

YOUNG SYSTEMATISTS' FORUM

1st December 2010, Flett Theatre, Natural History Museum, London, UK

08.30	Registration	(Please put posters up as early as possible from 08.30)
09.20	Welcome	David Bass
09.30	Richard Thompson	Phylogeny of the ankylosaurian dinosaurs (Ornithischia: Thyreophora)
09.48	Jazmin Hernandez-Kantun	Maërl beds, phylogeny and taxonomy of free-living coralline algae (Corallinales: Rhodophyta) in Europe
10.06	Mark Young	The evolution of super-predatory behaviour in metriothynchid crocodylians
10.24	Anne O'Connor	Age rank/clade rank congruence through geological time and across higher taxa: an empirical study of potential biases
10.42	Anna Kurapova	Periodically warmed up soils of Mongolia and Russia as a bank of thermophilic and thermotolerant actinomycetes
11.00	Coffee and posters	
11.30	Tricia Goulding	Thorny-headed worms infecting mole crabs: cosmopolitan marine parasite or cryptic species complex?
11.48	Andrea Zamora	Phylogeny of the family Aglajidae (Gastropoda: Cephalaspeida) and systematic revision of the genus <i>Chelidonura</i> : preliminary results
12.06	Thérèse Holton	The effective balance of modern tree reconstruction methods
12.24	Seda Sengun	The <i>Vitex trifolia</i> species complex: a truly complex group of plants
12.42	María Aguilar	Integrating environmental niche models into the phylogeography of the myxomycete <i>Badhamia melanospora</i>
13.00	Lunch and posters	
14.00	Jordi Paps	Evolution of animals' closest relatives: a multigenic analysis unveils the phylogenetic positions of Apusozoa and the Opisthokonta <i>incerta sedis</i>
14.18	Lahcen Campbell	Minuscule tardigrades, microRNAs and phylogenomics reveal velvet worms as the arthropod sister group
14.36	Nathan Whelan	Life history evolution of <i>Leptoxis</i> (Gastropoda: Pleuroceridae)
14.54	Ross Mounce	The (continued) growth of phylogenetic information
15.12	Tea and Posters	
15.40	Aodhán Butler	Placing enigmatic species on the centipede tree: a total evidence approach integrating molecules, morphology and non-destructive analysis of historical type specimens
15.58	Dino McMahon	The origin of parasitism in Strepsiptera (Insecta) is associated with a burst of molecular evolution
16.16	Mónica Joyce Moniz	Understanding the phylogeny of the green algal order Prasiolales (Trebouxiophyceae, Chlorophyta)
16.34	David Legg	Arthropod phylogeny: historical perspective and future prospects
16.52	Simon Segar	Presenting the global phylogeny of Sycorytine fig-wasps: implications for speciation in the parasitoids of an obligate mutualist
17.10	Poster session	
18.00	Presentation of Prizes and Reception	Juliet Brodie/Ellinor Michel
19.00		

Organized by **David Bass** (Zoology, NHM), **Ellinor Michel** (Zoology, NHM), and **John Todd** (Dept Palaeontology, NHM), with support from:



TALK ABSTRACTS

Phylogeny of the ankylosaurian dinosaurs (Ornithischia: Thyreophora)

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Ankylosauria is a diverse clade of quadrupedal ornithischian dinosaurs whose remains are known from Middle Jurassic to latest Cretaceous sediments worldwide. Despite a long history of research, ankylosaur interrelationships remain poorly resolved and existing cladistic analyses suffer from limited character and taxon sampling. Here, we present the most comprehensive phylogenetic analysis of the group attempted to date. The traditional ankylosaurid-nodosaurid dichotomy is maintained. Ankylosauridae forms a well-resolved clade, which includes Zhongyuansaurus, the first ankylosaurid known to lack a tail club. Nodosauridae includes a number of taxa that were resolved either as 'polacanthids' or basal ankylosaurids in previous analyses. The use of a broader character sample allows analysis of the interrelationships of all valid ankylosaur species: this has revealed several previously unrecognised relationships. Stegosauria is recovered as the sister taxon to Ankylosauria, while Scelidosaurus is found to be a basal thyreophoran. Dedicated methods for coding continuous characters could be used in future to improve the resolution of ankylosaur phylogeny, particularly in order to explore the relationships within the poorly resolved nodosaurid clade.

Maërl beds, phylogeny and taxonomy of free-living coralline algae (Corallinales: Rhodophyta) in Europe

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Maërl-forming species are red algae of the order Corallinales. In Europe, *Lithothamnion corallioides* and *Phymatolithon calcareum* are recognized as the most abundant maërl-forming corallines and they are included in an international list as habitat-forming organisms that require protection (Annex V of the EU Habitats Directive). For these species, the taxonomy and identification is based on the shape and the anatomy (cells arrangement) of the specimens. Nevertheless, an update in the taxonomy and phylogeny of these important habitat-forming organisms is necessary. So far, our actual molecular information is represented by samples from Ireland, North Ireland, Scotland, England, Spain (Atlantic and Mediterranean) and France (Mediterranean and Atlantic). The phylogeny and some taxonomic remarks are presented based on psbA and 18S rRNA genes. Species such *Lithophyllum dentatum*/L. *fasciculatum* and *Lithothamnion glaciale*/L. *corallioides* showed no variation on the previous genes, suggesting a possible synonym that require further analysis.

