Young Systematists' Forum

VIRTUAL CONFERENCE

Friday 14th November 2025

Sponsors

Royal Botanic Gardens Kew

THE Systematics ASSOCIATION

Natural History Museum

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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 Start	Session	Title	Speaker	Session	Title	Speaker
10:00	**OPENING REMARKS**					
10:15	**Introduction to the Systematics Association from the SA President, Dr Davide Pisani** **TALKS BEGIN AT 10:30 GMT**					
10:30	Flash A1	Disentangling the taxonomy and population genomics of the *Hieracium tomentosum* L. group	Calzoni	Flash B1	Exploring hidden richness: unveiling the undocumented pyrenocarpous lichen of Southern Philippines	Taer
10:35		Microsnails and how to find them: A morpho-taxonomic survey of marine microgastropods (Mollusca: Gastropoda) in Panglao Island, Bohol, Philippines using lumon-lumon as experimental probe	Caril		To trim or not to trim; the effect of alignment trimming in phylogenomic analysis	Baron
10:40		*Fritillaria yakutiae* sp. nov. (Liliaceae) from Surkhandarya, Uzbekistan	Karimov		Phylogenetic, biogeographic and ecological enquiry into deciduousness	Jahan
10:45		From hidden retreats to phylogenetic trees: resolving the evolutionary history of Iberian red devil spiders	Nava		A comprehensive study of *Ophiorrhiza* in India: Taxonomy, Systematics and Ethnomedicinal Relevance	Chanu
10:50		Optical Traits as Taxonomic and Evolutionary Markers for Microbial Identification and Phylogenetics	Chatragadda		Exploring the use of large language models (LLMs) as an aid for botanical monograph compilation	Fiddes

10:55		The taxonomic structure of the Green Crested Lizard, *Bronchocela cristatella* (Kuhl, 1820), in Sabah, Malaysia	Searle-Webb		How about we dive deeper? Understanding the role of whale falls in the context of deep-sea species evolution. Azorean case study for conservation guidelines	Debost Mallevialle
11:00		New insights into the root of Metazoa using multiple matrices	Galán Luque		Transcriptome Skimming unlocks Biological Diversity	Arya
11:05		Optimising the use of COI and ITS2 markers for molecular delimitation of *Ooencyrtus* (Hymenoptera, Encyrtidae)	Jugariu-Vicoleanu		Systematics of sphenomorphin Skinks in Western Melanesia: A Phylogenomic Approach	Pal
11:10		The Syntomini of Madagascar: more diverse than we expected, less surveyed than we thought (Lepidoptera: Noctuoidea: Erebidae: Arctiinae)	Wiorek		Phylogeographic patterns of *Rana temporaria* (common frog) in the UK.	Grimason
11:15		The complete mitochondrial genome of the brachyuran *Pilumnus spinifer* H. Milne-Edwards, 1834: a new molecular tool for the family in the Mediterranean	Giacobelli		The PhyloODB Pipeline for generating scalable phylogenetically informative datasets using BUSCO and OrthoFinder	Jones
11:20		Taxonomic review of species of the genus *Narcine* Henle, 1834 distributed in the Southwestern Atlantic Ocean (Chondrichthyes: Batoidea: Torpediniformes)	Oliveira		Investigating tardigrade communities across elevational and urbanisation zones with environmental DNA (eDNA)	Dash
11:25		Open data for understanding potential issues in species identification in non-model species: a case study with the genus *Chordodes* (Phylum Nematomorpha, Class Gordioida)	De Vivo		Divide et vinces. Systematic advances and challenges of the Andricus oak gall wasp genus (Hymenoptera: Cynipidae: Cynipini).	Cuesta-Porta

11:30	**BREAK (10 min) TALKS RESUME AT 11:40 GMT**					
11:40	Full A1	Diversity of agar-producing red seaweed *Gracilaria* Greville (Gracilariales, Rhodophyta) from Luzon, Philippines	Viloria	Full B1	Phylogenomics supports the monophyly and internal relationships of Brachiopoda	Yang
11:55		Unravelling the Spiny Secrets of *Pallisentis nagpurensis* (Bhalerao, 1931) Baylis, 1933 from the Snakehead Fish	Sarkar		Patterns of plant diversity in high Andean Peru revealed by iNaturalist and expert-curated datasets	Lombard
12:10		Data-Driven Reanalysis Resolves Nuclear-Plastid Discordance in Mesangiosperm Phylogeny	Low Wood		Genome skimming phylogeny of cyclostome bryozoans	Reinisch
12:25		Unravelling the Spiny Secrets of *Pallisentis nagpurensis* (Bhalerao, 1931) Baylis, 1933 from the Snakehead Fish	Akdogan		Diversity, taxonomy, and evolutionary history of Hymenophyllaceae in China: a focus on the subgenus *Mecodium* (genus *Hymenophyllum*)	Zhao
12:40	**LUNCH (1 hour) TALKS RESUME AT 11:40 GMT**					

13:45	Full A2	The systematics and taxonomy of a diverse plant radiation on a remote oceanic island	Brook	Full B2	Revisiting *Acalypha* medicinal interest: ethnobotany, experimental studies, and the implications of taxonomic misuse pitfalls	Villaescusa-González
14:00		Competing methods of divergence time estimation recover diverse evolutionary timescales	Davies		Tell me about your DNA and Tubercles: A Reverse Taxonomy Approach Confirms *Eurynome aspera* (Pennant, 1777) and *Eurynome spinosa* Hailstone, 1835 (Decapoda: Majoidea) Living Syntopycally in the Mediterranean Sea	Tanduo
14:15		Planarians cryptic diversity in Cuba: evidence from molecular phylogeny	Catalá		Hiding behind a giant – Untangling the gemsnakes of the *Liophidium torquatum* complex from Madagascar	Fleck
14:30		Improving Divergence Time Estimation for Groups with Scarce Fossil Record	Reinales		Family drama in Tardigrada: DNA reveals *Ursulinius cameruni* (Isohypsibioidea) breaks from tradition	Dey
14:45	**BREAK (10 min) TALKS RESUME AT 14:55 GMT**					

14:55	Full A3	Diversity of Okinawan nudibranchs of the family Phyllidiidae assessed by DNA barcoding and creation of a reference collection	Labarthe	Flash B2	Biogeographic History, Ecological Drivers of Speciation, and Floral Trait Evolution in *Calochortus* (Liliaceae): a focus on the Mexican clade	Harden
15:00					Integrative taxonomy in the morphological circumscription of *Souroubea guianensis* Aubl. (Marcgraviaceae: Ruyschieae)	Carvalho
15:05					Tetrigidae of Ethiopia: First Species Delimitation via DNA Barcoding and Description of Three New Species	Fite
15:10		More than it seems: integrative taxonomy unveils cryptic speciation in the Caribbean Metalmark *Dianesia carteri* (Riodinidae), a unique butterfly lineage of the West Indies	Álvarez		Sequencing of global *Penicillium* isolates recaptures speciation in Fleming's fungus and related species	Hatmaker
15:15					Historical Biogeography of *Tristerix* (Loranthaceae)	Carmona-Gallego
15:20					Unravelling the phylogeny of the Greek snake skink, *Ophiomorus punctatissimus*: Cryptic lineages and evolutionary patterns revealed by preliminary mtDNA data	Chatzaki
15:25		Phylogeny and Systematics of *Calymenina* (Trilobita)	Camus		Deep-river knifefishes: Linking craniofacial form and lineage diversity	Allen
15:30					Confirmation of the North American mountainheath hybrid Phyllodoce × intermedia *(*Ericaceae)	Maclachlan
15:35						
15:40	**Summary comments and thanks from the Systematics Association Thanks and farewell comments from the YSF organisers**					

