

# XI<sup>TH</sup> YOUNG SYSTEMATISTS' FORUM

2nd December 2009, Flett Theatre, Natural History Museum, London, UK

## Programme

09.00	Registration	
10.00	<b>Welcome</b>	David Bass / Tom Richards
10.05	Opening comments	Juliet Brodie (Department of Botany, Natural History Museum, London and President Elect of the Systematics Association).
10.20	Omar Rota Stabelli	Arthropods phylogenomics supports a clade of myriapods, crustaceans and hexapods reconciling molecules and morphology.
10.40	Cuong Tang	Determining the relative importance of abiotic and biotic drivers of diversity in a Western Cape plant genus ( <i>Sparaxis</i> , Iridaceae).
<b>11.00</b>	<b>Coffee and posters</b>	
11.30	Thérèse A. Holton	Towards resolving the eukaryotic tree of life using complete and partial genomes.
11.50	Elizabeth A. Snell	Placing the ancient Phylum apusozoa in the eukaryotic tree using multigene phylogenomic analyses.
12.10	Jamie Harrison	Pinpointing The Evolutionary Ancestry Of The "Orange" Algal Plastid.
12.30	Ed Glucksman	The novel marine gliding zooflagellate genus <i>Mantamonas</i> (Mantamonadida ord. n.: Apusozoa).
<b>12.50</b>	<b>Lunch and posters</b>	
14.00	Martin Hughes	Pteropods: a study of shells and sequences
14.20	Anne-Claire Lautredou	The genus <i>Trematomus</i> (family of Nototheniidae)
14.40	Alex Papadopulos	In situ speciation of vascular plants on an isolated oceanic island.
<b>15.00</b>	<b>Tea and Posters</b>	
15.50	Maarten Vanhove	<i>A comparative approach to parasite evolution under host adaptive radiation</i>
16.10	João Iganci	Taxonomic diversity and conservation of <i>Abarema</i> Pittier (Leguminosae, Mimosoideae) in the Atlantic Domain, Brazil
16.30	Carla Cummins	TIGER - a new method for site rate identification.
<b>16.50</b>	<b>Closing comments / presentation of prizes</b>	Tom Richards / David Bass
<b>17.15</b>	<b>Reception and Posters</b>	
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<b>19.00</b>		

Organized by **David Bass** (Dept. Zoology, NHM) and **Tom Richards** (School of Biosciences, University of Exeter) with support from:



# ABSTRACTS

## ORAL PRESENTATIONS

### **Arthropods phylogenomics supports a clade of myriapods, crustaceans and hexapods reconciling molecules and morphology.**

**Omar Rota Stabelli**, Henner Brinkmann, Greg Edgecombe, Hervé Philippe, & Max Telford  
University College, London

The advent of molecular systematics has linked myriapods with chelicerates (Myriochelata or Paradoxopoda hypothesis) despite the strong morphological resemblance between myriapods, insects and crustaceans (named Mandibulata hypothesis after the mandible found in all groups). We suggest that this conflict derives from systematic errors in previous tree reconstruction, in particular long-branch attraction (LBA). To confirm this hypothesis we assembled a phylogenomic dataset of 198 genes from 30 taxa covering the main groups of Ecdysozoa and including new data for the previously undersampled myriapods. Analyses of these data support Mandibulata. Analyses designed to reduce the effects of LBA – less saturated data, exclusion of outgroups with long branches, removal of the fastest evolving positions and the use of the best available evolutionary models – consistently result in increased support for Mandibulata over Myriochelata. Our results reconcile the molecule-based phylogeny of arthropods with the known distribution of most morphological characters.

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### **Determining the relative importance of abiotic and biotic drivers of diversity in a Western Cape plant genus (*Sparaxis*, Iridaceae)**

**Cuong Tang**<sup>1</sup>, Paul Rymer<sup>1,2</sup>, & Vincent Savolainen<sup>1,2</sup>

<sup>1</sup>Imperial College London, Silwood Park Campus; Ascot, Berkshire SL5 7PY; <sup>2</sup>Royal Botanical Gardens, Kew; Richmond, Surrey TW9 3AB

*Sparaxis* is a Western Cape plant genus with high variability in pollination syndromes and bioclimatic conditions. Using a species-level molecular phylogeny reconstructed from one nuclear and three plastid genes from 35 taxa, we investigated the relative importance of abiotic and biotic factors as drivers for diversification. We completely sampled species and subspecies of *Sparaxis* (40 accessions), in addition to the 15 outgroups, to confirm this genus is monophyletic and test species delimitation. Nuclear and plastid phylogenetic analyses highlight incongruences, indicating potentially different evolutionary histories. The optimisation of ancestral pollinator syndrome and terrestrial ecoregion states on to the phylogeny identifies nine ecological shifts. Shifts in pollinator (6) and ecoregion (6) are equally frequent; with three shifts in both traits. These findings indicate that a geographical mosaic might be responsible for driving speciation in this Cape clade.

