



6th Young Systematics Forum

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Thursday, 9th December 2004
 Flett Lecture Theatre
 The Natural History Museum
 London, UK



Organisers: Dr. Mark Carine and Dr. Angie Newton

Images from the 5th Biennial poster.
From the top;

seed, unknown origin
(*Bignoniaceae* sp.)

palm fruit, Phillipines
(*Metroxylon sagu*)

barley, UK
(*Hordeum distichon*)

fossilised sea urchin, Tunisia
(*Mecaster* spp.)

cockle shell
(*Cardium edule*)

flower beetle, Kenya
(*Gnathocera trivittata*)

grass vole skull, UK
(*Microtus* sp.)

butterfly, South America
(*Heliconius melpomone*)

purple sea snail, worldwide
(*Janthina janthina*)

beetle, unknown origin
(*Sagra bouqueti*)

butterfly, UK
(*Pieris rapae/ Anthocharis cardamines*)

ammonite, UK
(unknown sp.)

sea urchin, Greece
(*Arbacia lixula*)

pheasant feather, UK
(*Phasianus colchicus*)

fossilised shark tooth, USA
(*Isurus* sp.)

money cowrie, Indo-Pacific
(*Cypraea moneta*)

whitebait, UK
(*Clupea sprattus*)

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Introduction

The annual **Young Systematists' Forum**

represents an exciting, setting for postgraduate students and young postdoctoral researchers to present their data, often for the first time, to a scientific audience interested in taxonomy, systematics and phylogenetic inference. The meeting provides an important opportunity for budding systematists to discuss their research in front of their peers within a supportive environment. Supervisors and other established systematists are also encouraged to attend.

There is space for up to 15 speakers with additional places available for those wishing to present a poster. A prize will be awarded for the most promising oral and poster presentations as judged by a small panel on the day.

Registration is **FREE**. Please let us know if you wish to attend. Send applications by email to **Dr. Mark Carine** (m.carine@nhm.ac.uk), supplying your name, contact address and stating whether or not you wish to give an oral or poster presentation. Space for either will be allocated subject to availability and for a balanced programme of animals, plants, molecular and others research.

Abstracts must be submitted by email in English no

flower, unknown origin
(*Euphorbia fulgens*)

lichen, Austria
(*Letharia vulpina*)

seed, South America
(*Erythrina lanceolata*)

artwork by:
Diccon Alexander
T: 00 44 (0)7906 078658
E: (diccona@hotmail.com)
www.diccon.com

later than 10th November 2004. The body text should not exceed 150 words in length. If the presentation is co-authored, then the actual speaker (*oral*) or presenter (*poster*) must be clearly indicated in **BOLD** text.

All registered attendants will receive by e-mail further information about the meeting, including abstracts, one week in advance. This information will also be displayed on the Systematics Association website (www.systass.org).

Programme

9.30 Registration

10.00 Welcome and introduction

Laura Kelly & Alastair Culham The Development of Low Copy Nuclear Gene

10.10 Regions for Inferring the Pattern and Process of Evolution in Plants:

Digitalis/Isoplexis as Exemplars

10.30 **Barbara Rinkel** Revising the taxonomy of the green algal genus *Acrochaete* (Chlorophyta) using molecular techniques in conjunction with morphology

Meredith Murphy Thomas, N.C.

Garwood, W.J. Baker, S. Henderson, D.R.

10.50 **Hodel, S.J. Russell & R.M. Bateman** A Molecular Phylogeny of the Palm Genus *Chamaedorea*

11.10 **Maria S. Vorontsova, P. Hoffmann & M.W. Chase** Evolution of the *Andrachne* clade (Phyllanthaceae or Euphorbiaceae s.l.)

11.30 Tea, coffee and posters

12.00 **Ruth Eastwood** The Domestication of *Lupinus mutabilis*

12.20 **Kehan Harman, J. Moat, E. Nic Lughadha, J. Dransfield, R. Magill, B. Thiers & A. Paton** Accelerating the Production of Preliminary Conservation Assessments

12.40 **Gayle Philip** Supertree analyses reveal that the classical Plant-Animal-Fungi relationship may be correct

13.00 Lunch

14.00 **Rajith Dissanayake** A taxonomic revision of the Genus *Funambul* (Sciuridae)

