



4TH Young Systematics FORUM

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Thursday, 5th December 2002
 The Flett Theatre
 The Natural History Museum
 London SW7 5BD, UK

The **Young Systematist's Forum** represents an exciting, annual 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, and hopefully supervisors too, within a supportive environment.

A molecular phylogeny of *Drosera* L using Nad1 and TrnL-F sequences with emphasis on biogeographical interpretation

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The carnivorous genus *Drosera* (Droseraceae) has a cosmopolitan distribution with centres of diversity in the southern hemisphere. The chloroplast DNA region TrnL-F and the mitochondrial DNA region Nad1 were used to create a phylogenetic hypothesis of the genus. TrnL-F was found to be the most informative region. Three main clades were identified, two of which consisted of Australian species and the other of South African, American and European taxa. Strong evidence was found for a Gondwanan origin with a secondary colonisation of Australian species after a widespread extinction event. The current intrageneric classification is supported.

Biodiversity, biogeography and phylogeny of the Phylum Cercozoa (Protozoa)

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The novel protozoan phylum Cercozoa Cavalier-Smith 1998 comprises several groups previously of obscure affinity, including Cercomonadida, Thaumatomonadida, chlorarachniophyte algae, euglyphid testate amoebae, plasmodiophorid plant pathogens, and the parasitic Ascetospora. Many previously unclassified genera also belong to this phylum, including Helkesimastix, Sainouron, and Bodomorpha. Cercozoa exhibit a wide range of morphologically and ecologically diverse forms, including most soft-surfaced biciliate zooflagellates (e.g. Cercomonas, Heteromita), zooflagellates with silicious scales and emergent pseudopodia (e.g. Thaumatomonas, Allas), amoebflagellate algae (e.g. Chlorarachnion), syncytial parasites (e.g. Plasmodiophora, Haplosporidium), most filose amoebae, typically testate (e.g. Euglypha, Cyphoderia), some reticulose amoebae (e.g. Gymnophrys, Biomyxa), colonial flagellates (e.g. Spongomonas), and numerous small gliding flagellates (e.g. Allantion, Bodomorpha, and many not yet named).

Ribosomal RNA trees suggest that Cercozoa are related to Foraminifera (also supported by actin trees) and Radiolaria. We aim to identify and distinguish between genotypes that are cosmopolitan and those with more restricted distributions, and to test the hypothesis that most eukaryote species below a certain size are cosmopolitan they are small and abundant enough to be dispersed on a global scale (therefore allopatric speciation rarely or never occurs) and have very wide ecological tolerances (so ecological speciation rarely occurs). The consequences of this hypothesis are that the ratio of local to global species richness approaches unity.

Our results are summarised as follows. Although morphotypes (morphospecies) appear to be mostly cosmopolitan, some environmental sequences group only with those from the same locality or/and similar ecological conditions. In contrast, other sequences are very similar or identical to those sampled from different ecological conditions or/and widely separated sampling sites. This suggests that some taxa are less rapidly dispersed relative to their rate of evolution/mutation than others, and that in some cases distributions are ecologically restricted.

Winner of best poster.

Tropical diversity - the problem of large genera: *Cyrtandra* (Gesneriaceae)

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Large genera pose a problem for taxonomists - they are too big to revise as a whole within a reasonable timeframe and therefore remain understudied, yet they form a substantial and important component of tropical diversity. Effective ways of tackling large genera by dividing them into manageable portions are needed not only from a purely taxonomic point of view; information gained from these genera can be very useful in biogeographic studies, and in identifying priority areas for conservation. *Cyrtandra*, with probably more than 600 species, is one of the most species-rich understorey genera in South East Asia. It is a common element of the Indo-Malayan rain forest and has a high capacity for producing local endemics. The advantages and disadvantages of three different approaches to the genus *Cyrtandra*, each involving both alpha taxonomy and molecular phylogenetics, are discussed: local (*Cyrtandra* of Mount Kerinci); regional (Peninsular Malaysia) and monographic (section *Dissimiles* C.B. Clarke).

Variation in trilobite terrace ridge patterns using extended eigenshape analysis

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Many trilobites have cuesta-like structures, known as terrace ridges, on both the dorsal and ventral surfaces of the exoskeleton. These structures are relatively poorly studied and their function is controversial. Although terrace ridges all appear to have the same basic construction, they are highly variable and several types are known, including long, continuous forms with asymmetric profiles running subparallel to the margin and symmetrical forms which bear a qualitative similarity to fingerprints.