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### **Towards resolving the eukaryotic tree of life using complete and partial genomes**

**Thérèse A. Holton**

National University of Ireland Maynooth

Establishing the phylogenetic relationships of eukaryotes persists as one of the principal challenges in evolutionary biology. At present the consensus view of the eukaryote tree, arrived upon by both morphological and molecular analyses, recognises six distinct 'supergroups'. While the branching order of these major groups remains largely unclear, this scheme is further limited by the strength of evidence for each of these branches. The accumulation of molecular sequence data, sampling across eukaryotic diversity, suggests that the reconstruction of a eukaryotic phylogeny addressing these limitations is effectively within our grasp. Here we endeavour to provide a framework for the eukaryote tree of life using all available complete genomic and EST sequences. Using a supertree approach we reconstruct the phylogeny of over 500 eukaryotic species.

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## **Placing the ancient Phylum apusozoa in the eukaryotic tree using multigene phylogenomic analyses.**

Elizabeth A. Snell

Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS, UK

The phylum Apusozoa comprises an under-studied collection of gliding heterotrophic, bi-flagellate bacteriovores found in marine, freshwater and soil environments. The phylum has two main groups – Apusomonadida (six genera) and the Planomonadida (one genus). Ultrastructural analyses and (for apusomonads) a characteristic gene fusion previously suggested that apusozoans are bikonts, but gene sequence trees have been poorly resolving and contradictory. Indeed, the phylogenetic position of Apusozoa remains unclear and whether it is monophyletic remains questionable. To resolve their placement among basal eukaryotes, we have conducted large-scale, random EST sequencing on five apusozoan species (two apusomonads and three planomonads) and compared them to other eukaryote EST and genomic datasets. Preliminary results place all members of the Apusozoa within unikonts, with apusomonads as sister to Opisthokonts and planomonads basal to all unikonts. Resolution of the monophyly of the group will be determined with the subsequent addition of more data to the dataset in these ongoing studies.

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## **Pinpointing The Evolutionary Ancestry Of The “Orange” Algal Plastid.**

James Harrison, Meredith Jones, & Thomas Richards

Centre for Eukaryotic Evolutionary Microbiology, University of Exeter, School of Biosciences, Geoffrey Pope, Stocker Road Exeter EX4 4QD

“The picobiliphytes” a recently discovered novel group of photosynthetic algae, branch with the cryptomonads in the chromalveolate clade based on SSU rDNA gene phylogenies. We used environmental DNA methods, bioinformatic techniques and fluorescence in situ hybridization microscopy to identify the 16S gene of the picobiliphyte plastid and investigate its evolutionary ancestry. Environmental DNA was analysed using group specific PCR producing a diverse range of target group sequences from marine locations and, for the first time, from oligotrophic freshwater habitats suggesting a highly diverse phototrophic group. Phylogenetic analysis showed the plastid of the target group originated from the red algal endosymbiotic event that also gave rise to the plastids of other chromalveolate taxa, therefore suggesting the plastid has been transmitted by vertical descent from the original chromalveolate secondary endosymbiosis event. This evidence confirms the presence of novel phototrophic life in diverse aquatic habitats and demonstrates its evolutionary history, significantly increasing the diversity of the phototrophic microbial biosphere.

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## **The novel marine gliding zooflagellate genus *Mantamonas* (Mantamonadida ord. n.: Apusozoa)**

Edvard Glücksman<sup>1</sup>, Elizabeth A. Snell<sup>1</sup>, Cédric Berney<sup>1</sup>, Ema E. Chao<sup>1</sup>, David Bass<sup>2</sup>, & Thomas Cavalier-Smith<sup>1</sup>

<sup>1</sup>Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, UK; <sup>2</sup>Natural History Museum, Cromwell Road, London SW7 5BD, UK

*Mantamonas* is a novel genus of marine gliding zooflagellates probably related to apusomonad and planomonad Apusozoa. Using phase and differential interference contrast microscopy we describe the type species *Mantamonas plastica* sp. n. from coastal sediment in Cumbria, England. Cells are ~5 µm long, ~5 µm wide, asymmetric, flattened,

biciliate, and somewhat plastic. The posterior cilium, on which they glide smoothly over the substratum, is long and highly acronematic. The much thinner, shorter, and almost immobile anterior cilium points forward to the cell's left. These morphological and behavioural traits suggest that *Mantamonas* is a member of the protozoan phylum Apusozoa. Analyses of 18S and 28S rRNA gene sequences of *Mantamonas plastica* and a second genetically very different marine species from coastal sediment in Tanzania show *Mantamonas* as a robustly monophyletic clade that is very divergent from all other eukaryotes. On 18S rRNA trees its precise position varies with the phylogenetic algorithm and/or taxon and nucleotide position sampling; with the dataset shown here *Mantamonas* is weakly but consistently sister to Planomonadida (Apusozoa). On 28S rRNA and joint 18/28S rRNA phylogenies (including 11 other newly obtained apusozoan/amoebozoan 28S rRNA sequences) it strongly groups with Apusomonadida (Apusozoa). Our trees suggest that Apusozoa may be unikonts.

