

# YOUNG SYSTEMATISTS' FORUM

29<sup>th</sup> November 2013, Flett Theatre, Natural History Museum, London, UK

08:30-9:30	<b>Registration</b>	<b>(Please put up posters as early as possible from 08:30)</b>
09:30	<b>Welcome, opening remarks</b>	<b>Robert Scotland, SA President and YSF team</b>
09:40	Viviana Peña	Alpha species diversity of Coralline algae: numbering species based on molecular data
09:58	Kevin Gori	Clustering Genes by Phylogenetic Similarity
10:16	Arash Sotoodeh	Molecular phylogeny of Turkish and Iranian <i>Artemisia</i> using ITS and ETS
10:34	Manja Voss	Revision of the Halitheriinae and a new classification concept for the order Sirenia (Mammalia)
10:52	<b>Coffee and attended posters (even numbers)</b>	
11:30	Konstantinos Angelis	Bayesian estimation of the nonsynonymous/synonymous rate ratio and sequence distance between two protein-coding sequences
11:48	Patrícia dos Santos	Floral development of <i>Lewisia</i> Pursh (Montiaceae) investigating patterns of perianth and stamen diversity
12:06	Amr Aswad	Paleovirology and metagenomics reveal hidden biodiversity in genome data
12:24	Elisabeth Biersma	Evolutionary History of the Antarctic Flora
12:42	Jing-Wei Yap	Patterns of introgressive hybridisation and putative homoploid hybrid speciation in the evolution of the Malesian slipper orchids ( <i>Paphiopedilum</i> section <i>Barbata</i> )
13:00	<b>Lunch and poster session</b>	<b>(Light lunch provided for registered attendees)</b>
14:00	Sofia Hauck	Multilocus sequence typing whole genome analysis of <i>Bordetella</i> species
14:18	Maxim S. Nuraliev	Towards a phylogenetic system of the Asian <i>Schefflera</i> Clade (Araliaceae): revealing taxonomically significant morphological characteristics
14:36	Antonia G. Ford	Diversification of East African soda lake cichlids
14:54	Thomas Dejado	Integrative species delimitation reveals complex evolutionary history in Alpine jumping bristletails
15:12	<b>Tea and attended posters (odd numbers)</b>	
15:50	Fouad el Baidouri	The <i>Leishmania</i> genus: genetic structure and evolutionary mechanisms
16:08	Joanna Baker	Detecting Cope's rule in extant mammals
16:26	Orlando Schwery	The influence of leaf traits and mountain association on species richness in Ericaceae
16:44	María Camila Gómez-Gutiérrez	Speciation in the high-altitude Páramo ecosystem
17:02	Konstantin B. Gongalsky	An inventory of woodlice (Crustacea, Isopoda, Oniscidea) fauna of the former USSR
17:20	<b>Poster session</b>	
18:00-19:00	<b>Reception</b>	<b>Presentation of prizes, closing remarks</b> Robert Scotland, President of the Systematics Association and YSF team, reception in the NHM Gallery "From the Beginning" (Evolution through Time Fossil Gallery)

Organised by Ellinor Michel (Dept. Life Sciences, NHM), Maria Vorontsova (RBG Kew), Jane Droop (RBG Edinburgh) & Xavier Aubriot (NHM), with support from:



# TALK ABSTRACTS

## Alpha species diversity of Coralline algae: numbering species based on molecular data

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Coralline algae represent an outstanding group of marine benthic algae. The high phenotypic plasticity has led to many descriptions of new species. Nowadays, Corallinales is one of the most diverse orders of red algae, with 1600 taxa proposed of which 600 are currently recognized as valid names. The advent of molecular systematics has unravelled cryptic diversity within this order and enabled the analysis of phylogenetic relationships among species. In particular, the use of DNA barcoding has propelled molecular systematics of the Corallinales world wide. we provide an estimation of the coralline species diversity at global and regional scales, based on both COI-5P sequences available in GenBank and BOLD as well as our own data. The generalized mixed Yule-coalescent model is applied for the species delimitation. The results obtained are compared with the species diversity previously reported in the literature.

## Clustering Genes by Phylogenetic Similarity

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Abundant sequence data has the potential to make phylogenetic inference more accurate through the analysis of multiple loci at once. However, if the loci do not share the same history due to events such as horizontal gene transfer, it is misleading to only report a single tree. I will present a method, called treeCl, that uses clustering and maximum-likelihood inference to infer a number of trees summarising the various evolutionary histories present in multi-locus data. I show a means of visualising distributions of trees in tree-space, an assessment using simulation of the accuracy of the clustering methods used by treeCl, an optimiser framework to improve upon an initial result, and a means of determining the number of clusters. I apply the method to a set of yeast transcription factors.

