

YOUNG SYSTEMATISTS' FORUM

20th November 2015, 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	Lucy Holloway	Out of ice: Extant global turtle biodiversity is a consequence of the Eocene-Oligocene global cooling event
09.58	Aime Rankin	A polar protean: characterisation of a deep-water moss from a perennially ice-covered lake in Antarctica
10.16	Elisabeth Biersma	First evidence of multi-million year persistence of plants in Antarctica
10.34	Nathan Christmas	The evolution of cold tolerance in cyanobacteria
10.52	Coffee & Posters (attend even numbers)	Attended posters (even numbers) should be presented by the author
11.30	Stephanie Sang	Towards predicting accurate morphological character sets in turrnellines
11.48	Max Stockdale	Matrix-Representation Parsimony of the Crocodylomorpha
12.06	Ciara O'Donovan	Reconstructing how the Dinosaurs radiated across the globe
12.24	Jack Oyston	What Limits the Morphological Disparity of Clades?
12.42	Richard Dearden	The early evolution of the cartilaginous fishes: what makes a chondrichthyan chondrichthyan?
13.00	Lunch and posters	(Light lunch provided for registered attendees)
14.10	Péter Kóbor	New <i>Germalus</i> species from New Guinea and the Solomon Islands (Heteroptera: Geocoridae)
14.28	Marcos Roca-Cusachs	Testing ecological release and species boundaries in multi-island species with contrasting levels of trophic specialization: The case of the genus <i>Dysdera</i> (Araneae: Dysderidae) in the western Canary Islands.
14.46	Warut Siriwut	An integrative approach to centipede systematics: a case study on the genus <i>Scolopendra</i> Linnaeus, 1758 in mainland Southeast Asia
15.04	Carlos Leiva	Phylogenetic relationships and genetic connectivity of a new <i>Pterocirrus</i> species (Annelida, Polychaeta) from the shallow-water Southern Ocean
15.22	Coffee & Posters (attend odd numbers)	Attended posters (odd numbers) should be presented by the author
16.00	Georgia Ward	Paramyxids: enigmatic but emerging parasites of marine invertebrate
16.18	Maria Longakit	The oculata clade of the Order Haplosclerida (Demospongiae: Porifera)
16.36	Chris Barratt	Phylogenetic Endemism of a highly threatened biodiversity hotspot
17.00	Poster session	
17.45- 19.00	Reception	Presentation of prizes and closing remarks

Organised by Ellinor Michel, Ross Mounce, and Xavier Aubriot, with support from:



TALK ABSTRACTS - listed in speaking order

Out of ice: Extant global turtle biodiversity is a consequence of the Eocene-Oligocene global cooling event

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A large molecular dataset was used to reconstruct a dated phylogeny for extant turtles (Testudines), using maximum likelihood and Bayesian models. Multiple fossil data sets provided temporal calibrations. The monophyly of the two extant testudine lineages, Cryptodira and Pleurodira, and that of all extant testudine families was supported. Relationships between these families was resolved with the exception of the marine turtles (Cheloniidae). Speciation rates were calculated. The majority of divergence events occurred after the Cretaceous-Palaeogene mass extinction event with rates increasing sharply after the rapid global cooling event at the Eocene-Oligocene boundary. Ancestral preferences for temperature and precipitation were reconstructed for Trionychidae, a Cryptodira family. Minimum tolerance levels for both variables have fluctuated throughout the evolutionary history of this family. It is likely that this cooling event impacted extant biodiversity within Testudines. This is significant with regards to conservation efforts in the current period of anthropogenic mass extinction.

A polar protean: characterisation of a deep-water moss from a perennially ice-covered lake in Antarctica

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Submerged bryophytes are difficult to identify due to developmental plasticity obscuring their characteristic features. In 1980, a deep-water moss population of uncertain identity was found growing within the perennially ice-covered Lake Vanda, Antarctica. Through phylogenetic analysis of the nuclear ribosomal region ITS, the moss was identified as *Bryum pseudotriquetrum*. SEM revealed adaptations to an aquatic life not known for this species, such as extraordinarily thin cell walls. Another new character for the species was the production of rhizoidal knots in contaminated, low nutrient media. The knotting behaviour was thought to manifest from interactions with Lake Vanda's algal mat. The moss is trapped within the second of three convection cells in the lake and the absence of any mosses in the surrounding area adds mystery to the provenance of the population. The findings will therefore assist conservation management and understanding the response of biodiversity to climatic change in Antarctic ice-covered lakes.

First evidence of multi-million year persistence of plants in Antarctica

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How long has life persisted on Antarctica? Glaciological reconstructions estimate thick ice sheets covered most terrestrial areas of the Antarctic during the Last Glacial Maximum (~22–18ka), as well as previous glaciations, suggesting no terrestrial life could have survived in Antarctica throughout these periods. However, recent studies show most groups of the contemporary Antarctic terrestrial fauna have a hundred thousand to multi-million year persistence on the continent. The most dominant group of Antarctic flora – the bryophytes (mosses) - seems to stand distinct from these patterns. Their low species number, low endemism levels, and distribution patterns suggest today's moss biota are recent colonists. Alternatively, bryophytes may have a long persistence in Antarctica, but their presence has previously been underestimated. Using the nuclear Internal Transcribed Spacer (ITS) and the plastid trnL-F region combined with Bayesian inferences and molecular dating methods we examined the global phylogeography of the cosmopolitan species *Bryum argenteum*, and several bipolar species of *Polytrichum*. The analyses showed high genetic variation and long-term in situ isolation of mosses in Antarctica, with genetic dating methods revealing a multi-million year persistence of bryophytes in the Antarctic. This study suggests that, despite the harsh polar climate during glaciation periods, mosses may have had a much longer persistence in Antarctica than previously thought.