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## Planktonic snails: a study of shells and sequence

Martin Hughes

Pteropods, aka 'marine butterflies', are a cosmopolitan grouping of holoplanktonic marine gastropods, defined in part by their modified foot that functions as 'wings' permitting them to actively swim in the pelagic zone. The majority produce aragonitic shells, contributing to a pteropod fossil record spanning the last ~58MA, over which time various shell morphologies have evolved. Recently there has been considerable topical interest since Arctic pteropods are predicted to be one of the first significant groups of organisms to be severely affected by ocean acidification, as a result of their shell composition. Therefore understanding current levels of diversity for these organisms is important. Although aspects of their biology, including their physiology, have been studied in detail, debate continues over their position in the gastropod evolutionary tree and even as to whether the group is monophyletic. Traditional taxonomy of this group is based on morphological, chiefly conchological, characters. Recent molecular phylogenetic studies support pteropod monophyly but this is based on only a handful of sequences. Even less information is available for internal relationships. Our project, using material collected during the Atlantic Meridional Transect Cruise 18 of 2008, amplified Cytochrome oxidase I from 36 individuals from across 5 families; representing the majority of pteropod families. Our results show that COI gene trees correspond well with traditional taxonomy at generic level but show major discrepancies at higher taxonomic levels. The implications of this work will be discussed.

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## The genus *Trematomus* (family of Nototheniidae)

Anne-Claire Lautredou

The genus *Trematomus* (family of Nototheniidae) is central to our understanding of the marine antarctic ecosystem, but ecological studies are hindered by identification problems. Barcoding approaches are therefore welcome and the present study is testing the suitability of the COI gene as a Trematominae barcode. First, we decided to test species delineation in the genus *Trematomus* comparing nuclear (rhodopsin retrogene) and mitochondrial markers, as a previous study (Kuhn & Near in press) failed to recover monophyletic *Trematomus* species. We show from a rich specimen sample that two pairs of species (*T. vicarius*-*T. bernacchii* and *T. loennbergii*-*T. lepidorhinus*) might have a species delimitation problem. Except for these two pairs, COI is a promising tool to identify *Trematomus* species when the method by position on the tree is used. Moreover, we show that reminiscent polymorphism affects alleles of the *Pkd1* nuclear gene, suggesting that all nuclear markers are not suitable.

KUHN K.L. & NEAR T.J., 2009. Phylogeny of *Trematomus* (Notothenioidei: Nototheniidae) inferred from mitochondrial and nuclear gene sequences. Antarctic Science. In press.

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## In situ speciation of vascular plants on an isolated oceanic island

Alex Papadopoulos

Investigating the patterns and processes which govern the formation of new species (speciation) is key to understanding and explaining the incredible diversity of organisms found on the planet. Theoretical models have established that sympatric/parapatric ecological speciation in the face of ongoing gene flow is both possible and

plausible, however, there are few convincing examples in nature. A recent study of the evolution of two palm species (*Howea belmoreana* and *Howea forsteriana*) on Lord Howe Island (LHI) provided complete evidence of a sympatric speciation event giving rise to morphologically and ecologically distinct species. Here a general framework is implemented by which the influences of colonisation, anagenesis and in situ cladogenic speciation on the composition of the flora of LHI have been assessed. Further incidence of in situ speciation events on LHI have been identified, supporting the idea that sympatric/parapatric speciation may be more common than previously thought.

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## **A comparative approach to parasite evolution under host adaptive radiation**

**Maarten P.M. Vanhove**<sup>1,2</sup>, Tine Huyse<sup>1</sup>, Jos Snoeks<sup>1,2</sup>, & Filip A.M. Volckaert<sup>1</sup>

<sup>1</sup> Laboratory of Animal Diversity and Systematics, Katholieke Universiteit Leuven, Charles Debériotstraat 32, 3000 Leuven, Belgium; <sup>2</sup> Department of African Zoology, Royal Museum for Central Africa, Leuvensesteenweg 13, 3080 Tervuren, Belgium

While the evolutionary mechanisms leading to an explosive speciation in fish have been well studied for several model systems, parasites occurring under such circumstances have received almost no attention. Monogenean flatworms provide an excellent target as their direct life cycle and host specificity ensure a close relationship with their host species. We investigated the molecular and morphological diversity of monogenean parasites in two cases of fish adaptive radiation. Our model systems are textbook examples of fish species flocks, whose Monogenea were never recorded: lake Tanganyika Tropheini cichlids and sand gobies of the eastern Mediterranean. We believe this comparison is a unique occasion to disentangle general patterns in Monogenea speciation and in wildlife disease evolution in general. Meanwhile, relating our findings to the history of the fish hosts and their environment, we are able to add to the knowledge of those understudied ecosystems as a whole.

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## **Taxonomic diversity and conservation of *Abarema* Pittier (Leguminosae, Mimosoideae) in the Atlantic Domain, Brazil**

**João R. V. Iganci**<sup>1</sup> & Marli P. Morim<sup>2</sup>

<sup>1</sup>Programa de Pós-Graduação em Botânica, Universidade Federal do Rio Grande do Sul, RS, Brasil ([joaoiganci@gmail.com](mailto:joaoiganci@gmail.com)); <sup>2</sup>Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Diretoria de Pesquisa Científica, Rio de Janeiro, RJ, Brasil ([mpires@jbrj.gov.br](mailto:mpires@jbrj.gov.br)).

