

# YOUNG SYSTEMATISTS' FORUM

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23<sup>rd</sup> November 2018, Flett Theatre, Natural History Museum, London, UK

08.45	<b>Registration</b>	<b>(Please put posters up as early as possible from 08:45)</b>
09.45	<b>Welcome</b>	<b>Mark Wilkinson, President of the Systematics Association</b>
09.55	Sandra Álvarez-Carretero	Bayesian Estimation of Species Divergence Times Using Correlated Quantitative Characters
10.15	Filipa Sampaio	An island radiation of burrowing snakes (Serpentes: Uropeltidae)
10.35	Leah Fitzpatrick	Untangling the web-using novel methods to explore the evolution of spider (order Araneae) venom
10.55	Vanina Tonzo	An old love affair: Genomic data reveal past hybridization and suggest evolution of reinforcement in sympatric populations of two montane grasshoppers from the Iberian Peninsula
11.15	<b>Coffee &amp; Posters (attend even numbers)</b>	<b>Attended posters (even numbers) should be presented by the author</b>
12.00	Pablo Muñoz-Rodríguez	Genomic insights into the origin and evolution of the sweet potato
12.20	Rowena Hill	Exploring the evolution of the lichenicolous lifestyle within the Ascomycota
12.40	Alan Beavan	What can relationships between genes tell us about events in genome evolution?
13.00	<b>Lunch and posters</b>	<b>(Light lunch provided for registered attendees)</b>
14.00	Katherine Short	A new comprehensive phylogeny of the Tardigrada may alter the hypotheses for their colonisation of Antarctica
14.20	Edmund Moody	Inferring the temperature at which the Last Universal Common Ancestor lived
14.40	Samuel Abalde	Molecular systematics of cone snails (Gastropoda: Conidae)
15.00	Rhiannon Williams	King or Royal Family? Multilocus Phylogeography and Species Delimitation in the King Cobra ( <i>Ophiophagus hannah</i> )
15.20	<b>Coffee &amp; Posters (attend odd numbers)</b>	<b>Attended posters (odd numbers) should be presented by the author</b>
16.00	Alexander Bowles	Phylogenomic analyses reveal the genomic novelties accompanying the major transitions of plant life
16.20	Angelo Moerland	Target enrichment provides deeper insight in phylogenetic relationships in <i>Saxifraga</i> despite use of degraded DNA
16.40	Annabelle de Vries	Seed size evolution and biogeography of Ptychospermatinae (Arecaceae)
17.00	Juniper Kiss	Phylogenetic signal in subgenus <i>Rubus</i> (brambles, blackberries) leaflet shape using geometric morphometrics
17.20	<b>Summing up</b>	<b>Mark Wilkinson, President of the Systematics Association</b>
17.25	<b>Poster session</b>	
18.00-19.00	<b>Reception</b>	<b>Presentation of prizes and closing remarks (please remove all posters before the reception)</b>

Organised by Ellinor Michel, Karen Siu Ting, Yvette Harvey and Xavier Aubriot, with support from:



## TALK ABSTRACTS - LISTED IN ALPHABETICAL ORDER

### **Molecular systematics of cone snails (Gastropoda: Conidae)**

**Samuel Abalde**<sup>1</sup>, Manuel J. Tenorio<sup>2</sup>, Rafael Zardoya<sup>1</sup>

<sup>1</sup>Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, Spain

<sup>2</sup>Departamento CMIM y Q. Inorgánica-INBIO, Facultad de Ciencias, Universidad de Cadiz, Cádiz, Spain

Cone snails are one of the most diverse groups of marine animals, including more than 900 species in all tropical and subtropical seas. This astonishing diversity, as well as the beauty of their shells, has attracted the interest of biologists, naturalists and collectors, who have dedicated years to study and classify them. Molecular systematics has been an important tool on these studies, defining new species and synonymizing others. However, this tool relies on the accuracy of the databases. Analyzing the more than 2000 COI sequences of cone snails available on Genbank we have seen that between 10-20% of them are incorrectly identified, which could potentially affect all the downstream analysis based on these sequences. On this talk, I will try to identify the reasons that have led to this situation. This study can also provide valuable information, which could help us, hopefully, to prevent making the same mistakes in the future.

### **Bayesian Estimation of Species Divergence Times Using Correlated Quantitative Characters**

**Sandra Álvarez-Carretero**<sup>1</sup>, Anjali Goswami<sup>2,3</sup>, Ziheng Yang<sup>2</sup>, Mario dos Reis<sup>1</sup>

<sup>1</sup>School of Biological and Chemical Sciences, Queen Mary University of London, London E1 4NS, UK.

<sup>2</sup>Department of Genetics, Evolution and Environment, University College London, London WC1E 6BT, UK.

<sup>3</sup>Department of Life Sciences, The Natural History Museum, London SW7 5DB, UK.

Discrete morphological data have been widely used to study species evolution, but the use of quantitative (or continuous) morphological characters is less common. We have implemented a Bayesian method to estimate species divergence times using quantitative characters, following the Brownian diffusion model with character correlation and character variation within populations. Through simulations, we demonstrate that ignoring the population variation and the correlation among characters leads to biased estimates of divergence times and rate. We apply our new method to the analysis of cranium landmarks and molecular data from carnivoran mammals. Our results show that time estimates are affected by the type of data analysed and whether the correlations and population noise are accounted for or ignored in the analysis. Our method is implemented in the program MCMCTree for Bayesian inference of divergence times.