The evolution of cold tolerance in cyanobacteria

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The importance of cyanobacteria as primary producers in polar and alpine environments is well understood, yet less is known about their tempo and mode of evolution. To begin to clarify this we constructed a phylogeny from over 250 high quality SSU rRNA sequences from throughout the cryosphere, coupled with over 250 sequences from temperate and tropical environments. Deep branching relationships were maintained by enforcing a backbone topology determined through phylogenomic analysis of cyanobacterial strains with complete or near complete genome sequences. This tree confirms observations that the cryosphere hosts considerable diversity from throughout the cyanobacteria. Bayesian ancestral state reconstruction was used to statistically delimit lineages of cold tolerant cyanobacteria, revealing 20 lineages with positive support for a cold tolerant ancestor. These included lineages both unique to particular cryo-environments and shared between them, suggesting multiple incursions of cyanobacteria into cold environments by multiple mechanisms.

Towards predicting accurate morphological character sets in turritellines

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Despite the ubiquity of molecular data, morphological characters remain the only source of phylogenetic information for fossils. However, we require methods of validating and understanding the accuracy of the information. In cases where molecular and morphological phylogenies conflict, the morphological characters may not be a reliable signal. Using turritellines, a group of morphologically-similar marine snails, we generate a computational method that predicts which morphological characters to use for analysis. Our method heuristically searches different combinations of morphological characters. It then finds the character set that produces the morphological tree most similar to the molecular tree.

Matrix-Representation Parsimony of the Crocodylomorpha

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The Crocodylomorpha have undergone a dramatic loss of diversity since their inception. They are represented by just 23 extant species, all of them amphibious ambush predators limited to the tropics. This is in stark contrast to the fossil diversity of the Crocodylomorpha, which is represented by over 400 species including marine and terrestrial forms, insectivores, omnivores and herbivores. Placing this diversity in to a phylogenetic context presents challenges: the majority of examples are extinct and therefore beyond the reach of molecular approaches. Fossil remains are often fragmentary, making encoding morphological characters difficult. Here we present the first comprehensive phylogeny of the Crocodylomorpha, assembled using the Matrix Representation Parsimony method. This meta-analysis approach allows for the construction of supertrees using parsimony of virtual characters. The completed supertree opens new vistas of research for studying large-scale evolutionary processes among crocodylomorphs.

Reconstructing how the Dinosaurs radiated across the globe

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Following their origination over 200 million years ago in South America the Dinosaurs radiated rapidly and within 30 million years had a cosmopolitan distribution – here we present a novel method of studying how this occurred. We consider geographical location as a continuous trait that can diffuse over a three-dimensional, spherical Earth and allow the speed of migration to vary among the branches of a phylogeny. Our results reveal that Sauropods travelled significantly greater distances than Theropods and Ornithischians. Theropods showed the fastest rates of movement – with Aves showing particularly rapid speeds which has implications for the timing of powered flight. Overall, there is a strong and significant trend towards a slow-down in the rates of movement in all three of the major dinosaurian clades over time. Taken together these results provide a new view of dinosaur biogeography where dinosaurs underwent rare but extreme migrations interspersed with smaller, localised dispersal events.

What Limits the Morphological Disparity of Clades?

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Variation in form within clades is decoupled from estimates of diversity. Animals and plants frequently maximise morphological disparity early, even if diversity is low. This suggests a 'restricted morphospace', consistent with an observed decrease in the rate of origination of novel bodyplans, higher taxa and character states over time. We used published phylogenies of 93 clades of animals to test whether this character exhaustion is widespread among animal clades. We also investigated the possibility that character exhaustion can account for early high disparity by testing whether a simple relationship exists between the level or rate of exhaustion in character states up a phylogeny and the shape of a clade's disparity profile. The result has profound implications not only for the link between the evolution of novel characters and overall morphological disparity but also suggests that while evolution is shaped by constraint, some constraints have a greater importance than others.

The early evolution of the cartilaginous fishes: what makes a chondrichthyan chondrichthyan?

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Sharks and their relatives (Chondrichthyes) have long been perceived as evolutionarily conservative and key to understanding ancestral conditions in jawed vertebrates. However, like any group, chondrichthyans express a combination of primitive and derived traits. Recent palaeontological investigations have upset the long-standing view that their external skeletons, formed from tiny scales, exhibit an ancestral vertebrate state. Nonetheless, the relationships and significance of many fossil chondrichthyan-like taxa remain mysterious, owing to a fragmentary fossil record. In light of recent shifts in phylogenetic thinking on early gnathostomes, we review the problematic areas of early chondrichthyan evolution and investigate how this impacts the evolution of the group and inferences about general gnathostome anatomical conditions. We critically review morphological characters that could place problematic fossils within the total and crown groups. We highlight problems in delimiting the chondrichthyan crown and propose characters that could be useful in uniting fossils with the component living lineages.

