

YOUNG SYSTEMATISTS' FORUM

29th November 2012, Flett Theatre, Natural History Museum, London, UK

08.30	Registration	(Please put posters up as early as possible from 08.30)
09.30	Welcome	YSF team
09.40	Claire R. Peart	Biodiversity and evolutionary relationships of Claroteid catfish from Lake Tanganyika
09.58	Marylaure de la Harpe	Do genetic, geographical or ecological factors play a major role in the distribution of the Western European <i>Alyssum montanum</i> polyploid complex?
10.16	Patrick Knopf	Origin and phylogeny of Podocarpaceae (Coniferopsida)
10.34	Bhanubong Bongchewin	A phylogenetic study of the tribe Gomphostemmatae Scheen & Lindqvist (Lamiaceae)
10.52	Coffee and attended posters (even numbers)	
11.30	Simon Maddock	Living in Paradise: systematics and biogeography of Seychelles amphibians
11.48	Karen Siu Ting	Taxonomic placement of <i>Ericabatrachus baleensis</i> (Amphibia: Anura: Ranoidea) and a proposal for inclusion of data in phylogenetic analyses.
12.06	Sarah Parks	The effect of long branches on Maximum Likelihood tree reconstruction
12.24	Wasiu A. Akanni	Developing a Maximum Likelihood and Bayesian supertree
12.42	Anaïs Grand	3ia swims with the fishes: a comparison of 3ia and parsimony phylogenies of Gadiform fishes
13.00	Lunch and posters	
14.00	Richard S. Thompson	Locked in the bones: the production of a large molecular systematic dataset from museum specimens.
14.18	Bethany Williams	Foundation Monograph of <i>Convolvulus</i>
14.36	Haris Saslis-Lagourdakis	Phylogenies reveal predictive power of traditional medicine in bioprospecting
14.54	Zoë Goodwin	Species discovery in <i>Aframomum</i>
15.12	Tea and attended posters (odd numbers)	
15.50	Nicola Susanne Heckeberg	How combining morphological and molecular data improves positioning of fossil taxa in cervid (Ruminantia, Artiodactyla) phylogenies
16.08	Sérgio Henriques	The advantages and challenges to the study of camel spiders (Solifugae, Arachnida).
16.26	Krzysztof M. Kozak	Marker incongruence and signal consistency in the hyperdiverse <i>Heliconius</i> butterflies (Lepidoptera: Nymphalidae)
16.44	Ana Rita Mendes	The <i>Myosotella</i> 'myosotis-denticulata' complex: untying a morphological knot
17.02	Martin R. Smith	Deep molluscan relationships: reconciling morphology and molecules
17.20	Poster session	
18.00	Presentation of Prizes and Reception	Robert Scotland/Maria Vorontsova
-19.00		

Organized by **Ellinor Michel** (Dept Life Science, NHM),
Jon Todd (Dept Earth Science, NHM), **Jane Droop** (RBG, Edinburgh) & **Maria Vorontsova** (RBG, Kew), with support from:



TALK ABSTRACTS

Biodiversity and evolutionary relationships of Claroteid catfish from Lake Tanganyika

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Lake Tanganyika (LT) is home to a diverse array of endemic radiations, including at least three endemic catfish radiations, but to date only the genus *Synodontis* has been studied in some detail. Catfish in the sub-family Claroteinae have also diversified and this work seeks to address the evolutionary relationships within the Claroteinae, using a multi-gene approach. The novel phylogeny reveals a large-scale LT radiation, however, the morphologically divergent species *Chrysichthys brachynema* is paraphyletic with respect to this radiation. In addition this analysis reveals cryptic diversity within the endemic genera *Phyllonemus* and *Lophiobagrus*. These results indicate that LT claroteid species may be locally restricted and highlights the need for fine-scale sampling. The limitations of fossil calibrations for molecular dating in this group and diversification scenarios will also be discussed.

Do genetic, geographical or ecological factors play a major role in the distribution of the rare *Alyssum cuneifolium* polyploid complex?

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Alyssum cuneifolium L. (Brassicaceae) aggregate is an endangered orophyt endemic to European mountain ranges. Taxa circumscriptions within this evolutionary unit remain problematic, most likely due to edaphic dynamic and the occurrence of three cytotypes ($2n = 2x, 4x, 6x$), and geographically close related *Alyssum* species. The cytotypes occur on subalpine and alpine screes on various mountain ranges, while close related species are found on xeric, oligotrophic, and open grasslands on all vegetation stages. The phylogeographic history of this polyploid complex in Western Europe is inferred using DNA fingerprinting (AFLP) and sequencing (cpDNA and nDNA) methods on 239 individuals representing 61 populations. Results are analyzed using Bayesian clustering methods for the AFLPs and phylogenetic inferences for the DNA sequences. Fine scale bioclimatic and substrate variables were included to explore their influence clusters distribution. Molecular results revealed geographical patterns incongruent with taxonomy in most cases. Moreover, statistical analysis demonstrated significant ecological speciation.

