

# YOUNG SYSTEMATISTS' FORUM

25<sup>th</sup> November 2016, Flett Theatre, Natural History Museum, London, UK

08:45	<b>Registration</b>	<b>(Please put posters up as early as possible from 08:45)</b>
09:45	<b>Welcome</b>	<b>YSF team</b>
09:55	Holly Betts	Estimating a timescale for the Tree of Life: Is it time to leave behind a literal interpretation of the fossil record?
10:13	Steven Müller	Finding minimal clade specific orthologous gene sets within the Metazoa
10:31	Hanwen Zhang	On the difficulties of understanding Elephantid systematics from isolated teeth
10:49	Arn R. Jensen	Using modern systematics to explore an extinct rove beetle
11:07	<b>Coffee &amp; Posters (attend even numbers)</b>	<b>Attended posters (even numbers) should be presented by the author</b>
11:50	Marloes Tump	DNA barcoding of hyperiid amphipods along an Atlantic Meridional Transect
12:08	Marla Spencer	Taxonomy and biogeography of deep-sea peracarid crustaceans of the African continental margin
12:26	Adam G. Ciezarek	Substitutions in the glycogenin-1 gene are associated with the evolution of endothermy in sharks and tunas
12:44	Cecilie S. Svenningsen	Microbiomes across the Insecta (Heteroptera, Orthoptera & Odonata)
13:02	<b>Lunch and posters</b>	<b>(Light lunch provided for registered attendees)</b>
14:15	Kamil Hupała	Diversity and origin of freshwater gammarids from Crete and Peloponnese
14:33	Nikol Kmentová	Parasites of pelagic fishes in Lake Tanganyika: A marine phenomenon in a freshwater lake
14:51	Theodor S. Poettinger	Molecular phylogeny and the geographic origins of neotropical freshwater crabs of the family Pseudothelphusidae (Crustacea, Brachyura)
15:09	Christopher J. Owen	Changes in arctic freshwater prokaryotic diversity across a latitudinal gradient (56-83 <sub>o</sub> N)
15:27	<b>Coffee &amp; Posters (attend odd numbers)</b>	<b>Attended posters (odd numbers) should be presented by the author</b>
16:10	Mathilde Delaunay	How do people see biodiversity? The use of a digital identification key for a citizen science program
16:28	Robert Leigh	Using gene remodelling events to reconstruct the fungal tree of life
16:46	Charley McCarthy	Whole-genome phylogenetic analysis of the oomycetes using multiple supertree methods
17:04	Thais N.C. Vasconcelos	Phylogeny and biogeography of Myrteae (Myrtaceae)
17:22	<b>Poster session</b>	
18:00-19:00	<b>Reception</b>	<b>Presentation of prizes and closing remarks (please remove all posters before the reception)</b>

Organised by Dr Ellinor Michel, Dr Anne Jungblut and Dr Xavier Aubriot, with support from:



# TALK ABSTRACTS - LISTED IN SPEAKING ORDER

## Estimating a timescale for the Tree of Life: Is it time to leave behind a literal interpretation of the fossil record?

**Holly Betts**

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The timescale of life's early history on Earth remains one of the last areas where our understanding is guided by literal interpretations of the fossil record. However, more accurate estimates of divergence times can potentially be gained using molecular clocks. These rely on carefully constructed calibrations, the choice of which must be conservative, finding the oldest definitive member of a group. Here, we establish a suite of calibrations for some of life's fundamental divergences and use them to infer a holistic evolutionary timescale. Integrating across the uncertainties yields an imprecise timescale for life's history, but one that is more accurate than a timeline based on a literal interpretation of the fossil record. We establish a framework that can be updated as new fossil and molecular data are revealed. Our findings show the prokaryotic crown lineages appearing almost in parallel prior to 3 Ga, with crown Eukarya established around 1.8 Ga.

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## Finding minimal clade specific orthologous gene sets within the Metazoa

**Steven Müller**, Philipp H. Schiffer and Maximilian J. Telford

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Clade specific gene events may have influenced phenotype. We are interested in genes that are unique to certain clades within the Metazoa as an explanation of the evolution of these clades. Testing previously published bilaterian and deuterostome "core orthologous gene sets" by broader taxonomic sampling showed instances of false positives. To reduce the number of false-positives we establish a set of putative orthologous groups using three orthology prediction programs using 36 metazoan and 3 choanozoan species and merging the resulting groups. Taxon sampling bias was addressed with a check against the RefSeq database. Non-clade homologues that group within orthologous groups after alignment and gene tree reconstruction were discarded. Finally we rejected clade specific groups if any of the the closest non-clade homologues were associated with a clade member as reciprocal bi-directional best BLAST hits. We consider the remaining orthologous groups to be minimal clade specific "core orthologous gene sets".

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## On the difficulties of understanding Elephantid systematics from isolated teeth

**Hanwen Zhang**<sup>1,2</sup> and Adrian Lister<sup>2</sup>

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The Elephantidae has been the poster child for rapid evolutionary rate and phyletic morphological transitions in the established literature. However, most of their scientifically scrutinised fossil record is restricted to isolated molars, due to the low preservation potential of craniomandibular materials and comparatively un-diagnostic postcrania. Whereas different criteria of dental morphology such as lamellar number, hypsodonty index and enamel figure shape are informative of elephantid evolution, they have always been susceptible to a high degree of parallelism throughout the evolutionary history of the elephantids. Furthermore, a unique horizontal tooth replacement system, involving very large molars that are durable for long periods, creates considerable intraspecific variations in dental morphology, as a result of differences in wear stages and positions in tooth rows. This catalogue of caveats obscures phylogenetic signals to an extent that a robust cladistic analysis of elephant phylogeny remains to be achieved. Understanding the nature of dental homoplasies and sources of metrical errors will be crucial towards a modern, quantitatively testable understanding of elephantid evolution.

