

# YOUNG SYSTEMATISTS' FORUM

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22<sup>nd</sup> November 2019, 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>David Williams, President of the Systematics Association</b>
09.55	Watchara Arthan	Dissimilar but closely related? An unexpected example from dominant savannah grasses <i>Heteropogon</i> and <i>Themeda</i> (Poaceae:Andropogoneae)
10.15	Guilherme Roxo	Integrating biogeographical data and cytogenomic variation to elucidate the Apiaceae and Brassicaceae evolution within the Macaronesian islands
10.35	Miguel Angelo Brilhante	Do inflorescence height and genome size explain geographic range size of the Macaronesian <i>Aeonium</i> genus (Crassulaceae)?
10.55	Sonia Molino	The challenge of making the monograph of <i>Parablechnum</i> C.Presl, the largest genus within the family Blechnaceae (Polypodiopsida)
11.15	<b>Coffee &amp; Posters (attend even numbers)</b>	<b>Attended posters (even numbers) should be presented by the author</b>
12.00	Ali Budhi Kusuma	Biosystematics of bioactive actinobacterial strains isolated from Indonesian extreme environments: a pioneering study
12.20	Hend Abu Elmakarem	Phylogenomic and genomic analyses of anaerobic free-living eukaryote reveal the presence of a Hydrogenosome
12.40	Theo Llewellyn	Revisiting generic concepts in the Teloschistaceae (lichen-forming Ascomycota) using molecular phylogenetics, algorithmic taxa delimitation and molecular networks
13.00	Emily Phelps	Evidence for the underestimation of genetic diversity within an Afrotropical crab genus ( <i>Potamonantes</i> )
13.20	<b>Lunch and posters</b>	<b>(Light lunch provided for registered attendees)</b>
14.20	Nathan Vranken	Exploring the cichlid diversity of Lake Edward (East Africa)
14.40	Heleen Maetens	The <i>Enteromius</i> species (Cyprinidae) from the Lake Edward system (East Africa): geographic variation or cryptic diversity?
15.00	Joan Ferrer Obiol	Resolving recent radiations: phylogenomics of shearwaters
15.20	Karina Vanadzina	Global drivers of variation in cup nest size and parental effort in passerine birds
15.40	<b>Coffee &amp; Posters (attend odd numbers)</b>	<b>Attended posters (odd numbers) should be presented by the author</b>
16.20	Ahmed Hubini	Taxonomy and diversification of <i>Cyclamen</i> L. using next-generation sequencing approaches
16.40	Benedikt Kuhnhäuser	Targeted sequencing of 976 nuclear genes elucidates evolutionary relationships within the palm subfamily Calamoideae
17.00	Marcelo de Santis	The explanation problem in systematics
17.20	Ana Serra Silva	Looking for rogue taxa in supertrees by taking advantage of matrix representation
17.40	<b>Summing up</b>	<b>David Williams, President of the Systematics Association</b>
17.45	<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, Pablo Muñoz-Rodríguez and Xavier Aubriot, with support from:



**Dissimilar but closely related? An unexpected example from dominant savannah grasses *Heteropogon* and *Themeda* (Poaceae: Andropogoneae)**

**Arthan, Watchara**<sup>1,2,\*</sup>, Guillaume Besnard<sup>3</sup>, Luke T. Dunning<sup>4</sup>, Elizabeth A. Kellogg<sup>5</sup>, Jan Hackel<sup>1</sup>, Caroline E. R. Lehmann<sup>6</sup>, Jonathan Mitchley<sup>2</sup>, Maria Vorontsova<sup>1</sup>

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*Heteropogon* Pers. and *Themeda* Forssk. are ecologically critical pantropical grass genera, dominating savannah environments in Africa, America, Asia and Australia. Genome-skimming data acquired from herbarium specimens across the genera was used to generate a large dataset of plastome and nuclear genes. Phylogenomic trees revealed that *Heteropogon* and *Themeda* are polyphyletic groups. Phylogenetic positions of *Heteropogon* species are difficult to reconcile with traditionally studied morphological characters which record grass spikelets and inflorescence structure. Some *Heteropogon* are nested with *Themeda* clades. *Themeda* is split into several lineages which can be differentiated by the number of spikelets. Discordance among gene trees implies evolutionary mechanisms such as polyploidization and hybridization within the groups. The results challenge traditional classification into two genera. This work will also use species traits to understand niche evolution and contribute to the study of global savannah ecosystems and their response to climate change.

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**Integrating biogeographical data and cytogenomic variation to elucidate the Apiaceae and Brassicaceae evolution within the Macaronesian islands**

**Roxo, G.**<sup>1\*</sup>, M. Brilhante<sup>4</sup>, M. Moura<sup>3</sup>, M. Menezes de Sequeira<sup>2,3</sup>, A. Pereira<sup>1</sup>, J. Duque<sup>1</sup>, J.C. Costa<sup>1</sup>, P. Talhinas<sup>1</sup>, M.M. Romeiras<sup>1,4</sup>

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The families Apiaceae and Brassicaceae are represented by 35 and 64 endemic taxa, respectively, in the Macaronesia region. Genome-size analyses is an effective method in taxonomy and evolutionary biology. Using flow cytometry, we analysed the genome size of 93 species (52 from the Apiaceae family, and 42 from the Brassicaceae family) from all the Macaronesian archipelagos and Mainland Portugal. Our results revealed a tendency towards smaller genome sizes in insular endemic species, comparing with the continental species. Moreover, some native species (e.g. *Angelica lignescens* Reduron & Danton, *Crithmum maritimum* L., *Erysimum bicolor* (Hornem.) DC.) present population-level genomic diversity. Our data also support the ancestral relationships between the genera *Daucus* L. and the endemic monotypic genus *Melanoselinum* Schrad. & J.C.Wendl., and *Monizia* Lowe from the Madeira archipelago and the endemic genera *Tornabenea* Parl. from Cabo Verde.

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## Do inflorescence height and genome size explain geographic range size of the Macaronesian *Aeonium* genus (Crassulaceae)?