# Molecular phylogeny of Turkish and Iranian *Artemisia* using ITS and ETS

Arash Sotoodeh<sup>1</sup>, Murat Kürsat<sup>2</sup>, Semsettin Civelek<sup>3</sup>, Farideh Attar<sup>4</sup>, Céline Pelissier<sup>1</sup>, Kamuran Aktas<sup>5</sup> & Laure Civeyrel<sup>1</sup>

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*Artemisia* belongs to Asteraceae, and comprises about 500 taxa. The centres of diversity of *Artemisia* are in the Northern hemisphere, in the temperate and cold regions of Eurasia, North America and Asia. The genus is divided into subgenera or sections depending on authors: *Absinthium*, *Artemisia*, *Dracunculus*, *Seriphidium*, *Tridentatae*. We have sampled all known taxa from Turkey (26) and Iran (22), and we sequenced both ITS and ETS. The sequences were incorporated into a large phylogeny based on published sequences from Genbank. The Iranian and Turkish species of *Artemisia* belongs to four subgenera, but the majority of them are in subgenera *Artemisia* or *Seriphidium*. The evolutionary history of these two subgenera is different: Iranian and Turkish species in subgenus *Artemisia* have a long history with accumulation of mutations, whereas species in subgenus *Seriphidium* have known a very rapid radiation and are hardly distinguished from each other with ITS and ETS data.

## Revision of the Halitheriinae and a new classification concept for the order Sirenia (Mammalia)

Manja Voss

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Sirenia, or sea cows, are a group of mammals that re-adapted to aquatic lifestyles more than 50 Ma ago. Their monophyly is well corroborated, but the higher-level phylogeny and systematics consider mostly paraphyletic groups, which accordingly lack reliable definitions. Sirenians are conventionally divided into the extinct “Prorastomidae” and “Protosirenidae”, and the “Dugongidae” and Trichechidae with extant representatives. Paraphyly specifically refers to the extinct dugongid subfamily “Halitheriinae”. Revising this group resulted in the hitherto most comprehensive phylogeny of Sirenia. Though homoplasly based, the main nodes of this phylogeny are well supported by often more than one synapomorphy, good bootstrap values, and biogeographic data. As there have been made very few changes to the traditional classification, the taxonomic concept for the whole order is revised and expanded promoting amongst others a consequent differentiation between a paraphyletic stem group and a monophyletic crown group. The crown group is thereby further subdivided.

## **Bayesian estimation of the nonsynonymous/synonymous rate ratio and sequence distance between two protein-coding sequences**

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The nonsynonymous/synonymous rate ratio ( $\omega = dN/dS$ ) is an important measure of the mode and strength of selection acting on protein-coding genes. The simplest analysis is the estimation of the  $\omega$  ratio and the distance ( $t$ ) between two sequences with both counting methods and maximum likelihood (ML) method based on a codon substitution model widely used. However, these methods do not have nice statistical properties, as the estimates can be zero or infinity in some datasets, so that their means and variances are infinite. In large genome-scale comparisons, such extreme estimates of  $\omega$  and  $t$ , are common. We implement a Bayesian method to estimate  $\omega$  and  $t$  in pairwise sequence comparisons. A combination of computer simulation and real data analysis, shows that the Bayesian estimates have better statistical properties than the ML estimates, because the prior on  $\omega$  and  $t$  shrinks the posterior of those parameters away from extreme values. The new method is computationally efficient and may be useful for estimation of  $\omega$  and  $t$  in genome-scale comparisons of protein-coding sequences.

## **Floral development of *Lewisia* Pursh (Montiaceae) investigating patterns of perianth and stamen diversity**

**Patrícia dos Santos**

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The Portulacinae (Portulacaceae sensu lato) is a clade of Caryophyllales whose members share a bipartite perianth consisting of two outer median bracteoles and usually five petaloid organs. *Lewisia* (Montiaceae) is a peculiar group genus among the Portulacinae considering the floral ontogeny, particularly the development of the perianth and androecium. Unlike other taxa, the petaloid perianth of this group seems to be derived from two different kinds of tepals but has the same appearance at maturity. The growth pattern of the outer tepals is similar to other related groups and alternate with the two median bracteoles. However, the inner tepals arise much later than the outer tepals and tend to be variable in position and number. We studied the floral development of seven species of *Lewisia* to understand the reasons for this divergence between outer and inner tepals. Different options are analysed as to whether outer and inner tepals are morphologically distinct, or whether differences are related to genetic influences of neighbouring organs during development.

# Paleovirology and metagenomics reveal hidden biodiversity in genome data

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*Herpesviridae* is a family of DNA viruses that have characteristically large and complex genomes. This defining feature is also why sequencing difficulties and considerable bioinformatic challenges complicate Herpesvirus genomics. This is coupled with a need to explore Herpesvirus diversity, by increasing the rate of viral discovery in order to understand pathogenesis within an evolutionary context. Using methods intended for the identification of endogenous viral elements, and combing them with perspectives from metagenomics, we identify three Herpesviruses within the genome data of their primate hosts. All three viruses are closely related to important human pathogens and two of them are entirely new species. Both comparative molecular biology and evolutionary analysis were applied to examine our results for their clinical relevance and to delineate their taxonomy. Furthermore, we demonstrate how this analytical approach was also used for the data collection itself, by treating nucleotide databases in their entirety as a single metagenomic resource.

## Evolutionary History of the Antarctic Flora

Elisabeth Biersma<sup>1,2</sup>, J. Jackson<sup>1</sup>, K. Linse<sup>1</sup>, H. Griffiths<sup>2</sup> & P. Convey<sup>1</sup>

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Ice sheet reconstructions suggest that thick ice sheets covered most terrestrial areas of Antarctica during the Last Glacial Maximum (LGM; ~22–18 ka), as well as during previous glaciations. This suggests that most contemporary biota must have (re-)colonised Antarctica since the LGM. However, recent biogeographic research suggests that much of the contemporary terrestrial biota has a long-term history in situ in Antarctica, with timescales of persistence ranging through pre-LGM to Gondwana-breakup (~65 mya). Mosses, a major component of the Antarctic flora, currently stand distinct from these patterns. Their low endemism levels (5-10%) and distribution patterns suggest today's moss biota are recent colonists. Alternatively, the evolutionary divergence processes may be very slow in mosses, making it difficult to observe a possible long-term persistence on Antarctica. Results of population structure and phylogenetic relationships of several target moss species are presented, giving an insight into the evolutionary history and origin of Antarctic mosses.