The evolution of super-predatory behaviour in metriorhynchid crocodylians

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Metriorhynchid crocodylians represent the apex of marine specialisation within Archosauria. Over the last decade, a series of comprehensive studies have begun to elucidate metriorhynchid phylogenetic relationships, revise their taxonomy, and provided us with a thorough understanding of craniodental morphology and how this indicates trends in feeding behaviour. Despite this surge of interest in functional traits and comparative morphology, there has been little focus on the evolution of super-predatory behaviour in the subclade Geosaurini. The genera in this subclade famously display unusual features, such as: tyrannosaur-like and shark-like teeth, the oldest confirmed evidence of true ziphodonty in any secondarily marine clade and bullet-shaped skulls with a foreshortened snout. Using a varied toolkit of techniques (cladistics, scanning-electron microscopy and biomechanical analyses) we found Geosaurini possessed serrated dentition and a distinct biomechanical biting profile. However, a new Middle Jurassic taxon from England shows many of the craniodental adaptations to hypercarnivory pre-date Geosaurini.

Age rank/clade rank congruence through geological time and across higher taxa: an empirical study of potential biases

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A number of studies have shown congruence between the order of fossils in rock strata and cladistic branching sequences. However, the strength and significance of this is variable through geological time and across higher taxa (e.g., congruence is greatest in the Mesozoic, while vertebrates then to have better congruence than arthropods). It has been shown that most measures of stratigraphic congruence are logically or empirically biased by several factors including tree size, tree balance and the temporal extent of clades. Statistical modeling methods are used to assess the influence of these biases on the Gap Excess Ratio (GER) for a dataset of 650 published cladograms. Some taxonomic groups still show a congruence signature that is probably a product of their preservation potential. Once sources of bias are factored out, there is no clear residual trend through time.

Periodically warmed up soils of Mongolia and Russia as a bank of thermophilic and thermotolerant actinomycetes

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Periodically warmed up soils of Mongolia and Russia characterized by extreme environmental conditions. Such as low humidity and high temperature of soil surface. It is possible to intend a presence of thermophilic and thermotolerant mycelial actinobacteria – actinomycetes in this soils.

In our work we consider dry steppes and semi-deserts soils of Mongolia and volcanic soils of Kamchatka as a bank for allocation of thermophilic and thermotolerant actinomycetes. We study a complex of thermotolerant and thermophilic actinomycetes of investigated soils (using a FISH method and method DGGE), show a predominance of thermotolerant and thermophilic actinomycetes over mesophilic in these soils, and isolate both actinomycetes of *Streptomyces genea*, and "rare" genes of actinomycetes, such as *Streptosporangium*, *Actinomadura*, etc. Using a phylogenetic analysis of nucleotide sequences from 16S rDNA we isolate a new strain of *Streptomyces genea* and deposit it in the GenBank sequence database (NCBI, <http://www.ncbi.nlm.nih.gov/>).

Thorny-headed worms infecting mole crabs: cosmopolitan marine parasite or cryptic species complex?

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Parasites are the most common mode of animal life, yet we are just beginning to understand the vast biodiversity of this group. Systematically, many parasites with broad host use or wide distribution have been identified as multiple cryptic species. Acanthocephalans (thorny-headed worms) are considered their own phylum by some parasitologists, and unlike many parasites, are not known to reproduce asexually in their life cycle. We expected that in the marine acanthocephalan, *Proflicollis altmani*, lack of clonal reproduction would result in increased genetic diversity compared to marine trematodes. In contrast, when we examined genetic divergence between *P. altmani* populations in mole crabs in the Atlantic, Pacific and Gulf of Mexico we found shared haplotypes and low divergence (0-1.8% COI and 0% ITS). These results suggest there is significant dispersal of this parasite and that *P. altmani* is not a cryptic species complex, but a generalist parasite with a wide geographic range.

Phylogeny of the family Aglajidae (Gastropoda: Cephalaspidea) and systematic revision of the genus *Chelidonura*: preliminary results

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Aglajidae is a family of marine opisthobranchs occurring worldwide in tropical and temperate habitats, inhabiting coral reefs, rocky shores, and soft bottoms. Systematic work has been based mostly on the description of the external morphology whereas data on the anatomy and internal shells remain poorly known for most species. Description of species based on juvenile forms and chromatic variations have been common and this lead to a confusing taxonomy with high numbers of synonym names. The genus *Chelidonura* is the most diverse of the family, with over fifteen species worldwide. A multilocus coalescent Bayesian framework (based on mitochondrial COI, 12SrRNA, and 16SrRNA genes and nuclear 28SrRNA and Histone-3 genes) will be used to infer species trees. This will be combined with morphological, and anatomical information in order to discriminate between species and generate species-level phylogenies to hypothesize on the origin, diversification patterns, and biogeography of the Aglajidae. Here, we present a preliminary molecular phylogeny obtained from COI sequence data largely gathered from Genbank. Characters of the external morphology and new anatomical data of *Chelidonura* species are discussed and a summary on the present knowledge of Aglajidae systematics is given. This project is funded through a doctoral grant to the first author by the Consejo Nacional de Ciencia y Tecnología (CONACYT- México), fellowship BAZS/188890/2010.

