

YOUNG SYSTEMATISTS' FORUM

1st December 2011, Flett Theatre, Natural History Museum, London, UK

08.30	Registration	(Please put posters up as early as possible from 08.30)
09.30	Welcome	YSF team
09.40	Peter Mark	Systematic and taxonomic significance of the pollen morphology of Violaceae
09.58	Hugo Dutel	Lineages of giant Mesozoic coelacanths
10.16	Antje Donner	Phylogenetic and morphological analysis of <i>Chroococcidiopsis</i> , the Pleurocapsales and related heterocyte-forming Cyanobacteria
10.34	Anaïs Grand	Bio-ontologies: An unambiguous way to represent subjective knowledge
10.52	Coffee and attended posters (even numbers)	
11.30	Kyle Freeman	A morphometric study of mandible shape change in the evolutionary lineage of <i>Mammuthus</i>
11.48	Alice Burridge	Shells, shapes and sequences: An integrated morphological, molecular and biogeographic study of Cuvierinidae (Gastropoda, Thecosomata)
12.06	Olivia Cheronet	Quantitative geometric morphometric assessment of the disparity of Lake Tanganyika's endemic gastropod fauna
12.24	Bram Knegt	Are marine lakes inside-out islands? Population divergence of <i>Brachidontes</i> (Bivalvia, Mytilidae) and <i>Nerita</i> (Gastropoda, Neritidae) from Indonesia
12.42	Laura Michie	Sympatry in fiddler crabs (genus <i>Uca</i>) at their Wallacean hotspot of diversity
13.00	Lunch and posters	
14.00	Carly Benerfer	Genetic diversity and phylogenetic relationships of economically important click beetle species
14.18	Krzysztof Kozak	Conflict between species tree methods in estimating and dating the phylogeny of the adaptive radiation of Heliconiini butterflies
14.36	Andrew Briscoe	Promises and pitfalls of the amplification of whole mitochondrial genomes: A case study within the Araneae
14.54	Elizabeth Cooke	Systematics and phylogeography of the emerging model plant <i>Cardamine hirsuta</i>
15.12	Tea and attended posters (odd numbers)	
15.50	Mark Harrison	The application of next generation sequencing technology in phylogeography and population genetics: A test case using Antarctic brittle stars
16.08	Julien Massoni	Evolutionary history of a 10,000-species clade of angiosperms: Reconstructing the phylogeny of magnoliids a whole
16.26	Rick Thompson	The calculation and interpretation of hidden support in combined analysis phylogenetics
16.44	Claire Morgan	Inferring the mammalian phylogeny using a heterogeneous approach
17.02	Roberto Feuda	The complexity of rooting the animal tree of life using nuclear encoded genes: Outgroups and compositional effects
17.20	Poster session	
18.00 – 19.00	Presentation of Prizes and Reception	Juliet Brodie/Ellinor Michel

Organized by **Ellinor Michel** (Dept Zoology, NHM),
Jon Todd (Dept Palaeontology, NHM) & **Maria Vorontsova** (RBG, Kew), with support from:



TALK ABSTRACTS

Systematic and taxonomic significance of the pollen morphology of Violaceae

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This study focuses on the pollen morphology of Violaceae Batsch, a family of 825-900 species in approximately 23 genera. The current taxonomic understanding of the family (Hekking, 1988) has been considerably challenged by the multi-genomic molecular phylogeny of Tokuoka (2008). In order to seek morphological characters that may aid the characterization of clades, and hence any future circumscriptions of taxonomic groups, exine characters from 21 taxa throughout the range of Violaceae were described using SEM and LM, and optimized on Tokuoka's phylogeny. The results indicate that, at the current level of taxon sampling, it is difficult to conclude if the pollen of Violaceae has any significant systematic/taxonomic potential, either in isolation or as part of a suite of characters, including non-palynological characters. However, a number of potential synapomorphies have been identified, which would merit further investigation, particularly those that may aid the delimitation of lineages within the defunct genus *Hybanthus* Jacq.

References:

- Hekking, W.H.A. (1988) Flora neotropica monograph 46, Violaceae Part I – *Rinorea* and *Rinoreocarpus*. New York Botanical Garden, NY.
- Tokuoka, T. (2008) Molecular phylogenetic analysis of Violaceae (Malpighiales) based on plastid and nuclear DNA sequences. *J. Plant Res.* 121: 253-260.

Lineages of giant Mesozoic coelacanths

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Coelacanths (Actinistia) are usually considered as a very conservative group that have experienced very few anatomical changes during their evolution. However, when the fossil record is carefully taken in account, coelacanths display a significant morphological and ecological diversity. Among fossil coelacanths, the largest specimens described have been referred to the genus *Mawsonia*. These non-marine coelacanths, from the Late Jurassic and Lower Cretaceous of South America and Western Africa, were estimated to reach 4m in length. Based on the redescription of the giant coelacanths *Megalocoelacanthus* (Upper Cretaceous, North America) and *Trachymetopon* (Lower Jurassic, Germany) I here show that giant coelacanths evolved in several lineages during the Mesozoic in both marine and non-marine environments. These new fossils shed new light on the paleobiogeography of the Mawsoniidae and the ecological diversity of Latimeriidae.

Phylogenetic and morphological analysis of *Chroococcidiopsis*, the Pleurocapsales and related heterocyte-forming Cyanobacteria

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The classification of Cyanobacteria is still largely based on morphological data, which does not necessarily reflect their evolutionary history. The order Pleurocapsales, for example, are characterized by a unique mode of reproduction, and traditionally include the genus *Chroococcidiopsis*. Recent studies indicate that *Chroococcidiopsis* may be a sister group to the heterocyte-forming Cyanobacteria instead. We analysed three genes (16S rDNA, *rpoC1*, *gyrB*) with a focus on the Pleurocapsales, *Chroococcidiopsis* and heterocyte-forming cyanobacteria. The available data from GenBank and completed genomes were combined with new sequences and analysed for approx. 100 strains using Maximum Likelihood and Bayesian methods. In addition, scanning electron microscopy was used to examine the thylakoid structures as a morphological character of selected taxa. Our results support the hypothesis that *Chroococcidiopsis* is related more closely to heterocyte-forming Cyanobacteria, and confirm the non-monophyly of the Pleurocapsales.

