its placement as sister group of the Scorpionoidea s. str. remains uncertain. The validity of *Brandbergia* (recently synonymized) was confirmed based on morphology; it was placed sister to other bothriurid genera, and must be reinstated. The monophyly of *Brachistosternus* and its current division into three subgenera were confirmed, and its position as the sister group of other bothriurids (excepting *Brandbergia*, *Lisposoma* and *Thestylus*) was established. *Bothriurus* and *Orobbothriurus* were polyphyletic: three new genera must be created. *Brazilbothrius* is placed deeply inside the *bonariensis* clade of *Bothriurus* and must be synonymized. *Vachonia* and *Timogenes* grouped as sister taxa, in a monophyletic group with the inermis clade of *Bothriurus*. *Tehuanka* was closely related to *Centromachetes* and (*Cercophonius* + *Urophonius*). The position of *Phonioecercus* is unstable: it groups with *Tehuanka* and related genera or with (*Pachakutej* ('*Bothriurus*' (*Vachonia* + *Timogenes*))). Genera presenting the most plesiomorphic characters, *Brandbergia*, *Lisposoma*, and *Thestylus*, display distributions congruent with vicariance events associated with the breakup of Gondwana.

Phylogeny of *Archiseopsis* Silva (Diptera, Sepsidae) using three different weighting approaches. Ramon L. Mello^{1*} and Vera C. Silva². ¹Museu de Zoologia da Universidade de São Paulo, MZSP; Avenida Nazaré, 481; 04263-000 São Paulo, SP, Brazil; ²Depto de Ciências Biológicas, Faculdade de Ciências e Letras de Assis—UNESP São Paulo State University; Av. Dom Antonio, 2100; 19.806-900 Assis, SP, Brazil

The Neotropical Sepsidae have received little attention during the last century, and many taxa remain to be described. The genus *Archiseopsis* has been proposed recently by Silva, 1993, for eight species. At present, 13 valid species are recognized for the genus distributed mainly in the Neotropical Region with some species reaching the Nearctic Region. In the cladistic analysis, a data matrix with 27 adult morphological characters, treated as unordered, was used. Two outgroup species were used, the Palearctic *Nemopoda nitidula* (Fallen) and the Neotropical *Lateosepsis laticornis* (Duda). The characters were treated under three different weighting approaches: equal (EW), successive (SW) and implied weighting (IW). EW and SW were obtained using NONA version 2.0. The IW was done with TNT, with

concavity constant (*k*) between 3 and 6. EW analyses resulted on 11 trees with 50 steps, with the consensus tree collapsed on six nodes with *Lateosepsis laticornis* inserted within *Archiseopsis*. SW found a single tree with 48 steps, with *Archiseopsis* monophyletic (without the addition of *L. laticornis*). For IW, all *k* values applied produced the same two trees, differing only in the position of *A. polychaeta*, and both with *Archiseopsis* monophyletic. Based on this, the consensus tree of IW is chosen to represent the evolutionary history of the genus as follows: ((*A. discolor*) + ((*A. umbrifer*), (*A. ecalcarata* + *A. pusio*)), ((*Lateosepsis laticornis*), (*A. polychaeta*), (*A. armata* + *A. excavata*), (*A. diversiformis* + *A. priapus*)), (*A. peruana* + (*A. pleuralis* + (*A. bolivica* + *A. hirsutissima*))))).

Molecular phylogeny of *Allograpta* (Diptera, Syrphidae) reveals diversity of lineages and non-monophyly of phytophagous taxa. Ximo Mengual^{1*}, Gunilla Ståhl² and Santos Rojo¹. ¹Dpto. de Ciencias Ambientales/Instituto Universitario CIBIO, Universidad de Alicante, Apdo 99, E-03080 Alicante, Spain; ²Finnish Museum of Natural History, PO Box 17, FI-00014 University of Helsinki, Finland

Phylogenetic relationships of the genera *Allograpta*, *Sphaerophoria* and *Exallandra* (Diptera, Syrphidae) were analyzed, based on sequence data from the mitochondrial protein-coding gene cytochrome c oxidase subunit I (COI) and the nuclear 28S and 18S ribosomal RNA genes. The three genera are members of the subfamily Syrphinae, where nearly all members feed as larvae on soft-bodied Hemiptera and other arthropods. Phytophagous species have recently been discovered in two subgenera of *Allograpta*, sg *Fazia* and a new subgenus from Costa Rica. Phylogenetic analyses of the combined datasets were performed using parsimony, under static alignment and direct optimization, maximum likelihood and Bayesian inference. Congruent topologies obtained from all the analyses indicate paraphyly of the genus *Allograpta* with respect to *Sphaerophoria* and *Exallandra*. *Exallandra* appears embedded in the genus *Sphaerophoria*, and both genera are placed within *Allograpta*. The distribution of phytophagous taxa in *Allograpta* indicates that plant feeding evolved at least twice in this group.

Phylogenetic position of the tribe Cyphostyleae and the genus *Physeterostemon* within the Melastomataceae: Understanding fruit evolution and homologies. Fabián A. Michelangeli^{1*}, María Eugenia Morales², Heriberto David³, Andre Amorim⁴ and Renato Goldenberg⁵. ¹The New York Botanical Garden, NY, USA; ²Universidad Tecnológica y Pedagógica de Colombia, Tunja, Boyaca, Colombia; ³Herbario de la Universidad de Antioquia, Medellín, Antioquia, Colombia; ⁴Centro de Pesquisas do Cacau, Herbário CEPEC, Itabuna, Bahia, Brazil; ⁵Universidade Federal do Paraná, Curitiba, Paraná, Brazil

Melastomataceae is a mostly tropical family of 150–160 genera and 4500–5000 species. The family exhibits a wide variety of fleshy and dry fruits, ranging from the extreme forms of berries and capsules to several intermediate types such as dry berries, fleshy capsules and woody berries. Most berries (and related types) are found in taxa with partially to totally inferior ovaries, while capsules (and related types) are present in taxa with superior ovaries. However, in the New World only six of the close to 100 genera deviate from this pattern. *Alloneuron*, *Allomaieta*, *Physeterostemon*, *Tateanthus*, *Tessmanianthus* and *Wurdastom* all have capsular fruits derived from flowers with inferior or partially inferior ovaries. In the present study, we conducted a family wide phylogenetic analysis of *ndhF* and *rbcL* sequence data that included all three species of *Physeterostemon* and ten species of *Cyphostyleae*. *Alloneuron*, *Allomaieta*, and *Wurdastom*, with less than 20 species in total, form the tribe Cyphosteleae, which at times has also been included in the tribe Miconieae based on ovary position. The Cyphostyleae are resolved as monophyletic, and within a polytomy that includes some New World representatives of the tribe Bertolonieae, all of which have capsules derived from superior ovaries. *Physeterostemon* is a recently described genus with three species endemic to Eastern Brazil for which no affinities have been proposed.

Physeterostemon is resolved as a monophyletic genus, sister to the also Brazilian endemic *Eriocnema*. *Eriocnema* has capsular fruits derived from superior ovaries. This *Eriocnema* + *Physeterostemon* clade is sister to the large tribe Miconieae, which has berries and flowers with partially to totally inferior ovaries. Fruit evolution in the Melastomataceae will be discussed in the context of these phylogenetic results.

Measuring phylogenetic diversity on cladograms: a new index based on the Gromov transform with reference to the root. Nobuhiro Minaka^{1*}, Takashi Suemura² and Kouki Machii². ¹Ecosystem Informatics Division, National Institute for Agro-Environmental Sciences, Tsukuba, Ibaraki 305-8604, Japan; ²Turaltec Company Limited, Kasama, Ibaraki 309-1717, Japan

The phylogenetic diversity index (PD) has inspired various applied studies on conservation biology and community ecology in recent years. However, PD as a metric opens many theoretically interesting problems, which are worth further exploring mathematically and statistically. Indices of phylogenetic diversity defined on a phylogenetic tree, including Faith's original definition of phylogenetic diversity index (Faith 1992), are briefly reviewed. Faith's phylogenetic diversity ('PD') of a subset of taxa is equal to the sum of the lengths ($d(*,*)$) of all those branches that are members of the corresponding minimum spanning path. The subtree that minimally covers a subset of terminal nodes (OTUs) with their associated internal branches has no explicit reference to the root of the full tree. The Gromov transform of phylogenetic diversity index is proposed which is defined for any triplet (x, y, r) such that x and y are terminal OTUs and r is the root of the full tree. For any pair of terminal nodes (OTUs), x and y , and a reference node (root r), the Gromov product is defined as follows: . The Gromov product distinguishes between derived and primitive pairs of nodes with reference to the root (r). Several other properties of the transformed index are discussed. Our software ('BALANCE') for estimating large-scale molecular phylogenetic trees under the principle of parsimony implements the new function of calculating the Gromov-based phylogenetic diversity index.