Research is underway investigating terrace ridge shape variation across the class Trilobita, using a recently developed morphometric technique, extended (landmark-registered) eigenshape analysis (MacLeod, 1999). Major trends in the variation of simplified terrace ridge arrays are currently being explored, both within and between the terrace ridge-bearing orders. Preliminary results show that analysis of pygidial doublural terrace ridge arrays gives good taxonomic separation and can differentiate both phylogenetically and ecologically coherent groups. In particular, this analysis appears to separate pelagic and benthic terrace ridge-bearing forms, potentially providing an independent morphological test for trilobite mode of life hypotheses based on other aspects of morphology.

Assessing the phylogenetic utility of four mitochondrial genes and a nuclear intron in the Asian pitviper genus, *Trimeresurus* : separate, simultaneous, and conditional data combination analyses.

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A number of methods have been proposed addressing how to optimally analyze multiple datasets from different gene partitions in the pursuit of robust organismal phylogenies. The present study used separate, simultaneous and conditional data combination methods to analyse 3135 b.p. of data from four mitochondrial partitions, and a nuclear intron in the Asian pitviper genus, *Trimeresurus sensu stricto*. Despite the detection of heterogeneity of phylogenetic signal between the mitochondrial and nuclear partitions, the simultaneous analysis represented the best supported topology of all the data. The resulting tree helped to resolve the phylogenetic relationships of taxa which were unresolved throughout all individual gene trees, and tentatively supports the existence of morphologically and genetically distinct clades within the genus. Based upon a combination of homoplasy indices, partitioned Bremer support, and topological appraisals, the relative phylogenetic utility of all gene partitions for intrageneric analyses are also discussed.

A Central-American origin for *Guatteria* (Annonaceae) based on 5 chloroplast markers.

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The Neotropical genus *Guatteria* is one of the largest woody plant genera in the world and the largest within the family of Annonaceae, comprising approximately 260 species. Revision of this genus dates back to 1939, when Fries made a treatment based on few macromorphological characters. He divided the genus into 30 sections. Up to now it is the only major genus of Neotropical Annonaceae that awaits revision. Because of its homogeneity in many morphological characters it is very difficult to understand the systematics and evolution of the genus. The lack of a taxonomic framework and of a classification of the genus severely hampers the evaluation of the large quantities of new material that have been collected throughout recent years. This research started to unravel the classification of *Guatteria* by using molecular markers.

In this study a parsimony analysis was performed on 47 taxa of *Guatteria* using DNA sequence data of the plastid genome (*rbcl* region, *matK* region, *trnL-F* spacer and *trnL* intron and

psbA-trnH spacer). Although these data are still insufficient to resolve the relationships between all closely related species, they do show that *Guatteria* is a very well supported monophyletic group. Furthermore, the genus seems to have its origin in Central-America, rather than in South-America.

A new supertree construction algorithm with associated measures of reliability of phylogenetic hypotheses

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The notion of a tree uniting all of life is attributable to Haeckel in the 19th century. This concept, although generally accepted by most biologists, was difficult to demonstrate for prokaryotes, with many different conflicting phylogenetic signals coming from different characters. However, with the arrival of molecular methods and ribosomal RNA sequencing, a prokaryotic phylogenetic system was incorporated and the issue was considered to be closed. More recently, the availability of complete genome sequences has revealed conflicting tree topologies when using different genes and once again the notion of a prokaryotic phylogenetic tree has come under scrutiny. In our work, we use a dataset of 3,200 phylogenetic trees to construct a phylogenetic supertree of the prokaryotes. We have developed a new supertree construction algorithm with associated measures of reliability of phylogenetic hypotheses. We assess the strength of signal supporting this phylogenetic tree and the possibility that this tree could be constructed from random fundamental trees. Our results show strong support for a prokaryotic phylogeny and this phylogeny is not very different from trees drawn using ribosomal RNA genes. Not all gene trees agree with this tree and some are considerably different. We discuss our results in light of notions of vertical and horizontal gene transfer.

Winner of best talk.

