

# YOUNG SYSTEMATISTS' FORUM

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## Day 1

Monday 23<sup>rd</sup> November 2020, Zoom [all timings are GMT+0]

11.50	Opening remarks	David Williams, President of the Systematics Association
12.00	Rodrigo Vargas Pêgas	Species Concepts and the Anagenetic Process Importance on Evolutionary History
12.15	Katherine Odanaka	Insights into the phylogeny and biogeography of the cleptoparasitic bee genus <i>Nomada</i>
12.30	Minette Havenga	Association among global populations of the Eucalyptus foliar pathogen <i>Teratosphaeria destructans</i>
12.45	David A. Velasquez-Trujillo	Phylogenetic relationships of the whiptail lizards of the genus <i>Holcosus</i> COPE 1862 (Squamata: Teiidae) based on morphological and molecular evidence
13.00	<b>Break</b>	<b>10 minutes</b>
13.10	Arsham Nejad Kourki	The Ediacaran <i>Dickinsonia</i> is a stem-eumetazoan
13.25	Flávia F.Petean	The role of the American continent on the diversification of the stingrays' genus <i>Hypanus</i> Rafinesque, 1818 (Myliobatiformes: Dasyatidae)
13.40	Peter M.Schächinger	Discovering species diversity in Antarctic marine slugs (Mollusca: Gastropoda)
13.55	Alison Irwin	Eight new mitogenomes clarify the phylogenetic relationships of Stromboidea within the gastropod phylogenetic framework
14.10	<b>Break</b>	<b>20 minutes</b>
14.30	Érica Martinha Silva de Souza	The lineages of foliage-roosting fruit bat <i>Uroderma</i> spp. (Chiroptera: Phyllostomidae)
14.45	Melissa Betters	Rethinking Informative Traits: Environmental Influence on Shell Morphology in Deep-Sea Gastropods
15.00	J. Renato Morales-Mérida-	New lineages of <i>Holcosus undulatus</i> (Squamata: Teiidae) in Guatemala
15.15	Roberto S. Probst	Speculating on evolutionary determinism: <i>Myrmelachista</i> ants (Hymenoptera) as a case of extreme convergent evolution
15.30	J. S. Silviria	Demystifying the extinct stilt-legged horse <i>Equus (Harringtonhippus) francisci</i> (Mammalia, Perissodactyla, Equidae, Equini)
15.45	<b>Break</b>	<b>10 minutes</b>
15.55	Poster breakout	60 minutes
16.55	<b>Break</b>	<b>10 minutes</b>
17.05	Discussion breakout	55 minutes
18.00	Close of Day 1	

## Day 2

Tuesday 24<sup>th</sup> November 2020, Zoom [all timings are GMT+0]

Welcome		
09.00	Mya Bhone Maw	Taxonomic studies on <i>Begonia</i> (Begoniaceae) in Myanmar: New Discoveries in Northern Myanmar
09.15	Cristian C. Lucañas	Review of the Arboreal Darkling Cockroach, <i>Dorylaea</i> Stal 1877 (Blattodea: Blattidae)
09.30	Raden Pramesa Narakusumo	Hundreds out of thousands: progress on the taxonomy of hyperdiverse <i>Trigonopterus</i> weevils (Coleoptera : Curculionidae) in the Wallacea region of Indonesia
09.45	George P. Burton	Systematics of <i>Myrcia</i> sect. <i>Calyptranthes</i> (Myrtaceae): a case study in resolving the taxonomy of complex genera in the Neotropics
10.00	<b>Break</b>	<b>10 minutes</b>
10.10	M. Brunetti	Cryptic diversity in phytophagous insects species: the case of <i>Psylliodes chalconera</i> (Coleoptera: Chrysomelidae)
10.25	Frederik W. Becker	Cape <i>Oxalis</i> polyploids show no evidence of "Gigas" effect.
10.40	K. Murray	Climatic predictability vs. phylogenetic relatedness: what drives the evolution of seed recalcitrance in SA <i>Oxalis</i> ?
10.55	Amy Jackson	Hybridisation and ecological speciation in the evolutionary history of Canary Island <i>Descurainia</i> (Brassicaceae)
11.10	<b>Break</b>	<b>20 minutes</b>
11.30	Marc Domènech	Building a robust, densely-sampled spider tree of life for ecosystem research
11.45	Adrià Bellvert1	Nature or nurture? Convergent evolution in predation traits in <i>Dysdera</i> spiders of the Canary Islands
12.00	Werner De Gier	An ecomorphological review of pea crabs (Decapoda: Brachyura: Pinnotheridae)
12.15	Juliana L. Segadilha	Phylogenetic analysis of Typhlotanaidae (Crustacea, Tanaidacea) based on morphological characteres, with description of a new species from Brazil
12.30	<b>Break</b>	<b>10 minutes</b>
12.40	Poster breakout	60 minutes
13.40	<b>Break</b>	<b>10 minutes</b>
13.505	Discussion breakout	60 minutes
14.50	<b>Close of Day 2</b>	Closing remarks and prizes
15.15	End of meeting	

Organised by Ellinor Michel, Karen Siu Ting, Yvette Harvey, Pablo Muñoz-Rodríguez and Katie Collins, with support from:



## YSF 2020 Poster presentations

Three concurrent sessions on 15:55-16:55 Monday 23<sup>rd</sup> and two sessions Tuesday 24<sup>th</sup> 12:40-13:40

### Monday Session 1 – Zoology - Chordates

Presenter	Title of poster	No.
Pino, Kateryn	Neotropical origin of free-tailed bats (Chiroptera: Molossidae): An integrative paleontological and molecular approach to re-evaluate a classic hypothesis	1
Brown, Emily	Assessing conflict between early neornithischian tree topologies	2
Ortega, Rose Chinly Mae	Metabarcoding of Dermal Microbial Community Structure of Hippocampus barbouri using 16S rRNA gene, Next Generation Sequencing : A tool for Seahorse Conservation	3
Gwilt, Annie	Mitogenomic by-products: Systematics of Seychelles caecilian amphibians from nontarget mitochondrial reads	4
Ribeiro-Silva, Luis	Molecular Sistematics revels cryptic species in the Neotropical fish genus Iguanodectes Cope 1872 (Teleostei, Characiformes)	5
O'Connell, Darren	Uncovering new species in a Wallacean "great speciator" lineage: congeneric island colonisers with very different origins	6
Boivin, Myriam	Total-evidence phylogeny of giant chinchilloids (Rodentia, Caviomorpha)	7
Meneses, Camila	Redescription and the First Molecular Phylogenetic Estimates of Evolutionary Affinities in Two Secretive, Endemic Reptiles from the Romblon Island Group, Central Philippines	8

### Monday Session 2 – Zoology – Insects

Ferreira, Wellington	Bayesian methods applied to the phylogenetic inference of morphological data: a study using solitary wasps (Hymenoptera, Vespidae, Eumeninae)	1
Gandhi, Monika	Sub-species Discrimination of Stingless bees (Meliponini) using Wing Geometric Analysis in Coimbatore district, Tamil Nadu, India	2
Zhang, Miles	One hundred and sixty years of taxonomic confusion resolved: Belonocnema Mayr (Hymenoptera: Cynipidae) gall wasps associated with live oaks	3
Orlov, Igor	Total Evidence Backbone Phylogeny of Aleocharinae (Coleoptera: Staphylinidae)	4
Salnitska, Maria	Integrative taxonomy and species limits in the Quedius umbrinus complex (Coleoptera: Staphylinidae)	5
Gillett, Conrad	Macroevolution and shifts in the feeding biology of the New World scarab beetle tribe Phanaeini (Coleoptera: Scarabaeidae: Scarabaeinae)	6
Magoga, Giulia	Factors affecting the efficiency of molecular species delimitation in a species-rich insect family	7

### Monday Session 3 – Zoology - Other

Riquelme, Franklyn Cala	New genus and species revealed by phylogenetic analyses of Antillattus (Salticidae: Euophryini)	1
Magalhaes, Ivan	Incorporating topological and age uncertainty into biogeographic inference in Neotropical sand spiders (Araneae: Sicarius)	2
Souto, Camilla	Dispersal, endemism and extinction shaped the cassiduloid echinoid's (Echinodermata) evolutionary history	3
Sosa, Irene de	Helter skelter: phylogeography of Eiseniella tetraedra (Oligochaeta) in the Iberian Peninsula.	4
Gharbi, Kamilia	Taxonomic study of Helminth parasites of digestive tract of two congeneric goatfish Mullidae Rafinesque, 1815 from off the Algeria coast	5
Bhowmik, Moumita	Current status of marine annelids (polychaete) taxonomy in India and its perspective	6
Bouguerche, Chahinez	Neither host specific nor has a vagina! An integrative study of Pseudaxine trachuri (Platyhelminthes, Monogenea) leads to a better understanding of the systematics Pseudaxine and related genera	7
Omura, Giovanna	Comparing partitioning strategies of Gastropoda discrete morphological characters using Bayesian and Maximum Likelihood approaches	8

## YSF 2020 Poster presentations

Three concurrent sessions on 15:55-16:55 Monday 23<sup>rd</sup> and two sessions Tuesday 24<sup>th</sup> 12:40-13:40

### Tuesday Session 1 – Botany

Presenter	Title of poster	No.
Holzmeyer, Laura	Generic recircumscription of <i>Dysoxylum</i> Blume ex Raspail (Meliaceae)	1
Olivar, Jay Edneil	Taxonomic analysis reveals correct usage of <i>Cyrtandra villosissima</i> Merr. (Gesneriaceae) and a new species	2
Nge, Francis	Southern hemisphere biogeography of Pomaderreae (Rhamnaceae) in Australasia	3
Landoni, Beatrice	The biogeography of <i>Linum bienne</i> Mill., a crop wild relative with a wide distribution	4
Fonseca, Luiz	Mining molecular data to infer a comprehensive phylogeny of the plant order Lamiales	5
Pauli, Maria	Rediscovery of <i>Mollinedia myriantha</i> (Monimiaceae, Laurales) after 123 years: implications for the taxonomy	6
Naive, Mark Arcebal	Complete plastid genome and phylogenetic analysis of selected Philippine <i>Etlingera</i> (Zingiberaceae) including the discovery of a remarkable new endemic species	7
González-Toral, Claudia	What hides in the heights? The case of <i>Bromus</i> (Poales) in Picos de Europa	8
Thiesen, Julia Faillace	Molecular phylogeny of the genus <i>Palisota</i> Rchb. ex Endl. (Commelinaceae)	9
Zavatin, Danilo	Can the genome size be informative to circumscribe species in <i>Macropopus</i> Perkins (Mollinedioideae, Monimiaceae, Laurales)?	10

