

16TH YOUNG SYSTEMATISTS' FORUM

21st November 2014, Flett Theatre, Natural History Museum, London, UK

Programme

09.00	Registration	
09.30	Welcome	Ellinor Michel (NHM)
09.35	Opening comments	Robert Scotland, President of the Systematics Association
09.50	Jose Barba-Montoya	Angiosperm divergence times: A phylogenetic analysis of genome-scale data sets
10.10	Steven Dodsworth	Using genomic 'rubbish': Repeat abundances contain phylogenetic signal
10.30	Ivana Piližota	Fast inference of homologs and their application to identifying split genes in low-quality genomes
10.50	Jacqueline Heckenhauer	DNA barcoding and community structure assessment in a tropical forest: a 25 ha mixed dipterocarp forest at Kuala Belalong Brunei Darussalam as a model
11.10	Coffee and attended posters (even numbers)	Attended posters should be presented by the author
11.40	Ladislav Hodac	Cryptic sexuality and stress response in asexual plants: A case study on <i>Ranunculus carpaticola</i> clones based on microsatellite data
12.00	Hibbah Auf	Evolution of tandem repeats in chromosomally extremely variable <i>Prospero autumnale</i> complex (Hyacinthaceae)
12.20	Mariana de Oliveira Büniger	Systematics of <i>Eugenia</i> sect. <i>Phyllocalyx</i> (Myrtaceae)
12.40	Isuru Kariyawasam	Classical plant taxonomy complementing molecular phylogenetics: A taxonomic revision of <i>Oligotrichum</i> DC. in Lam & DC. (Polytrichaceae) in the Sino-Himalaya
13.00	Lunch and poster session	(Light lunch provided for registered attendees)
14.00	Peter Moonlight	Is <i>Begonia</i> an adaptive radiation? The ecology of diversification in a mega-diverse genus
14.20	Deniz Aygoren Uluer	Resolving intrafamilial relationships: how to build a robust phylogeny of the Angiosperms
14.40	David Pattinson	Phylogeny, paleontology, and primates: Do incomplete fossils bias the Tree of Life?
15.00	Andrew Helmstetter	Repeated evolution of viviparity greatly increases diversification rates in the order Cyprinodontiformes
15.20	Coffee and attended posters (odd numbers)	
15.50	Daniel Marquina	Internal anatomy and molecular data support the colour-based identifications in polyclad flatworms
16.10	László Zsalakovics	Relation between <i>Orbellis</i> and some <i>Neolethaeus</i> species (Heteroptera: Lygaeoidea: Rhyparochromidae)
16.30	Alastair Tanner	A phylogenomic approach to cephalopod evolutionary history
16.50	Luke Parry	Reconstructing the ancestral annelid: Reconciling fossils, morphology and molecules
17.10	David Attenborough Field Award	Flash Talk by recipient David Kipling
17.20	Closing comments / presentation of prizes	Robert Scotland & Ellinor Michel
17.35-	Wine reception and	
19.00	Posters	

Organized by **Ellinor Michel** (NHM), **Xavier Aubriot** (NHM), **Ross Mounce** (University of Bath) and **Peter Olson** (NHM) and sponsorship from:



ABSTRACTS

ORAL PRESENTATIONS

Angiosperm divergence times: A phylogenetic analysis of genome-scale data sets

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The explosive increase of molecular sequence data has produced unpredicted opportunities for addressing a number of evolutionary problems. In this study we are exploring the use of molecular sequence data, combined with statistical summaries of the fossil record, to date species divergences. In particular we are examining the origin and divergences of angiosperms (flowering plants) and evaluating the effects of different types of molecular data, including temporal information from fossils, and using different molecular clock methods. The project involves compilation of sequence and fossil datasets and phylogenetic analysis of genome-scale datasets.