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# Using modern systematics to explore an extinct rove beetle

**Arn R. Jensen**

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The extinct *Cafius gigas* (Coleoptera, Staphylinidae), is a flightless and phylogenetically puzzling rove beetle from the subtribe Philonthina from Lord Howe Island, a remote tiny volcanic island with very interesting biogeography. Like several other endemics, *C. gigas* became extinct due to predatory pressure of the human introduced rats. Preliminary examination suggested that this species is not a member of the genus *Cafius*, but is closely related to *Hesperus dolichoderes*, another endemic species to the island. Morphology-based phylogenetic analysis confirmed the placement of *C. gigas* outside *Cafius* and inside the so-called 'Hesperus-complex' together with *H. dolichoderes*. The next step is a combined phylogenetic analysis with the complete morphological and molecular data for *H. dolichoderes* and morphology-only data for extinct *C. gigas*. Lastly we extracted ancient DNA in a non-destructive way from 130 years old *C. gigas* specimens that will be added to the analysis, if sequencing is successful.

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# DNA barcoding of hyperiid amphipods along an Atlantic Meridional Transect

**Marloes Tump**<sup>1</sup>, Alice K. Burrige<sup>1,2</sup>, Kevin Beentjes<sup>1</sup>, Ronald Vonk<sup>1,2</sup>, Erica Goetze<sup>3</sup> and Katja T.C.A. Peijnenburg<sup>1,2</sup>

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Hyperiid amphipods are an exclusively pelagic group of crustaceans that have close associations with gelatinous plankton. Numerous studies have focused on the morphological characteristics of hyperiid species, however little is known about their genetic diversity. We examined genetic diversity using DNA sequences of the mitochondrial cytochrome oxidase subunit I (COI) gene of hyperiids collected along a latitudinal transect from 34°N to 45°S in the Atlantic Ocean. In order to validate morphologically identified species, we collected COI sequences of 120 specimens representing 65 morphologically identified hyperiid species belonging to 35 genera. The mitochondrial gene tree was largely congruent with morphologically identified taxa, with three putative novel species. We also found phylogeographical patterns within species along the Atlantic transect that were congruent with distinct oceanographic provinces and differences in morphology. Although the COI barcode region showed too much variation to resolve higher level taxonomic arrangements, we found it a valuable marker for hyperiid species identification and discovery.

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# Taxonomy and biogeography of deep-sea peracarid crustaceans of the African continental margin

**Marla Spencer**<sup>1,2,3</sup>, Tammy Horton<sup>2</sup>, Andrew Gates<sup>2</sup>, Lawrence Hawkins<sup>1</sup>, Miranda Lowe<sup>3</sup> and Gordon Paterson<sup>3</sup>

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The biodiversity of the deep sea is poorly understood, yet human disturbance of this environment, e.g. from oil exploration, mineral extraction, is on the increase. Environmental impact Assessments (EIAs) are a legal requirement for companies exploiting marine resources and have generated substantial macro-faunal data and corresponding environmental data. EIAs samples from the African Continental Margin form the basis of my PhD data. The diversity and distribution of macro-faunal marine species vary spatially and temporally, with responses varying amongst faunal groups and habitats. These patterns are likely the result of both historical evolutionary influences and current environmental conditions, however, information on the relative importance and interactions of these drivers is limited. This work focuses on the peracarid component of the EIA samples, in particular one family of amphipods, the Phoxocephalidae for detailed work on the taxonomy and biogeography to better understand the differences in diversity on a regional basis. Peracarid crustaceans, including amphipods and isopods, are abundant in deep sea-floor sediment communities and have important nutrient recycling roles. Peracarids are subject to frequent cryptic speciation, so new peracarid species are regularly discovered, especially in deep waters. Consequently analyses are hampered by rare and undescribed taxa and inaccurate taxonomic identifications. In order to understand the distribution patterns and the phylogenetic relationships of this group, we must ascertain which species is which. My aim is to improve the taxonomy of these poorly known fauna, and in turn, advance the knowledge of global patterns of peracarids. Here we present results from an extensive survey of the benthic environment along the continental slope of the Angolan Margin.

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## Substitutions in the glycogenin-1 gene are associated with the evolution of endothermy in sharks and tunas

Adam G. Ciezarek<sup>1</sup>, Luke T. Dunning<sup>1,2</sup>, Catherine S. Jones<sup>3</sup>, Leslie R. Noble<sup>3</sup>, Emily Humble<sup>1,4</sup>, Sergio Stefanni<sup>5</sup> and Vincent Savolainen<sup>1</sup>

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Despite 400-450 million years of independent evolution, a strong phenotypic convergence has occurred between two groups of fish: tunas and lamnid sharks. This convergence is characterised by centralisation of red muscle, a distinctive swimming style (stiffened body powered through tail movements) and elevated body temperature (endothermy). Furthermore, both groups demonstrate elevated white muscle metabolic capacities. These traits are likely to have evolved to support their fast-swimming, pelagic, predatory behaviour. Here we tested the hypothesis that their convergent evolution was driven by selection on a set of metabolic genes. Using RNA-seq data from 26 shark and bony fish species, we constructed phylogenetic trees and carried out analyses of gene selection. We inferred several genes relating to metabolism to be under selection. We found that the same gene, glycogenin-1, evolved under positive selection independently in tunas and lamnid sharks, providing evidence of convergent selective pressures at gene level possibly underlying shared physiology.

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## Microbiomes across the Insecta (Heteroptera, Orthoptera & Odonata)

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Bacteria and insects are known to form complex symbioses, which has drastically shaped the evolution of both groups. Hemiptera have been studied thoroughly for bacterial symbiosis, but the origin of the diverse endosymbionts within the suborder Heteroptera has remained unclear. Through sequencing of bacterial 16S rRNA from the gut, eggs and body from species of the heteropteran infraorders Nepomorpha, Gerromorpha and Pentatomomorpha, as well as from Orthoptera and Odonata, the microbiota composition of the various insect species will be estimated. Bacteria and host phylogenies will be compared to elucidate how bacteria and their hosts may have evolved, and to provide clues to the origin and diversification of symbiotic associations.