A preliminary cladistic analysis of the genera of Bembicini (Hymenoptera: Crabronidae). María Alejandra Molina CONICET—Instituto Superior de Entomología (INSUE), Miguel Lillo 205, CP 4000, San Miguel de Tucumán, Argentina

The females of sand wasps (Bembicini) are typically predators of Diptera, Odonata, Lepidoptera, and Hemiptera nymphs; after the prey is paralyzed, it is used to feed the larva. The females usually nest in sandy or loamy soils, and the nest consists of a simple burrow with a single enlarged cell with a larva. The Bembicini includes 15 exclusively American genera. Additionally, the Neotropical genera, like *Rubrica*, *Trichostictia*, *Selman*, *Editha*, *Hemidula*, *Zyzyx*, *Bicyrtes*, *Carlobembix* and *Sticia*, contain a huge number of species. In the 1950s Willink carried out a systematic revision of this group, which included morphological and behavioural characters. Later, Evans (between 1957 and 1970) made several contributions on behaviour. Finally, Genise during the 1980s added behavioural observations for several Bembicini species, as well as new adult and larval morphological traits. After the study of Bohart and Menke (1976), which consists of a hand-made cladogram of Bembicini, the only study of the Bembicini appears to be the phylogenetic study of Alexander (1992) on Sphecidae. In this contribution, new and well-known characters of morphology (40 characters) and behaviour (4 characters) of Bembicini are used to analyze the relationships of the genera of Bembicini (18 taxa). This preliminary cladistic analysis is compared with the hypothesis of Bohart and Menke.

Spatio-temporal tracking and phylodynamics of a DENV-3 outbreak in a city from Brazil. Adriano Mondini^{1*}, Roberta Vieira de Moraes Bronzoni¹, Silvia Helena Pereira Nunes¹, Francisco Chiaravalloti-Neto^{1,2}, Eduardo Massad³, Wladimir J. Alonso⁴, Pablo Marinho de Andrade Zanotto³ and Mauricio Lacerda Nogueira¹. ¹Faculdade de

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The dengue virus has a single-stranded positive-sense RNA genome of ~ 10 700 nucleotides with a single open reading frame that encodes three structural (C, prM and E) and seven nonstructural (NS1, NS2A, NS2B, NS3, NS4A, NS4B, NS5) proteins. It possesses four antigenically distinct serotypes (DENV 1–4). Many phylogeny studies addressed particularities of the different serotypes using convenience samples that were not conducive to a spatio-temporal analysis in a single urban setting. We describe the pattern of spread of distinct lineages of DENV-3 circulating in São José do Rio Preto, SP (Brazil) during 2006. Blood samples from patients presenting dengue-like symptoms were collected for DENV testing. We performed M-N-PCR using primers based on NS5 for virus detection and identification. The fragments were purified from PCR mixtures and sequenced. The positive dengue cases were geocoded. To type the sequenced samples, 52 reference sequences were aligned. The dataset generated was used for iterative phylogenetic reconstruction with the maximum likelihood criterion. The best demographic model, the rate of growth, rate of evolutionary change and Time to Most Recent Common Ancestor (TMRCA) were estimated. The basic reproductive rate during the epidemics was estimated. We obtained sequences from 82 patients among 174 blood samples. We were able to geocode 46 sequences. The alignment generated a 399 nucleotide-long dataset with 134 taxa. The phylogenetic analysis indicated that all samples were of DENV-3 and related to strains circulating in the isle of Martinique in 2000-01. Sixty DENV-3 from SJRP formed a monophyletic group (lineage 1), closely related to the remaining 22 isolates (lineage 2). We assumed that these lineages appeared before 2006 on different occasions. By transforming the inferred exponential growth rates into the basic reproductive rate, we obtained values for lineage 1 of $R_0 = 1.53$ and values for lineage 2 of $R_0 = 1.13$. Under the exponential model TMRCA, lineage 1 dated 1 year and lineage 2 dated 3.4 years before the last sampling. The possibility of inferring the spatio-temporal dynamics from genetic data has been generally little explored and it may shed light on DENV circulation. The use of both geographic and temporally structured phylogenetic data provided a detailed view on the spread of at least two Dengue viral strains in a populated urban area (Financial support: Capes; CNPq and FAPESP).

Evolutionary biogeography of Chilean vascular plants: tracks, regions and prospects. Andrés Moreira-Muñoz Instituto de Geografía, Pontificia Universidad Católica de Chile, Av. Vicuña Mackenna 4860, Casilla 306-Correo 22, Santiago, Chile

Different approaches and methods proliferate and to some extent rival nowadays in the biogeographic arena. Some see a crisis of the discipline; others interpret this 'plethora of methods' as a field in constant evolution. In this context two novel programs arise: 'comparative biogeography' (Parenti and Ebach 2009), and 'evolutionary biogeography' (Morrone 2009). Both programs offer a comprehensive empirical framework for discovering and interpreting the patterns and processes of the distribution of life on Earth. The present work is an attempt to apply this systematic framework to the analysis of the Chilean vascular flora. Biotic components have been recognized through track analysis for the 815 genera of the vascular flora: seven floristic elements and ten generalized tracks were identified, accounting for several disjunct distribution patterns. Furthermore, a hierarchical arrangement or biogeographic regionalization has been established by means of the program NDM/VNDM (Szumik and Goloboff 2004). Two groups were selected as case studies: the genus *Alstroemeria* and the Asteraceae, the richest Chilean family at both genus and species level. The distribution data were obtained from the National Herbarium (SGO). The results yielded three areas of endemism for *Alstroemeria*, and nine areas for

the Asteraceae. Also, PAE was applied to the data set, since it has the advantage of permitting a hierarchical arrangement of the areas; in this case the preliminary results were not satisfactory due to the existence of many collection gaps (on a 1×1 degree grid). The improvement of the data base by augmentation of the collection effort and the exploration of distribution modelling techniques has been undertaken. The systematization of the areas of endemism (*sensu* Ebach et al. 2008) is also being explored.

Phylogeny of the Paniceae (Poaceae: Panicoideae) integrating chloroplast DNA sequences and morphology. Osvaldo Morrone¹, Lone Aagesen^{1*}, M. Amalia Scataglini¹, Diego Salariato¹, Silvia S. Denham¹, M. Amelia Chemisquy¹, Silvina Sede¹, L.M. Giussani¹, E.A. Kellogg² and Fernando O. Zuloaga¹. ¹Instituto de Botánica Darwinion (IBODA)- CONICET, Labardén 200, B1642HYD San Isidro, Buenos Aires, Argentina; ²Department of Biology, University of Missouri–St Louis, One University Blvd, St Louis, MO 63121, USA

The tribe Paniceae currently includes approx. 110 genera and 2000 species distributed world-wide. The Paniceae exhibits a great morphological and physiological variability that makes it difficult to establish generic boundaries among its members; recent molecular studies lead to a new classification of several genera of the tribe. The present study aims to analyze all genera of the tribe combining morphological and ndhF sequence data in order to delimit the tribe within the Poaceae, and to establish generic relationships within it. As found in earlier studies monophyly of the Paniceae was not supported. The Paniceae is divided in two major clades, recognized as the $x = 9$ and $x = 10$ clades. The ndhF sequences support a sister-group relationship between the $x = 10$ clade and the tribe Andropogoneae. The $x = 10$ clade is defined by a 6 base-pair long insertion in the ndhF sequences. The basal dichotomy divides the group into a small clade integrated by minor genera from Australia, India, and Africa, and a major clade including American taxa only, some genera, such as *Paspalum* and *Axonopus*, with a high number of species. The distribution of the $x = 9$ clade is mainly Pantropical. Within this clade the basal dichotomy separates a small clade including the genus *Digitaria* and three small genera previously related to taxa of the 'Bristle clade': *Antheplora* and related genera. This clade is well supported and defined by a 24 base-pair long deletion within the ndhF sequences. Main clades within the $x = 9$ clade are the 'Bristle clade' that among other genera includes *Setaria*, *Pennisetum* and *Cenchrus*, the PEP-ck clade, with *Urochloa* and genera with a similar anatomic and photosynthetic syndrome, and the *Panicum* clade characterized by having a NAD-me photosynthetic subtype. Although the morphological characters were homoplastic and decrease the branch supports, they proved useful for placing several taxa for which DNA sequence data were not available.