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*Aeonium* Webb. & Berthel. is considered the most speciose radiation of Macaronesia occupying a great diversity of habitat types. The genus encompasses a wide range of morphological diversity, including some species with more restricted ecological preferences (specialists) and others with more ubiquitous distributions (generalists). This study aims to relate inflorescence height and genome size of several *Aeonium* species endemic to the Canary Islands, comprising the natural distribution of specialists and generalists. We applied a holistic approach to explain the geographic range size of several *Aeonium* species based on reproductive traits and flow cytometry. According to the reproductive trait measure analysis, we observed that species that invest in taller inflorescences and more reproductive units have wider distributions. The cytogenomic results reveal that *Aeonium* species with larger genomes tend to have smaller occurrence areas corresponding to the most threatened species of the genus.

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## The challenge of making the monograph of *Parablechnum* C.Presl, the largest genus in the family Blechnaceae (Polypodiopsida)

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Blechnaceae is a fern family which comprises ~250 species whose centers of diversity are mostly found in tropical, subtropical and temperate areas of the southern hemisphere, although it also has representatives in the northern hemisphere. In the past, the family was considered to have 9-11 genera, but recent studies have reclassified the family into 25 genera, being *Parablechnum* C.Presl the largest, with ~67 species distributed throughout tropical-subtropical America, Austropacific and South Africa. The current classification of the genus may not be reliable enough for reasons such as the restrictive and local distribution of some species and the lack of a complete, worldwide phylogeny. We aim to delve into the systematics of *Parablechnum*, proposing a complete monograph and a molecular phylogeny of the genus that, as a whole, resolve its infra-generic taxonomy, as well as a molecular dating and historical biogeographic analyses.

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## Biosystematics of bioactive actinobacterial strains isolated from Indonesian extreme environments: a pioneering study

**Kusuma, Ali B.**<sup>1,2,\*</sup>, Imen Nouioui<sup>1</sup>, Michael Goodfellow<sup>1</sup>

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Two hundred thirty-nine presumptive actinobacterial strains were isolated from 12 different extreme environments in Indonesia that covers arid lands, hot-neutral, hot-alkaline, acidic/hot-acidic and hypersaline habitats using several selective isolation techniques. Representatives of colony types growing on the isolation plates were assigned to 88 different colour-groups and numerous DNA fingerprint profiles. Phylogenomic analysis showed that one-third of the representative strains formed distinct lineage in the genus of *Streptomyces* and the remaining strains represented new members of rare genera: *Dermococcus*, *Arthrobacter*, *Pseudonocardia*, *Kocuria*, *Nonomuraea*, *Microbacterium*, *Gordonia*, *Janibacter*, *Mycobacterium*, *Micromonospora*, *Rhodococcus*, *Nocardioides*, *Actinospica*, *Cellulosimicrobium* and *Amycolatopsis*. Many strains were found to inhibit the growth of one or more of a panel of six wild type microorganisms while some of them can inhibit the synthesis of cell envelope, cell wall, fatty acid and RNA synthesis. This finding indicates that taxonomically diverse actinobacteria from Indonesian extremobiosphere could potentially give significant contribution in drug discovery campaign.

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## Phylogenomic and genomic analyses of anaerobic free-living eukaryote reveal the presence of a hydrogenosome

**Abu Elmakarem, Hend<sup>1\*</sup>**, Stephen J. Taerum<sup>2</sup>, Celine Petitjean<sup>1</sup>, Xyonane Segovia<sup>2</sup>, Christopher Kay<sup>1</sup>, Gillian H. Gile<sup>2\*</sup>, Tom A. Williams<sup>1\*</sup>

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The origin and evolution of eukaryotes is inextricably linked to the rise of oxygen following the Great Oxidation Event, but some modern eukaryotes flourish without oxygen by having mitochondrial-related organelles (MROs). The Parabasalia are an ancient anaerobic lineage, and the most speciose lineage of Metamonada, a major lineage of eukaryotes. The most well-studied metamonads are parasites including *Trichomonas vaginalis* and *Tritrichomonas foetus*, but we lack any genome data for free-living members of the group. Here, we sequenced the genome and transcriptome of *Pseudotrichomonas keilini*; a free-living metamonad. Through phylogenetic and computational analyses, we identified key hydrogenosomal proteins in *P. keilini* like Pyruvate:ferredoxin oxidoreductase (PFO) which provides strong support for the presence of hydrogenosomes in *P. keilini*. Hydrogenosomes are MROs producing energy from hydrogen and not oxygen and are usually found in parasites. This discovery would change the way we see the evolution of MROs in microbial eukaryotes.

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## Revisiting generic concepts in the Teloschistaceae (lichen-forming Ascomycota) using molecular phylogenetics, algorithmic taxa delimitation and molecular networks

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In systematics, delimitation of genera is constantly changing as taxonomic units above species level are not standardised. The Teloschistaceae, a diverse family of lichenised fungi, represents an extreme example of this where the number of genera has increased tenfold in the last decade. Many of these genera are based solely on molecular clades which makes the current classification confusing for taxonomists and impenetrable for non-experts. Here we show that at least 37 Teloschistaceae genera are either polyphyletic or nested within other genera and that the subfamily Brownlielloideae is invalid due to use of contaminated and misidentified DNA sequences. Algorithmic taxon delimitation and molecular networks show clear signal at the genus level, suggesting both as useful additions to the taxonomic toolkit for delimiting higher taxa. This study represents a starting point for delimiting stable, standardised genera in the Teloschistaceae with the aim of producing an intuitive, natural classification of the family.

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## Evidence for the underestimation of genetic diversity within an Afrotropical crab genus (*Potamonautes*)

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It is increasingly important to have accurate estimations of biodiversity and an understanding of the speciation process to mitigate elevated extinction rates. We have resolved the relationship between two closely related species from *Potamonautes*, a freshwater crab genus. A phylogeny, reconstructed using ddRAD-seq data, showed '*P. lirrangensis* (Rathbun, 1904)' (Decapoda) from Lake Malawi are nested within one of two riverine *P. montivagus* (Chase, 1953) (Decapoda) clades, that are geographically separated by the African Rift Valley. The clustering is indicative of a speciation event suggesting the Lake group constitutes an endemic species derived from a riverine ancestor. Furthermore, the reconstruction indicates that the Lake group is not part of *P. lirrangensis*, the holotype of which is in the Congo. These findings are important both taxonomically and in assessing the conservation status of species within *Potamonautes*, as endemics are more vulnerable to extinction due to their limited range.