### Tuesday – Session 2 - Micro, Myco & Other

Presenter	Title of poster	No.
Chaber, Katarzyna	Delimitation of species in <i>Lepocinclis ovum</i> complex (Euglenida)	1
Fells, Alicja	A study in water - an exploratory look into the phylogenetics of Euglenid loricate taxa	2
Marková, Patrícia	Microbiome of the cooling towers: Case study on cyanobacteria from Slovakia Nuclear Power Plant	3
Villanueva, Sariah	A Species Listing of Bark-associated Crustose Lichens in Angat Watershed Forest Reserve, Northern Philippines	4
Ewers, Isabelle	Re-analysis of the SSU-rRNA colpodean ciliate phylogeny	5
Araújo, João	Phylogenetic Diversity and Ecological Plasticity in Fungi	6
Łukomska-Kowalczyk, Maja	<i>Flexiglana</i> , a new genus in the autotrophic euglenids (Euglenida)	7
Silva, Ana Serra	The Effects of Tree Islands on Consensus	8
Mlungu, Zizile	Taxonomic revision of the highly cryptic monotypic genus of Sternophysingidae (Crustacea, Amphipoda)	9

## Species Concepts and the Anagenetic Process Importance on Evolutionary History

Vargas Pêgas, Rodrigo<sup>1,\*</sup>, Gomes de Souza, Lucy<sup>2</sup>

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Under the Unified Species Concept, species are lineages that evolve independently, but accounting for them as explanatory hypothesis for the fixation of characters on a tokogeny. Under many views, cladogenesis and heterobaty play major roles in speciation. Yet, as originally defined, anagenesis is the process responsible for generating change (including autapomorphies), irrespective of tokogenetic branching. Heterobaty could occur when (1) autapomorphies appear in two recently-branched lineages, or (2) when, in a continuum of two species, the second species loses the first's autapomorphies plus gains a new one. Therefore, heterobaty and tokogenetic branching are not prerequisite of each other. A third scenario: paraspecies coexists with a phyletic branch that gained an autapomorphy, without heterobaty. The validity of such heterobaty-less species is debated; yet, the processes behind the origin and fixation of autapomorphies are the same in all three scenarios. Therefore, heterobaty should not be viewed as a requisite for speciation.

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## Insights into the phylogeny and biogeography of the cleptoparasitic bee genus *Nomada*

Odanaka, Katherine<sup>1</sup>, Branstetter, Michael<sup>2</sup>, Rehan, Sandra<sup>1</sup>

<sup>1</sup>Department of Biology, York University, Toronto, CA

<sup>2</sup>Department of Biology, University of Utah, Salt Lake City, UT, USA

Previous morphological work of the cleptoparasitic bee genus *Nomada* (Hymenoptera: Apidae) established 16 distinct species groups, however the validity of these groups has not been confirmed using molecular data. Additionally, there are two competing hypotheses regarding *Nomada* biogeography: one suggesting an origin in South America and another suggesting a South African origin. Using molecular techniques, we 1) test the validity of the 16 species groups, 2) use fossil calibration points to determine the age, and 3) use ancestral state reconstruction to infer the biogeography of *Nomada*. Ultraconserved elements are used to construct a phylogenetic tree representing each of the 16 species groups and cover every ecoregion for biogeographic analyses. These data support 15 of the 16 species groups and suggests the need for revising the remaining group. Here we present the first molecular phylogeny and historical biogeography for the *Nomada*; these results provide an important foundation for understanding their diversification.

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## Association among global populations of the *Eucalyptus* foliar pathogen *Teratosphaeria destructans*

Havenga, Minette<sup>1,3\*</sup>, Wingfield, Brenda D.<sup>1</sup>, Wingfield, Michael J.<sup>1</sup>, Dreyer, Léanne L.<sup>2</sup>, Roets, Francois<sup>3</sup>, Aylward, Janneke<sup>1,3</sup>

<sup>1</sup> Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, ZA

<sup>2</sup> Department of Botany and Zoology, Stellenbosch University, ZA

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The aggressive leaf pathogen *Teratosphaeria destructans* (Wingfield & Crous) Wingfield & Crous causes widespread damage to *Eucalyptus* L'Hér. plantations in tropical and sub-tropical regions of South East Asia and South Africa. Little is known regarding the genetic diversity, origin or dispersal pathways of this pathogen. To date, only the asexual state of *T. destructans* has been found. This study investigated the genetic diversity and global relatedness of seven populations of *T. destructans*. All populations were independently introduced into their sampling region from an unknown source and the origin remains unknown. The Malaysian population had the highest genotypic diversity, isolates grouped in an independent cluster and had signs of recombination which suggests the existence of a cryptic sexual state in this plantation. The other six populations had low levels of genetic diversity, high numbers of clones and grouped into three distinct clusters, which highlight the strong influence of asexual reproduction.

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## Phylogenetic relationships of the whiptail lizards of the genus *Holcosus* COPE 1862 (Squamata: Teiidae) based on morphological and molecular evidence

Velasquez-Trujillo, David A.<sup>1,\*</sup>, Bolivar-Garcia, Wilmar<sup>1</sup>, Arias, Federico<sup>2</sup>

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<sup>2</sup> Consejo Nacional de Investigaciones Científicas y Técnicas de Argentina, AR

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*Holcosus* is a genus of recently resurrected lizards of the family Teiidae. It contains ten species with neotropical distribution that goes from Mexico to Ecuador. We present a hypothesis of the phylogenetic relationships, based on morphological and molecular evidence. Four loci and 34 morphological characters were analyzed. We sampled a total of 47 terminals of the internal group that represent 80% of the species diversity and the entire distribution of this group, plus 80 terminals of the external group with representatives of all genera of the Teiidae family were included. The results obtained showed *Holcosus* monophyletic divided into three clades: Clade 1 (*H. anomalus*, *H. bridgesii*, *H. festivus*, *H. quadrilineatus*), Clade 2 (*H. leptophrys*) and Clade 3 (*H. undulatus*). *H. festivus* was paraphyletic, formed by three clades, Magdalena valley, Caribbean and Chocó, populations of Colombia showed a genetic distance between them of 7%.

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## The Ediacaran *Dickinsonia* is a stem-eumetazoan

Nejad Kourki, Arsham<sup>1,\*</sup>, Vinther, Jakob<sup>1,2</sup>

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The evolution of key early metazoan characters is currently hotly debated. Traditionally, inferring these evolutionary steps has relied heavily on evidence from comparative morphology and embryology of modern taxa, and more recently from developmental genetics. However, direct evidence of ancestral characters can only come from the fossil record. *Dickinsonia* is a macroscopic, benthic, heterotrophic extinct genus from the Ediacaran which has long been hypothesised to be of metazoan origin. Here, we reassess the suite of characters possessed by *Dickinsonia* and the closely related *Yorgia* through analogy with extant metazoans, followed by reconstructing a phylogeny of metazoans incorporating *Dickinsonia* and *Yorgia*. Our results strongly support the placement of these genera as stem-eumetazoans. This finding provides the groundwork for reconstructing key steps in the evolution of eumetazoans, especially their body plans, without over-reliance on neontological evidence. It also strongly raises the possibility that bilateral symmetry evolved independently of gastric cavities or cephalisation.

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## The role of the American continent on the diversification of the stingrays' genus *Hypanus* Rafinesque, 1818 (Myliobatiformes: Dasyatidae)

Petean, Flávia F.<sup>1,\*</sup>, Lei Yang<sup>2</sup>, Corrigan, Shannon<sup>2</sup>, Maia Queiroz de Lima, Sergio<sup>1</sup>, Naylor, Gavin J.P.<sup>2</sup>

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Marine stingrays of the genus *Hypanus* Rafinesque, 1818 currently encompass nine valid species distributed in the Atlantic and Pacific oceans. To assess the genus' monophyly and evaluate species divergence times and possible routes of dispersion, we sequenced whole mitochondrial genomes of all putative species using the gene capture methodology and performed calibrated phylogenetic Bayesian Inferences. We tested lineages' diversifications and correlated them to the American continent constraints, which were divided into four types of barriers: land, represented by the Isthmus of Panama and Florida Peninsula; salinity and sediments by the Amazon river outflow; depth and distance by Mid-Atlantic and Eastern Pacific ridges; and temperature by northern and southern high latitudes. The genus originated 33.97 Ma [26.13-36.09 HPD] and its diversification was probably related to a world cooling event when stingrays were restricted to tropical waters in Western Atlantic. *Hypanus* still harbours a hidden diversity that affects the conservation of species.

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## Discovering species diversity in Antarctic marine slugs (Mollusca: Gastropoda)

Schächinger, Peter M.<sup>1,2,\*</sup>, Schrödl, Michael<sup>1,2,3</sup>, Wilson, Nerida G.<sup>4,5</sup>, Moles, Juan<sup>2</sup>

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*Tritoniella* Eliot, 1907 is a genus of marine nudibranchs belonging to Tritoniidae Lamarck, 1809. Unlike most of the family, this genus was endemic to the Southern Ocean with presently a single valid species. Although originally found in the Ross Sea, here we obtained extensive material from several expeditions sampled by both bottom trawling and SCUBA diving in the Weddell Sea, Antarctic Peninsula, all islands around the Scotia Sea, and as far north as the Falkland Islands. All material was sequenced (CO1, 16S, and H3) and the phylogenetic relationships were analysed in the context of all other tritoniids. Species delimitation tests led to the identification of five new species. Here we will discuss their affinities in a biogeographic, morphological, and anatomic comparative framework. Not surprisingly *Tritoniella* is another example of a previously unrecognized cryptic species complex occurring in Antarctica.