## What can relationships between genes tell us about events in genome evolution?

Alan J. Beavan<sup>1</sup>, James W. Clark<sup>2,3</sup>, Davide Pisani<sup>1,2</sup>, Philip C. J. Donoghue<sup>2</sup>

<sup>1</sup>School of Biological Sciences, University of Bristol

<sup>2</sup>School of Earth Sciences, University of Bristol

<sup>3</sup>Department of Plant Sciences, University of Oxford

The coding content of genes can evolve by duplication, transfer, loss and *de novo* gene formation. Extreme examples of duplication and transfer are whole genome duplication and hybridisation respectively, which contribute to the evolution of populations by increasing the genetic material on which evolutionary forces can act. Here I apply methods which reconcile gene trees with an overarching species tree in order to estimate the rates of duplication, transfer and loss in three lineages proposed to have undergone whole genome duplication with hybridisation. These are wheat, oleaceae and eudicots, which represent progressively more ancient events. We show high rates of transfer from one branch to another, can be evidence for hybridisation and that this signal is strongest in more recent hybridisation events. We propose that these methods can be applied to whole genome duplication across the tree of life.

## Phylogenomic analyses reveal the genomic novelties accompanying the major transitions of plant life

Alexander Bowles<sup>1</sup>, Ulrike Bechtold<sup>1</sup>, Jordi Paps<sup>1</sup>

<sup>1</sup>University of Essex, UK

Identifying the genomic changes that have accompanied the origin of distinct plant groups is key to unravelling the molecular basis of biological innovations. In the last decade, the quantity and quality of complete genomes has dramatically increased, allowing for large-scale phylogenomic comparisons. Approaches that utilise a phylogenetic framework to perform comparative genomics will inform our understanding of the influences of speciation and duplication on gene family innovation, expansion and reduction. Using a phylogenomics pipeline incorporating data for 208 species, evolutionarily conserved gene innovations across the plant phylogeny were identified. Analyses has revealed large numbers of core gene novelties in the ancestors of Embryophyta and Streptophyta, likely involved in the transition of plants from water to land and the evolution of multicellularity. Gene Ontology analysis has identified the functional changes that have accompanied major plant developments. These results will help us to understand the influence of genomic innovations on plant diversification.

## **Seed size evolution and biogeography of Ptychospermatinae (Arecaceae)**

**Annabelle de Vries**<sup>1</sup>, Pablo Gómez Barreiro<sup>1</sup>, Peter van Welzen<sup>2,3</sup>, William Baker<sup>1</sup> & Sidonie Bellot<sup>1</sup>

<sup>1</sup>Royal Botanic Gardens, Kew, Richmond, Surrey, UK

<sup>2</sup>Naturalis Biodiversity Center, Leiden, The Netherlands,

<sup>3</sup>Institute Biology Leiden, Leiden University, Leiden, The Netherlands,

Seed size evolution can be influenced by habitat, plant size and dispersers size, and may in return constrain the biogeography of plant lineages. Palms (Arecaceae) occur in all tropical regions, including remote islands. Seed size varies more than one order of magnitude across the family, raising questions about the drivers and the biogeographical consequences of seed size evolution in palms. To better understand seed size evolution in the family we studied species of the subtribe Ptychospermatinae, which have fruits from <1 cm to 4.9 cm long, and are found in South East Asia, Australia and the Pacific Islands.

Ptychospermatinae seeds available in the Kew collections were measured using a non-destructive approach based on X-ray imaging of the fruits. Seed size, habitat, height and distribution of species were then analysed together in a phylogenetic context to test hypotheses about seed size evolution and biogeography in Ptychospermatinae. Our results show that seed size evolution was not influenced by plant height, habitat or species distribution. The ancestral fruit sizes before dispersal and the dispersals across oceanic gaps suggest the ancestral dispersers were small sized like flying mammals or birds.

## **Untangling the web-using novel methods to explore the evolution of spider (order Araneae) venom**

**Leah Fitzpatrick**

Imperial College London/Natural History Museum

The spiders (Araneae) are an order of arthropod whose success lies predominately within their application of venom. As a whole, the evolution of venom is poorly understood, yet alone within the spiders. A novel combination of programmes (PHYLIP, Multi Variate Statistic Package (MVSP) and PAJEK Networking) attempted to investigate the driving forces behind spider venom using unconventional methods. Focus is given predominately to the methods in this presentation, including a potential way of reviving distance matrices in modern systematics.

Output from the programmes concluded that despite venoms targeting an array of taxa, molecularly they are immensely conservative on an inter and intraspecific level. Using the results, it was concluded that this is because they evolved at the same time as their main prey (insects) and adapted themselves to exclusively target their synapses, which corroborates with current thinking.

## Exploring the evolution of the lichenicolous lifestyle within the Ascomycota

Rowena Hill<sup>1</sup>, Samantha Fernández-Brime<sup>2</sup>, Lucia Muggia<sup>3</sup>, David Hawksworth<sup>1</sup>, Ester Gaya<sup>1</sup>

<sup>1</sup>Comparative Plant and Fungal Biology, Royal Botanic Gardens, Kew, UK

<sup>2</sup>Department of Botany, Swedish Museum of Natural History, Stockholm, Sweden

<sup>3</sup>University of Trieste, Department of Life Sciences, Trieste, Italy;

Lichenicolous fungi are pathogens, saprotrophs or commensals which grow obligately on lichens. The lichenicolous habit has evolved many times, with species found in many families across the Ascomycota, the phylum to which the majority of lichenicolous fungi belong. They are, however, often missing from the general consciousness of fungal strategies, and so provide a novel avenue of research regarding fungal diversity and evolution. In this study, a range of lichenicolous fungi from various localities and lichen hosts have been sequenced - including novel species - and molecular data from previously sequenced lichenicolous fungi have been collated from literature. Species were resolved in a broad, multilocus phylogeny of the Ascomycota, alongside diverse taxa such as endolichenic, mycoparasitic and rock-inhabiting fungi, and an ancestral state reconstruction was performed to show how a lichenicolous perspective influences the big picture of fungal evolution within the Ascomycota.

