Young Systematists' Forum

VIRTUAL CONFERENCE

Friday 15th November 2024

Sponsors

Royal Botanic Gardens Kew

THE Systematics ASSOCIATION

Natural History Museum

CRC Press
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Organisers: Ellinor Michel (Natural History Museum London), Katie Collins (Natural History Museum London), Pablo Muñoz-Rodríguez (Universidad Complutense de Madrid), Ana Serra Silva (University College London), Kálmán Könyves (Royal Horticultural Society) and Peter Mulhair (University of Oxford) with the support of The Systematics Association Council.

Zoom session will open at 9:30 am, the event will start at 10:00.

Prizes for best talks will be awarded during the Systematics Association Annual General Meeting

https://systass.org/

The talk titles in the schedule are linked to the abstracts. Click on the title to go straight to the abstract

GMT	Session	Speaker	Title
10:00	**OPENING REMARKS**		
10:15	**Introduction to the Systematics Association from the SA President, Dr Pablo Muñoz-Rodríguez** **TALKS BEGIN AT 10:30 GMT**		
10:30	**1** Flash talks	Horenkamp	A global taxonomic revision of the deep-sea squid family Brachioteuthidae, starting with New Zealand species
10:35		Jorid	Petiole Anatomical Investigation of Some *Ficus* Species in Southeast Bangladesh and Their Taxonomic Significance
10:40		K	Biogeography and Phylogenetic Relationships of *Caridina fernandoi* in India and Sri Lanka, with the Discovery of Novel Western Ghats Endemics
10:45		Roy	An integrative taxonomic analysis reveals a new genus of freshwater mollusc from the Western Ghats, India
10:50		Jashmi Devi	Behold the rare: *Strobilanthes* from North Eastern Region of India
10:55		Kapsetaki	Cancer prevalence in relation to life history traits in birds
11:00		Declercq	Taxonomic revision of the *Ipomoea longituba-marmorata* complex; An African-endemic sweet potato crop wild relative group
11:05		Ferm	The Neotropical rainforest mimosoid genus *Zygia* P.Browne - Diversification and evolution based on phylogenomics and morphology
11:10		Rose	Evolutionary genomics analysis reveals a unique lineage of *Megachile pruina* found in an isolated population in Bermuda
11:15		Ojo	An Exploration of Trichome Diversity: A Morphological Study of Twenty African *Ipomoea* Species (Convolvulaceae) Using Herbarium Specimens

11:20	**BREAK (10 min) TALKS RESUME AT 11:30 GMT**		
11:30	**2** Full talks	Lazaro	Diversity of Ulvaceae (Ulvales, Chlorophyta) from northern Philippines including the description of a new *Umbraulva* species
11:45		King	Systematics of *Lepidagathis* Willd. (Acanthaceae: Barlerieae) in India
12:00		Sharma	Investigating cryptic speciation in Indian Blackbird (*Turdus simillimus* complex) using phylogenomics
12:15		Herath	Evolution of South Asian Mountain biota: dispersal, fine-scale biogeography, and phylogenetics of Nannenini of jumping spiders
12:30	**LUNCH (35min) TALKS RESUME AT 13:05 GMT**		

13:05	**3** Full talks	Bangal	Unravelling the Biogeography and Evolution of *Impatiens* (wild balsams) in Peninsular India
13:20		Röttgers	Species diversity and first phylogenetic relationship of the parasitoid wasp genus *Tamarixia* in Sweden
13:35		Leyton Rotella	Assessing mitogenomic gene order rearrangements and phylogeny of the parasitic family Stylopidae (Strepsiptera)
13:50		Arañó	Assembling the largest 18S ribosomal RNA curated data set for non-bilaterian animals
14:05		Sumlińska	Integrative redescription of *Minibiotus jonesorum* Meyer et al., 2011 (Tardigrada: Macrobiotidae)
14:20	**BREAK (10 min) TALKS RESUME AT 14:30 GMT**		
14:30	**4** Full talks	Shorter-Rodríguez	A new threat to the European marine environment: The exotic polyclad flatworm *Postenterogonia orbicularis* (Schmarda, 1859)
14:45		Nava	A timescale for the evolutionary history of sea spiders (Arthropoda: Pycnogonida)
15:00		Tianara	A revision to the ginger genus *Epiamomum* A.D.Poulsen & Škorničk.
15:15		García	Preliminary insights into the phylogeny of the “soldier spiders” (Araneae: Corinnidae: Corinninae)
15:30		Huacuja Barraza	Phylogenetic Discordance in True Eels (Anguilliformes): Use of Morphological vs. Molecular Data and Total Evidence

15:45	**BREAK (10 min) TALKS RESUME AT 15:55 GMT**		
15:55	**5** Flash talks	Campbell	*Anolis gingivinus* (Dactyloidae): revised description, sexual size dimorphism, and lessons learnt on the value of natural history collections.
16:00		Stewart	A new genus of ectoparasitic Myzostomida from the Pacific abyss
16:05		Rivas-Ferreiro	What actually is a “blusher”? Advances in delimiting the European species of *Amanita* series *Validae*
16:10		Fernandes	Blooming in the Shadow of Extinction: Taxonomy of the Brazilian Gumweeds (*Grindelia*, Asteraceae)
16:15		Popova	Taxonomic study of the genus *Chaenotheca* (Coniocybaceae, Ascomycota) in Bulgaria
16:20		Dalseng	A Phylogenetic Study of *Lemmus*
16:25	**Summary comments and thanks from the Systematics Association** **Thanks and farewell comments from the YSF organisers**		