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## Eight new mitogenomes clarify the phylogenetic relationships of Stromboidea within the gastropod phylogenetic framework

Irwin, Alison<sup>1,2,\*</sup>, Strong, Ellen E<sup>3</sup>, Kano, Yasunori<sup>4</sup>, Harper, Elizabeth M.<sup>5</sup>, Williams, Suzanne<sup>1</sup>

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Members of the gastropod superfamily Stromboidea are characterised by their elaborate shell morphologies and diverse eye structures. The large and complex eyes within families Rostellariidae, Seraphsidae and Strombidae provide surprisingly good vision in contrast with the small eyes of Aporrhaidae and Struthiolariidae. Stromboidea thus provides an excellent opportunity to study eye evolution; however, a robust phylogenetic framework is required. Although a few strombid mitochondrial genomes have been sequenced, data for other stromboid families are lacking. In this study we report seven new mitogenomes obtained from transcriptomic and genomic data, with taxonomic representation from each Recent stromboid family, including the first mitogenomes for Aporrhaidae, Rostellariidae, Seraphsidae and Struthiolariidae. We also report a new mitogenome for group Xenophoridae. We use these data, along with published sequences, to investigate the relationships among these families, as well as gastropod groupings at a higher taxonomic level, and indicate the transition point of large eye evolution.



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## The lineages of foliage-roosting fruit bat *Uroderma* spp. (Chiroptera: Phyllostomidae)

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The genus *Uroderma* (Peters, 1865) has been historically described as two species, and six subspecies. It has also been artificially split in chromosomal races, and recently in five species. Here, we revisited the diversification of *Uroderma* using molecular (*Cytochrome b* and *Cytochrome Oxidase subunit I*) and morphological data. Our data support the five species, and the occurrence of two structured populations of *U. bilobatum* (Peters, 1866) at South America. The diversification of genus has probably occurred during the Late Miocene (6.75 Ma) followed by an explosive diversification by: *U. bilobatum* (3.52 Ma), *U. convexum* (4.16 Ma), *U. davisii* (3.36 Ma), and *U. bakeri* (3.08 Ma). The discrete data revealed high levels of polymorphisms that may lead to misidentifications. These species represent a highly complex biological system involving chromosomal polymorphisms, hybridization, and patterns of population structure that may not be well understood with the lack of comprehensive analyses of multiple data.

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## Rethinking Informative Traits: Environmental Influence on Shell Morphology in Deep-Sea Gastropods

Bettors, Melissa J,<sup>1</sup> Cordes, Erik<sup>1</sup>

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Marine gastropod mollusks (Thiele, 1925) within deep-sea, chemosynthetic environments present unique challenges to taxonomic study because they are chronically under-sampled, yet are anomalously biodiverse along the ocean floor. While classifying this diversity often relies on shell morphology, the accuracy of shells in delineating species is no longer clear, as genetic evidence increasingly confirms intraspecific morphological variation. The extent of this variation, and how it arises in chemosynthetic environments, is still poorly understood. The heterogeneous abiotic landscape of hydrocarbon seeps, for instance, may affect shell formation and maintenance, and preliminary data show a diversity of morphotypes within seep genera. My research will examine how *Provanna laevis* (Dall, 1918) (Gastropoda) shell morphometry varies along environmental parameters associated with active hydrocarbon seepage, including substrate, oxidative reductive potential, and pH. This research aims to document intraspecific variation and critically assess the reliability of shell morphology as a data source for chemosynthetic gastropod taxonomy.

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## New lineages of *Holcosus undulatus* (Squamata: Teiidae) in Guatemala

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*Holcosus undulatus* is a lowland to middle-land lizard whose distribution is from Northern Mexico to Central America. In Guatemala it is considered to have three subspecies (Smith and Lafe, 1946) or three species (Meza-Lázaro and Nieto-Montes de Oca, 2015). In this work, 60 NADH subunit II mitochondrial sequences of individuals in the *Holcosus undulatus* group of South Mexico, Guatemala, and Honduras, were analyzed using Bayesian and Maximum Likelihood approaches to see if the populations respond genetically to the physiography. Six lineages for Guatemala were identified, four belong to previously described lineages and two are new lineages for the country. The phylogenetic analysis shows that the populations respond to the physiographic areas of Guatemala, which means that the volcanic and mountain chains are barriers for each population. These results show the complex history of lowland species, the unknown diversity, and the potential studies about the lowland species of Guatemala.

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## Speculating on evolutionary determinism: *Myrmelachista* ants (Hymenoptera) as a case of extreme convergent evolution

Probst, Rodolfo S.<sup>1\*</sup>, Longino, John Thomas<sup>1</sup>, Branstetter, Michael Gareth<sup>2</sup>

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Natural selection can promote repeatable outcomes in evolution, contributing to the idea of evolutionary determinism in different biological systems. Obligatory ant-plant symbiotic interactions have evolved multiple times. The ant genus *Myrmelachista* Roger, 1863 comprises ~60 species distributed throughout the Neotropical region. Within the genus, species can be divided into dead stem nesters or generalist inhabitants of live stems, and those engaged in tight associations with a set of similar plant species. We apply a phylogenomic approach (enrichment of ultraconserved elements) to reconstruct the evolutionary history of *Myrmelachista*. We use the phylogeny to investigate the evolution of nesting behavior within the genus, and our analyses suggest that the evolution of highly symbiotic relationships occurred several independently times among the Mesoamerican species. Our divergence timing analyses estimated the age of the independent evolutions of obligatory associations to be highly similar, suggesting a remarkable and relatively recent history of extreme convergent evolution.

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## Demystifying the extinct stilt-legged horse *Equus (Harringtonhippus) francisci* (Mammalia, Perissodactyla, Equidae, Equini)

Silviria, J.S.<sup>1,2,\*</sup>,

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The extinct "stilt-legged" horses of Pleistocene North America are commonly interpreted as a single polytypic species, *Equus (Harringtonhippus) francisci* (Hay, 1915) Heintzman *et al.*, 2017, based partly on low mitochondrial divergence. However, reanalysis of every major morphometric study on North American *Equus* since 1985 supports a more restrictive diagnosis for *E. francisci*, the most derived member of a speciose "stilt-legged" clade. Aside from extreme elongation of the metatarsal with respect to proximal breadth, no postcranial apomorphy unambiguously distinguishes the "*E. francisci*" clade from other *Equus*, and thus *Harringtonhippus* best considered a subgenus of *Equus*, rather than a separate genus. Morphological resemblances of the "*E. francisci*" clade to taxa from an ass/zebra clade, particularly the extant African plains zebra (*E. quagga* Boddaert, 1785) and the extinct Asian "suessmionines" (*E. ovodovi* Eisenmann & Sergej, 2011), cannot be ignored in future phylogenetic analyses.

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## Taxonomic studies on *Begonia* (Begoniaceae) in Myanmar: New Discoveries in Northern Myanmar

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Although the Northern Forest Complex of Myanmar is one of the most biodiverse areas in the world, our knowledge of species richness within these forests is very limited. Recently, new species and new records continue to be described especially from Northern Myanmar but the flora is still poorly known in this region. Consequently, the *Begonia* flora of Myanmar is amongst the least well studied worldwide and has not been revised due to the lack of resources, although the number of species in the genus *Begonia* is likely to be very high. Likewise, the updated taxonomic information and a complete recent revision on the genus *Begonia* are still lacking. On this talk, I will discuss our flora expedition in the northernmost parts of Myanmar, where access is limited due to its high topography, transportation, and political situation, and some new discoveries of *Begonia* we have found in this region.

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## Review of the Arboreal Darkling Cockroach, *Dorylaea* Stal 1877 (Blattodea: Blattidae)

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The Arboreal Darkling Cockroach, *Dorylaea* Stal, 1877 (Blattodea: Blattidae) is redefined. Despite being placed in Blattinae Latreille, 1810, the tarsal, and genital characters indicate closer affinity to the Australian *Methana* Stal, 1877 (subfamily Polyzosteriinae). Four species-groups are established based on based on pronotal patterns and tegminal coloration: -*brunneri* species group, -*flavicincta* species group, -*hosei* species group, and -*magna* species group. Of the 24 known species, 20 were placed in the established species groups, two remained unplaced, and two species were excluded from the genus. The genus is distributed throughout the Oriental Region, yet most species are narrowly distributed. Several undescribed, mostly sibling species are noted from the Philippines and surrounding countries.

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## Hundreds out of thousands: Progress on the taxonomy of hyperdiverse *Trigonopterus* weevils (Coleoptera : Curculionidae) in the Wallacea region of Indonesia

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*Trigonopterus* Fauvel 1862 (Insecta: Coleoptera: Curculionidae) is a hyperdiverse genus of hidden snout weevils (Crypthorynchinae) that inhabit the Indo-Australian Archipelago. The epicentre of *Trigonopterus* radiation is in New Guinea, and a recent biogeographical analysis shows that it dispersed unidirectionally from the east (Sahul) (~45 MYA), through Wallacea (~38 MYA) to Sundaland (~29 MYA). Sulawesi and Maluku acted as an important hub for *Trigonopterus* dispersal further west. Here we present a summary on *Trigonopterus* of Wallacea using an integrative turbo taxonomy approach, combining molecular data, i.e., the cox1 barcoding fragment, high-resolution digital images, and diagnostic descriptions to provide rapid descriptions of new species. At the start of this project, only three described *Trigonopterus* species were known from Wallacea and now there are 110 more, newly described species. Also, we present ancestral state reconstructions of the weevils' lifestyle which is either edaphic or on foliage. Finally, we discuss some features of the mitochondrial genome.

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## Systematics of *Myrcia* sect. *Calyptranthes* (Myrtaceae): a case study in resolving the taxonomy of complex genera in the Neotropics

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*Myrcia* (Myrtaceae) are a highly diverse genus of plants known for their aromatics and ecological prevalence across the Americas. The complex taxonomy of the group often makes it unmanageable for conservationists, and as an avenue to resolving this systematic impediment, this project focuses on improving understanding of *Myrcia* sect. *Calyptranthes* (Sw.) A.R.Lourenço & E.Lucas (2018) using several approaches. The group was first organised into three manageable geographical sections, and monographic work is now undertaken to resolve the group. Herbarium and extensive digital collections have been examined to consolidate taxonomy and distribution, and morphometric analyses used to untangle difficult species complexes. Alongside phylogenetic research, nomenclature has been clarified, including transfers into *Myrcia*. This research has underpinned assessments for the IUCN Red List, showing how complex genera can be tackled using immersive monography, providing a knowledge-base for wide-reaching collaborations.