The effective balance of modern tree reconstruction methods

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Examining the shape, and in particular, the balance of phylogenetic trees can disclose latent aspects pertaining to macroevolutionary processes. The observed balance of a phylogenetic tree, however, may be indicative of an inherent bias associated with the method of reconstruction, rather than a true reflection of underlying evolutionary forces. Tree estimation under parsimony has been suggested to have a tendency towards producing trees with a greater degree of imbalance than other methods. More recently, there has been evidence to suggest that the maximum likelihood method is culpable of producing imbalanced trees. Here, we undertake a comprehensive study of tree balance using a large molecular data set of 1,008 gene alignments. We consider the four most commonly utilised tree reconstruction methods in modern phylogenetics (i.e. parsimony, maximum likelihood, Bayesian analysis and neighbour joining) and evaluate their relative balance using tree balance specific metrics. Using a variety of statistical tools we show that there is a significant variance in the balance of trees produced by alternative tree reconstruction methods, with parsimony consistently producing trees with greater imbalance than other methods considered.

The *Vitex trifolia* species complex: a truly complex group of plants

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Vitex trifolia species complex consists of *V. agnus-castus* L., *V. pseudo-negundo* (Hauskn. ex Bornm.) Hand.-Mazz., *V. negundo* L., *V. trifolia* L. and *V. benthamiana* Domin. Although the complex is morphologically well defined within the genus and the complex form a monophyletic group, individual species are difficult to distinguish from one another. The current research aims to clarify the boundaries between individual species and to examine their medicinal uses. This presentation outlines the research and puts forward the questions that need to be answered.

Integrating environmental niche models into the phylogeography of the myxomycete *Badhamia melanospora*

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Protists tend to have wider distributions and lower degree of endemism than multicellular organisms. Their huge population sizes and efficient dispersion over large areas, facilitated by small cell size, would be the primary causes of these phenomena. Some authors defend the “everything is everywhere” hypothesis, which states that the protist species found in a given location would be a function only of habitat properties and not of restricted dispersion. Others defend the “moderate endemism” hypothesis, illustrating it with examples of geographically restricted species with a distinct and unmistakable morphology. The underlying question is to what extent the current geographic barriers and historical geologic events have restrained the dispersion, and if their influence can be traced in the distribution of the organisms that exist today. In other words: is it possible to find allopatric phenomena driving evolutionary change in this kind of organisms?

In this study we report an analysis of intraspecific DNA sequence variation in a global sample of *B. melanospora*, using a fragment of the small subunit ribosomal DNA (SSU rDNA). An attempt was made to sample from the entire known geographical range of the species, and to select specimens to obtain a final sample as representative as possible. It has also been made a more precise study of the morphology using scanning electron microscopy (SEM), to compare it with the genealogy previously obtained. The geographical distribution of the variants is also explored for a better understanding of the evolutionary history of the species. A random distribution of the variants in space would reflect an “everything is everywhere” scenario, while a strong spatial autocorrelation would be consistent with an intraspecific “moderate endemism” pattern. As a distinct geographic pattern has been found, the alternative hypothesis that clade-specific adaptations to locally different environmental conditions are operating has been explored by comparing environmental niche models.

Evolution of animals' closest relatives: a multigenic analysis unveils the phylogenetic positions of Apusozoa and the Opisthokonta *incerta saedis*

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Opisthokonta is one of the major eukaryotic groups that comprise the popular animals, fungi, and choanoflagellates, as well as lesser known single-celled eukaryotes. While the relationships between the popular groups are widely accepted, the position of the other opisthokont lines remains unresolved. This *incertae saedis* are organisms such as the enigmatic Apusozoa, Ichthyosporea, *Corallochytrium limasporum*, *Ministeria vibrans* or *Capsaspora owczarzaki*. Clarifying their position is vital to comprehend key evolutionary events, such as the genesis of multicellularity in the eukaryotes.

Here we present a study that aims to analyze the evolutionary position of those neglected unicellulars, building a dataset that balances both the sampling of taxa and number of markers. Our alignment contains 12,283 nucleotides for 63 taxa, and was analyzed under a probabilistic framework. The resulting phylogenetic tree provides a complete picture of opisthokont evolution, robustly placing the problematic organisms, and shedding new light into the flagella evolution.

Minuscule tardigrades, microRNAs and phylogenomics reveal velvet worms as the arthropod sister group

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Panarthropods (onychophorans, tardigrades, arthropods) are typically grouped together on the basis of morphology, e.g. all three clades within this superphylum have walking appendages. Recently, molecular phylogenies suggest that Panarthropoda might not be monophyletic, instead placing tardigrades and nematodes as sister clades within Cycloneuralia. However, this result is suspicious because the branches associated with both the Tardigrades and the Nematoda are very long, suggesting the nematode-tardigrade grouping might represent a long-branch attraction artifact. We tested alternative hypotheses of tardigrade relationships using two independent genomic data sets: a large EST data set and microRNAs for all relevant taxa. Each data set yielded congruent results, thus providing compelling evidence in favor of monophyletic Panarthropoda. Our results show that Onychophora is the sister group to Arthropoda, and Tardigrada to be the sister group of Arthropoda and Onychophora. These findings should thus provide a solid foundation to fully understand the process of "arthropodization".

Life History Evolution of *Leptoxis* (Gastropoda: Pleuroceridae)

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The critically imperiled freshwater snails of the genus *Leptoxis* of the southeastern United States have been traditionally overlooked in many systematic studies. As part of a total systematic revision of *Leptoxis*, I am performing a study concerning the life history strategies of the genus. Observations of life history strategies (i.e. period of oviposition, egg laying strategies, shape and size of egg clutches) for each *Leptoxis* species will be made in order to provide novel insights concerning the evolution of *Leptoxis* and to find synapomorphic and autapomorphic characters for the genus. In addition to the life history analyses, for the first time a phylogeny of *Leptoxis* is being created with adequate taxon sampling and a multi-locus approach. Preliminary data from molecular phylogenetics shows that egg clutch laying is the more derived life history strategy. Furthermore, preliminary data suggests *Leptoxis* is not monophyletic and morphologically cryptic species as been found.