-7	-6	-3	GMT	+1	+2	+5.5	+6	+8	+13	Session	Speaker
03:00	04:00	07:00	10:00	11:00	12:00	15:30	16:00	18:00	23:00	**OPENING REMARKS**	
03:15	04:15	07:15	10:15	11:15	12:15	15:45	16:15	18:15	23:15	**Introduction to the Systematics Association from the SA President, Dr Pablo Muñoz-Rodríguez** **TALKS BEGIN AT 10:30 GMT**	
03:30	04:30	07:30	10:30	11:30	12:30	16:00	16:30	18:30	23:30	**1** Flash talks	Horenkamp
03:35	04:35	07:35	10:35	11:35	12:35	16:05	16:35	18:35	23:35		Jorid
03:40	04:40	07:40	10:40	11:40	12:40	16:10	16:40	18:40	23:40		K
03:45	04:45	07:45	10:45	11:45	12:45	16:15	16:45	18:45	23:45		Roy
03:50	04:50	07:50	10:50	11:50	12:50	16:20	16:50	18:50	23:50		Jashmi Devi
03:55	04:55	07:55	10:55	11:55	12:55	16:25	16:55	18:55	23:55		Kapsetaki
04:00	05:00	08:00	11:00	12:00	13:00	16:30	17:00	19:00	00:00		Declercq
04:05	05:05	08:05	11:05	12:05	13:05	16:35	17:05	19:05	00:05		Ferm
04:10	05:10	08:10	11:10	12:10	13:10	16:40	17:10	19:10	00:10		Rose
04:15	05:15	08:15	11:15	12:15	13:15	16:45	17:15	19:15	00:15		Ojo
04:20	05:20	08:20	11:20	12:20	13:20	16:50	17:20	19:20	00:20	**BREAK (10 min) TALKS RESUME AT 11:30 GMT**	
04:30	05:30	08:30	11:30	12:30	13:30	17:00	17:30	19:30	00:30	**2** Full talks	Lazaro
04:45	05:45	08:45	11:45	12:45	13:45	17:15	17:45	19:45	00:45		King
05:00	06:00	09:00	12:00	13:00	14:00	17:30	18:00	20:00	01:00		Sharma
05:15	06:15	09:15	12:15	13:15	14:15	17:45	18:15	20:15	01:15		Herath
05:30	06:30	09:30	12:30	13:30	14:30	18:00	18:35	20:35	01:35	**LUNCH (35min) TALKS RESUME AT 13:05 GMT**	

06:05	07:05	10:05	13:05	14:05	15:05	18:05	19:05	21:05	02:05	**3** Full talks	Bangal
06:20	07:20	10:20	13:20	14:20	15:20	18:50	19:20	21:20	02:20		Röttgers
06:45	07:45	10:45	13:45	14:45	15:45	19:15	19:45	21:45	02:45		Leyton Rotella
06:55	07:55	10:55	13:55	14:55	15:55	19:25	19:55	21:55	02:55		Arañó
07:05	08:05	11:05	14:05	15:05	16:05	19:35	20:05	22:05	03:05		Sumlińska
07:20	08:20	11:20	14:20	15:20	16:20	19:50	20:20	22:20	03:20	**BREAK (10 min) TALKS RESUME AT 14:30 GMT**	
07:30	08:30	11:30	14:30	15:30	16:30	20:00	20:30	22:30	03:30	**4** Full talks	Shorter-Rodríguez
07:45	08:45	11:45	14:45	15:45	16:45	20:15	20:45	22:45	03:45		Nava
08:00	09:00	12:00	15:00	16:00	17:00	20:30	21:00	23:00	04:00		Tianara
08:15	09:15	12:15	15:15	16:15	17:15	20:45	21:15	23:15	04:15		García
08:30	09:30	12:30	15:30	16:30	17:30	21:00	21:30	23:30	04:30		Huacuja Barraza
08:45	09:45	12:45	15:45	16:45	17:45	21:15	21:45	23:45	04:45	**BREAK (10 min) TALKS RESUME AT 15:55 GMT**	
08:55	09:55	12:55	15:55	16:55	17:55	21:25	21:55	23:55	04:55	**5** Flash talks	Campbell
09:00	10:00	13:00	16:00	17:00	18:00	21:30	22:00	00:00	05:00		Stewart
09:05	10:05	13:05	16:05	17:05	18:05	21:35	22:05	00:05	05:05		Rivas-Ferreiro
09:10	10:10	13:10	16:10	17:10	18:10	21:40	22:10	00:10	05:10		Fernandes
09:15	10:15	13:15	16:15	17:15	18:15	21:45	22:15	00:15	05:15		Popova
09:20	10:20	13:20	16:20	17:20	18:20	21:50	22:20	00:20	05:20		Dalseng
09:25	10:25	13:25	16:25	17:25	18:25	21:55	22:25	00:25	05:25	**Summary comments and thanks from the Systematics Association** **Thanks and farewell comments from the YSF organisers**	

Assembling the largest 18S ribosomal RNA curated data set for non-bilaterian animals

Javier Arañó Ansola*

University of Barcelona, Spain

*Corresponding author: jaranoan7@alumnes.ub.edu

The small subunit ribosomal RNA (SSU rRNA), named 18S in eukaryotes, is a gene universally present across the Tree of Life (ToL) that has been instrumental to solve the most ancient relationships. Furthermore, it serves as a molecular identifier of biodiversity in environmental DNA studies. Despite its significance, specialised 18S databases still contain errors. This challenge hinders the assembly of reliable reference phylogenetic trees needed to identify novel environmental 18S sequences. This work focuses on curating the 18S sequences of non-bilaterian animals in the Protist Ribosomal Reference Database. Through this curation process, we generated the largest backbone phylogenetic tree for non-bilaterians, essential for the taxonomic identification of 18S sequences within this group. Furthermore, we reaffirmed that 18S can recover most well-known animal clades to the phylum level. Lastly, we confirmed that incorporating 18S secondary structure information into sequence alignment positively impacts the topology of the inferred animal ToL.

Unravelling the Biogeography and Evolution of *Impatiens* (wild balsams) in Peninsular India

Yogesh Bangal, Rengaian Ganesan*

Ashoka Trust for Research in Ecology and The Environment (ATREE), Bengaluru, India

*Corresponding author: rganesan@atree.org

The genus *Impatiens* (Balsaminaceae), known for its biogeographical complexity, likely originated in southern China or Southeast Asia, followed by migration. However, the historical biogeography of Peninsular Indian *Impatiens* remains unclear, complicated by India's unique geological history. This research investigates the biogeography of the seven *Impatiens* groups endemic to the Western Ghats, initially classified by Hooker J.D. in the Flora of British India based on habit and habitat. By integrating molecular and morphological analyses, we aim to determine whether each of the seven groups is monophyletic and to trace the phylogeography and evolutionary history of Peninsular Indian *Impatiens*. Using molecular biogeography methods, preliminary findings suggest a migration route from southern China or Southeast Asia to Peninsular India, with potential evolutionary links between African species in Annuae and Microsepalae groups. This study provides insights into migration and evolutionary patterns among *Impatiens* species at the Peninsular Indian level and globally.