Origin and phylogeny of Podocarpaceae (Coniferopsida)

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Podocarpaceae, the second largest gymnosperm family (18 genera, 205 taxa), shows a great diversity in morphology, anatomy, and ecology. The disjunctive distribution of the recent taxa as well as the fossil documentation supports a strong Gondwanan relationship. The present study is focused on detecting the origin of Podocarpaceae and the migration of the species in time and space. However, long-distance dispersal also may have influenced the distribution pattern. A comprehensive anatomical and morphological study ensured the accurate identification of the sampled specimens. An extensive phylogenetic reconstruction using *rbcL*, *matK*, *nrITS1* and *NEEDLY* intron2 sequences of more than ¾ of all Podocarpaceae was done. A comprehensive biogeographical analysis using a relaxed molecular clock approach (implemented in BEAST) and an ancestral area reconstruction (S-DIVA) was performed. Our results support the origin of Podocarpaceae in the Austral Realm, where two major migration routes to South America/Africa and Australasia started.

A phylogenetic study of the tribe Gomphostemmateae Scheen & Lindqvist (Lamiaceae)

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Phylogenetic relationships between members of the tribe Gomphostemmateae Scheen & Lindqvist (Lamiaceae), which includes three genera, *Gomphostemma* Wall. ex Benth., *Chelonopsis* Miq. and *Bostrychanthera* Benth., have been studied by analysis of morphological, chemical and DNA-sequence data. The classification of *Gomphostemma*, proposed by Prain (1891) and based on morphological characters, has been evaluated with reference to chemical (flavonoid and some phenolic characters) and phylogenetic (two chloroplast DNA regions; *trnL-F* and *rpL32F-trnL(UAG)* and two nuclear ribosomal regions; ITS and ETS) data. Our results are only partially congruent with those of Prain, and support a combined *Chelonopsis-Bostrychanthera* clade, within which *Chelonopsis* is paraphyletic, and relationships within *Gomphostemma* are further resolved.

Living in paradise: systematics and biogeography of Seychelles amphibians

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Island archipelagos provide good opportunities to investigate evolutionary patterns and processes. The Seychelles archipelago, due to its partly Gondwanan history, harbours recent and ancient endemic amphibians. We investigated genetic variation in (1) a relatively recent endemic, the Seychelles tree frog *Tachycnemis seychellensis* (Hyperoliidae) thought to have arrived in the Seychelles via transoceanic dispersal 11–21 million years ago, and (2) a small ancient endemic caecilian radiation that has been on the Seychelles for at least 65 million years. We generated DNA sequence data for these taxa using multiple mitochondrial and nuclear markers. We found surprisingly low genetic variation in most of the caecilians and the tree frog, even among the different islands, and high variation in two of the caecilians. Comparison of different amphibians and reptiles suggests that diversity within and among Seychelles islands is likely to be influenced by dispersal ability, response to environmental change, and duration of occupancy.

Taxonomic placement of *Ericabatrachus baleensis* (Amphibia: Anura: Ranoidea) and a proposal for inclusion of data in phylogenetic analyses

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Ericabatrachus baleensis (Lagen, 1991) is the only species in its genus and is endangered and endemic to Ethiopia. During a recent field expedition, the species was rediscovered after 25 years. There is great uncertainty regarding its phylogenetic placement in Ranoidea. Previous proposals have tentatively assigned this taxon to the families Petropedetidae, Phrynobatrachidae, Pyxicephalidae, based on morphological evidence. The objective of our study is to resolve the phylogenetic position of this taxon within Ranoidea. We sequenced five molecular markers (12S, 16S, 28S, RAG1 and H3A) to carry out this analysis and combined them with data from previously published works. To account for problems associated with combining genes with such different evolutionary mechanisms we assessed the effect of using different partitioning schemes based on saturation of the different gene partitions and codon positions. Here, we shall present the results of the phylogenetic relationships of *Ericabatrachus baleensis* within Ranoidea.