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## Cryptic diversity in phytophagous insects species: the case of *Psylliodes chalconera* (Coleoptera: Chrysomelidae)

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Individuals of the flea beetle *Psylliodes chalconera* (Illiger, 1807) were observed feeding both on *Centaurea solstitialis* L., 1753 and species in the genus *Onopordum* L., 1753 and *Carduus* L., 1753. To investigate whether this species is polyphagous or it is comprised of host races or cryptic species, several individuals were collected in Bulgaria, Italy, Russia and Turkey. A fragment of the *cox1* mitochondrial gene was sequenced to study the population structure and investigate the divergence among populations feeding on different plant species. The results indicate that at least three different groups are present: 1) associated with *C. solstitialis*, 2) associated with *Onopordum* spp. and 3) associated with *Carduus* spp., *Onopordum* spp., and possibly *C. solstitialis*. Adult specimens indicated a possible fourth group. Our results suggest that at least some of these groups could represent incipient species and could be evaluated as prospective candidates for classical biological control of weeds.

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## Cape *Oxalis* polyploids show no evidence of “Gigas Effect”

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The process of polyploidisation has profound effects on morphological, ecological and evolutionary attributes of plant lineages. Two well-recognised effects of whole genome duplication are the Gigas Effect: a significant increase in the size of polyploid organisms, and an increase in invasive capability. Despite the assumed ubiquitous nature of the Gigas Effect, recent work has not consistently supported size increase. We have investigated the Gigas Effect in South African *Oxalis*, a lineage (<230 spp.) with high levels of within-species polyploidy and many invasive species. Classically-used Gigas Effect measurements such as pollen and stomatal guard cell size show no obvious polyploidy-related increase; nor is there correlation between these measurements. Our results suggest that the Gigas Effect is not a reliable outcome of polyploidisation. We discuss these results with respect to this highly polyploid lineage, as well as the relationship between polyploidy and invasiveness.

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## Climatic predictability vs. phylogenetic relatedness: what drives the evolution of seed recalcitrance in SA *Oxalis*?

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Seed recalcitrance is commonest in aseasonal, tropical habitats - a pattern challenged by species of South African *Oxalis*. Species in this genus, distributed across semi-arid habitats, display a spectrum of seed germination strategies from ancestral desiccation-tolerance to multiple origins of desiccation-sensitive recalcitrance. In this study, we propose that the predictability of winter-rainfall growing conditions may drive seed recalcitrance evolution, and test for relationships between predictability of climatic variables and seed mass - a proxy of recalcitrance related to water content. Preliminary results using - phylogenetically corrected methods - show that for larger seeds, mass (and therefore recalcitrance) is indeed related to environmental predictability. This pattern however is sensitive to several large seed mass outliers, resulting in very different predictors for seed mass (mean annual temperature, mean annual precipitation). These results urge recognition of environmental predictors for this system, and suggest further exploration of seed functional traits for future research.

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## Hybridisation and ecological speciation in the evolutionary history of Canary Island *Descurainia* (Brassicaceae)

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Along with geographic isolation and ecological shifts, a growing body of genomic evidence have suggested that hybridisation has played an important role in the evolution and diversification of oceanic island flora. However, hybridisation is challenging to detect due to confounding evolutionary processes, such as incomplete lineage sorting (ILS). Here, we used genotyping-by-sequencing (GBS) data collected from all seven *Descurainia* (Brassicaceae) species endemic to the Canary Islands to investigate the contribution of hybridisation to the diversification of the group. Phylogenetic relationships were inferred and three instances of ecological speciation were inferred using climatic-niche characteristics. Gene flow between taxa was examined using three approaches, D-statistics, species networks and ABC models, and indicate a likely ancient hybrid origin, as well as an introgressive origin. Our study highlights the necessity to use phylogenetic network approaches that can simultaneously accommodate ILS and gene flow when studying groups that are prone to hybridisation.

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## Building a robust, densely-sampled spider tree of life for ecosystem research

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Understanding the non-random loss of species with respect to phylogeny is essential to determine how species and communities evolve across time and space and for making better-informed conservation decisions. However, several factors are known to influence phylogenetic reconstruction and, ultimately, phylogenetic diversity metrics. In this study, we use the largest spider tree of life in terms of taxa to empirically test how some of these factors affect phylogenetic resolution and phylogenetic diversity metrics. We found that the incorporation of the 28S nuclear gene to the COI mitochondrial gene of local taxa and the use of a backbone matrix had the highest impact on tree

topology, followed by the time information and the use of topological constraints. Incorporating all, some or none of these treatments/data will depend on either data availability or trade-offs between time and resource costs for generating data and the potential downstream benefit.

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## Nature or nurture? Convergent evolution in predation traits in *Dysdera* spiders of the Canary Islands

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Ever since Darwin, understanding the origins and identifying the processes that shaped biodiversity have been major questions in biology. Adaptive radiations in oceanic islands offer the experimental conditions and multiple replicates required to unravel the underlying patterns of species proliferation and, untangle the role of adaptive change and phylogenetic constraints in assembling local communities.

The nocturnal hunter *Dysdera* spiders have colonized and diversified in the Canary Islands. Endemic species have evolved a large array of chelicerae shapes, which has been suggested to be linked to levels of dietary specialization and capture strategies. In this study, we characterize chelicera types using geometric morphometric techniques, and investigated their evolution in the most up-to-date phylogeny of the group.

We identified 7 different chelicerae types that evolved multiple times independently in different islands, supporting the hypothesis that convergent evolution in predation related traits played a major role in the radiation of Canarian *Dysdera*.

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## An ecomorphological review of pea crabs (Decapoda: Brachyura: Pinnotheridae)

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Almost all species in the crustacean “pea crab” family (Pinnotheridae) are classified as obligatory endo- or ectosymbionts, living in a mutualistic or parasitic relationship with a wide range of invertebrate hosts. While pea crabs are regarded as one of the most morphologically adapted groups of symbiotic crabs, the functionality of these adaptations in relation to their lifestyles has not been reviewed before. In this presentation, the wide range of morphological diversity within the family will be showcased, and comparisons will be made between crab species associated with soft-bodied hosts (like bivalves and ascidians) and hard-bodied hosts (like echinoderms). Additionally, the proposed functionality of some of these adaptations will be discussed.

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Phylogenetic analysis of Typhlotanaidae (Crustacea, Tanaidacea) based on morphological characteres, with description of a new species from Brazil

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Typhlotanaidae Sieg, 1984 is a cosmopolitan family of Tanaidacea (Crustacea). Herein, we present a morphological cladistic analysis of this family performed using the program TNT and based on a data matrix of 107 characters x 86 terminal taxa (80 from the ingroup, including all 14 known genera). Two most parsimonious trees were obtained from a phylogenetic analysis under implied weights and *strict consensus* tree was calculated. Typhlotanaidae was corroborated as monophyletic, as well as ten non-monotypic genera of the family. *Typhlotanais* Sars, 1882, as currently composed, is proved to be polyphyletic, where some groups were rearranged. *Typhlotanais* species with pereopods 1–3 coxal spur present were transfered to *Antiplotanais* Bamber, 2008 (new combination). Moreover, two morphogroups (*trispinosus*- and *spinicauda*-groups) and two well-supported clades are designated as new genera. One of the new genera includes an undescribed species from Brazil. The family is now composed by 114 species in 18 genera.

### Phylogenetic diversity and ecological plasticity in Fungi

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Entomopathogenic fungi are parasitic organisms that evolved the ability to use the insect body as food source and sporulate from it, transmitting to the next host. Although insect parasitism emerged multiple times along the evolution of Fungi, the order Hypocreales (Ascomycota) contains the greatest diversity of extant entomopathogenic lineages. Hypocrealean fungi parasitizes 12 orders of insects and spiders, plants and other fungi, with few groups exploiting nematodes and also endosymbionts of plants and insects. The emerging picture then is of a large order of microbes that is remarkably diverse. This raises important questions for evolutionary studies which is if some evolutionary pathways (e.g. parasitic to mutualistic life-style, or Coleoptera to Hymenoptera association, etc) are more likely to occur than others? Why some host groups act as “islands of biodiversity” for parasitic lineages, while others remain uninfected? How the hosts and the environment shape morphological and ecological adaptations in parasitic microbes?

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### Current status of marine annelids (polychaete) taxonomy in India and its perspective

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India is a megadiverse country with global biodiversity hotspots, but has severe impediments for strengthening the taxonomic knowledge of marine annelids (polychaetes). This has a cascading effect on biodiversity assessment and conservation policy because polychaetes are exceptionally diverse with crucial roles in marine ecosystems. Due to a chronic scarcity of taxonomic experts and museum collections, the proper upgradation of polychaete field guides and databases need updating. However, copious ecological articles on Indian polychaetes are available, but a few taxonomic articles and monographs. Additionally, the concept of cosmopolitanism has created another critical issue in historical perspective and as a result, the number of questionable species deserves clarification. Therefore, extensive faunistic studies, field guides, and taxonomic revisions are highly encouraged in order to find out the hidden biodiversity of Indian polychaetes.

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## Total-evidence phylogeny of giant chinchilloids (Rodentia, Caviomorpha)

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Although not being a species-rich taxonomic group today, the Chinchilloidea present an astonishing past diversity including the largest rodents of all times. We studied a new chinchilloid skull from the Miocene of Tucumán, Argentina. Through a comprehensive matrix including 473 cranio-dental and 11,211 molecular characters for 54 taxa, a total-evidence phylogenetic analysis of the chinchilloids was performed to unveil the relationships of their giant representatives and the phylogenetic position of this new material from Tucumán. We used both maximum-parsimony and probabilistic approaches, and additional analyses were realized on the morphological characters solely. Our Bayesian inferences support the creation of a new extinct family, the Tetrastylidae, with the taxon from Tucumán being a representative of the family. Our analyses further provide different phylogenetic relationships for the Tetrastylidae and Neopiblemidae (also extinct), either close to the Dinomyidae or to the Chinchillidae.

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## Assessing conflict between early neornithischian tree topologies

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The phylogenetic position of the 'hypsilophodonts' remains one of the key questions in dinosaur research, having implications for the evolution of several derived ornithischian clades. Recent phylogenetic analyses have recovered two conflicting hypothetical placements for these taxa: (H1) within Cerapoda, as a paraphyletic assemblage of ornithopods; and (H2) outside of Cerapoda, within the clade Thescelosauridae. Here we assess three independent neornithischian phylogenetic studies from the last five years that have recovered topologies congruent with either H1 or H2. H1 matrices are stable and retain hypsilophodonts within Cerapoda throughout all analyses, while the H2 matrix is highly influenced by taxon and character sampling. Our findings show no significant relationship between the completeness of input taxa or characters and tree resolution, suggesting that future analyses can confidently include incomplete taxa. The phylogenetic position of the hypsilophodonts remains largely enigmatic, but our study highlights problems that should be addressed in future analyses.