Bio-ontologies: An unambiguous way to represent subjective knowledge

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Literature in natural science is full of identical terms which are not always related to the same concepts, making a review of the terminology laborious. We present here the interest of ontologies for a controlled terminology on one hand and for transparency of a researcher's choices and interpretations on the other hand. Ontologies consist in representing knowledge (i.e. concepts and their relations) into a standard language (such as OWL) enabling requests and "data mining". They may have applications in many disciplines, with various scopes of expectations. We mention here their application to a well-formalized descriptive model allowing for subjectivity to be unambiguous. This work on descriptors may also be the starting point for a work on homology. Would homology then be a relation or a concept within the ontology? We present the interoperability between Xper2 (ontology-structured management tool for descriptive knowledge) and LisBeth (phylogenetic software) developed in Paris (UMPC, MNHN).

A morphometric study of mandible shape change in the evolutionary lineage of *Mammuthus*

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The Pleistocene *Mammuthus* evolutionary lineage is well researched from *Mammuthus meridionalis* to the most recent *Mammuthus primigenius*. The evolutionary pattern of the mandible in this succession from ancestor to descendant indicates an overall deepening of the horizontal ramus and shortening of the rostrum, presumably to accommodate the increasingly deepening molar roots associated with increasing hypsodonty. This study used a Principal Components Analysis (PCA) on datasets of Procrustes aligned 3D landmarks as well as linear measurement datasets with the purpose of analysing potential ontogenetic and evolutionary shape change. The linear measurement results suggested an overall width of the mandible to be the most influential factor of shape change; however, the landmark analysis suggested ramus depth to be more influential. However, due to the limited number of specimens as well as the high levels of missing data present in this study, there is a limit to the reliability of the data.

Shells, shapes & sequences: An integrated morphological, molecular and biogeographic study of Cuvierinidae (Gastropoda, Thecosomata)

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Pteropods, holoplanktonic gastropods, are of increasing interest as a group which may be especially vulnerable to ocean acidification due to their highly soluble aragonitic shells. Developing meaningful species concepts, however, for the group is an essential prerequisite to their use as critical indicators of ocean changes. This multidisciplinary study has examined species boundaries in the family of Cuvierinidae, linking phenotypic, genetic, and biogeographic information (using Geographic Information Systems). This approach proved to be highly effective in the discrimination of taxa. All taxa described within the group could be distinguished based on geometric morphometric analyses of shell outlines applied to several hundred museum and fresh specimens from the Pacific, Atlantic and Indian Oceans. Furthermore, we found highly congruent patterns based on mitochondrial and ribosomal DNA sequences of 74 fresh specimens.

Quantitative geometric morphometric assessment of the disparity of Lake Tanganyika's endemic gastropod fauna

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Lake Tanganyika's cerithioid gastropod radiation is claimed to be the most morphologically diverse monophyletic freshwater gastropod radiation. We tested this assertion using geometric morphometrics.

Through coordinate-point extended-eigenshape analyses, we characterised morphology, calculated disparity metrics, and contrasted the Tanganyikan radiation with two other diverse fossil radiations: the East African Albertine Rift Valley cerithioids and South American Pebas Formation gastropods.

Morphospace occupied by the Tanganyikan fauna represents a biologically more favourable uniform growth region with few adult modifications (shifts in geometry associated with sexual maturity). Although phylogenetic correlation is generally poor, a few groupings are evident. A negative relationship between within-taxon disparity and taxonomic diversity suggests more experimentation within species-poor clades.

Morphospace occupation was largely similar among comparative groups. One could hypothesise a common morphospace-filling mechanism in Tanganyika and Pebas, with dominant taxa and other species-poor taxa undertaking greater morphological experimentation. It nevertheless remains evident that the Tanganyikan radiation is morphologically extremely variable.

Are marine lakes inside-out islands? Population divergence of *Brachidontes* (Bivalvia, Mytilidae) and *Nerita* (Gastropoda, Neritidae) from Indonesia

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Marine lakes are isolated bodies of seawater surrounded by land. Can these lakes be considered as marine counterparts of islands? To analyse geographic isolation, we sampled two benthic invertebrates: the mussel *Brachidontes* sp. and snail *Nerita* sp. from nine Indonesian marine lakes and four adjacent marine habitats. We first assessed species boundaries and next revealed significant intraspecific structure in these taxa using geometric morphometric and genetic (mitochondrial and nuclear) markers. Three *Brachidontes* lineages (15% divergence) and two *Nerita* lineages (1% divergence) were found based on mitochondrial Cytochrome Oxidase 1 sequences. Most lakes contained only one mitochondrial lineage, suggesting that marine lakes harbour isolated populations. Since the marine lakes sampled in this study are no older than 10,000 years, our results suggest that either divergence can accumulate rapidly in marine lakes, or anciently diverged lineages have colonized different lakes.

Sympatry in fiddler crabs (genus *Uca*) at their Wallacean hotspot of diversity

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Fiddler crabs (genus *Uca*) occur in tropical and temperate intertidal habitats; they are gregarious and are often found living in groups of hundreds or thousands. On the island of Kaledupa (Indonesia), at the interface between a mangrove forest and a mudflat, nine species of fiddler crabs coexist, many more than at any other known site in the world. The main objective is to understand how these species manage to coexist with the key focus being on resource partitioning. Research includes behaviour observations, sediment composition analysis and the examination of mouthparts to determine whether the different species are consuming different resources. This research will help establish whether species alter their behaviour when living sympatrically, and by extension, contribute to general understanding of how different ecologically-equivalent species manage to coexist.

Genetic diversity and phylogenetic relationships of economically important click beetle species

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Click beetle (Coleoptera: Elateridae) larvae (wireworms) are economically important crop pests in Europe and North America. In Canada there are several damage-causing species that are morphologically difficult to identify, but lack sequence data. However, accurate knowledge of the species involved in damage and their relationships, population genetics and phylogeography will aid the targeting of sustainable pest management strategies. Wireworms were collected from areas of significant crop damage across Canada, morphologically identified, and sequenced at the 16S rRNA region of mitochondrial DNA. For one re-emerging pest of the prairies there was a significant relationship between genetic and geographic distance. High intraspecific genetic distances between some samples suggested the possibility of cryptic species. Phylogenetic analyses using all available Elaterid 16S rRNA sequence data from GenBank indicated the likely taxonomic grouping of these unknown species. These data provide a starting point for assessing the evolutionary relationships and classification of elaterid pest species.