## Phylogenetic signal in subgenus *Rubus* (brambles, blackberries) leaflet shape using geometric morphometrics

Juniper B. Kiss<sup>1</sup>, Dániel G. Knapp<sup>2</sup>, Gábor M. Kovács<sup>2</sup>, Michal Sochor<sup>3</sup>, Nigel Cooper<sup>4</sup>

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<sup>4</sup>Anglia Ruskin University, Global Sustainability Institute, Cambridge, UK

Subgenus *Rubus* (brambles, blackberries) is one of the most taxonomically challenging groups of dicots and their morphology-based classification has not been consistent with their molecular phylogeny. Here, we combined geometric morphometrics with molecular analysis to test whether leaf morphology is a reliable identification character. A total of 230 leaves were imaged from different environments in the UK. We conducted a three-loci molecular analysis using *ITS*, *matK* and *trnL-trnF* regions for 23 representative samples. Using Canonical Variate Analysis (CVA), the five-foliolate leaf shapes clustered according to the different environments of each bramble haplotype. Using squared-change parsimony, the molecular phylogeny of the haplotypes was projected into the leaflet morphospace and a phylogenetic signal was statistically significant ( $P < 0.05$ ) in between different haplotypes. These results suggest that each haplotype has different shapes in different environments, while the overall leaf shape differences of haplotypes could be explained by their phylogeny.

## Target enrichment provides deeper insight in phylogenetic relationships in *Saxifraga* despite use of degraded DNA.

Michelangelo S. Moerland<sup>1,2</sup>, William J. Baker<sup>1</sup>, Julie A. Hawkins<sup>2</sup>, Jurriaan M. de Vos<sup>1,3</sup> & Wolf L. Eiserhardt<sup>1,4</sup>

<sup>1</sup>Comparative Plant and Fungal Biology, Royal Botanic Gardens, Kew, Richmond, Surrey, UK

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<sup>4</sup>Department of Bioscience, Aarhus University, Aarhus, Denmark

The species-rich genus *Saxifraga* L. (> 440 spp.) is a long-standing model for the study of evolutionary histories of arctic-alpine flora, but is additionally well-known for its complex genetic patterns resulting from radiations and hybridization. Previous phylogenetic studies based on Sanger sequencing resolved relationships among clades, while species-level relationships are obscured by polytomies and polyphyletic taxa. Furthermore, silica collected sample acquisition is often limiting in species-level phylogenetics for large genera. To overcome both limitations, we employed a target enrichment approach to resolve phylogenetic relations within *Saxifraga*, using mostly DNA from herbarium accessions. We used custom RNA baits to capture 329 putative single-copy nuclear loci. Subsequently we inferred phylogenetic relationships of 313 accessions. In >150 year old herbarium material over half of target loci could still be sequenced, thus eliminating the need for an infeasible fieldwork campaign. A new species tree and its implications are presented and informative markers are identified for future studies. While target enrichment has recently become a popular method we confirm its benefit in building trees with closely related species with a complex coalescent history.

## Inferring the temperature at which the Last Universal Common Ancestor lived

Edmund R. R. Moody<sup>1</sup>, Tom. A. Williams<sup>1</sup>

<sup>1</sup>University of Bristol

Cellular life is incredibly diverse, and although split into different domains, shares a common ancestor. Reconstructing the Last Universal Common Ancestor (LUCA) is key to understanding how early life evolved. Here, we reconstruct LUCA by comparing extant organisms and applying statistical models of genome evolution to determine which genes and proteins were present at the root of the tree of life. Amino acid content can be used as an indicator of the optimal growth temperature of prokaryotes, even when only a subset of the proteome is known. Amino acid compositions of extant organisms were examined and used to predict their growth temperature. These predictions were compared against values from the scientific literature and a strong correlation was found. We then reconstruct a proteome for LUCA, using an improved phylogenetic model. We conclude LUCA was adapted to cooler temperatures, whereas the last archaeal and bacterial common ancestors were hyperthermophiles.

## Genomic insights into the origin and evolution of the sweet potato

**Pablo Muñoz-Rodríguez**<sup>1</sup>, Tom Carruthers<sup>1</sup>, John R.I. Wood<sup>1</sup>, Robert W. Scotland<sup>1</sup>

<sup>1</sup>Department of Plant Sciences, University of Oxford, South Parks Road, OX1 3RB Oxford, United Kingdom

Despite being one of the most important crops in the world, most questions pertaining to the origin of the sweet potato (*Ipomoea batatas* (L.) Lam.) have never been satisfactorily answered. Our contribution presents the results of a comprehensive study of the group of species closely related to the sweet potato using genomic data. We generated a robust phylogenetic framework that allowed us to investigate the origin and evolution of the crop. We identified the wild species from which the sweet potato most probably evolved and revealed that this species had a dual role in the origin of the crop through an ancient hybridisation event. Furthermore, we provide a timeframe for the evolution of the sweet potato and its storage root. These results have important implications in our understanding of sweet potato evolution and its domestication, as well as for the potential use of wild species in breeding programmes.

## An island radiation of burrowing snakes (Serpentes: Uropeltidae)

**Filipa L. Sampaio**<sup>1,2</sup>, Julia J. Day<sup>2</sup>, David J. Gower<sup>1</sup>

<sup>1</sup> Department of Life Sciences, Natural History Museum, London, UK

<sup>2</sup> Department of Genetics, Evolution and Environment, University College London, London, UK

Uropeltidae, commonly known as shieldtails, is a family (8 genera, 55 species) of poorly studied, small fossorial (burrowing) snakes distributed in southern India's Western Ghats and Sri Lanka. Uropeltids show morphological adaptations to fossoriality, including strongly reinforced skulls for headfirst burrowing. Their diverse snout shapes are likely associated with distinct digging behaviours, habitat use and/or diets. All Sri Lankan uropeltids belong to the genus *Rhinophis*, and are considered to be the result of a single colonisation event from India. This biotic dispersal and subsequent adaptation to a seemingly wider range of island environments than inhabited by their mainland relatives might have promoted diversification of shieldtails in Sri Lanka. Insights will be presented into the morphological, environmental and species diversity and diversification of *Rhinophis*, based on quantitative analyses of traits in the context of a new molecular phylogeny.