New *Germalus* species from New Guinea and the Solomon Islands (Heteroptera: Geocoridae)

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The genus *Germalus* (Stal 1862) from the family Geocoridae (Heteroptera: Lygaeoidea) is distributed from the Afrotropical to Pacific biogeographic region with 34 known species. The taxonomy of this genus is less known, most researches ended in the 1950's. Recently only the Australian members of the taxa are studied by M. B. Malipatil and his colleagues. During the study of the specimens of European museums six new *Germalus* species were found: three from New Guinea and three from the Solomon Islands (Bougainville, Guadalcanal and Santa Isabel). The only species known from New Guinea was *Germalus fuscovittatus* (Malipatil 2013), its presence was confirmed by further identified specimens. From the Solomon Islands there was no data on presence of the genus. Our results will be used by the general revision of the genus.

Testing ecological release and species boundaries in multi-island species with contrasting levels of trophic specialization: The case of the genus *Dysdera* (Araneae: Dysderidae) in the western Canary Islands.

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The spider genus *Dysdera* has undergone a remarkable diversification in the volcanic archipelago of the Canary Islands. The species *D. calderensis* and *D. silvatica* are sympatrically distributed in La Gomera, where they coexist with 8 additional species, and in the younger islands of La Palma and El Hierro, where they coexist with just one species. Using geometric morphometric tools, we tested whether *D. calderensis* and *D. silvatica* undergone ecological release following colonisation of the younger islands, measured as the range of variation in morphological traits. Our prediction is that species in islands with less competition, ie. lesser conspecifics, will show higher morphological variation. As predicted, *D. silvatica* on La Palma exhibited larger phenotypic variation than its counterpart from La Gomera. However, *D. calderensis* showed the opposite pattern. The combination of the geometric morphometric data with molecular phylogenetic analysis revealed that the over-dispersion of phenotypic characters in La Gomera was the result of mixing two overlooked evolutionary lineages occurring in separate parts of the island. Here we present further evidence that they represent two different species.

An integrative approach to centipede systematics: a case study on the genus *Scolopendra* Linnaeus, 1758 in mainland Southeast Asia

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Centipedes in the genus *Scolopendra* are well known and are used commercially in SE Asia. The *Scolopendra subspinipes* subspecies complex, which ranges throughout SE Asia, has resisted a stable classification using traditional external morphology alone. The broad distributional range suggests that geographical variation might affect morphology as is known for other centipede groups. To resolve ambiguities about intra- and interspecific variability, an integrative approach involving geometric morphometrics, molecular phylogenetics, and external morphological characters was applied. Morphometrics was based on landmark methods using shapes of the coxosternite, cephalic plate and tergite 21. Canonical Variance Analysis identified clusters that correspond to morphologically diagnosed species that are monophyletic in ML and Bayesian phylogenetic trees based on COI, 16S rRNA and 28S rRNA sequences. In addition to revealing genetic differentiation between species, genetic structure at a broad sampling scale explained local endemism within species of *Scolopendra* in different parts of their geographic ranges.

Phylogenetic relationships and genetic connectivity of a new *Pterocirrus* species (Annelida, Polychaeta) from the shallow-water Southern Ocean

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Despite Antarctic shallow-water polychaetes have been widely studied, still new species are often discovered. Here, we describe a new and abundant upper-infralitoral Antarctic phyllodocid of the genus *Pterocirrus* Claparède, 1868. Morphologically, this species is characterized by the position of the median antenna, the tentacular cirri arrangement, and by the lack of nuchal organs. Our Maximum Likelihood and Bayesian Inference phylogenetic analyses, based on 2 nuclear (*18S* and *28S*) and 2 mitochondrial (*COI* and *16S*) markers, place the new *Pterocirrus* as a basal species within its genus. The haplotype network obtained from the analysis of 91 *COI* sequences suggests that the populations sampled within the Antarctic Peninsula and the South Shetland Islands present panmixis, likely due to the presence of planktotrophic larvae allowing for the long-distance dispersal of the species. Future studies will be directed to establish a robust phylogeographic hypothesis for the species in the light of past climatic events.

Paramyxids: enigmatic but emerging parasites of marine invertebrate

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Paramyxida is an order of Rhizarian protists that parasitise marine molluscs, annelids, and crustaceans. They include notifiable pathogens of bivalves and other taxa of economic significance for shellfish production. The diversity of paramyxids is poorly known, particularly outside of commercially important hosts, and their phylogenetic position is unclear due to their extremely divergent 18S rDNA sequences. However, paramyxean lineages are increasingly being detected in a wide range of invertebrate hosts. Environmental DNA (eDNA) sequencing using paramyxid-specific primers shows that paramyxids are associated with a wider range of hosts and habitat types than previously known, and reveals two novel clades. We review the diversity, host affiliations, and geographical ranges of all known paramyxids, present a comprehensive phylogeny of the order, and clarify its taxonomy. We also use *in-situ* hybridisation to associate sequence data with genera previously known only from morphological studies.