Phylogenetic position of *Dinomys branickii* Peters (Dinomyidae) in the context of Caviomorpha (Hystricognathi, Rodentia). Norma Lidia Nasif INSUGEO-CONICET, Facultad de Ciencias Naturales e Instituto Miguel Lillo, Universidad Nacional de Tucumán, Miguel Lillo 205, 4000, Tucumán, Argentina

Dinomys branickii Peters, commonly known as the 'pakarana', is the only extant species of the Dinomyidae (Caviomorpha, Hystricognathi, Rodentia). *Dinomys branickii* is restricted to forest areas of the eastern Andes of Brazil, Perú, Ecuador, Bolivia, Venezuela and Colombia. Dinomyids, however, were highly diverse and widely distributed in South America with Miocene-Pliocene forms known from the northwestern, northeastern and south (Patagonia region) of Argentina. Living dinomyids are medium-sized, whereas some of the extinct forms are the largest rodents currently known. The monophyly of the Dinomyidae was never questioned, but there is controversy concerning the relationships of Dinomyidae with remaining caviomorphs. This group has been considered as related to Erethizontidae, Dasyproctidae and Chinchillidae on the basis of different lines of evidence. A cladistic analysis is presented here with the aim of determining the phylogenetic

placement of *D. branickii* and its relationships to caviomorphs. The data matrix has a total of 184 characters including craniodental features, chromosomal morphology and reproductive and gestation patterns. The in-group includes nine taxa that represent eight of the 12 families recognized in living caviomorphs: *Coendu* (Erethizontidae), *Dasyprocta* (Dasyproctidae), *Myocastor* (Myocastoridae), *Ctenomys* (Ctenomyidae), *Pediolagus* (Caviidae), *Hydrochoerus* (Hydrochoeridae), *Lagostomus* and *Lagidium* (Chinchillidae) and *Dinomys* (Dinomyidae). *Thryonomys*, the only living genus of the Thryonomyidae, was chosen as the out-group, as this is a representative of the African Hystricognathi, a group closely related to the South American caviomorphs. The program TNT was used for the analysis. The tree search strategies included heuristic searches, use of implied weights, and treatment of multistate characters as additive and non-additive. Bremer support was calculated to evaluate the monophyly of each clade. One most parsimonious tree resulted from each analysis, varying only in the placement of the most basal taxa. In all MPTs dinomyids are basal, whereas the majority of the trees show a sister-group relationship between *Dinomys* and *Coendu*. This hypothesis is used to explain the affinities of *Dinomys* in the context of living caviomorphs and to discuss its placement in previous classifications.

Are the Baetidae subfamilies (Insecta: Ephemeroptera) natural groups? Carolina Nieto^{1*} and Jean-Luc Gattolliat². ¹CONICET-INSUE. Fac. de Cs. Naturales e I.M.L. Tucumán, Argentina; ²Museum of Zoology, Place de la Riponne 6, CH-1014 Lausanne, Switzerland

Ephemeroptera (mayflies) are the most primitive winged insect Order; it encompasses presently about 40 families, 400 genera and 3000 species. With almost cosmopolitan distribution, mayflies inhabit almost all kinds of lentic and lotic freshwater habitats. The nymphs are aquatic; together with larval Diptera and Trichoptera, they are among the most abundant and diverse insects in running waters throughout the world. The family Baetidae was established in 1815 by W.E. Leach. Recent phylogenetic studies based on molecular data of the Ephemeroptera (Ogden and Whiting, 2003) and Paleoptera (Hovmoller et al., 2002) consistently place Baetidae as the sister group of all other mayflies. The oldest fossil records belong to the upper Cretaceous (Kluge, 1997). With 97 genera and 894 species (one fourth of the global mayfly diversity), Baetidae are one of the most diversified families, with a world-wide distribution except New Zealand and Antarctica. Three subfamilies are generally recognized in Baetidae: Baetinae Leach, Callibaetinae Riek and Cloeoninae Kazlauskas. These groups were proposed based on wing venation, mouthpart characters and ornamented cuticle. Here we present a global phylogeny of the family including almost all genera (96) and 136 morphological characters. The families Nesameletidae and Siphlaenigmatidae were selected as outgroups. We analyzed the matrix using parsimony analysis (TNT) and Jackknifing was used to calculate the group support. Preliminary results do not recover the three subfamilies as monophyletic groups; the clades obtained in the analysis mainly reflected biogeography.

***Caytonia* fossils as blank slates for verifying angiosperm origins.** Kevin C. Nixon L.H. Bailey Hortorium, Department of Plant Biology, Cornell University, Ithaca, NY 14853, USA

Caytonia is a well-known mesozoic 'seedfern' with incurved cupules that contain several flattened seeds. Numerous theories have been proposed that place *Caytonia* as an ancestral angiosperm precursor. These theories have either suggested that the cupule of *Caytonia* is homologous with the carpel of angiosperms, or that the cupule is homologous with an (anatropous) second integument of an angiosperm seed. The latter theory requires several steps to travel from a *Caytonia*-like ancestor to a primitive angiosperm. These steps include, but are not limited to, reduction of the number of ovules in the *Caytonia* cupule to a single ovule, including morphological changes that would produce an angiospermous micropyle (*Caytonia* has a

rather typical gymnospermous pollen chamber, in which pollen has been found in situ). Additionally, the *Caytonia* cupules, which are arranged along a naked axis, would need to be placed on an angiospermous placenta, with some kind of enclosing vegetative structure that would be homologous with the carpel. The conifer-like alveolate, bisaccate pollen of *Caytonia* would also need to be radically changed to accommodate any of the extant or projected basal types of pollen in angiosperms, none of which are saccate. Overall, it appears that the superficial resemblance of the *Caytonia* cupule to an anatropous ovule has clouded interpretations of these structures, and resulted in direct coding of the cupule as homologous with the second integument of some angiosperms. Combined with biased coding of other features, this is nothing more than verificationism. Other features of associated fossils (e.g., typical gymnospermous venation in *Sagenopteris* leaves) do not suggest an angiosperm relationship, and overall, *Caytonia* appears to have greater morphological similarity to some clades of conifers, such as Podocarpaceae, which have an anatropous fleshy envelope of single seeds and bi-saccate alveolate pollen. Variations on existing and new cladistic analyses of *Caytonia* will be presented.

On the cell provisioning and oviposition process (POP) of the stingless bees seen in a phylogenetic perspective (Hymenoptera, Apidae, Meliponini): A preliminary approach. Fernando B. Noll^{1*} and Ronaldo Zucchi². ¹Departamento de Zoologia e Botânica; Instituto de Biociências, Letras e Ciências Exatas, UNESP, Rua Cristóvão Colombo, 2265; 15054-000, São José do Rio Preto, SP; Brazil; ²Departamento de Biologia, Faculdade de Filosofia Ciências e Letras de Ribeirão Preto, Universidade de São Paulo, Brazil.

Behaviour is an important source of information for phylogenetic reconstructions. Stingless bees are part of a highly controversial clade, the corbiculate Apinae (Chavarría & Carpenter, 1994). In this taxon, stingless bees (Meliponini) present a highly intricate sequence of the cell provisioning and oviposition process (POP), comprising a very stereotyped dance, in which workers respond actively to queen's signals. Several papers have tried to better understand POP behaviour in an evolutionary perspective but never within a phylogenetic perspective. The major problem was the lack of a reliable phylogeny, originally because morphological phylogenies were highly controversial. More recently, molecular studies produced trees that at least reconstruct a biogeographical pattern. Based on these new insights, we show that behavioural characters are useful in phylogenetic reconstructions for stingless bees and show that the POP evolved from a less integrated to a highly integrated process.

Phylogenetic relationships of glossiphoniid leeches and host-bacteria evolution within *Haementeria* and *Placobdella* clades. Alejandro Ocegüera-Figueroa* and Mark E. Siddall The American Museum of Natural History, Central Park West at 79th, New York, NY 10024, USA

Leeches of the genera *Placobdella* and *Haementeria* feed on blood of a wide variety of vertebrates, particularly in the New World. Contrary to the jawed medicinal leeches, members of *Placobdella* and *Haementeria* possess a long eversible proboscis and a complex system of salivary gland cells. Characteristic of these groups is the presence of bacteria-bearing structures called mycetomes. Recently, it has been shown that even though species of *Placobdella* and *Haementeria*, together with *Helobdella* species, form a monophyletic group, they are associated with a completely different kind of Proteobacteria. (Gamma and Alfa-proteobacteria respectively) suggesting different origins of association. Detailed information about the symbiotic association between leeches and bacteria is not at hand, but a vertical transmission of bacteria from parents to offspring is expected. In order to study common evolutionary patterns between leeches and bacteria, we conducted a phylogenetic analysis of *Placobdella* and *Haementeria* species, as well as of their associated bacteria. Phylogenetic hypotheses were investigated with parsimony methods using DNA sequences (Mitochondrial 12S,

COI, ND1 for leech phylogenies and 16S rDNA for associated bacteria). Comparison of phylogenetic hypotheses of both partners of the association show common branching patterns, suggesting that species of *Haementeria* and *Placobdella* and their respective symbionts share a common history. This hypothesis seems to be preferred over alternative explanations like geographical proximity of the leeches with similar bacteria or different leeches parasitizing the same vertebrate host harbouring the same kind of bacteria.