Opuntioid cactus evolution and systematics; inferences from DNA sequence data

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The ITS and trn regions were sequenced for 100

representatives of the Cactaceae subfamily Opuntioideae, and 10 outgroup taxa from the subfamilies Cactoideae, Maihuenioideae and Pereskioideae. Parsimony analysis of these data supports the following relationships: The Opuntioideae form well-supported sister clade to the remaining Cactaceae; relationships among remaining subfamilies are unresolved; Maihueniopsis is sister to the remaining Opuntioideae, which includes two clades marked by terete or flattened stem morphology. Two independent reversals to persistent leaves within the terete-stemmed Opuntioideae (and no leaf persistence within the flat-stemmed clade) suggest that selection for increased surface area may be an important factor in the evolution of the Opuntioideae; also, terete stems appear to be homoplastic. These data support a South American origin for both terete- and flat-stemmed Opuntioideae. Proposed classification of Opuntioideae will include six morphologically and molecularly cohesive tribes. Currently recognized circumscriptions of many genera in Opuntioideae appear to recognize non-monophyletic groups.

The evolution of Australian trypanosomes

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Trypanosomes are protozoan parasites of which several species cause important diseases of humans and domestic livestock. Little is known about the trypanosomes of indigenous Australian mammals. We have undertaken a survey of trypanosomes in Australian vertebrates and invertebrates. Nested PCR using primers specific to the ssu rRNA gene was used to detect trypanosomes in marsupials and blood-sucking invertebrates. Trypanosomes isolated from three species of marsupial (a kangaroo, a wallaby and wombat) were included within in a phylogeny of trypanosomes based on the ssu rRNA gene. These trypanosomes from marsupials fell in three different clades, being more closely related to mammalian trypanosomes from placental mammals outside Australia than they are to each other, suggesting divergent evolutionary origins of these parasites. Trypanosomes were detected in a high proportion of haemadipsid leeches, from Australia, Sri Lanka and New Guinea. This suggests that terrestrial leeches may be important vectors of marsupial trypanosomes in South East Asia and Australia.

Evolutionary Relationships and Biogeography in the Myricaceae (bog myrtles)

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In this study molecular tools have been used to clarify relationships within the Myricaceae (bog myrtles or wax myrtles). The family is disjunctly distributed throughout the world but uniformity of gross morphology has made both generic and species delimitation problematic. The ITS region of the nuclear genome and the trnL-F region of the chloroplast genome were sequenced for a number of species representative of the major groups and areas of distribution of the family. A preliminary phylogeny based on a combined analysis of the two data sets confirmed the monophyly of the family, including a species endemic to New Caledonia of questionable affinities. The molecular data also support the recent erection of a new genus, *Morella*. The Macaronesian taxa are found to be sister to a clade containing African species which conflicts with the current classification.

The phylogeny and diversity of the centrohelid Heliozoa

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Heliozoa are protozoa with radiating axopodia, but this condition is probably polyphyletic. Centrohelid heliozoa are the most clearly defined order within the phylum, based on scale morphology, and we have sequenced 18s rRNA genes from several cultured species of centrohelids. As they are difficult to grow in pure culture, although often abundant in environmental samples, we have devised centrohelid specific primers for pcr amplification of the 18S rRNA gene from mixed cultures. We present a phylogeny of the order and discuss its evolutionary position among eukaryotes. As the specific primers amplify centrohelid 18S genes from total genomic DNA extracted from environmental samples, we are using them to study the diversity of the Centrohelida. Preliminary results from a small lake in Cumbria and marine samples are presented. Finally, using the absence of indels in the protein ubiquitin, the position of centrohelid heliozoa within the eukaryotic tree is considered.

Multiple origins of the rock fern *Asplenium majoricum*

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Asplenium majoricum Litard. (Aspleniaceae) is an allotetraploid

fern derived from *Asplenium x protomajoricum*, the F1 hybrid between the diploids *Asplenium fontanum* and *Asplenium petrarchae* subsp. *bivalens*. *Asplenium majoricum* is a rare Spanish endemic, known from only a few sites on the island of Majorca and in the south of Valencia province on the mainland. At certain sites in Valencia, *A. majoricum* and *A. x protomajoricum* are found growing together with *A. fontanum* and *A. petrarchae* subsp. *bivalens*. This sympatry of the allopolyploid and the F1 hybrid with both parental taxa provides a unique system for the study of speciation in action. We have collected extensively from these sites in 1999 and 2002, and are using allozyme electrophoresis and cpDNA sequencing to test the hypothesis that there have been multiple independent origins of *A. x protomajoricum* and *A. majoricum*. We are also investigating the relationship between mainland and Balearic *Asplenium majoricum* - did the latter colonise from Valencia, or arise de novo on Majorca?