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## Diversity and origin of freshwater gammarids from Crete and Peloponnese

Kamil Hupalo<sup>1</sup>, Tomasz Mamos<sup>1</sup>, Weronika Olszewska<sup>1</sup>, Marta Świdnicka<sup>1</sup>, Ioannis Karaouzas<sup>2</sup>, Wanda Plaiti<sup>3</sup> and Michał Grabowski<sup>1</sup>

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Islands are considered to be natural laboratories of evolution and the Mediterranean Region is one of the most precious biodiversity hotspots in the world. Given the high cryptic diversity discovered recently in European gammarids and scarcity of studies upon insular species, we conclude that number of species already reported is underestimated. Our main goal is to reveal the diversity, phylogeny and origin of freshwater gammarids inhabiting Crete and Peloponnese. We have revealed presence of five freshwater species on Crete. Four of them could be identified as *Echinogammarus* species already known from Crete and one being a species new for science and belonging to *Gammarus*, genus that has not been yet described from Cretean freshwaters. Additionally, we revealed presence of ten freshwater species of *Gammarus* on Peloponnese. Several both mitochondrial and nuclear markers were used for the time-calibrated phylogeny reconstruction to reveal the origin of freshwater gammarids inhabiting Crete and Peloponnese.

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## Parasites of pelagic fishes in Lake Tanganyika: A marine phenomenon in a freshwater lake

**Nikol Kmentová**<sup>1\*</sup>, Maarten Van Steenberge<sup>2</sup>, Joost Raeymaekers<sup>3</sup>, Stephan Koblmüller<sup>4</sup>, Pascal Hablützel<sup>3</sup>, Fidel M. Bukinga<sup>5</sup>, Theophile M. N'sibula<sup>5</sup>, Pascal M. Mulungula<sup>5</sup>, Milan Gelnar<sup>1</sup> and Maarten Vanhove<sup>1,2,3,6</sup>

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Lake Tanganyika, the biggest freshwater ecosystem in Africa, is famous for its species richness. While the global diversity of parasites is assumed to be impressive, only some parasite species have been described in the lake to date including 28 mostly specialist monogenean species, mainly from the littoral. But have monogeneans also specialised to the hosts inhabiting the pelagic zone? We examined 14 pelagic fish species including cichlids, clupeids and latids. Samples originated from localities including all three subbasins of the lake. Parasites were analysed using morphometric, geomorphometric, phylogeographic and phylogenetic approaches. The analyses revealed a lower monogenean host specificity (compared to the littoral) in all examined fish families. Reported parasite species belong to two families (Dactylogyridae, Diplectanidae). The results correspond with previous studies performed in marine systems suggesting a broader parasite host range in the pelagic habitat. They also indicate some typically marine parasites adapted to freshwater environments.

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## Molecular phylogeny and the geographic origins of neotropical freshwater crabs of the family Pseudothelphusidae (Crustacea, Brachyura)

**Theodor S. Poettinger**<sup>1</sup>, Sebastian Klaus<sup>2,3</sup> and Christoph D. Schubart<sup>1</sup>

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The historical biogeography of Neotropical freshwater systems received much attention during the last decades. The phylogenetic patterns of freshwater crabs are considered good biogeographic indicators as they often reflect the palaeogeographic or palaeoenvironmental history of their range. However, the phylogenies of the two Neotropical freshwater crab families Trichodactylidae and Pseudothelphusidae were not approached from a molecular perspective so far. The Neotropical Pseudothelphusidae are distributed from Mexico in the north to the southern tributaries of the Amazon, also occurring on the Greater Antilles (Cuba, Hispaniola, Puerto Rico; excluding Jamaica) and on the Lesser Antilles. Lacking a robust phylogeny, only scarce knowledge of pseudothelphusid origins and range evolution is available. We present the first molecular phylogeny of the Pseudothelphusidae, with the aim of (a) evaluating the different morphology-based phylogenetic hypotheses of the family's relationship, and (b) testing the corresponding biogeographical scenarios against a time-calibrated phylogeny. The taxonomic system of Rodríguez, i.e. the recognition of two subfamilies Epilobocerinae on the Greater Antilles and the Pseudothelphusinae on the mainland is mostly supported by the present molecular phylogeny. Also the biogeographic scenario for pseudothelphusid range evolution as proposed by the present data is close to the hypothesis put forward by Rodríguez. In contrast, the system of Bott has to be rejected.

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# Changes in arctic freshwater prokaryotic diversity across a latitudinal gradient (56-83°N)

**Christopher J. Owen**<sup>1,2</sup>, **Connie Lovejoy**<sup>3</sup>, **Warwick F. Vincent**<sup>3</sup> and **Anne D. Jungblut**<sup>2</sup>

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Benthic microbial mat communities dominate the biodiversity of freshwater habitats in the Polar Regions. Few biogeographical patterns have been identified for Polar freshwater microorganisms past the Baas-Becking hypothesis that "everything is everywhere, but the environment selects"; overall, little is still known about latitudinal diversity gradients (LDG) in microbial biodiversity. We therefore carried out the first high-throughput small-subunit 16S rRNA environmental gene survey of Bacteria and Archaea in freshwater microbial mats from the Sub- to High Arctic (56-83°N) to describe communities and evaluate biogeographical patterns. Our work showed a significant inverse relationship between latitude and species richness and suggests the presence of a LDG in Arctic freshwater benthic microbial communities. Temperature trends best explained the relationship, supporting the physiological-tolerance hypothesis that invokes climate-dictated limits on metabolic kinetics. Monitoring of changes in species assemblages in the Arctic microbial LDG may prove valuable in tracking climate-driven change in these unique freshwater ecosystems.