The effect of long branches on Maximum Likelihood tree reconstruction

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Long branch attraction (LBA), describes a propensity for long branches to be placed together in estimated trees. LBA has been claimed to affect all major phylogenetic reconstruction methods, even statistically based methods such as Maximum Likelihood (ML). Despite the widespread use of the term LBA, its causes and exact nature are poorly understood. Studies of LBA have focused on the effect of two long branches on tree reconstruction. However none have checked the effect of one long branch, a factor that may have an impact on LBA. In this study we look at the effect of one long branch on three-taxon tree reconstruction and show counterintuitive results. We build upon these results to look at the effect of two long branches on four-taxon trees. The results illustrate that small model trees are still useful for understanding phylogenetic methods and that LBA is a complicated phenomenon that deserves further study.

Developing a Maximum Likelihood and Bayesian supertree method

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Supertrees can be used to combine partially overlapping trees and generate more inclusive phylogenies. It has been proposed that Maximum Likelihood supertrees could be developed using an exponential probability distribution to model errors in the input trees (given a proposed supertree). When the tree-to-tree distances used in the ML computation are Symmetric Differences, the ML supertree has been shown to be equivalent to a Majority Rule Consensus supertree, and hence, exactly as the latter, it has the desirable property of being a median tree (with reference to the set of input trees). The ability to estimate the likelihood of supertrees, allows implementing Bayesian MCMC approaches, which have the advantage to allow the support for the clades in a supertree to be properly estimated. We developed the first software for the estimation of Maximum Likelihood and Bayesian supertrees, and used it to reanalyze a variety of datasets including the datasets for the Metazoa, the Carnivora and we also recovered the first Bayesian supertree-based phylogeny of the Eubacteria and the Archaeobacteria. Here, results from these analyses will be presented and properties of these new supertree methods discussed, with reference to other, well-known supertree methods like Matrix Representation with Parsimony.

3ia swims with the fishes: a comparison of 3ia and parsimony phylogenies of Gadiform fishes

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Within cladistics, two methods of phylogenetic reconstruction are implemented: parsimony (in various programs as PAUP) and three-item-analysis (3ia, in the single LisBeth software). Since LisBeth has newly been published (2012), no empirical study allowing for the comparison of parsimony and 3ia has yet been conducted. I present the application of both methods to a set of morphological characters among Gadiform fishes, based on previous works published by Endo (2002). Characters are unordered in Endo's publication (analyze A) and transcribed into hierarchies (rooted trees) in 3ia (analyze B). I also run a parsimony analysis from ordered characters (analyze C). Since hierarchical and ordered characters carry more hypotheses than unordered characters, one could expect for analyses B and C to reconstruct trees that best fit. In order to test this intuition, I suggest a new index allowing for the comparison of trees. I also compare different kinds of summaries (consensus and intersection-tree).

Locked in the bones: the production of a large molecular systematic dataset from museum specimens

OR: Rick's adventure in a deoxyribonucleic acid wonderland

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Due to their taxonomic breadth and relative ease of access, museum collections act as an exceptional repository for morphological information crucial to our understanding of evolution, systematics and taxonomy. Furthermore they provide a vast repository of DNA, which remains largely untapped despite its potential to greatly enhance our understanding of the tree of life. Over the past decade the extraction of DNA from museum specimens has become increasingly commonplace; however, the potential damage to the morphological data, which such valuable and rare specimens were collected to preserve, remains a major obstacle to the exploitation of this resource. Here I review a methodology used to non-destructively sample DNA from 22 distinct genera of insectivoran mammals (Mammalia: Lipotyphla), and the subsequent treatment of this degraded genomic DNA extract to produce a systematically informative dataset for the group. This procedure uses a capture array to enrich the genomic DNA for desired target loci, essentially increasing their representation in the combined sample of all DNA extracts. This enrichment allows the exploitation of high-throughput next-generation sequencing technologies, ultimately enabling the production of roughly a gigabase of raw sequence data from a single sequencing run. If completely successful, this study could produce over 40kb of data for each taxon under study for less than £3000. Such a high yield of data from some obscure mammalian taxa could only be achieved through the use of taxonomically rich museum collections, and will greatly increase our understanding of the lipotyphlan order for a monetary investment well within the capabilities of most researchers.

Foundation Monograph of *Convolvulus*

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As the biodiversity crisis escalates there is an ever-greater need for global treatments of large plant genera, to address the high levels of synonyms and the lack of species identification keys. The Foundation Monograph is proposed as a pragmatic approach to overhaul the taxonomy of large, problematic plant groups. This initial study aims to produce a monograph of *Convolvulus* – a genus of approximately 200 species – in a short timeframe with limited funds, by integrating both traditional and modern resources, with the focus on species delimitation. An overview is presented here of the sequencing success when utilising herbarium specimens and a comparison of the performance of *matK*, *rbcL* and ITS to discriminate species within *Convolvulus*. Also presented are examples of how the molecular data has helped guide taxonomic decisions and how the Foundation Monograph Approach offers a pragmatic solution to the problem of how to accelerate the pace of taxonomy.