Using genomic ‘rubbish’: Repeat abundances contain phylogenetic signal

Steven Dodsworth^{1,2}, Mark W. Chase^{2,3}, Laura J. Kelly^{1,2}, Ilia J. Leitch², Jiří Macas⁴, Petr Novák⁴, Mathieu Piednoël⁵, Hanna Weiss-Schneeweiss⁶ and Andrew R. Leitch¹

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A large proportion of genomic information, particularly repetitive elements, is usually ignored when researchers are using next-generation sequencing. Here we demonstrate the usefulness of this repetitive fraction in phylogenetic analyses, utilising comparative graph-based clustering of next-generation sequence reads, which results in abundance estimates of different classes of genomic repeats. Phylogenetic trees are then inferred based on the genome-wide abundance of different repeat types treated as continuously varying characters; such repeats are scattered across chromosomes and can constitute a majority of nuclear genomic DNA. In six diverse examples, five angiosperms and one insect, this method provides generally well-supported relationships that agree with previous results from standard markers. We propose that this methodology may prove useful in groups where there is little genetic differentiation in standard phylogenetic markers. At the same time as providing data for phylogenetic inference, this method additionally yields a wealth of data for comparative studies of genome evolution.

Fast inference of homologs and their application to identifying split genes in low-quality genomes

Ivana Piližota

Department of Genetics, Evolution and Environment, University College London, London, UK

A key prerequisite of phylogenetic analyses entails identifying genes of common ancestry—homologs—as they can be used to infer trees and study the evolution of gene families. However, major challenges lie in computationally prohibitive data processing and poor quality of assemblies. In the first part, I will present a new approach to homology inference, a computational bottleneck in large-scale analyses. Our algorithm increases speed by considering subsequence-level homology and the transitivity of homology. This is particularly relevant to large, complex, and highly redundant plant genomes. In the second part, I will discuss how homologous sequences can be used to improve plant genomes. Specifically I will describe a new likelihood-based statistical test to infer split genes—parts of the same gene wrongly annotated as paralogs. I will present preliminary results in the wheat genome and outline plans to turn this approach into a generic tool.

DNA barcoding and community structure assessment in a tropical forest: A 25 ha mixed dipterocarp forest at Kuala Belalong Brunei Darussalam as a model

Jacqueline Heckenhauer¹, Rosabelle Samuel¹, Kamariah A. Salim², Ovidiu Paun¹, Mark W. Chase³, Toby Pennington⁴ and Michael Barfuss¹

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Species diversity in tropical rain forests is maintained by various ecological and evolutionary processes. However, there is a lack of community phylogenetic analyses based on DNA barcoding for the Southeast Asian tropical rainforest. Here, we present first insights into the community structure of a 25 hectare forest dynamics plot at Kuala Belalong, which is one of the sites set up by the Center for Tropical Forest Science (CTFS) in collaboration with University of Brunei Darussalam for investigations. Considering different ecological niches, all individuals (> 1 cm dbh) of several subplots were sampled. For barcoding, plastid regions *rbcL* and *matK* were sequenced as recommended by the Consortium for the Barcode of Life (CBOL). These DNA barcode sequences are used to reconstruct evolutionary relationships, which are compared with existing phylogenetic patterns (APG III) to examine the presence or absence of phylogenetic clustering. FWF (Austrian Science Fund) project AP26548-B22 funded to Prof. Rosabelle Samuel.

Cryptic sexuality and stress response in asexual plants: A case study on *Ranunculus carpaticola* clones based on microsatellite data

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Asexual reproduction via seeds, or apomixis, was traditionally associated with the presumption of strict clonality of the offspring derived from an asexually reproducing mother plant. Therefore, many studies handled apomicts as if they were completely lacking sexuality and the evolutionary advantage of recombination. Here we present a study on sexual diploid *Ranunculus carpaticola*, compared with asexual hexaploid hybrids (*R. carpaticola* × *cassubicifolius*) from the Carpathians. We use six microsatellite loci derived from transcriptome data to (1) validate the clonality of siblings produced in self-pollination experiments from apomictic mother plants; (2) to search for genetic variability within the clones which might have arisen either via recombination or through accidental mutations; (3) to test an increase of genetic variability within clones for a correlation with experimentally induced environmental stress. Results suggest variable, partly environment-dependent cryptic sexuality in apomictic genotypes.