Novel analyses of the butterfly tribe Heliconiini (Lepidoptera: Nymphalidae) produce conflicting species tree hypotheses and unexpectedly recent divergence estimates

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The ability of multi-locus coalescent methods to produce species trees of taxa with complex evolutionary histories remains unclear. We use diverse approaches to analyse the systematics of the neotropical Heliconiini butterflies, which for over 150 years have served as a crucial model for the study of adaptation and selection in the wild. We sequenced 12.5 kilobase pairs of DNA spanning 16 nuclear and two mitochondrial loci from 87 individuals in all genera of the tribe. Tree reconstructions using concatenated loci (TNT, BEAST) and species coalescent based on both sequence alignments (BEST) and gene trees (MDC, STEM) yielded conflicting hypotheses. Although the relationships within major genera are recovered with high consistency, the proposed intergeneric relationships differ widely between the phylogenies. Furthermore, a dating of the radiation using the relaxed clock model in BEAST shows an outburst of rapid speciation in the diverse genus *Heliconius* between six and four mya. This contrasts the previous mtDNA-based estimate, which suggests gradual diversification between 15 and five MYA. Our work demonstrates surprising uncertainties in the systematics of an important model group, thus highlighting the significance of analytical choices in species tree reconstruction and the perils of relying solely on concatenation-based approaches.

Promises and pitfalls of the amplification of whole mitochondrial genomes: a case study within the Araneae

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As more sequence data becomes available, large-scale sequencing efforts and interrogation of expressed sequence tag (EST) libraries are yielding impressive numbers of nuclear markers for use in phylogenomics. However, true phylogenomic analyses are still not practical for larger numbers of taxa that lack *de novo* sequenced transcriptomes. A compromise between traditional phylogenetic methods and phylogenomics lies in the analysis of whole mitochondrial genomes. Whilst the advent of second-generation sequencing technologies is likely to facilitate *en mass* sequencing capability, there is still an apparent bottleneck associated with the amplification of whole mitochondrial genomes, with

current mitogenomic studies being limited to incomplete or nominally intra-specific datasets. Here, we focus on the exploration and optimisation of both PCR-based and Whole Genome Amplification (WGA) methodologies, in order to test the utility of complete mitochondrial genomes in resolving complex evolutionary relationships, using the Araneae (true spiders) as a model order.

Phylogeography of the emerging model plant *Cardamine hirsuta* L.

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Cardamine hirsuta (Brassicaceae) is an emerging model system in developmental genetics. These studies seek to understand the genetic basis of morphological traits, in the context of natural genetic variation within *C. hirsuta*. However, currently there is limited knowledge of the geographical structure or genealogical history of genetic variation within *C. hirsuta*. A published study, using two markers, found little genetic variation within *C. hirsuta*, despite wide geographic sampling. This current study seeks to increase character (nucleotide) and taxon (individuals) sampling by identifying chloroplast and nuclear regions with intraspecific variability and sampling from across the entire native range of *C. hirsuta*, primarily using DNA extracted from herbarium specimens. This strategy has revealed clear geographic structuring of genetic variation within *C. hirsuta* with congruent patterns between chloroplast and nuclear markers. A chloroplast phylogeny indicates an early split within *C. hirsuta* between Eurasia and the East African High Mountains. The Eurasian lineage then diversified into six major haplogroups, four are geographically restricted in their distribution to floristic regions: the Atlantic fringe, the Atlas Mountains, and two in Irano-Turanian, and two haplogroups are widespread, co-occurring across Europe. The phylogeographic structure of *C. hirsuta* in Eurasia is suggestive of Pleistocene range dynamics.

The application of next generation sequencing technology in phylogeography and population genetics: A test case using Antarctic brittle stars

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A general limitation in molecular evolutionary biology and systematics is that often only one or few genetic markers are employed which may lead to biases as single marker investigations are generally unrepresentative of true organismal evolutionary histories or phylogenies.

We are developing a new protocol for generating multiple markers at affordable costs and on a reasonable time-scale. We are achieving this by combining AFLP and cDNA fragment generation methods with standard laboratory enrichment procedures and taking advantage of next generation sequencing techniques. Having a high number of markers will allow (1) combined analyses on different evolutionary levels, i.e. phylogeny and population genetics & (2) high resolution analyses which will help assess systematic relationships and genetic diversity much more robustly.

We will be demonstrating this by testing the protocol on two complex problems involving Antarctic brittle stars: the contended systematics of the family 'Ophiuridae' and geographic structuring of *Ophioperla koehleri*.

Evolutionary history of a 10,000-species clade of angiosperms: reconstructing the phylogeny of magnoliids as a whole

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Magnoliids are an early-diverging clade of angiosperms consisting about 10,000 species. Current understanding of deep relationships within magnoliids relies mostly on higher-level analyses of angiosperms with limited sampling of magnoliids. In an effort to address evolutionary questions in this clade, we assembled a large molecular data set of three plastid markers (*rbcL*, *matK*, and *ndhF*) and 205 species representing >75% of magnoliid genera. Phylogenetic analyses of this combined data set yielded well resolved trees consistent with previous higher-level and family-level studies. In particular, magnoliids appear to consist of two large clades: [Piperales+Canellales]; [Laurales+Magnoliales]. On the other hand, our analyses resolved a number of long-standing polytomies. These results highlight the importance of a large taxonomic and molecular sample to resolve both deep and shallow phylogenetic relationships within magnoliids. This study is the first step toward a robust and accurate phylogenetic framework needed to reconstruct patterns of floral evolution in this clade.

The calculation and interpretation of hidden support in combined analysis phylogenetics

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In phylogenetic analysis, support for a given clade is "hidden" when in the analysis of isolated partitions the clade in question is not as well supported as in the combined dataset. In such simultaneous analyses, signal common to the majority of partitions should come to dominate the topology, at the expense of any signal idiosyncratic to each partition. This process is often referred to as synergy, and is commonly used to validate the combination of disparate data partitions. We investigate the behaviour of hidden branch support and hidden synapomorphy as measures of hidden support using artificial, real and experimentally manipulated datasets. Our analyses demonstrate that high levels of both metrics can be obtained by combining data with little shared phylogenetic signal. This finding agrees with the original intent of hidden support metrics, which quantify the extent of dataset interaction, both through the dispersion of homoplasy and revelation of underlying shared signal.

Inferring the mammalian phylogeny using a heterogeneous approach

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Sixty-five million years ago marked a period of rapid speciation and diversification in the Mammalia. As a consequence resolving the order in which these species of Mammalia arose has proven extremely difficult. There are currently four major competing hypotheses for the topology of mammals each of which have been generated using molecular data and various phylogenetic approaches. From decades of phylogenetic research we know that the quality of data, taxon sampling, and reconstruction methods, impact hugely on the phylogenetic outcome. More recently, the development and implementation of Next Generation Sequencing technologies has resulted in a surge of mammalian genomes being completed to a far higher quality. We are now at an exciting juncture in the understanding of mammalian evolution. With greater availability of higher quality data and novel heterogeneous models of sequence evolution, along with a greater understanding of the evolutionary process, we have addressed the longstanding question of mammalian phylogeny.

