



**8<sup>TH</sup> YOUNG SYSTEMATISTS'  
FORUM**

*7<sup>TH</sup> DECEMBER 2006, FLETT THEATRE,*

*Natural History Museum, London*



# PROGRAMME

## 09.00 Registration

- 09.35 Introduction Juliet Brodie (NHM)
- 09.40 Welcome and Introduction Richard Bateman  
(President, Systematics Association)
- 09.50 Taxonomic escapades with the moss genus *Macromitrium* Joanna Wilbraham
- 10.10 Origin, diversity and evolutionary potentials of apomixes Ovidiu Paun
- 10.30 Large punctuational contribution of speciation to evolutionary divergence at the molecular level Chris Venditti
- 10.50 Floral morphology and ontogeny in Fabales: towards a hypothesis on interfamilial relationships Maria Angelica Bello

## 11.10 Coffee and posters

- 11.40 From Africa to India or vice versa? - Revision and phylogenetic analysis of the genus *Anogeissus* (Combretaceae, Myrtales) based on morphological and anatomical data Gesche Hohlstein
- 12.00 Taxonomic revision of the Mesozoic marine crocodylians Metriorhynchidae, a morphometric and phylogenetic approach Mark Young
- 12.20 The early diversification of the species rich tropical genus *Begonia*: a phylogenetic perspective Will Goodall-Copestake
- 12.40 The morphological and molecular signatures of three red algal *Acrochaetium* spp.: the *A. secundatum* / *A. virgatulum* / *A. luxurians* complex Susan Leta Clayden

## 13.00 Lunch and posters

- 14.00 The phylogeny of Juncaginaceae, a cosmopolitan wetland/coastal family Sabine von Mering
- 14.20 Functional morphology of the genitalia in longhorn beetles (Coleoptera: Cerambycidae) Lasse Hubweber

- 14.40 Phylogeny of the genus *Cordia* L. (Boraginaceae) and systematics of neotropical *Cordia* section *Myxa* (Endl.) DC. Maria de Stapf
- 15.00 Strong divergence between mitochondrial lineages of the Mexican black spiny tailed iguana (*Ctenosaura pectinata*) Eugenia Zarza-Franco
- 15.20 Tea and Posters**
- 15.50 Resolving the base of the brown algal tree (using complete *rbcL* and *psaA* sequence data) with special reference to the Dictyotales Lucie Bittner
- 16.10 Comparative morphology of the gynoeceum in Anacardiaceae and Burseraceae Julien Bachelier
- 16.30 Giant-Pill Millipede Phylogeny and Plate Tectonics (Diplopoda, Sphaerotheriida) Thomas Wesener
- 16.50 Phylogeny of Mediterranean *Lithodora* Griseb.: Some insights into the resolution of the "catch-all" taxon *Lithospermum* L. s.l. Daniel Thomas
- 17.10 Closing comments and presentation of prizes for best oral and poster presentations**
- 17.25 –19.00 Reception**

# TALKS

## Taxonomic escapades with the moss genus *Macromitrium*

**Joanna Wilbraham**

Department of Botany, The Natural History Museum, Cromwell Road, London, UK.

This presentation aims to describe my taxonomic work towards a treatment of the moss family Orthotrichaceae in the Bryophyte Flora of Uganda, which is currently being produced by the British Bryological Society (BBS). This flora will provide the first full account for many genera of the Orthotrichaceae in Tropical Africa.

The Orthotrichaceae is divided into two subfamilies, the Orthotrichoideae and the Macromitrioideae. The subfamily Macromitrioideae contains predominantly tropical genera and is in particular need of revision in Africa. The large and complex genus *Macromitrium* belongs here and this talk will focus on my recent work with this taxon. My research has been based on collections made by the BBS during expeditions to Uganda and Malawi. In the course of identifying this material many interesting discoveries have been made that support new synonymy and extended distribution ranges.

The genus *Macromitrium* could provide interesting research opportunities in biogeography and molecular studies, though the supporting taxonomic work should be completed first. The initial results of this project highlight the importance of further floristic work on bryophytes in under-researched regions, such as the African tropics. This is particularly important considering the valuable role that mosses play in tropical forests and the need for data on bryophyte diversity and endemism for global conservation initiatives.

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## Origin, diversity and evolutionary potentials of apomixis

**Ovidiu Paun**<sup>1</sup> and Elvira Hoerandl<sup>2</sup>

<sup>1</sup>Molecular Systematics Section, Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, UK.

<sup>2</sup>Department of Systematic and Evolutionary Botany, University of Vienna, Rennweg 14, A-1030 Vienna, Austria.

The origin and evolutionary maintenance of apomictic lineages remain largely under debate. Here we review studies on *Ranunculus auricomus* complex using various molecular markers (isoenzymes, AFLPs, microsatellites, DNA sequencing), aiming (1) to validate the role of hybridization, auto- or allopolyploidy, and introgression of apomixis genes in the origin of apomictic lineages; (2) to estimate the different impact of the main factors creating genetic diversity, i.e. ancestry, backcrossing to sexual relatives, residual sexuality, and mutational change; and (3) to outline the evolutionary and ecological implications of genetic variation in the persistence of facultative apomictic complexes.

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## Large punctuational contribution of speciation to evolutionary divergence at the molecular level

**Chris Venditti** and Mark Pagel

School of Biological Sciences, University of Reading, UK.