Evolution of tandem repeats in chromosomally extremely variable *Prospero autumnale* complex (Hyacinthaceae)

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Prospero autumnale is a species complex exhibiting a spectacular array of chromosomal variation, encompassing four diploid cytotypes, each with unique combination of chromosome base number ($x = 5, 6$ or 7) and structure, genome size as well as numerous polyploids. Next generation sequencing of the repeatome revealed one tandem repeat (satDNA) shared by all cytotypes. The aim of this study was to infer the evolutionary history of two other satDNAs, CL138 and CL147 in *P. autumnale* genomes. The dynamics of these repeats in allopolyploids in comparison to their diploid progenitors was also assessed using cytogenetic and molecular approaches. Each of the two new satDNAs was preferentially amplified in one specific cytotype. They were, however, present in lower copy numbers in some related cytotypes. Although there was no evidence of post-polyploidization intergenomic spreading of satDNAs in allopolyploids, their distribution patterns in polyploids were not additive and deviated from parental patterns. This study was supported by Austrian Science Fund project P21440 to HWS.

Systematics of *Eugenia* sect. *Phyllocalyx* (Myrtaceae)

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Eugenia (Myrtaceae, Myrteae) is a predominately Neotropical genus, with some 1000 species and ca. 60 species in Africa. 55 % of the diversity of the genus is reported to be in Brazil (ca.500 spp). The most recent *Eugenia* classification recognizes nine well supported clades. One such clade corresponds to *Eugenia* sect. *Phyllocalyx* O.Berg, a group of c. 21 species occurring in the Brazilian Atlantic rainforest, Amazon and Cerrado. We sampled c. 80% of the species and applied molecular techniques to infer their relationships and to date diversification of and within the group. Results of this work demonstrate 1) *Eugenia* sect. *Phyllocalyx* to be paraphyletic 2) the taxonomic consequences of the phylogenetic relationships and 3) a dated biogeographic hypothesis for *Eugenia* sect. *Phyllocalyx* that indicates migration routes between the Atlantic Forest and Cerrado biomes.

Classical plant taxonomy complementing molecular phylogenetics: A taxonomic revision of *Oligotrichum* DC. in Lam & DC. (Polytrichaceae) in the Sino-Himalaya

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Traditional taxonomic revision remains the most efficient tool for species circumscription in many groups. The moss genus *Oligotrichum* had not previously been studied in the Sino-Himalaya and many herbarium specimens were incorrectly identified. Light and scanning electron microscopy were used to explore taxonomic characters relevant to species delimitation. Eight species are confirmed from the study area, and one, *O. hercynicum*, is excluded. New observations are reported on characters critical for resolving taxonomic controversies. Keys, descriptions, synonymy, typification, ecological notes and new geographical records are reported. *O. aristatulum* Broth., *O. semilamellatum* var. *darjeelingense* Gangulee and *O. semilamellatum* var. *edentatum* Gangulee are newly synonymised with *O. semilamellatum* (Hook.f.) Mitt. The previously unknown sporophytes of *O. glaciale* are described, corroborating molecular evidence suggesting that it should be excluded from *Oligotrichum*. Newly identified collections of this species in turn now permit more extensive molecular studies, highlighting the synergetic relationship between herbarium and molecular work.

Is *Begonia* an adaptive radiation? The ecology of diversification in a mega-diverse genus

Peter Moonlight

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Begonia is the sixth largest genus of flowering plants with over 1650 species distributed throughout the tropics of Africa, Asia, and the Americas. The timing, rates, and geography of its diversification are well known following more than 10 years of molecular phylogenetic work but the drivers of that diversification are less well understood. *Begonia* is widely cited to be a group with one niche, the tropical humid forest understory, but is this the case or is today's *Begonia* diversity the result of adaptive radiation through different ecological niches? I will present methods based upon MaxEnt niche modelling, molecular phylogenetics, field and herbarium data that will be used to test whether *Begonia* shows ecological diversification patterns consistent with an adaptive radiation or niche conservatism consistent with neutral processes acting on isolated populations in similar niches?

Resolving intrafamilial relationships: How to build a robust phylogeny of the Angiosperms

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Uncertain interfamilial relationships have been reported for many Angiosperm orders, and pose a significant challenge to the assembly of a robust phylogeny of this important group. The prevailing view is that more data will reveal well-supported, stable relationships. Our case study is of the Fabales, an order comprising four families (Leguminosae, Polygalaceae, Surianaceae, and Quillajaceae), amongst the best-studied Angiosperm orders yet clearly exemplifying uncertain interfamilial relationships. We present an overview of past studies of the order, and describe the suite of analyses we have carried out using a 680 taxa supermatrix to reveal “root sensitivity” but not Long Branch Attraction (LBA). In the light of these analyses we discuss the deficiencies of a more-data approach, and the strategies which might be applied more generally to identify and address “root sensitivity” problems.