- 14.20** **Nigel J. Marley** Cosmopolitan taxa in the Phylum Tardigrada - Fact or Fiction?
Boris F. Striffler Speciation in the
- 14.40** afrotropical scorpion genus *Pandinus* Thorell, 1876 (Scorpiones, Scorpionidae)
Adriaan Gittenberger, E. Gittenberger, &
- 15.00** **B.W. Hoeksema** Mushroom corals and associated gastropods: phylogenies and distributions
- 15.20** Tea
Shelah Morita Phylogeographic structure of tongue length in the long-tongued
- 15.50** horsefly pollinator *Philoliche aethiopica* (Diptera: Tabanidae)
Shen-Horn Yen, C. Lopez-Vaamonde, I. Sims & D.R. Davis Evolution of Sexual
- 16.10** Dimorphism, Host Use and Female Case Architecture in Bagworm Moths
Andrea Waeschenbach Reconstructing
- 16.30** the phylogeny of a ctenostome bryozoan genus, or not
Birgit H M Meldal Morphological evolution
- 16.50** of the Phylum Nematoda - molecular phylogeny versus environmental signal
Closing comments and presentation of
- 17.10** prizes for best oral and poster presentations Dr Barry Leadbeater, President of the Systematics Association
- 17.25**
- Reception
- 19.00**
-

Abstracts

Oral Presentations

A taxonomic revision of the Genus *Funambulus* (Sciuridae)

Rajith Dissanayake
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Asian Palm squirrels (*Funambulus* spp) include highly conspicuous mammals from the Indian subcontinent. Yet they

are much in need of taxonomic revision. Of the five recognized species, *F. palmarum* (the common palm squirrel) has been allocated to some 12 taxa in India and Sri Lanka. This species intergrades with its relative *F. tristriatus* currently in three problematic subspecies. Very little is known about *F. sublineatus* and *F. layardi*. New morphometric analyses presented here from NHM material help clarify races of *F. palmarum* and reveal that *F. tristriatus* is unnatural and should be split into at least two taxa, including a new species. Another new squirrel in Sri Lanka allied to "*F. tristriatus*" has been discovered. The current names would need revising on the basis of the validity of types present. The number of known *Funambulus* species is thus set to increase, with similar implications for understudied tropical mammals and birds.

The Domestication of *Lupinus mutabilis*

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Plant domestication spans diverse families and geographic areas. Despite the overwhelming importance of crops for mankind the origins of many remain unknown, leaving fundamental questions about domestication processes unanswered. Domestication also provides an unusual opportunity to investigate direct ancestor descendent relationships. One region where the crops have been poorly documented is the Andes, a global hotspot of early independent domestication. My D.Phil aims to investigate the origin of an Andean pulse crop *Lupinus mutabilis* and quantify the morphological changes which have accompanied it's domestication. ITS, GPAT and CYC gene trees will be presented that resolve the position of Andean lupins within the genus for the first time but reveal that the majority form a large unresolved clade in which *L. mutabilis* is nested. Lack of resolution stems directly from low sequence variation. Low molecular variation in combination with high morphological diversity is characteristic of both domestication and rapid species diversification.

Mushroom corals and associated gastropods: phylogenies and distributions

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Mushroom corals (Fungiidae) and their parasitic snails (Epitoniidae and *Leptoconchus* spp.) are ideal model taxa to study the evolution of host-parasite associations in relation to species diversity. These corals and their parasitic snails were collected throughout the Indo-Pacific and conserved for DNA-sequencing. The resulting "molecular" phylogenies show far more gene-pools among the gastropods than had been distinguished as species on the basis of morphology. This was most obvious in *Leptoconchus* snails, which live inside corals and do not show much, if any, interspecific differences in shell morphology. Although 9 "morpho-species" are characterized in literature (Massin, 2003), molecular data indicate 18 species, which are restricted to their own host species. A similar pattern was found for wentletraps (Epitoniidae). Although 6 species were recognized based on morphology (Gittenberger et al., 2000), molecular analysis suggests 12 species. Most species have large ranges and are found both in the Indian and the Pacific Ocean.

Accelerating the Production of Preliminary Conservation Assessments

Kehan Harman, Justin Moat, Eimear
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Currently only about 3% of plant species have conservation assessments. To meet the targets of the Global Strategy for Plant Conservation (all species assessed by 2010) the rate of assessment needs to be increased massively. Analysing specimen data within a GIS can rapidly produce preliminary assessments and help address this need. We correlated conservation status with the number of herbarium specimens at three institutes for a plant species. Both existing data and newly generated assessments were used to do this. We found the repeated trend that the majority of threatened species had few specimens, and species with few specimens represented the majority of all species. The implications of this are that by databasing only 10 to 20% of collections, targeting those with fewer specimens (10-15) per species, we can assess conservation status for up to 60 % of species and 90% of threatened species globally.