Preliminary insights into the phylogeny of the "soldier spiders" (Araneae: Corinnidae: Corinninae)

Fabián García[1,2,*], Alexandre Bonaldo[1,2]

[1] Laboratório de Aracnologia, Coordenação de Zoologia, Museu Paraense Emílio Goeldi, Belém, Brazil
[2] Programa de pós-graduação em Zoologia, Universidade Federal do Pará & Museu Paraense Emílio Goeldi, Belém, Brazil

*Corresponding author: Falgaroo97515@gmail.com

The subfamily Corinninae, within the family Corinnidae, is primarily distributed in the Neotropics and includes spiders that mimic ants. Although taxonomic advances have clarified some aspects of their diversity, hypotheses regarding intergeneric relationships have yet to be evaluated phylogenetically. This study constructs the first phylogeny of Corinninae using five molecular markers (COI, 12S, 16S, 18S, 28S), revealing that Corinninae is not monophyletic due to the inclusion of the genera *Mesappus* and *Ianduba*, previously suggested as sister groups to Corinninae. Two main groups were identified: the first comprises *Megalostrata*, the *Corinna aenea* group, and *Mesappus*, while the second includes a clade formed by the *Corinna kochi* group, *Paradiestus*, the *Corinna capito* group, and the *Creugas gulosus* group, along with *Falconina*, *Septentrinna*, *Methesis*, *Parachemmis*, *Tupirinna*, *Stethorrhagus*, and the *Creugas belliator* group. These results are not yet conclusive, and efforts are ongoing to include new molecular data.

Evolution of South Asian Mountain biota: dispersal, fine-scale biogeography, and phylogenetics of Nannenini of jumping spiders

Thakshila Herath[1], Athira Jose[2], Ambalaparambil V. Sudhikumar[2], Suresh P. Benjamin[1,3,*]

[1] National Institute of Fundamental Studies, Kandy, Sri Lanka

[2] Centre for Animal Taxonomy and Ecology, Department of Zoology, Christ College, Irinjalakuda, Kerala, India

[3] Alexander Koenig Research Museum of Zoology, Bonn, Germany

*Corresponding author: suresh.benjamin@gmail.com

Nannenini jumping spiders are confined to the intact tropical rainforests of South and Southeast Asia, with most species being point endemics found in high-elevation cloud forests. This distribution offers a valuable opportunity to study the effects of geography and historical climate change on species diversification. In this study, we explored their phylogenetic relationships to understand their evolutionary history. DNA extracted from leg tissue was sequenced for mitochondrial (CO1, H3) and nuclear (28S, 18S) genes. Phylogenetic analyses, integrating molecular data and time-calibrated trees, revealed distinct clades and key divergence events during the Oligocene and Miocene epochs. The results suggest that Nannenini spiders dispersed during the Late Oligocene, with climatic shifts promoting speciation. Montane environments likely served as refugia, maintaining biodiversity during adverse climates and facilitating later expansion, highlighting the crucial role of Sri Lanka’s central highlands in its biodiversity.

Phylogenetic Discordance in True Eels (Anguilliformes): Use of Morphological vs. Molecular Data and Total Evidence

Sebastián Huacuja Barraza[1,*], Kleyton Magno Cantalice Severiano[2]

[1] Posgrado en Ciencias Biológicas UNAM, México

[2] Instituto de Geología UNAM, México

*Corresponding author: sebastian_huacuja@ciencias.unam.mx

True eels (Anguilliformes) are a group of cylindrical and elongated fishes. While their monophyly is supported by osteological characteristics, defining the internal relationships within the group solely through morphology presents challenges. Moreover, the inclusion of Cretaceous fossils increases uncertainty about the evolutionary history of the osteological traits traditionally used to define true eels. This study describes a new species of eel from the Paleocene of Mexico and explores the use of total evidence analysis to understand the evolution of morphological characteristics in true eels, assessing their utility in defining suborders and families. Additionally, it evaluates the phylogenetic affinities of ""primitive"" eels from the Cretaceous with ""modern"" forms from the Cenozoic.

Systematics of *Lepidagathis* Willd. (Acanthaceae: Barlerieae) in India

Anishkar F J King, Gunadayalan Gnanasekaran*

Department of Botany, Madras Christian College, Chennai, India

*Corresponding author: gnanasekaran@mcc.edu.in

Lepidagathis Willd. (Acanthaceae: Barlerieae) is distributed in pantropical regions of the world with 151 accepted species. In India, it is represented by 29 species and two varieties, of which 21 species are endemics. The results of the present systematic study based on morphology (gross, pollen and seed) and molecular (*rbcL* and *trnS* (GCU)–*trnG* (UCC)) characters coupled with scrutiny of all the earlier publications to date and examination of herbarium specimens housed in Indian and foreign herbaria will be discussed. They are: (i) updated circumscription for all species with dichotomous keys, illustrations, photo plates, and extinction risk; (ii) taxonomic and nomenclatural novelties; (iii) evidence for subsuming nine names; (iv) type designation for many names; (v) systematic significance of pollen and seed micromorphology; and (vi) evolution and phylogeny with morphological synapomorphies and biogeography.

Diversity of Ulvaceae (Ulvales, Chlorophyta) from northern Philippines including the description of a new *Umbraulva* species

Christine Marie M. Lazaro*, John Michael Lastimoso, Wilfred John E. Santiañez

Gregorio T. Velasquez Phycological Herbarium and The Marine Science Institute, College of Science, University of the Philippines, Philippines

*Corresponding author: cmlazaro@msi.upd.edu.ph

Members of the green seaweed family Ulvaceae are economically and ecologically important. Of these, the cosmopolitan genus *Ulva* inhabits shallow waters, while *Umbraulva* species are typically found in deeper, colder waters. Both genera are easily confused as most possess bladed thalli but are discriminated based on distinct molecular phylogenetic positions and the presence of siphonaxanthin in *Umbraulva*. Here, we report new records of *Ulva* in the Philippines and the first record of the genus *Umbraulva* in the country. For the latter, we described a new *Umbraulva* species based on morpho-anatomical observations and molecular phylogenetic analyses based on *tufA* gene sequences. Our work highlights the need to continuously explore tropical waters which often results in the discovery and descriptions of taxa new to science, a foundational knowledge for advancing initiatives on resource conservation and in support of a sustainable blue economy.