Phylogeny, palaeontology, and primates: Do incomplete fossils bias the Tree of Life?

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Paleontological systematics relies on morphological data that have undergone decay and fossilization (taphonomy). We measured the impact of taphonomy on phylogeny relative to a known topology. We compiled a morphological and molecular matrix for living primates and reconstructed a robust topology with two methods. We then simulated the extinction of a single taxon, repeated the phylogenetic analysis, and compared the result to the known topology. Unsurprisingly, we found a positive correlation between fossil completeness and phylogenetic accuracy. Artificial extinction was based on actual fossils, whereby characters missing in a real fossil (all molecular and a subset of morphological) were treated as missing in the artificial fossil; therefore, inference on preservational bias in specific fossils can be made. For example, *Darwinius masillae* outperformed taxa with similar levels of missing data, due to its even character sampling across morphological partitions.

Repeated evolution of viviparity greatly increases diversification rates in the order Cyprinodontiformes

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In order to understand the macro-evolutionary processes that generate diversity, we must determine the relationships between taxa, establish when changes in diversification rates have occurred and correlate these changes with factors that may have stimulated speciation. The Cyprinodontiformes are an order of 1243 ray-finned fish species found worldwide, several of which are used as model organisms in aging, pollution tolerance and evolutionary research. Two remarkable life-history traits have evolved within the group, viviparity and annualism. However, the extent to which these innovations have affected diversification is unknown. We present the first time-calibrated genus-level molecular phylogeny of the Cyprinodontiformes. Using this we show that both viviparity and annualism evolved multiple times but only viviparity is correlated with multiple instances of increased diversification rates. Our results demonstrate that a change in reproductive strategy can lead to an increase in biodiversity

Internal anatomy and molecular data support the colour-based identifications in polyclad flatworms

Daniel Marquina

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The family Pseudocerotidae is known for the generalised homogeneity in the internal anatomy of the reproductive system, result of a process of simplification due to the copulation mechanism. Taxonomists have solved this problem establishing a system of identification based solely in the distinctive colour pattern of the species. This identification system is often ambiguous and some taxonomists and systematics do not agree. Combining morphological information (colour pattern and an exhaustive internal anatomy examination) with molecular data (sequences of the mitochondrial genes COI and 16S) the validity of the mentioned system have been tested in *Pseudoceros* and *Pseudobiceros*, the two most diverse genera of the family Pseudocerotidae. The results support the identification through colour pattern. However, for the current taxonomy, a detailed description of the internal anatomy is necessary. Complete morphological information not only helps for a solid identification, it can also be used to solve phylogenetic conflicts and evolutionary events.

Relation between *Orbellis* and some *Neolethaeus* species (Heteroptera: Lygaeoidea: Rhyparochromidae)

László Zsalakovics and Előd Kondorosy

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The tribe Lethaeini was created with 4 other tribes by Stål in 1872. Before the establishment of the tribes the subfamily Rhyparochromidae was chaotic and therefore hard to study. *Orbellis* was described by Distant (1913) as a monotypic genus with the only species *Orbellis typicus* from the Seychelles Islands, later the genus was synonymized with *Lethaeus* by Bergroth in 1916. In 1967 Scudder restored it as genus. Slater and O'Donnell (1999) described three new *Neolethaeus* species from Madagascar: *Neolethaeus polhemi*, *N. madagascariensis* and *N. maculosus*. After examining the type specimens of both *Orbellis* and the three Madagascarian *Neolethaeus* we found that *O. typicus* and *N. polhemi* are very similar and are probably synonyms thus need to be revised. The other two *Neolethaeus* species are closely related to *N. polhemi* and probably have to be revised as well. The main differences between the genera are the broadness of the head and the pronotum.