The complexity of rooting the animal tree of life using nuclear encoded genes: Outgroups and compositional effects

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It is now generally agreed that the Animalia and the Bilateria are monophyletic. On the contrary, rooting the metazoan tree is proving difficult, and the interrelationships of the non-bilaterian metazoans appear unresolved. Uncertainty on non-bilaterian metazoan relationships revolve around whether the sponges are the monophyletic sister group of all the Metazoa, or a paraphyletic assemblage. We used two different datasets: a new version of Sperling et al. (2010) and a modified version of the EST data set of Pick et al. (2010) to investigate the effect of outgroup selection and compositional heterogeneity on our understanding of early metazoan evolution. As expected, our results confirm that both can have a powerful influence on the results of phylogenetic analyses. With reference to early metazoan evolution, our results illustrate that, despite a large body of evidence accumulated in recent years favoring sponge monophyly whether sponges are monophyletic or paraphyletic is still uncertain.

POSTER ABSTRACTS

1)

Phylogeny: a tool to investigate the evolutionary mysteries of the palm flower

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Palms (Arecaceae) are an emblematic family of the monocots comprising 183 genera and around 2400 species distributed on all continents. Palm flowers are usually considered as rather dull. They are small (a few centimetres), trimerous, often unisexual, colourless (white or greenish) and grouped in huge inflorescences that probably function as the reproductive unit. However palms exhibit a large diversity in flower setting within the inflorescence and a large diversity in stamen number, diversity that is still poorly understood. Male and female flowers can be variously distributed within and among inflorescences (monoecy), or even among individuals (dioecy). Stamen number ranges between a few units (oligandry) to several dozens and even several hundreds of units (polyandry). We studied the evolution of inflorescence organisation and flower morphology using maximum parsimony optimization of these characters on a phylogeny of palms derived from morphological and molecular data (supermatrix recently published).

2)

Differential diagnosis within Araucariaceae Henkel & W. Hochst.

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The Araucariaceae consist of 3 genera with at least 37 species (*Agathis* Salisb., *Araucaria* Juss. and *Wollemia* W. G. Jones, K. D. Hill & J. M. Allen, Farjon 2010). These are distributed in Malesia up to the South West Pacific; except *Araucaria angustifolia* and *A. araucana* in South America (Golte 1993). Since vegetative material is difficult to identify, older keys (De Laubenfels 1972) are usually based upon characters of male cones. Even though the cones are useful for species identification, they are often not available. Vegetative macromorphological features, however, tend to be highly variable even within a taxon. Therefore our studies focus on leaf anatomy.

So far, anatomical structures of the leaves of 88 accessions of *Agathis* were analysed with several microscopic techniques. Characters valuable for identification are, e.g., size and distribution of resin canals, stomatal distribution, structure of stomatal plugs and of the hypodermis. These characters were used to develop dichotomous and interactive keys for all taxa of *Agathis* Salisb., the first ones primarily based on anatomic attributes of the leaves.

3)

The identification of putative dihydrofolate reductase (DHFR) duplicates and their phylogenetic distribution

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Dihydrofolate reductase (DHFR) is an enzyme essential for the conversion of dihydrofolate to tetrahydrofolate. As such, this enzyme is important for DNA synthesis and until recently it was thought that it was coded for by a single gene. A number of processed pseudogenes have been identified in human and one of these (DHFR1) has been shown to serve the same function as DHFR (McEntee et al. 2011).

This discovery raises an important question: are there multiple functional copies of this essential enzyme in organisms such as mouse and rat upon which we rely heavily to model human DNA related disorders such as cancer?

We have identified additional DHFR like pseudogenes/sequences (DHFR1s) across the vertebrata and have investigated their phylogenetic distribution. The known pseudogenes in human have arisen from separate retroposition events. Other DHFR1s we have identified have emerged in multiple species across the Eutheria - seemingly in independent events.

Reference:

McEntee G, Minguzzi S, O'Brien K, Ben Larbi N, Loscher C, Ó'Fágáin C & Parle-McDermott A (2011). The former annotated pseudogene dihydrofolate reductase-like 1 (DHFR1) is expressed and functional. *PNAS*, **108**(37): p.15157–15162.

4)

Climatic disturbances and their effect on the evolution of Southern Ocean gastropods

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This PhD intends to elucidate the long-term effects of climate change on the evolution of gastropods, with a particular focus on species from the Southern Ocean. The family Buccinidae is a globally widespread and speciose group (1500+ species) of carnivorous marine molluscs. Due to the diverse nature of the group a detailed phylogenetic investigation into the higher taxonomy of the Buccinidae has not yet been performed and there is still disagreement as to the familial placement and subfamilial structure of the Buccinidae. We aim to address the following questions regarding the phylogenetic inter-relationships and patterns and timing of divergence within buccinids. Is it possible to establish the time of origin and evolutionary radiation of the Antarctic buccinids? Can ages obtained from the fossil record calibrate molecular trees? Did any modern groups originate in the Paleocene, or earlier? Are the Antarctic genera monophyletic? When were the major buccinid radiations and do they correlate with major climatic disturbances? Phylogenetic approaches, including Maximum Likelihood, maximum parsimony and Bayesian methods, will be used to answer these questions. We will utilise morphological characteristics and multiple genetic loci sequenced from both Antarctic and non-Antarctic taxa. Additionally, fossil taxa will be chosen to provide constraints on the molecular phylogeny so that species divergence times and diversification rates can be estimated. If these fossil taxa can be used to calibrate molecular

trees of modern whelks it should be possible to indicate when major radiations of Antarctic marine taxa occurred. These dates can then be considered in the wider context of past global climate change. This will allow hypotheses regarding the evolution of Antarctic buccinids to be assessed.

5) **The evolutionary status of *Tragopogon* hybrids in London**

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The hybridization of two species in the plant genus *Tragopogon* (Asteraceae), *T. porrifolius* and *T. pratensis*, produces the homoploid hybrid *T. x mirabilis*, often recognised by its intermediate floral morphology. Flow cytometry shows these hybrids have C-values intermediate between those of parents (*T. porrifolius* mean $2C = 6.2pg$, *T. pratensis* mean $2C = 5.1pg$, *T. x mirabilis* mean $2C = 5.6pg$). Morphometrics suggest *T. x mirabilis* exhibits heterosis, (e.g. hybrid mean height = 74.7 cm, compared to 67.8 cm and 49.9 cm for *T. porrifolius* and *T. pratensis* respectively).