Assessing mitogenomic gene order rearrangements and phylogeny of the parasitic family Stylopidae (Strepsiptera)

Carlos Leyton Rotella[1,*], Meri Lähteenaro[2,3], Daniel Benda[4], Jakub Straka[4], Johannes Bergsten[2,3]

[1] Department of Biology Education, Faculty of Science, Stockholm University, Sweden
[2] Department of Zoology, Swedish Museum of Natural History, Stockholm, Sweden
[3] Department of Zoology, Faculty of Science, Stockholm University, Sweden
[4] Department of Zoology Faculty of Science Charles University, Czech Republic

*Corresponding author: leytonrotella@gmail.com

The mitochondrial genome has been widely used to investigate evolutionary relationships due to its unique features. While mtDNA gene arrangements are generally conserved in arthropods, particular groups such as some parasitic taxa, can exhibit high variability in gene order. Previous research has shown that Strepsiptera, an insect order characterized by a parasitoid lifestyle, displays some mtDNA rearrangements. Our results obtained from newly assembled mitogenomes from seven of the eight different Stylopidae genera (*Crawfordia*, *Eurystylops*, *Halictoxenos*, *Hylecthrus*, *Kinzelbachus*, *Melittostylops* and *Stylops*) demonstrates that each genus has a distinct gene order. The holarctic genus Stylops exhibits the most highly rearranged mitochondrial genome, including rearrangements of protein-coding genes (PCGs) not previously documented in Strepsiptera. Furthermore, the mitochondrial genomes from 41 different Stylops species reveal that all share the same highly rearranged gene order. Phylogenetic analyses, using all 37 mitochondrial genes, provide support for previous phylogenetic conclusions on Stylops based on nuclear data.

A timescale for the evolutionary history of sea spiders (Arthropoda: Pycnogonida)

Morena Nava[1,2,*], Sandra Álvarez-Carretero[3], Russell J. Garwood[4,5], Philip C. J. Donoghue[3], Romain Sabroux[3], Davide Pisani[2,3]

[1] Department of Biotechnology and Biosciences, University of Milano-Bicocca, Italy
[2] Bristol Palaeobiology Group, School of Biological Sciences, University of Bristol, UK
[3] Bristol Palaeobiology Group, School of Earth Sciences, University of Bristol, UK
[4] The Natural History Museum, London, UK
[5] Department of Earth and Environmental Sciences, University of Manchester, UK

*Corresponding author: morena.nava@hotmail.it

Sea spiders (Arthropoda: Pycnogonida) are an ancient lineage of marine chelicerates represented by ca. 1,400 extant species distributed worldwide. While they are currently represented by a single order (Pantopoda), the fossil record testifies that their diversity was once much higher. To better understand their diversification through time, we used MCMCtree to conduct timetree inference analyses with a set of 13 mitochondrial protein-coding genes, 18S rRNA sequences, and 98 Ultra Conserved Elements from 198 pycnogonid taxa. Following the most recent interpretations of the fossil record, we used five fossil specimens to constrain the node ages of our phylogeny. Our results indicate that pycnogonids diverged from other arthropods during the Cambrian (539-510 Ma), suggesting 100 Myr between Pycnogonida origin and pantopod diversification. In addition, Pantopoda diversified between the Silurian and the Late Devonian (435-367 Ma), thus preceding the appearance of the first pantopod fossil by ~206.5 Myr.

Species diversity and first phylogenetic relationship of the parasitoid wasp genus *Tamarixia* in Sweden

Lucie Röttgers[1,2,*], Emma Kärrnäs[1], Søren Faubry[2], Niklas Wahlberg[1]

[1] Department of Biology, Lund University, Sweden

[2] Department of Biological & Environmental Sciences, University of Gothenburg, Sweden

*Corresponding author: lucie.rottgers@biol.lu.se

Insects are negatively affected by anthropogenic stressors, leading to a rapid decline in their biodiversity. For battling this loss, knowledge on the diversity of species – which is largely lacking for insects, is crucial. This knowledge gap is particularly pronounced in parasitic wasps (Hymenoptera), a highly understudied yet ecologically and economically important insect group. Although 153,000 species of Hymenoptera are currently described, estimates suggest their numbers exceed one million, with >90% of these being parasitic wasps. Our study aims to enhance the understanding of the diversity of parasitic wasps in Europe, focusing on the Swedish species in the wasp genus *Tamarixia* (Eulophidae: Tetrastichinae). Using both DNA barcoding and whole-genome sequencing data, we infer the first phylogenetic relationships within *Tamarixia*. Here, I present the first molecular species delimitation for *Tamarixia*, based on barcode data of 64 specimens. Analysis from four different methods suggest the discovery of 6 new *Tamarixia* species.

Investigating cryptic speciation in Indian Blackbird (*Turdus simillimus* complex) using phylogenomics

Archita Sharma[1,*], Naman Goyal[1], Vinay KL[2], Dhyey Shah[3], Sampath Seneviratne[4], VV Robin[1]

[1] Indian Institute of Science Education and Research (IISER) Tirupati, India

[2] Louisiana State University, USA

[3] Maharaja Sayajirao University of Baroda, India

[4] University of Colombo, Sri Lanka

*Corresponding author: architasharma@students.iisertirupati.ac.in

In the peninsular part of India (25° - 8° N), landscape and climatic barriers have resulted in as many as 200 subspecies of birds. This study uses ultraconserved elements (UCEs) to reassess the taxonomy of the Indian Blackbird (*Turdus simillimus*) with four subspecies found across India and Sri Lanka. We systematically collected genetic samples from the field for 1 to 5 individuals per sub-species. For 21 samples (including outgroup *T. boulboul*), we extracted DNA from blood and prepared 5060 tetrapods UCE-enriched libraries. We did maximum likelihood tree construction, species delimitation, and divergence dating analysis. UCE data revealed 3 monophyletic clades (subsp. *nigropileus*, subsp. *kinnisii*, and subsp. *bourdilloni*+*simillimus*). Dating analysis revealed that migratory subsp. *nigropileus* diverged earlier (~2.49 mya) from non-migratory subsp. *bourdilloni* and *simillimus*. We have also done multivariate analysis of morphological, song and environmental niche data to assess divergence, applying an integrative taxonomy approach.