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## Exploring the cichlid diversity of Lake Edward (East Africa)

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Many of the East African Great Lakes are renowned for their extraordinary diversity of haplochromine cichlids. These perch-like fishes evolved through adaptive radiation and explosive speciation. Their large species richness coupled with subtle interspecific differences resulted in many cichlid species remaining undescribed. This is especially true for Lake Edward of which only 32 of the 60–100 species have been formally described. We performed a systematic revision of the species of *Haplochromis* Hilgendorf, 1888 from Lake Edward. For each trophic group, we carried out a morphometric study and delineated and (re)described species. Within six of these groups, we discovered 28 species, 20 of which remain undescribed. These include five species of paedophages that steal eggs from other cichlids, three species of oral snail-shellers with stout jaws to crush snails, and twelve species of piscivores with sharp teeth and contrasting colour patterns.

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## The *Enteromius* species (Cyprinidae) from the Lake Edward system (East Africa): geographic variation or cryptic diversity?

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*Enteromius* is a genus of small African diploid barbs and the third largest fish genus in the world. Recently it has become clear that the species diversity in this genus is not well-known. Based on a combined morphometric and genetic (COI, mtDNA) approach, we were able to delineate five *Enteromius* species from the Lake Edward system (Congo, Uganda): *E. alberti*, *E. cf. mimus*, *E. cf. pellegrini*, *E. cf. kerstenii* and *E. cf. apleurogramma*. The first two species are morphologically highly similar, but genetically clearly different. The last three species can easily be distinguished morphologically. Remarkably, within each of these three species, we found two lineages, which were highly similar in morphology. Hence, four morphological groups, but eight genetic lineages were found. Furthermore, we found a sixth species in the system, *E. portali*, which has been regarded as a synonym of *E. neumayeri*.

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## Resolving recent radiations: phylogenomics of shearwaters

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Seabirds and in particular procellariiformes are among the most endangered bird groups on the planet. Their populations are jeopardized by threats in their breeding areas (habitat loss, predation by invasive species) and in their foraging areas (bycatch, overfishing). Their conservation requires a good understanding of the processes that drive diversification and speciation. Unfortunately, our current understanding of these processes in the procellariiformes is very limited. Here, we generate genomic data (UCE and ddRAD) to resolve the recent radiation in the shearwaters. We evaluate the use of different phylogenetic methods with two different datasets. Four fossil species are used to calibrate the molecular clock in a Bayesian analysis with a relaxed clock. We test different biogeographical scenarios and we study the role of introgression during speciation. We show that founder effects are an important speciation mechanism and that introgression is rare but important in some speciation events.

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## Global drivers of variation in cup nest size and parental effort in passerine birds

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What determines the size of a nest that a songbird species normally builds? How does it relate to other aspects of parental care? Field studies of common blackbirds have shown that northern populations build larger nests with thicker walls compared to birds that nest in the south. It is currently not known if this environmental signal persists at an interspecific level. An increase in nest size could also be driven by post-mating sexual selection as size can act as a signal of parental quality and lead to longer periods of care in species where both parents build. As part of this phylogenetic comparative study, I investigate the global drivers of variation in nest size and parental effort using the largest species-level dataset of cup-building passerines compiled to date. I employ Bayesian phylogenetic mixed models to analyse the relationship between nest size, a set of environmental variables and parental investment.

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## Taxonomy and diversification of *Cyclamen* L. using next-generation sequencing approaches

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The genus *Cyclamen* is well-defined, with at least 23 species, that has attracted scientists to examine and investigate speciation rate, climate change impacts, and most importantly questions of taxonomic status. Over the past 80 years, many morphological and phylogenetic studies have been published on *Cyclamen*. The number of species in the genus *Cyclamen* continues to change as the species concept remains equivocal. However, next-generation sequencing can allow us to sequence the entire genome (chloroplast, mitochondrial, and nuclear), enhancing our understanding of speciation rates and phylogenetic relationships. We sequenced total genomic DNA of 25 samples and assembled and annotated chloroplast genomes. The plastid genome of the samples ranged in size from 151,712bp (*C. rhodium* subsp. *viduum*) to 158,166bp (*C. hederifolium* subsp. *crassifolium*) with the typical quadripartite structure. This will form the basis for a new phylogeny.

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## Targeted sequencing of 976 nuclear genes elucidates evolutionary relationships within the palm subfamily Calamoideae

**Kuhnhäuser, Benedikt**<sup>1,2,\*</sup>, Sidonie Bellot<sup>2</sup>, Guillaume Chomicki<sup>3</sup>, Wolf L. Eiserhardt<sup>2,4</sup>, Simon Hiscock<sup>1</sup>, William J. Baker<sup>2</sup>

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The palm subfamily Calamoideae contains approximately 650 species in 17 genera, accounting for one quarter of all palms (Arecaceae). Calamoid palms are of pantropical distribution with the centre of diversity in Southeast Asia, where they form the basis of a multi-billion dollar trade in rattan canes. Because of their high diversity, exclusive occurrence in rainforests, and climbing habit of most species resulting in the obligate reliance on canopy trees for support, calamoid palms are an ideal group to study rainforest assembly through time and space. However, a solid phylogenetic framework for Calamoideae has been lacking, preventing this endeavour. Using targeted sequencing of 976 genes from 117 species systematically chosen to represent the taxonomic diversity within calamoid palms, we provide such a framework. Specifically, we test the monophyly of all calamoid genera, elucidate their evolutionary relationships, and validate recent taxonomic changes within the highly diverse subtribe Calaminae.

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## The explanation problem in systematics

**De Santis, Marcelo D.**<sup>1\*</sup>, Silvio S. Nihei<sup>1</sup>

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How does scientific explanation work in systematics? The usual answer is that explanatory power is gained from the apparent asymmetrical relationship between a phylogeny being able to explain homology, as characters derived from a recent common ancestor, with instances of homoplasy merely being *ad hoc* hypotheses and to be avoided. Given this understanding, most cladists transformed Hempel-Popper's model of scientific explanation by constructing a deductive-nomological model by subsuming under a universal law. In this presentation, however, I will show that both of these strategies fail. Then, I will offer an alternative solution that is based on a teleological-causal explanation for the evolution of each character (homology) using a functional analysis study that can be incorporated after reconstructing a phylogeny to confirm each instances of homology.