Taxonomic novelties in the *Verbena* complex inferred from cpDNA and nuclear ETS/ITS sequences. Nataly O'Leary¹, Yao-Wu Yuan², Amelia Chemisquy^{1*} and Richard G. Olmstead². ¹Instituto de Botánica Darwinio, Labardén 200, San Isidro, Argentina; ²Department of Biology, University of Washington, Seattle, WA, USA

The '*Verbena* complex' includes three genera, *Verbena*, *Glandularia* and *Junellia*, and is a rapidly diversifying group. *Junellia* is distinguished by its shrubby habit, woody rootstock and reduced, sometimes spiny, leaves, and a basic chromosome number $x = 10$; being *Glandularia* and *Verbena* leafy herbs or subshrubs, without woody rootstock nor spines. *Verbena* differs from *Glandularia* principally by its basic chromosome number being $x = 7$ and $x = 5$, respectively, as well as several morphological and anatomical characters. *Junellia* is a South American genus, distributed all along the arid Andean region, from Perú, Bolivia, Chile and Argentina. *Verbena* and *Glandularia* are distributed in temperate regions of both South America and North America. *Junellia* comprises 39 species, *Verbena* 44 species and *Glandularia* 84 species. For cladistic analyses 73–75 terminals, representing 19 *Junellia* taxa, 18 *Verbena* taxa, 22 to 33 *Glandularia* taxa, plus *Urbania pappigera* were sequenced; *Lippia* and *Aloysia* were used as outgroup taxa. Seven non-coding chloroplast regions were sequenced, these include intergenic spacers and/or introns in trnD-trnT, trnS-trnG, trnS-trnM, trnT-trnL, trnG, trnL, and trnL-trnF, totalling ca. 5.3 kb (365 informative characters). The nuclear ITS and ETS were also sequenced (310 informative characters). Parsimony analyses were performed separately on the combined cpDNA dataset and on the nuclear ETS/ITS dataset. All phylogenetic analyses were conducted using TNT 1.1. This extensive sampling, together with previous studies, suggest that *Junellia*, as traditionally conceived, is paraphyletic and 'ancestral' among the three genera. *Junellia* should be restricted to the monophyletic group where *Glandularia* sect. *Paraglandularia* and the genus *Urbania* are nested. The rest of the species of *Junellia* integrate a monophyletic group that should be separated as a different genus, *Thryothamnus*. *Verbena* and *Glandularia* (excluding *Glandularia* sect. *Paraglandularia*, which is nested within *Junellia*) are monophyletic, but relationships within each genus are extremely difficult to resolve; nevertheless there is evidence that South and North American *Verbena* might be both monophyletic. Non-monophyly of *Verbena* and *Glandularia* recovered by cpDNA data is due to chloroplast transfer, as reported in previous studies. *Verbena* and *Glandularia* are sister groups, and together they are sister to the newly classified *Junellia*. *Thryothamnus* is sister to the group comprising all the three genera *Verbena* + *Glandularia* + *Junellia*.

Phylogeny of *Dziedzickia* Johannsen (Diptera: Mycetophilidae), with emphasis in the Neotropical Region. Sarah Siqueira Oliveira^{1*} and Dalton de Souza Amorim². ¹University of Sao Paulo, Brazil FAPESP; ²University of Sao Paulo, CNPq Research Fellowship, Brazil

The family Mycetophilidae (Diptera, Bibionomorpha) is a well corroborated monophyletic group with world-wide distribution, containing 135 extant genera and about 4100 species. In the Neotropical region it encompasses approximately 50 genera and 1000 species. Mycetophilidae is represented in the fossil record since the Cretaceous (145–65 million years ago). Sciophilinae, Gnoristinae, Mycomyiinae, Leiinae, Manotinae, and Mycetophilinae s.s. are currently accepted as valid subfamilies within the family. Gnoristinae includes 26 genera, but in the Neotropical region is represented only by species of *Austrosynapha*, *Coelosia*, *Dziedzickia*, *Schnusea* and *Synapha*. There are not

phylogenetic studies about the subfamily Gnoristinae. *Dziedzickia* was erected for a species from Russia (Palearctic region), although the genus is nowadays known to occur predominantly in the Neotropical region (38 extant species, plus five undescribed). Members of *Dziedzickia* also inhabit the Palearctic (3), Nearctic (7), Oriental (1), and Afrotropics (5). *Dziedzickia* is known from Cretaceous and Eocene/Oligocene (55–23 million years ago) from one and five fossilized species, respectively. A phylogenetic analysis of this genus was performed with 37 morphological characters of adults in a taxonomic sampling of 52 terminal taxa, comprising 41 species of *Dziedzickia* (39 Neotropical and two Afrotropical), *Schnusea* (all the five species of the genus), and six outgroups, including three species of other genera of Gnoristinae, and one species of Mycomyinae, Sciophilinae and Keroplatidae. The Neotropical genus *Schnusea* (initially described for a specimen from Peru), presents apomorphic features, like an absence of M1+2—plesiomorphic for the species of *Dziedzickia* suggesting that *Dziedzickia* would be paraphyletic in relation to *Schnusea*. A heuristic search was performed by using the implied weighting procedure, implemented in TNT, version 1.1. The monophyly of the subfamily Gnoristinae and of the genus *Dziedzickia* was corroborated. *Schnusea* is a monophyletic group inside *Dziedzickia* suggesting the former should become a synonym of the latter, in order to compose a monophyletic group and to reflect the obtained topology. Besides the clade *Schnusea*, supported by the absence of M1+2, oblique r-m, and spines in the gonostyles, other clades were recognized. One of them, sister-group of the Afrotropical species, characterized by reduced mouth parts, corroborates the idea that the genus has different subgroups with intercontinental disjunction. Two other subclades with well-circumscribed distributional patterns in the Neotropical region were recovered: one including species from southern South America (Chile, Argentina, and Brazil) and one constituted by species from northern South America and Caribbean Region.

The Northern-Andes: a biogeographic reconstruction based on events. Erika Jazmín Parada-Vargas* and Daniel Rafael Miranda Esquivel Laboratorio de Sistemática y Biogeografía, Universidad Industrial de Santander, Bucaramanga, Colombia

The Northern-Andes ranges from the high mountains in north Colombia and Venezuela to the mountains in south Ecuador. This portion of the Andes harbors a high diversity that has been studied based on few groups or a narrative perspective. In order to elucidate the historical relationships among the North-Andean areas, we performed a biogeographic analysis based on events. Thirty-seven phylogenies from different taxa in 19 Neotropical areas were taken from the literature. The set of in-group areas is composed by the Merida Cordillera (CM), the Eastern Cordillera of Colombia (CE), the Western and Central Cordilleras of Colombia (CW), the South of Colombia (SC), the North of Ecuador (NE), Central and South Ecuador (SE) and the North of Peru (NP). The analysis was performed under the treefitting approach, using the widespread optimization recent and the TREEFITTER 1.3b default set of costs. The North-Andean areas are grouped into two main clades; the former contains SC and NP, and the latter the remaining ingroup areas. NP, which is the North-Central-Andean limit, is more related to Amazonia; and SC is located at the base of the non-Andean clade. The second clade, (CM, (CE, CW), (Central-Andes, (NE, SE))), shows the Merida Cordillera as the sister area of the North and Central Andes. The results presented here show that although the North-Andes is not a biogeographic unit, some of its areas behave as a unit together with the Central-Andes.

Endemicity analysis of hypogean and epigeal freshwater Eumalacostraca Crustacea in South America. Marcela Peralta^{1*} and Luis E. Grosso². ¹Fundación Miguel Lillo, Miguel Lillo 251, Tucumán (4000), Argentina; ²CONICET, Fundación Miguel Lillo, Miguel Lillo 251, Tucumán (4000), Argentina

Some paleozoic groups of Crustacea, widely distributed in the old oceans, are now reduced taxa in the subterranean freshwater of South America. These ancient lineages, with relictual distributions and limited dispersal ability, are good candidates for biogeographic studies. In addition to the subterranean taxa, a high diversity of epigeal Aeglidae and Parastacidae (Decapoda) are endemic malacostracan groups of southern South America. How restricted are the subterranean relictual areas relative to other epigeal freshwater taxa of Crustacea? Here, we identify areas of endemism for epigeal and hypogean Eumalacostraca with the endemicity analysis of Szumik & Goloboff (2004) (EA), implemented in the programs NDM-VNDM. With 1218 georeferenced records from 172 species (lotic, lentic and subterranean) of 15 crustacean families, from 7 to 56°S, we presence/absence grid (0.8° × 0.8°). Twenty five areas of endemism (defined by two or more species) with maximum endemicity index resulted: 7 with hypogean non-Decapoda species, 8 with epigeal species, and 10 with both epigeal and hypogean sympatric faunas. Areas in La Rioja-S. Juan (ARG) and Mato Grosso do Sul (BR), are new areas for hypogean crustaceans. Other areas are partially coincident with the Decapoda epigeal areas previously proposed by Morrone & Lopretto (1994). With respect to the eight areas found with epigeal species, the four Brazilian ones cover the same geographical regions and do not correspond to the Uruguay River and southern Brazil disjunct Decapoda areas of Morrone & Lopretto; the Chilean area is nearly coincident with their central Chile area. New areas of endemism for epigeal species are reported in the Titicaca Lake and Central Perú. The areas with epigeal and hypogean sympatric fauna are partially coincident with some of the known distributional patterns of freshwater Decapoda. The possibility that the western areas of endemism for hypogean fauna would be the consequence of Late Paleozoic or Late Cretaceous-Tertiary marine transgression is discussed.