A longstanding debate in evolutionary biology concerns whether species diverge gradually through time or by rapid punctuational bursts at the time of speciation. From an analysis of 122 published gene-sequence alignments we find that approximately twenty-two percent (22±3.6%) of substitutional changes in phylogenetic trees can be attributed to punctuational bursts of evolution, when such effects are present, the remainder accumulating from normal background gradual divergence. Punctuational effects are more common in plants (56.7±7.8%) and fungi (71.4±16.0%) than in animals (20.6±4.7), possibly owing to differences among these groups in rates of polyploidy and hybridization, but the proportion of total divergence attributable to

punctuational change does not vary among taxa. The size of the punctuational contribution predicts ( $r=0.79$ ,  $p<0.0001$ ) departures from a clock-like tempo of evolution, suggesting punctuational changes should be accounted for in deriving clock-based dates from trees. Punctuational episodes of evolution may play a larger and more widespread role in promoting evolutionary divergence at the molecular level than has been previously appreciated.

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## **Floral morphology and ontogeny in Fabales: towards a hypothesis of interfamilial relationships**

**Maria Angelica Bello**<sup>1,2</sup>, Julie A. Hawkins<sup>1</sup> and Paula J. Rudall<sup>2</sup>

<sup>1</sup>School of Biological Sciences, University of Reading, UK.

<sup>2</sup>Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, UK.

After more than a decade of molecular-based phylogenetic hypotheses of the Angiosperms, some taxa remain unresolved, poor or controversially supported. Particularly, the interfamilial relationships within the economically important order Fabales remain uncertain, despite recent attempts to infer a phylogenetic hypothesis using chloroplast sequences. Fabales includes the species-rich families Leguminosae and Polygalaceae, as well as Quillajaceae and Surianaceae. This circumscription, supported by molecular-based phylogenies, raises questions regarding morphological evolution, such as the potential homologies between papilionate flowers of Polygalaceae and Leguminosae, the origin and development of radially symmetrical flowers of Surianaceae and Quillajaceae, and the evolution of the sepaloid identity of petals and carpel merosity in the order. Sampling representatives of the four families, we compare floral morphology and ontogeny in Fabales to provide new insights into character evolution. The phylogenetic reconstruction within Fabales, potential primary homologous traits, and future perspectives of combined molecular-morphological cladistic analyses will be discussed.

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## **From Africa to India or vice versa? - Revision and phylogenetic analysis of the genus *Anogeissus* (Combretaceae, Myrtales) based on morphological and anatomical data**

**Gesche Hohlstein**

Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany.

The paleotropical genus *Anogeissus* comprises about nine species, which are trees of ecological and economic importance in savannahs and monsoon forests. Evaluation of morphological characters used in floras and a previous revision for species identification revealed a frequent lack of reliability, due to high variability. This study compares 246 morphological characters, several investigated for the first time, resulting in revised species concepts. 33 phylogenetically informative characters were selected for a cladistic analysis including ten ingroup and ten outgroup taxa. The resulting 15 most parsimonious cladograms support the monophyly of *Anogeissus*, but its position within the subtribe *Terminaliinae* remains unclear due to paraphyly of *Terminalia*. Phylogenetic relationships within *Anogeissus* are resolved, yielding two well-supported clades. The basal position of *A. leiocarpa* relating to these two clades is probably a result of hybridization. Hypotheses about the origin of and character evolution, migration and speciation within the genus are discussed within a palaeontological context.

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## **Taxonomic revision of the Mesozoic marine crocodylians Metriorhynchidae, a morphometric and phylogenetic approach**

**Mark Young**<sup>1, 2</sup>

<sup>1</sup>The Natural History Museum, Cromwell Road, London, UK.

<sup>2</sup>Faculty of Life Sciences, Imperial College London, UK.

The interrelationships of Metriorhynchidae, a group of highly marine-adapted crocodylians from the Middle Jurassic to Early Cretaceous, are investigated and taxonomy revised. The study aimed to characterise the dorsal aspect cranial geometry using geometric morphometrics, and reconstruct the group's evolutionary history using cladistics.

Cranial shape is found to be divergent within Metriorhynchidae, with two forms; brevirostrine and longirostrine. This divergence becomes most extreme in the Late Jurassic between *Dakosaurus* and *Geosaurus*.

Phylogenetic analysis found *Teleidosaurus* to be the least marine adapted genus within Metriorhynchidae and the sister taxon to all other genera. This clade, here named Metriorhynchinae consists of a dichotomous split, with one tribe Dakosaurini, containing *Dakosaurus* and the brevirostrine *Metriorhynchus*; and the second, Metriorhynchini, consisting of the longirostrine *Metriorhynchus*, *Geosaurus* and *Enaliosuchus*. With *Metriorhynchus* found to be paraphyletic the resurrection of *Suchodus* Lydekker, 1890 is proposed for the *Metriorhynchus* brevirostrine forms, whilst *Metriorhynchus* is retained for the longirostrine forms.

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## **The early diversification of the species rich tropical genus *Begonia*: a phylogenetic perspective**

**Will Goodall-Copestake**<sup>1,2</sup>, Dave Harris<sup>1</sup>, Pete Hollingsworth<sup>1</sup>, Rod Page<sup>2</sup>

<sup>1</sup>Royal Botanic Garden Edinburgh, 20A Inverleith Row, Edinburgh, Scotland.

<sup>2</sup>Division of Environmental and Evolutionary Biology, University of Glasgow, Scotland.