The (continued) growth of phylogenetic information

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In 1993, Sanderson et al (Syst. Biol.) tried to get a handle on just how much new phylogenetic information was being published each year. They found an overwhelming amount of data. The rate of growth of information published was and still is increasing rapidly. There are easily thousands of novel datasets published each and every year across thousands of disparate journals, of which only a tiny fraction are archived in publicly-accessible online electronic databases (e.g. TreeBase). I argue, this needs to change, particularly for morphological/paleontological data. For the benefit of supertree research, comparative cladistics, and all other usages that re-purpose primary data and also for the benefit of transparency and repeatability. Finally, it shall also be pointed out, that the vast majority of phylogenetic research is governmentally or charitably-funded (e.g. academic societies), so there should be a strong moral imperative for the results and the data behind this research to be made accessible.

Placing enigmatic species on the centipede tree: a total evidence approach integrating molecules, morphology and non-destructive analysis of historical type specimens

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House centipedes (Scutigermorpha) endemic to New Guinea have until now been omitted from phylogenetic assessment due to a lack of modern morphological or molecular sequence data. The tribe Ballonemini, originally established for *Ballonema* Verhoeff, 1904, and *Parascutigera* Verhoeff, 1904, based on similar tergal prominences is reappraised. *Ballonema* is resolved either in a grade of Scutigerae or as sister to all other Scutigerae + Thereuoneminae. Confocal laser scanning microscopy of the types of *B. gracilipes* demonstrates the utility of this technique for non-destructive imaging of historical museum material at a resolution comparable to SEM. A possible record of *Ballonema* in the Seychelles is dismissed; a new collection samples a member of Thereuoneminae described as *Seychellonema gerlachi* gen. nov. sp. nov. Morphological data, analysed with six genes from other Scutigermorpha, ally *Seychellonema* with the Oriental-Australian genus *Thereuopoda*, but its novel autapomorphies merit recognition of a new genus.

The origin of parasitism in Strepsiptera (Insecta) is associated with a burst of molecular evolution

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Understanding the relationship between genotypic evolution and selection at the phenotypic level is a key area of research. This is investigated in Strepsiptera, an order of endoparasitic insects whose evolutionary biology is poorly understood. Using multiple phylogenetic approaches, we investigate the association between the evolution of the unusual strepsipteran phenotype and the history of: a) molecular substitution rate, and b) lineage diversification. A significant burst in the rate of molecular and morphological evolution at the origin of Strepsiptera is followed by a return to a low and even order-wide substitution rate, and a period of relative phenotypic stability. These data support a decrease in selective constraint during the onset of endoparasitism in Strepsiptera. The period of molecular rate elevation precedes the main phase of strepsipteran diversification. These results have implications for Strepsiptera phylogeny, knowledge of the evolutionary corollaries of parasite diversification, and the causes of molecular evolutionary rate variation.

Understanding the phylogeny of the green algal order Prasiolales (Trebouxiophyceae, Chlorophyta)

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The Prasiolales are one of the few algal groups with marine, freshwater and terrestrial representatives and are easily identifiable by the observation of their stellate axial chloroplast with a central pyrenoid. These algae are widespread in colder regions and marine species living in the two hemispheres are geographically disjunct. I am analyzing the phylogeny of the more speciose genera *Prasiola* and *Rosenvingiella* using the chloroplast genes *rbcL* and *psaB* and adding, in comparison to previous studies, taxa from non-European regions such as China, Antarctica, Australia, New Zealand and Mexico to better understand the biogeography of this order. Phylogenetic trees from these genes are in agreement and show that some species within this order need reevaluation, namely *Prasiola crispera* and *Prasiola calophylla*. Studies like this bring us closer to understand how this group, which apparently has diversified quickly, conquered very different environments and understand which was the primitive habitat.

Arthropod phylogeny: historical perspective and future prospects

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With over 1,000,000 currently recognised species, arthropods are the most speciose phylum on Earth. Four distinct major extant clades are recognised: Chelicerata (spiders, scorpions, ticks), Myriapoda (centipedes and millipedes), Hexapoda (insects), and Crustacea (crabs, ostracods, brine shrimp, etc). Although the monophyly of these clades is often well supported, their relationships to each other are hotly debated – with nearly every conceivable grouping proposed. In morphological analyses, the main problem is identifying homologous structures amongst the different clades. New evidence from molecular and fossil data is helping to resolve these problems and establish a consensus. The importance of these techniques for determining patterns of arthropod head segmentation is given as a case study and highlighted as an area for future research.

Presenting the global phylogeny of Sycorytine fig-wasps: implications for speciation in the parasitoids of an obligate mutualist

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The relationship between the genus *Ficus* and its pollinating wasps (Chalcidoidea: Agaonidae) is one of the only obligate mutualisms. Alongside pollinating wasps fig fruit are utilised by six other Chalcid sub-families with a variety of trophic roles. Having a solid phylogeny for these sub-families allows us to test hypotheses on co-evolution across multiple trophic levels. Little is known about the evolution of the globally distributed parasitoid sub-family Sycoryctinae, a large and ecologically important group. We recreate its evolutionary history using over 100 taxa and three independent loci. Using this phylogeny we discuss the implications for speciation and co-evolution of the group with *Ficus*. We put forward a revised classification and additionally we discuss the divergent modes of speciation in two major Old World genera, test the idea that host-shifts within genera are constrained by fig section and investigate the geographic origin and age of each genus.