A phylogenomic approach to cephalopod evolutionary history

Alastair R. Tanner

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Cuttlefish, octopuses and squid – the coleoid cephalopods – highlight the breadth of diversity exhibited by marine invertebrates. Adaptations ranging from exquisite camouflage and mimicry to indications of sentience lend the group particular celebrity amongst the wider molluscan phylum. Although the fossil record has been crucial in tracing the earlier evolutionary history from monoplacophoran-like Palaeozoic ancestors, shell-loss in the coleoid crown-group has diminished preservation potential and impeded effective palaeontological insight. Here we apply a phylogenomic approach to cephalopod relationships and evolutionary origins. We recover monophyly congruent with morphological systematics uniting groups in both the oegopsid and myopsid squid, and the incirrate and cirrate octopuses. Origins of the Decapodiformes and the Octopodiformes are recovered as occurring ~ 150 Ma and ~ 182 Ma respectively, concurrent with the view that cephalopods diversified in parallel with teleost fish, and should be viewed as a phenomenon of the Mesozoic Marine Revolution.

Reconstructing the ancestral annelid: Reconciling fossils, morphology and molecules

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The relationships of the annelid classes, Polychaeta and Clitellata, have been a source of controversy over the past century. The treatment of either group as 'primitive' has resulted in radically different reconstructions of the annelid ancestor. Phylogenetic reconstructions of polychaete relationships have also proved problematic, as multiple independent losses of key characters have plagued studies of morphological characters. Molecular phylogenies suggest that clitellates are nested within polychaetes, rendering the latter paraphyletic. This is corroborated by the fossil record, with the oldest annelids from the early Cambrian possessing well-developed parapodia, chaetae and head appendages. We report a morphological phylogeny of fossil and living annelids. The inclusion of ancient stem group fossils correctly polarizes morphological characters, breaks long branches and recovers a topology more in agreement with sequence data. However, fossils provide the only direct evidence of ancestral morphologies and significant conflict still exists between recent phylogenomic studies and the fossil record.

Poster Abstracts

Developing new SSR markers for male-specific in date palm (*Phoenix dactylifera* L.)

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Phoenix dactylifera L. is an important crop in North Africa, Middle East, dioecious, the female individuals produce fruits. There was no way to identify the sex of date palm plants before reproductive age, which is 6-8 years or more from seed. The first genetic linkage map for date palm with a gender identify region mapped was published in 2014, which facilitated the development of reliable markers for sex determination. Sex-linked SSR were developed of the gender regions. We screened these new markers in 56 male and 40 female, collected over a wide geographical area. Suitable softwares were used to visualize the discrimination power of each locus, and compared gender markers with overall genetic diversity. We observed Male-specific alleles at two loci, absent in females, which allowed identification of the gender of date palm samples successfully and with 100% accuracy. These markers will facilitate ratification sex in offshoots, selected female individuals, seedlings can be more readily grown on and screened for good agronomic properties.

Estimating the timeline of animal evolution

Mario dos Reis¹, Yuttapong Thawornwattana¹, **Konstantinos Angelis¹**, Maximilian J. Telford¹, Philip C.J. Donoghue², Ziheng Yang¹

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Current molecular studies place the origin of Metazoa during the Cryogenian period (635 to 850 million years ago (Ma)) which is further supported from recent fossil findings. However, the evidence for the diversification of Bilateria remains controversial. Molecular studies place the origin of Bilateria during the Ediacaran period (541 to 635 Ma) but the fossil record suggests a massive radiation of Bilateria phyla after the Ediacaran-Cambrian boundary (~541 Ma). We conduct a Bayesian molecular study to estimate early animal divergences using 203 amino acid nuclear coding genes from 54 metazoan species in combination with 34 recent fossil calibrations. Results suggest that the divergence of Metazoa occurred 834–681 Ma during the Cryogenian and most of the crown-group bilaterian phyla diverged during the Ediacaran. However, the time estimates are sensitive to the fossil calibrations used, to different phylogenetic hypotheses and to the degree of data partitioning.

HGT between viruses: Perspectives from paleovirology

Amr Aswad and Aris Katzourakis

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Paleovirology is the study of endogenous viral elements (EVEs) - genomic features that result from the accidental integration of viral genetic material in the host germline. EVEs have predominantly been used as 'genetic fossils' that inform us about the evolution of the viruses, but recent studies have recognized the importance of a functional subset, co-opted to benefit the host. Conversely, there are host-derived genes in viruses, a phenomenon that has primarily been observed in large double stranded DNA viruses. Although exceptionally rare, gene flow between unrelated viruses also occurs. Our most recent work has demonstrated that virus-to-virus gene transfer can occur in a convergent evolutionary manner, demonstrating that a particular underlying evolutionary mechanism is at play. The principles of paleovirology can be used to study horizontal gene transfer between viruses as well as between viruses and their hosts under the same evolutionary framework.