# Patterns of introgressive hybridisation and putative homoploid hybrid speciation in the evolution of the Malesian slipper orchids (*Paphiopedilum* section *Barbata*)

Jing-Wei Yap<sup>1,2</sup>, Laura J. Kelly<sup>1,2</sup>, Andrew R. Leitch<sup>2</sup>, Ilia J. Leitch<sup>1</sup>, Lee Yung-I<sup>3</sup>, Jutta Babczinsky<sup>4</sup>, Günter Gerlach<sup>4</sup>, Bert Kline<sup>1</sup> & Mike F. Fay<sup>1</sup>

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The *Paphiopedilum* (Cypripedioideae: Orchidaceae) are an early diverging group of terrestrial orchids for which homoploid hybrid speciation is suspected on the basis of morphological data. We use sequence data from the low-copy nuclear gene *Xdh* and four plastid [*psaAycf3ex*, *trnF(GAA)-ndhJ*, *matK*, *ycf1*] regions and sampled multiple-individuals per taxon to evaluate the phylogenetic relationships within *Paphiopedilum* section *Barbata*, a biologically diverse and the most derived section of *Paphiopedilum*, to test the hypothesis that hybridisation plays a role in speciation processes in *Paphiopedilum*. We uncovered signals of phylogenetic incongruence as early molecular evidence for historical and on-going hybridization in the evolution of *Paphiopedilum* section *Barbata*. This research has improved phylogenetic resolution between *Barbata* taxa and illustrates the importance of using extensive sampling and multiple independent assorting loci when using phylogenetic data for analysing species relationships.

## Multilocus sequence typing whole genome analysis of *Bordetella* species

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Despite widespread vaccination and low diversity, *Bordetella pertussis* remains endemic globally, and recent pertussis outbreaks have included other *Bordetella* as co-infections and co-occurring outbreaks. To examine the relationships between species of the *Bordetella* genus and changes to the *B. pertussis* genome over time, 102 genomes were analysed using two multilocus sequence typing (MLST) schemes, one based on universal ribosomal genes and another on the core *Bordetella* genome. The two analyses showed similar topology, supporting the ribosomal scheme as representative of the whole genome, and confirming the usefulness of the MLST method as a scalable, backwards compatible and phylogenetically consistent microbe identification system. *B. bronchiseptica* was shown to be polyphyletic, forming three groups that may be separate species. The clonality of *B. pertussis* was confirmed. *Bordetella* species appeared to have evolved to infect human hosts independently at least three times, most recently perhaps to fill the niche that vaccination has emptied.

# Towards a phylogenetic system of the Asian *Schefflera* Clade (Araliaceae): revealing taxonomically significant morphological characteristics

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The Asian *Schefflera* clade represents a recently recognized monophyletic group within the family Araliaceae. The taxonomic status of this clade and its delimitation are to be developed during the ongoing revision of the family. Basing on original ITS molecular phylogenetic analysis, we have examined the diversity and evolution of several previously suggested or newly investigated morphological characters for usefulness in the description of subgeneric taxa within the genus *Schefflera*. We found a single character (lamellate or entire stem pith), that is congruent with subdividing of the Asian *Schefflera* Clade into two subclades. Several other features show more complicate and often homoplastic evolution, but can be used in combination for describing minor groups of species within the subclades. These features include the type of partial inflorescence and floral merism which were traditionally used for delimitation of sections and even genera within the *Schefflera* s.l. complex.

## Diversification of East African soda lake cichlids

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Cichlid fishes have radiated in many freshwater lakes; however, uniquely they have also colonised the East African soda lakes (Lakes Natron and Magadi). The *Alcolapia* species flock includes three sympatric species in Lake Natron (*A. alcalicus*, *A. latilabris*, *A. ndalalani*) and a further species (*A. grahami*) restricted to Lake Magadi. Here, we aim to characterise this radiation to investigate whether colonisation and speciation occurred in ancestral freshwater conditions or more recently, in hypersaline conditions. Stable isotope analysis indicates trophic niche segregation between *A. alcalicus* and other species at sympatric sites, and geometric morphometric analysis demonstrates significant morphological differences between all described species. However, phylogenetic analysis using mtDNA failed to resolve species relationships, and analysis of genome-wide variation using RAD-Seq data reveals shallow divergences between species, indicating a young radiation with large ecological and morphological diversification. Methods for dating the divergence will be examined in testing between alternative colonisation scenarios.