POSTER ABSTRACTS

Developing Bayesian and Maximum Likelihood supertrees

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There is very little work on the development of supertree methods in the Likelihood and Bayesian frameworks. Recently, it has been proposed that Maximum Likelihood supertree method could be developed by using an exponential probability distribution to model the probability that the input trees could be erroneous. The Maximum Likelihood approach has

been suggested to return a Majority Rule consensus supertree (i.e. a median tree) when the distance used to estimate similarity between the proposed supertree and the input tree is the Symmetric Difference. However, distribution different from the exponential might be used to model uncertainty in the input collection of trees, and other distance measures could be used to estimate the difference between the supertree and the input trees, and it is currently unknown which distance and probability distribution should be used to recover Maximum Likelihood supertrees.

We are currently developing the first software for the estimation of Maximum Likelihood and Bayesian supertrees. The program is being written in Python and will exploit the capabilities of the Crux and Dendropy libraries. Here we will present our software, and present a simple case study in which, given a set of input trees ML and Bayesian supertrees are estimated. When completed, we expect our software to be able to recover supertrees using MCMC and implement a variety of tests that make use of the recovered supertree (e.g. diversification rate analyses).

The Brazilian Atlantic forest biodiversity hotspot: land planarians as model organisms for fine-scale phylogeographic studies

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The Brazilian Atlantic Forest is one of the richest biodiversity hotspots as well as one of the most damaged by human activities. In recent years, with the aim to preserve the small remaining forest fragments, the Brazilian authorities have supported the creation of protected areas based on biodiversity studies of this region. Some paleoclimatic modeling studies have predicted two stable regions in the central part of the Atlantic Forest while southern regions might have suffered strong instability during glaciations. Molecular phylogeographic and endemism studies show, nevertheless, contradictory results: some data support these predictions, while other indicate that paleoclimatic models fail to predict areas with stable rainforest in the south. Most of these studies however, have been conducted using species with relatively high dispersal rates, whereas taxa with lower dispersion capacity will likely be better predictors of habitat stability.

Here, we have used two land planarian species as model organisms to analyze the patterns and levels of nucleotide diversity on a locality in the Southern Atlantic Forest. We find, in both species, high levels of genetic variability without the molecular footprint of recent colonization or population expansions. The results reflect, therefore, a long-term habitat stability scenario for this region. This result gives support to the existence of stable areas, maybe glacial refuges, also in the southern Atlantic Forest, and at the same time show the suitability of land planarians to understand current patterns of biodiversity.

Ancestral or Derived? A total evidence analysis of Antilopinae challenges the view of “primitive” dwarf antelopes

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Gazelles and their allies and some dwarf antelopes form a well known monophyletic group called Antilopinae (Bovidae, Mammalia). Their ecological adaptations and social systems are

remarkably diverse, ranging from monogamous browsers (dikdiks) to small mixed feeders living in family groups (Beira antelope) to polygamous grazers that live in large migrating herds (Saiga antelope) or in temporal male territories (Springbok). The phylogenetic relationships of Antilopinae were much debated in the past. I present the results of a new supermatrix analysis with molecular, morphological and behavioural data. The well resolved tree is used to reconstruct ancestral body mass, territoriality, and tooth crown height of Antilopinae. The results challenge the traditional view that the dwarf species represent ‘primitive’ remnants of the first radiation of African antelopes. Instead their minute body size is very likely a derived feature. It also supports the Gerenuk being the only known example for a reversal from high-crowned back to low-crowned teeth.

Tree School – a new initiative for engaging schools in cutting edge science

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Given the current decline in the popularity of science among school children, there is growing concern about a future shortage of scientifically literate and trained professionals. Scientists at the Natural History Museum, London, have been working in collaboration with the Cothill Educational Trust to offer pre-GCSE school children the opportunity to be involved in relevant and cutting-edge scientific research. Tree School enables the pupils to learn about and actively participate in current biodiversity research, instilling long-lasting enthusiasm for the natural world. The children are taught to identify plants using traditional techniques (e.g. keys) and DNA based methods of plant identification (specifically DNA barcoding). All the data generated by the school children are then analyzed by NHM scientists and submitted to the Barcode of Life Data Systems (BOLD). Here we outline the aims and benefits of Tree School and present provisional results from the DNA barcode data generated to date.

Supermatrix or supertree? A comparison of supertree and supermatrix methods using the landfowl (Aves: Galliformes)

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There are two distinct methods available to construct large-scale trees: supermatrix and supertree. Each has advantages and disadvantages, but supertrees in particular have come under heavy criticism from some authors. Supertrees are secondary constructions, built from individual phylogenetic trees, whereas a supermatrix is constructed from primary data collated into a single, large matrix. We look at the supertree vs. supermatrix “controversy” in order to assess which, if either, is a more suitable method for building large phylogenetic trees. We plan to do this by building both a supertree and a supermatrix based on the same set of molecular data downloaded from GenBank. Each tree will be compared to the input source trees of the supertree using different comparison metrics in order to assess how well each tree represents the input data.

