



Abstracts of the 23rd Annual Meeting of the Willi Hennig Society. “Phylogenetics and Evolutionary Biology”

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The 23rd annual meeting of the Willi Hennig Society took place in Paris with the support of Muséum national d'Histoire naturelle and CNRS (Centre National de la recherche Scientifique), from the 18th to the 23rd of July 2004. Ninety four participants from 16 countries presented 67 talks and 11 posters. The symposia comprised both methodological contributions and strong analyses of case studies, focusing on hot topics in systematics, methodological advances in phylogenetic analysis, epistemology, phylogenetic analysis of behavioral and ecological traits, phylogeny and coevolution of microbial symbioses, taxon and character sampling, biogeography, and the evolution of arthropods. The student participation was very high with 30 student talks (45%) distributed among all symposia, showing the same healthy trend seen in previous meetings. The present abstracts show how much systematics and phylogenetics are scientifically growing and contribute significantly to all research fields of evolutionary biology in the framework of comparative biology.

The Student Awards Committee (Cyrille D'Haese, Diana Lipscomb, John Wenzel) nominated the following winners: Johannes Bergsten, the Hennig Prize (\$1000) for “Antagonistic coevolution between the sexes in diving-beetles (Coleoptera: Dytiscidae); phylogeny and experiments in reciprocal illumination”, Mahé Ben Hamed, the Brundin Prize (\$500) for “Reconstructing the history of Chinese through lexicon. Cladistics, distances and trees” and Lara Lopardo, the Rosen Prize (\$250) for the poster “Chilean Anapids and Their Webs, a Phylogenetic Approach (Araneae, Anapidae)”.

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How did pentastomids get there? Mikaël Agolin* and Cyrille D'Haese. FRE 2695 CNRS, Département Systématique et Évolution, Muséum national d'Histoire naturelle, 45, rue Buffon, 75005 Paris, France

Pentastomids constitute a group of about 130 described species of worm-like parasites of the respiratory tract of tetrapod vertebrates. Their phylogenetic affinities have remained enigmatic until recently. Consequently, the evolution of the group is unclear and none of the previously proposed evolutionary scenarios was ever tested through a phylogenetic framework. More and more evidence has been found to conclude that Pentastomida is an arthropod group, closely related to the free living ectoparasite Branchiura (Crustacea: Maxillopoda). In order to address evolutionary questions concerning pentastomids, we first sequenced the complete 18S gene for *Raillietiella* sp. and *Kiricephalus* sp. and a fragment of 16S rDNA for *Kiricephalus* sp. Then the morphological matrix produced by Giribet et al. (in press) was completed and slightly modified

according to the literature on pentastomids morphology and anatomy. We performed a class-level total evidence phylogenetic analysis including 54 taxa for 2 genes and 358 morphological characters, using direct optimization with a Sensitivity Analysis plus Tree Fusing strategy. The inferred topology shows a robust sister group relationship between Pentastomida and Branchiura, forming the clade Ichthyostraca. The relationships between Ichthyostraca and Ostracoda remains unclear, since our taxonomic sampling includes only one Podocopa, no Myodocopa. Our results do not support previous publications arguing Pentastomida is a basal arthropod group, making the hypothesis of a very ancient origin of the group based on Cambrian fossils attributed to the phylum Pentastomida unsupported.

Taxonomic position of *Nipponolejeunea* (Steph.) Hattori. Inkeri Ahonen. Botanical Museum, Finnish Museum of Natural History, University of Helsinki, PO Box 7, 00014 University of Helsinki, Finland

Liverwort genus *Nipponolejeunea* is morphologically intermediate between genus *Jubula* and the family

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data decreases the ambiguity regarding the placement of the root and provides a resolved phylogeny of extant penguins.