Preliminary cladistic analysis of the Thysanoptera families Aeolothripidae and Melanthripidae. Verónica V. Pereyra CONICET, Instituto Superior de Entomología 'Dr. Abraham Willink', Miguel Lillo 205, Tucumán, Argentina

The insect Order Thysanoptera has nearly 6000 described species (Mound, 2007) in two suborders: Terebrantia and Tubulifera. Eight families are recognized in Terebrantia (2400 species) and a single family in Tubulifera (3500 species). Melanthripidae, Merothripidae and Aeolothripidae are considered basal families of Terebrantia with numerous plesiomorphies. Biologically, these three families are very different: merothripids are fungus-feeders, melanthripids are flower-feeders, and aeolothripids are usually facultative or obligate predators on other arthropods. Aeolothripidae is distinguished from the other two families because females have completely lost the eighth abdominal sternite, while in Merothripidae and Melanthripidae it is retained as a pair of lobes on the posterior margin of the sternite VII. For many years, Melanthripidae was considered a subfamily of Aeolothripidae, because they have relatively broad fore wings with several cross veins. This study explores the relationships between these families. A data matrix with 80 morphological characters scored for 146 taxa was analyzed under parsimony. The optimal trees obtained recovered the monophyly of Merothripidae, Melanthripidae and Aeolothripidae. In Melanthripidae, *Melanthrips* Haliday appears as sister group of *Ankothrips* Crawford, and *Dorythrips* Hood as the sister group of *Cranothrips* Bagnall. The relationships between genera of Aeolothripidae are unclear. *Orothrips* Moulton, *Ripidothrips* Uzel and *Dactuliothrips* Moulton are the basal groups of this family. *Aeolothrips* Haliday appears as the monophyletic sister group of *Allelothrips* Bagnall. *Frankliniothrips* Backs appears as paraphyletic in terms of *Corynothripoides* Bagnall and *Mymarothrips* Bagnall is the sister group of both. *Desmothrips* Hood appears as paraphyletic in terms of *Desmidiothrips* Mound, and *Stomatothrips* also appears as paraphyletic in terms of *Erythrothrips* Mound & Marullo. *Erythrothrips* Moulton appears as monophyletic and in the basal section of the tree. The relationships between the other Aeolothripidae genera remain unresolved.

Plant mitochondrial phylogenetics and the problem of paralogy. Gitte Petersen* and Ole Seberg Laboratory of Molecular Systematics, The Natural History Museum of Denmark, Sølvgade 83, opg. S., DK-1307 Copenhagen K, Denmark

Sequence data from the mitochondrial genome have only recently been applied in higher plant phylogenetics. In contrast to animal mitochondrial genes, the plant mitochondrial genes usually have an extremely slow substitution rate, thus mainly being informative at the deep taxonomic level. However, the increasing amount of plant mitochondrial sequence data has revealed drastic differences in substitution rates among clades. Additionally, the plant mitochondrial genome is characterized by a high level of RNA editing and insertion of 'processed paralogs'. RNA editing affects specific sites in the genes or intergenic regions such that a particular nucleotide in the mRNA becomes substituted by another nucleotide, usually C to U. Thus, the amino acid sequence can not be directly predicted from the DNA. Edited sites tend to be more homoplasious than other sites, but we consider that a minor problem. Processed paralogs are created when reverse transcribed copies of mRNA from mitochondrial sequences are inserted in the mitochondrial or nuclear genome. If a gene does not include edited sites or introns, the original gene and its processed paralog will be identical. If the sequence undergoes editing or intron excision it will be different from its source gene. Thus, occurrence of edited sites becomes an aid in identifying paralogy, which may affect phylogenetic reconstruction. Using the Asparagales as an example we will illustrate the consequences of RNA editing and potential occurrence of processed paralogs on phylogenetic reconstruction. Three mitochondrial genes (*atp1*, *cob*, *nad5*) have different levels of RNA editing, thus genes and processed paralogs differ from each other to different extents. As occurrence of processed paralogs is largely clade specific exclusive use of mitochondrial data may produce severely misleading phylogenetic results.

Evolution of Crocodyliformes (Archosauria) in the Southern Hemisphere during the Mesozoic and early Cenozoic. Diego Pol CONICET-Museo Paleontológico Egidio Feruglio, Avenida Fontana 140, Trelew 9100, Chubut, Argentina

A wide diversity of fossil crocodyliforms have been recently discovered in Jurassic, Cretaceous, and Paleogene beds of Gondwana. Most of these forms have plesiomorphic characters that indicate their basal position within Mesoeucrocodylia (e.g., 'mesosuchian' palate, amphicoelic presacral vertebrae) in combination with highly modified and diverse rostral and dental anatomy. This diversity of fossil archosaurs is reviewed and their phylogenetic relationships are analyzed through a cladistic study of 101 taxa scored across 296 characters. The most significant results of this analysis indicates the presence of a large monophyletic clade (Notosuchia) that clusters more than 80% of the known diversity of crocodyliforms from the Cretaceous of Gondwana. This group is one of the largest clades within Crocodyliformes and is the one that has the most diverse dental anatomy, including multicusped, ziphomorph, zipodont, and conical tooth morphologies. Furthermore, sebecids are depicted in this analysis as late representatives of this clade that survived the Cretaceous–Paleogene boundary, being one of the few large terrestrial vertebrates that survived this mass extinction event.

Phylogeny of the genus *Leptodactylus* (Anura, Leptodactylidae) based on characters of morphology and mode of life. María Laura Ponssa^{1*}, W. Ronald Heyer² and Rafael de Sá³. ¹CONICET, Instituto de Herpetología, Fundación Miguel Lillo, Argentina; ²Amphibians and Reptiles, National Museum of Natural History, Smithsonian Institution, USA; ³Department of Biology, University of Richmond, USA

The leptodactylid frog genus *Leptodactylus*, with 86 species, is predominantly Neotropical (a few species have colonized the southern Nearctic region), and ranges from Texas to Argentina and certain Caribbean islands. The genus has been considered a clear example of

transition from a life history closely tied to water to a more terrestrial ecology. Based on morphology and behaviour, Heyer (1969) divided the genus *Leptodactylus* into five species groups (*L. fuscus*, *L. melanonotus*, *L. ocellatus*, *L. pentadactylus* and *L. marmoratus* groups), which were later redefined by Maxson and Heyer (1988). The recent study by Frost et al. (2006) reallocates the genus *Adenomera* within *Leptodactylus*, proposing the subgenus *Leptodactylus* (*Lithodytes*) to encompass the former genera *Adenomera* and *Lithodytes*. Recently, some authors have been using the *Leptodactylus marmoratus* species group to refer to this clade of frogs. Previous analyses exemplify the need to test the monophyly of the genus *Leptodactylus*, and to corroborate currently recognized species groups. With the objective of testing the monophyly of the species groups and exploring their interrelationships, a cladistic analysis was performed. A matrix of 157 characters scored across 75 taxa was constructed, employing 38 characters of external morphology, 75 from osteology, 18 from larval chondrocranium and 26 from mode of life. The data set was analysed under implied weighting with TNT. In the consensus tree, two major clades are evident. One includes most of the species of the *fuscus* group, paraphyletic as it excludes *L. albilabris* and the sister species *L. labrosus*–*L. ventrimaculatus*. This last group is nested in the other main clade. The second clade includes two monophyletic groups, one that contains the species of the *melanonotus* and *ocellatus* groups, which are para- and polyphyletic, respectively. On other hand, the *pentadactylus* group is monophyletic. In the base of the tree are the species of the subgenus *Lithodytes*, which results paraphyletic.