The “Supertree Tool Kit” (STK) and a supertree of fossil birds

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Creating supertrees containing thousands of taxa requires hundreds of input trees. Managing and processing these data in a systematic and error-free manner is challenging and will become even more so as supertrees contain increasing numbers of taxa. Protocols for processing input source phylogenies have been proposed to ensure data quality, therefore any tool for processing source phylogenies should enable these protocols to be followed. The aim of the STK is to aid in the collection, storage and processing of source trees for use in supertree analysis. We have added meta-data to each tree that contain information such as the bibliographic information for the tree and how the data were derived, including the character data used. Here we demonstrate the efficiency and ease of use of the STK by creating a supertree of fossil birds from a subset of data derived from a large avian dataset of over 6000 taxa.

Molecular phylogenetics of *Chroococidiopsis* and heterocyst-forming cyanobacteria

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Cyanobacteria are a challenge for systematics and taxonomy. Their classification is traditionally based on morphological data, which often does not reflect the evolutionary history. Molecular studies in cyanobacteria can be difficult due to secondary products, various polypeptides, or polysaccharide sheaths. One particularly interesting group of cyanobacteria are the Pleurocapsales, characterized by a unique reproduction through multiple fission and specialized cells called baeocytes. Based on morphological traits, the genus *Chroococidiopsis* has been traditionally classified within the Pleurocapsales, but recent molecular studies indicate that the Pleurocapsales are paraphyletic, and that *Chroococidiopsis* is a sister group to heterocyst-forming cyanobacteria. This is in strong contrast to the close morphological similarity of *Chroococidiopsis* to other members of the Pleurocapsales. However, many molecular studies show a very limited taxon sampling, lack statistical support, or are based on the analysis of single genes only. In order to overcome these problems, our project aim is finally to analyse three genes (16S rDNA, *rpoC1* and *gyrB*) of approx. 70 strains with a focus on Pleurocapsales, *Chroococidiopsis*, and heterocyst-forming groups. Data from GenBank and from available genomes was combined and analysed using Maximum Likelihood and Bayesian methods. Preliminary results support the hypothesis that *Chroococidiopsis* is related to the heterocyst-forming cyanobacteria and confirm the paraphyly of the Pleurocapsales. Our results also indicate that several strains (*Chroococidiopsis* and others) from culture collections are misidentified.

Chloroplast phylogeny indicates a single origin of nickel hyperaccumulation in *Alyssum*

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Nickel hyperaccumulation in the genus *Alyssum* L. (Brassicaceae) is a useful model system for investigating the origin of complex adaptive traits. This genus comprises 201 species, of which 53 are largely restricted to small areas of serpentine soils (which are rich in nickel) and have the ability to accumulate nickel to very high concentrations in shoot tissue. My research addresses the number of origins of this trait within *Alyssum*, and the ecological causes and evolutionary consequences of its appearance. A Bayesian analysis of sequence data was carried out for four chloroplast loci (*trnL-F*, *rps16-trnK*, *MatK*, *trnD-trnT*) and 126 species of *Alyssum*. Hyperaccumulation status was optimised onto the tree using parsimony. Results are consistent with a single origin of nickel hyperaccumulation in *Alyssum*, possible subsequent rapid species radiation, and a separate origin of nickel hyperaccumulation within the closely related genus *Bornmuellera*. These results provide evidence for phylogenetic niche conservatism and extensive geographic dispersal of nickel hyperaccumulation within *Alyssum*, rather than multiple origins in separate locations. The evolution of the ability to hyperaccumulate nickel, allowing colonisation of isolated areas of serpentine soil, may have been instrumental in triggering subsequent rapid diversification of local endemics.

Gene-sharing networks define species groups in prokaryotes

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In prokaryotic systematics, there is no species concept, instead there are species definitions based largely on molecular data. We assess whether there is a meaningful species definition for prokaryotes based on complete genome comparisons. In bacteria, genes can be exchanged across the species boundary resulting in taxa that have genes with diverse evolutionary histories. The “tree of life” metaphor suggests that evolution is a homogenous process with vertical inheritance being dominant. If we wish to describe species incorporating both horizontal and vertical inheritance of genes then we need to describe a genome by its connectivity to other genomes. Phylogenetic studies are now looking to network representations of gene sharing and exchange. Our network represents all homologous relationships between a set of bacteria. The data are filtered by similarity level and thus ability to recombine, providing an insight into gene sharing, species boundaries and the vertical and horizontal components of inheritance.

The morphology and SSU rRNA gene based phylogeny of two new marine euplotids, *Diophrys nigricans* spec. nov. and *Paradiophrys zhangii* spec. nov. (Ciliophora, Euplotida)

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The morphology, infraciliature and molecular phylogeny of two new marine eulotids, *Diophrys nigricans* spec. nov. and *Paradiophrys zhangii* spec. nov., isolated from a sandy beach near Qingdao, China, were investigated. *D. nigricans* is characterized by a combination of the unique, single and very short undulating membrane, a flat and inconspicuous buccal field, as well as the dorsal kineties shortened at both ends. The new species *P. zhangii* is similar to the type species *P. irmgard* but can be recognized by having smaller size, lower number and different arrangement of the frontoventral cirri. The small subunit rRNA (SSU rRNA) gene was sequenced, which firmly supports the distinction of both new species. Phylogenetic analyses indicate that *D. nigricans* is most closely related to its congeners *D. scutum* and *D. apoligothrix*, while *P. zhangii* clusters first with a morphologically diverse form, *Apodiophrys ovalis* with different bootstrap support, and then groups with two of its congeners.