Genetic diversity and population structure of *Galium glaucum* group (Rubiaceae) in Eastern Europe

Alexey A. Borisyuk

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There are three species from *Galium glaucum* group in an area of our study: *G. xeroticum* Soo, *G. biebersteinii* Ehrend., *G. octonarium* Pobed. Only *G. xeroticum* have a good morphology character. We investigate ISSR markers variability in 20 natural populations. A high variability was observed in all populations (65% of variance in populations, 35% among them). We have found unique bands for regions and for one of species. A genetic discontinuity was found around *G. xeroticum* populations and in chalky soil areas. There are two main clusters in STRUCTURE version 2.3.4. The first is *G. xeroticum* cluster. The second is other populations cluster. There is a common genetic pool for *G. octonarium* and *G. biebersteinii* in Eastern Europe. Moreover, we observe a *G. xeroticum* genetic impact in nearest populations of other species. This influence corresponds with geographic distance.

Molecular systematics of the genus *Phoxinus* Rafinesque, 1820 (Actynopterygii: Cyprinidae) in the Iberian Peninsula

Irene Cobo and Ignacio Doadrio

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Since the early 20th century, it has been accepted that there is a single species of the genus *Phoxinus* in western Europe, *Phoxinus phoxinus* (L., 1758). A current systematic revision (Kottelat, 2007) based on morphological characters differentiated three European species, *P. bigerri*, France and Spain, *P. septimaniae*, France, and *P. strymonicus*, Greece. Kottelat and Freyhof (2007) warn that the identification of the Iberian minnow populations as *P. bigerri* is tentative, as Kottelat did not analyze Iberian samples. Thus, systematic of genus *Phoxinus* is based only on morphological characters. This work provides the first systematic revision of this genus in the Iberian Peninsula based on molecular data. For this purpose, both mitochondrial (Cytochrome b) and nuclear (S7) DNA of 241 individuals were studied. Phylogenetic (ML and NJ) and phylogeographical (Haplotypes network) analysis was performed with these sequences. The results show several well-differentiated groups. That suggests the possible existence of different species.

A cryptic species of freshwater fishes in Southern Spain is found by way of molecular analysis of the genus *Squalius* Bonaparte, 1837 (Acanthopterygii, Cyprinidae)

Marta Cobo-Simón, Silvia Perea and Ignacio Doadrio

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The taxonomy of the Spanish freshwater fishes was mainly precluded for the monumental work of Lozano Rey (1935). This work considered the same origin to the Iberian and the rest of European fish fauna. Differences in morphology many times were assigned to small local variations and Spanish populations were attributed taxonomically to subspecies of well recognized central and north European species. This vision of Spanish freshwater fishes has changed because of molecular systematics, which found a high diversity and different origins to this fish fauna. The number of species was increasing since 1980 and an endemic cyprinid, *Squalius malacitanus* (Doadrio and Carmona, 2006), was currently described. As consequence of a phylogeographical approach to all populations of *Squalius malacitanus* using nuclear and mitochondrial molecular markers, we found two deep divergent groups. These two groups have higher divergences than other Spanish species of same genus.

New Afrotropical species of *Rhyparothesus* (Heteroptera, Lygaeoidea, Rhyparochromidae, Rhyparochromini)

Anita Fábics and Előd Kondorosy

Department of Animal Science, Pannon University, Hungary

The tribe Rhyparochromini is the largest tribe (about 350 known species in 46 genera) of the family Rhyparochromidae of the true bugs (Heteroptera). In the 19th century were only few genera described with numerous species, which now belong to different genera. E.g. *Aphanus* was a collecting genus including many species. For *A. orientalis* Distant Scudder (1962) described the genus *Rhyparothesus* and later (1967) he transferred other 6 species to this genus without explanation. The distribution area of the group is very special: six species (*Rhyparothesus* sp. 1-6) are Oriental (from Nepal to Sri Lanka and Thailand); but one species (*Rhyparothesus atomarius*) is Afrotropical, specifically from South Africa. During the revision of the genus we realized, that more than one species live in Africa. The most important species-level attributes, which differ the African from the Asian species are: colours of antennal segments, head, legs, membrane; and male genitalia (pygophore and paramere).