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## Looking for rogue taxa in supertrees by taking advantage of matrix representation

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A property of phylogenetic trees that has been used in supertree building is the ability to encode trees as binary character matrices. While the use of matrix representation (MR) for tree building has been shown not to be ideal due to multiple analytical biases and artefacts, its similarity to morphological data matrices opens the possibility of using MR to test the source trees for unstable taxa. Using the Concatabominations (Siu-Ting et al. 2015) pipeline, we tested a MR of 25 gene trees of caecilian taxa, and identified one unstable taxon, *Hypogeophis montanus*. An inspection of the source trees revealed this to be due to non-effective overlap between trees, which was resolved by adding *H. montanus* to one of the most taxon-rich gene trees. Thus, while MR may not be the best method to build supertrees, it can be used to identify problems of taxonomic instability in sets of source trees.

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**Estimating the divergence of dire wolves from their common ancestor with living canids using a Bayesian dating approach**

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The dire wolf is thought to be the most widespread carnivore in Pleistocene America, yet relatively little is known about its evolution or extinction. To further explore this, we generated a molecular alignment with both extinct (dire wolf ancient DNA) and extant canid species and used the software MCMCtree to date the canid's phylogeny.

First, we carried out a simulation test to evaluate the impact that deamination could have on the time estimates. Then, we performed a Bayesian model selection analysis on both simulated and real data sets to decide which topology and evolutionary rates model best fitted the data. Last, we proceeded with divergence times estimation in MCMCtree under the model supported by the Bayes factors. Our results indicate that errors in simulated data sets (deamination) had a minimal impact on times estimates and that dire wolves parted from their common ancestor with living canids ~5.5 million years ago.

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**New insight into the evolution of terrestrial planarians' mitogenomes (Geoplanidae, Platyhelminthes) inferred from two Brazilian Atlantic Forest species**

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Here we present the mitogenomes of the Brazilian terrestrial flatworm species *Cephaloflexa bergi* (Graff, 1899) and *Imbira marcusii* (Marcus, 1951). This taxonomic group includes species established as model organisms in biodiversity assessment studies and is rich in invasive species introduced all over the world, with their consequent economic impact. The mitochondrial sequences were extracted from NGS genomic data. As described for the few Tricladida species already sequenced, the two new mitogenomes have a high A + T content. One of the strengths of our study is the detection of the gene coding for atp8, whose existence had already been predicted in previous flatworm analyses but not confirmed before in terrestrial planarians. We provide new molecular data to develop new markers for future phylogeographic and systematic studies that can also be used as tools for detection of invasive species before they can be detected visually in imported plants.

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**Is alpha taxonomy still needed? The case study of *Hyptidendron* Harley (Hyptidinae-Lamiaceae, Angiosperms), endemic of South America**

**Antar, Guilherme M.**<sup>1,\*</sup>, Raymond Mervyn Harley<sup>2</sup>, José Floriano Barêa Pastore<sup>3</sup>, Paulo Takeo Sano<sup>1</sup>

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*Hyptidendron* Harley, one of the 19 genera recognized for Hyptidinae, comprises 19 species endemic to South America with highest diversity in Brazil. The most up-to-date, comprehensive taxonomic treatment of the genus was done in 1949 by Carl Epling. Based on herbarium material examination and extensive fieldwork we propose a new taxonomic revision of the genus. Whilst 91 specimens were examined when the genus was last revised, we examined 1060 specimens of which 41% were newly determined. We detected an average of 24 years from the gathering to proper determination of specimens. Six new species are recognized of which three are based on collections made in the last ten years. This taxonomic revision highlights the need for alpha taxonomy and fieldwork to be conducted in the Neotropics. Although funding and credibility for these are scarce, without alpha taxonomy no accurate conservation measurements or evolutionary and biogeographic studies are possible.

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**Phylogenetics and mitogenome organisation in black corals (Anthozoa: Hexacorallia: Antipatharia): An order-wide survey inferred from complete antipatharian mitochondrial genomes**

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Black corals (Anthozoa: Antipatharia) are an ecologically and culturally important group of deep-sea cnidarians, vulnerable to overexploitation due to their commercial use in jewellery and medicine. Molecular approaches to black coral systematics have previously been limited in scope due to the availability of only a small number of published mitochondrial genomes (mitogenomes). Using next generation sequencing, eighteen complete and five partial antipatharian mitogenomes were assembled. This includes species from four families previously unrepresented, enabling the first family-level, full mitochondrial gene analysis over the whole order.

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## Hagfish genome illuminates vertebrate genome evolution and phylogeny

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The phylogenetic position of hagfish (Myxini) has been the source of debate among systematists. Morphological analyses traditionally place them as the sister of all other vertebrates, whereas molecular evidence suggests they are the sister group of lampreys, in a clade called cyclostomata. We readdress this question using the newly sequenced genome of a hagfish *Eptatretus burgeri*. We compare the likelihoods of inferred gene trees under competing species tree hypotheses to show that monophyletic cyclostomes is supported by our data. Further, we use the discordance between gene trees and species tree to refine our understanding of vertebrate genome evolution. We compare models allowing whole genome duplication events with null models forbidding them. The likelihoods of the gene trees under these models can be compared. While this work is ongoing, it appears to suggest genome duplications immediately before and after the divergence of cyclostomes as well as a lamprey specific duplication.

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## Conservation genomics applied to the Balearic shearwater

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The Balearic shearwater (*Puffinus mauretanicus* P.R. Lowe, 1921) is the most threatened bird in Europe. Listed as critically endangered by the IUCN, the species population undergoes an annual decline of 7.4-14% and some studies predict that the species could become extinct by 2070. We assembled a high-quality *P. mauretanicus* genome (N50 of 2.1 Mb, BUSCO completeness of 94.8%) to scrutinize the genomic effects of the population decline, reconstruct its historical demography and gain insight into the molecular evolution of Procellariiformes. We inferred the historical population size of the species with PSMC<sup>1</sup>, which reveals that the human colonization of the Balearic Islands circa 5000 years ago halved the *P. mauretanicus* population. This reference genome will be the keystone for future fine-scale studies of the species population genomics based on resequencing of 28 individuals plus 6 *Puffinus yelkouan* Acerbi, 1827 as sister species and 2 *Puffinus puffinus* Brünnich, 1764 as outgroup.