Unravelling the *Haploniscus hydroniscoides* species complex through integrated methods of taxonomy and molecular analyses

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Recent studies discover an increasing number of “cryptic” species complexes amongst deep-sea isopods – even taxa already known to science – are growing. However, species delineation often faces problems of ambiguity, underlining the necessity of using integrative taxonomy to unravel these cryptic taxa. Molecular data hinted at the existence of a potentially undiscovered species complex within the abundant and widely distributed deep-sea isopod *Haploniscus hydroniscoides* Birstein, 1963 from the North Pacific. To test this hypothesis an integrative taxonomical approach combining morphological analyses such as geometric morphometrics with molecular barcode data (16S, COI) was applied. This approach revealed the existence of seven distinct, yet closely related species, each characterized by unique biogeographic distributions spanning abyssal to hadal depths. The taxonomic description of these novel taxa and their diagnostic features further provide important insights into the systematics of the family Haploniscidae Hansen, 1916, a group known for requiring a thorough taxonomic re-evaluation.

More than it seems: integrative taxonomy unveils cryptic speciation in the Caribbean Metalmark *Dianesia carteri* (Riodinidae), a unique butterfly lineage of the West Indies

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The monotypic genus *Dianesia* (Riodinidae) is a distinctive yet poorly known element of the West Indies butterfly fauna, composed by two subspecies inhabiting Bahamas and Cuba. Phenotypic variability between their allopatric populations suggested that the genus could contain multiple species. In this work, we examined data from adult and larval morphology, DNA barcodes and natural history, to test whether these populations were different species. Our results indicate that *Dianesia* is composed at least of nine species, eight of them endemic to Cuba. All species are reciprocally monophyletic except two of them, which were still recovered as independent species by species delimitation analyses. These species remained undetected due to their morphological resemblance. The habitat-rich mosaic of the Cuban and Bahamian landscapes proved a perfect scenario for this neglected radiation. Further research will clarify their biogeographical history, life cycle and major threats for their survival.

Transcriptome Skimming unlocks Biological Diversity

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Meiofauna are microscopic invertebrates which pass through 1mm meshes. Two-thirds of all animal taxa are represented by at least one meiofaunal species. Many species remain underrepresented in databases, and many require taxonomic revision. Abundance, phyletic diversity, and intricate interspecific interactions position meiofauna as unique monitors for ecological changes, especially in habitats threatened by anthropogenic change. Here, we use low-depth, long-read sequencing of transcriptomes (transcriptome skimming), which provides ~10,000 reads per sample at a low cost and with relatively little labour, and captures any symbionts or gut contents per individual. We provide proof-of-concept that this method effectively assembles high-quality transcriptomes for these samples, extract meaningful phylogenetic markers, iteratively build phylogenetic trees, and identify many species concurrently at a community level. Automated techniques such as these will be transformative for meiofaunal study in a time of rapid environmental change.

The systematics and taxonomy of a diverse plant radiation on a remote oceanic island

Theodore S. Brook[1,2,*], Ian J. Hutton[3], Alexander S.T. Papadopulos[4], Lesley Elkan[5], Trevor C. Wilson[5], Sue Bower[6], Martin Bidartondo[1,2], Vincent Savolainen[1,2]

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The genus *Coprosma* (Rubiaceae) on Lord Howe Island (LHI) provides a striking example of island diversification, with an endemic ration of six species. Here, we present a systematic revision of this group, describing new species and clarifying the taxonomy of others. Previously hidden within a cryptic species complex, these taxa are now distinguished using morphological, ecological, and molecular evidence. Alongside important conservation implications, our work has broader evolutionary significance. Molecular analyses reveal that hybridisation and introgression have been central to diversification in *Coprosma* on LHI, providing a convincing example of speciation with gene flow and lending support to the syngameon hypothesis. Our work into *Coprosma* highlights the role of taxonomy and systematics in uncovering both biodiversity and evolutionary processes on oceanic islands.

Phylogeny and Systematics of *Calymenina* (Trilobita)

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Calymenina Swinnerton, 1915, is a suborder of trilobites with generally cosmopolitan distribution, ranging from the earliest Tremadocian to the middle Givetian. Traditionally composed of five families, the phylogenetic structure of the suborder has never properly been explored. Here, we present an extensive phylogenetic analysis to resolve relationships between families, test the monophyly of the different groups, and to explore topology within each clade. Four distinct cladistic analyses, performed under both equal and implied weighting were carried out, including 239 species distributed among 56 genera. Following previous work, the alokistocarid *Elrathia* Walcott, 1924, and the eulomids *Euloma* Angelin, 1854 & *Proteuloma* Sdzuy, 1958, were used as outgroups. The traditional Bravarillidae Sdzuy, 1957, Bathycheilidae Přibyl, 1953, Homalonotidae Chapman, 1890 and Calymenidae Burmeister, 1843 have been recovered as monophyletic, while "Pharostomatidae" is rendered paraphyletic by "*Pharostomina*". Prionocheilidae is instead proposed, and Reedocalymeninae, elevated to the familial rank, is also recovered monophyletic.

Microsnails and how to find them: A morpho-taxonomic survey of marine microgastropods (Mollusca: Gastropoda) in Panglao Island, Bohol, Philippines using lumon-lumon as experimental probe

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This study employed experimental sampling method, lumon-lumon, to evaluate the biodiversity of micromollusks at two distinct sites in the waters surrounding Panglao Island, Bohol, Philippines. Our sampling apparatus and methodology integrate traditional knowledge with scientific innovation, particularly in difficult-to-sample areas. We retrieved three of these nets and collected a total of 379 individuals, representing 50 species across 22 families and spanning 12 superfamilies. LMN01 recorded the highest species richness and estimated diversity, indicating rich micromollusk assemblage and further suggesting the presence of numerous undetected species. While LMN02 and LMN03 showed markedly lower richness. LMN01 exhibited high diversity and moderate evenness, indicating a balanced distribution of individuals across many species and a more equitable community. In contrast, LMN02 and LMN03 were dominated by a few species or even a single taxon. This study is the initial result of our experimental sampling methodology and contributes new records of micromollusk diversity.