Phylogenies reveal predictive power of traditional medicine in bioprospecting

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There is controversy about whether traditional medicine can guide drug discovery, and investment in bioprospecting informed by ethnobotanical data has fluctuated. One view is that traditionally used medicinal plants are not necessarily efficacious and there are no robust methods for distinguishing those which are most likely to be bioactive when selecting species for further testing. Here, we reconstruct a genus-level molecular phylogenetic tree representing the 20,000 species found in the floras of three disparate biodiversity hotspots: Nepal, New Zealand, and the Cape of South Africa. Borrowing phylogenetic methods from community ecology, we reveal significant clustering of the 1,500 traditionally used species, and provide a direct measure of the relatedness of the three medicinal floras. We demonstrate shared phylogenetic patterns across the floras: related plants from these regions are used to treat medical conditions in the same therapeutic areas. This finding strongly indicates independent discovery of plant efficacy, an interpretation corroborated by the presence of a significantly greater proportion of known bioactive species in these plant groups than in random samples. We conclude that phylogenetic cross-cultural comparisons can focus screening efforts on a subset of traditionally used plants that are richer in bioactive compounds, and could revitalize the use of traditional knowledge in bioprospecting.

Species discovery in *Aframomum*

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The current and unprecedented loss of species due to manmade habitat destruction and climate change adds a desperate urgency to the need to describe and conserve the remaining undiscovered species. Our ability to understand, measure and evaluate the extent of this 'biodiversity crisis' is hampered by our lack of knowledge of how many species there are on Earth. Even for 'well-known' groups of organisms such as the seed plants an inventory of all species is yet to be completed. The African genus *Aframomum* (Zingiberaceae) is typical of many large tropical groups in that it has been frequently collected yet largely neglected taxonomically. During this presentation I will review the history of species discovery in *Aframomum* up to the completion of a recent revision, and discuss why the production of taxonomic monographs is more important than ever if we are to complete the inventory of seed plants.

How combining morphological and molecular data improves positioning of fossil taxa in cervid (Ruminantia, Artiodactyla) phylogenies

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A number of successive adaptive radiations since their first appearance in the fossil record 19 million years ago (early Miocene) made cervids the second most diverse family of large living mammals today. Despite their long evolutionary history, many questions regarding intrafamilial phylogenetic relationships remain. Furthermore, only little is known about the relationship of fossil to modern cervids; e.g. is there a stem group among fossil cervids? In this study, morphological data, consisting of 120 craniodental characters and molecular data from fossil and living cervids are compiled for the first time to get more insight into phenotypic and genotypic evolution. Three different optimisation criteria, Maximum Parsimony, Bayesian Inference and Maximum Likelihood, were used for phylogenetic analyses and compared with each other. A more robust placing of fossil taxa on the tree could be observed when molecular and morphological data were combined.

The advantages and challenges to the study of camel spiders (Solifugae, Arachnida)

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Solifugae, commonly known as camel spiders, are a poorly studied meso-diverse arachnid order. Often under-represented in scientific collections and generally overlooked in biodiversity assessments, they can in fact, be impressively diverse, with many new species waiting for decades to be described even in some of the world's most prestigious museums. This group has evolved to be uniquely adapted to arid and desert habitats, and this environmental adaptation makes them very promising. Biogeographically it means they are inhabitants of the land version of the lakes, but also makes them potentially valuable indicators for accessing the advancement of desertification and the impact of global warming. So why do we know so little about them? We will present and debate some of the promising work done with this group in the last decade, including the Global Survey and Inventory of Solifugae:

<http://www.solpugid.com/Global%20Survey%20and%20Inventory.htm>.

Marker incongruence and signal consistency in the hyper-diverse *Heliconius* butterflies (Lepidoptera: Nymphalidae)

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The neotropical butterfly genus *Heliconius* has emerged as a model system for genetics, ecology and evolution, culminating in the publication of the *H. melpomene* genome earlier this year. To understand the relationships between over 40 species, we combine Sanger sequencing, ancient DNA techniques and a novel approach based on de novo assembly of whole genome resequencing data. Our dataset comprises 22 loci sampled from multiple individuals of 63 species of *Heliconius* and allies, balancing alignment length with taxonomic representation. We also present a whole mitochondrial alignment for 31 species. Multiple analyses of individual genes reveal high levels of incongruence between the loci. Despite this conflict, MP, ML and Bayesian phylogenies based on nuclear and whole-mitochondrial supermatrices show nearly identical, well-supported topologies. Multispecies coalescent methods (*BEAST, BUCKy, MDC, MP-EST) produce the same results with lower support, reflecting varied gene histories. This incongruence is further illustrated by a highly reticulate distance network. We suggest that the observed patterns result from incomplete lineage sorting during bursts of rapid speciation and from unusually high levels of gene flow in *Heliconius*. Our study elucidates the history of a novel model system and highlights the relative merits of recently developed phylogenetic techniques.