Although hybrids showed low seed set per head (14% of average parental seed set), this is partly offset by higher numbers of seed heads per plant (102% more than the parental average), giving potential for gene flow between parental species. Studies of pollen viability and seed germination will provide more information on hybrid stability. Molecular markers and GISH will be used to detect introgression.

6) **Systematics and biogeography of *Senna* (Leguminosae) in the Arabian Peninsula**

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Senna is pantropical and comprises c.350 species. This project provides a taxonomic revision and biogeographic study of *Senna* in the Arabian Peninsula. Herbarium specimens were examined and field observations were made in Saudi Arabia, Oman and Yemen. Current research indicates approximately 17 taxa in the Arabian Peninsula. PADME software has been used to store specimen and character data and will be used to generate taxonomic descriptions. Phylogenetic analyses of chloroplast *matK* sequence data indicate that *Senna* is monophyletic. All Arabian samples are placed in a clade except for those of *Senna sophera* which were placed with New World *Senna* accessions.

7)

Population connectivity between upper stream populations of *Gammarus fossarum* and *Sericostoma personatum* in a German mountain range

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Gene flow between populations of freshwater organisms is determined by extrinsic (geographic distance, landform, hydrological barriers) and intrinsic (dispersion potential of a species) factors. Especially in the case of isolated mountain stream populations it is unclear whether gene flow is possible at all or to what extent.

In this study the genetic connectivity of a crustacean, *Gammarus fossarum* (aquatic), was compared to that of a caddisfly, *Sericostoma personatum* (aquatic larvae & terrestrial imagos), in a German mountain range. This was achieved by analysing the genetic polymorphisms present within a fragment of *cox1* in 260 individuals from 25 different populations in different catchments.

The caddisfly revealed a much higher genetic diversity (35 versus 7 haplotypes) and an overall higher connectivity between populations than *G. fossarum*. We propose that the higher connectivity of *S. personatum* is linked to its ontogeny allowing a genetic exchange over land.

8)

Morphological and molecular evolution of the sea butterflies (Gastropoda, Thecosomata)

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Thecosomes, commonly known as sea butterflies, are planktonic shelled gastropods which occur throughout the world's oceans. The group shows highly diverse shell morphologies and are the only metazoan plankton with a good fossil record. These attributes make them an ideal group to study morphological as well as molecular evolution of marine zooplankton. We present a molecular phylogeny of the Thecosomata with representative outgroups based on complete 18S and partial 28S rDNA sequences. We find that genera level groupings are consistent with conventional taxonomy, however, deeper level groupings are not. Preliminary results based on the application of a relaxed molecular clock using fossil calibration points suggest that a major radiation of morphological diversity took place in the Miocene.

9)

Monophagous gall midges on Reed (*Phragmites australis* (Cavan) Trin ex Steudel)

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Decay of reedy areas is a worldwide known problem. There has been limited research carried out in Hungary on the arthropod fauna of reeds. One of our aims was to describe the gall midge species found by our former colleagues and in addition to quantify the harmful Diptera species on reeds. This unnamed gall midge may cause 20-50% damage of reeds. It causes problems especially in closed reed-beds 50-60 meters far from coastal areas. One of the most serious problems caused by this species is that the damaged plant does not grow a panicle. Galls containing larvae and pupae were also discovered at the beginning of August 2011 so two generations per year may be possible. *Platycephala planifrons*, *Giraudiella inclusa* and some *Lipara* spp. were also found in this area.

10)

Morphology, anatomy and systematics of the Southern African and Madagascan Podocarpaceae

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The Podocarpaceae are the family with the greatest diversity within the Pinales. The extensive number of genera indicates the large morphological variability of this family. The Podocarpaceae presently consist of 18 to 20 genera with 174 to 204 taxa (Farjon 2001, 2010; Knopf et al. in prep.; The Plant List 2010). The inconsistent conception of different authors shows the difficulty of systematic classification within this family. The present study implies a dichotomous key for the Podocarpaceae of Southern Africa and Madagascar. It is the first key solely based on anatomical characters of the leaves. The basis of this key is the data of several microscopic techniques. Examples for characters valuable for identification are the size, the distribution and the number of resin canals and the stomatal distribution. An additional objective of this study was to provide a full leaf anatomical description of each taxon of Podocarpaceae from Southern Africa and Madagascar.

11)

Comparative phylogeny within Podocarpaceae (Coniferopsida)

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The second largest gymnosperm family, the Podocarpaceae, consists of more than 200 taxa and shows strong Gondwanan relationships. Weakly supported groups or taxa which had uncertain positions were shown in previous molecular phylogenetic analyses. To address this need we used sequence analyses of *rbcL*, nrITS1 and *NEEDLY* intron2 of over 75% of all Podocarpaceae species (183 accessions of 145 taxa). Furthermore, a comprehensive anatomical and morphological study ensured the accurate identification of the investigated taxa and provided features that support clades within the molecular analyses. Two reconstruction methods (Bayesian inference and parsimony (TNT 1.1)) were used to detect method-independent monophyletic groups. Our results show three major clades: the prumnopytidioid, dacrydioid, and podocarpoid clades. In total, 20 new prominent groups, including 10 new monophyletic groups within the formerly poorly resolved genus *Podocarpus*, were discovered. The monotypic *Sundacarpus* is placed back within *Prumnopitys* and Phyllocladaceae are subsumed into the Podocarpaceae again.

12)

Phylogenetics of Caprifoliaceae s.l. tribe Linnaeae (Dipsacales)

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Linnaeae, with seven genera is a small group of dicotyledonous shrubs distributed mainly in China. Many taxa from the tribe are highly prized in horticultural circles (e.g., *Abelia* and *Kolkwitzia*). The group displays a diverse range of inflorescence morphology, from reduced to compound thyrses, often with accrescent bracts and organs recaulescence. We present a molecular phylogenetic analysis indicating that the genus *Abelia* is not monophyletic and forms two distinct clades. This led us to reevaluate morphological characters and discover that a new group exists with two good synapomorphies (terminal paired flowers and clavate nectaries). We subsequently described this clade as the new genus *Diabelia*. In our future work we intend to use amplified fragment length polymorphisms (AFLPs) to study selected commonly cultivated plants from Linnaeae. This study will aim to clarify the variability between and within taxa and establish a more robust nomenclature.