# Integrative species delimitation reveals complex evolutionary history in Alpine jumping bristletails

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Jumping bristletails (Order Microcoryphia) are a heavily understudied group of wingless insects. Filling the phylogenetic gap between basal hexapods and winged insects, they are eligible to address important questions in insect systematics and evolution. Here, we focus on the genus *Machilis*, which underwent a recent radiation in European alpine regions – possibly influenced by Pleistocene climatic oscillations. Species limits in this genus are currently based on questionable phenotypic characters, thus hindering the species' use in biological research. We sampled specimens from 26 nominal species throughout the Eastern Alps and applied morphometrics, karyotyping, genome-size measurements and mitochondrial and nuclear markers to infer their speciation history. In doing so, we were able to 1) redefine species limits of previously unknown or wrongly delimited species and, 2) get a glimpse on their evolutionary history including hybridisation, polyploidisation and parthenogenesis, all of which likely have contributed to speciation events in this genus.

## The *Leishmania* genus: genetic structure and evolutionary mechanisms

Fouad el Baidouri<sup>1</sup>, Laure Diancourt<sup>2</sup>, Vincent Berry<sup>3,4</sup>, François Chevenet<sup>3,4,5</sup>, Francine Pratlong<sup>6</sup>, Pierre Marty<sup>7</sup>, Christophe Ravel<sup>6</sup> & Stuart Humphries<sup>1</sup>

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The mechanisms of genomic and genetic evolution in the *Leishmania* order, a protozoan group that contains about twenty pathogenic species, are the focus of much debate. Although these parasites have been considered for years to reproduce clonally, recent research has demonstrated both experimental and *in natura* intra- and inter-specific hybrids. Interspecific exchanges should be sources of plasticity and adaptation to new parasitic cycles. In this work we used a MultiLocus Sequence Analysis approach to analyse 222 *Leishmania* strains that belong to different species and were isolated in African and Eurasian foci. This analysis classified the different strains in seven robust genetic clusters that showed remarkable congruence of the phylogenetic message between them. From a taxonomic point of view, the seven clusters overlapped with most of the biochemical taxonomic groups currently in use, except for species causing visceral



forms of leishmaniasis. Contrary to what was expected, we did not detect traces of interspecific recombination and genetic exchanges between the different species. Finally, these results should have consequences on the taxonomy, on our understanding of the epidemiology and on the therapeutic management of these infections.

## Detecting Cope's rule in extant mammals

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The tendency for species to increase throughout geological time, termed Cope's rule, is a phenomenon which has received much attention in the literature. Paleontological evidence for Cope's rule exists in a number of taxonomic groups, but the most robust support for this controversial idea is provided by the fossil record of mammals. Despite this, studies using extant data have failed to provide any support for Cope's rule across any group examined, including mammals - in stark contrast to results from the fossil record. Here we take a novel phylogenetic approach to studying Cope's rule in extant mammals that does not assume homogenous rates of morphological evolution. Contrary to some previous suggestions, we show that it is possible to uncover evolutionary trends using only extant data. Our results show that patterns in body size evolution can be inferred from extant mammals and are in line with both Cope's rule and fossil evidence.

## The influence of leaf traits and mountain association on species richness in Ericaceae

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Angiosperm diversity is unevenly distributed across lineages, but the factors that affect changes in a lineage's diversification rate are not yet well understood. Here, we hypothesise that the interaction of functional leaf traits and habitat can influence diversification rate. We investigate this question in the Angiosperm family Ericaceae, which has a worldwide distribution with around 4000 species in various habitats from sea level to >5000 m elevation. We predict that the interaction of low specific leaf area (SLA) and the environmental conditions of mountain habitat might be correlated to accelerated diversification rate in the respective lineages. A molecular phylogeny based on *rbcl* and *matK* sequence data was built and dated using fossil calibrations and molecular clock estimates. Using a variety of methods, the relations of trait and habitat states and diversification rates were investigated. Our results suggest that ecological opportunity and phenotypic adaptation are important drivers of diversity.

## Speciation in the high-altitude Páramo ecosystem

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Páramo is a unique Neotropical high-altitude ecosystem with an island-like distribution along the mountain tops of the northern Andes mountain range. Its likely young geological age and extremely high plant diversity makes it a suitable model for studying plant phylogeography so as to elucidate the patterns and processes behind speciation. Representatives of its flora were selected based on their distribution patterns, different life histories and the fact that a dated phylogeny exists: *Castratella piloselloides* (Melastomataceae), and the five species within the American clade of *Oreobolus* (Cyperaceae). Preliminary results for two chloroplast markers (*trnL-F* and *trnH-psbA*) and one nuclear region (ITS) have been obtained while other markers still under test, in the search for highly variable intra-specific ones. Measures of genetic diversity will be performed as well as tests related to demographic history, geographic structure and population history.

## An inventory of woodlice (Crustacea, Isopoda, Oniscidea) fauna of the former USSR

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An inventory of woodlice fauna of the former USSR yielded in 192 species. The most species-rich genera are *Armadillidium* (11 species), *Cylisticus* (16), *Hemilepistus* (16), *Ligidium* (11), *Protracheoniscus* (39), and *Trachelipus* (13). According to cartographic analysis, the distribution of free-living terrestrial isopods over the areas excluding mountains is explained by the temperature. No woodlice records were found outside the isoline of 120 days a year with the temperature above 10°C. The major species diversity was found between the isolines of 180 and 210 days. These areas correspond to forest-steppe and steppe zones.

## POSTER ABSTRACTS

1.

### **Angiosperm Divergence Times: a phylogenetic analysis of genome-scale data sets**

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The explosive increase of molecular sequence data has produced unpredicted opportunities for addressing a number of evolutionary problems. For my PhD research project we are exploring the use of molecular sequence data, combined with statistical summaries of the fossil record, to date species divergences. In particular we are examining the origin and divergences of angiosperms, and attempt to resolve the apparent conflict between the molecular dates and fossil evidence. The project involves compilation of sequence and fossil datasets and phylogenetic analysis of genome-scale datasets.