*Begonia* is one of the largest Angiosperm genera with ca. 1500 herb and shrub species distributed throughout tropical Africa, America and Asia. Relationships between continental level assemblages of *Begonia* species remain obscure due to poorly resolved basal internal nodes in previous phylogenetic studies. To try to resolve these relationships, five chloroplast (ca. 7Kbp) and five mitochondrial (ca. 6Kbp) DNA regions were sequenced from a small sample of exemplar taxa in order to generate duplicate organellar phylogenies. Using a new relaxed phylogenetic approach, key nodes covering continental level *Begonia* relationships were resolved and dated in both organellar phylogenies. Taken together, the results indicated that one or more inter-specific hybridization events occurred early on during the evolution of *Begonia*. Furthermore, comparisons with life history, geological and climatic data suggested that adaptation to seasonal environments and long distance dispersal played a key role during the inter-continental diversification of *Begonia*.

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## **The morphological and molecular signatures of three red algal *Acrochaetium* spp.: the *A. secundatum* / *A. virgatulum* / *A. luxurians* complex**

**Susan Leta Clayden** and Gary W. Saunders

Department of Biology, University of New Brunswick, Fredericton, N.B. E3B 6E1 Canada.

Diminutive, often microscopic, filamentous red algae, with relatively simple vegetative and reproductive features broadly describe members of the related orders Acrochaetiales and Colaconematales. Within the Acrochaetiales, the type genus is *Acrochaetium*, and type species *Acrochaetium secundatum*. For over a century there has been debate in both Europe, and North America, whether this species is synonymous with a similar, less common taxon, *A. virgatulum*. Accounts of the former, *A. secundatum*, often indicate that it has smaller individual cells, and is diminished in overall size and spread of colonies, with respect to *A. virgatulum*,

features with which we concur from our Canadian isolates. A third taxon has also been associated with this species pair, *A. luxurians*, characteristically forming a dense fringe on leaves of the seagrass *Zostera*. We report molecular results (nuclear ribosomal and mitochondrial barcode sequences) for algae fitting each of these morphological descriptions, to test for their synonymy or distinctiveness.

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## **The phylogeny of Juncaginaceae, a cosmopolitan wetland/coastal family**

**Sabine von Mering** and Joachim W. Kadereit

Johannes Gutenberg-Universität Mainz, Institut für Spezielle Botanik und Botanischer Garten, Bentzelweg 9a/b, 55128 Mainz, Germany.

Juncaginaceae is a small, little known family within the basal monocot order Alismatales. This family contains 4-5 genera with about 30 species, which are mostly found in coastal and wetland areas. *Triglochin* (incl. *Cycnogeton*), the largest genus of the family, is distributed almost worldwide. The geographical distribution of Juncaginaceae, with Australia as their centre of diversity and several Southern hemisphere taxa (*Tetroncium*, *Maundia*, *Lilaea*), plus its old age, suggest that the family is of Gondwana origin.

Morphological and molecular characters (*rbcl*, ITS) were used to clarify the delimitation of the family and inter- and intrageneric relationships within Juncaginaceae. First results suggest that (1) *Lilaea*, a genus often placed in its own family based on its divergent floral morphology, falls within *Triglochin*; (2) *Triglochin procera* agg. (Water-ribbons), a monophyletic group from Australia, is sister to the rest of *Triglochin*, and could be segregated as *Cycnogeton*.

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## **Functional morphology of the genitalia in longhorn beetles (Coleoptera: Cerambycidae)**

**Lasse Hubweber**

Zoologisches Forschungsinstitut und Museum A. Koenig, Adenauerallee 160, 53113 Bonn, Germany.

Genitalia of beetles, especially male genitalia, are often used as characters in articles on taxonomy and phylogeny, because of their complex structure and divergent evolution. Very curious is the fact that there are almost never hypotheses concerning the function of the different elements. In my ongoing PhD-project I try to close this gap. After describing different methods of collecting beetles in copula and dissecting them, I will give an introduction on the complexity and terminology of genitalia, followed by some ideas on the possible function of different structures such as the internal sac and tegmen. The tegmen consists of a tegminal strut and parameres. These parameres can be quite variable in appearance, but there are many unsolved questions on their function. The internal sac or endophallus is the intromittent organ in cerambycids, everted during copulation. Therefore, it comprises different sclerites for distinct functions.

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## **Phylogeny of the genus *Cordia* L. (Boraginaceae) and systematics of neotropical *Cordia* section *Myxa* (Endl.) DC.**

**Maria Natividad Sanchez de Stapf**

Universidade Estadual de Feira de Santana, Brazil / Smithsonian Tropical Research Institute, Panama.

The genus *Cordia* L. (Boraginaceae) comprises about 350 species with distribution pantropical. Centres of diversity are in tropical America and Africa. It is characterized for the woody habit, a twice-bifid style, undivided endocarp and cotyledons plicate. Most modern authors have recognized six sections in the genus. *Cordia* sect. *Myxa* (Endl.) DC. is the largest section of the genus with approx. 130 species, the majority of the species (ca. 80 species) in the Neotropics and, recent molecular studies confirmed the monophyly of the section. The section is difficult taxonomically and it has not been treated in a comprehensive manner for the new world since de Candolle (1845). The aims of my research are to evaluate the infrageneric relationships of *Cordia* using molecular and morphological data and, the taxonomic revision of the genus *Cordia* sect. *Myxa* for the neotropical.