A total-evidence phylogeny of megachiropteran bats. Norberto Giannini* and Nancy Simmons. Department of Mammalogy, American Museum of Natural History, Central Park West at 79th street, New York, NY 10024-5192, USA

The suborder Megachiroptera comprises > 160 species of fruit bats (Pteropodidae). Molecular phylogenetic results have generally contradicted most currently recognized taxonomic groups, implying high levels of morphological homoplasy, particularly in traits related to feeding habits. However, a recent study has shown that the alleged conflict between morphology and molecular data may be less significant than previously thought. To further investigate this, we generated a morphological matrix of over 200 characters for 44 representative megachiropterans and six microchiropteran outgroups. We combined this matrix with sequences from the 12S, 16S, t-valine, cyt b and the nuclear c-mos oncogene from previous studies. We used direct optimization under equal weights. Exploratory analyses using implied weights suggest that maximal topological congruence between the combined analysis and trees based on separate data sets can be achieved using strong concavities (k equal to 3 or 4). The combination of the two sources of evidence easily accommodated the morphological and molecular signals, yielding a well-resolved, well-supported phylogeny of the Megachiroptera that agrees remarkably well with the current taxonomy of the group.

Continuous characters analyzed as such. Pablo A. Goloboff*, Camilo I. Mattoni and Andrés Sebastián Quinteros. Instituto Superior de Entomología 'Dr Abraham Willink', Miguel Lillo 205, 4000 S.M. de Tucumán, Argentina; Diversidad Animal I, F.C.E.F.y N., Universidad Nacional de Córdoba, Av. Velez Sarsfield 299, 5000 Córdoba, Argentina; Cátedra de Anatomía Comparada, Facultad de Ciencias Naturales, Universidad Nacional de Salta, Av. Bolivia 5150, 4400 Salta, Argentina

Continuous characters have rarely been included in cladistic analysis of morphological data; when included, they have always been discretized, using a variety of ad hoc methods. Since continuous characters are typically additive, they can be optimized with well known algorithms and thus they could be easily analyzed without discretization. TNT has recently incorporated continuous characters, and three real matrices (for scorpions, spiders, and lizards) are analyzed to study the performance of continuous characters analyzed as such. One of the problems that has been pointed out (Farris, 1990) with some existing methods for discretization is that they

can assign terminals that do not differ significantly to different states. With the implementation in TNT, this problem can be easily avoided by simply assigning to each terminal a range that goes from the mean minus one standard deviation to the mean plus one standard deviation; given normal distributions, terminals that do not overlap thus differ significantly (more significantly if using more than one standard deviation). One of the matrices has a reduced number of continuous characters, and thus continuous characters cannot be analyzed by themselves; adding the continuous characters to the discrete characters, however, increases the support of several groups. The other two matrices have larger numbers of continuous characters, so that the results of separate analyses for the discrete and the continuous characters can be more meaningfully compared. In both cases, the continuous characters (analyzed alone) result in trees that are relatively similar to the trees produced by the discrete characters alone. These results suggest that the continuous characters carry indeed phylogenetic information, and that (if they have been observed) there is no real reason to exclude them from the analysis.

Transaptation, a new concept to describe historical continuity of function with change of the associated structure. Philippe Grandcolas*, Laure Desutter-Grandcolas, Tony Robillard, Frédéric Legendre and Jérôme Murienne. FRE 2695 CNRS, Département Systématique et Evolution, Muséum national d'Histoire naturelle, 45 rue Buffon, 75005 Paris, France

From the early times of systematics and evolutionary biology, structure and function have been considered as related concepts. More or less tightly coupled, they have always been associated within the definition of adaptation, preadaptation and more recently, exaptation. In the last decades, several seminal papers have shown that phylogenetics is absolutely necessary for the study of the historical component of these adaptational concepts. Phylogenetics permits us to reconstruct whether an apomorphic/plesiomorphic structure is associated with an apomorphic/plesiomorphic function at a given phylogenetic node. In that way, adaptation can be distinguished from preadaptation or exaptation, all concepts invaluable to the study of evolution which show how organisms can evolve little but adapt significantly. However, one case of combination of character's states of structure and function has not been characterized until now: an apomorphic structure with a plesiomorphic function. That case has been evoked indirectly in the literature while it appears to be widespread and potentially biologically meaningful. Therefore, we propose the name of 'transaptation' for that adaptational situation where the same function is continuously present, 'trans-cending' a change of structures or 'aptations'. The evolutionary significance of this concept is discussed in the light of several examples. It refers to the 'recruitment' of structures in the