Phylogeny of *Dussia* (Leguminosae-Papilionoideae) illuminates the affinities of the Chocó and the influence of the Andean uplift and closure of the Panama Isthmus

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Dussia is a small, taxonomically complex, neotropical tree genus. Its distribution in rain forests spanning the Andes and throughout Central America makes it ideal to address two key issues of neotropical biogeography: the influence of the Andean orogeny and the Panamá Isthmus closure. Furthermore, *Dussia* has endemic species in the Chocó biogeographical region—a hyper-wet rain forest, isolated by the Andes on the north-west South American Pacific coast—meaning it's also ideal to examine the relationships of that region. A new phylogeny for *Dussia* species was dated and demonstrated that: i) the uplift of the Andean mountains created a biogeographical barrier to migration; ii) migration between South America and Central America occurred before the closure of the Panamá Isthmus indicating that for *Dussia* the Pacific Ocean was less of a barrier than the Andes; iii) the biogeographic affinities of *Dussia* species from the Chocó lie with Colombian Inter-Andean valleys and Central America.

Genetic structure, genetic diversity and phylogeography of the western populations of the eastern imperial eagle (*Aquila heliaca*)

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The eastern imperial eagle is a globally threatened raptor species. Its large, migrating populations breed in Russia and Kazakhstan, but it has separated small non-migrating populations in the western part of its distribution: the Carpathian Basin, the Balkan Peninsula, the Ukraine and Asia Minor. Using genetic information of the mitochondrial control

region and nine microsatellite loci, we tried to reveal the genetic structure of these western populations. Genetic diversity was lowest in the Carpathian Basin and highest in Turkey and Caucasus region. MtDNA haplotypes formed two clades, but this split didn't match to the geographic pattern. We found evidence for gene flow to the Carpathian Basin from the eastern and the southern regions as well. Inside the Carpathian Basin, microsatellites predicted differences between western and eastern subpopulations, but this was not supported by the mtDNA data. The Balkan populations showed definite subdivision, with larger genetic distances between Bulgarian and the nearby Macedonian population compared to the Central Turkish population.

Morphological and molecular analysis of *Anacanthorus* sp. and *Mymarothecium viatorum* (Monogenea: Dactylogyridae) from *Piaractus mesopotamicus* in fish farms from São Paulo state, Brazil

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The monogenean genera *Anacanthorus* and *Mymarothecium* are commonly found in high quantities in farmed fish in Brazil. These parasites represent a potential risk for productivity and can cause high mortality of fishes. The objectives of this work were to examine the phylogenetic position, histopathology and epidemiological aspects of *Anacanthorus* sp. and *Mymarothecium viatorum*, which commonly infect *Piaractus mesopotamicus*, an endemic species from the Paraguay-Paraná River. A total of 278 fishes were collected between February 2008 and March 2010. 13.140 parasites were removed from gills and used for morphological identification and histopathological studies. The epidemiological results showed prevalence 85.9% and intensity of infection 54.9 worms/fish. In order to establish the positions of these species within a phylogenetic framework on monogenean parasites, complete 18S and partial 28S rDNA was sequenced from representative specimens and analysed with published data.

Problems in the systematics and biogeographical history of salamanders

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Living salamanders are diverse and, with the exception of two recent southward migrations, are limited to northern continents. After more than a century of morphological and molecular analysis, some phylogenetic consensus has been reached, but the relationships of some clades (e.g. sirenids) remain controversial, in part because of widely prevalent pedomorphosis. The earliest fossil salamanders date from 165 mya, with crown group taxa appearing shortly after. Most fossil remains are fragmentary, making classification difficult, but exceptional Early Cretaceous Chinese and Spanish material offers the potential for more rigorous phylogenetic analysis. Like living taxa, fossil salamanders are mainly restricted to northern continents (ancient Laurasia) suggesting a northern origin. However, a small number of aberrant fossil salamanders are known from the Cretaceous and Paleogene of

Africa and South America (ancient Gondwana) raising the question as to whether early salamanders, like frogs, might have been more widely distributed.

Phylogenetic studies on *Paraboea* (Gesneriaceae)

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Paraboea comprises about 100 species distributed throughout Southeast Asia, from China to Sulawesi. The genus is highly diverse in fruit and inflorescence morphology, including straight- and twisted-fruited species and species with terminal, subterminal and axillary inflorescences. *Paraboea* has a characteristic matted indumentum on the lower leaf surface which distinguishes it from *Boea*. Although preliminary molecular studies have indicated a potential paraphyly of *Paraboea* with *Trisepalum*, the latter is morphologically distinguishable by the calyx and the stigma. It also has narrower distribution, being found mainly in Thailand and Burma. Here we present an extended molecular investigation on the clade containing *Paraboea*, *Trisepalum* and closely allied genera, the *Boea* group. The DNA regions examined are the chloroplast *trnL-F* intron-spacer and the nuclear ITS. The data have been analysed using maximum parsimony and Bayesian inference. The study will shed light on the species and genus relationships within the *Boea* group.

Molecular systematics of *Pyramidula* (Gastropoda, Pulmonata)

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Pyramidula is a genus of terrestrial gastropods whose distribution in the Palaearctic Region extends to almost all Europe, Mediterranean area and Central Asia and includes six species. Until now, the identification of the species has been based exclusively on shell parameters because there are not differences in the reproductive system. Some of the shell parameters are correlated so the morphological criteria seem to be not enough to deduce the taxonomy and the need for complementary characters become evident. The aim of the present study is to review the taxonomy and phylogeny of the genus using molecular markers. DNA sequences will be compared with the currently established morphospecies. At present, four species of the genus are being analyzed but future studies will include all the species of the genus and samples from the whole geographical range.