## A new comprehensive phylogeny of the Tardigrada may alter the hypotheses for their colonisation of Antarctica

**Katherine Short**<sup>1,2</sup>, Sandra McInnes<sup>1</sup>, Davide Pisani<sup>2</sup>, Chester Sands<sup>1</sup>, Peter Convey<sup>1</sup>

<sup>1</sup> Biodiversity, Evolution and Adaptation Team, British Antarctic Survey, UK

<sup>2</sup> School of Earth Sciences, University of Bristol, UK

Internal phylogenetic relationships within the Tardigrada are poorly resolved, and the studies that have been undertaken in this area are generally restricted to certain groups within the phylum, as well as rarely including molecular analyses of divergence times. In this ongoing study, we infer the phylogeny of the phylum using 18S, 28S and CO1 sequences obtained from GenBank. To investigate the colonisation history of tardigrades in Antarctica, further newly-available sequences for *Acutuncus antarcticus* and *Mesobiotus furciger* for different geographical regions were added. Trees were created using Maximum Likelihood and Bayesian methods, with divergence times estimated using a relaxed clock model. These were then mapped to a biogeography matrix to estimate biogeographic patterns. Ongoing analyses suggests that the biogeographic history of *A. antarcticus* and *M. furciger* may be different to that previously proposed with lineages being much older than previously thought.

## An old love affair: Genomic data reveal past hybridization and suggest evolution of reinforcement in sympatric populations of two montane grasshoppers from the Iberian Peninsula

Vanina Tonzo<sup>1,3</sup>, Anna Papadopoulou<sup>2</sup>, Joaquín Ortego<sup>1</sup>

<sup>1</sup> Department of Integrative Ecology, Estación Biológica de Doñana (EBD-CSIC); Av. Américo Vesputio 26 – 41092; Seville, Spain

<sup>2</sup> Department of Biological Sciences, University of Cyprus; Kallipoleos 75 – 20537; Nicosia, Cyprus

<sup>3</sup> Dept .de Biologia Animal, Facultat de Biologia; Universitat de Barcelona; Av. Diagonal 645 - 08028; Barcelona, Spain

When two closely related species get into secondary contact can experience hybridization. Under certain circumstances, however, this process may promote the evolution of reproductive isolation by increasing the selective pressure against hybrids in a process known as reinforcement. *Omocestus minutissimus* and *O. uhagonii* are two Montane grasshopper species of the subgenus *Dreuxius*, showing partially overlapping distributions in the Central Mountain System of the Iberian Peninsula. To reconstruct the evolutionary history of these taxa we sampled sympatric and allopatric populations of both species. We used the RAD-seq approach to obtain SNPs information and then applied coalescent-based modeling techniques to evaluate alternative scenarios of contemporary/past hybridization and disruption of gene flow. Our results support a scenario where, despite the occurrence of past, episodic strong gene flow, reproductive barriers have probably consolidated because of a reinforcement process that prevents contemporary hybridization. This evidence support that speciation-with-gene-flow may be more prevalent in nature than formerly acknowledged.

## King or Royal Family? Multilocus Phylogeography and Species Delimitation in the King Cobra (*Ophiophagus hannah*).

Rhiannon Carys Williams<sup>1</sup>, Gowri Shankar<sup>2</sup>, Wolfgang Wüster<sup>1</sup>

<sup>1</sup>Molecular Ecology and Fisheries Genetics Laboratory, School of Natural Sciences, Bangor University),

<sup>2</sup>Agumbe Rainforest Research Station

King Cobras (*Ophiophagus hannah*) are widely distributed across Asia, often in areas of high endemism. This study aims to determine if *O. hannah* represents a cryptic species complex and to contextualise observed diversity via population biogeography.

A maximum likelihood phylogenetic tree was produced using mitochondrial DNA loci (16s, nd4, cytb). Nuclear DNA loci (rag1, prlr, nt3) were used to test if mitochondrial clades denoted independent organismal lineages. Haplotype sharing was assessed in Network and genetic distance estimated using POFA. Bayesian species delimitation was undertaken in BPP3 and congruence with mtDNA clades tested. The mitochondrial phylogeny supports 4 major clades. BPP also supports the mtDNA clades as separate species. Our results thus suggest that *O. hannah* represents a species complex. However, further analysis is necessary prior to species delimitation. As *O. hannah* populations are decreasing rapidly across its range, widespread conservation of this vulnerable species is vital to preserve cryptic diversity.

## POSTER ABSTRACTS - LISTED IN ALPHABETICAL ORDER BY FIRST AUTHOR

### **1. African affinities of the mangrove flora of the Farasan Islands, Saudi Arabia as revealed from the molecular phylogeny of *Avicennia marina* (Forssk.) Vierh**

**Samah Alharbi<sup>1</sup>** & Alastair Culham<sup>1</sup>

<sup>1</sup>School of Biological Science, University of Reading, UK

The Farasan Archipelago in the southeastern part of the Red Sea is at the northern range margin of *Avicennia marina*. The islands host the best stands of *A. marina* in the area, which are fragmented and show poor growth due to the harsh conditions prevailing in the Red Sea. These forests play a significant role in the conservation of biological diversity in the islands and serve as nesting sites for migratory birds. Recently, the accelerating development in the Archipelago has led to many healthy mangrove areas becoming endangered communities. This pressure, coupled with global climate change and sea level rise, may lead to increase the loss of the islands' populations. This research aims to assess the affinities of *A. marina* in the islands using combined nuclear DNA phylogeny and Bayesian dating analysis. The result suggests a closer relationship to Eastern Africa, which may have colonised the islands in the late Pleistocene.