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## **Strong divergence between mitochondrial lineages of the Mexican black spiny tailed iguana (*Ctenosaura pectinata*)**

**Eugenia Zarza-Franco**, Victor H. Reynoso and Brent C. Emerson

School of Biological Sciences, University of East Anglia, Norwich, UK.

The threatened iguana species *Ctenosaura pectinata* is endemic to Mexico and lives in a wide variety of environments along the Pacific Ocean coast, the Río Balsas Basin, and on several islands. Although currently recognised as a single species, *C. pectinata* exhibits geographic variation in morphology suggesting a possible complex evolutionary history. Mitochondrial phylogenetic trees and haplotype networks indicate strong genetic divergence between five evolutionary lineages detected within *C. pectinata*. Some of these lineages form zones of secondary contact, and one *C. pectinata* lineage forms a contact zone with *C. hemilopha*, with genetic evidence of hybridisation. Relatively small genetic distances have been found between populations of *C. acanthura* and *C. pectinata*, bringing into question the taxonomic status of *C. acanthura*. Nested Clade Phylogeographic Analysis of mitochondrial and nuclear gene sequences, combined with coalescent based analyses, are being used to infer the likely factors responsible for the observed phylogeographic structure.

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## Resolving the base of the brown algal tree (using complete *rbcL* and *psaA* sequence data) with special reference to the Dictyotales

Lucy Bittner<sup>1</sup>, C. E. Payri<sup>2</sup>, F. Rousseau<sup>1</sup> and B. Reviere<sup>1</sup>

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To improve deep phylogenetic relationships within the brown algae, both available *rbcL* and *psaA* sequences from EMBL/Genbank and 63 new sequences were analysed. A particular sampling effort was done on the Dictyotales since they were previously poorly represented in phylogenetic analyses. Maximum parsimony, maximum likelihood and bayesian inference analyses were performed using 74 taxa (including 38 Dictyotales) and 2500 bases pairs length (1100 bp *rbcL*, 1400 bp *psaA*). For the first time, early divergent orders (e.g. Dictyotales, Onslowiales, Syringodermatales, Sphacelariales) are evidenced, specifically Onslowiales is always sister of Dictyotales whereas Onslowiales was previously tentatively included in the Sphacelariales using morphological criteria. Moreover, excellent resolution was obtained at interspecific level within dictyotalean species.

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## Comparative morphology of the gynoecium in Anacardiaceae and Burseraceae

Julien B. Bachelier and Peter K. Endress

Institute of Systematic Botany, University of Zürich, Switzerland.

Traditionally, Anacardiaceae and Burseraceae have been distinguished on the basis of the ovule number and orientation in the ovary locules. Recently, molecular and morphological phylogenetic studies indicated that Anacardiaceae and Burseraceae are both monophyletic families and in addition, that they form a well-supported clade nested within Sapindales. Floral morphology and anatomy has been studied into some detail only in Anacardiaceae and but is poorly known in Burseraceae. In addition, a broad comparative study of the two families and structural support for this new clade was lacking.

Our results indicate that the gynoecium, and especially the position of the centre of the former floral apex, is very similar in some basal Anacardiaceae (Spondioideae incl. *Spondias*, *Dracontomelon* and *Pleiogynium*) and the basalmost Burseraceae, *Beiselia*. In addition in both families, similar evolutionary trends may be seen with a reduction of the carpel number and an increase of their synorganisation.

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## Giant-pill millipede phylogeny and plate tectonics (Diplopoda, Sphaerotheriida)

Thomas Wesener

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Giant-pill millipedes of the order Sphaerotheriida belong to the Ophistandria, and their sister taxa are the well-known Glomerida in the northern hemisphere. The giant-pill millipede family Sphaerotheriidae has a disjunctive distribution in South-Eastern Australia, India, South Africa and Madagascar.

A first phylogenetic analysis revealed a sister-group relationship between Malagasy and Indian taxa. As a result of this, stridulation organs in giant-pill millipedes are not homologous but evolved independently, three times in fact. Stridulation organs in the Malagasy-Indian subfamily Arthrosphaerinae evolved separately in males and females. The meaning of those stridulation organs is mostly unstudied, but they seem to play an essential role in mating behavior. Furthermore, such stridulation organs are probably the cause for the high number of species which can occur sympatrically on Madagascar.

The current distribution of the clades of Sphaerotheriidae corresponds perfectly to the time when Gondwana broke into several continents approximately 180 – 90 millions years ago. This means that the present clades are presumably old, dating back to the Paleozoic Era.

Dispersal seem to play only a minor role in the current distribution of giant-pill millipedes. Those limited dispersal abilities seem to be the cause for the small area of distribution found recently in the Malagasy giant-pill millipede species of the genera *Zoosphaerium* and *Sphaeromimus*. Two other features only displayed in Malagasy giant-pill millipedes are female gigantism and Batesian mimicry.