Historical Biogeography of *Tristerix* (Loranthaceae)

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Tristerix Mart. is a plant genus with 13 accepted species, distributed from northern Andes to southern Andes, inhabiting diverse environments. It has been proposed that the Andean cordillera influenced the diversification in the genus; however, biogeographic hypotheses have not been presented before. To understand the biogeographic history in *Tristerix*, we perform a phylogenetic analysis, divergence time estimation and ancestral area reconstruction using chloroplast and nuclear DNA, including *Tristerix* species and related taxa from the tribe Psittacantheae. *Tristerix* had its origin during the Eocene, in southern Andes, splitting into a Central-South clade and a Central-North clade which diversified in the Early Miocene and the Middle Miocene, respectively. Climatic events associated to the Andean uplift match the timing of diversification events in this taxon.

Planarians cryptic diversity in Cuba: evidence from molecular phylogeny

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Planarians diversity has been little study in Cuba with only two species reported the endemic *Girardia cubana*, and the invasive *G. sinensis*. Here a molecular identification of freshwater planarian populations collected from 26 locations in Cuba is presented. Mitochondrial (COI) and nuclear (EF1-α, 18S, and 28S) markers were sequenced, and maximum likelihood and Bayesian inference methods were employed. The molecular phylogeny reconstruction of *Girardia* suggested two colonization events. A divergent lineage within the sinensis group was detected. The remaining populations constitute a clade, the Cuban group, structured into at least three lineages. In addition, a lineage belonging to the suborder Cavernicola was identified, for which there are no previous records in the Antilles. The results showed that the richness of planarians in Cuba has been underestimated, and new species could be described, providing relevant biogeographic information about the group in the Caribbean.

Optical Traits as Taxonomic and Evolutionary Markers for Microbial Identification and Phylogenetics

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Microbial optical traits such as bioluminescence, fluorescence, pigmentation, and iridescence are widely distributed across bacteria, fungi, yeasts, cyanobacteria, and other microbial groups. The potential of optical traits as integrated, combinatorial markers for microbial taxonomy and evolutionary lineage tracing remains underexplored. Recent findings highlight that when considered together, these traits provide robust phenotypic signatures that can complement molecular approaches for microbial identification. This research emphasizes the importance of studying the synergistic occurrence and coupling of optical traits as novel taxonomic markers and evolutionary indicators. By mapping these combinations, we propose new frameworks for understanding microbial diversity, phylogenetic relationships, and adaptive strategies to light environments. Furthermore, harnessing optical traits has significant implications for rapid, non-invasive microbial identification and for applications in biotechnology, medicine, ecology, and environmental monitoring. Filling this critical research gap will advance our ability to classify microbes, trace their evolutionary trajectories, and explore their societal applications.

Divide et vinces. Systematic advances and challenges of the Andricus oak gall wasp genus (Hymenoptera: Cynipidae: Cynipini).

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Cynipini wasps (commonly called oak gallwasps) offer an excellent opportunity to study evolutionary dynamics processes due to their intimate ecological relationships with host plants, and roles as keystone species supporting rich communities of associated parasitoids and inquilines. An update on the classification of oak gall wasps is needed. Part of the outdated and erroneous genus-level boundaries have been re-defined for the last 10 years, yet the most complex genera remain unresolved. The greatest challenge now is tackling the *Andricus* Hartig, 1840 genus. Several phylogenetic studies have shown the polyphyly of *Andricus*, and part of my PhD has transferred some of the independent lineages into new genera and re-established valid genera. We propose several hypotheses on how to resolve the *Andricus* classification including the options of re-establishing the genus *Adleria* in the Western Palearctic or removing *Andricus* from the Nearctic and Neotropical fauna.

Competing methods of divergence time estimation recover diverse evolutionary timescales

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The imperfect nature of the fossil record has led researchers to seek alternative methods for calibrating evolutionary events to geological time in the form of molecular clock analyses. Such methods include node-calibration, where select lineage divergences are constrained using user-specified probability densities, or tip-calibration, where divergence times are extrapolated from both the phylogenetic position and age ranges of extinct taxa. More recently, the fossilised birth-death process (FBD) has been proposed as a solution for estimating more realistic divergence times while retaining an explicit model-based approach. Does this suite of methods estimate evolutionary time equally well? Beyond rhetoric, only a handful of studies have attempted to benchmark the relative efficacy of competing approaches in an empirical context. We assessed relative performance among methods using crocodilians as a model system, a group with a mostly uncontroversial phylogeny of living species and a well-sampled, intensively studied fossil record.

Open data for understanding potential issues in species identification in non-model species: a case study with the genus *Chordodes* (Phylum Nematomorpha, Class Gordioida)

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With more available genomic open data, we can try to recognize morphological similar species. Horsehair worms (phylum Nematomorpha) could be used as an example for this, since data is starting to be available for the group and their species recognition is usually regarded as very hard. For checking this, I extracted COXI sequences from an RNAseq dataset labelled as belonging to *Chordodes fukuii*. I then evaluated the correctness of such species ID using a mix of a previously released ddRADseq sequences plus the RNA-seq ones. Accordingly, two different groups were present in the RNA-seq dataset, *C. formosanus* and *C. japonensis*; however, two individuals identified by COXI as *C. japonensis* clustered with *C. formosanus* specimens in the ddRAD-RNAseq dataset, indicating potential past mitochondrial introgression or ILS. My work shows the usefulness of open data for evaluating species delimitation and potential needs in DNA barcoding for avoiding future misidentification.

How about we dive deeper? Understanding the role of whale falls in the context of deep-sea species evolution. Azorean case study for conservation guidelines

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Whale falls are biomass hotspots in the deep sea. Being a source of food for all organisms, they decompose and host a succession of dynamic communities. In 2015, a juvenile sperm whale was artificially sunk in the Azores. In 2021, the last visit was carried out. Imagery was analysed to assess state, composition, and associated species. A vertebra was sampled to determine the species community composition. In-lab analyses combined classical invertebrate taxonomical identification, as well as DNA analysis of key species. Based on the presence of the *Bathymodiolus azoricus*, the whale fall was determined to be in a chemosynthetic stage featuring specific sulphur-oxidising organisms. Species identified were put in a larger context to evaluate the role of whale falls as stepping stones across the Atlantic Ocean. This study provides information for management, highlighting the significance of studying deep-sea habitats threatened by anthropogenic impacts and in need of protection.

Family drama in Tardigrada: DNA reveals *Ursulinius cameruni* (Isohypsibioidea) breaks from tradition

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Tardigrades, the microscopic "water bears," are famous for their resilience and evolutionary quirks. Tardigrade taxonomy is full of surprises and *Ursulinius cameruni* (Iharos, $^{1}9^{6}9$) might be one of the biggest. Once shuffled between *Hypsibius*, *Isohypsibius*, and *Ursulinius*, this species seemed settled until DNA had its say. Using molecular phylogenies from Indian and Australian populations, we found that *Ursulinius* aff. *cameruni* actually belongs within Hypsibioidea, not Isohypsibioidea as previously thought. The results reveal a lineage so distinct it could represent a new genus, or even a new family. Remarkably, these findings highlight cryptic diversity across continents and suggest that similar lineages may have gone undetected elsewhere. Our study demonstrates that in tardigrades, family ties can get complicated and that DNA evidence continues to reshape our understanding of their evolutionary relationships, emphasizing the importance of integrating molecular data into classical taxonomy.