### **2. A Taphonomic Analysis of Mammalian Fossils Excavated from the Cemeteries and Rock-Cut Tombs of Qau el-Kebir, Egypt**

**Nicolas Baird<sup>1,2</sup>**, Pip Brewer<sup>2</sup>, Spyridoula Pappa<sup>2</sup>

<sup>1</sup>Dept. of Life Sciences, Imperial College London

<sup>2</sup>Dept. of Earth Sciences, NHM

A series of excavations in the early 1900s at grave sites near Qau el-Kebir, Egypt recovered hundreds of vertebrate fossils that represent the only surviving remains of an unknown deposit. This study describes the taxonomic composition and taphonomic history of the mammalian remains. Taphonomic variables were analysed to determine the nature of the original deposit(s) and understand the impact of biotic and abiotic factors on the assemblage. The mammalian remains were identified to skeletal element and taxon, and taphonomic variables including weathering, abrasion, surface modifications, fracturing, and fragmentation were recorded and compared among taxa. The Qau collection is dominated by Artiodactyla, and signs of both carnivore activity and human-mediated selection are present. The distributions of taxa, skeletal elements, and taphonomic variables imply site formation in a near-shore environment. The collection is interpreted as a combination of remains derived from multiple deposits throughout the Late Pleistocene.

### 3. Phylogenomics of the camaenid land snails, a shuffling of subfamilies

**Gizelle A. Batomalaque**<sup>1,2,3</sup>, Adnan Moussalli<sup>4</sup> and Gary Rosenberg<sup>1,2</sup>

<sup>1</sup>Malacology Department, Academy of Natural Sciences of Philadelphia, Drexel University, Philadelphia, Pennsylvania, USA

<sup>2</sup>Department of Biodiversity, Earth and Environmental Science, College of Arts and Sciences, Drexel University, Philadelphia, Pennsylvania, USA

<sup>3</sup>Institute of Biology, College of Science, University of the Philippines-Diliman, Quezon City, Philippines

<sup>4</sup>Sciences Department, Museum Victoria, Melbourne, Australia

Camaenidae is a hyperdiverse family of land snails. Recent molecular evidence showed that the camaenids are restricted to the Old World and are confamilial with the Bradybaenidae. There are four recognized subfamilies—Bradybaeninae, Camaeninae, Hadrinae, and Helicostylinae. Using exome sequences, we show that all subfamilies except for Hadrinae are paraphyletic or polyphyletic. We thus present a reorganization of the species belonging to each camaenid subfamily. In terms of their geographic ranges, Bradybaeninae and Camaeninae are comprised of species in continental Asia, Japan, and the Philippines. Helicostylinae is restricted to the Philippines, Taiwan and small islands off the coast of Borneo and Sulawesi, while Hadrinae now has the Philippines as its northern limit. Furthermore, we show that Polygyridae is the sister clade of the Camaenidae.

### 4. Plants of the Caribbean – Unraveling the phylogeny and systematics of *Casearia* Jacq.

**Astrid de Mestier**<sup>1\*</sup>, Jorge Gutiérrez Amaro<sup>2</sup>, Grisca Brokamp<sup>1</sup>, Marcela Celis<sup>3</sup>, Thomas Borsch<sup>1</sup>

<sup>1</sup>Freie Universität Berlin, Botanischer Garten Botanisches Museum Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany; \* ademestier@zedat.fu-berlin.de

<sup>2</sup>Universidad de La Habana, San Lázaro y L. Plaza de la Revolución, La Habana, Cuba

<sup>3</sup>Universidad del Norte, Departamento de Química y Biología, Km. 5 Vía Puerto Colombia, Área Metropolitana de Barranquilla, Colombia

The Caribbean region, a mosaic of islands and coasts, is one of the global biodiversity hotspots. Nevertheless, few phylogenetic studies are available to retrace the evolutionary history of this region. Here, we are reconstructing the phylogeny of *Casearia* Jacq. whose systematic placement still remains uncertain. 70 of its 180 species are found in the Neotropics and all around the Caribbean. Thus, it is an ideal model group to increase knowledge on the species diversification patterns that formed today's biodiversity of the region. Preliminary results from maximum parsimony, maximum likelihood, and bayesian inference analyses of trnK-matK, rpl16, and rps4-trnLF sequences indicate that the genus is not monophyletic. Future analyses of divergence time estimates and biogeographical methods will likely reveal key aspects in the species diversification of this plant lineage and by that part of the evolutionary history of the region.

## **5. Comparative genomics and Phylogenetics of low nutrient environment carnivorous plant species**

**Wessam Felemban<sup>1</sup>, Alastair Culham<sup>1</sup>**

<sup>1</sup>School of Biological Science, University of Reading

Next-generation sequencing (NGS) technologies have improved the understanding of many aspects of comparative evolution, including the relationships between taxa at varying levels of classification. The life-history, including remarkable morphological, physiological, and ecological features, make carnivorous plants an ideal model for studying a wide range of ecophysiological and ecological evolutionary processes. Two sister lineages of Caryophyllales Droseraceae (194 species), with hermaphrodite flowers and very little interspecific hybridization, and Nepenthaceae (130 species), with unisexual flowers and numerous fertile hybrids found in the wild are both carnivorous. This offers the opportunity to understand rates and patterns of speciation under challenging environmental conditions, but fundamentally different breeding patterns. Affordable genomics approaches offer the tools to study these groups from a phylogenetic perspective.

In this study, we will use Illumina HiSeq data to resolve the phylogenetic relationships between Droseraceae and Nepenthaceae. At the same time, the whole chloroplast genome analysis data will be used to build subsequent phylogenetic trees based on the patterns of differences in these alignments.

## **6. Untangling the web-using novel methods to explore the evolution of spider (order Araneae) venom**

**Leah Fitzpatrick**

Imperial College London/Natural History Museum

The spiders (Araneae) are an order of arthropod whose success lies predominately within their application of venom. As a whole, the evolution of venom is poorly understood, yet alone within the spiders. A novel combination of programmes (PHYLIP, Multi Variate Statistic Package (MVSP) and PAJEK Networking) attempted to investigate the driving forces behind spider venom using unconventional methods. Focus is given predominately to the methods in this presentation, including a potential way of reviving distance matrices in modern systematics.

Output from the programmes concluded that despite venoms targeting an array of taxa, molecularly they are immensely conservative on an inter and intraspecific level. Using the results, it was concluded that this is because they evolved at the same time as their main prey (insects) and adapted themselves to exclusively target their synapses, which corroborates with current thinking.