Preliminary phylogenetic analysis of otters (Carnivora, Mustelidae, Lutrinae) combining morphology and molecular data. Francisco Juan Prevosti^{1*} and M. Amelia Chemisquy². ¹División Mastozoología, Museo Argentino de Ciencias Naturales 'Bernardino Rivadavia', Av. Angel Gallardo 470, C1405DJR, Buenos Aires, Argentina; ²Instituto de Botánica Darwinion (IBODA)-CONICET, Labardén 200, B1642HYD San Isidro, Buenos Aires, Argentina

The otters are a group of aquatic carnivores that appeared in the Miocene and are currently represented by 13 species, which inhabit all continents, except Antarctica and Oceania. The Lutrinae are deeply nested in Mustelidae and recent DNA studies showed that Lutrinae is the sister group of the genus *Mustela*. Previous phylogenetic analyses of this subfamily showed three main clades, *Pteronura*, *Lontra*, and *Aonyx* + *Lutra* + *Enhydra* + *Lutrogale* + *Hydrictis*. Those studies were based on mitochondrial and nuclear DNA, leaving other sources of data aside, like osteological and soft anatomy. Thus, those analyses did not include the numerous taxa known from the rich fossil record of the group. In this contribution, we present a preliminary analysis based on cranial, dental and postcranial characters and their combination with nuclear and mitochondrial DNA sequences, of all the living otters plus some fossils, and several outgroups. Our preliminary results showed high incongruence between morphological and DNA partitions. The morphological matrix supported the monophyly of Lutrinae as the sister clade of *Mustela* + *Galictis*. *Amblonyx* is the most basal taxon inside Lutrinae and the remaining Lutrinae are grouped in two clades: (*Lontra* + *Lutra*) and ((*Lutrogale* + *Pteronura*) (*Aonyx* + *Enhydra*)). The fossils *Satherium* and *Enhydritherium* are grouped with *Enhydra lutris* and *Pteronura brasiliensis*, respectively, but *Mionictis* is placed outside the clade Lutrinae + (*Mustela* + *Galictis*). The combined phylogeny with equal weighting showed a monophyletic Lutrinae but with low resolution, and only with a few small clades solved (e.g., *Lontra*; *Satherium* + *Pteronura*). With implied weighting we obtained the clades recognized in the published DNA studies, but several with very low branch supports. The low resolution and/or the low support values are generated by two fossils, *Aonyx aonychoides* and *Mionictis* and the living species *Aonyx congica*, the three lacking DNA data. Excepting for these, the position of the other fossils mostly agrees with previous expectations.

Use of ontologies to document characters. Martín J. Ramírez^{1*}, Wayne Maddison² and Jonathan A. Coddington³. ¹Museo Argentino de Ciencias Naturales ‘Bernardino Rivadavia’–CONICET, Avenida Angel Gallardo 470, C1405DJR, Buenos Aires, Argentina; ²Department of Zoology, 6270 University Blvd, University of British Columbia, Vancouver, BC V6T 1Z4, Canada; ³Entomology, Smithsonian Institution, PO Box 37012, NMNH E529, NHB-105, Washington, DC 20013-7012, USA

Documenting characters and states in phylogenetic datasets is becoming an onerous task. As scholarship advances, no single person can know all relevant anatomical structures, much less all the interpretations of those structures. A person scoring cells in a dataset needs at least a succinct documentation for each character state, especially in a multi-author project. Composing such character documentation is however not trivial. In large-scale, encyclopedic projects, the list of characters may easily scale up to hundreds or thousands, hence the associated documentation becomes monograph-sized by itself. There are several factors by which proper documentation of characters is rarely done, among others: (1) it is hard for phylogeneticists to keep pace with publications relevant to characters, especially on functional morphology and experimental development; (2) character documentation usually duplicates, to a large extent, previous work; (3) it is therefore hard to transform the monumental work of character documentation into a regular publication; (4) if the documentation is published, it is hard to convert and maintain free text publications (paper-based or digital) into machine readable formats to document future phylogenetic datasets. It turns out that there is a simple way to convey community-based repositories of biological data into phylogenetic datasets, thus alleviating a significant part of their documentation. Dataset editors such as Mesquite and MX can make use of ontologies to document characters. We present an application of this idea in Mesquite, using ontologies in Obofoundry. These ontologies are structured via controlled vocabularies with definitions, synonyms, and relationships between terms, curated by a community of experts, machine readable, and exposed in public repositories. The basic idea is to associate characters with the relevant terms in an ontology, thus allowing Mesquite to display the information in the ontology relevant to each character. By this simple operation, a large part of character documentation and related functionality can rely on an external repository, opening channels for interaction between communities working with model organisms and with diversity.

Conflation of truth and knowledge in the inference of clade posteriors. Christopher Randle^{1*} and Kurt Pickett². ¹Department of Biological Sciences, Sam Houston State University, Huntsville, TX 77341-2116, USA; ²Department of Biology, University of Vermont, Marsh Life Science Building, 109 Carrigan Drive Burlington, VT 05405, USA

The objective Bayesian approach in phylogenetics relies on the construction of prior distributions that reflect ignorance. When topologies are considered equally probable *a priori*, clades cannot be. Several justifications have been offered for the use of uniform topological priors in Bayesian inference. (1) They do not inappropriately influence Bayesian inference because they are uniform. (2) Although clade priors are not uniform, their undesirable influence is negated by the likelihood function, even when data sets are small. (3) The influence of non-uniform clade priors is unavoidable and appropriate. The first two justifications have been addressed previously, and found to be questionable. We address the final justification, which is inconsistent with the first two justifications and objective Bayesian philosophy itself. If uniform priors arrived at by convention do not represent knowledge, but rather are mathematical placeholders to allow the estimation of posterior distributions, extension of these uniform priors to non-uniform priors of composite hypotheses is not warranted. In other words, if priors on clades must be either informative or incoherent, use of any prior distribution on clades precludes an objective interpretation of the posterior. We propose and discuss several potential solutions: (1) Bayesian inference can be abandoned in

favor of other methods of phylogenetic inference. (2) The topology with the greatest posterior probability, which is also the tree of greatest marginal likelihood, can be accepted as optimal, with clade support estimated using other means. (3) The objective Bayesian philosophy can be abandoned in favour of a subjective interpretation. (4) A modified Bayes factor can be used to assess differences between prior and posterior beliefs introduced by the data at hand.

Areas of endemism of Southern South America: an example using a large data base of insect distributions. Germán San Blas*, Cecilia Domínguez, Federico Agrain and Sergio Roig Juñent Laboratorio de Entomología, CCT-Mendoza, CC 507, CP 5500, Mendoza, Argentina

The definition of Patagonian and Subantarctic subregions (Morrone, 2001) has been based mainly on its floristic composition and only a few studies were based on mammal or insect distributions. The present study is to our knowledge, the largest of this kind for the area. The original matrix (with 19 845 records for 1041 species) was filtered by eliminating single-locality species. The final matrix has 999 species of insects and over 12 000 georeferenced data entries of Coleoptera and Hymenoptera. This information was gathered from systematic revisions and collections of the main museums and institutions of Argentina, Chile and Brazil. NDM ver. 2.2 was used to analyze the matrix with different grid sizes and fill options. Five analyses were made: (a) 1° × 1° grid without fill, (b) 1° × 1° grid with fill of 30, (c) 0.5° × 0.5° grid, (d) 1° × 0.5° (West–East oriented grid) and (e) 0.5° × 1° (North–South oriented grid). Nested areas, conflictive areas and disjunctive areas were identified. The results for 1° × 1° with fill of 30 was selected for a more detailed analysis. This search was selected because it recognizes the largest number of not superimposed areas, 17 in total. The results without fill recognized six more areas not found in the first analysis. The other searches did not recognize additional areas. Four of the seven areas recognized by Domínguez et al. (2006) for the Patagonian steppe were recovered here. Furthermore, six areas matching with only one ecoregion (Valdivian forest, Chilean matorral, Magallanic subantarctic forest, Patagonian steppe), several areas with associations of two or more ecoregions that were also proposed in previous studies (e.g., Patagonian steppe–Low Monte), and two major areas that cover most of Chile and part of western Argentina were recovered. The use of a large dataset allowed us to identify a larger number of areas of endemism with higher scores (i.e., a higher number of endemics). The use of different grid sizes increased the sensitivity of the analysis (e.g., the use of 1 × 0.5 grid identified areas within the Maule region of Chile). Nevertheless, there are still many downfalls in identification of areas of endemism, mostly from lack of information for large areas (e.g., eastern region of Argentine Patagonia). This problem does not arise in Chile, which is better known.