Tetrigidae of Ethiopia: First Species Delimitation via DNA Barcoding and Description of Three New Species

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Tetrigidae is a caeliferan family of Orthoptera constituting a diverse group of small Orthopterans, which has its greatest diversity in tropical and subtropical areas. However, to date, few studies have been conducted on the identification and description of Tetrigidae species in Ethiopia. Hence, we performed the first species delimitation study via DNA barcoding of species belonging to the genera *Paratettix*, *Leptacrydium*, *Dasyleurotettix*, and *Morphopoides* from Ethiopia. We show that Ethiopian Tetrigidae can be successfully delineated using DNA barcodes; the gene was strongly congruent with the phylogenetic tree. We report three species, *Dasyleurotettix infaustus*, *Morphopoides tessmanni*, and *M. folipes*, from Ethiopia for the first time. In addition, we describe three new species: *Paratettix tanai* sp. nov., *Paratettix geminus* sp. nov., and *Leptacrydium naqamteensis* sp. nov. Future integrative taxonomic studies, including more material from diverse regions and additional genetic loci, need to be performed to understand the diversity of Tetrigidae across Africa.

Hiding behind a giant – Untangling the gemsnakes of the *Liophidium torquatum* complex from Madagascar

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Liophidium torquatum (Boulenger, 1888) is a species of gemsnakes (Pseudoxyrhophiidae) endemic to Madagascar, but considered to be widespread over large parts of the island. New phylogenetic data revealed that this taxon is paraphyletic, with one clade of the *L. torquatum* species complex being more closely related to *Liophidium mayottensis*, an island giant endemic to the Comoran island of Mayotte, than to other populations of the taxon. We herein demonstrate that *Liophidium torquatum* in its broad current definition needs to be split into three species based on differentiation in (I) multiple mitochondrial and nuclear markers, (II) colour patterns, (III) hemipenal structures, and (IV) distinct distribution ranges of each species. Thus, we recover the true *L. torquatum* as a monophyletic taxon and will describe two species new to science. We also shed light on the evolutionary history of *L. mayottensis*, proposing its colonization of Mayotte from Madagascar via the South Equatorial Current.

New insights into the root of Metazoa using multiple matrices

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The phylogenetic root of Metazoa is one of the most debated questions in evolutionary biology, with studies alternately placing ctenophores or sponges as the earliest-branching animal lineage. These conflicting results often depend on factors such as which species are included, the genes analyzed, and the evolutionary models applied. We propose a workflow to assess the robustness of phylogenetic results using multi-protein, clade-specific matrices containing different taxa and different genes. This included reducing the number of species per lineage to allow the use of complex mixture models. Furthermore, we tested multiple strategies to explore how dataset composition and analytical choices affect results, such as the effect of outgroup selection and applying amino acid recoding. By comparing outcomes across these approaches, we evaluated how phylogenetic topology and support values change under different conditions, providing a framework for assessing the robustness of competing hypotheses about the early evolution of animals.

Phylogeographic patterns of *Rana temporaria* (common frog) in the UK.

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Amphibians are the most threatened vertebrate group globally and recent assessments of UK amphibians have documented declines of once common species. There have been anecdotal reports of declines in the widespread common frog, *Rana temporaria*, in the UK. Limited published genetic data exists for *R. temporaria* in the UK; however, a further investigation of this information could better aid in conservation assessments and management in the future. In this presentation we fill this knowledge gap by extending previous genetic work. Buccal swabs were collected from >40 populations across England, Scotland, and Wales. Sequence data was generated for two mitochondrial loci: 16s rRNA (541 bp) and cytochrome b (546 bp). Data was analysed using maximum likelihood and Bayesian inference phylogenetic trees, haplotype networks, and genetic diversity measures. Our data recover very little mitochondrial diversity in *R. temporaria* populations across the UK, with the highest diversity recorded in Scotland.

Sequencing of global *Penicillium* isolates recaptures speciation in Fleming's fungus and related species

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Penicillin-producing fungi *Penicillium chrysogenum* and *Penicillum rubens* were considered the same species until *P. rubens* was defined in the early 2010s. Several cryptic species were also proposed from the *P. chrysogenum* complex, but these species lack genome assemblies. Therefore, we still do not understand speciation or species relationships within the complex. We collected >80 isolates from an array of ecological niches, sequenced their genomes, and downloaded public data for additional isolates. Some isolates identified as *P. chrysogenum* were found to be other species. *P. chrysogenum* and *P. rubens* both formed monophyletic clades in our phylogenies, but we also discovered additional clades possibly representing cryptic species. We were unable to classify the unidentified isolates as previously identified cryptic species, possibly indicating new species in the complex. Although further phenotyping is needed to characterize variation of our so-called cryptic species, our work sheds light on the complexities within the *Penicillium* genus.

The PhyloODB Pipeline for generating scalable phylogenetically informative datasets using BUSCO and OrthoFinder

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The rapid expansion of genomic data in repositories such as NCBI offers unprecedented opportunities for large-scale phylogenomic analyses. However, the continuously growing repository presents challenges for building robust phylogenetic datasets. While genome-wide superalignments are computationally intensive, a set of single-copy ortholog alignments may provide a more efficient and accurate approach for species tree inference (Pisani et al., 2022). The BUSCO pipeline (Simão et al., 2015) is widely used to assess genome completeness, but recent studies reveal limited overlap with other orthology tools such as OrthoFinder (Emms and Kelly, 2015; Liu et al., 2024). Here we present an automated system that continuously monitors new genome uploads on NCBI and generates phylogenetic datasets. To improve ortholog detection, we introduce a 'core BUSCO' set defined as the intersection of single-copy orthologs shared between BUSCO and OrthoFinder across a set of high-quality proteomes spanning a clade of interest.

Diversity of Okinawan nudibranchs of the family Phyllidiidae assessed by DNA barcoding and creation of a reference collection

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The Phyllidiidae are a frequently observed family of nudibranchs on Indo-Pacific coral reefs. However, it remains understudied, particularly in Okinawa, a biodiversity hotspot. This study provides a first estimate of specific diversity of Phyllidiidae around Okinawa main island, combining morphology-based taxonomic identification with DNA barcoding and phylogenetic analyses. We examined 60 specimens from 12 sites around Okinawa Island and analyzed using these integrative methods. A total of 21 distinct genetic entities (molecular operational taxonomic units, MOTUs) were identified, nine of which corresponded to described species and 12 to undescribed species or cryptic complexes, mainly within the genus *Phyllidiella*. In addition, two species are recorded for the first time from Okinawa; *Phyllidiopsis shireenae* Brunckhorst, 1993 and *Phyllidiella rudmani* Brunckhorst, 1993. These results underline the importance of using integrative taxonomy with morphological and molecular identification to reveal biodiversity and provide a first baseline for Phyllidiidae in southern Japanese waters.