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## Three new species of *Oocephalus* (Hyptidinae, Lamiaceae) from Chapada dos Veadeiros National Park, Goiás, Brazil

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*Oocephalus* (Benth.) Harley & J.F.B.Pastore has 20 species and is almost entirely endemic to the Brazilian Campos rupestres, especially in Cadeia do Espinhaço (Bahia and Minas Gerais state) and in the Brazilian Central Plateau, in Goiás state. Here, we present three new species from Chapada dos Veadeiros National Park, Goiás, Brazil. *Oocephalus griseus* sp. nov. is similar to *O. viscaria*, being immediately differentiated by the absent the viscid indument and the rotund leaves; *O. longipetiolatus* sp. nov. can be recognized by the possession of long petioles and long peduncles, while *O. foliosus*, the closest morphological species, has sessile leaves and short peduncles; *O. queirozii* sp. nov. could be confused with *O. grazielae*, leaves ovate with serrate-dentate margin and cymes 1–3-flowered distinguishes it from the later species, which has rotund to broadly ovate leaves and sub-crenate margin.

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## An endemic radiation of deer in the Late Pleistocene of Malta

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The origin of island endemics provides outstanding opportunities to investigate evolutionary adaptation and diversification. This research focuses on a little-studied yet remarkable radiation of deer from the Pleistocene of Malta. A large sample of teeth, bones and antlers from Għar Dalam Cave was subjected to detailed analysis of metric variables and qualitative morphological traits. Comparisons with variation in extant deer plus cluster analysis identified at least three size groups; morphological character analyses strongly indicate that all groups derive from red deer (*Cervus elaphus*). All size-classes demonstrate allometric grade shifts in limb bone proportions, plus differences in antler-base morphology. The inclusion of juvenile bones illustrates the ontogenetic trajectory for each taxon. A critical sample of *in situ* fossils at Għar Dalam demonstrates probable contemporaneity of the taxa, which together with the presence of only a single red deer size-class on Sicily (the likely source area), implies cladogenetic speciation on Malta itself.

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## Who's the real "False Widow"? Investigating the phylogenetic relationships within the Latrodectinae spiders using Bayesian and Maximum Likelihood

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The Theridiidae subfamily Latrodectinae contains the medically significant spiders *Latrodectus* (Black Widows) with envenomation responsible for symptoms in humans such as vomiting or abdominal cramps. Due to the similarities in their morphology, the related but much less medically significant genus *Steatoda* (False Widows) has been confused with *Latrodectus*, leading to panic by laypersons. Despite notoriety, minimal research has been undertaken on the taxonomic relationship between *Steatoda* and *Latrodectus*. Here we present a consensus tree on the phylogeny of 22 specimens representing eight Latrodectinae species, using three genes (16s, 18s, 28s) and two different methods (Bayesian and Maximum Likelihood). The results present a consensus tree that places *Steatoda* as paraphyletic with *Latrodectus* as a monophyletic clade placed within *Steatoda*. This tree presented throws the taxonomy of Latrodectinae into question, with the implication that *Latrodectus* and *Steatoda* genera may be one monophyletic clade as opposed to two distinct genera.

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## Discovering dicyemid genetic diversity.

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Dicyemids, belonging to the group of Mesozoa, are tiny marine parasites living in renal organs of benthic cephalopods. Their body is very simply built of approximately 40 cells and they lack "hard morphological features". Current taxonomy is based mostly on their shape, the number of cells and overall size. However, dicyemids may be morphologically plastic in all of these traits. We present an outline of a study where we will employ 18S amplicon sequencing to create metagenomic profiles of multiple cephalopod hosts. In this way, we will assess dicyemid species diversity across a wide spectrum of cephalopod species but also within individual host species.

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## How-to-guide for phage taxonomy and phylogenetics

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Currently the knowledge of bacteriophage evolution is as patchy as the mosaicism in bacteriophage genomes. Unlike many well-studied organisms that have suitable markers to study evolution, such as 16S ribosomal genes for bacteria and archaea, there is no single marker acceptable to use for bacteriophages. Whilst the term “phage” is loosely given to any virus predatory on prokaryotes, but most commonly bacteria, this name actually encompasses a number of different viral families. This poster aims to gather and present a summary of the current understanding of phage taxonomy, phylogenetics and phylogenomics. It will evaluate the current methods for analysing phage evolution and relationships. Finally, it will offer an opportunity to gauge responses and take suggestions from the audience on possible ways forward to improve this knowledge.

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## An objective pipeline for the selection of genes for phylogenomic analyses

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The recent increase in the availability of genomic and transcriptomic data has led to the emergence of phylogenomics, the inference of phylogenies using whole-genome information. A key step of this approach is the selection of the most phylogenetic-informative genes from a pool of homologous groups, a procedure that must be as objective and stringent as possible. We have developed a pipeline that processes the results of an orthology inference and returns a curated list of single-gene alignments that can be used as input to a phylogenomic analysis. The whole procedure focuses on the identification and removal of potential paralogous sequences, a fundamental step in order to reduce misleading phylogenetic signal. We have tested our new approach on a dataset composed of nematoid taxa and here we report the resulting number and nature of genes, as well as the topology. Future steps include the comparison of this workflow to other established protocols for paralog filtering.

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## Evolution of gall-induction and host-plant associations in Phyllanthaceae-feeding *Caloptilia* (Lepidoptera: Gracillariidae)

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Gall-induction has repeatedly evolved insects. However, most lineages of gall-inducers contain a reduced number of species. Therefore, it is difficult to assess whether gall-induction should be considered as an evolutionary dead-end or a key innovation that contributes to evolutionary success. Insect groups that include species either capable or not capable of inducing galls are good models to infer the transition of feeding habit. We focused on species of the *Caloptilia* genus (Lepidoptera: Gracillariidae) associated with Phyllanthaceae and that currently comprises a single species of gall-inducer. However, previous works have suggested the existence of multiple undescribed gall-inducing *Caloptilia*, which indicating a possible adaptive radiation of gall-inducing moths. We sampled 16 species of *Caloptilia* associated with *Glochidion*, including 9 undescribed, and inferred phylogenies from Ultra Conserved Elements. The phylogeny showed that gall-inducers form a well-supported monophyletic group. The monophyly of *Caloptilia* species associated with Phyllanthaceae and *Glochidion* was also strongly supported.