On reciprocal illumination and biogeographical consilience in cladistic biogeography. Charles Morphy Dias dos Santos* and Renato Soares Capellari Faculdade de Filosofia, Ciências e Letras de Ribeirão Preto, Universidade de São Paulo, Avenida Bandeirantes, 3900, Cidade Universitária, CEP 14040-901, Ribeirão Preto, SP, Brazil

In a broad sense, to comprehend the spatial distribution of organisms is to comprehend evolution as a whole. According to such perspective, biogeography is not only the application of a straightforward method to explain a certain distributional problem: the intent of biogeography is to depict the reality of the evolutionary process, especially regarding its spatial component. To this end, every biogeographical analysis should consider two steps often lacking in published studies: a reciprocal illumination step, and a consilience step. In general, incongruence is the main source of ambiguities in biogeographical analyses, particularly when the problems are considered under different analytical methods. Besides the difficulties to delimit the biogeographical unities, and how past and present events affect the distributional patterns, the existence of widespread taxa, redundancy, and missing areas also lead to non-congruence. Last, but not least, some biogeographical methods are intrinsically flawed. Even if these

challenges were successfully handled, resulting in a completely resolved area cladogram, the obtained pattern is not necessarily meaningful in biogeographical terms—it needs a continuous test in the light of external hypotheses. For this reason, a concept analogous to Hennig's reciprocal illumination is valuable, as well as a sort of biogeographical consilience in Whewell's sense. Firstly, through the search for different classes of evidence, somehow congruent with the biogeographical hypothesis under test, information useful to improve the hypothesis can be accessed via reciprocal illumination. Following, a more general hypothesis would arise through a biogeographical consilience process, revealing that the coincidences are not stochastic, the cases of congruence being part of a more general biogeographical theory. To be consilient, a biogeographical hypothesis must explain phenomena that were not contemplated during its construction, like other taxonomic group distributions, existence (or absence) of fossil groups, and phylogeny of groups distinct but with shared distributional patterns. Biogeographical consilience is an evaluative criterion for the robustness of biogeographical hypotheses as scientific theories, and not as purely descriptive patterns. In a nutshell, biogeography is a fusion of phylogenetic patterns, definition of areas of endemism, delimitation of area relationships, explanations of processes and mechanisms, and geological patterns; reciprocally illuminated, every biogeographical hypothesis has the possibility to explain other phenomena that were not contemplated earlier. Such wide explanations are reliable descriptions of how life changes its form both in space and time, putting historical biogeography close to Croizat's statement of evolution as a tridimensional phenomenon.

Transposable elements and homology. Ole Seberg* and Gitte Petersen Laboratory of Molecular Systematics, The Natural History Museum of Denmark, Sølvgade 83, opg. S., DK-1307 Copenhagen K, Denmark

Transposable elements—DNA sequences that possess the ability to change their genomic location—are ubiquitous in higher plants, but their evolution is not well understood. Given the lack of direct observational data relating to transposition of Stowaway miniature inverted repeat transposable elements (MITEs), phylogenetic methods may provide a means of generating data that adds to our knowledge of these elements. In a phylogenetic framework the evolutionary history of homologous elements may be traced, and the nucleotide sequence of elements at or close to the time of insertion can be reconstructed. Based on a phylogeny of the diploid species of the genus barley (*Hordeum*) we explore evolutionary aspects of four non-homologous groups of Stowaway elements inserted into three nuclear genes: nucellin, xylose isomerase, and barley leucine zipper 1. The data illustrate how elements starting from a high degree of sequence similarity between terminal inverted repeat regions gradually degrade, and confirm previous notions about preferential insertion at particular TA target sites. It is shown how creation of consensus sequences as estimates of ancestral elements may be positively misleading.

Phylogenetic analysis of *Hasemania* Ellis, 1911 (Characiformes, Characidae). Jane Piton Serra* and Francisco Langeani UNESP—Universidade Estadual Paulista, Instituto de Biociências, Letras e Ciências Exatas, câmpus de São José do Rio Preto, Departamento de Zoologia e Botânica, Rua Cristóvão Colombo, 2265, 15054-000, São José do Rio Preto, São Paulo, Brazil

Hasemania is a small genus of small-sized Characidae fishes restricted to the Brazilian Shield rivers. The genus is presently composed by six species: *H. nana* (Lütken, 1875), from the São Francisco basin; *H. melanura* Ellis, 1911 (type-species) and *H. maxillaris* Ellis, 1911, from the Iguçu basin; *H. hanseni* (Fowler, 1949), from an unknown locality in Goiás state; *H. crenuchoides* Zarske & Géry, 1999, from the upper Paraná, and *H. nambiquara* Bertaco & Malabarba, 2007, from the upper Tapajós. The genus, proposed by Ellis (1911), is characterized by: small size; two rows of premaxillary teeth; maxillary with no or few teeth in its upper angle;

lateral line incomplete; caudal fin naked, adipose fin absent, and pectoral fin frequently archaic (= poorly developed) in small specimens. The phylogenetic relationships of *Hasemania* are not known and the characters that define the genus are not unique, which raises doubts about its monophyly. Therefore, the objectives of the present paper are to test the monophyly of *Hasemania* and the phylogenetic relationships within Characidae and among included species. The phylogenetic analysis was based on osteological and morphological characters; all nominal species of *Hasemania* were examined (except *H. maxillaris*) and also species of many other genera of Characidae and Characiformes. The data matrix was analyzed under PAUP*'s heuristic search. The results present *Hasemania* as monophyletic, comprising three among all valid species for the genus (*H. melanura*, *H. nana* and *H. hanseni*), plus four new species from Tocantins-Araguaia basin (2), Jequitinhonha basin and upper Paraná basin, and *Hyphessobrycon negodagua*. *Hasemania crenuchoides* and *Hasemania nambiquara* were outside the clade composed by the other *Hasemania*; *H. crenuchoides* together with a new species from the upper Paraná may constitute a new genus; *H. nambiquara* on the other hand, appears more closely related to a clade composed by *Bryconella pallidifrons*, *Coptobrycon bilineatus* and *Grundulus cochae*, which should be better evaluated in the future. The clade formed by the species of *Hasemania* appears as the sister group of a clade formed by *Hasemania nambiquara*, *Bryconella pallidifrons*, *Coptobrycon bilineatus* and *Grundulus cochae*.

Phylogenetic analysis of Sandokanidae (Arachnida, Opiliones, Laniatores): Evaluating the independence of associated gene regions. Prashant Sharma^{1*} and Gonzalo Giribet². ¹Department of Organismic & Evolutionary Biology and Museum of Comparative Zoology, Harvard University, Cambridge, USA; ²Department of Organismic & Evolutionary Biology and Museum of Comparative Zoology, Harvard University, Cambridge, USA

Though the suprafamilial level phylogeny of Opiliones has received some attention, comparatively little is known about the familial and generic level phylogeny of Laniatores, the most diverse suborder of Opiliones. We investigated the internal phylogeny of the family Sandokanidae (formerly Oncopodidae) (Arachnida, Opiliones, Laniatores) on the basis of sequence data from eight molecular loci: the complete sequence of 18S rRNA, the D1–D3 regions of 28S rRNA, 12S rRNA, 16S rRNA, cytochrome c oxidase subunit I (COI), histone H3, histone H4, and U2 snRNA. Exemplars of four recognized genera of Sandokanidae, as well as a putative new genus, were included. Data analyses were based on a direct optimization approach using parsimony as the optimality criterion. For parsimony analysis, a sensitivity analysis of 13 parameter sets was undertaken, and character congruence was used as the optimality criterion to select among competing hypotheses. The results obtained include the monophyly of Sandokanidae and its stability under a variety of parameter sets and methods. The internal phylogeny is similarly robust to parameter choice and demonstrates the monophyly of all described genera, corroborating morphological observations of external anatomy and male genital characters. The exemplar of the putative new genus does not cluster with any established genera, validating its designation as a separate genus of Sandokanidae. Furthermore, it is observed that pairs of associated genes expected to undergo similar selection pressures (e.g., histones H3 and H4; 12S rRNA and 16S rRNA) do not necessarily yield identical, or even similar, topologies. The topologies of the constituent eight molecular loci and their scales of resolution are discussed in the context of sandokanid evolution.

Molecular phylogenetics of *Nesobasis* and *Melanesobasis* (Odonata: Coenagrionidae): exploring the evolution of a large insular insect radiation. Jeffrey H. Skevington^{1*}, Christopher D. Beatty², Hans Van Gossom³, Thomas W. Donnelly⁴, Thomas N. Sherratt⁵, Arash Rashed⁶ and Scott Kelso¹. ¹Agriculture and Agri-Food Canada, Canadian National Collection of Insects, Arachnids and Nematodes, 960 Carling Avenue, Ottawa, ON, K1A 0C6, Canada; ²Grupo de

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In 1990 Nick Donnelly revised a large part of the Fijian damselfly fauna. An unusual anomaly was discovered—some species appeared to be heavily female biased. In an effort to better understand this phenomenon, we decided to create a phylogenetic hypothesis for the two large, near-endemic, Fijian genera, *Nesobasis* and *Melanesobasis*. These putative sister taxa had never been studied phylogenetically; however, Donnelly postulated the existence of several species groups and some sister species relationships based on a few characters. We refute the concept that *Nesobasis* and *Melanesobasis* are sister taxa and provide quantitative evidence supporting most of Donnelly's perceptions about relationships within *Nesobasis*. Two mitochondrial genes (COI and 12S) and one nuclear gene complex (ITS1 and ITS2, and ribosomal 5.8S rDNA) were sequenced for 45 taxa in our analysis. This represents most of the extant species of *Nesobasis* and *Melanesobasis* and all of the numerous undescribed species. Female-biased species were found in more than one lineage. Results and analytical methods will be discussed and ecological traits will be explored in light of our phylogenetic hypothesis.