The *oculata* clade of the Order Haplosclerida (Demospongiae: Porifera)

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Haliclona oculata is the type species of a diverse sponge genus resulting from a previous amalgamation of 26 sponge genera. The genus currently contains six subgenera one of which contains sponges of the 'oculata' group. Molecular data distribute species of this genus across five major clades of a large order of marine Haplosclerida. Simplicity in skeletal elements and the high plasticity in form could explain the wide gap in both morphological and molecular taxonomy. Here we focus on the *oculata* clade and show that while molecular and morphological data are congruent regarding the close relationships between two species; *H. oculata* and *H. urceolus*, another member of the group *H. simulans* is not postulated to be closely related to this pair via molecular data unlike recommendations from morphology. We will present the data and approach for these species and discuss possible new synapomorphies that may strengthen their relationship.

Phylogenetic Endemism of a highly threatened biodiversity hotspot

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The Coastal Forests of East Africa are a highly threatened global biodiversity hotspot in imminent danger of being completely destroyed. There is an urgent need to prioritize areas for conservation efforts. Unfortunately, biodiversity patterns are poorly known with few comparative studies able to scientifically inform on where biodiversity rich areas might be and therefore what is more worth protecting. We outline a project aimed at sampling across the whole region using phylogenetic data of whole amphibian assemblages. Using this data we investigate the distribution of biodiversity using Phylogenetic Endemism (PE) and derived metrics. Using Categorical Analysis of Neo and Paleo Endemism (CANAPE) allows us to statistically test the significance of the PE results. Preliminary results show the identification of areas for future conservation efforts based on criteria of those areas that preserve the greatest amount genetic diversity.

POSTER ABSTRACTS

Taxonomic revision and phylogeny in the genus *Leptogenys* (Hymenoptera: Formicidae) from the Oriental region

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Leptogenys Roger, 1863 is the largest ponerine genus and contains over 300 species from the world's tropics and subtropics. Recently, species from the Afrotropical region and New World are revised taxonomically. However, this genus in the Oriental region has not been studied comprehensively. To explore its diversity and evolution in this region, we revised the Oriental species and reconstructed their phylogeny using a DNA dataset. We recognized 13 species groups and about 173 species including 100 undescribed. Our molecular analysis revealed that this genus is divided into the two clades. A clade comprising of three species groups can be called "army ants". Their mandibles have distinct teeth at the masticatory margin. All of the other clade do not have teeth, and are not army ants. Additionally, the relative length of the masticatory margin to the basal margin is significantly different between species in the two clades.

New citations of free living marine nematodes from Costa da Morte and Carnota-Monte Pindo, Galicia (NW Iberian Peninsula)

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The knowledge about free living marine nematodes from Galicia is limited. Actually, checking available literature, there are only few publications with some relevant information of this group of organisms. Nowadays, the checklist of Galician free living marine nematodes consists of 17 genera and 21 species, less than other countries from Europe. The sampled area consists in two sample points from Costa da Morte and other two sample points Carnota-Monte Pindo. Both areas are in the west coast of Galicia (NW of Spain) and opened to the North Atlantic Ocean. We found 159 specimens, which belong to 10 different families and 25 different genera. With the results obtained in this study, the checklist of Galicia increases its number by 1 new family, 2 new subfamilies and 13 new genera. Therefore, the actual checklist is 30 genera and 21 species.

Establishing a timescale for the Tree of Life

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Molecular divergence time estimation has, somewhat paradoxically, focussed on lineages with rich fossil records. No scions of the Tree of Life are in need of greater age constraint than the most fundamental of all, the last universal common ancestors of the principal domains of life. This is mostly because there is little evidence on which to derive constraint; few ancient rocks are available for sampling and still fewer have survived deformation over time. Nevertheless, there is still a diversity of evidence available, including degraded organic molecules, isotope fractionation, sediments, and microfossils that can be interpreted to establish minimum constraints. For instance, a minimum age constraint on the last universal common ancestor (LUCA) can be established based on evidence of oxygenic photosynthesis. Soft maximum constraints on clade ages are more problematic but using the moon-forming impact to date LUCA could be an option as it would have effectively sterilised Earth.

The phylogenetic position and diversity of the enigmatic mongrel frog genus *Nothophryne* Poynton, 1963 (Amphibia, Anura)

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The knowledge of African amphibian fauna is relatively poor. Specifically, there is great uncertainty in the taxonomic delineation and identification of many taxonomic categories of African amphibians. The mongrel frog *Nothophryne broadleyi* Poynton, 1963 is the only member of its genus and the phylogenetic position of this taxon remains unresolved. Herein we conduct a broad phylogenetic analysis, followed by a small-scale analysis using a refined dataset for precise investigation of the phylogenetic position of *Nothophryne*. Additionally we provide new data about this taxon's current distribution and diversity. We address questions on whether these newly discovered populations represent the currently described taxon (e.g. *N. broadleyi*) or new species, and make predictions of possible new areas of discovery based on ecological niche models.

An ecological view of a taxonomic problem: is the high conservation-priority species *Pseudocyphellaria lacerata* really in Britain?