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# How do people see biodiversity? The use of a digital identification key for a citizen science program

**Mathilde Delaunay**, Régine Vignes-Lebbe and Romain Nattier

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"Spipoll" is a French citizen science program about pollination. To assist the volunteers, a multi-access identification key is available on the Spipoll website. The pictures, identifications and series of steps followed by the participants have been recorded since September 2015. These data allow to study the behaviour of the citizens when they observe an insect, and to deduce the taxonomic confusion and the misunderstanding of character states. The identification paths give elements on how the entomofauna diversity is perceived. Which morphological traits are chosen most frequently? Are the most noticeable characters selected to the detriment of those which need advanced entomological skills? Here we show that some morphological parts are perceived more easily than others, and that people are sensitive to the quality of character descriptions in the keys. These elements must be taken in account in order to improve identification tools, in particular those used by the general public.

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# Using gene remodelling events to reconstruct the fungal tree of life

**Robert Leigh**

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Gene remodeling is the biological process of genetic rearrangement that may result in the formation of novel protein coding genes. Gene remodeling may occur due to point mutations, chromosomal rearrangement or mosaic events. Genetic mosaicism describes a gene remodeling event where two or more protein coding genes may undergo a fusion event to form a composite protein-coding gene, or undergo a fission event leading to one or more independent protein coding genes. By assessing mosaicism in phylogenetic relationships, protein association networks, gene neofunctionalisation and distribution patterns we can hypothesize evolutionary pressures behind these events and how these events may have conferred advantages to their host. We have investigated the degree of mosaicism across 113 taxa from the Fungal Kingdom. Our analyses show high rates of gene remodeling amongst these species. Using mosaic genes as phylogenetic markers we have uncovered the established species phylogeny within fungi. We are currently investigating the biological significance of mosaic families and uncovering their evolutionary significance.

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# Whole-genome phylogenetic analysis of the oomycetes using multiple supertree methods

**Charley McCarthy** and David Fitzpatrick

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The oomycetes are a class of microscopic, filamentous eukaryotes within the Stramenopiles-Alveolate-Rhizaria (SAR) supergroup which includes ecologically significant animal and plant pathogens, most famously *Phytophthora infestans*. Single-gene and concatenated phylogenetic studies of both individual genera and the larger class have drawn conflicting conclusions for species phylogenies within the oomycetes. Supertree phylogenies combine large numbers of potentially disparate trees to determine evolutionary relationships that cannot be inferred from individual phylogenies alone, and have had successful application in many large-scale eukaryotic phylogenetic analyses. With a sufficient amount of genomic data now publically available, we have undertaken the first whole-genome phylogenetic analysis of the oomycetes using data from 39 species. In our analysis, we have used both established and cutting-edge methods to generate supertree phylogenies from ubiquitous, orthologous and paralogous gene families. We compare the results of our different phylogenetic methods and their resolution of the evolutionary relationships within the oomycetes.

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## Phylogeny and Biogeography of Myrteae (Myrtaceae)

**Thais N.C. Vasconcelos**<sup>1,2</sup>, Gerhard Prenner<sup>1</sup>, Astrid Wingler<sup>2,3</sup> and Eve J. Lucas<sup>1</sup>

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Myrteae is the largest tribe of Myrtaceae and one of the most ecologically important groups of Angiosperms in the Neotropics containing several large, cryptic genera. A robust phylogenetic hypothesis was reconstructed by this study, towards conclusive systematics and evolutionary understanding of the tribe. Dates of diversification events were estimated using a selection of fossil calibrations and the subsequent topology was analysed for biogeographical patterns. Results present strong statistical support for ten clades, one exclusively Australasian sister to nine mostly Neotropical ones. Biogeographic patterns show early divergence events of Myrteae occurring in Zealandia with colonization to the Neotropics happening just once, likely via an Antarctica bridge, in the middle Eocene. Results provide systematic background and emphasize the importance of high latitudes in the evolutionary history of a current mainly tropical lineage.

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# POSTER ABSTRACTS - LISTED IN ALPHABETICAL ORDER

1

## An online updated checklist of The Farasan Archipelago Flora

**Rahmah AlQthanin** and Alastair Culham

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The Farasan islands flora comprises approximately 10% of Saudi Arabia plant species. These Islands have a number of threats to plant biodiversity and the Farasan islands flora now seriously out of date, following the enormous amount of research on the Islands flora generally, and the large realignments of higher level classification as a result of the APGIV, 2016. This study presents an electronic updated Checklist flora of the Farasan islands follows current taxonomic trend and including their geographical distribution at islands level. The Checklist includes a total of 250 taxa belonging to 146 genera in 50 families. Six Families have become synonyms of other families. Four families are now new names for the Farasan Archipelago. In addition 48 Species that have been updated to new accepted names and the plant checklist recommends updates to the generic circumscription of several genera in the Farasan Islands flora.

2

## PCR-based evidence for the presence of dicot rDNA in a monocot plant genome: Implications for a horizontal gene transfer?

**László Bartha**<sup>1</sup>, Terezie Mandáková<sup>2</sup>, Horia L. Banciu<sup>1</sup>, Lujza Keresztes<sup>1</sup>, Martin A. Lysak<sup>2</sup> and Aleš Kovařík<sup>3</sup>

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Horizontal gene transfer (HGT) has been extensively documented among different types of living organisms; however, examples of HGT of ribosomal DNA (rDNA) are rare. In eukaryotes, the single case of HGT of rDNA so far has been documented in microorganisms. Here we report the consistent PCR amplification of a dicot type internal transcribed spacer (ITS, part of rDNA) from the genome of the monocot plant *Erythronium dens-canis*, originating from specific populations. The research was repeated in different laboratories using different plant parts as the source material. Quantitative PCR experiments revealed that there were approx. 1,000 times less dicot than monocot ITS copies in the *Erythronium* genome, whereas for RNA/cDNA sequences this ratio was several tens of thousands times lower. Cloning and sequencing showed that the dicot ITS type of *E. dens-canis* was similar to the ITS of *Potentilla*, thus revealing a potential candidate donor genus of HGT of rDNA. The results open up new avenues for studies of HGT from dicots to monocots at the level of rDNA. This study was supported by a grant of the Babes-Bolyai University, project number GTC-31778-2016.