The *Myosotella* ‘*myosotis-denticulata*’ complex: untying a morphological knot

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Myosotella myosotis (Draparnaud, 1801) is a morphologically highly polymorphic heterobranch gastropod (Ellobiidae). Two forms have, however, long been kept separate: the typical thick-shelled, paucidentate *M. myosotis* and the thin-shelled, denticulate *M. denticulata* (Montagu, 1803). Both forms are common in marshes and among rolled stones above the supratidal. Yet, *M. myosotis* lives more closely to terrestrial habitats, whereas *M. denticulata* prefers exposed habitats near the high tide mark. Both forms live in the Azores, with *M. myosotis* having been described as *Auricula bicolor* Morelet, 1860 and *M. denticulata* as *A. vespertina* Morelet, 1860, both from the same locality in Pico island. Using a holistic approach based on ecological, morphological, anatomical and molecular data we attempted to assess the taxonomic status of both forms. Preliminary results suggest the separation of the European *M. myosotis* and *M. denticulata*, whereas the two Azorean forms refer to one endemic species. However, evidence points to additional species in the Azores.

Deep molluscan relationships: Reconciling morphology and molecules

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The molluscs are the second most diverse animal phylum, but their origin is poorly constrained. Morphological studies suggest a stepwise evolution from the shell-less Aplacophora, via the armoured slug-like Polyplacophora, to more familiar shell-bearing Conchifera such as clams, snails, and cuttlefish. Molecular studies instead group the worm-like Aplacophora and Polyplacophora into a clade, “Aculifera”, the sister group to Conchifera. A new supermatrix of 965 morphological characters addresses this dilemma. Analysis using parsimony methods upholds the traditional morphological hypothesis. But Bayesian analysis – the preferred method of molecular systematists – recovers the “molecular” topology. The analytical methods, rather than the data themselves, seem to be responsible for the divergence between morphological and molecular trees. I argue that the morphological hypothesis represents an artefact of parsimony methods, not the molluscs’ true evolutionary history. As such, the “Aculiferan” hypothesis now finds support from both morphological and molecular datasets. Regrettably, its balanced topology means that extant taxa do little to constrain early molluscan evolution. The inclusion of exceptional soft-bodied fossils from the earliest periods of molluscan evolution makes it possible to directly constrain the ancestral molluscan body form and the origins of the modern molluscan groups.

POSTER ABSTRACTS

1. *Galium glaucum* group cline - vicariant species or illusion?

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Gaps in morphological or genetic variability call for taxonomic level interpretation. These interpretations are sometimes far from being satisfactory. For example two vicarious species in the *Galium glaucum* group, *G. hexanarium* Knjazev and *G. octonarium* (Klokov) Pobed., show the morphological variability gap in the Ciscaucasia region. This phenomenon was known from 19th century, yet morphology and climatic variability comparison reveal a high level correlation. Moreover, climatic-based models have a higher percentage of explained variability than geographic-based. There is a common cline along climatic gradients for both "species". The gap in morphological variability is an artifact of bedstraw's geographic distribution and climatic gradient direction change in the Ciscaucasia region. That variability gap does not imply the existence of a taxonomic border.

2. A database for a lichen collection from Sardinia (Italy)

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A database is an important tool for managing information on the specimens kept in natural history collections. The data gathered give not only information on specimens but also on the flora of a region and on its changes through space and time. The University of Sassari has created a database for the lichen specimens kept in SS herbarium. GBIF-2001, TDWG-2007 guidelines and the nomenclature as in Cabi Bioscience (2012) were followed. The database contains data on over 3,580 samples belonging to 360 lichen taxa, and it is going to be used for managing information on other organisms as well. The following fields were selected: taxon, organism type, State, municipality, locality, geographical coordinates, collecting date, substratum, collector, determinavit, herbarium code, determinavit code, picture, notes. Data are constantly updated to include information on new collections and it is aimed to provide an online search interface soon.

Biodiversity Information Standards – TDWG, 2007. <http://www.tdwg.org/Cabi>.

Bioscience Species Fungorum, 2012. <http://www.speciesfungorum.org/>.

Global Biodiversity Information Facilities – GBIF, 2001. <http://www.gbif.org/>.