## 7. Molecular palaeobiology of Ecdysozoa

**Mattia Giacomelli**<sup>1</sup>; Richard J. Howard<sup>3</sup>; Jesus Lozano-Fernandez<sup>1,2</sup>; Matt Wills<sup>4</sup>; Gregory D. Edgecombe<sup>3</sup>; Philip Donoghue<sup>1,2</sup> & Davide Pisani<sup>1,2</sup>

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Ecdysozoa is a superclade uniting eight phyla of protostome animals, which together constitute the overwhelming majority of extant Metazoa. Whilst phylogenetically robust, its internal topology remains unresolved; of particular concern is the validity of the clade Cycloneuralia, a group uniting Scalidophora and Nematoida. Furthermore, the timing of ecdysozoan lineages divergences in geological time is under debate, with molecular clock analyses predating the first appearance of ecdysozoan fossils. To address these obstacles, we assembled a large phylogenomic dataset adding data from ecdysozoan taxa with poor molecular data and applied Bayesian methods to infer the phylogeny and divergence times of ecdysozoan lineages. Our phylogenetic analysis support a sister group relationship between nematoids and panarthropods (rendering Cycloneuralia paraphyletic), and our fossil-calibrated relaxed molecular clock analyses show that the lag between genetic isolation of the ecdysozoan lineage and its representation in the fossil record is not as considerable as has been previously purported.

## 8. Unearthing the Taxonomic History of the “Great Goldilocks Moss”

**Isuru U. Kariyawasam**<sup>1,2</sup>, Michelle J. Price<sup>3</sup>, Jaakko Hyvonen<sup>4</sup>, Neil E. Bell<sup>1</sup>, David G. Long<sup>1</sup>, Robert Mill<sup>1</sup>

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The binomial *Polytrichum commune* Hedw. (Bryophyta, Polytrichaceae) was coined by Linnaeus (1753) and validated by Hedwig (1801) in his *Species muscorum frondosorum*, the starting point of moss nomenclature (excepting the Sphagnaceae). The taxon had previously been identified and illustrated by Dillenius (1747) as the “Square-headed great Goldilocks Moss” and referenced in the works of many other pre-Linnaean European botanists. However, even 200 years after its valid publication, *P. commune* remains to be precisely typified. The interesting element of this work has been to establish the roots of the entity understand how the concept has developed over time and outline its taxonomic circumscription based on the validating description, as well as to link the name to a physical specimen selected from a diverse mixture of stems mounted on a single herbarium sheet. The *P. commune* concept has now been established and a lectotype chosen from the original material.

## 9. Phylogenetic relationships of the tribe Neospartoneae (Verbenaceae) based on molecular data

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Neospartoneae is a small tribe in Verbenaceae, native to southern and central Andes. It comprises seven species in three genera: *Diostea*, *Lampayo* and *Neosparton*. Previous chloroplast DNA phylogenetic studies first identified Neospartoneae as a clade. However, due to the limited sampling and molecular data, evolutionary relationships within Neospartoneae remain unclear. In this study, plastid and nuclear DNA were used to reconstruct phylogeny with almost complete taxon sampling. Maximum likelihood and Bayesian analyses were conducted using single-locus and concatenated datasets to generate gene trees. Species tree was reconstructed by Bayesian multispecies coalescent analyses. The generic relationships are well resolved and confirm the monophyly of this Neospartoneae and each genus under this tribe. The topologies show that *Diostea* is sister to *Lampayo* and has a more distant phylogenetic relationship with *Neosparton*. This study presents a first species-level phylogeny of Neospartoneae and provides insight to character evolution of this tribe.

R. G. OLMSTEAD ET AL. Phylogeny of Neospartoneae (Verbenaceae)

## 10. Evolution and Distribution of *Boeckella* (Calanoida: Copepoda) in the Southern Hemisphere

Claudia S. Maturana<sup>1,2</sup>, Sebastian Rosenfeld<sup>3</sup>, Javier Naretto<sup>1,2</sup>, Jennifer Jackson<sup>4</sup>, Peter Convey<sup>4</sup>, Ian Duggan<sup>5</sup>, Ian Hogg<sup>5,6</sup> and Elie Poulin<sup>1,2</sup>

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*Boeckella* is a calanoid copepod genus that currently includes 42 described species. The genus has a Gondwanan distribution. We studied the evolution and distribution of the species within the genus using molecular approaches applied to specimens previously identified using classical morphological taxonomy. We used a combination of molecular markers, targeting one fast-evolving mitochondrial (*cox1*) and two slow-evolving nuclear markers (28S and ITS). Phylogenetic reconstructions were prepared using Maximum Likelihood and Bayesian Analyses. Nuclear and mitochondrial data generally confirmed the classical species identifications, and identified distinct South American and Australasian clades. Within South America, *cox1* showed the presence of new evolutionary units within specimens morphologically assigned to *B. poppei*.

## **11. Molecular systematics and phylogeography of the South African mole-rat genus, *Cryptomys***

**Hana Merchant**<sup>1</sup>, Nigel Bennett<sup>2</sup> & Chris Faulkes<sup>1</sup>

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The African mole-rat family (Bathyergidae) are an extensive sub-Saharan radiation of subterranean rodents. Historically, their systematics have been confused due to convergence in phenotype, and one of the six genera, *Cryptomys*, has not been subject to recent revision. This project analysed 46 DNA samples from *Cryptomys* populations across their entire South African range, using sequence data from four genes: mitochondrial cytochrome b, and nuclear BRCA1, TTR, and vWF. Following phylogenetic analysis, we inferred seven novel genetically distinct monophyletic clades, indicating between five and seven potential species within the genus, with the possibility of a number of sub-species. The phylogeography of the genus will be discussed in the context of changes in the vegetative and drainage systems across South Africa since the divergence of *Cryptomys*, 12-10 million years ago. This provides new insight into the validity of species within the genus, and their current geographical patterns of distribution.