Patterns of plant diversity in high Andean Peru revealed by iNaturalist and expert-curated datasets

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Containing 70% of all tropical glaciers and shaped by unique geologic and climatic conditions, the high Andes of Peru are a region of exceptional endemism and taxonomic interest. Given mounting threats of mining and climate change to Peru's alpine habitats, and with no nationwide assessment of plant communities ever conducted in this region, the window to assess these communities is closing. Using specimen datasets from [12] taxonomists, curated iNaturalist observations, and Infomaps Bioregions, we analysed occurrence maps of [24] plant genera across high Andean Peru, identifying three bioregions and two biogeographical barriers. Six collection gaps, which are endangered by mining and lack protection, are recommended for priority assessment. The success of this study in using high-quality iNaturalist observations to augment expert-curated specimen data strengthens an argument for greater engagement of taxonomists with the iNaturalist community to help fill biodiversity knowledge gaps at a time of great urgency.

Data-Driven Reanalysis Resolves Nuclear-Plastid Discordance in Mesangiosperm Phylogeny

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Deciphering the evolutionary relationships among the three largest mesangiosperm clades (monocots, eudicots, and magnoliids) remains a central challenge in angiosperm phylogenetics. Conflicting signals in plastid and nuclear analyses have obscured mesangiosperm topology, leading to hypotheses of ancient hybridisation or ILS events. Through data-driven, comparative reanalysis of the largest available nuclear and plastid datasets, I demonstrate the first consensus between the two data sources. Both concatenated and coalescent methodologies resolved well supported phylogenetic trees with a high degree of consistency. In these analyses, monocots diverge first, with magnoliids and eudicots forming a sister clade, contrary to the longstanding APGIV supported topology. However, the positions of Chloranthales and Ceratophyllales remain enigmatic, reinforcing the need for further investigation. Overall, these findings provide a robust framework for future angiosperm phylogenetic studies, underscoring the value of re-examining large phylogenetic datasets with rigorous methodology that addresses systematic biases.

Systematics of sphenomorphin Skinks in Western Melanesia: A Phylogenomic Approach

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Western Melanesia is one of the most interesting yet understudied hyper-diverse regions on Earth. The dynamic geological history has led to extreme topographic heterogeneity and complex evolutionary histories for the region's biota. Despite, extremely high diversity and endemism, the origins of most taxonomic groups in the region remain poorly studied. This is especially true for range-restricted taxa such as reptiles. Represented by 11 genera, sphenomorphin skinks represent a significant proportion of the region's lizard diversity. The evolutionary relationships within this group remain poorly understood. In this study, we address this knowledge gap by employing high-throughput sequencing methods to generate genetic data for over 40 sphenomorphin skinks. DNA was extracted using established protocols from fresh and historical samples, and novel squamate conserved loci (SqCL) sequence data was generated. Our preliminary results highlight the complexity in this highly diverse group, and the paraphyly of multiple genera.

Improving Divergence Time Estimation for Groups with Scarce Fossil Record

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Divergence time estimation is required in most evolutionary studies because generates phylogenetic trees in absolute time, separating branch lengths into evolutionary rate and time by using time priors as calibrations, a clock model, and a model for tree evolution. Specifying the nature and number of calibration points is challenging and depends on the available time information. We evaluated different node calibration strategies to estimate divergence times for clusioids clade exploring two recently developed approaches for setting calibration priors: the conflation of time distributions, which summarises previous estimates into a single prior distribution to be used as secondary calibration; and stratigraphic intervals, a flexible method for estimating lineage origination and extinction times, based on the full available fossil record. Using multiple calibration points reduced the effect of the prior distribution on the posterior, and improved the precision of time estimates compared with analyses using few points.

Genome skimming phylogeny of cyclostome bryozoans

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Cyclostomatida represents the sole extant order of class Stenolaemata. They exhibit high phenotypic plasticity, resulting in homoplasious characters that complicate morphology-based phylogenetic analyses and potentially obscure true evolutionary relationships. These challenges highlight the need for molecular approaches to reveal insights into their evolution. This research constructs a molecular phylogeny from ~60 different cyclostome taxa across 15 families using mitogenomes and nuclear ribosomal RNA genes as molecular markers. Scanning Electron Microscope (SEM) images serve as complementary data to assess morphological diversity and provide phylogenetic corroboration, with skeletal ultrastructure polymorphisms offering key support for some molecular results. The mitochondrial genome analysis further demonstrates the complexity of bryozoan mtDNA, heavily infiltrated with interrupted protein-coding genes. This project expands upon limited existing molecular work on cyclostomes, providing new phylogenetic insights into this evolutionarily significant bryozoan group.

Unravelling the Spiny Secrets of *Pallisentis nagpurensis* (Bhalerao, 1931) Baylis, 1933 from the Snakehead Fish

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Pallisentis nagpurensis was originally described from *Channa striata* in India, though early records lacked details on sexual dimorphism. The present study redescribes *P. nagpurensis* collected from *C. striata* during a six-month survey in the Hooghly and Bardhaman districts of West Bengal. Specimens were examined using light and scanning electron microscopy (SEM). Distinct proboscis hook patterns, collar and trunk spines, and well-defined reproductive structures were observed. SEM analysis clarified the arrangement of hooks and unique posterior features. Comparative evaluation with related taxa confirmed the identity as *P. nagpurensis*. These findings enhance knowledge of the morphology, taxonomy, and distribution of this acanthocephalan parasite.

Tell me about your DNA and Tubercles: A Reverse Taxonomy Approach Confirms *Eurynome aspera* (Pennant, 1777) and *Eurynome spinosa* Hailstone, 1835 (Decapoda: Majoidea) Living Syntopycally in the Mediterranean Sea

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Eurynome species have long-standing taxonomic, phylogenetic, and biogeographic challenges due to their rarity, small-sizes, and complex ornamentations. Using reverse taxonomy on specimens from Mediterranean Sea, this study addressed unresolved issues concerning the two pseudocryptic taxa *Eurynome aspera*, type species of the genus, and its syntopic species *Eurynome spinosa*. Newly generated molecular data (mitochondrial and nuclear), integrated with existing markers, identified two distinct operational taxonomic units and confirmed conspecificity between Atlanto-Mediterranean populations, whereas phylogenetic analyses supported their placement within Majoidea and Majidae. Reverse taxonomy led to updated descriptions of the species and the identification of traits distinguishing juveniles and adults. This study provides a basis for revising the genus, recommending broader geographic sampling and potential neotype designation. It also underscores the need for further research on related genera to verify the correct classification of taxa from other biogeographic regions within *Eurynome*.

Revisiting *Acalypha* medicinal interest: ethnobotany, experimental studies, and the implications of taxonomic misuse pitfalls

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Acalypha L. (Euphorbiaceae) is a pantropical genus of approximately 450 species, many traditionally used to treat human and animal ailments. However, ethnobotanical interpretations have been hindered by misidentifications, outdated names, and the lack of study for many species, limiting their potential to inform pharmacological and conservation studies. This study presents the first global synthesis of medicinal uses in *Acalypha*, based on peer-reviewed literature, databases, and historical sources. Sixty-two species with reported uses in 55 countries were identified, including applications in human and veterinary medicine, rituals, and plaguicides. Experimental studies revealed antibacterial, antifungal, antioxidant, and anti-inflammatory effects. All reported uses were classified and standardised using WHO and national disease classification systems, and scientific names were taxonomically reviewed. Nearly 25% of studies contained taxonomic errors, highlighting the need for improved taxonomic rigour. This review provides a taxonomically validated framework and identifies gaps for future phytochemical and pharmacological research.