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In Britain, several high conservation priority species have a high degree of taxonomic uncertainty, which in some cases may be attributable to morphological plasticity due to habitat factors, among other competing explanations. An increasing number of molecular studies show that taxonomy based on morphological and chemical characters is not always sufficient to accurately determine species. This is especially the case for ‘difficult’ or ‘specialist’ groups such as the lichenized fungi. The need for a critical revision of species concepts is most acute where uncertainty surrounds conservation priority species, that are thought to be threatened, and which draw on a limited conservation resource. This study critically evaluates the status of the lichen *Pseudocyphellaria lacerata* Degel., a rare Biodiversity Action Plan (BAP) species distinguished by the details of its asexual reproductive propagules. However, variation in these features suggests that it may in fact be a luxuriant or anomalous growth of the more common *P. intricata* group, representing an ecological morphotype. Extensive fieldwork was carried out across the UK to collect fresh material for *P. lacerata* and its con-generics: *P. intricata*, *P. norvegica* and *P. crocata*. The project uses a combination of sequence data from multiple genetic markers (mtSSU, MCM7, RPB1), including the official fungal barcode (ITS), together with complimentary analysis of morphological, chemical and ecological data to ask whether the conservation priority species *P. lacerata* is in fact a distinct species in Britain, or whether morphological variability is attributable to phenotypic plasticity associated with ecological conditions.

In search for the female of a new species of *Dicopomorpha* (Hymenoptera, Mymaridae) from Costa Rica, and phylogeny of *Alaptus* group genera

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Discovery of a diminutive male parasitoid which lacks wings, eyes and mouthparts, belonging to the genus *Dicopomorpha* (Hymenoptera, Mymaridae), provides an opportunity to try to associate extremely dimorphic sexes using molecular markers only. While searching for the female of the apterous male more than 200 specimens of *Dicopomorpha* and closely related genera were sequenced, targeting the 28S D2-D3 region of nuclear ribosomal DNA. Non-destructive DNA extraction also allows the specimens to be mounted as a permanent reference specimen. Sequences were used to construct neighbour-joining and parsimony trees which show the phylogeny of several *Alaptus* group genera. Evidence is obtained for *Litus* being a member of the *Alaptus* group, contrary to the most recent classification, and a potential female of the *Dicopomorpha* species was found.

New species and key of the genus *Narbo* Stål, 1865 (Heteroptera, Lygaeoidea, Rhyparochromidae, Rhyparochromini)

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The genus *Narbo* from the Oriental Region is related to the genera *Metochus* and *Dieuches*; the main differences: e.g. width of the lateral margin of the pronotum, length of the hairs and shape of it; tooth-like spines beneath anterior part of the first femora. Four valid species have been described in the genus until now: *longipes* Stål 1867 as type of the genus, *biplagiatus* Walker, 1871, *fasciatus* Distant, 1901 and *nigricornis* Zheng, 1981. We have found further 3 new species (sp.1-2-3). We made a key for the separation of the 7 species. The main species-level attributes are e.g. dentation of the first and second femora; pale spots of the scutellum, corium and membrane; dorsal and lateral shape of the pronotum, width of the lateral pronotal margin, projection on back edge on the posterior lobe of pronotum; length of the rostrum and elytra.

Using different tools to solve taxonomic problems in *Anemopaegma* (Bignoniaceae, Bignoniaceae): *Anemopaegma arvense* species complex as a case study

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Considering that species are the main units of ecological and evolutionary studies, the identification of boundaries among closely related species is a essential target of current systematic studies. *Anemopaegma* is the third largest genus of the tribe Bignoniaceae, the largest tribe of Bignoniaceae, with most of its taxa presenting problematic delimitations. In this context, the main goal of our research is to delimit species of *Anemopaegma* that compose species complex based on multiple lines of evidence. At first, we delimited the taxa from the literature and morphology. The study of leaf anatomy showed that *Anemopaegma arvense* and *A. glaucum* are consistent species; however, *A. acutifolium* individuals may represent several hybrids between *A. arvense* and *A. glaucum* or they may belong to different species. The reproductive biology study showed interspecific compatibility and the evaluation of the diversity of transposable elements showed that each species has a different composition of TEs.

Insect diversity through a crisis: effects of the end-Triassic mass extinction on the British entomofauna

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Mass extinctions are a key process in macroevolution and have provided opportunity for the evolution of many modern forms of insects. The end-Permian mass extinction saw the demise of many Palaeozoic insect orders and the subsequent rise in the Triassic of many modern groups. The end-Triassic mass extinction was devastating for many terrestrial and marine clades but estimates for the effects of the event on insects are probably inaccurate due to limited taxonomic work essential for the accuracy of datasets. This PhD seeks to build a taxonomically accurate dataset of insect diversity across the extinction event and here presented are several chunks of that larger project. This research allows us to make more accurate estimations of species ranges across the event and to estimate how robust these insects were to extinction leading to greater understanding of the current crisis.