A new threat to the European marine environment: The exotic polyclad flatworm *Postenterogonia orbicularis* (Schmarda, 1859)

Emma Shorter-Rodríguez[1], Ricardo López-Alonso[1], Esteban Pascual-Parra[1], Claudia González-Toral[1,6], Ana del Cerrob, Marta Muñoz[3], Verónica Soto-López[4], Deva Menéndez-Teleña[4], Iris Carrera-Rodríguez[4], Jesús Ángel García-Maza[4], Eduardo Cires [1,5], Andres Arias [1,*]

[1] Department of Organisms and Systems Biology, University of Oviedo, Oviedo, Spain
[2] Regional Agrifood Research and Development Service (SERIDA), Department of Animal Health, Gijón, Spain
[3] Regional Agrifood Research and Development Service (SERIDA), Department of Genetics and Animal Reproduction, Gijón, Spain
[4] Department of Nautical Science and Technology, University of Oviedo, Gijón, Spain
[5] Institute of Natural Resources and Land Planning, Mieres, Spain
[6] Department of Functional Biology, University of Oviedo, Oviedo, Spain

*Corresponding author: UO282970@uniovi.es

Harbours are key locations for early detection of Non-Indigenous Species (NIS) due to marine traffic and habitat degradation. Among NIS, polyclad flatworms are predators of bivalves, threatening marine ecosystems and aquaculture. This study reports the first morphological and molecular identification of a new NIS polyclad species native to the Pacific Ocean, in the Cantabrian Sea, Bay of Biscay. Morphological traits, such as the ruffled pharynx and cephalic eyes are consistent with *Postenterogonia orbicularis*. Phylogenetic analysis using the mitochondrial COI marker placed the specimens from Avilés and Gijón, along with *Idiostylochus tortuosus* from Arcachon Bay (France), within the *P. orbicularis* clade (Ilyplanidae family). Our results suggest that *I. tortuosus* may be synonymous with the New Zealand species *P. orbicularis*. Finally, we discuss possible ecological impacts of its introduction and provide some management recommendations for controlling its influx in the recipient environments.

Integrative redescription of *Minibiotus jonesorum* Meyer et al., 2011 (Tardigrada: Macrobiotidae)

Aleksandra Sumlińska[1,*], Jacob Loeffelholz[2], Alejandro López-López[1], Łukasz Michalczyk[1]

[1] Department of Invertebrate Evolution, Institute of Zoology and Biomedical Research, Faculty of Biology, Jagiellonian University, Kraków, Poland
[2] University of Wyoming, Department of Molecular Biology, Laramie, USA

*Corresponding author: a.sumlinska@student.uj.edu.pl

The taxonomy of tardigrades has undergone significant changes over the past two decades, primarily due to molecular techniques. However, despite the dynamic development of this branch of zoology, the phylogenetic position of most species remains unknown. A notable example is the genus *Minibiotus*, whose high morphological diversity raises the possibility of polyphyly. However, extremely limited genetic data and frequent lack of detailed morphological information hinder the verification of relationships within this genus. In this study, we provide an integrative redescription of *Minibiotus jonesorum* based on a newly discovered population in Wisconsin, USA. Our approach combines traditional taxonomic methods, including morphological and morphometric analyses using PCM and SEM, alongside genetic data for four markers: 18S rRNA, 28S rRNA, ITS-2, and COI. Additionally, for the first time, we constructed a concatenated phylogenetic tree for all available sequences of *Minibiotus* using Bayesian inference, providing new insights into the enigmatic evolution of the genus.

A revision to the ginger genus *Epiamomum* A.D.Poulsen & Škornick.

Alexander Tianara[1,2], Jana Leong-Škorničková[3,4], Flávia Fonseca Pezzini[1], Mark Hughes[1], Axel Dalberg Poulsen[1,*]

[1] Royal Botanic Garden Edinburgh, Edinburgh, United Kingdom
[2] Herbarium Depokensis (UIDEP), Department of Biology, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Indonesia
[3] Herbarium, Singapore Botanic Gardens, Singapore
[4] Department of Biological Sciences, National University of Singapore, Singapore

*Corresponding author: axel@dalbergpoulsen.com

The genus *Epiamomum* (Zingiberaceae) was established in 2018 including six species endemic to Borneo. The phylogeny, however, only sampled two species (*E. angustipetalum* and *E. roseisquamosum*), thus the aim to sample the remaining species to test the monophyly of the genus. In total, 101 *Epiamomum* herbarium collections from twelve herbaria were included. Ten samples were used in phylogenetic analyses producing nrITS and *matK* sequence data. Bayesian Inference of the nrITS dataset confirmed monophyly with two subclades. A dated phylogeny suggests that the common ancestor of the genus originated around Early- to Mid-Miocene (17.5 Mya). Our taxonomic treatment accepts six species, proposes one new synonym (*E. hansenii*), one new combination (*E. bilabiatum*), and detects several probable new species. Ninety-four distribution records from collections reaffirmed Epiamomum's endemism to Borneo. Conservation status re-evaluation resulted in all species are threatened due to habitat decline caused by agriculture and logging.

Anolis gingivinus (Dactyloidae): revised description, sexual size dimorphism, and lessons learnt on the value of natural history collections.

Ellen Campbell

University College London, UK

*Corresponding author: campbell.emc@gmail.com

Despite natural history collections providing an incredible resource for researching life on Earth, appreciation for their value is declining. This study endeavoured to examine a collection of 184 unidentified anole specimens from the Grant Museum of Zoology, UCL. Through extensive data collection on size measurements and 32 squamation traits, specimens were identified as *Anolis gingivinus* from the Lesser Antilles, and the species description was revised. Data was analysed using PCA, Mann-Whitney U tests, and ANOVAs to examine the extent of sexual dimorphism within the species. Sexual size dimorphism (SSD) was significant and large within this collection (1.36). However, following size correction using SVL, only head width and shank length showed significant sexual dimorphism. No dimorphism in squamation was present, though variation was much higher than reported previously. Continued efforts to revise descriptions and improve the coverage of natural history collections are crucial to maintaining their value for future research.

A Phylogenetic Study of *Lemmus*

Carmen C. T. From Dalseng*

Natural History Museum, University of Oslo, Norway

*Corresponding author: ccdalsen@student.ibv.uio.no

The phylogeny of *Lemmus* is not fully understood and no consensus has yet been reached on species delimitation within the genus. Changes in the nomenclature of the genus through history, can be viewed in light of changing taxonomical approaches. The most recent phylogenetic studies of *Lemmus* are largely based on mitochondrial data. One such study reported the discovery of a new subspecies, *L. lemmus chernovi*, on the Russian islands of Novaya Zemlya. This insular population is geographically closest to the mainland species *L. sibiricus* and morphologically very similar to it. Using whole-genome data, for the first time from *Lemmus*, we see that there is incongruence in mitochondrial and nuclear signals; that although mitochondrial data supports the splitting of *L. sibiricus* into two separate species, the nuclear data does not; and that there is not support for recognizing the lemmings of Novaya Zemlya as a subspecies of *L. lemmus*.