The genus *Abarema* belongs to the tribe Ingeae (Leguminosae, Mimosoideae) comprising about 50 neotropical species. The main centre of diversity of the genus is the Amazonic Domain (33 species), followed by the Atlantic Domain. This work presents a study of the extra-Amazonian Brazilian species (Eastern Brazil) of *Abarema*, analyzing the Botanic collections, re-evaluating the diagnostic characters and the taxonomic limits among these species. Thirty five herbaria were examined, including types and/or photos of types, concomitantly field expeditions to the main regions of occurrence of the taxon were carried out. It was found 10 species of *Abarema*, occurring in dense ombrophillous forest and coastal scrubs (restinga) of the Atlantic Domain. Only one species occurs also in the Cerrado Domain. Another species is the unique that presents disjunct distribution between Amazonic Domain and Atlantic Domain. Three new species were recognized. A key to identification is presented along with descriptions and illustrations.

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## **TIGER - a new method for site rate identification.**

**Carla Cummins** & James O. McInerney

Sites (columns) in alignments can evolve at different rates, naturally producing a range of variation amongst all sites. In many situations the variation found is too great for models to adequately describe. Removal of sites serves to narrow the spectrum, allowing improved model fit and, subsequently, better estimations. As fast evolving sites account for most noise in datasets, they present the best candidates for removal. Previous methods have used the fit of the data to trees as a measure of evolutionary rate, however we have shown that this can incur notable

biases towards the tree. Our method uses patterns within the data, such as split conflict, as a proxy for evolutionary rate.

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## POSTER ABSTRACTS

### [1] **Phylo-MCOA: Visualizing Concordance among Gene Trees in Phylogenomics using Multiple Co-Inertia Analysis**

Damien M. de Vienne, Sébastien Ollier, & **Gabriela Aguilera**

Full genome datasets are currently being explored on a regular basis to infer phylogenetic trees, but there are often discordances among the trees produced by different genes. This variability is commonly treated as noise and different methods are employed to find the more likely tree species given the different gene trees. However, doing so may lead to the loss of a wealth of information on potentially interesting biological processes, such as incomplete lineage sorting, hybridization, and horizontal gene transfers. Here we propose a visualization tool to explore the genomic tree space based on multiple co-inertia analysis (MCOA), which efficiently captures and compares the similarities in the phylogenetic topologies produced by individual genes. Our method allows the rapid identification of sets of topologically similar gene trees as well as outliers; it shows how different the compared topologies are and it identifies which species and genes explain those differences. Phylo-MCOA builds a consensus typology by extracting the similarities, in terms of the pairwise distances, between all the species in all the trees simultaneously. This is achieved by using MCOA, which finds successive decomposition axes from individual ordinations (i.e., distance matrices) that maximize a covariance function. The tool has a user-friendly interface that produces a plot grouping the species and the genes jointly and a histogram ranking the genes by the average distance separating them from the consensus typology built by MCOA. It is also available online at <http://www.ese.u-psud.fr/phyloMCOA/index.html>.

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### [2] **Biodiversity and evolutionary history of mastacembelid eels from Lake Tanganyika**

**Katherine J Brown**<sup>1,2</sup>, Lukas Rüber<sup>2</sup>, & Julia J. Day<sup>1</sup>

<sup>1</sup>Department of Genetics, Evolution & Environment, University College London, Wolfson House, 4, Stephenson Way, London NW1 2HE, UK; <sup>2</sup>Department of Zoology, The Natural History Museum, Cromwell Road, London SW7 5BD, UK

Lake Tanganyika (LT) is the oldest of the African Rift Lakes and is one of the richest freshwater ecosystems on Earth, with high levels of faunal diversity and endemism. The endemic species flocks that occur in this lake, such as cichlids, gastropods, catfish and crabs, provide unique comparative systems for the study of patterns and processes of speciation. Mastacembelid eels (Teleostei: Mastacembelidae) are a predominately riverine family of freshwater fish, occurring across Africa and Asia, but which also form a small species flock in LT. A combined matrix of nuclear and mitochondrial genes recovers LT *Mastacembelus* as monophyletic, and reveals rapid diversification of five main lineages. Relaxed molecular clock dating provides age estimates for the LT flock as ~7–8 Ma, older than other LT faunal groups of a similar taxonomic level (e.g. *Synodontis* catfish and *Platythelphusa* crabs). Our analyses also reveal undescribed diversity within and beyond the lake.

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### [3] **Sponges are not Eumetazoans: Complete mitochondrial genome support for a sister group relationship between Porifera and the other animals.**

**Lahcen I. Campbell** & Davide Pisani

Metazoan monophyly is well established; yet the relationships among the basal Metazoa are unresolved. Studies focusing on Porifera (sponges), Cnidaria (corals and jellyfishes), and Placozoa produced conflicting results. Morphology groups the sponges into a monophyletic clade representing the sister group of the other animals. This

is followed by Placozoa, Cnidaria, and Ctenophora, as progressively closer sister groups of Bilateria. Molecular data suggests that sponges can either be (1) the monophyletic sister group of all the other animals, (2) a paraphyletic assemblage of basal metazoan, or (3) the sister group of Cnidaria. The latter result is strongly supported by complete mitochondrial genomes. Here we show that signal in complete mitochondrial genomes supporting a sister group relationship between Porifera and Cnidaria represents a bias (resulting from compositional heterogeneity and long branch attraction). Sponges most likely represent the (possibly paraphyletic) sister group(s) to all the other animals.