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## **Phylogeny of Mediterranean *Lithodora* Griseb.: Some insights into the resolution of the “catch-all” taxon *Lithospermum* L. s.l.**

**Daniel C. Thomas**, Maximilian Weigend and Hartmut H. Hilger

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*Lithodora*, a Mediterranean genus of the Boraginaceae, tribe Lithospermeae, comprises nine species of often narrowly endemic dwarf shrubs and shrubs. Phylogenetic relationships of *Lithodora* were investigated with ITS1 and *trnL<sub>UAA</sub>* intron sequences using parsimony and likelihood analyses. The results strongly indicate a polyphyly of *Lithodora*. The majority of species forms a monophyletic clade (“*Lithodora* I”) in a well supported trichotomy together with a *Lithospermum* s.s. clade and a Buglossoides clade. A smaller number of species (“*Lithodora* II”) falls into another monophylum in a well supported clade including the monotypic genera *Paramoltkia*, *Mairetis* and *Halacsya*. A critical reevaluation of carpological characters traditionally used to delimit *Lithodora* corroborates the results of the molecular analysis, and indicates the homoplasy of the mericarp appendages and cupulate areoles found in the genus. The phylogenetic resolution here obtained is formalized by the establishment of *Glandora* gen. nov. incorporating “*Lithodora* I.”

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## **POSTER ABSTRACTS**

### **Phylogeny of *Chilades* Moore, 1881 (Lepidoptera, Lycaenidae, Polymmatinae) inferred from mtDNA sequences of *COI* and *COII*: Evolution of convergent wing patterns and hostplant associations**

**Li-Wei Wu**<sup>1</sup>, Shen-Horn Yen<sup>2</sup> and Yu-Feng Hsu<sup>1</sup>

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<sup>2</sup>Department of Biological Sciences, National Sun Yat-Sen University, Kaohsiung, Taiwan

Previous studies showed that each species of *Chilades* butterflies use distinctly different hostplants. Some of these butterflies feed on *Cycas* plants, the members of the ancient gymnosperms, but the others feed on angiosperms such as Fabaceae or Rutaceae. Multiple species in the currently defined *Chilades* are known to be associated with the cycads. It is well documented that very few butterflies are capable of utilizing gymnosperms as larval hosts, thus it should be interesting to investigate the origin of the cycad-feeding within a phylogenetic framework. Three questions we hope to elucidate are: (1) whether the genus *Chilades* is a monophyletic group; (2) to decide the number of colonization events to cycads for these lycaenids; and (3) the direction of hostplant switches among these butterflies.

We sampled lycaenid butterflies currently place within the genus *Chilades* and members of a number of polymmatine genera that are considered closely related to *Chilades* by various authors. Fragments of the mitochondrial *COI*+*COII* (about 1900bps) sequence data were obtained employing standard PCR

procedures, and maximum parsimony (MP) was used as the criteria for the phylogenetic analysis. The results reveal that (1) The members of *Chilades* sensu lato as currently defined do not form a monophyletic assemblage, but if the members of *Freyeria* are removed from *Chilades* sensu lato, the remaining taxa forms a monophyletic *Chilades* sensu stricto; (2) The *Chilades* species that are known to be specialized on cycads do form a monophyletic group within *Chilades* sensu stricto, suggesting the colonization of cycads occurred just once in the evolutionary history of these lycaenids; (3) the results indicates the cycad-association was derived from legume association, while the Rutaceae-association is an independent event unrelated to the colonization of cycads. Our results support the idea that colonization of gymnosperms from angiosperms remains a rare event in butterflies as any butterfly groups known to be specialists on gymnosperms succeeded the colonization processes just once in the evolution of their host-associations.

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## The evolution of sepal-petal differentiation in basal angiosperms

Kate A. Warner<sup>1,2</sup>, Paula J. Rudall<sup>2</sup> and Michael W. Frohlich<sup>1</sup>

<sup>1</sup>Department of Botany, The Natural History Museum, Cromwell Road, London, UK.

<sup>2</sup>Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, UK.

The conventional concept of an "undifferentiated perianth" obscures the fact that individual perianth organs may be differentiated into sepaloid (sepal like) and petaloid (petal like) regions. We have observed such differentiation in genera from several families including the basal angiosperms *Nuphar* and *Nymphaea* (Nymphaeaceae). In *Nuphar* the perianth organs traditionally called sepals exhibit both yellow petaloid and green sepaloid patches that show anatomical distinctions in addition to color differences. In *Nymphaea* the perianth organs near the boundary between "sepals" and "petals" are often subdivided into sepaloid and petaloid regions, rather than being intermediate in morphology over their entire surfaces. Our data suggest that the environment of a perianth organ helps specify these regions. The traditional concept of "sepal" and "petal" includes a hidden assumption that we believe is false: that sepalness and petalness must refer to whole perianth organs. We suggest a novel theory of perianth evolution, in which differentiation of the perianth into sepals and petals was predated by the evolution of sepalness and petalness.

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## Finding and testing gene fusions as evolutionary markers

Guy Leonard and Thomas A. Richards

University of Exeter, Hatherly Laboratories, Prince of Wales Road, Exeter, Devon, UK.

Recently the eukaryote phylogeny was re-rooted using the DHFR-TS gene fusion character, moving the root from the amitochondrial-excavate branch (*Trichomonas* & *Giardia*) to between the unikonts (opisthokonts & Amoebozoa – DHFR and TS unfused) and the bikonts (Excavata, Cercozoa, Plantae & chromoalveolates - DHFR-TS fused). However, horizontal gene transfer (HGT), endosymbiont gene transfer (EGT) or hidden paralogy in the DHFR-TS gene families was not investigated. This poster re-examines this rooting using phylogeny to test the validity of DHFR-TS as an evolutionary synapomorphy and offers a new program fdfBLAST for the detection of gene fusions and duplications for evolutionary analyses. The DHFR-TS analyses did not support unikont or bikont monophyly but demonstrated the phylogenies were weakly supported with some evidence of HGT, EGT and ancient paralogues suggesting that the DHFR-TS fusion character may be an unreliable evolutionary synapomorphy. fdfBLAST was used to compare ten highly divergent genomes and detected 24 differentially distributed gene fusions. The results of the program fdfBLAST did not show strong support for bikont/unikont rooting. However, it is likely that a large proportion of the characters detected represents evolutionary noise and therefore are not currently useful for inference of a new eukaryote root or tree topology without further investigation.