2.

### **Historic and new collections: complementary data reveals ‘hidden’ species diversity in an endemic gastropod radiation (Lake Tanganyika; Cerithioidea: Paramelania)**

**James D. Burgon**<sup>1,2</sup>, J. A. Todd<sup>3</sup> & E. Michel<sup>1</sup>

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What are the relative values of historic and new collections in documenting biodiversity? Lake Tanganyika, East Africa, has a species-rich, ‘superflock’ of endemic gastropods that, despite its fame, remains poorly systematised. The iconic genus *Paramelania* has been known for 130 years but, until now, has never properly been revised and historically thought to comprise 2-5 morphologically variable species. To re-assess its species diversity we first undertook phylogenetic analyses using CO1 and 16S of all available samples with well-preserved tissue (new SCUBA samples). These revealed five robust clades congruent with a priori fine-scale shell-based species. We used this correspondence to assess species diversity in three historic collections (NHM, RBINS and RMCA), comprising shells only. These had >7500 shells in 323 lots from over 96 lake-wide locations, including the currently inaccessible Congo coast. Study revealed 17 species (12 undescribed). We compared this with two modern research collections, largely from the Tanzanian coast (2116 shells, 301 lots, 44 sample sites), comprising 15 species (12 undescribed). Historic and new collections shared only ten species from a total of 22. Compositional differences in part reflect the geographical occurrence of frequent short-ranged species. Nonetheless, a few sites with both historic (dredge: deep) and modern

sampling (SCUBA: shallow) capture bathymetric and substrate differences between species. Our results emphasise that in this lake species discovery needs to be undertaken on both modern and historical collections for the most accurate view of biodiversity.

3.

### **New species of *Grossander* (Heteroptera: Rhyparochromidae: Drymini) from the oriental region**

**Anita Fábics & Előd Kondorosy**

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The tribe Drymini is part of the family Rhyparochromidae of true bugs (Heteroptera). Gross (1965) revised the Australian Drymini, describing several new genera and species. These genera were believed to be endemic until now. We found two new species (one from New Guinea, the other from the Sunda Islands, Thailand) belonging to genus *Grossander* Slater, 1976. The new species shows similarity to Palaeartic *Taphropeltus* Stål, 1872, Australian *Brentiscerus* Scudder, 1962 and some Ethiopian genera (*Ibexocoris* Scudder, 1963; *Bexiocoris* Scudder, 1969; *Salaciola* Bergroth, 1906). The most suitable genus for the new species is *Grossander* Slater, 1976. The two new species are rather different from the known species, and we should create a new subgenus for them, which can be easily separated through species-level attributes: stalked eyes, the long antecular and postocular part, the thick pronotal collar and the impunctate hind arm of the triradiate scutellar keel.

4.

### **Paraphyly of the Malagasy genus *Carphalea* (Rubiaceae, Rubioideae, Knoxiaceae) and its taxonomic implications**

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The Malagasy genus *Carphalea* of the coffee family (Rubiaceae) as defined by Kårehed and Bremer (2007) consists of six species (*C. angulata*, *C. cloiselii*, *C. kirondron*, *C. linearifolia*, *C. madagascariensis* and *C. pervilleana*) of woody shrubs or small trees, and is recognised by its distinctly lobed calyces. These authors showed that the genus is paraphyletic with respect to the genus *Triainolepis* based on combined chloroplast (rps16 and trnT-F) and nuclear (ITS) analyses. On the other hand, the ITS analysis resolved *Carphalea* as monophyletic with moderate support. *Carphalea linearifolia*, rediscovered in 2010, has not previously been included in any molecular phylogenetic studies of Rubiaceae. This study further investigated the monophyly of the genus *Carphalea* using sequence data from chloroplast (rps16 and trnT-F) and nuclear (ITS and ETS) markers and parsimony and Bayesian methods. The newly collected *C. linearifolia* was also added

in the analyses. *Carphalea* resolved in two clades (the *Carphalea* clade I and II), with *Triainolepis* as sister to the latter clade. *Carphalea linearifolia* grouped with *C. madagascariensis* and *C. cloiselii* in the *Carphalea* clade I. A new genus needs to be described to accommodate the species in the *Carphalea* clade II. *Carphalea* should be restricted to include only the members of *Carphalea* clade I. Finally, the conservation status of *C. linearifolia* was assessed using the IUCN criteria as critically endangered.

5.

## **Digeneans of cetaceans under a taxonomic and phylogenetic perspective**

**Natalia Fraija**, Francisco Javier Aznar, Juan Antonio Raga & Mercedes Fernández

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The taxonomic study of digeneans of cetaceans has traditionally suffered from two major problems. Firstly, few specimens are available for study and are often collected in very poor condition because they usually come from stranded hosts. Secondly, only the adult stage is known because life cycles develop presumably in the pelagic realm. Thus, there is a gap of information about the evolution of life cycles and host – parasite associations. We illustrate here how the combination of thorough study of morphology and molecules can alleviate these problems, allowing the description of new taxa, and how molecular markers and cophylogenetic analyses can help us to understand the origin of host – parasite associations. Overall results suggest that the associations between cetaceans and their digeneans would have originated via colonization from other marine hosts, supporting the hypothesis that the ancestors of cetaceans lost parasites of terrestrial origin during the hosts' transition to the sea.