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#### **[4] Effect of habitat type on avifauna diversity and distribution in Arabuko - Sokoke forest, Kenya**

**Chiawo David**, Katana Baya, Scolastica Ndegwa, Henry Karanja, Mary Warui, Bernard Soi, Titus Adhola, Samuel Njuki, Paul Omenge, Mathias Templin, & Mulwa Ronald.

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##### **Presented in absentia**

**Abstract:** Arabuko-Sokoke forest is rich in biodiversity, including endemic and endangered avifauna. It is a recognized IBA and ranked as one of the most important forest for conservation of threatened bird species in mainland Africa. More than 230 bird species have been recorded, including 6 globally threatened species. The main objective was to assess the effect of habitat type on bird species richness and distribution. Sampling was done in the three habitats; mixed forest, brachystegia and cynometra. 81 point counts were located along 9km transect. Daily survey started at 0645hrs – 1000hrs. Bird identification was aided by calls and sight according to Zimmermann 1999 and Stevenson 2002. At each point count vegetation assessment was expressed as % vegetation cover. Species richness was highest in brachystegia and lowest in Cynometra, There was Significant difference between brachystegia and cynometra;  $F_2, 78 = 6.051, p = 0.004$ . However, species distributions among the three habitats overlap.

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#### **[5] Origin and Diversification of Clathrin Mediated Endocytosis**

**Luigi Cibrario**, Nicholas J. Talbot, & Thomas A. Richards

Centre for Eukaryotic Evolutionary Microbiology, School of Biosciences, Geoffrey Pope Building, University of Exeter, Stocker Road, Exeter, EX4 4QD, UK.

Clathrin-mediated endocytosis (CME) is a key endocytic mechanism which performs a central role in regulating synaptic activity in neurons and has been studied extensively in yeast and the metazoa. Because clathrin is universally present in eukaryote taxa, it is proposed that CME is an ancient eukaryote acquisition and critical for eukaryote cell evolution. Here we investigate the origin and diversification of CME with a taxonomically broad comparative genomic and phylogenetic study. Our results show that while a set of core components such as clathrin and AP2 protein families are universally present and diversified anciently, most of the known interactome is of relatively recent origin. We propose three key stages in the origin and expansion of the CME interactome's complexity. The last common eukaryote ancestor acquired a basic form of CME. The last common animal, fungi and amoebozoan ancestor evolved integration of CME with membrane bending mechanisms and actin cytoskeleton. Finally, the last common metazoan/choanoflagellate ancestor increased its signal recognition specificity and evolved modulation of dynamin activity at the later stage of vesicle formation. Together this data suggests that endocytosis is highly diversified across the eukaryotic phylogeny.

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#### **[6] Reweaving the tapestry: A species-level supertree of birds**

**Davis, K. E.** and Page, R. D. M.

DEEB, FBLS, Graham Kerr Building, University of Glasgow, Glasgow, G12 8QP, UK

Supertrees are a useful method of constructing large-scale phylogenies by assembling numerous smaller phylogenies that have some, but not necessarily all, taxa in common. Supertrees have now been produced for a

diverse range of taxa including dinosaurs, mammals and crocodiles. Birds are an obvious candidate for supertree construction as they are the most abundant land vertebrate on the planet and no comprehensive phylogeny of both extinct and extant species currently exists. Here, a species-level supertree has been constructed containing 5274 taxa from 757 source trees. The tree shows generally accepted relationships between the main groups, with only a few novel clades, most of which can be explained by a lack of information regarding those taxa. The tree was constructed using a strict protocol, which ensures robust, accurate and efficient data collection and processing. Additionally, it was constructed in a collaborative fashion by placing the source trees and MRP matrix on the World Wide Web for the scientific community to download. No shorter trees were found using this community-based method of tree-building but it still proved invaluable in the identifying of taxonomic errors that would otherwise have had a negative impact on the resultant supertree.

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## **[7] Phylogenetic significance of morphological characters in the taxonomy of *Alloxysta* (Hymenoptera, Cynipoidea, Figitidae, Charipinae) species**

**Dávid Fülöp<sup>1</sup>**, István Mikó<sup>2</sup>, Péter Bihari<sup>1</sup>, Miklós Bozsó<sup>1</sup>, Juli Pujade-Villar<sup>3</sup>, Jordi Paretas-Martínez<sup>3</sup>, George Melika<sup>4</sup>, & Zsolt Péntzes<sup>1,5</sup>

<sup>1</sup>Institute of Genetics, Biological Research Center, Szeged, Hungary; <sup>2</sup>Insect Museum, Department of Entomology, North Carolina State University, USA; <sup>3</sup>Universitat de Barcelona, Facultat de Biologia, Departament de Biologia Animal, Barcelona, Spain; <sup>4</sup>Pest Diagnostic Laboratory, Plant Protection & Soil Conservation Directorate of County Vas, Tanakajd, Hungary; <sup>5</sup> Department of Ecology, Szeged University, Szeged, Hungary

Members of the genus *Alloxysta* (Förster 1869) are parasitoids of hymenopteran natural enemies of economically important aphid species. Most of the species are hardly distinguishable morphologically and it is impossible to determine if the variability is intra- or interspecific. According to some authors there are only a few, very variable and generalist *Alloxysta* species whereas others suggest that the genus contains much more species which are less variable but more specialized. The hypothetical relationships among the species are based on the same, often questionable morphological characters. In this study, many of these morphological characters were mapped on a phylogenetic tree reconstructed from region of the cytochrome-c-oxidase I (COI) and the ribosomal 28S D2 genes. The above mentioned morphological characters may have evolved in parallel in different species groups of *Alloxysta* and, taken alone, may be unsuitable for a subgeneric division of the genus, however, are suitable for species differentiation.