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## Evolutionary history of eisosomes

Luigi Cibrario and Thomas Richards

School of Biosciences, Geoffrey Pope Building, University of Exeter, Stocker Road, Exeter, UK.

Endocytosis, the ability for cells to 'swallow', was one of the most important evolutionary acquisitions by the eukaryote cell. Recently, the eisosome was identified as an anchor for endocytosis in yeast, predetermining sites for endocytosis. Eisosomes consist of two paralogous cytoplasmic proteins, LSP1 and PIL1 and a third transmembrane protein SUR7. The three eisosome proteins are known to interact with a number of endocytic effectors, including RVS167, which features a BAR and a SH3 domain gene architecture homologous to mammalian endocytic protein endophilin. In this study we test the presence of eisosome genes across a wide diversity of eukaryotic taxa as well as studying the phylogeny of eisosome associated proteins. Our results show that eisosome proteins are specific to Fungi, which suggests that eisosomes have evolved as a fungal innovation probably in concordance with the origin of the fungal cell wall. We therefore propose eisosomes to be a cladistic character of the fungi.

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## Phylogeny of *Triglochin* (Juncaginaceae) in South Africa

A. Valerie Köcke<sup>1</sup>, Sabine von Mering<sup>1</sup>, Joachim W. Kadereit<sup>1</sup> and Ladislav Mucina<sup>2</sup>

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*Triglochin*, the largest genus of Juncaginaceae (Arrow-grass family) with about 25-30 species, has an almost worldwide distribution. The most recent treatments of the genus in South African floras recognise only two species of *Triglochin*, *T. bulbosa* and *T. striata*. The species of the genus are mainly found in coastal salt marshes and tidal mud flats under a regular tidal flooding regime, but some populations also occur in (temporarily) moist, sandy, saline depressions such as inland salt pans or reed beds and freshwater wetlands.

The *Triglochin bulbosa* complex in South Africa shows great variation in, e.g., leaf anatomy, fruit characters and morphology of underground parts. Our study focuses on the systematics, phylogeny and evolution of *Triglochin* in South Africa using morphological anatomical and molecular (ITS, matK) data.

First results are

- (1) The genus *Triglochin* in South Africa is not monophyletic;
  - (2) The *Triglochin bulbosa* complex consists of 4-5 species; and
  - (3) The *Triglochin bulbosa* complex originated in the Mediterranean area.
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## Outgroup misleading effect and new arthropod phylogeny

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There are at least two main questions regarding arthropod phylogeny still under strong debate. First, are the hexapods a monophyletic group or, for instance, has the six-legged body plan evolved independently at least two times? Second, is the Mandibulata a monophyletic clade or should we rather believe in the Paradoxopoda hypothesis (chelicerates plus myriapods) recently proposed based on molecular analyses? Mitochondrial and nuclear based phylogenies give support for conflicting hypothesis and morphological data seem to contradict both sources of molecular evidence. Interestingly, as far as hexapods monophyly is concerned, conflict is even present between different mitochondrial based phylogenetic reconstructions.

In order to analyze the relationships among basal arthropods and to understand the conflict among different mitochondrial base reconstructions we have investigated the impact of compositional heterogeneity in these sequences and the impact of outgroup choice on the inference of phylogenetic trees.

We show that outgroup affects the topology of the reconstructed ingroups phylogeny and that the misleading effect is correlated with high genetic divergence and compositional properties of outgroups. We suggest that support for Hexapod monophyly and Paradoxopoda clade from the analysis of concatenated mitochondrial coding regions is likely to be an artifact of shared compositional bias and inappropriate outgroup choice rather than a true phylogenetic signal.

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## Evolutionary history of the alpine *Ranunculus alpestris* group in the European Alps and the Carpathians

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<sup>5</sup>Current address: Molecular Systematics Section, Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, UK.

Phylogeographic and phylogenetic analyses on AFLPs and *matK* sequence variation were used to assess the evolutionary history of *Ranunculus alpestris* s.l. (including the endemics *R. bilobus* and *R. traunfelneri*). Analyses of AFLP data split the 90 populations studied in three groups. The endemic species, both restricted to Southern Alps, together with south-eastern-most populations of *R. alpestris* formed one group, while the rest of the later species was split in a western and an eastern group (including the Carpathian populations). Chloroplast DNA sequences showed substantial intraspecific variation and confirmed the split of the endemics from *R. alpestris* s.s., estimated to have happened ca. 2.3 MYA. The lack of a synapomorphic 6 bp deletion in some accessions of *R. bilobus* might indicate that *R. traunfelneri* has evolved from within *R. bilobus*. Despite the clear high level of variation in AFLPs, there is no divergence of cpDNA between western and eastern *R. alpestris* s.s.