3. Systematic placement of the the Egyptian *Salvia* L. (Lamiaceae) species.

Achmed El-Banhawy

Ahmed El-Banhawy^{1,2}, Alastair Culham¹, El-Sayda Gamaleldin² & Wafaa Kamel²

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Large genera such as the widely distributed *Salvia* (≥ 950 spp.) are challenging subjects for the systematist. To study a geographically defined subset of the species is common practice but often does not allow assessment of whether the geographic group is a natural or monophyletic group and this limits the conclusions that can be drawn. Preconditions for such studies are a broad taxonomic knowledge of the group and a well-supported phylogeny, if the species are to be put in proper context. The present project is a part of an international collaboration involving Reading University, UK, and Suez Canal University, Ismailia, Egypt to reconstruct evolutionary tendencies in the assumed 350 Old World *Salvia* spp., with emphasis on the Mediterranean species. The molecular phylogenetic work has been done in UK, while taxonomic and phenotypic data were completed in Egypt. In Egypt 9–10 *Salvia* species are known. However, almost nothing is known about their biology, i.e. their habitat conditions, adaptation to environmental constraints and phylogenetic tendencies. Thus, the aims of the project are to a) establish the phylogenetic position(s) of *Salvia* in Egypt, b) to collect phenotypic and ecological data and c) to reconstruct the speciation events within this geographic group. Here the placement of the Egyptian species in a broader phylogeny of *Salvia* is presented based on phylogenetic analyses of chloroplast *psb-A*, *trnL-F* and the nuclear ITS sequence data.

4. Planktonic dispersal suggests a homogeneous genetic structure over large geographic scale. Is it mandatory?

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Marine invertebrates with planktonic-dispersing larvae are assumed to be good dispersers over long distances. This high dispersal capacity implies a high gene flow between populations and a homogeneous population genetic structuring over wide geographic scales. The marine gastropod *Melarhaphe neritoides* has a long-lived planktonic larval dispersal stage and allozyme data suggest that it is genetically homogeneous over its whole European distribution area. In contrast, preliminary mtDNA sequence data uncovered a remarkable degree of genetic diversity and genetic structuring on smaller geographic scales. In order to explore this mtDNA diversity and structuring in *M. neritoides* we started to survey sequence variation at COI and 16S rDNA all over the Azores archipelago. These data reveal that the Azorean populations share very few haplotypes. Hence, it seems that *M. neritoides* with its long-lived planktonic larval stage nevertheless shows a strong local population genetic structuring and thus challenges the current paradigm that correlates modes of larval development with levels of genetic structuring. It also stresses the importance of the sampling intensity (both in terms of numbers of specimens and genetic markers) to avoid experimental biases when assessing genetic diversity.

5. A new checklist and analysis of thirty plant families from the Libyan flora

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The Libyan flora is currently recorded in a series of volumes published between 1911 and 1977. Since then there has been substantial realignment of family boundaries and the discovery of new species. Due to the fact that no update or revision has been conducted in the Libyan flora since (1977-1980), this suggests that the Libyan Flora is out of date and requires reassessment using modern technologies so that current estimates of biodiversity can be made and that the conservation status of species can be estimated. Here we report initial efforts to provide an updated checklist covering 30 families, 138 genera and 210 species. The families Tiliaceae, Sterculiaceae, Bombacaceae, Guttiferae, Coridaceae, Vahliaceae, Leonticaceae, Violaceae and Illecebraceae have been updated and included in their current places in APGIII. Four families are now recorded in the Libyan Flora for the first time. This work forms the first part of the development of a toolkit to guide studies of Libyan floristics.

6. Monophagous gall midges on reed (*Phragmites australis* (Cavan) Trin ex Steudel)

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Decay of reedy areas is a problem known worldwide. There have been only a few studies carried out in Hungary investigating the arthropod fauna of reeds. One of our aims was to describe the gall midge species which has been already found by our former colleagues and, in addition, to get to know the harmful Diptera species on reed. This unnamed gall midge may cause 20–50% all damage on reeds. It causes problems especially in closed reed-beds 50–60 meters from coastal areas. One of the most serious problems caused by this species is that the damaged plant does not grow a panicle. Galls containing larvae and pupae were also discovered at the beginning of August 2011 so two generations per year may be possible. *Platycephala planifrons*, *Giraudiella inclusa* and some *Lipara* spp. were also found in this area.