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## What’s all the buzz about? Pollination-mediated selection in the buzz-pollinated plant genus *Solanum*

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*Solanum* L. is one of the largest angiosperm genera and exhibits a wide range of morphological diversity. This study aimed to test whether different evolutionary forces have driven the reproductive and vegetative trait evolution in *Solanum*. Because all *Solanum* species share a general floral form (‘Bauplan’) linked to buzz-pollination, variation in floral morphology within the genus has been little explored. Buzz-pollination is considered a generalist pollination strategy and pollination-related morphological traits were expected to show low rates. Ancestral trait reconstruction of 17 taxonomically important vegetative and reproductive morphological traits showed generally low transition rates in vegetative characters, with the exception of two. Five reproductive traits, including three traits linked to pollination (corolla colouration, and anther and filament length) showed high transition rates, however, indicating strong role of pollinator-mediated selection. High rate of morphological evolution in pollination related traits is likely linked to the diversity of bees capable of sonicating buzz-pollinated flowers.

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## A sessile and tube-dwelling Cambrian Lobopodian

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*Facivermis yunnanicus* Hou & Chen, 1989 is an enigmatic bilaterian fossil from the early Cambrian Chengjiang Biota of Yunnan Province, China. *F. yunnanicus* possessed a worm-like body, with five pairs of spiny anterior arms and a swollen hook-bearing posterior. This unusual bodyplan has prompted diverse taxonomic interpretations, including annelid, lophophorate, pentastomid, and most popularly lobopodian (the fossil grade panarthropod from which phyla derive). The lobopodian hypothesis suggests *F. yunnanicus* represents a transitional form between cycloneuralian worms and more typical lobopodians. We described new material of *F. yunnanicus*, and report new morphological characters including characteristically lobopodian ocelli and a dwelling-tube. Phylogenetic analyses indicate a derived systematic position of *F. yunnanicus*, revealing a series of unique character changes to facilitate a sessile, tube-dwelling lifestyle. We conclude that *F. yunnanicus* appears basal/transitional only due to secondary losses, and instead represents a rare Cambrian example of secondary adaptation to a specialised lifestyle.

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## The evolution and diversification of vision in strombid gastropods

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The large, conspicuous camera eyes in gastropod family Strombidae are thought to provide surprisingly good visual acuity, second only in Mollusca to the predatory Cephalopoda and Pterotracheoidea. These complex eyes vary enormously in size and structure across Strombidae and even more so within superfamily Stromboidea. However, the diversity and evolution of strombid eyes have not yet been investigated, which this project will address by integrating morphological, molecular and behavioural approaches within a phylogenetic framework. We will use Sanger sequencing to recover a phylogenetic history of the family Strombidae, and map morphological traits onto the phylogeny, obtained by computed tomography and histological methods. This approach will show that eye structure varies across families in Stromboidea, and within Strombidae. Our data will enhance the current understanding of strombid visual capabilities, giving a new perspective on how strombids see their surroundings, and add to our knowledge of the evolution of vision in Mollusca.

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## The evolution of multicellularity, microchimerism, and transmissible cancers

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My cells are trapped cooperators inside a community, my body. They have sacrificed their ability to reproduce independently outside the multicellular community. They can only leave their genes in the next generation by helping their neighbouring family cells reproduce, the germ cells. Back in evolutionary time, however, they used to live a lonely independently-reproducing lifestyle. The transition from one level of individual, a single cell, to another higher in complexity individual, a multicellular organism, is termed a major transition in individuality. By definition, the word “major” states that this transition is irreversible. But do transmissible cancers and microchimerism defy this rule? What drives multicellular reversal to unicellularity? What drives cancer transmissibility? Here we present insights from evolutionary biology towards a deeper understanding of multicellularity, microchimerism, and cancers across all multicellular species in the tree of life.

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## Central-European phylogeographic crossroads: phylogeography of *Monachoides incarnatus* (Mollusca: Gastropoda: Pulmonata)

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*Monachoides incarnatus* (O. F. Müller, 1774) is an abundant euryvalent land snail limited from east and west to Central Europe. The genus is further represented by two other accepted species *M. vicinus* (Rossmässler, 1842) and *M. bacescui* Grossu, 1979 and some potentially valid nominal taxa from the Velebit (Croatia) and the southern Alps. The first results of phylogenetic analyses (COI mitochondrial gene) indicate the origin of *M. incarnatus* and glacial refugia south of the Alps and colonization of the Czech Republic by two groups – distributed predominantly in the west and south-east of its range, respectively. All the samples from the Alps fall within the diversity of *M. incarnatus*. *M. bacescui* is barely distinguishable from *M. incarnatus*, but we have yet to obtain samples for molecular analysis. Also, it appears that there is a fourth species in Slovenia and Croatia, for which there is probably no available name.

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## Summarizing the trade of the world's most trafficked animal species: A conservation view on pangolins in India over the last decade

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Pangolins are currently the world's most trafficked mammals. There are eight species worldwide, with two in the Indian subcontinent, the Indian pangolin, *Manis crassicaudata*, and Chinese pangolin, *Manis pentadactyla*. In the last decade populations of both declined rapidly from habitat distraction and poaching, which results from fallacious inferred medicinal value for their biological parts, mostly scales. We assessed 119 seizures from 2009-2019 in India through data in print and electronic media. Of the seizures, 11 contained meat, 13 living and 4 dead pangolins and 7500 kg scales. Based on standardized 1kg scales/individual and complete bodies, we estimate >7680 individuals were killed in a decade. From 2009-2014 northeast India had the maximum number of pangolin incidents. From 2015-2019 the maximum came from north-eastern and southern states. Trade route analysis indicates exports are to China and Myanmar through the northeastern states. Our results support law enforcement and policy interventions for fighting wildlife trade nationally and internationally.