Marine meiofauna: the most abundant and diverse benthic group in the marine realm, and their relationship to other components of the benthic biota

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Meiofauna are an important component of benthic habitats due to their small size, abundance and rapid turnover rates. They exhibit high abundance, diversity and productivity in many benthic habitats and play important roles in benthic food webs. Meiofauna feed on other mesopsammic organisms, benthic microalgae, other microbes, and detrital food sources and are, in turn, important food resources for shrimp and a variety of juvenile fish that utilize shallow water nursery habitats. Meiofauna have been used as environmental indicators of human activities and pollution. Nematodes are relatively insensitive to anthropogenic disturbances, while “Turbellaria”, harpacticoid copepods and Foraminifera are considered to be pollution sensitive taxa. My investigation present new species of the free-living flatworm of different taxa from the sandy shores of Australia, South Africa and the Mediterranean. It is very important to document and describe the global free-living Platyhelminthes biodiversity, as this group is poorly known worldwide.

Species discrimination and phylogeny of *Spalangia* Latreille: congruence of morphological and molecular data (Hymenoptera: Pteromalidae)

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We tested for species discrimination within *Spalangia* using morphological characters and molecular data, including a fragment of the cytochrome c oxidase subunit I (COI) gene that largely overlaps with the standard barcode region and the D2 and D3 expansion regions of the 28S rDNA gene. Molecular phylogenetic analyses largely support species discrimination using morphological characters except for three cases where cryptic species were detected. *Spalangia simplex* is represented by six clades (four from Congo and two from Korea) while specimens of *S. nigripes* and *S. fuscipes* from Greece and those from Central or Eastern Europe are molecularly very distinct. In all these cases mean between group p-distances are significantly larger than within group distances. The phylogenetic analysis of the 28S rDNA gene and subtle morphological characters support the cryptic species firstly detected using COI sequences. Financial support: Project RU-TE 2012-3-0057, funded by the Romanian National Council for Scientific Research.

Shell Evolution of *Georissa* (Gastropoda: Hydrocenidae) from Malaysian Borneo

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The study of gastropod shell characters is ideally suited to understand character evolution and evolutionary diversification. In this study I am proposing to explore the shell character evolution of minute land snails from the genus *Georissa* (Family: Hydrocenidae). This poorly-known genus occurs throughout Southeast Asia, and is particularly rich in shell-shape diversity in Borneo. The animals are known to occupy limestone hills, although they also occur, at lower density, on other rocky substrates. Extensive morphometric study is proposed by using micro-computed tomography on a μ CT-scanner and the application of recently-developed models for quantifying shell shape. This research will be carried out to give insights in the character evolution and diversification, long-term patterns and dynamics of adaptation, and conservation of these minute land snails.

Lessons from placing the root of the placental mammal tree

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Important considerations in phylogenetic analyses include data quality, structure, signal, alignment quality and length, and leaf sampling. If good quality data is poorly modelled then variation in rates of change across proteins and across lineages can lead to incorrect phylogeny reconstruction that can lead to downstream misinterpretation of the underlying data. The risk of choosing and applying an inappropriate model can be reduced with some critical yet straightforward steps. We use the question of the position of the root of placental mammals to illustrate the topological impact of model misspecification. Over the past decade or more the position of this node has proven contentious with multiple positions proposed. More recently, using data from the same sources, the possibilities were reduced to two alternative hypotheses thus raising a number of questions over data and model suitability. The results we present show strong support for the resolution of root of the placental mammal tree using a data driven modelling approach.

Best practice in morphological phylogenetics: methodology and data

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After a long period of molecular driven research morphological data had fallen to the sidelines outside of morphology driven fields such as palaeontology. In recent times a drive for holistic approaches in the construction of phylogenetic trees incorporating a range of characters from morphology to molecular data has come to the fore. Consequently the need to identify which methods are best able to analyse morphological data and how variants in the data can affect analysis are now important questions. By using Robinson and Fould distances across a collection of real morphological matrices it is clear that equal weight parsimony does not perform as well as other methods and large numbers of characters are less congruent than smaller numbers, numbers of taxa produce mixed results and fossils make trees more congruent. Morphological characters are of critical importance but consensus is needed to drive research objectives forward.

Polyphyletic origin of the planktonic foraminifera genus, “*Globigerinoides*”, identified using combined fossil and molecular genetic evidence

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Planktonic foraminifera are one of the most abundant and diverse protists in the oceans today and in the fossil record. Their exceptional fossil record has been extensively utilised for biostratigraphy, diversity and evolutionary studies. However, genetic evidence from modern morphospecies suggests significant ‘cryptic’ diversity, creating doubt over the morphospecies concept and inferred phylogenies in the fossil record. Here, we combine molecular genetic and fossil evidence to recognise the polyphyletic nature of the genus, “*Globigerinoides*”. We demonstrate that the group consists of two distinct lineages, evolving independently, despite being hitherto grouped into one genus. Phylogenetic analysis of small subunit (SSU) rDNA sequences of living representatives of “*Globigerinoides*”, clearly resolve two lineages. The two lineages, whilst exhibiting paralleled evolution of morphological traits (supplementary apertures), are separated using morphometric evidence from late Oligocene and early Miocene populations. The fossil record corroborates the phylogenetic analysis showing two lineages, and provides an independent stratophenetic phylogeny.