3

## Constraining the timing of whole genome duplication in the plant kingdom

**James W. Clark** and Philip C.J. Donoghue

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Whole genome duplication (WGD) has occurred in many lineages within the tree of life and invariably invoked as causal to evolutionary innovation, increased diversity, and extinction resistance. Testing such hypotheses is problematic, not least since the timing of WGD events has proven hard to constrain. Here we show that WGD events can be dated through molecular clock analysis of gene trees, calibrated using fossil evidence for the ages of species divergences that bracket WGD events. We apply this approach to dating the two major genome duplication events shared by all seed plants ( $\zeta$ ) and flowering plants ( $\epsilon$ ), estimating the seed plant WGD event at 408-377 Ma, and the angiosperm WGD event at 325-282 Ma. These events thus took place early in the stem of both lineages, precluding hypotheses of WGD conferring extinction resistance, driving dramatic increases in innovation and diversity, but corroborating and qualifying the more permissive hypothesis of a 'lag-time' in realising the effects of WGD in plant evolution.



## Phylogenetics of *Sus strozzi* and *Sus minor*: Confirming a long debated hypothesis and comments on *Sus* taxonomy

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*Sus* is the most-species rich genus in the family Suidae, and is currently divided into the '*scrofa*' group, with *Sus scrofa* as its only member, and the '*verrucosus*' group, which includes species from South-east Asia. This division is mainly due to morphological differences, but recent molecular studies confirm the monophyly of both groups. *Sus minor* and *Sus strozzi* are two extinct European species. Taxonomists noted closer affinities between these two species and the *verrucosus* group, but a phylogenetic relationship has never been tested using cladistic methods. In this study we obtained data from the literature and collected new characters from museum specimens, and demonstrate for the first time that *S. strozzi* and *S. minor* are nested within the *verrucosus* clade. Furthermore, we show that the main character (i.e. the morphology of lower canine) used by some authors to distinguish the *scrofa* and *verrucosus* groups does not carry phylogenetic signal.

## The branchial skeleton in stem-chondrichthyans: An insight into the earliest evolution of jawed vertebrates

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Consensus is building that the "acanthodian" fishes - long a source of contention amongst early vertebrate systematists - are in fact some of the very earliest relatives of living chondrichthyans (sharks, rays, chimaeras, and their kin). This places them in a systematically pivotal position for establishing how jawed vertebrates evolved morphological novelties such as teeth, jaws and paired fins. However their anatomy remains poorly understood, in particular that of their endoskeleton, a potentially rich source of morphological characters for phylogenetic analysis. Here we present novel information on the branchial endoskeleton of two stemchondrichthyans from the Devonian of the UK: the "acanthodians" *Diplacanthus* and *Ptomacanthus*. These data provide new information on the morphology of the branchial skeletons of other early vertebrates, reveal potential characters for future phylogenetic work, and challenge recent interpretations of the ancestral condition of the chondrichthyan branchial skeleton.

## Systematics, diversity and historical biogeography of neotropical synandrous mimosoids – the Ingeae tribe

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The delimitation of the legume tribe Ingeae, often referred to as synandrous (stamen filaments fused) mimosoids, have long been in a state of flux, with many segregate genera being proposed and/or merged with other genera. This study intends to investigate selected ingoid genera (*Cojoba*, *Punjuba*, *Zygia/Marmaroxylon* and *Zapoteca*) with questionable taxonomic status in relation to other genera in the tribe. The project is divided into several parts working at different taxonomical levels, exploring the phylogeny and taxonomy using both morphological and molecular data. With the phylogenetic hypothesis as a basis, the aim is to provide a classification as well as species and subspecies delimitations that reflect the evolutionary history of the group. The project also aims at exploring the historical biogeography of these species, mainly distributed in the West Indies, Mexico together with Central America, and South America, as well as the evolution of morphological structures and cues.

## An origin of sight: What the Tardigrada can tell us about the evolution of vision

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Photoreception is a sensory system utilised by individuals across Metazoa to interpret their surroundings. Colour vision, however, has only evolved twice - once in the Arthropoda, and once in the Vertebrata. The reason for this radical shift in the interpretation of light is unknown, but studying closely related clades can help to elucidate the reasons, process and timing behind this change. Tardigrada are a phylum of the Ecdysozoa well-known for their resilience - they have colonised freshwater, marine and terrestrial environments, and can survive high levels of radiation and vacuum exposure. However, our understanding of their visual capabilities is limited to one species - *Hypsibius dujardini*. Here, we present new opsins - visual proteins - from 4 tardigrade species, many of which previously lacked any molecular representation. Additional sampling paints a much more complicated picture of the history of tardigrade photoreception, and the history of ecdysozoan vision, than previously thought.

## Addition of poorly studied taxa elucidate Ecdysozoan tree of life

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Ecdysozoa is a clade of molting invertebrate animals composed of eight phyla: Arthropoda, Onychophora and Tardigrada (Panarthropoda); Nematoda, Nematomorpha, Priapulida, Kinorhyncha and Loricifera (Cycloneuralia). This systematic hypothesis has superseded the traditional view of protostome evolution, the Articulata concept, which allied panarthropods and annelids given their segmented body plan. Whilst the monophyly of Ecdysozoa has received strong support from morphological and molecular evidence, its internal relationships are still contended, in particular the phylogenetic position of Tardigrada and the relationships among Cycloneuralian phyla. In this study we improved the taxonomic sample for key clades with poor or no molecular data (Loricifera, Nematomorpha and Eutardigrada). Our preliminary phylogenetic analyses under the best-fitting amino acid model recover the monophyly of Panarthropoda, with Tardigrada sister group of Onychophora + Arthropoda. In addition this work supports Scalidophora, a clade formed by Kinorhyncha, Priapulida, Loricifera and Nematoida (Nematoda plus Nematomorpha), with the latter being sister of panarthropods.