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## **[8] Macroalgae as source of new species of microorganisms.**

**Franz Goecke<sup>1</sup>**, Tim Staufenberg<sup>1</sup>, Jutta Wiese<sup>1</sup>, Andrea Gärtner<sup>2</sup>, Vera Thiel<sup>2</sup>, Kerstin Nagel<sup>1</sup>, Martina Blümel<sup>2</sup>, Rolf Schmaljohann<sup>2</sup>, & Johannes F. Imhoff<sup>1,2</sup>.

<sup>1</sup>Kieler Wirkstoff-Zentrum (KiWiZ) at IFM-GEOMAR, Am Kiel-Kanal 44, D-24106 Kiel; <sup>2</sup>Leibniz-Institut für Meereswissenschaften IFM-GEOMAR, Düsternbrooker Weg 20, D-24105 Kiel, Germany.



It has been demonstrated that epiphytic bacterial communities of macroalgae are different in number and generic composition from those of seawater and the surrounding environment (1). Certain bacteria are consistently found as algal epiphytes suggesting that they can be highly specific and may express adaptations to utilize resources provided by algae (2). In our investigations we have observed that a specific bacterial community can be found associated with different groups of algae growing in the same habitat under the same environmental conditions (1,3). Worldwide, several new bacterial species, genera and orders have been described after isolation from seaweeds, indicating that algae represent a distinct source for new bacterial taxa, even if the origin does not necessarily include specific association (2). In our laboratory we study the microbial communities associated to seaweeds from the Baltic Sea by molecular and culture methods. So far, we described a new Alphaproteobacterium, *Kiloniella laminariae*, found associated to *Saccharina latissima* (4,5).

(1) Staufenberg T, Thiel V, Wiese J, Imhoff JF (2008) FEMS Microb Ecol 64:65-77, (2) Goecke F, Labes A, Wiese J, Imhoff JF (2009) Mar Ecol Prog Ser (submitted in), (3) Lachnit T, Blümel M, Imhoff JF, Wahl M (2009) Aquat Biol 5:181-186, (4) Wiese J, Thiel V, Nagel K, Staufenberg T, Imhoff JF (2009) Mar Biotechnol 11:287-300, (5) Wiese J, Thiel V, Gärtner A, Schmaljohann R, Imhoff JF (2009) Int J Syst Evol Microbiol 59:350-356

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## [9] Actinomycetes with indistinct taxonomic position from dry steppes and semi-deserts soils of Mongolia

A.I. Kurapova<sup>1</sup>, J. Norovsuren<sup>2</sup>, & G. M. Zenova<sup>1</sup>,

<sup>1</sup>Lomonosov Moscow State University, Soil Science Faculty, Moscow, Russia; <sup>2</sup>Laboratory of Microbiology, Institute of Biology, MAS, Ulan-Bator, Mongolia

### Presented in absentia

Now it is clear that actinomycetes can occupy natural niches characterized by extreme conditions, but in the modern literature still not enough data about prevalence and taxonomic position of soil's thermophilic and thermotolerant actinomycetes, particularly «rare» genes of actinomycetes (be a rarity in soils), such as *Actinomadura*, *Saccharomonospora*, *Saccharopolyspora*, *Streptosporangium* etc. In our work we consider dry steppes and semi-deserts soils of Mongolia, as a "source" for allocation of thermophilic actinomycetes and "rare" genes of actinomycetes. We study a complex of thermotolerant and thermophilic actinomycetes of investigated soils by means of traditional methods of plating and biomolecular methods of analysis such as method of fluorescent *in situ* hybridization (FISH) and denaturing gradient gel electrophoresis method (DGGE). In the course of the work we have allocated both actinomycetes of *Streptomyces* genera, and "rare" genes of actinomycetes with indistinct taxonomic position that can be of concern for systematic.

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## [10] Inferring the phylogeny of the kinetoplastids; a comparative genomics study using maximal genome content when few taxa are available

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Attempts to resolve the phylogeny of the human parasitic kinetoplastids has produced conflicting data. Here we describe a novel method of reconstructing species phylogeny using whole genomes and few taxa. We calculated a phylogeny for every gene family present in the *T. brucei* genome to identify reliable gene markers for large-scale analysis, recovering 75 gene families. All 75 datasets were then concatenated resulting in an alignment of 36,278 characters and subjected to six different phylogenetic methodologies and alternative topology tests. We then constructed a reduced dataset with additional species in order to break the long-branch outgroup. Meanwhile eight trees showed evidence of reciprocal kinetoplastid paralogue rooting, negating the need for an outgroup and were analysed using the same methodologies. We then subjected all phylogenetic datasets to analyses with serial stripping of fast evolving sites. Throughout our results we recovered near total support for the monophyly of *T. brucei* and *T. cruzi* pinpointing the major branching order of the kinetoplastids. We then used these results to map

gene loss events across the kinetoplastid phylogeny demonstrating, in contradiction to most models of parasite evolution, large scale gene loss coupled to the transition from an intracellular to an extracellular parasite.