Molecular phylogenetic insights into the diversification and historical biogeography of the Sun orchids (*Thelymitra*, Orchidaceae)

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Thelymitra (c. 120 species) is a characteristic component of the Australian terrestrial orchid flora, and has a recent history of rapid diversification and hybridization. The Sun orchids display a striking morphological diversity often difficult to interpret and our knowledge on how this fascinating diversity has been shaped over the time is still limited. Here we present a multi-locus phylogeny of *Thelymitra* based on nuclear (ITS) and plastid markers (*matK*, *psbJ-petA*, *ycf1*) based on a broad taxonomic sampling which identifies major clades within the genus and provides first insights into infrageneric relationships. We reconstructed the evolution of key floral characters to assess their taxonomic value, and compared previous taxonomic treatments with the molecular phylogenetic results. We estimated divergence times and examined biogeographical patterns of species divergence using time-calibrated phylogenies in order to elucidate the effect of past climatic oscillations, dispersal and geography on the diversification of this charismatic group.

‘Taxonomy and biogeography of deep-sea peracarid crustaceans of the African continental margin’

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Peracarid crustaceans are a diverse and important component of benthic communities, comprising >20% of individuals, structuring deep-sea sediments and recycling nutrients. Peracarids exhibit direct development, restricting distributions and accelerating cryptic speciation, making them notoriously difficult to identify. New deep-sea peracarid species are regularly discovered, however analyses are hampered by rare and undescribed taxa, inaccurate taxonomic identifications, and unbalanced geographic and bathymetric sampling. My PhD studentship will advance the knowledge of global patterns of peracarid diversity by compiling regional species data for the African continental margin by utilizing existing industry survey samples. This region has a very large and rapidly expanding deep-water oil & gas industry, which poses both a major problem and a significant opportunity for taxonomists. Appropriate environmental impact assessments are restricted by the “taxonomic impediment”. This PhD aims to overcome this impediment by sharing taxonomic data through digital scratchpads. Providing a benefit to regulators, industry and academic science.

Building the UK’s bee DNA barcode library

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The UK’s declining diversity and abundance of bees is a serious economic, cultural, and ecological issue. Pinpointing the drivers for these declines has revealed a complex network of interacting forces, which are largely anthropogenic in origin. To mitigate anthropogenic impacts on bees we need base line population data, which could be obtained with a large scale monitoring program. The implementation of such a program is slowed by the difficulty associated with identifying bee species using conventional morphological methods. Molecular techniques can be used to quickly and reliably identify species. By associating a DNA barcode with a morphologically identified species one could build up an authoritative reference library for the UK’s bee species. Here we describe the progress of building the UK’s bee DNA barcode library and introduce how we intend to use this database to assess bee diversity across the UK using Next Generation Sequencing technology.

The evolutionary history of coleoid cephalopods inferred through phylogenomics

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Coleoid cephalopods (cuttlefish, octopuses and squid) are marine molluscs important to ecosystems, as fishing stock, and as examples of the breadth of diversity exhibited by invertebrates. The fossil record has been crucial in tracing earlier cephalopod evolutionary history. However, shell reduction and loss in the coleoid crown-group has impeded palaeontological insight on the origins of modern coleoids. Here we employ phylogenomics to infer relationships among cephalopods, and through molecular clock analysis propose timings of their evolutionary origins. We recover monophyly of octopuses (*Vampyroteuthis* plus *Octopodiformes*) reciprocal to the squid (*Decabrachia*). Octopuses underwent relatively gradual diversification in the late-Palaeozoic to the early-Mesozoic, while squid radiated more abruptly in the mid-Mesozoic. The rise of squid is concurrent with the Mesozoic Marine Revolution, suggesting that their diversification was fuelled by ecological competition with teleost fish, while shelled cephalopods such as belemnites declined in response to the development of durophagy among marine predatory groups.

Molecular barcoding of the giant deep-sea Amphipod *Eurythenes* from the Porcupine Abyssal Plain and Clarion-Clipperton Fracture Zone

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It has recently emerged that the deep-sea amphipod *Eurythenes gryllus*, previously thought to have a cosmopolitan distribution, is comprised of a number of cryptic species, many of which are new to science. Recent studies combining molecular and morphological analyses have confirmed this, and so the full number of described species is seven, with three more suggested from molecular data. Here, we present our work which aims to confirm the identity of *Eurythenes* spp. from the Porcupine Abyssal Plain and Clarion-Clipperton Fracture Zone in the Pacific Ocean using molecular techniques. We will focus on the mitochondrial COI gene and nuclear 28S gene, alongside Genbank sequences from previous work. These analyses will allow us to confirm if our specimens belong to one of the already described species, or if they correspond to those identified from molecular data. This knowledge will allow us to identify the specimens in our collections and determine whether there are more undescribed species in this genus.