Taxonomic revision of the *Ipomoea longituba-marmorata* complex; An African-endemic sweet potato crop wild relative group

Marie Declercq G.[1,*], Kagame Samuel P.[1,2], Kathambi Vivian. [1,2], Ngima Simon W. [3], Mutiso Patrick [3], Muigai Anne W.T.[5], Juliana Cruz Jardim Barbosa [6], Chatrou Lars W.[1], Simões Ana R.G.[1,2]

[1] Systematic and Evolutionary Lab, Department of Biology, Ghent University, Belgium
[2] Royal Botanic Gardens, Kew, UK
[3] Department of Biology, University of Nairobi, Kenya
[4] East Africa Herbarium, National Museum of Kenya, Nairobi, Kenya
[5] National Defence University-Kenya, Nakuru, Kenya
[6] Núcleo de Pesquisa Curadoria do Herbário, Centro de Pesquisa em Plantas Vasculares, Instituto de Pesquisas Ambientais (IPA), São Paulo, SP, Brazil

*Corresponding author: mariegdeclercq@gmail.com

In this taxonomic work, nine related, East-African *Ipomoea* will be revisited. The clade is unified by its floral morphology and the presence of storage roots. They bear a tubular, mainly white flower, which opens in the morning and at night. The clades' taxonomy needs updating as it has not been revisited since the 1960's. This will simultaneously aid the classification of the *Ipomoea*, as it still includes many uncertainties; synonymy, paraphyly, and the associated frequent name changes. A clear species classification including comprehensible boundaries is essential for implementing conservation and protection measures, crucial for addressing pressing issues related to biodiversity loss and climatic change. Our objective is to develop a comprehensive overview and accurate diagnosis of the species within the clade. This is done based on a morphological analysis of herbarium specimens (BR, K, NAI, EA), complemented by observations from fieldwork in Kenya.

The Neotropical rainforest mimosoid genus *Zygia* P.Browne - Diversification and evolution based on phylogenomics and morphology

Julia Ferm[1,2,*]

[1] Department of Environment, Ecology and Plant Sciences, Stockholm University, Sweden
[2] Royal Botanical Garden Edinburgh, UK

*Corresponding author: jferm@rbge.org.uk

The Neotropical legume genus *Zygia* P.Browne comprises about 50 species, recognised as small cauliflorous trees. Species relationships within *Zygia* have been difficult to resolve based on data generated with Sanger sequencing (i.e. sequences up to 1200 bp), something which may indicate a recent evolutionary radiation. This project will investigate diversification and evolution in *Zygia*. Phylogenetic relationships and node ages will be resolved using massive amounts of nuclear DNA data produced by the target enrichment method. Moreover, this project will determine if *Zygia* has undergone a recent rapid diversification caused by highly effective dispersal and investigate to what extent hybridisation, introgression and polyploidy may explain evolution and diversification within the genus. Finally, extensive morphological studies of *Zygia* will be conducted, and in combination with the phylogenetic results, the taxonomy and classification of the genus will be updated.

Blooming in the Shadow of Extinction: Taxonomy of the Brazilian Gumweeds (*Grindelia*, Asteraceae)

Fernando Fernandes[1,*], Tatiana Teixeira Souza-Chies[1], Gustavo Heiden[2]

[1] Universidade Federal do Rio Grande do Sul, Brazil
[2] Embrapa Clima Temperado, Brazil

*Corresponding author: fnandes.oliveira@gmail.com

Grindelia (Asteraceae), with 70 species known as gumweeds and a temperate disjunct distribution in North and South America, are generally xerophilies and inhabit desertic and mountainous environments, while others thrive in brackish or subhumid soils. The southern Brazilian species are at the genus distribution edge, where they tend to be found in isolated populations restricted to well drained sandy soils and sandstone and basalt outcrops. The ongoing research on Brazilian *Grindelia* species involves a taxonomic revision, sampling for phylogenetic reconstruction, and conservation status. It also addresses the population genetics of *G. atlantica*, critically endangered and known from only two remaining populations. Additionally, two new species living in surprising habitats are described: one that is the first in the genus endemic to the Brazilian Atlantic Forest, and a second one which is a rheophile found attached to rapids riverbed rocks. Both are known from single populations and are likely facing extinction.

A global taxonomic revision of the deep-sea squid family Brachioteuthidae, starting with New Zealand species

Austin Horenkamp

Auckland University, New Zealand

*Corresponding author: Ahorenkamp10@gmail.com

The deep-sea squid family Brachioteuthidae Pfeffer, 1908 has representative species in all oceans. Unfortunately, specimens are rarely collected and often damaged upon capture, which has led to unstable taxonomy in this family. Therefore, the overall goal of the present study is to use an integrative taxonomic approach—using a combination of morphology and genetics—to resolve the global systematics of the Brachioteuthidae (one of the most taxonomically unstable cephalopod families). Morphological species descriptions will be written following standard guidelines for the description of cephalopods. In addition, three mitochondrial gene regions (cytochrome c oxidase subunit 1 [COI], 16S rRNA, and 12S rRNA) will be sequenced and used to support species delimitations and phylogenetic relationships between species. This talk will focus on a local revision of the brachioteuthids from New Zealand. The results of this thesis will be of international significance to the systematics of this unstable group of deep-sea squids.

Behold the rare: *Strobilanthes* from North Eastern Region of India

Rajkumari Jashmi Devi*, Biseshwori Thongam

Institute of Bioresources and Sustainable Development, Takyelpat, Manipur, India

*Corresponding author: rajkumjas@gmail.com

The genus *Strobilanthes* Blume of family Acanthaceae is represented by rarely collected plants. It is distributed mostly in Asia, extending to Japan and Korea in the north, Afghanistan and Pakistan in the west, and northern Australia in the south. They are poorly known due to their plietesial flowering pattern. Manipur is one of the states from North Eastern region of India falling under the Indo-Burma Biodiversity Hotspot. Two rare species of genus *Strobilanthes* were re-assessed from Manipur, India. They are *Strobilanthes auriculata* Nees, a lesser known plant having eight-year plietesial cycle, was re-collected in the year 2019. And *Strobilanthes recurva* C.B. Clarke, another rare species, was re-collected in the year 2022. *S. recurva* is reported from only five locations: four from North Eastern Region of India and one from Chittagong, Bangladesh. The present study will be useful in exploring and evaluating this rare genus *Strobilanthes*.