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## [11] Phylogenetic problems in an enigmatic reptilian group, Choristodera

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Choristoderes are an enigmatic group of freshwater aquatic reptiles. With new discoveries over the last three decades, the group has been shown to be widely distributed across Laurasia, with a long temporal range (Jurassic – Miocene), and considerable morphological diversity. Choristodera is generally recognized to belong to the Diapsida, but its precise phylogenetic position is uncertain. Recently, several studies have attempted to analyze the ingroup relationships, but there is disagreement as to the placement of basal taxa, at least in part because of the difficulty of selecting an outgroup. To address these problems, several analyses were run in which: extra outgroups were added (including aquatic sauropterygians) in different combinations; the existing character list was revised with redefinition of ambiguous characters; some missing data was added. Although the phylogeny remains uncertain, the results contribute to an understanding of the different factors causing the problems and demonstrate the importance of outgroup selection.

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## [12] Molecular evolution of *rbcl* in *Conocephalum* (Hepaticae, bryophytes)

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Bryophytes are small land plants with simple morphology. We can therefore expect the existence of several biologically distinct units or cryptic species within each morphological species. We found three *rbcl* types in *Conocephalum japonicum* (Hepaticae, Bryophytes), and found evidence suggesting that the three types were reproductively isolated cryptic species. We were also able to demonstrate that the six cryptic species of *C. conicum* were recognized by allozyme analyses and their *rbcl* sequences. As a result, we were able to discriminate the nine cryptic species of *Conocephalum* based only on their *rbcl* sequences. An excess of nonsynonymous substitutions over synonymous ones has been regarded as an important indicator of adaptive evolution or positive selection at the molecular level. We will report such a case for *rbcl* sequences among cryptic species in *Conocephalum*. This finding can be regarded as evidence of adaptive evolution in several cryptic species within the genus.

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## [13] Taxonomy and phylogeny of the complex thalloid liverwort family Cleveaceae

Rubasinghe, S. C. K., Long, D. G., & Milne, R.

Cleveaceae Cavers is a family of complex thalloid liverworts and it is supported as monophyletic in molecular and morphological studies. But there are problems in taxonomy and phylogeny of genera within the family. Three genera are currently recognized; *Athalamia* Falc. (syn. *Clevea*), *Sauteria* Nees and *Peltolepis* Lindb. The project aims to research the taxonomy and phylogeny of Cleveaceae, using the alpha taxonomic approach with specialist techniques of SEM and molecular phylogenetics. Preliminary results suggest competing classification systems with different generic concepts. According to molecular phylogeny from *rpoc1*, *psbA*, *rps4* and 26S data, Cleveaceae is strongly supported with four genera: *Peltolepis*, *Sauteria*, *Athalamia* and *Clevea*. This shows that, current generic delimitation within Cleveaceae does not reflect phylogenetic relationships and challenges generic identity of

*Athalamia* and *Clevea*. A revised classification system reflecting phylogenetic relationships will be the end result of this study.

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#### [14] Biodiversity of the silica-scaled chrysophyte, *Paraphysomonas*.

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Attempts have been made to estimate the numbers of species of protist throughout the world, but controversy remains amongst protistologists about the definition of species boundaries. The 'theory of ubiquity' states that all species of protist can be found globally and that they have no true geographical restriction, but delimiting factors need to be established before such claims can be made concerning the global diversity of protists. Clumping protist species over splitting the groups may support this theory, however, phylogenetics is showing how clumping is grossly underestimating the number of protist species. The Chrysophyte genus *Paraphysomonas*, with its silica scales, is used to see how their scale-morphology compares to its 18S genotype in the challenge to understand more about the group's diversity. Are the traditional methods of identifying species by their scale-type sufficient, and does this system correlate with their phylogenetic data? Is morphology enough?

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#### [15] The life cycle of *Nostoc ellipsosporum* (Cyanobacteria)