7. Biogeography and the origins of sinistral land snails

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Evolution of whole-body left-right reversal in snails is generally a compelling example of non-adaptive speciation, because variants with reversed chirality would suffer from reduced mating opportunities within a population. Despite this reproductive disadvantage, sinistral snail species have repeatedly originated from dextral ancestors in terrestrial pulmonates. Analysing the global biogeography of 995 genera across 84 stylommatophoran families, I found that snail speciation by reversal has been accelerated on oceanic islands and in the geographic range of pareatid snail-eating snakes. Because oceanic islands are relatively small land masses offering highly fragmented habitats for snails, they may have facilitated the fixation of the non-adaptive allele for speciation by reversal. In contrast, sinistral variants would have enjoyed survival advantages under "right-handed" snake predation. This study illustrates that a speciation gene can be fixed in populations by positive pleiotropic effects on survival and by genetic drift in small populations.

8. Isolating genomic DNA from *Lagenophrys tattersalli* (WILLIS, 1942): a new insight into lagenophryid taxonomy.

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Lagenophrys tattersalli (Ciliophora: Peritrichia) was observed attached to the marine amphipod *Echinogammarus marinus* in great numbers as part of a wider study into the parasite ecology. Lagenophryids belong to a genus of loricated, suspension feeding ciliates consisting of approximately 71 described species, all of which form obligate ectocommensal associations with marine, freshwater and terrestrial crustaceans. Subcellular anatomy, particularly the morphology of the pseudochitinous lorica, is used to classify lagenophryid species; however the molecular taxonomy of this genus is under-represented by comparison to other peritrich taxons. During the present study, scanning electron microscopy was used to identify *L. tattersalli* before a 742bp fragment of the 18S small subunit RNA gene was isolated and sequenced from the infestations attached to the gills of *E. marinus*. A preliminary analysis based on available sequences in the GenBank database indicates that lagenophryids are closely related to the peritrich genera *Usconophrys* and *Myoschiston* respectively.

9. Exploring species delimitation methods based on DNA barcoding in the land snail genus *Rumina* (Gastropoda: Pulmonata)

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Species is a universally accepted term, but there is still no generally accepted species concept applicable to all organisms. The present study aims to compare several species delimitation methods in the facultatively selfing terrestrial pulmonate snail genus *Rumina*. To this end, we first evaluated to what extent phenotypic differentiation in *Rumina* reflects evolutionary divergence that can be interpreted under a phylogenetic species concept, by performing a phylogenetic analysis of mitochondrial DNA (COI, CytB, 12S rDNA, 16S rDNA) sequences. These results yielded a priori haplotype groupings, which then were subjected to several species delimitation methods using COI only: (1) classical DNA barcoding gap analysis, (2) the Automatic Barcode Gap Discovery, (3) the species delimitation plug-in of the Geneious software, (4) the Genealogical Sorting Index, and (5) the General Mixed Yule Coalescent model. The different methods were compared with respect to their ability to delimit putative species within this dataset.

10. Patterns of diversification among the Hexapoda

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Our understanding of the patterns of diversification in the insects and their relatives have hitherto been limited by a lack of phylogenetic resolution and the absence of a suitable historical framework for the group as a whole. The aim of this project is to combine the recent expansion in molecular data with improvements in the fossil record and novel diversity modeling techniques in order to achieve fresh insights into the processes driving hexapod diversity. The impact of fossil data treatment on the apparent pattern of diversification will also be explored. The work presented here uses a draft family level tree and aims to explore the patterns leading to differences in the diversity of higher taxa and the application of alternative diversification paradigms to this highly diverse group.

11. The fossil continental mollusks from Sandelzhausen (Miocene, Germany)

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Sandelzhausen is a Miocene Lagerstätte in southeastern Germany and, despite its small size, harbours a rich and well-preserved fossil record, in which the mammals and continental mollusks are the highlight. The majority of the mollusks (tentative identification indicates ~70 species) is composed of pulmonate gastropods. This fauna was discovered in the 1960's, but the mollusks never received due attention: so far they do not even have their alpha taxonomy established. Sandelzhausen's fauna has great potential for many lines of work, however the first and foremost step is taxonomy. Therefore, our current project aims to formally describe all fossil mollusks from Sandelzhausen. Moreover, with a proper taxonomic knowledge, we also intend to improve the paleobiogeographic knowledge of its families and genera, as well as refine previous paleoecological/paleoenvironmental works. As Sandelzhausen was an ancient lake environment, the occurrence of different freshwater species along the formation's facies holds much promise for evolutionary studies.

12. The widely used small subunit 18S rDNA molecule greatly underestimates true diversity in biodiversity surveys of the meiofauna

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Environmental barcode studies (eDNA) are increasingly popular for surveying biodiversity. Most eDNA surveys use the 18S rDNA gene as a marker; however, different markers and metrics used for delimiting species have not yet been evaluated against each other or against morphologically defined species. We assessed more than 12,000 meiofaunal sequences of 18S and of the main alternatively used marker COI mtDNA and show that 18S reduced diversity estimates by a factor of 0.4 relative to morphospecies, whereas COI increased diversity estimates by a factor of 7.6. Moreover, estimates of species richness using COI were robust among three of four commonly used delimitation metrics, whereas estimates using 18S varied widely with the different metrics. We recommend against using 18S as a marker for biodiversity surveys and suggest that use of COI for eDNA surveys could provide more accurate estimates of species richness in the future.