13)

Fusion and duplication finder BLAST (fdfBLAST): A systematic tool to detect differentially distributed gene fusions and resolve trifurcations in the ToL

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Reconstruction of the ToL is often unresolved due to horizontal gene transfer, hidden paralogy, and long branch attraction. Alongside traditional phylogenetics, additional methods would provide better resolution in reconstructing the ToL. Gene fusions are useful characters that can help resolve contentious branching relationships. fdfBLAST compares genomes for the presence of differentially distributed gene fusions, which can then be polarised with the help of phylogenetics and used as synapomorphies on the ToL. fdfBLAST was tested against a previous study identifying fusion events between *A. thaliana* and *O. sativa*. Re-analysis of their results compared to fdfBLAST's analysis of the same genomes indicated relative rates of gene fusion/fission events were reversed compared to the original dataset and literature. This has implications for using gene fusions as evolutionary informative synapomorphies; the identification of lower rates of reversion suggests these characters are less likely to be homoplasious; therefore representing useful tools for polarising evolutionary relationships.

14)

Different patterns of variation of inflorescence structure in two species of *Ruppia* (Ruppiaceae, Alismatales)

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Despite extensive debates on taxonomy of *Ruppia*, most accounts recognize at least two species, *R. maritima* and *R. cirrhosa*. We compared inflorescence morphology and vascular anatomy in these two species. Apart from inflorescences of typical structure (open spikes with two flowers) both *R. maritima* and *R. cirrhosa* develop spikes with at least partially fused flowers. *R. maritima* has a tendency to reduction in the number of flowers to one, while *R. cirrhosa* tends to increase the number of flowers up to three. In both species, complete fusion of two lateral uppermost flowers results into a terminal flower-like structure of unstable morphology. The species differ in presence or absence of stamens with inverted polarity in abnormal inflorescences. Our results contribute to understanding possible pathways of evolutionary transformations in flowers and inflorescences.

15)

Revision of the genus *Caridops* (Heteroptera: Lygaeoidea, Rhyparochromidae)

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The Rhyparochromini is a large tribe within the family Rhyparochromidae, distributed worldwide. In the tribe the genus *Caridops* is one of the smaller genera with 11 described species. The species are known from China (four species), India (four species), Sumatra, Myanmar and Vietnam. We examined a larger number of unidentified specimens from collections of different European museums. In the material we found five new species. In addition we found some new combinations, there are the follows: *Caridops albomarginatus* (Scott, 1874) is transferred to the genus *Eucosmetus*, and *Eucosmetus formicarius* Breddin, 1907 to the genus *Caridops*. We described the male of the species *C. admistus* (Distant, 1909) and *C. formicarius* (Breddin, 1907) for the first time.

16)

The evolution of the folate biosynthesis gene fusions in the eukaryotes

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Shared derived genomic characters such as gene fusion events can be useful identifying deep-branching clades in the tree of life. We report a newly identified tri-fusion which encodes the consecutive folate biosynthesis enzymes: DHNA, HPPK and DHPS. Using comparative genomics and phylogenetics the HPPK-DHPS bi-fusion was identified as a putative synapomorphy for the eukaryotes with several subsequent losses in certain groups, the tri-fusion was identified as a possible synapomorphy for the unikonts (a holophyletic clade encompassing: Metazoa, Fungi, and Amoebozoa). Reversions of this gene fusion character were identified within the unikonts along with a tandem duplication of the DHNA domain in basidiomycetes and ascomycetes (Dikarya) and inter-domain HGT events. In conclusion, the DHNA-HPPK-DHPS tri-fusion is a putative synapomorphy for the unikonts, however the loss and transfer of this character makes it difficult to evaluate the reliability of this synapomorphy.

17)

Cryptic diversity in the European Wall-rue

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The European fern flora is arguably among the best-known floras globally, as a result of its small size of ca.100 species, extensive collections, exhaustive morphological studies for

more than 200 years, and the more recent application of biosystematics. However, here we show that DNA taxonomic approaches can still recover unrecognized fern diversity in the European fern flora. Wall-rue (*Asplenium ruta-muraria*) is among the most widespread and common ferns in Europe. The majority of wall-rue specimens are tetraploids, assumed to be the autopolyploid offspring of diploid Wall-rue (*A. dolomiticum*). Diploid Wall-rue occurs on calcareous, relictual areas in the south of the Alps. In this study, we show evidence for the occurrence of two cryptic diploid species with distinct distribution areas. This hypothesis is based on extensive sampling throughout Europe, examination of ploidy levels using spore size and cytoflowmetry, phylogenetic evidence using chloroplast DNA sequence data, and evidence for reproductive isolation using allozyme data.

18)

Notes on the natural history of *Pipa pipa* (Linnaeus, 1758), (Anura, Pipidae)

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Pipa pipa is an emblematic and endemic aquatic frog from the Amazonian Basin and much of its biology remains poorly known. In this paper we focused on some aspects of *Pipa pipa* natural history, such as sexual dimorphism, diet, reproduction and morphological geographic variation. Fifty six individuals of *Pipa pipa* were measured for 23 morphological variables and analyzed after a principal component analysis (PCA) and a Fischer's linear discriminant function (DF). Data on diet and gonad development were studied in one population. The morphometric study showed that forearm diameter and snout length are sexual dimorphic characters, both larger in males. The most abundant item found in the species diet was Cyclopoida, whereas Heteroptera represents the one with the highest occurrence in stomachs.

19)

Testing a purely morphological character matrix for salamanders

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Living salamanders are represented by over 580 species within 10 families but the relationships of many fossil taxa remain uncertain. Morphological characters are needed in order to fit the extinct taxa into a phylogeny with modern forms, but their use is complicated by the fact that salamanders are a diverse group including many convergent neotenic, aquatic and terrestrial taxa. A new morphological matrix was developed using representative members of living families coded for 100 osteological characters. This study compares the results from analyses of the data set (full and partitioned character sets) with the available molecular and combined evidence trees. This is to provide a test of the character set before extending the matrix to include fossil taxa. Preliminary results are mixed but show, for

example, that although the atlas vertebra is frequently used as a holotype in fossil taxa, its characters perform poorly in phylogenetic analysis.

20)

Evolution of asymmetrical glochidia in the Unionidae (Mollusca: Bivalvia)

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Glochidial morphology has been an important character in freshwater mussel systematics for over 100 years. Despite its demonstrated taxonomic significance, glochidial morphology has not been considered in most modern phylogenetic studies. For example, five Southeast Asian genera have been observed to possess asymmetrical glochidia, which have a prominent marginal process on one of the two glochidial valves. Furthermore, these genera have never been strongly supported in any phylogenetic study. Although many larval characters are homoplastic, we hypothesize that this asymmetrical larval morphology represents a novel synapomorphy that is in disagreement with the current classification. Our research uses a combined evidence approach that utilizes mitochondrial (CO1 and 16S) and nuclear (28S) genes, as well as morphology to test the monophyly of genera bearing asymmetrical glochidia. Tree estimation methods utilized include maximum parsimony, maximum likelihood and Bayesian inference. The results of this research will be discussed in the context of freshwater mussel larval evolution and classification.