The development of low copy nuclear gene regions for inferring the pattern and process of evolution in

plants: *Digitalis/Isoplexis* as exemplars

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There have been increasing calls for the use of a wider range of molecular character sources for phylogeny reconstruction in plants, not only to improve resolution and support, but also to provide independent assessments of species relationships. However, the number of low copy nuclear gene regions currently available for phylogenetic inference is relatively small, and evidence has shown that some of these genes are not suitable for use in all groups of plants. This study has aimed to develop novel regions for use in species level reconstruction, using the insular woody lineage *Digitalis/Isoplexis* as an example. Five genes were selected and a variety of regions developed for use in phylogeny estimation. The sequence data obtained were assessed for their utility comparative to conventional molecular character sources, and the potential to elucidate not only relationships among the study taxa, but also the processes shaping the evolution of these plants, was explored.

Cosmopolitan taxa in the Phylum Tardigrada - Fact or Fiction?

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There are almost 1000 described species in over 100 genera of waterbears (Animalia: Tardigrada), with specimens collected from almost every habitat on the planet. Of these described species, only a handful of terrestrial species appear to have a global cosmopolitan distribution. This paper addresses whether these species are truly global in their distribution or whether they have been misidentified. I reinvestigate several of these taxa and assess: 1) whether the morphological taxonomic characters used currently in identification are suitable; and 2) if additional reliable characters are available. Current descriptions for the genera and species were then assessed in light of the initial findings. New taxonomic characters are recommended to be included in all future descriptions of waterbear species from the examined genera. Several new taxa will be described using material from the present studies in the near future.

Morphological evolution of the Phylum Nematoda -

molecular phylogeny versus environmental signal

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Great progress has been made in recent decades in designing computer models simulating evolutionary histories. Whilst most models fit processes of molecular evolutionary reasonable well, the same models do not seem to be able to incorporate processes of morphological evolution to its full extent. Morphological traits in nematodes can be very versatile and specialized, in particular in parasitic taxa. Therefore, without an independently derived evolutionary history of this phylum homology assessments of morphological features remain problematic. A phylogenetic analysis of up to 180 morphological characters in a variety of combinations revealed that morphological evolution is greatly influenced by environmental factors. When the morphological phylogenies are compared to classical systems and molecular phylogenies habitat-related signals seem to be stronger than other signals, e.g. from molecular characters. It is suggested that this is due to a) parallel evolution and b) the inability of the computer algorithms to model some of the complex evolutionary histories of morphological characters.

Phylogeographic structure of tongue length in the long-tongued horsefly pollinator *Philoliche aethiopica* (Diptera: Tabanidae).

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Long-tongued horseflies (Diptera: Tabanidae) pollinate a variety of deeply throated flowers. There is substantial spatial variation in proboscis length within some species of these flies. Two possible explanations for this are local adaptation and/or the presence of cryptic species. Previous work shows that this geographic structure in proboscis length correlates with floral morphology over space. However, the evolutionary biology of this group of flies remains unexplored. I examine phylogeographic structure in proboscis length for *P. aethiopica* to determine 1) is there geographic structure in proboscis length?, and 2) if so, is this variation due to cryptic species or selection? Flies from 12 populations of *P. aethiopica* were sampled over the southern part of its range in eastern Africa and analyzed using the mitochondrial gene ND4. Preliminary data suggests that there is geographic structure in proboscis length that is not due to cryptic species.

Supertree analyses reveal that the classical Plant-Animal-Fungi relationship may be correct

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We have tested two controversial hypotheses concerning eukaryotic phylogenetic relationships: the placement of arthropoda and nematodes and the relationships of animals, plants and fungi. We have constructed phylogenetic trees from 780 gene families from 10 completed genomes and amalgamated these into a single supertree. We have also carried out a total evidence analysis on the five protein families that can accurately reconstruct the uncontroversial parts of the phylogenetic tree. We have used data controls and multiple analyses and in 24 out of 26 analyses we find strong support for the grouping of vertebrates with arthropods and plants with animals. The latter finding overturns an eleven year theory of Eukaryotic evolution. We also reanalyze the evolution of intron gain and loss in the *rpL14* gene and find that it is much more compatible with the hypothesis presented here than with the opisthokonta hypothesis.