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## The evolution of reproductive strategies in the European species of *Dicranum* (Dicranaceae, Bryophyta)

Nichola Hawkins, Niklas Pedersen and Angela Newton

Department of Botany, The Natural History Museum, Cromwell Road, London, UK.

The gametophyte-dominated life cycle is one of the most notable aspects of bryophyte biology, but within that basic life cycle, bryophytes have evolved many different reproductive strategies. In one strategy, pseudautoicy, dwarf male plants grow on female hosts, allowing cross-fertilisation where it would not otherwise be possible. In addition, several forms of asexual propagule are known.

The moss genus *Dicranum* encompasses variation in the occurrence of both pseudautoicy and specialised vegetative propagation.

A molecular phylogeny was obtained for European species of *Dicranum*. Evolution of reproductive strategies was investigated over that phylogeny, including likelihood-based tests for correlated evolution with habitat and morphological characters.

Both strategies appear to be associated with drier habitats, where fertilisation from free-living males is less likely, but evolving independently from each other, suggesting distinctly separate roles for sexual spore production and vegetative propagation. Furthermore, morphological evolutionary correlates support the importance of sexual reproduction in maintaining adaptive potential.

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## **Phylogenetic relationships and evolutionary divergence of *Asparagus* (Asparagaceae)**

**Maria Vibe Norup**<sup>1</sup>, Ole Seberg<sup>1</sup>, Gitte Petersen<sup>1</sup> & H. Peter Linder<sup>2</sup>

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*Asparagus* (Asparagaceae) is distributed in the Old World, but with a putative closest sister (*Hemiphylacus*) in Mexico. The genus includes several commercially important species, however, the exact number of species is unknown and controversial (170-300?). Many species are listed as rare or vulnerable, but the majority are insufficiently known. We aim to ameliorate this by focusing on the systematics, evolution, and ecology of a major subset of the genus (ca. 100 spp.), distinguished by their presence in the ecologically diverse region of South Africa. Based on a phylogenetic hypothesis we will trace the evolution of biological and ecological traits in the remarkably diverse genus *Asparagus* and assess the possible role of these traits in speciation and extinction. We will try to determine alpha-niche dividing characters that allow the co-occurrence of up to six species. Furthermore we will examine the biogeographical aspects of speciation in the genus and establish if South Africa may be the origin of radiation.

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## **Populations of the Caribbean: Assessing genetic variation in the New World screwworm fly in preparation for sterile insect technique-based control**

**Laura McDonagh** and Jamie Stevens

School of Biosciences, University of Exeter, Hatherley Labs, Prince of Wales Road, Exeter, Devon, UK.

Larval infestations of the New World screwworm fly (NWSF), *Cochliomyia hominivorax*, cause considerable economic loss of livestock through direct mortality and reduced production. Since the 1950s, NWSF populations in North and Central America have been the target of virtually continuous eradication by sterile insect technique (SIT). Nevertheless, in some areas, e.g. Jamaica, SIT control programmes have failed.

Accordingly, our research investigates intra-specific phylogenetic relationships and associated biogeographic patterns between NWSF populations from the Caribbean and South America, i.e. those populations earmarked for forthcoming SIT control. The study utilises both nuclear and mitochondrial sequence data, including elongation factor 1 alpha (nuclear), and cytochrome oxidase I+II (mitochondrial).

Phylogenetic analysis of these data, representing populations from across the Caribbean and South America, indicates substructuring of fly populations on several of the larger Caribbean islands. The importance of these findings in the light of proposed SIT programmes in the region are discussed.

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## **Towards a taxonomic revision of the green algae (Chlorophyta)**

**Barbara Rinkel** and Juliet Brodie

Department of Botany, The Natural History Museum, Cromwell Road, London, UK.

Many species of green algae can be found in the natural world living epiphytically on or endophytically in a variety of red, green and brown algal hosts, as well as in association with a number of other substrata, including chalk, shells, corals and wood. Although rarely found free-living in nature, many will grow independently in culture. These cultures are the source of many morphological observations on which taxonomic relationships of these species within the Chlorophyta have been based. The aim of this project is to utilise sequence data for two molecular markers (the nuclear marker ITS2 and the plastic marker *tufA*) to assess both the position of the epi-endophytes and the current taxonomy of the Chlorophyta. The results show the close relationship of the epi/endophyte species to each other as well as to the blade-forming genus *Ulva*. The data also highlight the need for taxonomic revision within the Chlorophyta.

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## An empirical comparison of genome phylogeny methods

Angela McCann

National University of Ireland, Maynooth, Ireland.

Conditioned Reconstruction (CR) represents a new method of phylogenetic reconstruction (Lake & Rivera, 2004) and it proposes to reconstruct the 'Tree of Life' even in the presence of extensive Horizontal Gene Transfer. The method involves the analysis of the presence and absence of shared genes to estimate similarity between genomes. Previous to this study no empirical analysis has been carried out implementing CR. Using 22 fully sequenced Archaeal genomes this study evaluates CR by assessing its performance in comparison to six other phylogenetic methods. These include two variants of the CR and the SHOT method (Korbel et al., 2002) a Supertree approach (Creevey & McInerney, 2005) and a phylogenetic tree derived from the 16S rRNA molecule. Comparisons were carried out using the Robinson-Foulds distance metric (Robinson and Foulds, 1981). Thus, we have used empirical data to test congruence across different analysis methods and to further our understanding of the evolutionary history of the Archaea.