21)

Ectomycorrhizal relationships and preliminary conservation assessments of the *Berlinia* clade (Leguminosae-Caesalpinioideae)

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Ectomycorrhizal relationships are mutualistic plant-fungus associations very frequent in temperate and boreal forest. Ectomycorrhizal relationships are also reported in tropical areas, such as the *Berlinia* clade (Leguminosae-Caesalpinioideae) which comprises about 180 tropical African tree species. IUCN Red List conservation assessments are available for one third of the *Berlinia* clade, whereas none of the fungal symbionts have been evaluated.

We assembled a data set (>10,000 herbarium specimens) for the *Berlinia* clade, but found similar data for the fungal symbionts lacking. From specimen data we estimated preliminary conservation assessments for the species in the *Berlinia* clade, and assessed the minimum number of specimens needed for a reliable range estimate. We also made an independent comparison between preliminary range-based assessments with full Red List assessments. In the light of these results, we make recommendations how to produce actionable conservation assessments for data-poor species.

22)

Genetic and morphologic data unveil two overlooked Southern Ocean lysianassoid species (Crustacea, Amphipoda)

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Species diversity is difficult to assess for Southern Ocean taxa due to patchy sampling and the frequent occurrence of cryptic or overlooked species. The amphipod superfamily Lysianassoidea is the most abundant and diverse amphipod taxon in the Southern Ocean. However, correct identification is hindered by rudimentary descriptions and the lack of diagnostic characters, in particular for the genera *Tryphosella* and *Uristes*. Hence, the number of lysianassoid species described may not represent the true diversity of the group. In a genetic case study, analyses of the mitochondrial CO1 and the nuclear 18S and 28S rRNA genes of *Uristes murrayi* (Walker, 1903) revealed three well-supported clades. In this study, detailed morphological investigations (morphometric, light- and scanning electron microscopic analyses) were performed in order to search for yet overlooked diagnostic morphological characters. The results from this integrative taxonomic approach reveal the presence of two distinct new species within nominal *U. murrayi*.

23)

A geometric morphometric analysis of ruminant (Ungulata: Artiodactyla) and ornithopod (Dinosauria: Ornithischia) snouts: comparative and functional ccomorphology

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Snout shape is a prominent aspect of herbivore ecology concerning feeding strategy, affecting forage selectivity and intake rate. Within ruminants, feeding classes are partially delimited based on snout shape, with grazing species attributed 'blunt' and browsing species 'pointed' snouts. Here, this aspect of functional ecology is analysed in a statistically rigorous geometry-based framework, principally testing whether feeding strategy is consistent with snout morphology using a two-dimensional profile of the premaxilla in ventral aspect. A secondary objective is to assess this approach using ornithopod dinosaurs, the putative extinct analogues of modern ruminants. It is revealed that when ruminants are classified based on assigned feeding strategies, they cannot be discriminated on the basis of their shape profile. Conversely, ornithopods are found to exhibit patterned shape variation between 'blunt' and 'pointed' shapes. This pattern exists in both a phylogenetic and temporal context, and may relate to browsing height and forage selectivity.

24)

A combined analysis approach to the phylogeny of the Talpidae

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The family Talpidae, consisting of 17 extant genera, exhibits some of the most pronounced apomorphies amongst mammals. Although best known for their fossorial specialisations, a number of genera exhibit semiaquatic adaptations (*Desmana*, *Galemys*, *Condylura*) or possess a more generalized body plan (*Urotrichus*, *Neurotrichus*, *Uropsilus* and *Dymecodon*). In 2006 Sanchez-Villagra et al. carried out a detailed morphological study of the Talpidae with the aim of elucidating the evolution of talpid fossoriality. They produced a genus-level phylogeny based on 157 morphological characters. This topology is tested herein by combining 8 loci from both mitochondrial and nuclear DNA to produce the most comprehensive molecular phylogeny of the Talpidae to date. Bayesian analysis is used to analyse a concatenated supermatrix of both molecular and morphological partitions in Mr Bayes. Analyses suggest an early origin for fossoriality in the Family, with convergence between the two highly fossorial clades.

25)

Systematics of *Paepalanthus* sect. *Diphyomene* Ruhland (Eriocaulaceae)

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A revision of the taxonomy and morphology of *Paepalanthus* sect. *Diphyomene* (Eriocaulaceae) is presented. This monograph is based on field and herbarium studies. The group, consisting of 18 species restricted to South America, is distinguished by the tribotryum-shaped inflorescence structure with terminal dibotrya and terminal basic unit, dolabriform sepals of the pistillate flowers, and completely reduced staminodes in the pistillate flowers. Most species are narrowly distributed and usually restricted to a single locality. The exceptions are *P. chiquitensis* and *P. erectifolius*, which are widely distributed in South America and along the Espinhaço Range, respectively. Populations of species of *Paepalanthus* sect. *Diphyomene* occur predominantly in savannas of Brazil, Bolivia, Colombia and Venezuela, although some are also distributed through the Amazonian “Campinas” and campos rupestres of the Espinhaço Range. Taxonomic and morphological diversity is concentrated in the “Chapada dos Veadeiros” in Goiás. Based exclusively on the extent of occurrence, 13 species are considered critically endangered, one endangered, two vulnerable, and two running no risk. Besides comments on the section, the taxonomic survey consists of an identification key, a group description and detailed descriptions of each species, with commentaries, distribution maps, photos, and line drawings.

26)

South East Asia biogeography: new insights with a new methodological approach

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Historical biogeography is going through an extraordinary revolution concerning its foundations, basic concepts, methods and relationships to other disciplines of comparative biology (Crisci, 2001). Cladistic approach was applied to historical biogeography since the work of Nelson G. J. and N. Platnick I. (1981), Nelson, G. J. and Ladiges P. Y. (1991a), Nelson, G. J. and Ladiges P. Y. (1992b).

We want to use the Three-Item Analysis method applied to biogeography in order to test and valid it. We focus on a region particularly complex and largely debated. The area around the Wallace's line is biologically and geologically a complex area located in the centre of the Indo-Australian Archipelago. The main goals of this study are a better understanding of a new methodological approach for biogeographic studies and an improvement of the knowledge of South East Asia biogeography. We present here preliminary results on a shorter sampling for this region.