## **12. Crossing the Speciation Threshold: Evolution in a Complex Archipelago**

**Fionn Ó Marcaigh**<sup>1</sup>, David J. Kelly<sup>1</sup>, Darren P. O'Connell<sup>1</sup>, Adi Karya<sup>2</sup>, Kangkuso Analuddin<sup>2</sup>, and Nicola M. Marples<sup>1</sup>.

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Ever since Darwin and Wallace, island populations have been pivotal in understanding how new species evolve. The birds of Sulawesi, Indonesia, represent an ideal study system to examine evolutionary processes across islands and species. A region of complex biogeography and high endemism, the systematics of Sulawesi's fauna remains poorly understood. We have been looking at genetic patterns in bird populations across southeast Sulawesi, using barcoding genes ND2 and ND3. Different species show different patterns of isolation, as certain species can more easily cross between islands. The genetic work is supported by analyses of morphology and song. The patterns of isolation suggest that wingspan is not the only important aspect of bird biology which determines movement. Awareness of the drivers of isolation may help predict which populations are most likely to undergo allopatric speciation. We hope our discoveries will inform conservation efforts of the unique ecosystems they reveal.

## 13. Information Content of Trees: Three-Item Statements Inference Rules and Dependency

**Valentin Rineau**<sup>1</sup>, René Zaragüeta<sup>2</sup> and Stéphane Prin<sup>2</sup>

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Several supertree and phylogenetic methods use three-item statements, minimal statements of degree of kinship relationship between items (taxa, biogeographic areas, etc...). Because of their fundamental role in phylogenetics, three-item statements are at the heart of much methodological research. We analysed the different possible interactions within a set of three-item statements in order to propose a classification of three-item statements couples and trace the link between them and the emergence of dependency. A better understanding of the dependency between three-item statements allows us to propose a procedure for suppressing this dependency by fractional weighting. The three-item statements weighted in this way reflect the phylogenetic information content of any hierarchical structure. Fractional weighting becomes necessary for any analysis and phylogenetic metrics using three-item statements.

## 14. Modelling the vulnerability of endemic montane flora to climate change in the Australian Wet Tropics

**Lizzie Rooble**<sup>123</sup>, Darren Crayn<sup>3</sup>, Jon Lloyd<sup>1</sup>

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While many species are responding to climate change by migrating polewards and upward in elevation, endemic species already living at or near mountaintops are particularly vulnerable to extinction under predicted climate scenarios. Due to the sensitivity of the cloud forest ecosystem, high rates of endemism, and isolation of habitats, plant species in the Australian Wet Tropics are highly sensitive to the effects of climate change. This study utilizes Maxent, a species distribution model, to predict the potential future distribution of 37 endemic mountaintop plant species at three time periods in the twenty-first century (2035, 2055, 2085) and for two climate scenarios: RCP 4.5 and RCP 8.5. The models created in this study provide quantitative predictions for species richness and available habitat through the rest of the century under two climate scenarios, which can help inform conservation decision-making in the Australian Wet Tropics. Endemic mountaintop flora are highly vulnerable to predicted climate scenarios and should be prioritized for ex-situ conservation.

## 15. Addressing Unresolved Taxonomic And Phylogenetic Questions In Australasian Dendroid Mosses

Diego S. Ganfornina<sup>1,2</sup>, Isuru U. Kariyawasam<sup>1,2</sup>, Mark Hughes<sup>1</sup>, Neil E. Bell<sup>1</sup>

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Bryophytes sit as highly successful descendants of the nexus between green algae and tracheophytes. Around 50% of bryophyta (mosses) derive from a rapid radiation in the pleurocarpous orders, which form a monophyletic group defined by a key innovation in reproductive branching. Previous studies identified an early-diverging order, the Hypnodendrales, which presents plesiomorphic characters informative for the evolution of pleurocarpy.

A dated phylogeny for the Hypnodendrales based on nuclear and plastid regions confirms its early-diverging position and generates hypotheses about extinction-driven current diversity.

An in-depth study targeting the Australasian *Hypnodendron vitiense*, *H. marginatum*, *Sciadocladus kerrii* and *S. menziesii* was undertaken using ITS2 and *rbcl*. *Hypnodendron vitiense* was found to be taxonomically tortuous and paraphyletic with respect to *H. marginatum* and taxonomic solutions are investigated. *Sciadocladus kerrii* and *S. menziesii* are resolved as monophyletic, concluding past taxonomic uncertainties. Studied taxa are hypothesised to present an intriguing evolutionary history with unique dispersal pathways.

## 16. A new Scaphander species from the Mar del Plata submarine canyon off Argentina

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*Scaphander* Montfort, 1810 is a genus of deep-sea soft-bottom gastropods composed of approximately 18 species distributed worldwide. Eilertsen and Malaquias (2013) revised the systematics of the genus in the Atlantic, and recognized eight valid species. Our study describes a new *Scaphander* species from novel samples obtained from the Argentine continental slopes, using morphological and molecular data. Shells, gizzard plates, radulae, and male reproductive systems were studied by optical and scanning electron microscopy, and compared with data from all other known *Scaphander* species. Bayesian molecular phylogenetics based on two mitochondrial (cytochrome *c* oxidase sub-unit I and 16S rRNA) and one nuclear (28S rRNA) genes, together with the molecular species delimitation method Automatic Barcode Gap Discovery were used to compare the novel samples with all known Atlantic species. Our results revealed that the Argentinian specimens have a distinct shell and penial papilla and are 13.1–13.9% distinct (COI uncorrected *p*-distance) from their closest relative, the northern amphi-Atlantic species *S. punctostriatus*.