## What can flower anatomy and inflorescence development tell us about the Neotropical hyper-diverse genus *Eugenia* subg. *Calycorectes* (O.Berg) Mattos?

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Floral morphology and anatomy are here examined to diagnose the clades and potential drivers of speciation of *Eugenia* L. (Myrtaceae), a large Neotropical genus (> 1000 species). Preliminary analyses show *Eugenia* comprises eight clades. This study focuses on *Eugenia* subg. *Calycorectes*, a clade of trees or shrubs from northwest and southeast South America. This group is distinguished by the fused calyx in bud but it is not clear that this group is monophyletic or if this character is homologous. A molecular phylogeny based on five DNA regions (one nuclear; four plastid) suggests the fused calyx has arisen at least twice in *Eugenia*. *Eugenia* subg. *Calycorectes* must be re-diagnosed; a clade with similar morphology, arising in the Brazilian Atlantic forest has arisen independently. Improved taxonomic resolution of large genera such as *Eugenia* is critical to manage the biomes in which they are found and to understand Neotropical diversification.

## A revision of the genus *Cheliplana* (Rhabdocoela, Schizorhynchia), with the description of five new species

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With more than 30 species occurring worldwide, the genus *Cheliplana* de Beauchamp, 1927 is one of the most species rich genera in the turbellarian taxon Schizorhynchia Meixner, 1928. Here we present a comprehensive revision of the genus. Five species new to science are described. The new species are chiefly distinguished from each other and from any known representative of *Cheliplana* by the organization of the reproductive system and the structure of the sclerotized parts of the reproductive system. Furthermore, *Cheliplana devorticula* Ax, 2008 is synonymized with *C. triductibus* Van Steenkiste, 2008. Moreover, the two subspecies of *Cheliplana asica* Marcus, 1952, *C. a. asica* and *C. a. terminalis*, are elevated to species level. We also provide an identification key to all members of the genus, based on morphological characters, which are easily assessed in the field.

## The intertidal foraminifer *Trochammina inflata* with a distinct morphotype in the White Sea, Russian Arctic: a local variety or new species?

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The cosmopolitan intertidal foraminifer *Trochammina inflata* (Montagu) is extensively used in both paleoenvironmental reconstructions and ecological surveys of salt-marsh foraminifera, and therefore it needs correct identification. Images published over years depict differences in test shape, umbilicus features, incurvation of sutures, and number of chambers in the last whorl. For instance, Montagu (1808) described a 5-chambered specimen; revised description of Williamson (1858) as well as the neotype description (Brönnimann & Whittaker, 1984) reported 6 chambers. Recent White Sea specimens — 7-chambered, otherwise similar — inspired Mayer (1962) to propose a new subspecies “*Trochammina inflata* (Montagu) subsp. n.?”, but this work was not finalised. Recently collected White Sea specimens of *T. inflata* perfectly fit to Mayer’s description. It raises the question whether it is possible to distinguish a new (sub)species based on the number of chambers or we are dealing with a local morph of *T. inflata*.

## The genomics of parallel adaptation in Macaronesian *Echium* (Boraginaceae)

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The 29 species of *Echium* endemic to Macaronesia display diverse morphology and ecology, making this plant radiation a great model system for studying island evolution and ecological adaptation. Three *Echium* species are restricted to the sub-alpine zones on Tenerife and La Palma. Their contrasting morphologies suggest multiple independent shifts to the sub-alpine zone have occurred, however relationships in the group are unclear as previous phylogenies have suffered from incongruence and poor resolution. This project aims to address the question: how was the sub-alpine zone colonized by *Echium*? To investigate this, next-generation sequencing is being used to establish phylogenetic relationships with which to infer geographic and temporal patterns of evolution. Transcriptomic data will be used to identify loci with signatures of divergent selection and expression between sister species with temperature-divergent niches. Comparison of these species pairs will reveal whether similar genetic mechanisms are involved in independent shifts to the sub-alpine zone.

## I wanna be like you: The prevalence of molecular convergence in closely related organisms

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The closest thing we currently have to 'laws of convergence' is a generally accepted assumption that homoplasy is less prevalent in molecular than morphological data, and that homoplasy is more common among organisms that are closely related. This study aims to test and formalise these concepts by comparing molecular data from organisms across the tree of life. Data types tested include nucleotide and amino acid sequences as well as protein families and presence-absence data for protein domains. Previous work using the same method of analysis on morphological data has demonstrated that morphological convergence is more likely to occur among more closely related organisms. Preliminary results from this study suggest that not only is homoplasy prevalent in molecular data, similar patterns of convergence can be seen in molecular as in morphological data. In particular, homoplasy of protein domains within Metazoa is more likely to be observed among more closely related taxa.

## Confusion by cryptic genera: When the same is not same

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Cyanobacteria are admirable and notable organisms; they have existed on the Earth for billions years, surviving severe global ice ages, the impacts of meteorites and times of drought. Nowadays, they occupy the most extreme environments on the planet such as hot springs, deserts, arctic areas etc. Although they possess a relatively high degree of morphological variability compared to other prokaryotes, there are still significant gaps in our knowledge of cyanobacterial diversity, which is unexplored and often overlooked especially in tropical areas. Traditionally, cyanobacteria were classified based only on morphological characters, but recent research demonstrates an abundance of cryptic diversity evidenced by molecular analyses, e.g. 16S rRNA gene and whole genome phylogeny. Here, we present novel, filamentous, tropical cyanobacteria described using polyphasic approach. They were named: *Pinocchia* from lake in rain forest from Vietnam, *Elainella* from temporary waterbody in the forest from Vietnam and *Onodrimia* from hot water spring from Java.