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27)

Revision of genus *Tachytatus* (Heteroptera, Pentatomomorpha, Lygaeoidea, Rhyparochromidae)

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True bugs (Heteroptera) are among the largest groups of insects with gradual metamorphosis, and are exceeded in species numbers only by the truly immense groups with complete metamorphosis. Altogether, there may be some 37,000 described species of Heteroptera, in which family Rhyparochromidae represented by 14 tribes and about 1950 species. The Oriental region is the least investigated area among the habitats of the seed bugs.

The Rhyparochromid tribe Ozophorini contains species from all over the world (Slater, 1964; Slater & O'Donnell, 1995). Most of these species live in tropical America and South-Eastern Asia. We are working on the Oriental genera of this group, e.g. on the genus *Tachytatus*. This genus described by Ewald Bergroth in 1918 with only one species *T. prolixicornis* from the Philippines. We borrowed rhyparochromid specimens from various European museums. Among them some belong to the genus *Tachytatus*. These are

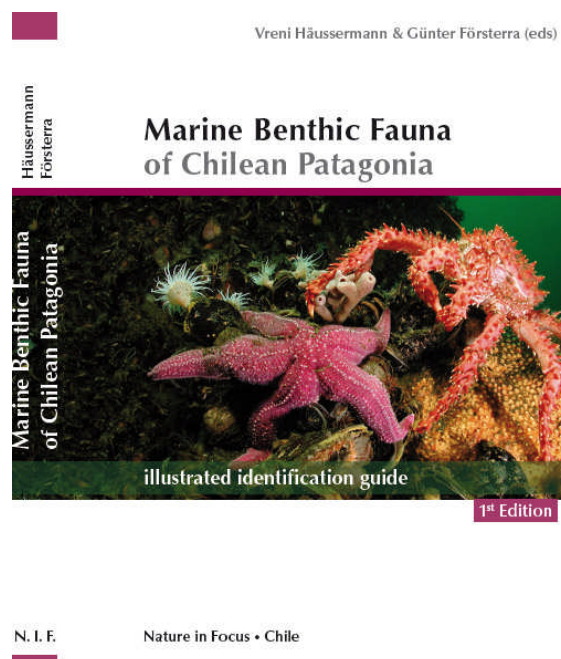
collected from the Oriental region: Philippines, Malaysia, Borneo, Sumatra, Celebes (Sulawesi) and are not conspecific with *T. prolixicornis*. Therefore we are describing four new species now.

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Prizes will be awarded for the most promising oral and poster presentation as judged by a small panel of systematists. Please inform the organizing committee if you wish to be excluded from consideration. Prizes include copies of the following volume:

Marine Benthic Fauna of Chilean Patagonia - illustrated identification guide

<http://www.PatagoniaMarina.info>

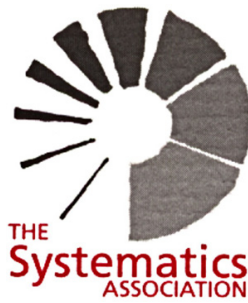


The Systematics Association is committed to furthering all aspects of systematic biology. It organises a vigorous programme of international conferences on key themes in systematics, including a series of major biennial conferences. The association also supports a variety of training courses in systematics and awards grants in support of systematics research.

Membership is open to amateurs and professionals with interests in any branch of biology, including microbiology and palaeontology. Members are generally entitled to attend the conferences at a reduced registration rate, to apply for grants from the Association and to receive Newsletters and mailings of information.

The Systematics Association was founded in May 1937 as the "Committee on Systematics in Relation to General Biology" to provide a forum for the discussion of the general theoretical and practical problems of taxonomy. An outline of the original objectives of the Association was published in *Nature* 140:163 (1938). The first of the Association's publications, *The New Systematics*, edited by the late Sir Julian Huxley, focused on new data from cytogenetics, ecology and other fields. Since then the Association has pioneered discussion on many new developments in systematics and more than 50 Special Volumes have been published. These have included systematic surveys of groups as diverse as haptophyte algae, tetrapods, lichens, free-living flagellates and haematophagous insects. Other volumes have explored fields such as phylogenetic reconstruction, systematics and conservation, genome evolution and the emergence of the biosphere. The Association also publishes books derived from training courses and on general aspects of systematics.

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



THE SYSTEMATICS ASSOCIATION MEMBERSHIP APPLICATION FORM

Title: _____ **Name:** _____

Institute: _____

Address: _____

City: _____ **Postal/Zip code:** _____

Country: _____

Email: _____

Research Interests:

We may occasionally contact you via email to publicise the Association's events such as talks or meetings. If you would prefer not to be notified by email please tick this box.

We will not pass your email to any other organizations.

Membership Rates:

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

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

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

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

Signature: _____

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Please return this form to: Dr. Jonathan Bennett, St. Paul's School, Lonsdale Road, LONDON, SW13 9JT, United Kingdom.

The Systematics Association is a registered charity.



The Systematics Association Gift Aid Declaration

For membership subscriptions and donations to the Systematics Association
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Details of Donor

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I would like the Systematics Association to treat all membership subscriptions and donations I have made in the last six years and all membership subscriptions and donations I make from the date of this declaration, until I notify you otherwise, as Gift Aid donations.

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Dr Jonathan Bennett, St. Paul's School, Lonsdale Road, London SW13 9JT

Please read the following notes before returning your Membership

1. You can cancel this declaration at any time by notifying the Systematics Association.
2. You must pay an amount of Income Tax and/or Capital Gains Tax at least equal to the tax that the Systematics Association reclaims from your membership subscriptions or donations in the tax year (currently 25p for each £1 you give).
3. If in the future your circumstances change and you no longer pay tax on your Income and Capital Gains equal to the tax that the Systematics Association reclaims, you can cancel your declaration.
4. If you are unsure whether your membership subscriptions or donations qualify for Gift Aid tax relief, then ask the Systematics Association or contact your local tax office for leaflet IR113 Gift Aid.
5. Please notify the Systematics Association if you change your name and address.

STANDING ORDER - The Systematics Association



AUTHORITY

Please complete the following and return to your bank if you wish to set up a standing order.

To: The Manager, Address of Bank or Building Society:

Instruction to your Bank or Building Society:

Please pay the sum of £20 annually on 1 June to the Systematics Association
Account No. 21539175, sort code 40-11-18 at HSBC., P.O. Box 68, 130 New Street,
Birmingham, B2 4JU.

Name of account to be debited: _____

Account number: _____

Sort Code _____

Signature: _____

Date: _____