Phylogenetic and phylogeographic patterns of *Silene ciliata*

Ifigenia Kyrkou^{1,2}, Alfredo García-Fernández² and José M. Iriondo²

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Silene ciliata is a species that inhabits the alpine mountains of the Mediterranean Basin, but with a highly disjunct distribution. We focused on testing the chloroplastic DNA variation in order to explain the observed disjunction and evaluate its phylogenetic origin. Particularly, we were interested in clarifying the long suggested division of *S. ciliata* into two subspecies. For this aim, we collected and extracted DNA from 25 populations. Major intraspecific variation was supported by all analyses. Plastid DNA evidence was in accordance with the division of *S. ciliata* into the two subspecies. Additionally, plastid DNA patterns are probably the result of a combination of geographic factors providing links and barriers, climatic adversities and evolutionary processes that took place during Quaternary glaciations.

Morphological and molecular variation in *Amblyosyllis* (Annelida, Syllidae)

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Amblyosyllis is a genre of the family Syllidae with cosmopolitan distribution, and it is present in samples from intertidal areas with moderate climates. The genre counts, nowadays with 8 valid species which present diverse morphologies. Some authors have suggested that these species can actually be a complex of cryptic species. The last phylogenetic reviews reveal that *Amblyosyllis* is an independent group, which can't be included in any of the subfamilies inside Syllidae. An intense bibliographic review has been carried out. To do the molecular analyses, mitochondrial COI genes of 110 specimens were sequenced as well as the nuclear 28S genes of 40 specimens. Maximum Likelihood analyses were carried out with the programme RAXML. The results indicate that *Amblyosyllis* is a monophyletic group with high support and is comprised by more species than the number thought up to date.

The biogeographic and floral evolution of Gesneriaceae (Lamiales)

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Angiosperm explosive radiation has been linked with floral diversification and ecological shifts amongst others factors. Gesneriaceae are an excellent model group to study the impact of these phenomena as they are a family with incredibly high floral diversity with many pollination syndromes. Gesneriaceae are a family of approximately 160 genera and more than 3200 species. The mechanisms responsible for the generation of this diverse group are still unclear. In this study we: (1) are constructing a phylogenetic and temporal framework for the family to understand and clarify diversification and taxonomy of the family, (2) will provide insights into the biogeography of Gesneriaceae and (3) will look for candidate genes that are regulating changes in pollination syndromes of the family using the transcriptome of two species and a hybrid of *Streptocarpus* and next generation sequencing.

Location of the Pleioplanidae family in the “fluid mosaic” of the Leptoplanoidea SFamily complex (Polycladida, Platyhelminthes)

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The Leptoplanoidea superfamily is one of the biggest complexes within the acotylean polyclads. In this work we locate the Pleioplanidae family, including new genus and species, in the fluid mosaic of this superfamily. The Pleioplanidae family finds its origins within the Notoplanidae family, which has experimented a number of changes in the last decades. Based on the anatomical reconstruction of the prostatic vesicle of *Notoplana atomata* Faubel erects the Pleioplanidae family in 1983, with this characteristic being the apomorphy which justifies its creation. This study presents a revision of this family, using material from different collections and molecular and histological techniques. The main conclusion of this work is the erection of a new genus in the Pleioplanidae family, as well as a new species within it. This study also serves as a preliminary approach in the reconstruction of the taxonomy, distribution and filogeny of the whole Leptoplanoidea complex.

Molecular characterization, DNA barcoding and conservation of arid-land Fabaceae in Nigeria

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Many plant species are threatened with extinction through human activity with no exception to the Nigerian species, this effect is more evident in the arid and semi-arid region of the northern part of Nigeria. To gain an overview of the severity of the problem and to potentially implement adequate conservation strategies, it has thus become imperative to understand the genetic variation within and between populations, this will help in the establishment of effective and efficient conservation practices for species. To achieve this, plant species of the bean family (Fabaceae), dominant in the arid zone of Nigeria is used as the model species. This research aims at characterizing the different arid legumes in Nigeria using morphological and molecular characters with a view of sharing the DNA sequence obtained as well as data about its voucher specimen in a public database. The expected output of this research will increase the public interest in biodiversity conservation issue, especially in the fragile paradise of Nigeria, contribute to the phylogeny of Fabaceae and subsequently conserve this species through DNA barcoding.