Revising the taxonomy of the green algal genus *Acrochaete* (Chlorophyta) using molecular techniques in conjunction with morphology

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A combination of morphological and molecular techniques is being employed to revise the taxonomy of the green algal endophytes currently assigned to the genus *Acrochaete*. Collections of a range of algal hosts from around the UK including the red algae *Chondrus crispus*, *Mastocarpus stellatus*, *Dumontia contorta*, *Osmundea pinnatifida*, *O. hybrida* and *O. osmunda*, and the brown algae *Chorda filum* and *Fucus serratus* have been made and the green algal endophytes isolated into culture. Preliminary sequence data of the ribosomal DNA ITS2 region confirm recent findings that the green endophytic algae are more diverse than traditionally thought at the intra- and inter-specific level and that some morphologically similar species belong to different genera. Furthermore, some species are host-generalists, whereas others appear to be host-specialists. The relationship of these endophytic green algae to the type of *Acrochaete*, *A. repens*, is being explored, and analysis of sequence data of regions of the plastid genome is being undertaken to provide further taxonomic resolution. Initial morphological observations have revealed differences in

species growth patterns but a more detailed study of morphological and reproductive structures is needed.

Speciation in the afrotropical scorpion genus *Pandinus* (Scorpiones, Scorpionidae) - from large forest dwellers to small desert species

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Taxonomic review of the genus *Pandinus* confirmed a high diversity in Eastern Africa (20 species) vs. a very low in Western Africa (3 species). Systematic analysis and palaeoclimatic conditions suggest (at least) two radiations causing the extant distribution of the genus. The first, Gondwanian, radiation is represented today only by the monotypic and most basal subgenus *Pandinopsis*. It can be regarded as a relict of the split from the Asian sister genus *Heterometrus*, conserved in the considerably stable rainforests of Cameroon and Gabon. Contrasting the stable environment in the West, East Africa underwent several climatic changes since Pleistocene. Arid periods were interrupted by intermittent humid periods causing habitat fragmentation through expansions and contractions of forests and deserts. At least one additional radiation has taken place since, so that about 20 *Pandinus* species evolved, varying from large forest dwelling species to advanced medium sized species in savannah and semiarid regions of North-Eastern Africa.

A Molecular Phylogeny of the Palm Genus *Chamaedorea*

Meredith Murphy Thomas¹, N.C.
 Garwood¹, W.J. Baker², S.
 Henderson¹, D.R. Hodel³, S.J.
 Russell¹, R.M. Bateman¹

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We conducted the first phylogenetic analysis of *Chamaedorea* (Arecaceae: Ceroxyloideae: Hyophorbeae), the largest neotropical genus of palms, using molecular data from the low-copy nuclear genes PRK and RPB2. The

monophyly of the genus and its placement within its tribe Hyophorbeae have not been systematically tested, nor have more than two of the approximately 100 species of *Chamaedorea* previously been included in a phylogenetic study of the palms. The prevalent current taxonomy of *Chamaedorea* recognizes eight subgenera (Hodel 1992), all based on floral characters, which provide a useful starting point to explore species-level systematics. Sequence data from 63 species, including representatives of all eight subgenera were analyzed using maximum parsimony and Bayesian inference optimality criteria. *Chamaedorea* is resolved as monophyletic with strong support in all PRK, RPB2 and combined analyses. However, at least two of the subgenera are resolved as non-monophyletic, including the two largest, *Chamaedorea* and *Chamaedoropsis*, which are distinguished from each other by the degree of connation in the staminate petals. Phylogenetic resolution among members of these two subgenera shows no pattern of congruence between relatedness and degree of staminate petal connation. Many of the well-supported clades resolved by these gene regions are unsupported by existing morphological evidence and define groups never before proposed within *Chamaedorea*. PRK is found to be more informative than RPB2, but both have proven useful for interpreting species-level relationships in palms. A paralogue of the desired copy of PRK is identified that could be a valuable source of phylogenetic information for future studies.

Evolution of the *Andrachne* clade (Phyllanthaceae or Euphorbiaceae s.l.)