## Identification of highly divergent small fragment of 12S and 16S rRNA genes in large felids: A practice in wildlife forensics

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Significance of using small amplicon with higher sequence variations or having fixed-state single nucleotide polymorphism (SNP) has a great potential in the field of conservation genetics and wildlife forensic. Because sample available (bones, claws, hair, scat, and tanned skins etc.) for use have failed to amplify the large size amplicon because that extracted DNA from varied parts/product of animals is in degraded form. Defining species boundary from such samples using the short fragment of any mitochondrial genes is challenge because it requires to target on level of variation and is little known on literature. In the wildlife forensic, large proportion of samples lost their morphology and required to identify through DNA based technology. Hence present study is aimed to identify highly divergent small fragment of 12S and 16S rRNA and assess its applicability in seven tanned-skins of leopard (*Panthera pardus*) which were seized under a wildlife offence. Though skins were of leopard but enforcement agencies have requested to confirm that these skins are of only leopard. Therefore we identify these skins using two universal primers of 12S 384bp & 16S rRNA (550bp) of mitochondrial genome and compare the level of species assignment using highly divergent (possess high number of polymorphic sites) fragment of 100 bp sequences selected from both genes. With the four applied computational methods (distance, character, topology, SNP) character attribute (CA) found helpful to identify species in the 16S rRNA. Whereas genetic variability in each 20 bp region of both 12S and 16S rRNA genes help to identify single nucleotide polymorphisms (SNP) in the amplified region. Comparing all these fragments, one best resolving 100 bp was selected which have required information to identify the species. Distance based (% sequence divergence) and topology also have the power to discriminate at species level using highly divergent of 100 bp region and found higher resolution power if compared with complete amplified regions of both genes.

## Insect response to environmental perturbation during the Upper Triassic and Lower Jurassic

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Several large-scale perturbations to the climate system have been proposed for the Upper Triassic and Lower Jurassic (Tr/J) including the end Triassic extinction (ETE). The intensity, longevity and even the occurrence of these events is still hotly debated. Abundant and highly diverse collections of fossil insects exist from throughout this period but they are often forgotten or deemed unimportant. But if developed taxonomically and stratigraphically they could provide an important dataset recording terrestrial diversity change throughout the Upper Triassic on a global scale. The current project aims to take a subset of this dataset to assess the impact of the ETE. Previous studies have not found dramatic changes in insect diversity at the ETE but they were based on unrevised taxonomy at family level. We provide updated taxonomy to species level for fossils from key localities around the ETE to better assess the impact of this event on insects.

## Pancrustacean phylogeny and the colonization of land by hexapods

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Animal life has marine origins, and early on Palaeozoic hexapods already have colonized land, giving origin to the largest animal clade. To identify how hexapods adapted to this new environment there is a need to robustly identify its aquatic sister group, and depending on the habitat (freshwater or marine), different inferences could be made. Molecular and morphological data supports a placement of hexapods within Crustacea, the Pancrustacea concept. Two main hypotheses rivaling regarding the specific sister group of Hexapoda, first suggests freshwater branchiopods and the second favours the marine cave-dwelling remipedes (and sometimes Cephalocarida). We used an expanded multigene dataset (>250 genes and >100 taxa), covering all pancrustacean main clades. Our preliminary results are still conflicting regarding the sister group of hexapods, either obtaining remipedes or branchiopods depending on parameters, although consistently recovers an alliance between Hexapoda, Branchiopoda, Remipedia and Cephalocarida. More species coverage is needed to robustly assess these relationships.

## Do proteins “know” anything about speciation? A lesson from littorinids (Mollusca: Caenogastropoda)

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We assessed evolutionary informativeness of proteomic data using 10 littorinid species from several geographic locations. The tree based on proteomes dissimilarities was compared with consensus molecular tree. Both trees were similar in shape, with interspecific differences being stronger than among locations. There were several minor inconsistencies between the trees. (1) The genetically distant species appeared relatively closer in the proteomic than genetic tree. This might be interpreted as proteomic homoplasy due to biotope sharing. (2) Proteomic distances were greater for close relatives, living in sympatry. This may reflect ecological divergence due to adaptation of species to their microhabitats, when ecology driven proteome specialization significantly “outruns” neutral genomic markers. Proteomics is less informative for inter-genera comparisons, because too many proteins are changed yielding poor grouping of the genera. Finally, the complementation of proteomic and genomic data can bring additional information with regard to closely related species, where proteomics has higher resolution.

## Multilocus phylogeography reveal rapid parallel morphological divergence in reed buntings *Emberiza scheniclus*

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In order to understand how the Pleistocene glacial cycles influenced the morphological diversification of Reed Buntings, we conducted a phylogeographic study by sequencing one mtDNA and two nuclear introns of birds from 32 breeding populations covering the species range. Two major clades that diverged in the mid Pleistocene and are segregated into East and West Eurasia were uncovered. Both clades showed signs of postglacial population expansion, but the Eastern populations had greater divergence between sub-populations than the western clade, which was more genetically homogeneous. Results strongly suggest the past existence of one glacial refugium in the west and two to three glacial refugia in the east. Our findings show that the neutral genetic variability does not correspond to the large number of described subspecies, and indicate that morphological divergence has occurred very rapidly, during the postglacial expansion, with some traits, in particular bill size and shape, probably evolving multiple times from different refugia.

## Integrated monography of the genus *Saxifraga* L. as a window on the evolution of the European Alpine flora

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Mountains can harbour high and unique plant diversity, but in spite of long standing scientific interest the fundamental principles responsible for the diverse mountain biota are not fully understood. This project aims to use the species-rich, predominantly alpine genus *Saxifraga* L. (ca. 440 spp.) as a model to elucidate the eco-evolutionary assembly of mountain floras, with emphasis on the European Alps. We are assembling a high-resolution phylogenetic tree of *Saxifraga* and to this end use next generation sequencing ("HybSeq") to obtain genome-wide data to overcome problems due to a lack of genetic variation among recently diverged species. Through the resulting phylogeny we will infer historic dispersal events and radiations, and the role of habitat- and trait evolution therein. Furthermore, many *Saxifraga* taxa are narrow endemics in sensitive alpine habitats. Our study also aims to unveil to what extent species diversity and functional diversity are at risk due to global climate change.