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## New genus and species revealed by phylogenetic analyses of *Antillattus* (Salticidae: Euophryini)

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An extensive ongoing survey of Caribbean arachnids continues to uncover, across multiple genera and families, greater species richness than hitherto appreciated. Here, we focus on a clade of jumping spiders endemic to the Caribbean, currently all placed in the genus *Antillattus*. Phylogenetic analyses were conducted on *Antillattus* s. l., and the group was revised based on the analyses. These analyses are based on molecular and morphological data, and include Cuban species, which were absent from previous analyses. A total of 125 morphological characters were scored for the group. Additionally, these data were used for species delimitation and identification. Our results indicate that several species formerly placed in *Antillattus* are misplaced in this genus and a new placement is proposed. One morphological synapomorphies and molecular data support the monophyly of the *Antillattus* clade and indicate that the genus as currently circumscribed actually comprises three divergent clades (*Antillattus*, *Pensacolatus* and *Bryanattus* **gen. nov.**). The monophyly of *Antillattus* (new circumscription) is supported by twelve morphological synapomorphies and is revised to include *A. gracilis*, *A. placidus*, *A. cambridgei*, *A. cubensis*, and *A. occultus* **sp. nov.** *Antillattus occultus* **sp. nov.** is genetically distinct from the other species but is morphologically cryptic. The genus *Pensacolatus* is revised to include *P. darlingtonia* **comb. nov.**, *P. electus* **comb. nov.**, *P. maxillosus* **comb. nov.**, *P. montanus* **comb. nov.**, *P. peckhami* **comb. nov.**, *P. scutiformis* **comb. nov.**, *P. surieli* **sp. nov.**, and *P. naranjoi* **sp. nov.** Finally, *Bryanattus* **gen. nov.** is proposed to include the type species *Bryanattus keyserlingi* **comb. nov.**, *B. mandibulatus* **comb. nov.**, *B. unispina* **comb. nov.**, *B. orientalis* **sp. nov.**, *B. thanos* **sp. nov.** and *B. sanchezi* **sp. nov.**

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## Delimitation of species in *Lepocinclis ovum* complex (Euglenida)

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Euglenids are eukaryotic microorganisms belonging to the supergroup Excavata. Together with heterotrophic flagellates (Kinetoplastida, Diplonemida, Symbiontida) they form the group Euglenozoa. There are two families of freshwater autotrophic euglenids: Euglenaceae and Phacaceae. The genus *Lepocinclis* is a part of Phacaceae family. *Lepocinclis ovum* (Ehrenb.) Lemmermann, 1901 is a cosmopolitan and common species, and *Lepocinclis globulus* Perty, 1849 is the type species of the genus. Even so, their correct identification is problematic. There are over 30 morphologically similar taxa in the literature, and no good diagnostic features exist to distinguish most of them. We used environmental sampling and whole genome amplification, and delimited species within the *Lepocinclis ovum* complex. Morphological and molecular features were analyzed for isolates from Poland and strains from algae collections. As a result, 15 species were distinguished and five taxa had their taxonomic ranks changed. For all verified species we designated epitypes.

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**Neither host specific nor has a vagina! An integrative study of *Pseudaxine trachuri* (Platyhelminthes, Monogenea) leads to a better understanding of the systematics *Pseudaxine* and related genera**

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The presence/absence and number of vaginae is extensively used for the systematics of Monogenea. This character distinguishes two genera: *Pseudaxine* Parona & Perugia, 1890 has no vagina whilst *Pseudaxinoides* Lebedev, 1968 has multiple vaginae. A study of *Pseudaxine trachuri* Parona & Perugia, 1890 yielded specimens with structures resembling multiple vaginae; comparison of their morphology and molecules (COI barcode) with specimens without vaginae revealed their conspecificity. Redescription of *P. trachuri* based on specimens from off Algeria and Museum specimens from off France demonstrate a male copulatory organ armed with a single hooks circle and a stylet involved in traumatic insemination.

Integrative study of specimens from *Trachurus trachurus* (type-host) and *B. boops* confirmed for the first time with molecular evidence, that *B. boops* is host of *P. trachuri*. The erection of *Pseudaxinoides* was based on an erroneous interpretation of structures that are not vaginae and consequently we transfer its species to *Pseudaxine*.

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**Helter skelter: phylogeography of *Eiseniella tetraedra* (Oligochaeta) in the Iberian Peninsula.**

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*Eiseniella tetraedra* (Savigny, 1826) is a parthenogenetic tetraploid and cosmopolitan earthworm with a riparian lifestyle.

We sampled 68 localities within the Iberian Peninsula and studied COI, 16S, and 28S rRNA markers. Bayesian inference tree showed 8 different lineages. Three of them are distributed all around the peninsula (lineages A, F, G). Clade B appeared in northeastern area mostly. We found clades C and D only in northwestern and central areas. Clades G (Balearic Islands mostly) and H (only present in one locality) showed limited distributions.

These results, together with the presence of these clades in other countries, suggest that phylogeography of *E. tetraedra* may have been shaped by anthropogenic introductions and that only the most resistant clades are able to colonize southern less areas of the Iberian Peninsula. However, the biogeographic pattern obtained from clades B, C and D seems to respond to ecoclimatic factors such as regularity of rainfall.

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## Re-analysis of the SSU-rRNA colpodean ciliate phylogeny

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Colpodeans form a major clade of ciliates and are found worldwide in both aquatic and terrestrial environments. They are united by similar somatic ciliature but differentiated by complex oral structures. Although there are four well supported colpodean subclades, there is disagreement in molecular phylogenetic inferences about their branching order. Using available nuclear SSU-rRNA sequences, we evaluated if the platyophryids or the bursariomorphids are sisters to the remaining colpodeans. We inferred the “platyophryids-early” topologies using different alignment and masking methods, but constrained analyses could not reject the “bursariomorphids-early” topology. Both platyophryids and bursariomorphids clades have a similar number of nucleotide positions shared with the outgroup, and both are interconnected with the outgroup in phylogenetic networks. Based on these discordant results, it is hard to determine which clade branched off first, although the “platyophryids-early topology” is also supported by mitochondrial SSU-rRNA data.

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## Molecular phylogeny of the genus *Palisota* Rchb. ex Endl. (Commelinaceae)

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*Palisota* Rchb. ex Endl. is the largest Commelinaceae genus endemic to Africa. Here, we present the first phylogenetic hypothesis for the genus; Bayesian and maximum likelihood analyses were performed on a sampling that included 24 out of the 33 species described to date. Molecular data used include four chloroplast regions (*matK*, *rp32-trnL*, *rps16-trnK* and *trnL-trnF*) and one nuclear spacer (ITS). Our results confirm the monophyly of *Palisota* and four clades were recognized within the genus. We then checked the phylogenetic distribution of 20 key morphological traits and we compared species geographical distribution between the clades. We found eight morphological traits potentially associated with the phylogenetic signal but no phylogenetic pattern was detected concerning species geographic ranges. We are working on adding more informative molecular data to provide a fully resolved phylogenetic backbone for *Palisota*; this will open the way towards formal biogeographical and diversification analyses of this still enigmatic genus.

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## A study in water – an exploratory look into the phylogenetics of Euglenid loricate taxa

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Euglenids are unicellular, cosmopolitan, autotrophic Eukaryotes. The loricate taxa – *Trachelomonas* (Ehrenberg, 1834) and *Strombomonas* (Deflandre, 1930) – are particularly of interest, due to creating metal-incrusted envelopes (lorica), used as their key diagnostic trait. However, as the lorica is sensitive to environmental and ontogenetic changes, and may even be lost in culturing conditions, rendering morphological identification impossible, other methods of distinguishing species are necessary. A molecular study of the 18S rDNA has been carried out, yielding a preliminary phylogenetic tree of over 50 new sequences, with newly emergent branches and some thought-provoking surprises. In order to avoid changes arising from culturing conditions, sequences have been obtained from environmental samples collected across Poland. The obtained results shed new light on the systematics of the loricate taxa and highlight the necessity for further improvement of the sequence databases.

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## Bayesian methods applied to the phylogenetic inference of morphological data: a study using solitary wasps (Hymenoptera, Vespidae, Eumeninae)

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In the history of Systematics morphological characters are an important source of data for phylogenetic inference. However, the variety of morphological data available still not explored with recent approaches, such as Bayesian methods, are abundant. The aim of this study was to evaluate the use of Bayesian inference upon matrices of morphological data already published for some genera of wasps (Hymenoptera, Vespidae, Eumeninae). Bayesian inferences were conducted with equal rates of character evolution and with rates under the gamma distribution, using the Mk model in both conditions. Resulted trees were compared to trees obtained by parsimony for the same data sets. Trees with lower topological resolution were obtained using Bayesian methods, but many of the relationships of the original studies were recovered. Even with the non-congruence of the results, the use of Bayesian inference is interesting because it reveals patterns that can elucidate misleading interpretations in the parsimony traditional analyses.

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## Mining molecular data to infer a comprehensive phylogeny of the plant order Lamiales

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Phylogenetic relationships within the plant order Lamiales have been the subject of study for over two decades, with a large accumulation of DNA sequences. These data are distributed throughout the order, but until now a comprehensive phylogenetic study in terms of number of species sampled is not available. Here we (i) infer the phylogeny of Lamiales using molecular data of all species available; (ii) use the phylogenetic framework generated to infer the evolution of key traits such as habit and presence of carnivory. For that, sequences for ten molecular markers were recovered, nine from chloroplast and the nuclear ITS. A total of 6910 species were included. Phylogenetic relationships between families are generally well supported and the current taxonomy was corroborated, with all recognized families emerging as monophyletic. The traits investigated were generally polymorphic with multiple evolutions of the herbaceous habit, and three independent transitions to carnivory in Lamiales.