Petiole Anatomical Investigation of Some *Ficus* Species in Southeast Bangladesh and Their Taxonomic Significance

Mohammad Jorid, Dr. Mohammad Harun ur Rashid*

University of Chittagong, Bangladesh

*Corresponding author: rashidmh@cu.ac.bd

This study investigated the petiole anatomy of 11 *Ficus* species to characterize their anatomical diversity and assess their potential for species identification. Microscopic examination of petiole cross-sections revealed variations in vascular bundle arrangement, trichome presence, and crystal type. While all species exhibited a single ring of vascular bundles, their number and arrangement differed significantly. Trichomes were found in some species but absent in others, suggesting potential ecological adaptations. Calcium oxalate crystals were observed in most species, with specific crystal types contributing to species-level identification. These findings demonstrate the utility of petiole anatomy as a diagnostic tool for *Ficus* species in southeast Bangladesh. Future research should explore the correlation between petiole anatomy and ecological factors to gain a deeper understanding of their adaptive significance.

Biogeography and Phylogenetic Relationships of *Caridina fernandoi* in India and Sri Lanka, with the Discovery of Novel Western Ghats Endemics

K Kunjulakshmi, Maclean Antony Santos, Sanjeevi Prakash*

Centre for Climate Change Studies, Sathyabama Institute of Science and Technology,
Chennai, Tamil Nadu, India

*Corresponding author: prakash.cccs@sathyabama.ac.in

The present study examines the phylogenetic relationships of freshwater shrimps between India and Sri Lanka, using *Caridina fernandoi* as a model organism. It has widespread distribution across India. Samples were collected from central Western Ghats (Mangalore) and southern Western Ghats (Calicut and Thrissur), with particular interest in locations across the Palghat gap. Analysis of mitochondrial genes (16S rRNA and COI) for phylogenetics and species delimitation revealed that India's *Caridina fernandoi* likely descended from diverse Sri Lankan mainland stock. Limited biotic exchange has led to high endemism, with species evolving into new taxa at higher altitudes of Western Ghats. Despite historical land bridges during low sea levels, faunal exchange between southern India and Sri Lanka has been restricted, with genetic exchange likely predating 500,000 years ago. The study suggests that treating the Western Ghats and Sri Lanka as a single biodiversity hotspot may overlook significant biogeographic structure.

Cancer prevalence in relation to life history traits in birds

Stefania E Kapsetaki[1,*], Zachary T Compton[1,2], Jordyn Dolan[1], Valerie K Harris[1], Walker Mellon[1], Shawn M Rupp[1], Elizabeth G Duke[3], Tara M Harrison[3], Selin Aksoy[1], Mathieu Giraudeau[4], Orsolya Vincze[5], Kevin J McGraw[1], Athena Aktipis[1], Marc Tollis[1,6,] Amy M Boddy[1,7], Carlo C Maley[1]

[1] Arizona State University, USA
[2] University of Arizona, USA
[3] North Carolina State University, USA
[4] Littoral Environnement Et Sociétés, France
[5] Hungarian Department of Biology and Ecology, Romania
[6] Northern Arizona University, USA
[7] University of California Santa Barbara, USA

*Corresponding author: stkapsetaki@gmail.com

Cancer affects multicellular life, including birds, yet it is unknown whether life history traits could explain the variation in their cancer prevalence. Based on life history theory, we would expect animals that invest more in reproduction to invest less in somatic maintenance such as cancer defenses. So, for example, species with a larger clutch may have higher cancer prevalence. In this study we collected cancer and neoplasia prevalence data from 5,729 necropsies across 108 bird species and used phylogenetically-controlled regressions to test whether body mass, lifespan, incubation length, clutch size, and/or sexually dimorphic traits, are correlated with neoplasia and cancer prevalence. We found that clutch size is positively correlated with cancer prevalence. However, no other life history trait was correlated with cancer or neoplasia prevalence. These results support a life history trade-off between somatic maintenance and reproduction in birds.

An Exploration of Trichome Diversity: A Morphological Study of Twenty African *Ipomoea* Species (Convolvulaceae) Using Herbarium Specimens

Funmilola Mabel Ojo[1,*], Ana Rita G. Simões[2], Vagner Augusto Benedito[3], Eloisa Vendemiatti[3]

[1] Department of Biological Sciences, Olusegun Agagu University of Science and Technology, Okitipupa, Nigeria
[2] Royal Botanic Gardens, Kew, London, UK
[3] Division of Plant & Soil Sciences, West Virginia University, USA

*Corresponding author: fm.ojo@oaustech.edu.ng

Trichomes, specialized epidermal structures, play vital roles in plant defense, ecology, adaptation, and systematics. This study investigates trichome morphology in Convolvulaceae, a family of 59 genera and 1,950 species. Twenty herbarium specimens from Royal Botanic Gardens, Kew, were examined using light and scanning electron microscopy. Results reveals significant variations in trichome shape, size, density, and distribution among species and genera. Three main trichome types were identified: simple non-glandular, glandular, and clustered. These trichomes correlate with leaf surface features and contribute to plant defense mechanisms. Simple non-glandular trichomes provide physical protection, while glandular trichomes secrete defensive compounds. Our findings underscore the taxonomic importance of trichome morphology in Convolvulaceae, shedding light on evolutionary adaptations and ecological interactions. This study provides a foundational understanding of trichome diversity, paving the way for future research on functional significance and applications in agriculture and conservation.