6.

## **Inter-archipelago comparisons of genetic and morphological diversity in *Pericallis* (Asteraceae): can we explain the 'Azores Diversity Enigma'?**

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A key question for biologists is why do different geographic regions harbour contrasting levels of diversity? Oceanic archipelagos typically host extensive radiations of flowering plants and are hotspots for biodiversity. The Atlantic archipelago of the Azores, however, represents an anomaly, with limited examples of in situ radiations and just one single island endemic (SIE) flowering plant, in comparison to the Canaries archipelago which hosts nearly 400 SIEs. This pattern is referred to as the 'Azores Diversity Enigma'. We investigated the patterns of morphological and genetic diversity and structuring within two relatively young clades (ca. 1 Myr) of *Pericallis*, endemic to the Azores and Canaries

respectively. *Pericallis* is an ideal case study to test key hypotheses to explain the Azores Diversity Enigma. Specifically, we test the hypothesis that the Azores Diversity Enigma is explained by a lack of our understanding of diversity in the Azores (taxonomic artefact) and the hypothesis that the Azores are too ecologically homogeneous to have facilitated diversification within *Pericallis*. The structuring of morphological diversity conflicted with genetic diversity patterns within each archipelago. Morphological diversity was largely consistent with taxonomy, however, morphological analyses revealed fewer SIEs in the Canaries compared to current taxonomic treatments. In contrast, genetic diversity was not consistent with current taxonomic treatments and suggested continued gene flow between islands and between currently recognized taxa. Therefore, genetic diversity patterns were much more complex than morphological diversity patterns within *Pericallis*. Our study suggests that the Azores Diversity Enigma cannot be explained by a taxonomic artefact alone. We revealed a significant role of ecology in the evolution of *Pericallis* within both archipelagos; therefore, we reject the hypothesis that the Azores are not too ecologically homogeneous to have facilitated diversification in the Azores. Our results contradict current hypotheses for the 'Enigma' and, in light of our findings; we propose novel possible explanations for the 'Azores Diversity Enigma'.

7.

## **Biogeography of woody species of Leguminosae in the caatinga of the Aiuaba Ecologic Station, Ceará State, Northeastern Brazil**

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Little is known concerning the flora and distribution patterns of species occurring in the caatinga, a xeric vegetation community present in Northeastern Brazil. A number of representative species of the Fabaceae family are found in this community. To better understand the geographic distribution of the species of the Fabaceae occurring in the caatinga and in other areas of the world, a floristic survey carried out at a Federal Conservation Unit (Aiuaba Ecologic Station in Ceará) was used as a basis for the study of distribution of the 34 woody species of Fabaceae. Specimens from the herbaria K, BM, OXF, FHO and E were examined. The results show that some species are present only in areas of caatinga, but that many of them occur also in dry forest formations throughout South and Central America. As a general rule, the distribution of the species studied in this study suggested that the caatinga can be considered as one of the nodes for migration between all the other dry areas of South America, and that the flow of species has probably occurred in two ways.

8.

## ***Pterocarpus rohrii* – How many species? A systematic study and revision of the *Pterocarpus rohrii* complex**

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This study investigated species limits of *Pterocarpus rohrii* Vahl, a neotropical tree species in the family Leguminosae, subfamily Papilionoideae, tribe Dalbergieae. Recent phylogenetic analysis suggests that *Pterocarpus rohrii* is polyphyletic and implies that there may be a conflict between the currently accepted species and its evolutionary relationships. Species limits were tested through a morphometric analysis of herbarium specimens using multivariate methods. Published phylogenies were examined to establish the degree of agreement between morphological entities and phylogenetic positions. The results suggest that *Pterocarpus rohrii* as previously delimited consists of several morphologically close but distinct species and support the reinstatement of nine *Pterocarpus rohrii* synonyms and the continuing recognition of one recently described species.

9.

## **Phylogeny and biogeography of the genus *Isoetes* L. from South America**

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*Isoetes* L. is a genus of heterosporous lycopsids which are aquatic or terrestrial associated with a seasonally inundated habitat. The east of South America is, with about 20 species, both a morphological and a taxonomical diversity centre. To understand the evolution of *Isoetes* is a challenge for several reasons: phylogenetic isolation from all other recent vascular plants; distinct divergence times within the genus; difficulties in rooting the phylogeny; allopolyploids; hybridization; and incomplete biogeographic species sampling. Here we present a phylogenetic reconstruction of the *Isoetes* species from eastern South America based on nrITS1 sequences using a maximum likelihood (ML) approach. The preliminary phylogenetic result revealed that the species complex from eastern South America is a paraphyletic group. These species form a clade together with three species from North America. This study is the first step towards a more robust phylogenetic framework that is needed to reconstruct the biogeographic pattern of the South American species.

10.