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## Sub-species Discrimination of Stingless bees (Meliponini) using Wing Geometric Analysis in Coimbatore district, Tamil Nadu, India

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In taxonomical studies of insects, geometric morphometrics can be applied for easy identification of species, as especially wing venation is a very important character used for insect identification. The following study has been conducted in a species of stingless bee (*Tetragonula iridipennis* Smith 1854) based on geometric patterns of venation of right forewing in Coimbatore district (five sampling areas were selected). Specimens collected from five different locations were assessed using wing geometric morphometric analysis to see discrimination among the same species of Stingless bee. Nine different landmarks on the right forewing were digitised which were used for geometric morphometric analysis. Visualization of digitised landmarks was used to find variations, if any, in same species from different locations by morphocluster formation. This study can help obtain correlation between phenotype and genotype within species and differentiate the occurrence of subspecies.



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## Taxonomic study of Helminth parasites of digestive tract of two congeneric goatfish Mullidae Rafinesque, 1815 from off the Algeria coast

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Goatfishes (Perciformes, Mullidae Rafinesque, 1815) are common marine teleosts of high commercial importance in numerous coastal areas. We investigated communities of Digenea species in two congeneric Mullidae hosts, collected from the Algerian coast, southern mediterranean. 298 *Mullus barbatus* (Linnaeus, 1758) and 88 *Mullus surmuletus* (Linnaeus, 1758) were examined, and a total of 239 Digenea were collected from their digestive tract, allocated to 5 species across 4 families: Opecoelidae Ozaki, 1925 represented by two species *Opecoeloides furcatus* (Bremser in Rudolphi, 1819) Odhner, 1928 and *Poracanthium furcatum* (Dollfus, 1948); an Hemiuridae Loss, 1988 *Lecithocladium excisum* (Rudolphi, 1819); a Fellodistomidae Nicoll, 1909 *Proctoeces maculatus* (Loss, 1901) and a single Fellodistomidae Nicoll, 1909), *Proctotrema bacilliovatum* Odhner, 1911.

An acute systematic study revealed an apparent overlap in morphometric data of the 5 Digenean species from two fish hosts. Consequently, the two fish hosts are likely to share the same Digenean community and the stenoxenic specificity of the Digenean parasites is briefly argued. We stress the gaps in the knowledge of systematics of Mullidae digeneans and the use of integrative systematics could reveal an additional digenean diversity.

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## Macroevolution and shifts in the feeding biology of the New World scarab beetle tribe Phanaeini (Coleoptera: Scarabaeidae: Scarabaeinae)

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The scarab beetle tribe Phanaeini contains coprophagous, necrophagous, mycetophagous and suspected myrmecophilous species. We analyse the largest molecular dataset assembled, incorporating for the first time the enigmatic monobasic genus *Megatharsis*, the *thalassinus* group of the subgenus *Coprophanæus* (*Metallophanæus*), and the subgenus *Dendropaemon* (*Eurypodea*) (formerly *Tetramereia*), unveiling their macroevolutionary history in light of Cenozoic abiotic changes and inferring shifts in feeding biology. We infer *Megatharsis* in a clade containing the myrmecophilous genus *Dendropaemon* and demonstrate that *Coprophanæus* (*Metallophanæus*) is polyphyletic. Our divergence time analyses and ancestral range estimation indicate an eastern South American tribal origin in the early Eocene, with subsequent Oligocene colonization of Central America, long before a Panamanian land-bridge. A shift to necrophagy in *Coprophanæus* is possibly linked to increasing Neotropical small vertebrate diversity since the Eocene and, astonishingly, myrmecophily evolved from necrophagy 35 Mya. These drastic shifts in lifestyle are unlinked to Quaternary extinction of large mammals.

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## What hides in the heights? The case of *Bromus* (Poales) populations in Picos de Europa

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The advances in molecular techniques have allowed their application to systematics leading to the detection of new species among botanic endemisms, which are common in mountainous regions. One example is *Bromus picoeuropeanus* Acedo & Llamas, 2019, a *Bromus* (Poales) population from the mountainous region of Picos de Europa (north of Spain), previously considered *Bromus erectus* Hudson, 1762. As this new species has been described based on its morphology and ecology, we aimed to determine whether the status of this endemism of Picos de Europa as species is supported by molecular data. We performed a preliminary phylogenetic analyses based on nuclear (ITS and ETS) and plastid (*trnL*) markers. The obtained topologies during the individual and combined (ETS-ITS-*trnL*) phylogenetic analyses placed the Picos de Europa *Bromus* in a clade with ambiguous relationships with *B. erectus*, depending on the molecular marker. This suggests further molecular studies are needed.

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## Mitogenomic by-products: Systematics of Seychelles caecilian amphibians from nontarget mitochondrial reads

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Ultraconserved elements (UCEs) are increasingly becoming common markers for systematic studies. UCEs are sequences of DNA that are highly conserved across species, allowing visualisation of evolutionary history. Targeting UCEs requires amplifying thousands of genomic regions and consequentially non-targeted DNA is present in subsequent sequence data, with many of these sequence reads of mitochondrial origin. Our study shows how these nontarget sequences can be used to reconstruct (near-)complete mitogenomes and used to perform phylogenetic analyses. Mitochondrial reads were extracted from a UCE dataset generated for Seychelles caecilian amphibians and (near-)complete mitogenomes reconstructed for seven of eight species. Although our phylogenetic analyses do not fully resolve the relationships, they do strengthen support for some undocumented evolutionary relationships. The data provides support for the convergence of two miniaturised forms, which morphologically look similar but do not form a sister relationship, and provides growing evidence that the groups generic level arrangements likely need revision.

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## Generic recircumscription of *Dysoxylum* Blume ex Raspail (Meliaceae)

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The hypothesized polyphyly of *Dysoxylum* Blume ex Raspail (Meliaceae) as currently circumscribed is tested. *Dysoxylum* has been one of largest genera of Meliaceae in Southeast Asia. Analyses based on nuclear ribosomal ITS, ETS, the plastid *trnL-trnF* intron and intergenic spacer, as well as the *rps15-ycf1* intergenic spacer clearly support the polyphyly and recover six strongly supported clades within *Dysoxylum* s.l., in large part supporting the classification of Harms (1940). Based on the largest molecular phylogenetic tree assembled to date, and morphological considerations, a revised disposition of the 95 currently recognised *Dysoxylum* species, is presented, re-instating the genera *Didymocheton* Blume, *Epicharis* Blume, *Goniocheton* Blume, *Prasoxylon* M.Roem. and *Pseudocarapa* Hemsl. Forty-four new combinations at species level and two at infraspecific are proposed.

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## The biogeography of *Linum bienne* Mill., a crop wild relative with a wide distribution

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*Linum bienne* (Miller, 1768) is an herbaceous species which belongs to the order Malpighiales. Its distribution spans the Mediterranean basin and the Atlantic coasts of Europe, from sea-level up to about 1000m. No comprehensive biogeography of the species exists, despite *L. bienne* is the wild ancestor of cultivated flax (*Linum usitatissimum*, Linnaeus, 1753), primarily used for fibre and oil. Natural variation for flowering time in *L. bienne* was fundamental to the adaptation of the crop to northern latitudes during domestication. The presence of natural variation for reproductive traits in *L. bienne* and its wide distribution make it an ideal species to study adaptation and plasticity across environmental gradients, but this requires a basic understanding of the species history. The description of *L. bienne* across its whole range from a genomic and phenotypic perspective is also a fundamental step in the improvement of the crop.

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## Phylogeny, morphology, and biogeography of *Myrcia* sect. *Aguava* (Myrtaceae), a complex Neotropical clade

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*Myrcia* (Myrtaceae) is a large Neotropical genus, including over 600 species divided into nine sections. *Myrcia* sect. *Aguava* is one of most complex groups of *Myrcia* due to extensive distribution range and high morphological variation of some of its species, notably the vexing *Myrcia guianensis* (Aubl.) DC. Combined high-throughput and Sanger sequencing data were used for phylogenetic inference. Divergence times and ancestral range distributions were estimated. *Myrcia* sect. *Aguava* is monophyletic, comprising 32 species with exclusively trilocular ovaries. Further diagnostic characters include leaves with raised adaxial midveins, symmetrical inflorescences, flowers with free calyx lobes, and glabrous discs. Three lineages that correspond to geography are observed within sect. *Aguava*, and multiple accessions of *M. guianensis* are non-monophyletic. *Myrcia* sect. *Aguava* apparently originated in the Cerrado during mid-Miocene, with subsequent late Miocene migrations to Atlantic Forest, Amazon and Caribbean, indicating transitions from open to forested areas that are uncommon in the Neotropics.

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## Incorporating topological and age uncertainty into biogeographic inference in Neotropical sand spiders (Araneae: *Sicarius*)

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Event-based biogeographic methods, such as dispersal-extinction-cladogenesis, have become increasingly popular for attempting to reconstruct the biogeographic history of organisms. Such methods employ distributional data of sampled species and a dated phylogenetic tree to estimate ancestral distribution ranges. Because the input tree is often a single consensus tree, uncertainty in topology and age estimates are seldom taken into account. We explore the effect of incorporating this uncertainty in a biogeographic analysis of the 21 species of sand spiders (Araneae: *Sicarius*) from Neotropical xeric biomes, based on a "total-evidence" phylogeny. Including uncertainty in ages gives insights into the age of colonization of the Galapagos Islands by this genus. Including topological uncertainty allows a more solid discussion on past connections among currently disjunct Neotropical dry forests. We argue that incorporating phylogenetic uncertainty in biogeographic inference is valuable, especially in the presence of rogue taxa or wide confidence intervals in age estimates.

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## Factors affecting the efficiency of molecular species delimitation in a species-rich insect family

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In the context of biodiversity loss, molecular species delimitation approaches can accelerate species discovery. In this study, the effect of intrinsic factors on the efficiency of the most used single-marker species delimitation methods (nucleotide distance threshold, ABGD, GMYC, mPTP) was tested on more than 90 empirical datasets, derived from 7,237 Chrysomelidae (Coleoptera) COI sequences. The considered factors were: number of haplotypes per species; geographic distance among conspecific collection localities; difficulty related to species morphological identification; taxonomic rank. Distance-based methods outperformed coalescent-based ones. A high number of haplotypes per species was found to negatively affect delimitation efficiency, whereas large geographic distances within species had a positive effect. ABGD, mPTP and distance threshold delimitations were negatively affected by species difficult to be morphologically identified. Only GMYC was influenced by the taxonomic rank, showing lower efficiency on genus datasets. Achieved results should be considered for obtaining more reliable delimitations through molecular methods.