Evolution and biogeography of the sweet vernal grasses (*Anthoxanthum* s.l.) American taxa

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In this study we aim to explain the evolution and biogeography of the sweet vernal grasses (*Anthoxanthum* s.l., Poaceae), with special emphasis in section *Ataxia* and the South American complex of former genus *Hierochloë* (now subsumed in *Anthoxanthum* s.l.). To achieve this, two plastid and two nuclear DNA regions were sequenced in 165 accessions of 38 taxa (8 South American *Hierochloë* species, 80% of the diversity of the genus in the sub-continent). Subsequently, a dated phylogenetic analysis was conducted using Bayesian methods and different networks were built in order to understand the parts of the phylogeny with low resolution. Our results reveal that *Anthoxanthum* section *Ataxia* results from a hybridisation event between the *Anthoxanthum* s.str. and the *Hierochloë* lineages. The South American *Hierochloë* are clearly monophyletic and very closely related, reflecting a recent diversification. Finally, different biogeographic patterns for *Anthoxanthum* s.l. are unravelled and introduced.

Guidelines for DNA taxonomy

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Resolved taxonomy is a prerequisite to investigating larger scale macroevolutionary patterns as well as being important for ecological and conservation practises, but describing biological diversity is not always a simple endeavour. The field of DNA taxonomy, i.e. the use of DNA to delineate species boundaries, can be used as a tool to alleviate the taxonomic crisis, which is so prevalent for groups such as the meiofauna where taxonomy is confounded by morphostasis, cryptic diversity, and a dearth of expert taxonomists. Here I present results from multiple meta-analyses exploring the effects of choice in gene, phylogenetic reconstruction methods, and species delimitation metrics, which provide better guidelines for DNA taxonomy. The analyses suggest that coalescent-based DNA taxonomy using the Generalized Mixed Yule Coalescent model in conjunction with the cytochrome oxidase 1 subunit c gene analysed in a Bayesian inference phylogenetic framework using BEAST, provides realistic and tangible species clusters (evolutionarily significant units).

Multiplying the number of small tropical parasitoid wasp species

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Small-bodied parasitoid wasps comprise one group of organisms whose tropical fauna remains remarkably understudied. One such group is the subfamily Orthocentrinae of the speciose family Ichneumonidae (Hymenoptera). Before the presented work, 38 orthocentrine species had been reported from the tropical regions, and 14 were known from the Neotropical region. The genus *Orthocentrus*, on the other hand, was presented by 49 species worldwide, and only one species was known from the Neotropical region. In our studies, the subfamily was first revealed to be one of the most abundant ichneumonid subfamilies in the Neotropics. Next, combined molecular and morphological species separation methods revealed at least 177 undescribed Neotropical orthocentrine species, some of which were probably morphologically cryptic species complexes. The best-represented genus was *Orthocentrus*. Last, we described 27 new species of *Orthocentrus* and proposed several species-groups for the Neotropical fauna to illustrate some of the extensive morphological diversity within the genus.

Phylogenetic relationships of *Lactuca* L. (Asteraceae) with a focus on African species

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We provide the first molecular phylogenetic reconstruction of *Lactuca* with a focus on African species, using two chloroplast DNA sequences (*ndhF* and *trnL-F*). In order to establish the affiliation of *Lactuca* within the Asteraceae sub-family Cichorioideae, we generated new sequences from herbarium samples and obtained Genbank data from the subfamilies of Asteraceae and conducted phylogenetic inference using both RAxML and Bayesian Inference (BI) analyses. For more detailed analyses of *Lactuca*, we selected 33 *ndhF* accessions representing 31 species, and 89 *trnL-F* accessions representing 47 species. This sampling covers 47% of the total African *Lactuca* species. The final RAxML and BI analyses of *ndhF* gene indicate that *Lactuca* is monophyletic if *L. tinctoriate* is excluded, while *trnL-F* gene trees imply that some *Melanoseris* species are mixed with *Lactuca* species with many polytomies. We also traced biogeographic and morphological character history over the RAxML trees and constructed consensus network and phylogenetic super network. We conclude that *Lactuca* could be divided into at least five groups: the crop clade, the Asian clade, the *Melanoseris* clade, the newly identified African clade and other species not included in former four clades. Additionally, the African scandent species are the sister group of other African species and form an independent sub-clade.

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