Diversity of agar-producing red seaweed *Gracilaria* Greville (Gracilariales, Rhodophyta) from Luzon, Philippines

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Gracilaria, valued for its ecological and economic significance, is the most diverse genus in the red algal family Gracilariaceae. Locally known as 'gulaman' in the Philippines, agar-producing *Gracilaria* species are wild-harvested or farmed and are sold in market as food products. Despite their importance, the taxonomy and molecular phylogeny of *Gracilaria* in the Philippines remain limited. Molecular techniques improve algal biodiversity studies by enabling accurate identification, complementing traditional morphological methods that are often prone to misidentifications. Our work fills in the gap in our knowledge on the biodiversity and systematics of Philippine *Gracilaria* by providing new *rbcL* sequences and corresponding morphological descriptions based on specimens collected in Luzon, Philippines. We report here a total of seven species, two of which represent putative new species. Our work highlights the need to conduct thorough assessment of red algal diversity in the Philippines, especially in the relatively colder waters of northern Luzon.

The Syntomini of Madagascar: more diverse than we expected, less surveyed than we thought (Lepidoptera: Noctuoidea: Erebidae: Arctiinae)

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The Syntomini tiger moths from Madagascar, with around 100 endemic species, belong to one of the largest evolutionary radiations among the island's insects. Still, the group is poorly studied and demands a modern revision. In my talk, I will present the outputs of the revision of the genera *Thyrosticta* and *Melanonaclia* (30 species in total), the topic of my recently defended PhD thesis, in large part based on museum collections. Both groups turned out to be polyphyletic and comprise nine separate lineages, of which seven are established as new genera. During the revision, three new species were discovered. Among them, the most intriguing is *Melanonaclia ranomafana*. The species belongs to the largest members of Madagascan Syntomini, and occurs in the Ranomafana National Park, one of the most intensively studied areas of Madagascar, yet is known only from three specimens, collected in 2004 and 2018.

Phylogenomics supports the monophyly and internal relationships of Brachiopoda

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Brachiopods, shelled invertebrates resembling bivalved molluscs, appeared early in the Cambrian and dominated Palaeozoic benthic marine environments, they possess one of the highest fidelity fossil records and present an outstanding opportunity to understand paleoecology and macroevolution of animals. However, persistent questions remain about brachiopod monophyly and brachiopod internal relationships. Here we present the first phylogenomic tree of Brachiopoda and their relatives, encompassing all five extant orders. We assembled a phylogenomic dataset using the novel BUSCO refining strategy and performed phylogenetic analyses using the across-site compositional heterogeneous model (CAT-PMSF). We found strong support for Brachiopoda as a monophyletic group within a clade of “true lophophorates” and as the sister group of Bryozoa plus Phoronida. Within Brachiopoda, we found support for the monophyly of inarticulate/articulated brachiopods,

phosphatic brachiopods are nested within the calcitic brachiopods. This result implies that there must have been multiple transition in primary skeletal mineralogy within Brachiopoda.

Diversity, taxonomy, and evolutionary history of Hymenophyllaceae in China: a focus on the subgenus *Mecodium* (genus *Hymenophyllum*)

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The Hymenophyllaceae, primarily thriving in warm and humid environments, are key components of tropical forest understories worldwide. Originating in the early Triassic, this fern family has undergone extensive diversification, making it important for understanding fern evolution. China harbors more than 60 species (out of about 434 globally), representing over 13% of the family's diversity and underscoring its regional significance. Due to the morphological complexity and still unresolved phylogenetic relationships, a comprehensive revision of Chinese Hymenophyllaceae remains needed. By integrating morphological data with molecular phylogenetic analyses, we provide an updated list of Chinese species and discuss their evolutionary relationships and diversification patterns. The subgenus *Mecodium* (Hymenophyllum) is presented as a case study to exemplify this integrative approach.

Deep-river knifefishes: Linking craniofacial form and lineage diversity

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The Navajini, a clade of Neotropical electric fishes (Apteronotidae), display striking craniofacial diversity shaped by ecological, developmental, and evolutionary forces. Using 3D geometric morphometrics, micro-CT, and phylogenetic comparative methods, we examined skull shape evolution across the clade. Ancestral reconstructions show that traits such as jaw elongation, opercle morphology, and maxilla orientation exhibit significant phylogenetic structure with clear ecological relevance. Sexual dimorphism strongly contributes to disparity in some lineages, where males evolve hypertrophied traits, while others retain conservative cranial architectures. Access to novel morphospace is associated with shifts in feeding ecology and developmental pathways, producing repeated convergent evolution among ecologically similar taxa. Our results suggest that cranial diversity in Navajini reflects both adaptive responses to ecological pressures and the influence of developmental constraints, offering insight into patterns of morphological evolution in Neotropical freshwater fishes.

To trim or not to trim; the effect of alignment trimming in phylogenomic analysis

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Although systematic error presents a major challenge to reconstructing evolutionary relationships, it can be reduced through careful analytical choices. Multiple sequence alignments (MSAs) are often trimmed in order to remove poorly aligned regions; however recent evidence has suggested this practice may result in less accurate trees. To investigate this, I estimated the accuracy of trees inferred from MSAs produced by different alignment trimming methods while controlling for alignment length. I showed that trimming can increase the phylogenetic signal per site, but this benefit is often outweighed by the overall loss of signal in shorter alignments. I also present some evidence that trimming may help reduce error caused by long branch attraction artifacts. Overall, despite its potential to reduce analytical accuracy, alignment trimming may play an important role in increasing computational efficiency and reducing systematic error in large phylogenomic datasets.

Disentangling the taxonomy and population genomics of the *Hieracium tomentosum* L. group

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Hieracium L. (Asteraceae) is one of the most diverse angiosperm genera. The wide range of morphological characteristics are caused by apomixis, extensive hybridization, and polyploidization. Current taxonomy is still largely based on morphological treatment, and lacks integration of modern approaches. We focused on the *H. tomentosum* group (group J of Flora Gallica), endemic to the Western Alps and northern Apennines, to reassess its taxonomy using morphology, cytology, and genomics. We analyzed around 16 taxa through chromosome counts, flow cytometry, and morphometrics. Moreover, ddRAD-seq genotyping was applied to 123 individuals of *H. tomentosum*, with an additional 185 samples collected in 2025. Diploid, triploid, and tetraploid populations of different taxa were identified. Diploid *H. tomentosum* showed clear genetic differentiation from triploids, which displayed locality-based structuring and reticulate evolution. These preliminary findings support taxonomic separation between *H. tomentosum* polyploid species and highlight the need for further comprehensive analysis and systematic revisions.