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## Microbiome of the cooling towers: Case study on cyanobacteria from Slovakia Nuclear Power Plant

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Cooling towers, used in electricity generation and industry, provide excellent conditions for the growth of many microorganisms, such as cyanobacteria. The wall surface of cooling towers provides very stable conditions for their growth. It offers microorganisms enough heat, nutrients, light and water to ensure an ideal environment for their reproduction. Cyanobacteria are usually found in growing clumps at the top and on the sides of the cooling tower. We focused on the microbial mats from lower part of the cooling tower V2 of the Jaslovské Bohunice Nuclear Power Plant, Slovakia. The majority of cyanobacteria are represented by species from orders Chroococcales, Synechococcales, Oscillatoriales. The most abundant were genera *Microcoleus*, *Gleocapsa*, *Aphanocapsa* and *Leptolyngbya*. They usually form filamentous morphotypes with firm hyaline sheath. Coccoid cells, on the other hand form massive mucilaginous colonies which could be potentially harmful for the functions of cooling towers.

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## Redescription and the First Molecular Phylogenetic Estimates of Evolutionary Affinities in Two Secretive, Endemic Reptiles from the Romblon Island Group, Central Philippines

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The Philippines possess a remarkable species diversity of amphibians and reptiles, the majority (80%) of which are endemic to this island archipelago. Recent investigations into the species diversity of two secretive, endemic lizards, false geckos (genus *Pseudogekko*) and semi-fossorial scincid lizard (genus *Brachymeles*) have revealed several cryptic species, highlighting the need for a more thorough understanding of diversity within these enigmatic genera of endemic Philippine reptiles.

We report on the first molecular estimates of phylogenetic relationships and present new data on phenotypic variation in these two poorly known taxa, endemic to the Romblon Island Group of the central Philippines. In this paper, we ameliorate both historical shortfalls. First, newly collected genetic data allowed novel molecular phylogenetic analyses aimed at explicating the evolutionary relationships of these lineages; secondly, with population level morphological data, allowed statistical characterization of interspecific and intraspecific phenotypic variation with congeners in both species for the first time.

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## Complete plastid genome and phylogenetic analysis of selected Philippine *Etilingera* (Zingiberaceae) including the discovery of a remarkable new endemic species

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Zingiberaceae are well known for their medicinal and economic significance across the world yet remained to be poorly known and studied and unfortunately considered as one of the most threatened plant families in the Philippines. Included is the genus *Etilingera*, where its taxonomy and nomenclature are much disputed particularly for several species in the archipelago. Here, we report the seven newly sequenced *Etilingera* plastomes obtained through genome skimming using next generation sequencing. All plastomes displayed a typical quadripartite structure and their size ranges from 161,289–164,641 bp which encoded 115 different genes (79 protein-coding, 32 tRNA and four rRNA genes). Gene content, gene order, and GC content were highly similar among these genomes. Maximum likelihood tree of the seven *Etilingera* and other related species showed that the plastomes can be used as

a super-barcode to identify *Etilingera* spp. and provides an important reference and solid foundation in the establishment of species identification and phylogeny of the family Zingiberaceae. In addition, recent fieldwork in Mindanao resulted in the discovery of a new species, *Etilingera dostseii* sp. nov., which is herein described and illustrated.

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### Southern hemisphere biogeography of Pomaderreae (Rhamnaceae) in Australasia

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Pomaderreae is Australasian endemic tribe of flowering plants within Rhamnaceae Juss. that contains c. 250 species. The majority of its species diversity is found across southern temperate Australia, with several species found in the northern Tropics, central arid Australia, and New Zealand. Here, we aim to: (1) assess the phylogenetic relationships, and (2) biogeographic and evolutionary history of the genus. We utilised a Next Generation hybrid capture sequencing approach to obtain 40 nuclear loci and near complete plastid genome for all species within the genus. Our phylogenetic analyses revealed major source and sink areas of dispersal across the region for this group, as well as asymmetric westward direction of dispersal. In addition, multiple independent long-distance dispersal events were detected from Australia to New Zealand across multiple species and clades within Pomaderris. The timing, significance, and drivers of these patterns are discussed.

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### Uncovering new species in a Wallacean 'great speciator' lineage: congeneric island colonisers with very different origins

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White-eyes (Zosteropidae) are known for their remarkable diversification and speed of evolution, particularly, on isolated islands. They are one of the 'great speciator' lineages, taxa known for their rate and tempo of speciation. Here we present evidence of two new white-eye species from the Wakatobi Islands in the Wallacea region. The Lemon-bellied White-eye (*Zosterops chloris*) is a widespread island colonising species. Its population on the Wakatobis are distinct from mainland populations in genetics, morphology, plumage and song. Even more remarkably we have discovered a completely novel white-eye species, found only on 155km<sup>2</sup> Wangi-wangi Island, with its closest relatives over 3000km to the east in the Louisiade Archipelago (*Zosterops griseotinctus* and *Zosterops murphy*). This species is estimated to have a population of <1000 individuals, giving impetus to efforts to have the Wangi-wangi white-eye recognised and protected. Our results demonstrate the uncharted biodiversity that remains in the Wallacea region.

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## Taxonomic analysis reveals correct usage of *Cyrtandra villosissima* Merr. (Gesneriaceae) and a new species

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New species often remain undetected and undescribed in herbaria unless detailed taxonomic work is conducted across the complete range of a taxon. Here, we review the application of the name *Cyrtandra villosissima* Merr. to specimens from the Philippines with erect suffrutescent habit and large, slightly falcate and densely hirsute leaves. Our taxonomic analysis revealed three other species sharing morphological similarities with *C. villosissima* Merr. which can be differentiated by their leaf symmetry and type of inflorescence. *C. villosissima* Merr. and *C. hirtigera* H.J. Atkins & Cronk are closely related and are distinguishable by their inflorescence, shape of calyx, and color of corolla. *C. ferruginea* Merr. is distinguishable by its anisophyllous leaves and sessile cymous inflorescences. The recently described species *C. argentii* Olivar, H.J. Atkins & Muellner is distinguishable from the other three by its cymose, pendulous compound inflorescence. This study highlights the importance of herbarium-based research and continuous field work to properly delimit species.

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## Comparing partitioning strategies of Gastropoda discrete morphological characters using Bayesian and Maximum Likelihood approaches

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The development of analytical strategies for discrete characters has gained renovated attention using reconstructions under parsimony, Maximum Likelihood (ML), or Bayesian Inference (BI). In this study, the performance of BI and ML was investigated under different analytical strategies and conditions on empirical morphological Gastropoda matrices (superfamily Cerithioidea, order Architaenoglossa Haller, 1890 and superfamily Stromboidea Rafinesque, 1815), by applying distinct evolutionary models, partition schemes, and under the presence or absence of invariable characters. IQTREE-ML preliminary results reveal higher likelihood values under unweighted characters and using invariable sites, and alternative evolutionary models did not result in significant differences. MrBayes-BI showed that using variable characters only, uncorrelated branch lengths, and implicit weights performed better than all other options. Applying different strategies in the analyses of discrete morphological characters can result in higher analytical reliability for future phylogenetic analyses, and our results might provide directions for data processing in modern programs.



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## Total Evidence Backbone Phylogeny of Aleocharinae (Coleoptera: Staphylinidae)

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Staphylinidae or Rove-beetles is the largest beetle family with over 72.000 described species arranged into 32 subfamilies. Among them, Aleocharinae is the largest and the most taxonomically challenging subfamily currently including 17.200 species in 61 tribes.

Phylogenetic studies of Aleocharinae, arguably and one of the largest and the least known insect lineages, are compromised by its enormous taxonomic diversity. Also, DNA is not available for numerous extant aleocharine species, hampering large scale phylogenomic studies. Using full body dissections and slide-mounting techniques for light microscopy supplemented by SEM, we constructed a matrix for 202 morphological characters across all major tribes of Aleocharinae and the outgroup subfamilies illustrated by 1.254 high-resolution microphotographs made available on-line. Parsimony- and model-based analyses of this matrix concatenated with earlier published DNA loci and including exemplar taxa lacking molecular data, brought a backbone phylogeny for Aleocharinae which resolved a number of outstanding phylogenetic controversies.

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## Metabarcoding of Dermal Microbial Community Structure of *Hippocampus barbouri* using 16S rRNA gene, Next Generation Sequencing : A tool for Seahorse Conservation

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*Hippocampus barbouri*, is one of the species of seahorse used in Traditional Chinese Medicine (TCM). Like any other species of seahorse, the dermal structure of this species is unique, characterized by flame cone cells which protrudes above the surface and covered by a prominent mucous cap. This structure can support epiphytic microbial growth. Identification of bacteria communities in the skin surface was done via 16S rRNA gene, Illumina NGS Workflow metabarcoding analysis. Result shows that there were 307,699 amplicon sequence reads representing all samples with corresponding 62 total operational taxonomic units. Phyla Proteobacteria, Fimicutes, Cyanobacteria, Bacteroidetes, Actinobacteria are the most prominent phylum observed with 16 classes, 25 orders, 43 families and 56 genera. These bacterial communities obtained from *H. barbouri* are greatly influenced by the host environment while few were exclusive. Findings could be a baseline data for groups of bacteria with medical potential that will need further tests and experimentation.

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## Rediscovery of *Mollinedia myriantha* (Monimiaceae, Laurales) after 123 years: implications for the taxonomy

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Mollinedia is a neotropical genus of flowering plants with c. 60 species. Some of them are endangered, rare or micro-endemic. The genus is extremely diversified in southeast Brazil in the Atlantic forest. *Mollinedia myriantha* Perkins was described from material collected in the Protected Area of Macaé de Cima, municipality of Nova Friburgo, Rio de Janeiro state, however was never seen after the type collection. Recently we rediscovered a male individual in the same area, after 123 years of the type. Some features unknown in the protologue were described for the first time: height of 8 m; DBH of 40 cm; corky bark and yellowish-green flowers. In 2019, the individual was found dead and no other individual was found. The present work reinforces the need for fieldwork and herbarium analysis, especially considering the environmental degradation, transforming the search for new species and the conservation of others in a race against time.