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## Systematics, genome size, chromosome number and a new species of *Macrotorus* (Monimiaceae, Laurales, Angiosperms)

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*Macrotorus* is a monotypic genus represented by *Macrotorus utriculatus* (Mart. ex Tul.) Perkins, an endemic species from Brazilian Atlantic forest. Recently, some herbaria specimens from Rio de Janeiro state came to our attention due to the atypical leaves, flowers and fruits characters that didn't fit in *M. utriculatus*. The study was based on fieldwork, morphological analyses, genome size estimation, chromosome numbers and CMA/DAPI-banding. We found four vegetative and ten reproductive characters to differentiate the two species, besides the divergent genome size and karyotype: while *M. utriculatus* showed  $2C = 5.545\text{pg}$  and 80 chromosomes, the *Macrotorus sp. nov.* showed  $2C = 2.644\text{pg}$  and 40 chromosomes. The tetraploiploid *M. utriculatus* presents a wide distribution across the states of Bahia, Espírito Santo, Rio de Janeiro and São Paulo, while the diploid new species is endemic from a narrow area in the central Rio de Janeiro state.

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## Parallel ddRAD analyses reveal a credible phylogenetic relationships of the four main genera of *Bambusa-Dendrocalamus-Gigantochloa* complex (Poaceae: Bambusoideae)

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Bambusoideae is one of the largest subfamilies of the grass family. It is the only major lineage of Poaceae that adapts to and diversifies in forest habitats, providing ecological, social, and economic benefits to local people. Bamboos now include 1680 species including three tribes: Olyreae, Arundinarieae and Bambuseae. The tribe Bambuseae is divided into the neotropical woody bamboos (NWP) and the palaeotropical woody bamboos (PWB). The *Bambusa-Dendrocalamus-Gigantochloa* complex (BDG complex) is the most diversified and phylogenetically recalcitrant group of the PWB. The lack of resolution based on previous molecular datasets has long confounded its phylogenetic estimation and generic delimitation. Here, we adopted a ddRAD-seq strategy to investigate phylogenetic relationships of the four main genera (*Bambusa*, *Dendrocalamus*, *Gigantochloa*, and *Melocalamus*) in BDG complex. A total of 102 species was sampled, and our analyses resulted in a well-resolved topology supported by morphological evidence such as the branches, rachilla, lodicules, filaments and stigma. We further generated and assembled whole plastid genomes of 48 representative species. However, the plastome and ddRAD-seq phylogenies are in conflict. Our study demonstrated that the BDG complex has undergone a complicated evolutionary history, possibly caused by incomplete lineage sorting and hybridization events among closely related species.

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## Predicting prokaryotic optimal growth temperature

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Prokaryotic life is incredibly diverse and inhabits a wide range of different environments from arctic ice-sheets to underwater volcanoes. What is it about the genomes of these organisms that allow them to thrive in such a broad, and occasionally extreme, range of conditions? Here, we introduce a relevance vector machine (RVM), that accurately predicts the optimal growth temperature of bacterial and archaeal species to within 4°C. Fitting the model to ~5000 prokaryotic genomes indicates that amino acid compositions, as well as certain dinucleotide combinations, are the most important features for determining optimal growth temperature. We also predict optimal growth temperatures for uncultivated species as well as consider the implications for inferring extinct ancestral species temperature preferences. Our results also demonstrate systematic biases in experimentally reported optimal growth temperatures. Our model might also be of use in other settings where observational data are used to predict biological parameters of interest.

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## **Integrative taxonomy of Brazil's national tree, *Paubrasilia echinata* (Leguminosae)**

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*Paubrasilia echinata* (Lam.) Gagnon, H.C.Lima & G.P.Lewis is the national tree of Brazil and an endangered species endemic to the Atlantic rainforest. Despite being a national symbol, the taxonomy of this species is still unclear. Three morphotypes are commonly identified based on the size of the leaflets but it is unclear if they represent distinct taxa or a single polymorphic species. A comprehensive morphometric study based on 74 geographically representative herbarium specimens from the entire distribution of the species was coupled with phylogenomic investigation of genotyping-by-sequencing data and multivariate ecological analyses of climate data. We found that the three morphotypes do not match separately evolving lineages. Rather, *P.echinata* is composed of five clades that are geographically structured and two lineages show signs of ongoing gene flow. We relate our findings to the practical aspects of conservation.

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## **The evolutionary history and diversity of the Mickey Mouse plants**

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The genus *Ochna* L. is the second largest genus in the family Ochnaceae with ca. 86 species. The species are of ecological and conservation importance as they constitute a significant element of woody vegetation in tropical dry forests which are severely under threat. The group has been treated in various regional floras, with the current infrageneric classification based solely on morphology. However, because the majority of specimens are collected in fruit when identification characters lie in the flowers, many specimens are left unidentified and taxonomic treatments incomplete. An integrated study using morphological and molecular data is used to provide insights into the relationships of the species and produce a well-supported classification. This dated phylogeny will enable an investigation into adaptive evolution in response to its environment and biogeographical distribution. Reconstruction of the ancestral character states and species ranges will provide insights into the potential drivers of speciation including different pollination specialisations.

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## Using reverse taxonomy to unmask cryptic speciation of *Eurythenes* amphipods in the Pacific Ocean

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The giant amphipod species, *Eurythenes gryllus* (Lichtenstein in Mandt, 1822), has recently been demonstrated to contain numerous genetically and morphologically distinct lineages. Here, *Eurythenes* diversity from the Pacific Ocean is investigated using Bayesian phylogenetic analyses of the sequence variance at the mitochondrial DNA 16S locus, combined with morphological analyses. These genetic data allowed phylogenetic lineages to be produced, demonstrating the existence of cryptic species within *E. gryllus*, several which occur in sympatry. In addition, morphological findings corresponded with the molecular genetic clades, indicating species level differentiations in anatomy. The *Eurythenes* sp. hadal morphospecies and the Eg8 clade were morphologically analysed to confirm their distinctness from the *E. gryllus* holotype. Numerous defining characteristics were identified, specifically regarding gnathopods 1 and 2. The biogeographic ranges of each clade are discussed with evaluation of possible factors influencing speciation within this genus, which is key for understanding factors influencing diversity in the deep sea.

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## The genus *Cranfillia* (Blechnaceae, Polypodiopsida): A proposal of natural sections for the genus

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The genus *Cranfillia* Gasper & V.A.O. Dittrich was created in 2016. Originally conceived as a genus of 12 species mainly framed by molecular data, the *Cranfillia* species has been subject of several taxonomic reviews, recombinations and new species have been described last years, reaching up to 22 species. This is probably because of the few diagnostic characters initially given to segregate *Cranfillia* from other phylogenetically related genera as *Austroblechnum* Gasper & V.A.O. Dittrich. Another systematic difficulty is the great morphological heterogeneity among its species that points to the need of a better morpho-anatomical revision of the genus. Our systematic results to date have led to new diagnostic characters, as well as anatomical traits to join *Cranfillia* species in phylogenetically supported sections. With all these characters, we have developed an identification key to the different taxa that we currently consider to be in *Cranfillia*.