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The *Andrachne* clade is a novel association comprising eight genera previously classified in five tribes and subtribes. *Actephila*, *Andrachne*, *Leptopus*, *Meineckia*, *Poranthera*, *Oreoporanthera*, *Zimmermannia* and *Zimmermanniopsis* contain 129 species of diverse life forms adapted to habitats ranging from tropical rainforest to desert margins and ericoid alpine meadows. Distributions of three genera are geographically disjunct between the Old and the New World. The preliminary results of our phylogenetic study using ITS and matK sequence data of 19 taxa are largely congruent. *Zimmermannia* and *Zimmermanniopsis* are embedded in the *Meineckia* clade. *Andrachne* and *Leptopus* are separate lineages, but *Andrachne cuneifolia* and *Andrachne ovalis* are distinct from both. Dating the nodes of the phylogenetic tree and performing a biogeographical analysis will contribute to a greater understanding of the evolution of these taxa in space and time, particularly their adaptation to specialised ecological niches.

Reconstructing the phylogeny of a ctenostome bryozoan genus, or not

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Bowerbankia is a common bryozoan genus found in the intertidal and shallow sublittoral of temperate shores. Unlike the majority of bryozoan species, *Bowerbankia* belongs to the order of uncalcified taxa (Ctenostomata). The lack of a calcareous exoskeleton, which in the calcified taxa yields numerous morphological characters, can make species identification and the assessment of species boundaries a tricky undertaking. This study set out to re-examine the phylogeny of the genus using cytochrome oxidase I (cox1) and 12S rDNA sequences and focussed in particular on two morphotypes, previously known as *B. gracilis* and *B. caudata* (synonymised as *B. gracilis* in 1956). Material was sampled from mainland UK, Orkney and Shetland Islands, Ireland and New England, covering extensive geographical ranges in order to establish species boundaries and variation in morphology across large geographic distances. The molecular dataset was severely confounded by nuclear mitochondrial pseudogenes, prohibiting the establishment of a clear molecular phylogeny. Cox1 pseudogenes could be readily identified by phylogenetic reconstruction, the presence of disruptive mutations and the examination of dN/dS and transition/transversion ratios. Pseudogene copies of 12S rDNA could not be unambiguously identified. The occurrence of identical pseudogene copies in members of the two suborders, Stolonifera and Carnosa, suggests a common ancestry, which, according to the fossil record, could lie back as far as 140 mya. Morphological and molecular data from a putative new species from New England, provides evidence for its synonymisation with the European *B. imbricata* species. A new *Bowerbankia* species was found in New England.

Evolution of Sexual Dimorphism, Host Use and Female Case Architecture in Bagworm Moths.

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The Family Psychidae contains approximately 600 species in over 300 genera distributed worldwide. This moth family shows one of the most extreme cases of sexual dimorphism within the order Lepidoptera. Males are winged whereas females can be winged, wingless, or very frequently, larviform. This larviform state has been hypothesized as the most derived condition. This extreme sexual dimorphism makes the classification of psychids notoriously difficult. We reconstruct a molecular phylogeny of over 30 species of Psychidae using a combination of 28S rDNA and Cyt *b* sequence data. We use this phylogeny to address the following issues: (1) to assess the validity of the current classification and in particular to test the monophyly of Micro and Macropsychina; (2) to reconstruct how host use and female case architecture have evolved through evolutionary time; (3) to test the hypothesis that ancestral Psychidae lineages had winged females and that the morphological reduction is a derived state and has occurred secondarily in several occasions.

Poster Abstracts

Some aspect of flower structure in *Ailanthus altissima* (Mill.) Swingle (*Simaroubaceae*), in Sardinia (Italy)

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Ailanthus altissima a deciduous trees commonly called Tree of Heaven, is native to Taiwan and central China. It was introduced in Europe by Pierre d'Incarville who sent seeds to England around 1751, and arrived in Italy, at *Padova* botanical garden, in 1760. The species, actually ranked as invasive throughout Europe, is generally described as polygamous, with perfect and male flowers in terminal or axillary panicles. Nevertheless, the flower structure and its features within and between individual and populations has not been investigated so far. This aspect may have important relationships with the spread of the species. Thirty plots has been located in different habitats in Sardinia, where *A. altissima* populations are growing in the wild. First results suggest that Sardinian populations have a peculiar distribution pattern of floral structure: clones with plants bearing only perfect flowers (thus producing vital seeds) are

spatially separated from clones with only male flowers, which propagate only vegetatively.