Taxonomic study of the genus *Chaenotheca* (Coniocybaceae, Ascomycota) in Bulgaria

Snezhina B. Popova[1,3,*], Veselin V. Shivarov[2]

[1] Faculty of Biology, Sofia University “St. Kliment Ohridski”, Bulgaria

[2] Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria

[3] National Museum of Natural History at the Bulgarian Academy of Sciences, Sofia, Bulgaria

*Corresponding author: snejina.b.popova@gmail.com

The genus *Chaenotheca* is a group of calicioid lichens, known for their pin shaped apothecia, small size and specific habitat preference. According to the Checklist of lichenized and lichenicolous fungi in Bulgaria (Denchev et al. 2022), nine species have been recorded for the country so far, six of which are known from single floristic regions. Our aim is to revise the existing materials, analyse literature data and collect new samples from poorly studied regions of the country. The materials will be analysed using taxonomic characters such as microchemical reactions, spore and apothecial morphology. The preliminary results from specimens collected by the authors from understudied regions show two new records for the country and three species are found in new floristic regions. This study aims to assess the taxonomic diversity, ecological preferences and distribution of the genus, as well as providing a key for identification of the *Chaenotheca* species in Bulgaria.

What actually is a “blusher”? Advances in delimiting the European species of *Amanita* series *Validae*

Mauro Rivas-Ferreiro[1,*], Paloma Morán[1], A. Martyn Ainsworth[2], Laura M. Suz[2]

[1] Centro de Investigación Mariña (CIM) – Department of Biochemistry, Genetics and Immunology, University of Vigo, Spain
[2] Royal Botanic Gardens, Kew, UK
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*Corresponding author: mauro.rivas@uvigo.gal

Amanita Pers. (1797) is a well-known genus of fungi with a global distribution and over 700 recognized species. One of the smaller clades within the genus is *Amanita* series *Validae* Fries (1854), which contains seventy-four validly published species, of which only four are native to continental Europe. Among these, we find a non-taxonomic group of species often called “blushers”, because of the bruising that occurs in their sporocarps. In Europe, these “blushers” are represented by two species: *Amanita rubescens* Pers. 1797 and *Amanita excelsa* (Fr.) Bertill. 1866, each with several recognized varieties. However, species delimitation in *A. rubescens* and *A. excelsa* has proven to be difficult, and DNA shows that there are cryptic species hidden under these names. In this presentation we will share our preliminary results in delimiting European “blushers” and propose potential solutions to address their complex nomenclatural issues.

Evolutionary genomics analysis reveals a unique lineage of *Megachile pruina* found in an isolated population in Bermuda

Jennifer Rose[1,*], M. Thomas P. Gilbert[1,2], Mark Outerbridge[3], Hernán E. Morales[1]

[1] Center for Evolutionary Hologenomics, The Globe Institute, University of Copenhagen, Denmark
[2] University Museum, Norwegian University of Science and Technology (NTNU), Trondheim, Norway
[3] Department of Environment and Natural Resources, Government of Bermuda, Hamilton Parish, Bermuda

*Corresponding author: jdrose08@gmail.com

The global decline in native bee diversity has raised concerns about the conservation status of many species. However, most bee species have not undergone taxonomic reassessment since their initial classification, complicating management efforts. In Bermuda's natural history, only three bee species have been recorded, including *Megachile pruina* Smith, 1853 (Hymenoptera: Megachilidae). This species is potentially the island's last native bee and is now restricted to an 11.5-hectare area. Despite being classified as "Vulnerable" under the Bermuda Protected Species Act, its taxonomic and evolutionary relationships remain uncertain. Through nuclear and mitochondrial genome analysis, we demonstrate that Bermuda's *M. pruina* population is genetically distinct from mainland U.S. populations, representing a unique evolutionary lineage confined to the island. In contrast, U.S. populations of *M. pruina* show no significant genetic differentiation from each other, contrary to previous classifications.

An integrative taxonomic analysis reveals a new genus of freshwater mollusc from the Western Ghats, India

Abhisikta Roy[1,2,*], Surya Narayanan[1], Aravind N.A.[1,3]

[1] Ashoka Trust for Research in Ecology and the Environment, India
[2] Manipal Academy of Higher Education, India
[3] Yenepoya (Deemed to be) University, India

*Corresponding author: abhisikta.roy@atree.org

The Western Ghats in India are home to a diverse freshwater molluscan fauna, with 14 genera from 10 families, including several endemic genera such as *Paracrostoma*, *Cremnoconchus*, and *Pseudomulleria*. Despite high diversity, much of the systematics of these molluscs remains unresolved. During research on *Paracrostoma*, we identified a unique specimen, which was revealed as a new genus through molecular analyses. Subsequent morphological and radula analyses confirmed it as a genus new to science, now represented by three species found in fast-flowing, perennial streams on the western slopes of the Ghats. This genus is endemic to the northern-central and southern-Northern Western Ghats. Phylogenetic studies suggest its closest relatives are in Southeast Asia, Australia, and South America, and further sampling may shed light on broader biogeographic patterns.

A new genus of ectoparasitic Myzostomida from the Pacific abyss

Eva C.D. Stewart[1,2,*], Naoto Jimi[3], Camille Moreau[4], Guadalupe Bribiesca-Contreras[1,5], Helena Wiklund[1,6,7], Adrian G. Glover[1]

[1] Life Sciences Department, Natural History Museum, London, UK
[2] School of Ocean and Earth Sciences, University of Southampton, UK
[3] Sugashima Marine Biological Laboratory, Graduate School of Science, Nagoya University, Japan
[4] Marine Biology Lab Université Libre de Bruxelles, Belgium
[5] National Oceanography Centre, Southampton, UK
[6] Department of Marine Sciences, University of Gothenburg, Sweden
[7] Gothenburg Global Biodiversity Centre, Sweden

*Corresponding author: e.stewart@nhm.ac.uk

The Myzostomida von Graff, 1887 are a small order of parasitic marine annelids associated with echinoderms, with around 170 species described to date. There are currently seven described families within the order, of which two – Asteriomyzostomidae and Asteromyzostomidae – are characterised by being endo- and ectoparasitic on asteroids respectively. Here we describe a new genus and two new species of Asteriomyzostomidae, the first species' of Myzostomida described from abyssal depths. Specimens were found infecting the dorsal surface of the starfish *Styracaster paucispinus* Ludwig, 1907, at abyssal depths in the equatorial Pacific Ocean, and on the dorsal surface of the starfish *Eremicaster crassus* (Sladen, 1883) in the Aleutian Trench. An integrative morphological and molecular taxonomic approach was undertaken, including microCT scanning of myzostomids and hosts allowing for a complete understanding of the species morphology.

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 the speakers 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 our meetings to date and there is no reason to expect this will change. 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, Katie Collins, Pablo Muñoz-Rodríguez, Ana Serra Silva, Kálmán Könyves or Peter Mulhair 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.