## 17. The signal of morphological evolution in Lake Tanganyika cichlid fishes

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Lake Tanganyika cichlid fishes are considered classic examples of adaptive radiation, as they display rapid phenotypic and ecological diversification. To investigate morphological evolution in this radiation we combined phylogenetic and geometric morphometric data applying disparity-through-time (DTT) and models for continuous character evolution to the three most diverse LT tribes (Ectodini, Lamprologini and Tropheini). The DTT analyses revealed a signal of morphological convergence when these tribes are analysed together. However, when analysed separately this signal was only found in the Ectodini and Lamprologini, whereas morphological evolution for the Tropheini was no different from Brownian motion, showing that for complex radiations a clade by clade approach may be more informative. These results suggest that the Tropheini, the most recent radiation into LT, may have radiated into an ecological niche unoccupied by previous radiations, while the Ectodini and Lamprologini likely repeatedly occupied similar niches across the lake.

## 18. Systematics Informed Synthetic Biology

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Synthetic biology aims to re-engineer biological systems. Rational biological engineering can be facilitated through an understanding of the evolutionary context of biological entities. As an example we present a study of the estimated site specific nucleotide substitution rates around the ribosome binding site (RBS) of proteins conserved across the *Enterobacteriaceae* family. The RBS is a DNA regulatory motif that is important for engineering synthetic genetic circuits with specific protein expression levels. Our study demonstrates significant variation in nucleotide substitution rates across sites which can inform re-engineering of an RBS. Furthermore we indicate other opportunities for systematics informed synthetic biology and the potential impacts of genetically modified organisms on systematics.

## 19. A review of the *Festuca amethystina* group (*Poaceae*) phylogeny – a new look at the old problem

**Przemysław Tomczyk**<sup>1</sup>, Marcin Kiedrzyński<sup>1</sup>, Agnieszka Rewicz<sup>1</sup>, Tomasz Rewicz<sup>2</sup>, Paweł Wąsowicz<sup>3</sup>

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*Festuca amethystina* group contain 4 species (and 7 cytotypes) with complex phylogenetic connections. *Festuca tatrae*, one of the species from this group, is probably an ancestor for *Festuca amethystina* (4x), but this is questionable for some part of its geographical range. Hence, relation between *Festuca amethystina* cytotypes (2x, 4x) is unclear. Studied group contain also *Festuca norica*, which occurs in the Alps and includes three cytotypes (2x, 4x, 6x) and *Festuca jacutica*, which, interestingly, occurs in Siberia. In the literature there are different views on the evolutionary relationship of these species and different views if described group is legitimate.

Our work reviews current ideas concerning *Festuca amethystina* group phylogeny and makes a comparison between these ideas and own preliminary results. Studied species, despite close relationship, has different ranges (e.g. *Festuca amethystina*, *tatrae*), hence such research is important in understanding of genetic mechanisms which are responsible for ecological success of grasses.

## 20. Amphipods from the Abyss: Two new scavengers from the Wallaby-Zenith Fracture Zone in the East Indian Ocean

**Johanna N.J. Weston**<sup>1</sup>, Rachael A. Peart<sup>2</sup>, Alan J. Jamieson<sup>1</sup>

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Scavenging amphipods (Amphipoda) are a model taxon for ultra-deep sea ecology (4000 – 11,000 m). The Wallaby-Zenith Fracture Zone in the Indian Ocean, a non-subduction hadal area, offers a unique location to test drivers of speciation and phylogeography. As morphological identification of amphipods is challenged by phenotypic plasticity, 16S and COI mtDNA regions were sequenced to support identification or initiate a reverse taxonomic approach. Eleven species were identified from 4932 to 6546 m, two are new species and one of which is potentially the holotype for a new genus in the Alicellidae family. *Stephonyx* sp. nov. can be distinguished by the sigmoid shape of the basis on pereopod 5 and 6. The other species can be identified from allied *Tectovalopsis* spp. by the nearly parallel and subchelate palm of gnathopod 1, the strongly oblique and concave palm of gnathopod 2, and the outer ramus of uropod 3 being longer than the inner ramus.

## 21. Data, time & money: what is the best strategy to resolve the phylogeny of non-model organisms?

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Increasing the number of taxa and characters can affect the robustness of phylogenetic inferences. With the advent of phylogenomics, transcriptomes and (reduced) genomes are now widely used, but sequencing, assembling and comparing them can be expensive, time consuming and complex for non-model organisms. Our goal was to identify the strategy that would represent the best compromise between costs, time and robustness of the resulting tree. We sampled 32 transcriptomes of marine molluscs of the family Turridae. From these data, we extracted the most commonly used genes in gastropod phylogenies (COX1, 12S, 16S, 28S, H3 & 18S), full mitogenomes, and reduced exome. With each dataset, we reconstructed phylogenies and compared their robustness and accuracy. We evaluated the impact of missing data, the use of supertree and supermatrix methods and the cost (time and money) in order to identify the best compromise for phylogenetic data sampling in non-model organisms.

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# MEETING POLICIES

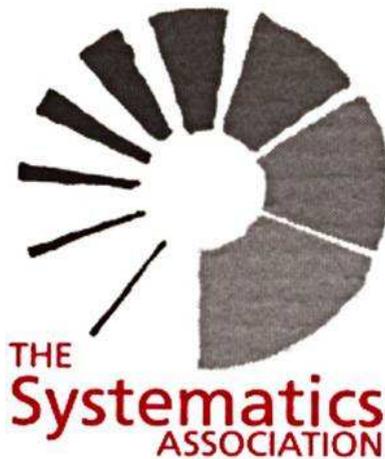
The Systematics Association Council wishes to promote a diverse programme of speakers and pool of registrants and has taken measures to encourage and support diversity. We welcome and encourage participation by everyone in the systematics community, and welcome feedback on how best to build on these 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 limit: **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, Yvette Harvey or Karen Siu Ting 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.

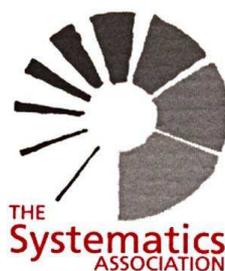


**The Systematics Association** is committed to furthering all aspects of systematic biology. It organises a vigorous programme of international conferences on key themes in systematics, including a series of major biennial conferences. The association also supports a variety of training courses in systematics 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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**Standard membership** - £20 (\$30 or €30) per year

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