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## Investigating the evolution of the 'Beetle Daisy' flower spot: Insights from gene characterisation, development, and molecular phylogenetics

Meredith Murphy Thomas<sup>1</sup>, Allan G. Ellis<sup>2</sup>, Paula J. Rudall<sup>2</sup>, Vincent Savolainen<sup>2</sup> and Beverley J. Glover<sup>1</sup>

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<sup>3</sup>Jodrell Laboratory, Royal Botanic Gardens, Kew, UK

Angiosperm flowers employ a wide variety of strategies for attracting their pollinators. One floral feature that has evolved many times across the flowering plants is the dark petal spot. The South African daisy *Gorteria diffusa* exhibits striking dark petal spots on its showy ray florets in a highly variable manner, resulting in a complex pattern of distinct morphotypes throughout its range. Pollination studies have shown that these flower spots attract a particular species of bee-fly, with the different morphotypes eliciting different behaviours in the flies, and may even act as a pollinator mimic. I intend to conduct a phylogenetic study to discover the underlying genetic diversity between the morphotypes of *G. diffusa* and also between *G. diffusa* and its sister species in order to interpret the evolution of the petal spot.

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## Evolution of direct development in caecilian amphibians

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Caecilians constitute one of the three extant orders of the Amphibia. We investigated development of the skull in the caeciliid caecilians *Gegeneophis ramaswamii* and *Boulengerula taitanus*. Both species develop directly, without a free-living larval stage. Hatchling *G. ramaswamii* have well ossified skulls that resemble the adult condition. In contrast, the distantly related *B. taitanus* has very immature hatchlings that have a similar degree of ossification to that of embryonic *G. ramaswamii* and free-living, aquatic larvae of more basal caecilians. These differences are correlated with differences in parental care provided to the offspring. In *G. ramaswamii*, young seem to get independent soon after hatching whereas female *B. taitanus* provide care to their offspring for several weeks during which juveniles increase in size substantially. Our study reveals a previously unsuspected degree of developmental diversity among direct developing caecilians. The available data imply several life history changes and independent evolution of derived reproductive traits within caecilians as a whole.

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## Evolution Of The Major Allopolyploid Sections In *Nicotiana*

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Phylogenetic relationships in *Nicotiana*, the sixth largest genus in Solanaceae, are complex due to polyploidy; 40 species are diploid (two sets of chromosomes), and 35 species are allopolyploid (more than two sets of chromosomes from different progenitor diploid species). We have studied molecular evolution at the DNA sequence level using a phylogenetic approach and at the chromosome level using fluorescent in-situ hybridization (FISH). Phylogenetic trees were constructed using three types of sequences: plastid loci (documenting the maternal lineage in allopolyploids), nuclear ribosomal loci (which exhibit conversion to one parental type in allopolyploids) and single copy nuclear loci (both parental copies present in allopolyploids). Here we focus on the three largest allopolyploid sections, *Suaveolentes*, *Repandae* and *Polydicliae*. Section *Suaveolentes* is the largest allopolyploid section with 26 species, all found in Australia except for one species in southern Africa. The progenitor diploids are all American. *Suaveolentes* forms a monophyletic group in all phylogenetic trees indicating that they have arisen from a single polyploidisation event, followed by dispersal and speciation. In some cases speciation has been accompanied by a reduction in chromosome number ( $n = 16, 18, 19, 20, 21$  &  $22$ ). Phylogenetic trees indicate that *N. sylvestris* and *N. obtusifolia* gave rise to the monophyletic section *Repandae*. The number of 45S ribosomal loci detected using FISH showed that members of sect. *Repandae* are not simply the sum of their two parental types, possibly due to diploidisation. Section *Polydicliae* contains just two North American species. Phylogenetic trees indicate that an ancestor of *N. obtusifolia* is the maternal parent, and a progenitor of the diploid section *Petunioides* is the paternal parent. Section *Polydicliae* is unique in that the allopolyploids are paraphyletic to their progenitor diploids, indicating they have arisen independently at different times from the same progenitor diploid lineages.

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# Systematics BURSARIES

*for the*  
**6th Biennial Conference of the Systematics  
Association**  
**'Celebrating the Tercentenary Carl Linnaeus'  
Birth'**

27-31 August 2007

Royal Botanic Garden Edinburgh  
20A Inverleith Row, Edinburgh EH3 5LR, UK

[www.systass.org](http://www.systass.org)

[edinburgh.biennial@systass.org](mailto:edinburgh.biennial@systass.org)

The Biennial conferences of the Systematics Association provide a forum for systematists from different disciplines to present and discuss their research. The Sixth Biennial Conference will be held at Royal Botanic Garden Edinburgh from 27 to 31 August 2007. The conference is open to everyone, especially research students and younger post-doctoral fellows, whatever their chosen subject in systematics.

To encourage student participation, competitive bursaries will cover registration, accommodation costs and the conference dinner (but not travel) for students giving a paper on their own research work. Current research students and those who have graduated since August 2006 giving a paper on their own research work are eligible to apply. Allocation of bursaries is competitive, based on assessment of an abstract that must be submitted by 31 December 2006, for decisions in January 2007. An online application form for those wishing to be considered for a bursary is available at the Systematics Association website, <http://www.systass.org/>

## Themes

- Two major themed symposia:
  1. Floras & Faunas Serving Biodiversity Research
  2. Speciation
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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 to be launched in 1997. 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.

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