Molecular phylogenetics of Ebenaceae inferred from plastid and low copy nuclear gene markers

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The pantropical family Ebenaceae comprises of three genera, *Diospyros* L.(c. 600 species) *Euclea* L.(c. 12 - 20 species) and *Lissocarpa* Benth. (8 species). The centers of diversity are in South East Asia, Madagascar, tropical Africa and South America. Few species are of temperate distribution. A preliminary phylogenetic investigation using plastid *matK*, *trnK* intron, *trnL* intron, *trnL/F* spacer, *trnS/G* spacer and nuclear ncp glutamine synthetase is in progress. Parsimony analyses of the *matK* and *trnK* intron clearly show that Ebenaceae are monophyletic and *Lissocarpa* is sister to *Euclea* and *Diospyros*. The subgeneric position of *D. maingayi* is clearly confirmed as indicated by Bakhuizen(1936 - 1955). However the subgeneric status of *Maba* is not well supported. Within subgenus *Eudiospyros* *matK* and *trnK* intron give better resolution for sections *Capanulata* Bakh., *Ebenaster* Bakh., *Glutinosa* Bakh., *Kurzella* Bakh., *Lotus* Bakh. and *Ptychocylix* Bakh.

Enigmatic endemics: molecular phylogenetic relationships of Lake Tanganyikan Crabs

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The endemic crabs from Lake Tanganyika in the family Platythelphusidae form a radiation of nine species, which are morphologically highly derived compared to other East African freshwater crabs. Taxonomic assignments and evolutionary inferences for these crabs have thus far been based exclusively on morphological data. In the present study, we carried out the first phylogenetic analysis of evolutionary relationships within the Platythelphusidae, using sequence data derived from 12S and 16S mtDNA. Our molecular analysis confirms monophyly of the Platythelphusidae, but indicates a recent, explosive divergence of these crabs within Lake Tanganyika and questions the status of some species. Rapid evolutionary branching and morphological diversification is a recurrent theme in ancient lake faunas and is often linked to adaptive radiation. Our molecular phylogenetic analysis provides the framework needed for future testing of hypotheses relating to processes of rapid speciation and striking morphological divergence in freshwater crabs.

Phylogeny of *Hygrohypnum* Lindb. based on molecular data

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The phylogeny of *Hygrohypnum* is reconstructed based on ITS, *trnL-trnF* and *atpB-rbcL* sequences. The analyses were conducted with 15 species of *Hygrohypnum* and 7 outgroup species selected on the basis of previous phylogenetic studies of *Amblystegiaceae s.l.* This study shows well support for two major clades, one with the two species included as representatives of *Amblystegiaceae s.str.* (*Drepanocladus polygamus* and *Palustriella decipiens*), *Hygrohypnum eugyrium* and *H. luridum* (the type of the genus), and the other one with the remaining species of the genus, *Platydictya jungermanniioides*, *Campylophyllum halleri* and the two taxa chosen as representatives of *Calliergonaceae* (Kanda) Vanderpoorten & al., *Calliergon cordifolium* and *Warnstorfia exannulata*. The results support the polyphyly of the genus suggested before based on morphology and molecular data. This study contradicts the close relationship traditionally established between *Hygrohypnum bestii* and *H. duriusculum-H. molle*, as show this taxon in a very well

supported clade (99% BS) with *H. ochraceum* and *H. polare*. *Hygrohypnum montanum* appears in a very well supported clade (95% BS) with *Campylophyllum halleri*, sister to the clade including the majority of species of *Hygrohypnum* (99% BS).

The circumscription of *Cynara* L. (*Compositae*, *Cardueae*): evidence from nrDNA ITS sequence variation