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## Plastid phylogenomics on the succulent group, *Euphorbia* sect. *Monadenium*

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As the second largest genus in flowering plants, *Euphorbia* L. contains around 850 succulent species *sensu stricto*. *Euphorbia* sect. *Monadenium* Bruyns, 90 spp in total, is a typical group of succulents to study growth forms variation and adaptation to drought. However, integrated taxonomy and molecular systematics upon this section are relatively poorly done. Previous research proposed to merge former genera, *Monadenium* Pax, *Synadenium* Boiss. and *Endadenium* Leach, and delimited them as a monophyletic clade within *Euphorbia* only based on ITS, *ndhF* and *matK* sequences. With more representative sampling, we sequenced plastid genome data for nearly half of the whole group using de novo assembly. Based on the robust phylogenetic tree, the monophyletic status of this section was confirmed, giving insight for the further infrasection division. Analysis of plastid genome structure illustrated the differences among both intersectional and infrasectional groups.

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## A giant in the deep: new species of *Eurythenes* from hadal depths of the Mariana Trench, Pacific Ocean

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*Eurythenes* (Smith in Scudder, 1882) are iconic scavenging amphipods that are found in every ocean across an extensive bathymetric range from the shallow polar waters to hadal depths in the Atacama Trench. While *Eurythenes* are large (maximum 154 mm), recent systematic studies illuminated cryptic speciation within the genus and the benefits of using a paired morphological and genetic identification approach. Since 2004, the genus has expanded from three to eight described species. In this study, we present a yet undescribed species that was recovered via baited traps from 6142 – 6949 m in the Mariana Trench in 2014. This new *Eurythenes* species was found to have distinct morphological characteristics and be a well-supported clade within a 16S and COI mtDNA phylogeny. As this species appears to be hadal depth endemic, this species sheds new light towards understanding the evolutionary and biogeographic history of *Eurythenes*.

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## Patterns of population co-diversification in Galápagos doves and their louse ectoparasites

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Galápagos represent an ideal natural laboratory for studying the processes of allopatric speciation. Here, we present a preliminary study on the mutual evolutionary history of *Zenaida galapagoensis* and its louse ectoparasites of the genera *Physconelloides* and *Columbicola*. Dove and ectoparasite samples were obtained from four Galápagos islands: Genovesa, Pinta, Darwin and Wolf. The level of population structure and genetic diversity in the parasites and their host were analysed using a homologous region of the cytochrome oxidase I gene. In accordance with the high mobility of doves, we found almost no specific haplotypes for any of the islands in any of the three taxa, showing that even 150 km of open sea do not represent a migration barrier. Furthermore, the overall low level of genetic diversity suggests that doves and their parasites colonized Galápagos relatively recently, experienced a strong bottleneck, and their genetic diversity that has not been fully restored yet.

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## Lethaeini of Madagascar (Hemiptera, Rhyparochromidae)

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Madagascar is a global biodiversity hotspot, being exceptionally rich in endemic animals such as true bugs, Heteroptera. We studied Madagascan specimens recorded as from the tribe Lethaeini in a number of European museums including Brno, Paris and London. This tribe can be recognized by the anterolateral trichobothria of the pronotum, iridescent spots on vertex and linear placement of the trichobothria on abdominal sternum V. Lethaeini is the second most species-rich Rhyparochromidae tribe of Madagascar with eight species described before 2019 but we found an additional 27 undescribed species. This makes Madagascar the most diverse country for Lethaeini species worldwide. Lethaeini of Madagascar now are placed in three genera. This year we described three new *Noteolethaeus* species (ZÁMBÓ ET AL. 2019) and we are working on five new Lethaeini genera. The work is supported by EFOP3.6.1-16-2016-00015 project. The project is co-financed by the European Union and the European Social Fund.

# MEETING POLICIES

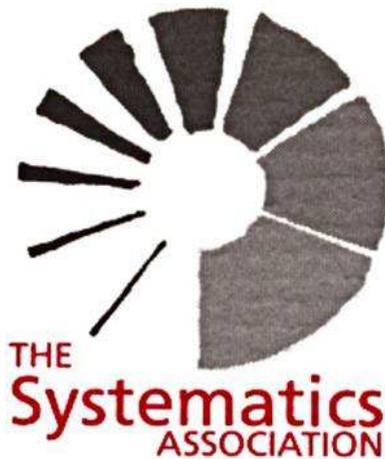
The Systematics Association Council wishes to promote a diverse programme of speakers and pool of registrants and has taken measures to encourage and support diversity. We welcome and encourage participation by everyone in the systematics community, and welcome feedback on how best to build on these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

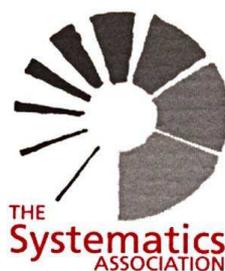


**The Systematics Association** is committed to furthering all aspects of systematic biology. It organises a vigorous programme of international conferences on key themes in systematics, including a series of major biennial conferences. The association also supports a variety of training courses in systematics 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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*We may occasionally contact you via e-mail to publicise the Association's events, such as talks or meetings. If you would prefer not to be notified by e-mail, please tick this box:*

Please don't contact me

*We will not pass your details to any other organisations.*

### **Membership rates:**

Payment may be made by cheque, cash or standing order. Cheques should be made payable to "The Systematics Association" and drawn on a UK bank account only. Non-UK based applicants may pay in Euros or US/Canadian dollars in cash only, or by PayPal (see website for details).

**Standard membership** - £20 (\$30 or €30) per year

**Student/retired/unwaged membership** - £10 (\$15 or €15) per year

I enclose as my subscription for \_\_\_\_\_ years / I have completed a standing order form and returned it to my bank/building society (delete as appropriate).

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In order to reduce costs and save resources, we send you our regular newsletter, The Systematist, in electronic format. If you would prefer to receive a paper copy, please contact our membership secretary to request one.

***The Systematics Association is a registered charity.***