## **Next generation sequencing for viral discovery, identification and food security**

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Plant disease is a constant threat to food security; plant viruses in particular cause significant damage and insidious viral diseases have no current treatment. Correct identification is therefore crucial to deploy effective control strategies. This poster presents the use of Next Generation Sequencing (NGS) as a rapid, universal and unbiased method for virus identification, improving upon the limitations of previous identification methods. The Illumina MiSeq was utilised to sequence diseased plants. Viruses were identified through similarity searching against Genbank, and confirmed using phylogenetic analyses. The results presented are an identified strain of Tobacco Mosaic Virus in *Tarenna Dallachiana*; a novel potyvirus in coriander; a previously described Potyvirus in phlox; and assays developed for future diagnostics. Furthermore we present the developments of a novel project starting in Kenya expanding the reach of NGS analysis. This technology will allow for new virus discovery whilst aiding food security.

11.

## **Central European Miocene land snails: taxonomy, paleobiogeography and paleoecology**

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The aim of the present work is to build a paleobiogeographic history of the land snails in Central Europe through the Miocene. A large database is being built based on the literature. Of course, there are many fossil sites whose faunas have either never been properly described or desperately need a revision. Unreliable data will harm any biogeographic analysis; thus, some of these faunas are currently being revised, for now restricted to the Early/Middle Miocene of Southern Germany: Sandelzhausen; Oggenhausen; Randeck Maar; Gündlkofen and Biberach. Moreover, this is also a good opportunity to study other aspects of these faunas, such as paleoecology. Sandelzhausen, for instance, dates from the Miocene Climatic Optimum, and the systematic collection of its fossils allows a precise study on faunal changes related to the environment. This study is being further complemented by isotope analyses (C, O, Sr), bringing new information for this important period.



12.

## Teaching taxonomy and systematics for children

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Facing a biodiversity crisis, researchers strive to reach “the broad public and policy makers”. It is tough to teach an old dog new tricks – the focus should be on teaching the importance of biodiversity to children. This, as everything in biology, starts with taxonomy and systematics. There are two points in taxonomy (that even some biologists fail to recognize) that should be the key in teaching it as a science: (1) it is a system built for the storage of a huge amount of information, which should be easily retrieved. This is achieved by a unique name for each species, to which all information is linked. (2) Each taxon is a hypothesis and thus much can be predicted regarding known and unknown species alike. School curricula in biology are often all about genes and a broader view of the living world, given by systematics and key for conservation, is lacking.

13.

## Molecular phylogenetics and phylogeography of neotropical salamanders (genus: *Bolitoglossa*)

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Plethodontid salamanders are among the most species rich families of the order Caudata. Furthermore, the majority of species within this family belong to the supergenus *Bolitoglossa*. While members of this genus are found in abundance throughout tropical Central America, comparatively few species are known from South America. This observation is somewhat paradoxical, given the greater landmass and the presence of mega-diverse habitats in South America. This has led to the formation of two major hypotheses: either that the observed lack of species richness in South America is a result of the recent arrival of bolitoglossine salamanders via the Panamanian land-bridge (estimated to have formed 3-4 million years ago); or that the real extent of species diversity is obscured by the presence of cryptic species. Previous attempts to quantify the distribution of genetic diversity as exhibited by members of this genus in Ecuador have revealed unsuspected levels of cryptic species diversity throughout the upper Amazon. Similarly, divergence time estimates have indicated an arrival of salamanders in South America that far precedes the completion of the contemporary land connection. The availability of molecular data for these species is at present largely restricted to Amazonian regions. In light of this, the purpose of this study is to investigate the distribution of genetic diversity of these salamanders in previously underrepresented coastal and Andean

regions of Ecuador in an attempt to better resolve the existing estimates of both species richness and time of colonisation in this area. Sequence data from four genes (two nuclear, two mitochondrial) are used to infer phylogenetic relationships of coastal and Andean specimens of bolitoglossine salamanders. Additionally, a time-calibrated phylogeny is implemented to estimate the time of arrival of salamanders into South America.

14.

## **Four deuterostome specific gene families found in Xenacoelomorpha genomes**

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Xenacoelomorpha (Acoela, Nemertodermatida, Xenoturbellida) are worms with a simple body plan and a blind gut. Even though morphological and embryological studies were not able to unambiguously place them on a tree of life, the latest molecular data group them together as Xenacoelomorpha and place them as a side branch of Ambulacraria within the deuterostomes. Here we report using full genome comparison studies, that four gene families conserved specifically throughout only deuterostomes are also present in genomes of Xenacoelomorpha. We further investigate the evolution and function of these proteins.

15.

## **The Pleistocene fauna of the island of Favignana (a preliminary study)**

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We are investigating the diversity of the Pleistocene fossil mammals from the island of Favignana (Egadi – Western Sicily). During the last ice age, the proximal islands in the Egadi archipelago (Favignana and Levanzo) were connected to mainland Sicily, and abundant pleistocenic remains can still be found on these islands. More importantly, the earliest examples of cave-art in Sicily (and the only examples across the entirety of central and southern Italy) are found on these islands (e.g. the famous Genovese cave in Levanzo). We started sampling the mammal diversity across these poorly studied islands, with the aim of clarifying the paleoecological and microclimatic aspects of western Sicily that presumably might have allowed (uniquely in the south eastern Mediterranean region) an early appearance human art. In this poster we shall present our project, and our very preliminary results.

16.