13. Taxonomic revision of the genus *Rostraria* (Poaceae)

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A comprehensive taxonomic revision of the genus *Rostraria* is presented. This treatment is based on observation of specimens from main herbaria (K, W, FI, MPU, PRC, MA, SEV, VAL, PI, K, SS), comparative study of morphological characters on these specimens by means of the analysis of their biometric variables, and, finally, the critical study of diagnostic characters of the described taxa. A key of the genus, description, distribution maps, habitat, chromosome number and an illustration for each species are provided.

14. Preliminary key for the oriental genera of Ozophorini (Insecta, Heteroptera, Rhyparochromidae)

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True bugs (Heteroptera) are among the largest groups of hemimetabolous insects, with approximately 37,000 described species. Many of the species feed on seeds, although many suck on plant leaves or are predators, and others feed on blood. In general they live on the ground or on plants, or in the forest litter. In Heteroptera the seed bug family Rhyparochromidae is represented by 14 tribes and about 1950 species. The Oriental region is the least investigated area of the seed bugs. The Rhyparochromid tribe Ozophorini contains species from all over the world. These animals are living on plants and feed on sap. Most of these species live in tropical America and South-Eastern Asia. We are working on the Oriental genera of this group. The genera belonging to Ozophorini are very diverse, but some of them are similar to each other. Revisions for some genera are ready yet, for example Slater and Zheng work on *Primierus* group. During our study of this group we made descriptions of new species and now the key for the genera.

15. A molecular approach to assessing the genus and species boundaries of the calcicolous lichen genus *Bagliettoa*

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Rock-inhabiting fungi are of significant interest because of their involvement in the deterioration of historically and culturally important monuments. Among these fungi is the genus *Bagliettoa* (Verrucariaceae), comprising a group of lichenized fungi that exclusively colonizes limestone surfaces and causes biopitting due to its endolithic growth form. This genus was recently resurrected for a group of eight endolithic species of *Verrucaria* based on molecular data. However, the type species *Bagliettoa limborioides* had not been included in previous studies. Moreover, the taxon sampling did not allow for testing species boundaries within the genus. In this study, specimens of *Bagliettoa* were collected from Southern France, Wales and the south of England and all known species of *Bagliettoa* including the generic type (*B. limborioides*) were represented. Specimens were morphologically identified and the ITS region was used to reconstruct the phylogenetic relationships between these taxa. Molecular data confirmed the placement of *B. limborioides* within the genus and supported the morphological-based delimitation of *B. cazzae*, *B. calciseda*, *B. limborioides* and *B. marmorea*. The high genetic variation found among specimens of *B. marmorea* suggests that this taxon might represent two cryptic species. For other species (*B. parmigera*, *B. baldensis*, *B. steineri* and *B. parmigerella*), the morphology-based delineation was not confirmed and further work will be needed to characterize these species.

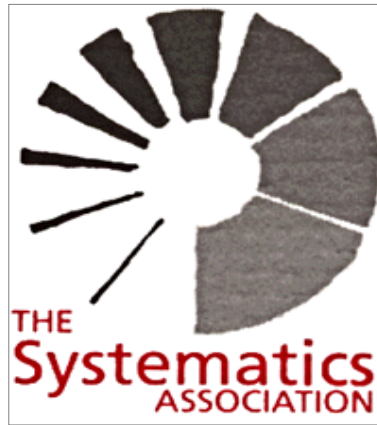
16. New Lethaeini genus (Insecta, Heteroptera, Rhyparochrominae) from the Oriental region

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The Lethaeini were recognized as an independent tribe in 1872 by Stål. It is currently part of the family Rhyparochromidae. Slater (1964) and Slater and O'Donnell (1995) listed 36 genera in this group. These insects can be found mostly in the tropical regions, therefore they are underrepresented in the Holarctic region. Today there are about 170 known species in the group. In the last fifty years, there were very few works about the Lethaeini of the Oriental region. The most recent work about these insects was the publication of Li et al. (2011) which reviewed the Chinese genera and species. Our work focuses on the Oriental region, and that is how we came across some specimens, which resemble no described genera. The almost even pronotal puncturation and the wide lateral margin on the pronotum is different from the described species. The examined specimens are from India, Vietnam, Laos and Thailand.



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