Molecular phylogeny of the genus *Ogasawarana* (Gastropoda: Helicinidae) – diversification on oceanic islands

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The *Ogasawarana* are a genus of endangered terrestrial snails, endemic to the Ogasawara oceanic island chain in the mid-west Pacific. The archipelago has an exceptionally high rate of gastropod endemism, and despite members of the genus being listed as either endangered or critically endangered, little is known about their evolutionary history and interspecies relationships. Representatives of 12 nominal species were sampled from 6 islands, and a combination of conserved and rapidly evolving loci were selected for phylogeny construction. The phylogeny reveals taxonomic discord, and suggests independent adaptive radiations occurred on each island cluster, rather than dispersal across the archipelago after a single radiation event. However, there are also distinct differences in phylogenetic pattern between island clusters. On one island, the phylogeny resolves well by species and sampling location. Yet on another, the species are poorly resolved, and there is evidence of extensive mitochondrial introgression in all nominal species sampled.

Taxonomic Revision of the Tribe Brontini (Insecta, Coleoptera, Silvanidae) of Japan and Taiwan

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The tribe Brontini is composed of 13 genera, and the species of this tribe are found from mainly under bark of dead trees (Thomas 2004, 2011). In Japan and Taiwan, four genera, *Dendrophagus*, *Macrohylita*, *Parahyliota*, *Uleiota*, and six species have been recorded previously (Halstead et al. 2007, Hirano 2009, 2010). However, there has been no taxonomic revision of the brontine species of both areas since Reitter (1889) and Grouvelle (1913). In addition, authenticity of the distributional records of *Dendrophagus crenatus* and *Macrohylita gracilicornis* from Japan is suspected by Hirano (2009, 2010). Here the brontine species are taxonomically revised, and five species including two new species were confirmed from Japan and Taiwan. Two species previously reported from these areas are turned out to be misidentified, and *D. crenatus* was not confirmed from these areas. In this presentation, we provide their morphology and diagnostic characters for each genus.

MEETING POLICIES

The Systematics Association Council wishes to promote a diverse programme of speakers and pool of registrants and has taken measures to encourage and support diversity. We welcome and encourage participation by everyone in the systematics community, and welcome feedback on how best to build on these intentions in the future.

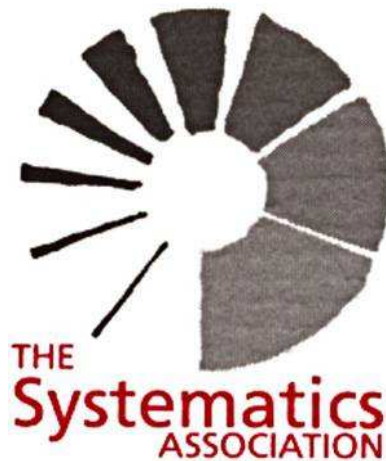
Photography and Social Media Policy

We want to promote and spread the word about the enormous range of work going on in the Systematics community, and we strongly encourage registrants and speakers to write about the meeting on blogs, social media, and via other media within the following limits:

- Please respect the wishes of speakers & poster presenters who ask for the content of their presentations not to be shared outside of the conference

Anti-Harassment Policy

To our knowledge, the Systematics Association has had no experience of harassment at any of their meetings to date, and we are not anticipating a change in this. Nonetheless, we wish to be proactive in ensuring that we make sure that we provide a welcoming environment for all and if any problems occur that attendees are supported appropriately. Behaviour and language that are acceptable to one person may be unwelcome and/or offensive to another. We will not tolerate harassment of conference participants in any form. Sexist language and potentially offensive human sexual imagery is not appropriate in a conference venue, including talks and posters. Any unwelcome conduct, verbal or physical, including when based on an individual's race, colour, gender, national origin, religion, age, disability, sexual orientation, status as a parent, gender identity, or physical appearance, should be reported to Ellinor Michel, Xavier Aubriot, or Ross Mounce as soon as possible. Reports do not have to be made by the recipient of the harassment, please report any such behaviour that you encounter. All reports will be recorded, and Council members will determine any action that needs to be taken, including the ejection of registrants responsible for such behaviour.

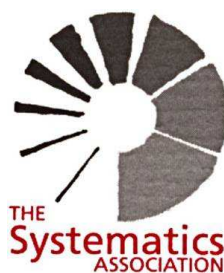


The Systematics Association is committed to furthering all aspects of systematic biology. It organises a vigorous programme of international conferences on key themes in systematics, including a series of major biennial conferences. The association also supports a variety of training courses in systematics and awards grants in support of systematics research. Membership is open to amateurs and professionals with interests in any branch of biology, including microbiology and palaeontology. Members are generally entitled to attend the conferences at a reduced registration rate, to apply for grants from the Association and to receive Newsletters and mailings of information.

The Systematics Association was founded in May 1937 as the "Committee on Systematics in Relation to General Biology" to provide a forum for the discussion of the general theoretical and practical problems of taxonomy. An outline of the original objectives of the Association was published in *Nature* 140:163 (1938).

The first of the Association's publications, *The New Systematics*, edited by the late Sir Julian Huxley, focused on new data from cytogenetics, ecology and other fields. Since then the Association has pioneered discussion on many new developments in systematics and more than 50 Special Volumes have been published. These have included systematic surveys of groups as diverse as haptophyte algae, tetrapods, lichens, free-living flagellates and haematophagous insects. Other volumes have explored fields such as phylogenetic reconstruction, systematics and conservation, genome evolution and the emergence of the biosphere. The Association also publishes books derived from training courses and on general aspects of systematics.

For more information, visit the SA website at <http://www.systass.org>



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