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## Neotropical origin of free-tailed bats (Chiroptera: Molossidae): An integrative paleontological and molecular approach to re-evaluate a classic hypothesis

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The free-tailed bats are among the most diverse groups of bats distributed in tropical and subtropical areas of the world. The relationships among the almost ~ 116 extant species, their timing of the origin, and geographic range evolution are not well understood. The only general hypothesis for this group proposes that the origin of this group is Paleotropical. We integrate paleontological and molecular evidence to infer their phylogenetic relationships and divergence times of extinct and extant lineages using the fossilized birth-death (FBD) method. Then we estimate the biogeographic range evolution using phylogenies that incorporate both extant and extinct lineages. Our results show that molossids (crown clade) originated during the Middle Eocene (45 Ma) in South America with several independent long-dispersal posterior events. These results contrast with all previous hypothesis of their origin and biogeographic history and showcase the necessity of integrating fossil and molecular data in these studies.

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**Molecular Systematics reveals cryptic species in the Neotropical fish genus *Iguanodectes* Cope 1872 (Teleostei, Characiformes)**

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The genus *Iguanodectes* Cope, 1872 include eight species distributed along the Amazon and Orinoco basins, and coastal Guyana rivers. Within this genus, a particular species, *Iguanodectes spilurus* (Günther, 1864), shows high level of morphological variation in external morphology and is widely distributed through hydrographic systems of South America. Therefore, the goal of our study is to use molecular and morphological tools to evaluate the existence of possible new species within *Iguanodectes*, mainly from the *Iguanodectes spilurus* group. The Principal Component Analysis (PCA), DNA barcode methods using cytochrome c oxidase subunit I (COI), associated with species delimitation methods demonstrated substantial intraspecific variation in both strains separating the *I. spilurus* species in four possible distinct groups. The results of the genetic distance of mtDNA COI sequences indicated high values with intraspecific variation between strains, *Iguanodectes* aff. *spilurus*–Nanay (16.8%), *Iguanodectes* aff. *spilurus*–Jari (17.9%), *Iguanodectes* aff. *spilurus*–Javari (18.2), which can be three cryptic species not yet described in *Iguanodectes*.

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**Integrative taxonomy and species limits in the *Quedius umbrinus* complex (Coleoptera: Staphylinidae)**

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The strong variability of various structures of morphology is quite an acute problem in the alpha-taxonomy of variousrove beetles including the large genus *Quedius*. A good example of such kind of species is *Quedius umbrinus* with the 12 hitherto known synonyms, originally described as separate species. Genitalia characters of *Q. umbrinus* appear in different morphological forms not corresponding to any patterns in external morphology. There seems to be some geographic pattern in the variability of morphology which, however, is not clear due to the complexity and gaps of the examined material. To properly study the variability of *Q. umbrinus*-complex, we are using methods of integrative taxonomy combining morphometric and single locus DNA data. Our preliminary results suggest that *Q. umbrinus* obviously represents a group of species which largely do not correspond with the subjectively defined 12 species that are currently in synonymy.

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## The Effects of Tree Islands on Consensus

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Phylogenetic analyses often yield multiple trees that can be interpreted as comprising distinct subsets based on the notion of adjacency in tree space, itself based on some notion/measure of the distance between two trees. Every pair of trees in the same 'island' are connected by a series of trees differing from each other by a single branch rearrangement and every tree in the series is present in the island. In a parsimony setting, the presence of tree islands with very disparate sizes can profoundly affect the commonly used majority-rule consensus (MRC), which can be dominated by groups in large islands. Using variations of the MRC, we show that it is possible to minimise island-size bias, while summarising the topological differences between all islands. We also explore how changing the branch rearrangement threshold can lead to multiple island subsets of the same tree distribution.

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## Dispersal, endemism and extinction shaped the cassiduloid echinoid's (Echinodermata) evolutionary history

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Cassiduloids are rare echinoids (Echinodermata) that live buried in coarse sediment and most likely originated in the Cretaceous. Despite their high diversity in the Paleogene, only seven cassiduloid species survived to the present. Previous studies revealed high levels of homoplasy and a dearth of novel traits in their evolutionary history. To detect informative morphological characters and improve phylogenetic resolution, I used microCT images of cassiduloid tests. The resulting time-calibrated phylogeny revealed a new family and showed that three of the living species are relicts of lineages from the Eocene. The temporal and spatial diversification of two cassiduloid clades were then analysed using a time-stratified likelihood model. Both clades had a Tethyan/NW Atlantic origin and their current distribution was established via initial range expansion, with highest speciation rate within the NW Atlantic during the Paleogene, followed by vicariance and geographically restricted extinction. Despite being brooders, living cassiduloids occur worldwide in allopatry.

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## *Flexiglena* – a new genus in the autotrophic euglenids (Euglenida)

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Autotrophic euglenids (Euglenida) belonging to supergroup Excavata are common and abundant unicellular algae, that occur in many freshwater habitats. Although taxonomic research on that group dates back almost 200 years, the molecular-morphological studies conducted in the 21st century have resulted in the description of two new genera: *Discoplastis* (Triemer, 2006) with two species and *Euglenaformis* (M.S.Bennett & Triemer, 2014) containing only one species. The goal of our study was to examine the two genera more closely by increasing the number of strains and taxa belonging to them and perform comparative morphological and molecular research. Our work resulted not only in enriching the *Discoplastis* and *Euglenaformis* genera with 5 new species, but also in discovery of a new phylogenetic line and description of the new genus *Flexiglena* (Zakryś & M.Łukomska, 2020).

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## A Species Listing of Bark-associated Crustose Lichens in Angat Watershed Forest Reserve, Northern Philippines

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The lichen symbiosis allows the fungal component (mycobiont) and its photosynthetic partners, to colonize any substrata including barks of living trees. In this study, we documented the crustose lichens associated with three host trees in Angat Watershed Forest Reserve in Bulacan, Northern Philippines. From the two hundred forty lichen specimens we collected from seventy host trees, we identified 10 species of corticolous lichens: *Anisomeridium polycarpum* (Müll. Arg.) R.C. Harris, *Bacidia inundata* (Fr.) Körb., *Fellhanera rhapsidophylli* (Rehm) Vězda, *Graphis caesiella* Vain., *Graphis scripta* (L.) Ach., *Lecanora chlorotera* Nyl., *Lecanora gangaleoides* Nyl., *Lecanora strobilina* (Spreng) Kieff., *Lepraria incana* (L.) Ach. and *Tephromela atra* (Huds.) Hafellner. Majority of the corticolous lichens were recorded from *Swietenia macrophylla* (L.) Jacq. This study serves as the first documentation of the lichen species within Angat Watershed Forest Reserve and provides baseline information on the diversity of crustose lichens in the region.

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## Do horny females prefer smaller males – sexual size dimorphism in the Arachnid sub-family Gasteracanthinae (Araneidae Clerck, 1757)

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Sexual size dimorphism (SSD) in spiders has been studied for many years. Species like the large orb-weavers from the genus *Nephila* Leach, 1815, are well known for the extreme sexual size dimorphism (eSSD) between the large females and small males. This eSSD is also apparent in the genus *Gasteracantha* Sundevall, 1833, located in the sub-family Gasteracanthinae. Gasteracanthinae are spiny orb-weavers, the larger females characteristically possessing large abdominal spines (or horns) while the smaller males often only reach a few millimetres in total length. In early trials using a phylogeny constructed from molecular and morphological data, the relationship of the female abdominal spine size to the male/female size ratio within the Gasteracanthinae, appears to have a positive correlation. This project ties in with worldwide research being done on other members of orb-weaving spiders and highlights the importance of museum and institution collections and why taxonomy is critical for interpreting molecular data.

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## Can the genome size be informative to circumscribe species in *Macropeplus* Perkins (Mollinedioideae, Monimiaceae, Laurales)?

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*Macropeplus* is an endemic genus from two hotspots in Brazil: Atlantic forest and Cerrado. It is composed by four dioecious species: *Macropeplus dentatus* (Perkins) I.Santos & Peixoto, *Macropeplus friburgensis* (Perkins) I.Santos & Peixoto, *Macropeplus ligustrinus* (Tul.) Perkins and *Macropeplus schwackeanus* (Perkins) I.Santos & Peixoto. The morphological features to circumscribe the species often overlap, hampering the precise taxa delimitation. In this sense, we need to use traits with lower intrinsic variation, as DNA amount, for example. Here, we define the genome size for two species:  $2C = 2.5$  pg in *M. dentatus* and  $2C = 16.4$  pg in *M. friburgensis*. The genome size varied eight times between these two species, being a promising technique to distinguish species, as proved before for another Monimiaceae genus, *Macrotorus*. Further studies with remaining two species will be performed to better understand the species delimitations and confirm the number of taxa in this problematic genus.

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## Taxonomic revision of the highly cryptic monotypic genus of Sternophysingidae (Crustacea, Amphipoda)

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Several freshwater amphipods have been shown to harbour cryptic diversity. The Southern African genus *Sternophysinx* (Sternophysingidae) has several species that appear to show cryptic diversity. For example, using traditional morphological diagnoses, *Sternophysinx transvaalensis* Holsinger & Straskraba, 1973 is reportedly occurring in four provinces, covering over 2000km, a highly improbable scenario. Species in this genus are generally narrow endemics, known only from one locality or several connected underground waters. There are three other species in this genus with a peculiar distribution. Consequently, this study is aimed at reviewing the morphological and genetic differentiation of this entire genus. Also, we will construct multi-locus phylogenies of this genus, complementing the DNA barcoding, to further clarify species boundaries and examine phylogenetic relationships among species to consider aspects of their biogeography and evolutionary history. Ultimately, this information will be used to prioritize taxa for conservation, based on measures of phylogenetic distinctiveness and distributions.

# MEETING POLICIES

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

## Photography and Social Media Policy

We want to promote and spread the word about the enormous range of work going on in the Systematics community, and we strongly encourage registrants and speakers to write about the meeting on blogs, social media, and via other media within the following limit: **please respect the wishes of speakers & poster presenters who ask for the content of their presentations not to be shared outside of the conference.**

## Anti-Harassment Policy

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



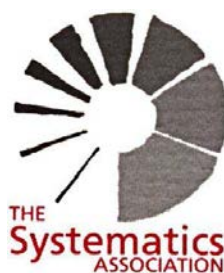


**The Systematics Association** is committed to furthering all aspects of systematic biology. It organises a vigorous programme of international conferences on key themes in systematics, including a series of major biennial conferences. The association also supports a variety of training courses in systematics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

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

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

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



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

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

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

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

**Signature:**

**Date:**

Please email this form to: [membership@systass.org](mailto:membership@systass.org)

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

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