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The ITS region of nrDNA in conjunction with morphological data has been used to study the monophyly and evolution of wild *Cynara* species. *Cynara* L. is a relatively small Mediterranean genus belonging to *Asteraceae*, comprising 8 wild species and the globe artichoke (*Cynara scolymus* L.) a widely cultivated food plant. All wild species are perennial and the genus is characterized by large spiny leaves and heads. The cardoon (*Cynara cardunculus* L.) is mainly Western Mediterranean in distribution but is also present in the Canary Islands and Madeira and has isolated populations in Cyprus and the Turkish part of the Red Sea; *Cynara algarbiensis* Cosson, *C. baetica* (Spreng.) Pau, *C. humilis* L. and *C. tournefortii* Boiss. & Reuter are principally Western Mediterranean in distribution; and *C. cornigera* Lindley, *C. cyrenaica* Maire et Weiller and *C. syriaca* Boiss. are distributed in the Eastern part of the Mediterranean. Parsimony analysis of the ITS data supports the monophyly of *Cynara sensu lato*, i.e. including the distinctive taxa *C. humilis* and *C. tournefortii*. This does not agree with the recent decision to create a new monotypic genus *Arcyna* for *C. tournefortii*. Multiple accessions show that ITS evolves in a complex manner within the genus and hybridisation is one possible explanation for this. However, evidence from morphological cladistic analysis and crossing experiments are contradictory as to the likely parents involved in such an event.

Drifted or relict endemics - the scorpion fauna of the Soqatra archipelago, Republic of Yemen (Scorpiones, Buthidae, Diplocentridae, Hemiscorpiidae)

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Soqotra archipelago is situated in the Indian Ocean close to the Horn of Africa and the border of three zoogeographic regions. The endemic scorpion fauna consists of five arid adapted species belonging to three scorpion families: Buthidae (*Hottentotta*, *Orthochirus*), Hemiscorpidae (*Hemiscorpius*) and Diplocentridae (*Heteronebo*). The tiny *Orthochirus* are exclusively desert adapted species from North Africa and the Southern tip of the Arabian Peninsula. Medium-sized *Hottentotta* are widespread within the African fauna extending across the Arabian Peninsula to India. Typical for Western Orientalis is *Hemiscorpius*, only known from isolated collection sites in Iran, Afghanistan, Arabian Peninsula and Somalia. Of special interest is the clearly monophyletic *Heteronebo* found only on the Soqotra archipelago and Caribbean Islands. This strange pattern is to the extant knowledge not found in any other animal but at least 2 plant genera (*Chapmannia* and *Thamnosma*) have a similarly strange distribution. Possible origins of these distribution patterns are discussed.

Endemic areas of *Psittacanthus* Mart. (Loranthaceae) in the Americas

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In order to carry out an area cladistic analysis, endemic areas for 70 species of *Psittacanthus* (Loranthaceae) have been estimated by using the computer program WORLDMAP* (Williams, 2002). Four groups of species have been clearly recognised. One group is comprised of those species which occur in Mexico with the southernmost ones reaching some parts of Northern Central America, together with two widespread species in these areas. A second group is comprised of South American species distributed in the Amazon basin, coastal areas of Northern Peru and Southern Ecuador, and Southeast Brazil. Two species of this group are also found in Panama and Southern Costa Rica. The third group is comprised of Central American species, all of them endemic to this area and restricted in distribution to small patches within some countries or next to the borders of neighbouring countries. The last group is comprised of three species endemic to some islands of the Lesser Antilles.

Geographical barriers such as mountain chains -The Andes in South America, Sierra Madre del Sur and Sierra Madre Occidental in Mexico- all seem to play an important role in delimiting the range boundaries for some taxa, whereas for other taxa rivers could have led to their geographical isolation and later speciation.

Reconciling Molecules and Morphology in a Definitive Phylogeny of the Order Haplosclerida, Phylum Porifera

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Sponges are of great importance in drug discovery and in the investigation of marine natural products, (producing antibiotic, antifungal, antiviral and cytotoxic substances). This has led to an increased but largely random collection of sponges for pharmaceutical investigations. Greater understanding of relationships within the Phylum Porifera (sponges) should lead to targeted searches for particular species of interest, which would in turn reduce destruction of sensitive marine habitats. Poriferan systematics has been problematical due to insufficient morphological characters and also because many sponge taxa are polymorphic for some characters e.g. surface texture and colour. Many molecular studies have been limited by employing too few taxa or only one gene region. Our aim is to reconstruct the first robust phylogeny of the Order Haplosclerida (important producers of secondary metabolites) by sequencing two to three genes from up to 140 different species. Morphological and other data will be assessed in view of the molecular phylogeny. To date DNA has been extracted from 103 different species. Forty-one partial 28s rRNA gene sequences, seventeen 18s rRNA gene sequences and thirty-six mt cox1 sequences have been aligned to other poriferan sequences downloaded from GenBank. The resulting trees are different from those expected under morphological methods but are in close agreement with each other, suggesting that major changes may have to be made in the classification of this group.

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Last Updated:

25 November, 2005

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