Integrative taxonomy in the morphological circumscription of *Souroubea guianensis* Aubl. (Marcgraviaceae: Ruyschieae)

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This project aims to taxonomically circumscribe *Souroubea guianensis* Aubl. (Marcgraviaceae), a species with significant morphological variability and poorly delimited subspecies. An integrative approach will assess whether this variability justifies the current infraspecific classification. Specimens from the three subspecies (*Souroubea guianensis* subsp. *amazonica*, *Souroubea guianensis* subsp. *cylindrica*, and *Souroubea guianensis* subsp. *guianensis*) will be collected from the Amazon and Northeastern Atlantic Forest. The methodology integrates morphometric analyses (Elliptic Fourier Descriptors for leaves, ImageJ for flowers), FT-NIR spectroscopy for chemical profiling, and anatomy to evaluate the taxonomic value of foliar sclereids. The study is expected to provide a robust basis for taxonomic delimitation, serve as a model for resolving other taxonomic complexes, and significantly contribute to understanding Neotropical biodiversity.

A comprehensive study of *Ophiorrhiza* in India: Taxonomy, Systematics and Ethnomedicinal Relevance

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The genus *Ophiorrhiza* represents an ecologically and therapeutically important group that is widely distributed in India. The study aims to bridge taxonomy with ethnomedicinal knowledge to develop a comprehensive account of *Ophiorrhiza* species found in the region. Through field visits and extensive literature surveys, 64 species were documented, of which 32 species might probably be endemic to India, along with a new recorded distribution for the region. Ethnobotanical documentation revealed that various species of the genus are traditionally used for treating snakebites, inflammatory conditions, wounds, body aches, gastrointestinal disorders, infections, cancer and other ailments, with some record of consumption as local food source. These observations contribute to a deeper understanding of the genus, underscoring its significant ethnopharmacological relevance and conservation importance of the genus within the region.

Unravelling the phylogeny of the Greek snake skink, *Ophiomorus punctatissimus*: Cryptic lineages and evolutionary patterns revealed by preliminary mtDNA data

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In this study, we investigate the phylogeny of *Ophiomorus punctatissimus* (Bibron & Bory de Saint-Vincent, 1833), an endemic limbless lizard of Greece. Previous studies have revealed the existence of distinct clades within the Peloponnese; however, their taxonomic status and evolutionary relationships remain unclear. We collected samples across the region, with particular emphasis on areas where clade diversification appears prominent and where previous sampling was limited and showed gaps. We analysed a mitochondrial marker to uncover potential cryptic lineages within the species, infer their geographic distribution, and reconstruct their phylogenetic relationships using Maximum Likelihood and Bayesian Inference methods. Species delimitation analyses were conducted to determine how many phylogenetic "species" are hidden within *O. punctatissimus*, and divergence times among them were subsequently estimated.

Investigating tardigrade communities across elevational and urbanisation zones with environmental DNA (eDNA)

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Microinvertebrate communities, especially tardigrades, play critical ecological roles but remain understudied locally. This study analyzed tardigrade diversity across paired forest and urban sites at two elevations in southern Poland using morphology and eDNA metabarcoding of 18S rRNA and COI markers in 73 moss samples. Elevation significantly influenced community composition, with high-elevation sites hosting specialist taxa nested within generalist low-elevation taxa. Urbanization reduced diversity, while forest habitats maintained richer, more stable communities. The 18S marker detected the highest genus-level diversity, outperforming COI and morphology, although species-level resolution was limited by incomplete reference databases. eDNA metabarcoding uncovered greater biodiversity and cryptic taxa undetectable by morphology. These results demonstrate the importance of integrating morphological and molecular approaches in tardigrade systematics and highlight the urgent need to enhance reference databases for improved species identification. This study advances understanding of how environmental changes affect tardigrade community structure and diversity.

Exploring the use of large language models (LLMs) as an aid for botanical monograph compilation

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Monographs are an essential tool for documenting plant diversity and distribution to ensure species conservation. Groups which lack a monograph face extinction threat before they can be conserved, but the compilation process can be slow and laborious. Automating parts of this process is a key element of RBG Kew's Science Strategy. We explore methods to automate the conversion of specimen-based trait matrices into textual species descriptions by leveraging the recent advances in Artificial Intelligence, specifically Large Language Models (LLMs). Utilising the comprehensive trait dataset and scoring criteria published with Henderson's 2020 Calamus monograph allows us to compare auto-generated and expert authored ("ground-truth") descriptions. Evaluation using widely-used natural language processing metrics show that auto-generated descriptions are very comparable to human written descriptions and shows great promise for integration of LLMs into the taxonomic process.

The complete mitochondrial genome of the brachyuran *Pilumnus spinifer* H. Milne-Edwards, 1834: a new molecular tool for the family in the Mediterranean

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Atlanto-Mediterranean crabs of the family Pilumnidae Samouelle, 1819 exhibit a complex taxonomic history, with persistent ambiguities regarding their true species boundaries and phylogenetic relationships. In this study, the complete mitochondrial genome of *Pilumnus spinifer* H. Milne-Edwards, 1834 was sequenced, representing the first mitogenomic record for Pilumnidae within the Atlanto-Mediterranean region. The mitogenome is composed of 16,410 base pairs and its overall nucleotide composition aligned with that of other brachyurans species. It included 13 protein coding genes, two ribosomal RNA genes, 24 tRNA genes, and a putative control region. A comparative analysis of its gene order against available data from related taxa revealed significant structural differences, including genes duplication, and thus offering new insights into the long-standing evolutionary debate surrounding this lineage. The present findings provide novel comparative tools, advancing the resolution of the taxonomy of this family in the area through the implementation of modern methodologies.

Biogeographic History, Ecological Drivers of Speciation, and Floral Trait Evolution in *Calochortus* (Liliaceae): a focus on the Mexican clade

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The Mexican clade of *Calochortus* (Liliaceae) provides a remarkable system to investigate the links between a species' biogeographic origins, morphological variation, and climatic niche evolution. We infer the ecoregion(s) in which the Mexican clade originated, describe species-level dispersal patterns, identify drivers of speciation, and evaluate if floral traits are correlated to the evolution of climatic niche. We find that the clade likely originated in central Mexico and that diversification can be attributed to a suite of ecological variables. Additionally, we demonstrate that the evolution of floral traits and climate niche are correlated. We find that each character state exhibits the same degree of niche conservatism when modelled with temperature variables, precipitation seasonality, and elevation. Lastly, the tempo of climatic niche evolution varies when character states are modelled with temperature variables. This study demonstrates the strengths of modelling niche and trait evolution when investigating the macroevolution of a speciose lineage.

Phylogenetic, biogeographic and ecological enquiry into deciduousness

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Deciduousness in tropical ecosystems is an understudied adaptive trait. How the evolution of novel traits in plants affects their niche and distribution is fundamental to our understanding of the historical assembly of the world's biomes. Multivariate comparative phylogenetic analysis has the ability to reveal processes that drive trait diversification – for instance adaptations to novel biomes as a response to changing climates. This research seeks to uncover the evolution of deciduousness of Dipterocarpaceae focused on tracing the number and geographic context of evolutionary transitions to deciduousness and assessing its ecological drivers through niche modelling and phylogenetic comparative methods.