## Assessing species boundaries in the open sea: Applying an integrative taxonomic approach to *Diacavolinia* pteropods

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To track changes in pelagic biodiversity in response to ocean change, it is essential to accurately define species boundaries. This can be achieved by an integrative taxonomic approach in which species are described not only based on morphological, but also on molecular, behavioral, ecological and/or geographic characteristics. A particularly suitable, yet challenging, group for integrative taxonomy is the holoplanktonic, shelled pteropod genus *Diacavolinia*. Numerous samples are available in museum collections and their shell shapes enable detailed geometric morphometric analyses. Although 24 morphological *Diacavolinia* taxa have been described, specimens are usually not identified below genus level. We designed an objective method for identifying species boundaries in *Diacavolinia* pteropods by linking incomplete and different datasets, including museum type specimens. We applied an integrative species concept based on congruence between Cytochrome Oxidase I and 28S sequence data, geometric morphometric analyses of shells, and geographic data to a total of 969 specimens and found evidence for reducing the number of species from 24 to 11 or 13 species. In the Atlantic Ocean the number of species should be reduced from seven to two species. In the Indo-Pacific we found at least nine species, comprising at least 13 of the originally described taxa. The most important biogeographic barriers were between the Atlantic and Indian oceans, between the East and Central Pacific, and between the Red Sea and Indian Ocean. Biogeographic distributions of revised *Diacavolinia* species were as follows: Atlantic (2 endemic species), South African waters (1 endemic species), Western Indian Ocean (4 species), Red Sea and Gulf of Aden (3 species), Indo-Polynesian (6 species, 1 endemic), Hawaiian waters (3 species, 1 endemic), Sino-Japanese waters (3 species), and East Pacific (3 endemic species). Given the high levels of genetic and phenotypic diversity found among *Diacavolinia* taxa, it is unlikely that different taxa will respond in the same way to future ocean changes.



## Insights into cichlid population history using whole genome data and bayesian computation

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Cichlids have contributed much to our understanding of evolutionary biology, demonstrating processes such as adaptive radiation, sexual selection, and speciation. This study is examining the population history of cichlids belonging to the genus *Astatotilapia* from crater lakes located in southern Tanzania. This interest stems from a case of ongoing sympatric divergence occurring in two ecomorphs in one of these crater lakes; Lake Massoko. Single nucleotide polymorphism (SNP) data used here is from whole-genomes sequenced in a previous study. Combined with demographic models and coalescence-based simulations in a framework of approximate Bayesian computation (ABC), this data is used to provide inferences into population history. Results are consistent with ongoing migration between Lake Massoko and the surrounding rivers. The nature of the migration rate between the two populations also appears to be skewed, with a larger flow of migrants originating from Lake Massoko and entering the surrounding rivers.

## Endorsing Darwin: Global biogeography of the epipelagic goose barnacles *Lepas* spp. (Cirripedia, Lepadomorpha) proves cryptic speciation

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Biogeographic compartmentation is known from marine species, but data from globally occurring species remains scarce. Already Darwin noted the large intraspecific diversity of the epipelagic rafting goose barnacle *Lepas* and speculated about distinct regional varieties. We analysed divergence within the globally occurring *Lepas* species using molecular phylogenetics. In *Lepas australis* we found genetically separate populations from coastal Chile and from circum-Antarctic waters. *Lepas anatifera* displays four distinct regional populations, and a global population which might be an ancestral stem-group. The differentiation reflects vicariance effects rooted in geological history: Neogene closure of the circum-equatorial Tethys in the Middle East and at the Panama Isthmus, installation of the cool Benguela Current, differing Pleistocene currents and temperatures, and modern current systems. The extreme ecological generalists *L. anatifera* and *L. pectinata* are not differentiated and might represent true global species. In conclusion, compartmentation of the oceans acts on species level according to ecospace limits.

## Constraining the timing of annelid terrestrialisation using phylogenomics and molecular clocks

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Annelid worms are diverse invertebrate phylum representing major components of nearly all ecosystems, from deep-sea hydrothermal vents to terrestrial soils. The terrestrialised annelids include earthworms and leeches and form the class Clitellata. Terrestrialisation is a major macroevolutionary transition, with plant, fungal and metazoan groups leaving their ancestral marine environments to become established on land. In the context of understanding the shift of complex ecosystems from marine to freshwater and continental environments, clitellate annelids (and in particular, earthworms) provide insight since the timing of their origins have bearings on the development of co-dependents and co-evolving lineages. Here we use a novel molecular dataset (58 taxa, 197 genes, ~40,000 amino acids) to investigate the timing of annelid terrestrialisation. We recover divergence times for earthworms in the late Carboniferous or early Permian, significantly more recent than previously thought. We suggest that earthworms coevolved with rooting systems of plants and their symbionts, and that this led to global ecological and geological change.



# MEETING POLICIES

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

## **Photography and Social Media Policy**

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

## **Anti-Harassment Policy**

To our knowledge, the Systematics Association has had no experience of harassment at any of their meetings to date, and we are not anticipating a change in this. Nonetheless, we wish to be proactive in ensuring that we make sure that we provide a welcoming environment for all and if any problems occur that attendees are supported appropriately. Behaviour and language that are acceptable to one person may be unwelcome and/or offensive to another. We will not tolerate harassment of conference participants in any form. Sexist language and potentially offensive human sexual imagery is not appropriate in a conference venue, including talks and posters. Any unwelcome conduct, verbal or physical, including when based on an individual's race, colour, gender, national origin, religion, age, disability, sexual orientation, status as a parent, gender identity, or physical appearance, should be reported to Ellinor Michel, Xavier Aubriot or Anne Jungblut 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.