## **The use of an AFLP fingerprinting method to differentiate similar *Chara* species (Charophyta)**

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Genetic variation of several species from the genus *Chara*: *Chara baltica*, *C. intermedia*, *C. hispida*, *C. polyacantha* and *C. rudis* – was investigated using AFLP techniques. Some of the species can be distinguished from the others by the presence or absence of numerous morphological characters. Because of the high variability of the morphological features and common occurrence of apparently transitional forms, many specimens of the five species were collected and analysed. The specimens were collected from various sites, including freshwater localities and sites in the Baltic Sea. Specimens were initially classified into the five species based on morphological features, and then analysed using AFLPs. The specimens formed two groups, but no consistent genetic differences were found between species within each of the two groups. Transitional forms of *C. hispida* and *C. rudis* were placed in a clade between individuals of *C. hispida* and *C. rudis* – this contradicts close similarities and close relations between them.

17.

## **DNA Barcoding in selected green algae from the genus *Chara* (Charophyta) – an ongoing project**

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DNA barcoding in plants and animals is a taxonomic method that uses a short genetic markers in an organism's DNA to identify it as belonging to a particular species. This is important not only for land animals, plant species and algae but for all those species with few or difficult to observe morphological characters. In the study presented here, we test the utility of several DNA barcoding loci in the Charophytes (genus *Chara*). All of the species tested are closely related algae and were treated as forms or varieties of *C. hispida* L., as markers that can distinguish closely related species in all groups of algae are not known (Hall et al. 2013). A study by Kim et al. (2013) demonstrates that DNA barcoding can provide an efficient method for species-level identifications. To test if species-level identifications can be possible in Charophytes, we proposed to use genes such as *matK*, *atpB* and *psaB*.

18.

## **Leaf epidermal characters of Iranian *Pyrus* (Rosaceae) and their taxonomic significance**

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*Pyrus* and *Malus* are two genera of great economic value in the Rosaceae. Half of the known wild species of *Pyrus* occur in Iran. In this study we have investigated leaf epidermal characters for 23 taxa of *Pyrus* plus one species of *Malus* as the closest relative to determine their taxonomical value among different species. We examined the shape of epidermal cells, patterns on anticlinal walls, stomatal size and type, cuticular ornamentation and epicuticular wax types. Scanning electron microscopy (SEM) and light microscopy (LM) were used for evaluation of epidermis features of the 24 taxa. We conclude that *Malus* is recognized easily from all species of *Pyrus* by stomatal density. Some characters, such as the distribution of stomata on abaxial and adaxial surfaces, shape and anticlinal wall pattern of epidermal cells, cuticular ornamentation and epicuticular wax types, are useful in the separation of *Pyrus* species. Moreover some characters such as shape of epidermal cells and anticlinal walls pattern are taxonomically useful at section level.

19.

## **A new genus of Lethaeini (Heteroptera: Rhyparochromidae) from New Guinea**

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A new genus with a single species (Heteroptera: Rhyparochromidae: Lethaeini) is described from New Guinea. Most members of this tribe are found in the tropical region. Currently there are 38 known genera, containing 176 species. Intensive Heteroptera research has been done in New Guinea since 1950. Gross published one of the earliest studies regarding the Rhyparochromidae family in this region in 1965, but more recent studies have also been done in this region dealing with various other families (Slater-Brailovsky 2006, Brailovsky 2011). After examining the specimens we discovered that they belong not only to a new species but to a new genus as well. After comparing them to other similar genera we concluded that this new genus is closest to the genus *Lethaeograndellus* Bergroth, 1918.

20.

## **Concatabominations: identifying unstable taxa in morphological and phylogenomic supertrees using Safe Taxonomic Reduction**

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Rogue taxa can be phylogenetically unstable because of limited and extensive missing data. Their inclusion in phylogenetic reconstructions often leads to unresolved topologies and an increase in run times. Safe Taxonomic Reduction (STR) has been proposed as an a priori method to determine the taxa that are potentially unstable and safe to exclude from an analysis, however it still has limitations. We developed a heuristic extension to STR called "Concatabominations" based on the experimental combination of data from pairs of "potential taxonomic equivalents" to create new "concatabominated" taxa. Compatibility estimates are then used to indicate if the concatabomination adds any homoplasy to the original data. Taxa that can be combined with many others without introducing any additional homoplasy to the data are candidate rogue taxa. A pipeline implementing the approach allows visualisation of taxonomic equivalence relations as connections between taxa in a network. We assessed performance using gap-rich paleontological and genomic MRP (Matrix Representation with Parsimony) datasets. Our approach outperforms STR in identifying rogue taxa in both and increases the resolution of the resulting phylogenies.

21.

## **The EDGE of conifers – an example for conservation strategies based on substitution rates**

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Due to the increasing threat of species and biodiversity loss, many species decline to critical levels. Numerous efforts are made to protect species in their natural habitat as well as in ex-situ collections. Species selection is mostly based on evaluations of the Red List commissions of the IUCN. Estimations are based on the reports of multiple member organizations. Many taxa are assigned to the categories "data deficient" and "least concern" because current data of frequency and distribution are only insufficiently available. Many species haven't yet been integrated into the evaluation process. Funds for taxon-specific studies are currently limited. Therefore, a pre-selection of taxa is important for the optimal utilization of available financial and human resources. This could be based on a phylogenetic approach. The present study uses the measuring of evolutionary diversity (ED) and the corresponding EDGE value. This method of pre-selection will be demonstrated and discussed for the Coniferopsida.

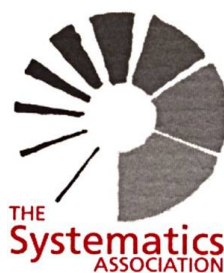


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