Optimising the use of COI and ITS2 markers for molecular delimitation of *Ooencyrtus* (Hymenoptera, Encyrtidae)

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DNA barcodes are a useful tool for species delimitation, complementing morphological methods, but the use of a single marker can lead to overestimation of the number of species due to introgression or geographical isolation. This study aims to complement the molecular marker COI with ITS2, in order to identify and characterize species of the genus *Ooencyrtus* and to eliminate the occurrence of pseudogenes through molecular cloning. The analysis was performed on several individuals collected from various regions of Europe. DNA was extracted using the DNeasy Blood & Tissue Kit (Qiagen), amplified by PCR with primers specific to the ITS2 region and cloned using the blue-white screening method with pGEM-T Easy Vector Systems (Promega). The sequences were processed using the Staden Package, analyzed in MEGA11 and compared with GenBank data by BLAST and phylogenetic analyses. The nuclear and mitochondrial trees were concordant, indicating the presence of a number of cryptic species.

Fritillaria yakutiae sp. nov. (Liliaceae) from Surkhandarya, Uzbekistan

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A new species, *Fritillaria yakutiae* (Liliaceae), is described from the Babatag Range in the Surkhandarya region of Uzbekistan. The species is placed in *F*. subg. *Rhinopetalum*. Morphologically, *F. yakutiae* closely resembles *F. bucharica* and *F. baisunensis* but differs in key floral characteristics, including the color and pattern of the perianth and anthers. Phylogenetic analyses based on complete chloroplast genome sequences confirms its placement within the Rhinopetalum clade, forming a strongly supported sister relationship with *F. bucharica, F. gibbosa* and *F. baisunensis*. The chloroplast genome of *F. yakutiae* has a total length of 151,757 bp and contains 130 annotated genes, including 84 protein-coding genes. The species is currently known only from its type locality, where approximately 300 mature individuals were recorded in 2020. Given the limited available data on its distribution and population trends, *F. yakutiae* is assessed as 'Data Deficient' (DD) under the IUCN Red List criteria.

Confirmation of the North American mountainheath hybrid *Phyllodoce* × *intermedia* (Ericaceae)

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Phyllodoce glanduliflora and *P. empetriformis* (Ericaceae) dominate the alpine and subalpine of northwest North America, respectively. Although the pair occupy distinct niches, a putative hybrid, *P.* × *intermedia*, is often observed where they overlap. To confirm the hybrid status and maternal parentage of *P*. × *intermedia*, I collected 57 tissue samples of the parents and hybrid from field locations within the Coast Mountains of British Columbia, Canada and extracted their DNA using a modified CTAB protocol. I sequenced the plastid *rbcL* locus and the nuclear ribosomal ITS region from the sample DNA to be analysed using phylogenetic invariants and maximum likelihood methods. Preliminary findings affirm the hybrid's status and suggest that *P. empetriformis* is more often the maternal parent, despite the hybrid's prevalence in *P. glanduliflora* dominated habitat. Future studies should investigate the ecological distribution of hybridizing populations and the impacts of hybridization on the fitness of the parents.

From hidden retreats to phylogenetic trees: resolving the evolutionary history of Iberian red devil spiders

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The spider genus *Dysdera* Latreille, 1804, is the most species-rich genus in the family Dysderidae, with 337 species, half of the currently described species. It includes ground-dwelling, nocturnal hunters with a Western Palearctic distribution, mainly limited to the circum-Mediterranean region and Macaronesian archipelagos, with at least one synanthropic species found worldwide. We present preliminary results of a multilocus phylogeny based on mitochondrial (COX1) and nuclear (18S) markers, covering 46 of 52 *Dysdera* species known from the Iberian Peninsula. Additionally, we describe six new species and a species complex, broadening our understanding of the group's hidden diversity. Most specimens of the new species described were collected during extensive fieldwork following optimized protocols, highlighting the importance of standardized sampling to improve biodiversity assessments and systematic resolution. This study provides a comprehensive molecular framework for *Dysdera* in the Iberian Peninsula and offers insights into its evolutionary history and diversification patterns.

Taxonomic review of species of the genus *Narcine* Henle, 1834 distributed in the Southwestern Atlantic Ocean (Chondrichthyes: Batoidea: Torpediniformes)

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Narcine brasiliensis (Olfers 1831) and *Narcine bancroftii* (Griffith & Smith 1834) are the two valid species of electric rays found in Brazil, with frequent identification problems. Overlaps on coloration, counts of teeth and body proportions reveal the need for deeper studies of their morphological variations. This study examined specimens of *Narcine* for morphometry, dorsal coloration and morphology of the neurocranium and clasper. Five distinct morphotypes were identified by the dorsal color pattern, related to both valid species and three potentially new species. Statistical analysis revealed great overlapping between *N. brasiliensis* and *N. bancroftii*, and significant differences between them and the other morphotypes. A morphological variation greater than previously known for *Narcine* species of the Southwestern Atlantic Ocean was identified, with the description of two possibly new species for Brazil. Due to overlapping in morphological characters and non-significant differences found between *Narcine brasiliensis* and *Narcine bancroftii*, this study proposes their synonymy.

The taxonomic structure of the Green Crested Lizard, *Bronchocela cristatella* (Kuhl, 1820), in Sabah, Malaysia

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Advances in next generation sequencing have allowed for near-complete inferences into the genomic relationships of diverging populations. However, whole genome sequences are underutilised as evidence for taxonomic decisions. The bright green agamid lizards of the genus *Bronchocela*, endemic to Southeast Asia, are considered taxonomically neglected and suspected to consist of multiple undescribed species. Recent descriptions from the genus have relied on single mitochondrial genes and morphology. We explored apparent cryptic speciation within *Bronchocela cristatella* (Kuhl, 1820) across elevational gradients in the Crocker Mountains, Sabah, Malaysia, through an integrative taxonomic method, incorporating whole genome sequences and complete morphological data. Multiple factor analysis highlights morphological divergence of montane populations, including at sympatric boundaries with lowland populations. Ongoing genomic analyses will determine phylogenetic relationships and the presence of admixture to further elucidate the taxonomic relationship of these putatively divergent populations, potentially resulting in the description of another montane endemic agamid for Sabah.

Exploring hidden richness: unveiling the undocumented pyrenocarpous lichen of Southern Philippines

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Despite recent advances in Philippine lichenology, the rich pyrenocarpous lichen diversity of Mindanao Islands remains largely unexplored, with species that have yet to be discovered and described, hence, the study was conducted. A series of transect walks and opportunistic sampling methods across seventeen study sites in the Southern Philippines revealed a total of 79 species, with 45 species and 5 genera as new country records. This discovery underscores the significant knowledge gaps in Philippine lichenology and indicates that Southern Philippines harbors considerably more pyrenolichen diversity than currently documented. The first dichotomous keys leading to the selected families, genera, and species were prepared. This study highlights the importance of unexplored regions in the Southern Philippines as repositories of unique and previously undocumented lichen taxa. Furthermore, integrative study and more collaborative efforts must be considered in the future to exhaustively document and understand pyrenocarpous lichens in the Philippines.

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.