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Nobody can say exactly how many *Nostoc* (Vauch.) Born. and Flah. species we have. The genus is problematic due to the absence of derived morphological characteristics. One way for correct species identification is to analyze adult colonies (which are rarely found in the nature), the other – to cultivate colonies or make molecular analyses (which is not always possible). In order to clear up the *Nostoc* identification problem and define characteristic features the colonies of the species were cultivated and stages of their life cycles were studied. *Nostoc* has complicated a multi-stage life cycle seldom described in the literature. The habitus of the early stage of all *Nostoc* species are similar and only adult colonies gather characteristic features. The life cycle of *N. ellipsosporum* (Rabenh.) Born. et Flah. was studied in 2008-2009. The adult colonies are spherical or expanded, 0.5-3.0 cm wide, of olive-green or yellowish-brown colour, forming a firm leathery outer layer. *N. ellipsosporum* colony was grown in well-water and the stages of its life cycle were studied. Water is an obligatory medium for terrestrial *Nostoc* species reproduction. The grown colony disintegrated into different length (1-20 cells) hormogonias. Akinetes started to germinate. Hormogonias developed in two ways: to colonies with visible trichomes and to colonies composed of densely located cells which later formed into regular trichomes. The further development of the young colonies is multifarious. Some oblong colonies segmented into two or more round or oval form colonies. In others the new microcolonies were formed in the periphery part. Some young colonies further proceeded by division of trichomes cells and new trichomes developed from the solitary cells, separated from the trichome. The common feature of the young colonies is thickly entangled trichomes which spread loosely during a further development of the colonies. Occasionally a colourless or brownish trichomes sheath was observed in larger young colonies. The adult colonies are compounded of flexuous, loosely entangled trichomes with a colourless or brownish individual sheath. Differences in the morphometric characteristics of the trichome cells were observed between young and adult colonies. Trichome cells of young colonies are barrel-shaped, 4.0-6.6 µm wide and 4.0-8.0 µm long; heterocytes are solitary or heterocytes are formed by three or more in a row; whereas cells of adult colonies are narrower, oblong, with rounded end or nearly cylindrical, 3.0-4.0 µm wide and 5.0-8.0 µm long; heterocytes are solitary; akinetes are oblong, 3.6-5.0 µm wide and 7-11 µm long.

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## **[16] Diversity and Lability of Floral Phyllotaxis in the Pluricarpellate Families of Core Laurales (Gomortegaceae, Atherospermataceae, Siparunaceae, Monimiaceae)**

**Yannick M. Staedler** & Peter K. Endress

Floral phyllotaxis of Laurales (Magnoliidae) is often poorly and sometimes conflictingly documented. In this study four types of floral phyllotaxis were recovered: Fibonacci spiral, simple whorled (decussate), complex whorled, and irregular. Whorled and spiral phyllotaxis occur in all families except Gomortegaceae and may vary within a species. Complex-whorled floral phyllotaxis (two or more organs in a position where only one is expected) and changes in merism are especially prominent in Atherospermataceae and Monimiaceae. The most elaborate complex-whorled phyllotaxis pattern (leading to 8-merous whorls) is present in flowers with a flat floral base. Presence of hyperstigma is correlated with double positions in the perianth. Flowers with few organs commonly have simple-whorled phyllotaxis; flowers with many organs have complex-whorled or irregular patterns. Spiral phyllotaxis occurs in flowers with a broad range of organ numbers. In Laurales, floral phyllotaxis diversity appears to have evolved from spiral phyllotaxis, independently in Atherospermataceae, Siparunaceae, and Monimiaceae.

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## **[17] Non-homogeneous phylogenetic models to detect host adaptation in Influenza**

**Asif Tamuri** & Mario dos Reis

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The natural reservoir of Influenza A is waterfowl. Normally, these viruses are not adapted to infect and spread in humans. Occasionally, genetic material from waterfowl viruses is introduced into the human population causing worldwide pandemics. Identifying which mutations allow viruses from avian origin to spread successfully in the human population is of great importance in understanding influenza pandemics. Here we describe a site-wise non-homogeneous phylogenetic model that explicitly takes into account differences in the equilibrium frequencies of amino acids in different hosts and locations. We identify 518 amino acid sites that show evidence of host adaptation. The sites that we identify provide a resource to experimental virologists studying host adaptation in influenza. We devise an index to measure the degree of adaptation of a flu virus to the human host, and apply it to historical data. This index should be helpful in predicting the pandemic potential of influenza strains.

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## **[18] Dinosaurs and the Cretaceous Terrestrial Revolution.**

**Graeme Lloyd**

Natural History Museum, London

The observed diversity of dinosaurs reached its highest peak during the mid-and Late Cretaceous, the 50Myr that preceded their extinction, and yet this explosion of dinosaur diversity may be explained largely by sampling bias. It has long been debated whether dinosaurs were part of the Cretaceous Terrestrial Revolution (KTR), from 125–80Myr ago, when flowering plants, herbivorous and social insects, squamates, birds and mammals all underwent a rapid expansion. Although an apparent explosion of dinosaur diversity occurred in the mid-Cretaceous, coinciding with the emergence of new groups (e.g. neoceratopsians, ankylosaurid ankylosaurs, hadrosaurids and pachycephalosaurs), results from the first quantitative study of diversification applied to a new supertree of dinosaurs show that this apparent burst in dinosaurian diversity in the last 18 Myr of the Cretaceous is a sampling artefact. Indeed, major diversification shifts occurred largely in the first one-third of the group's history. Despite the appearance of new clades of medium to large herbivores and carnivores later in dinosaur history, these new originations do not correspond to significant diversification shifts. Instead, the overall geometry of the Cretaceous part of the dinosaur tree does not depart from the null hypothesis of an equal rates model of lineage branching. Furthermore, we conclude that dinosaurs did not experience a progressive decline at the end of the Cretaceous, nor was their evolution driven directly by the KTR.



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