An improved view at arthropod relationships using site-heterogeneous models of sequence evolution

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Heterogeneous models of sequence evolution reduce the effect of systematic errors (due to violation of the homogeneity assumption by the data), thus promoting more reliable

phylogenies. This fact has been demonstrated for eukaryotes and for basal metazoan lineages, but has not been thoroughly applied to the problem of arthropod phylogeny.

We have explored the effect of using site-heterogeneous (CAT+Poisson and CAT+GTR) and site-homogeneous (empirically and mechanically derived GTR) models on four datasets encompassing various ranks of the arthropods: three phylogenomic datasets with up to 205 genes and a mitogenomic dataset including 5 new sequenced genomes.

Site-heterogeneous models fit all datasets better and recover (1) onychophorans and tardigrades as sister group of arthropods (Panarthropoda), (2) myriapods as sister of pancrustaceans (Mandibulata), (3) Paraneoptera sister of holometabolans (Eumetabola), and (4) branchiopods closer related to hexapods than to malacostracans. Heterogeneous models overturn results obtained using homogeneous models, reconcile molecules with morphology, and seem more apt to overcome the most notorious of the systematic errors, the Long Branch Attraction artefact.

Evolutionary and systematic implications of an AFLP study on endemic gastropod species of Lake Malawi

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The endemic species of the gastropod genus *Lanistes* of the African rift-lake Malawi show some remarkable morphological and behavioural adaptations to their respective niches: Facing predatory pressure from molluscivorous cichlid fishes, *L. solidus* developed the thickest shell of the entire genus. *L. nysassanus* burrows in the sandy substrate during daytime to avoid its predators and *L. nasutus* has escaped predation by living in deeper waters where molluscivorous fishes do not hunt. A recent study has shown that this endemic monophyletic group has evolved during the Pleistocene within the lake. Yet mitochondrial DNA fragments indicated no clustering into species. The present study uses high-resolution AFLP markers to investigate the phylogenetic relationship among the nominal species. It shows that genetic differentiation between these taxa is – despite their morphological and behavioural diversity – low and discusses evolutionary and systematic implications.

Morphology and phylogenetics of silica-scaled protists reveal increased diversity

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Protist taxonomy is an exciting and controversial area of research, which is growing in importance because of more environmental surveys to observe the micro-diversity within habitats around the world connected to concerns about 'climate change' theories. Electron microscopy of silica-scaled protists has revealed a level of diversity that has increased the number of new species within these scaled genera over the past 60 years. More recently, ribosome sequencing, to create phylogenetic relationships between isolates of the same genera, has revealed an even higher diversity than using the scales alone. In general, sequence data for protists far outweighs the microscopical data because of better sequencing facilities that make it easier to obtain genetic information without having to

culture protists in the laboratory. Culturing novel strains for sequencing, and observing these same strains in the electron microscope have married two sets of data for which the results have shaken the foundations of the taxonomical structure for these silica-scaled protists, as well as having direct implications to other non-scale bearing protists.

Pauropoda: our forgotten myriapods

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In 1867 Sir John Lubbock discovered the first 2 species of the class Pauropoda around the London area. Here *Stylopaupopus pedunculatus* and *Paupopus huxleyi* were described and the class Pauropoda was born. Pauropoda boasts the accolade of being one of the two classes primarily erected in Britain, making its origins firmly grounded within the UK. Despite this and the interest it received upon its discovery, this charismatic and mysterious class of Myriapod has been tragically understudied worldwide, especially in Britain, its initial birthplace. This study aims to build a basis for the continuous study of Pauropoda within the UK by producing a key of British species, extending habitat information and adding the description of new species. We also aim to raise the profile of these minute yet fascinating soil-dwelling creatures and give them the exposure they deserve.

The results of a new and still ongoing survey of the Pauropoda of England will be presented in this meeting. Of the 23 UK species hitherto described, 3 species from 3 genera (*Decapauropopus*, *Paupopus*, *Trachypauropopus*) and 2 different families (Pauropodidae, Eurypauropodidae) have been discovered in the Reading area. New localities and habitat data are added for *Trachypauropopus britannicus* and *Paupopus furcifer* (found in Berkshire) and *Decapauropopus distinctus* (found in Northamptonshire). In addition to the taxonomical studies, future outcomes aim to resolve questions about ecology, conservation, physiology and genetics of the Pauropoda.

Geographical variation in an endemic cichlid lineage from Lake Tanganyika

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In comparison with the species flocks of lakes Malawi and Victoria, the taxonomy of the estimated 250 species of Lake Tanganyika cichlids is relatively well known. It has only recently become clear that many of these species show a considerable amount of geographical variation in general morphology. The genus *Tropheus*, Boulenger, 1898, consist of highly stenotypic rock dwellers whose limited capacity for dispersal gave rise to over a hundred colour morphs. Notwithstanding their high chromatic and genetic differentiation, their morphology is assumed to have remained static. In this study, we investigated interpopulational morphological differentiation in *Tropheus duboisi*, Marlier, 1959. As this basal species shows only minor colour differences and is less stenotypic than its congeners, it is ideally situated to test the hypothesis of morphological stasis in *Tropheus*.

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