Commelinoids or palms up: facts, fantasies and fictions. Dennis Stevenson^{1*}, Jerrold Davis², Lisa Campbell¹, Christopher Hardy³ and Chelsea Specht⁴. ¹New York Botanical Garden, Bronx, NY, USA; ²Bailey Hortorium, Cornell University, Ithaca, NY, USA; ³Department of Biology, Millersville University, Millersville, PA, USA; ⁴Department of Plant & Microbial Biology, University of California, Berkeley, CA, USA

The results of numerous analyses of the monocotyledons, molecular, morphological and combined, have demonstrated the monophyly of the commelinoids sensu Dahlgren but including the palms and Dasygogonaceae and excluding Velloziaceae. The same is true for the Zingiberales, the Poales s.s., and the Cyperales. The constant reoccurrence of these lineages indicates that these relationships are stable and can be taken basically as fact. Thus, effort can be focused on solving other problems in monocot phylogenetic reconstruction. For some time, there were the fantasies of placing *Acorus* in the Typhales, finding a home for Hydatellaceae, and perhaps finding a home for *Hanguana* within the commelinoids. These seem to have solved in the former two but not the latter. For some reason there is the notion that the net-veined condition occurs in the commelinoids and that fleshy fruits are of no value in systematics and/or phylogenetic reconstruction. A close examination of these reveals that these are simply based upon a lack of knowledge of structure and development and as such are fictitious. Similarly, the Poales s.l. is based upon a fictitious notion that it is a useful construct for communication even though the group cannot be defined morphologically in contrast to a more conservative approach of using the Dahlgren orders. The latter allows circumscription and draws attention to interesting features in character evolution and underlying development.

Areas of endemism in Argentina: an analysis using 840 species of plants, mammals, reptiles, amphibians, birds and insects. Claudia Szumik^{1*}, Lone Aagesen², Vanesa Arzamendia³, Diego Baldo⁴, Dolores Casagrande¹, Fabiana Cuezco¹, Juan Manuel Diaz Gómez⁵, Adrián Di Giacomo⁶, Norberto Giannini⁷, Alejandro Giraud³, Pablo Goloboff¹, Cecilia Gramajo¹, Cecilia Kopuchian⁸, Sonia Kretzschmar⁴, Mercedes Lizarralde¹, Alejandra Molina¹, Marcos Mollerach⁷, Osvaldo Morrone², Fernando Navarro¹, Soledad Nomdedeu², Adela Panizza², María Sandoval⁶, Gustavo Scrocchi⁴, Leila Taher¹ and Fernando Zuloaga². ¹Instituto Superior de Entomología (INSUE-CONICET),

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The generalized notion of endemism implies distributional concordance of different groups of living taxa. The main goal of this work is to analyze in a surface of 1 000 000 km² (between the parallels 21°S and 32°S) whether it is possible to find areas of endemism supported by species of groups as diverse as those included in our data set. Then, the distribution of 820 species of plants (47 families), mammals (11 families), reptiles (6 families), amphibians (8 families), birds (19 families) and insects (21 families) is analyzed by using an optimality criterion to identify areas of endemism, implemented in the program NDM/VNDM. This is the largest study ever done in South America covering such an array of taxonomic diversity, and required the collaboration of numerous specialists. Unlike many other distributional studies, the present dataset contains only first-hand records provided by specialists in the respective groups. Almost all of these records are connected to a specimen in one of the major collections of Argentina, many of them collected by the authors. This implies that the ID and taxonomy are reliable (and subject to scrutiny), which is not the case for records downloaded from data bases on the www. Only those distribution patterns supported by several taxa are discussed, such as the Alto Andina area (supported by Camelids, Aves, Reptiles and Grasses) and the Yungas area (supported by 43–109 species from all the groups included).

Phylogenetic relationships of Neotropical species of the genus *Pohlia* (Bryophyta). Guillermo M. Suárez Fundación Miguel Lillo—CONICET, Miguel Lillo 251, San Miguel de Tucumán, Tucumán, Argentina

Pohlia is a genus of Bryaceae that includes 127 species distributed world-wide; its Neotropical representatives are distributed along the Andean corridor. Little is known about these species, besides the original descriptions. Shaw (1984) suggested the monophyly of the genus based on morphological data and divided the genus in three subgenera: *Nyholmia*, *Mniobryum* and *Pohlia*, the first group formed by Neotropical species. However his analysis included only 5 of the 36 Neotropical species. The aim of this study is to test the monophyly of the Neotropical species, through the study of gametophytic and sporophytic generations of all Neotropical species. A phylogenetic analysis was performed by parsimony under both equal and implied weights (with concavities ranging between 2 and 100). In all the analyses *Pohlia* (including *Mniobryum* and *Webera*) was paraphyletic, in terms of some *Leptobryum wilsonii*. In addition, none of the subgeneric divisions was confirmed. In all the analyses *L. wilsonii* was included in the *polisetous* group of *Pohlia*. Our results suggest the non-monophyly of the Neotropical species of the genus *Pohlia*. Future work including more taxa and characters are desirable, to test our results.

Trees, tree-shaped objects, super-trees, and support. Ward C. Wheeler Division of Invertebrate Zoology, American Museum of Natural History, USA

A distinction is made between trees, which possess observation-based optimality values, and tree-shaped objects, which look like trees but are not. Only trees can participate in hypothesis testing, and then only on the basis of their optimality scores. Several current implementations confuse this issue (e.g., Jackknifing, MrBayes), conflating support values and optimality. Other approaches, such as Super-Tree

analysis, optimize non-data based values. These techniques are better employed as measures of support, leaving tree reconstruction to hypothesis testing grounded in observation.

Differential rates of morphological diversification in *Feronista*, and the origins of the Pterostichine and Loxandrine fauna of New Caledonia. Kipling Will^{1*} and Geoff Monteith². ¹Essig Museum of Entomology and ESPM Dept., University of California, Berkeley, California, USA; ²Queensland Museum South Brisbane, Queensland, Australia

Feronista was relatively recently described for three species restricted to eastern Queensland. The genus is clearly placed in Loxandrine based on adult morphology and several sources of DNA sequence data. Preliminary analyses, including nearly 50 new species (25 from Australian and 23 from New Caledonia), strongly support a clade of New Caledonian species with the monophyly of a clade of Australian species equivocal. The significant difference in the number and type of morphological changes between Australian and New Caledonian species is one of the most interesting patterns in species of *Feronista*. The Australian taxa are relatively uniform in overall body-form, microsculpture, patterns of setation and genitalic features. The character states in these species are the same as in the near outgroup taxa and are presumably pleisiomorphic. This is in contrast to the high level of morphological diversity (apomorphic and synapomorphic) found in New Caledonian species. Species from New Caledonia have regions of prominent strigous microsculpture on the proepisternum, extensive loss and positional differences in chaetotaxy, etc.—all features that are normally conserved across loxandrine taxa. Most notable is the complete inversion of the male genitalia. The New Caledonian species appear to have or had a relatively greater rate of morphological change

when compared to Australian *Feronista* or even to other members of the Gondwanan Loxandrine. Most other groups in the tribe show remarkable morphological stasis (e.g., *Loxandrus* from Australia, South America and North America are nearly identical). Alternatively, it is possible that there have been significant selective forces acting on Australian *Feronista* resulting in extinction of variants or purifying selection acting on these characteristics. Preliminary phylogeny of Harpalinae carabids results in a polyphyletic Pterostichini (auct.) with several well supported clades that include assemblages of taxa with Gondwanan distributions. The majority of the flightless precinctive New Caledonian pterostichines are in clades where all close relatives, whose distributions span the Gondwanan continents, are also flightless. Flightlessness can be parsimoniously optimized to the ancestors of these clades, suggesting an inability to cross oceanic barriers. Therefore the present distribution of these taxa must be explained by ancient vicariance. This is further supported by the fact that none of these flightless Gondwanan groups is found on any islands except Tasmania, New Zealand, New Caledonia, New Guinea and Madagascar.

Web based matrix management using mx. Matthew Yoder Department of Entomology, Ohio State University, USA

Curiously, few general purpose web-based matrix management software packages (i.e., software that isn't custom built for a specific project or grant) exist. Possible reasons for this are discussed, and a countering example, 'mx', is overviewed. Mx is an experiment in open source software which seeks to build a community of like minded developers and users. Projects using mx, of a variety of sizes from individual graduate projects to larger scale international collaborations, are highlighted.