The herbaceous/woody divide: genetic changes in the evolution of island woodiness

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Evolution of arborescence is one of the classical patterns found in island plants. Recently, phylogenies inferred from molecular data have been constructed for several plant groups that include woody island species, however, these phylogenies have not always been fully resolved due to a lack of support and resolution in clades containing island species. Conventional sources of molecular data often provide too few informative characters for full resolution of relationships in island plant groups, it would appear that the pace of diversification in some insular groups has been too rapid for fixation of enough synapomorphic mutations to allow robust phylogenetic reconstruction. As a result, there is a need to identify new, more rapidly evolving gene regions that can be used as a source of additional phylogenetically informative characters. This study will develop new gene regions that can be used to create more robust phylogenies for plant groups containing woody island species.

Biogeography of the herpetofauna of the Eastern Arc Mountains, Tanzania (poster)

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The Eastern Arc (EA) is a fragmented chain of mountains in Kenya and Tanzania. They are characterised by a high number of species and high endemism. EA forests are thought to be ancient. An equatorial band of African forest is believed to have become fragmented in the late Miocene. Since then, EA forests appear to have been relatively isolated from each other and from forests of West and Central Africa. EA patterns of organismal distribution are thought to reflect this geographical history, but this has yet to be tested empirically. The historical biogeography of the EA is being investigated through molecular phylogenetics of selected amphibians. Phylogenies are being compared with existing area cladograms for other EA organisms, to assess patterns and their possible causes, including dispersal ability and climate fluctuations. Preliminary results suggest complex biogeographical histories, which do not correlate to just a simplistic model of fragmentation and isolation.

A cladistic analysis of whiteflies, subfamily Aleyrodinae (Hemiptera: Sternorrhynca: Aleyrodidae) (poster)

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Whiteflies are agricultural pests in most tropical and subtropical countries but the family is poorly studied taxonomically, particularly from a phylogenetic aspect. This study is an attempt to construct the first phylogenetic classification at genus level for the subfamily Aleyrodinae on a world wide basis. At the time of writing 111 genera plus 3 out-group genera from the subfamily Aleyrodinae (Hemiptera: Aleyrodidae) have been examined and used to define character systems. Ninety-four morphological characters (71 binary and 23 multistate), all of which were derived from the pupal case, were scored and subjected to maximum parsimony analysis. In order to avoid considering the genera as monophyletic units, several representative species of each were selected and then treated separately in the analyses giving a total of over 400 terminal taxa. Based on these analyses, 23 genera were recovered as monophyletic, but several of the economically important genera such as *Aleurolobus*, *Bemisia* and *Dialeurodes* were found to be para- or polyphyletic.

Bear Hunting in Devon (Tardigrada) (poster)

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All tardigrades species are aquatic, requiring a film of water to cover them in order to be active. The British tardigrade fauna has been poorly surveyed. The results of 12 years of sampling are summarised here, including one species new to science, 7 species new to Britain and 16 species new to Devon.

Phylogenetics of nematodes - an overview of an advanced system

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Historically, the classification of nematodes has been based solely on the interpretation of the evolutionary history of morphological characters, resulting in a set of mutually incompatible systems. Molecular phylogenetics offer the promise of being able to resolve conflicts in this field by measuring relatedness using a single metric and verifiable, model-driven analysis. Until recently, phylogenetic analyses of nematodes using partial small subunit ribosomal DNA gene sequences were able to show that the "Secernentea" are the most derived group within nematodes, but due to a lack of available sequences from the "Adenophorea", the relationships of its sub-taxa to each other and to the "Secernentea" could not yet be established. Analyses including new "adenophorean" sequences give us the opportunity to identify the interrelationships of nematodes in more detail. New ideas of the phylogenetic systematics of nematodes from molecular data will be compared to the classic systems derived from morphological analyses.

The Vahona (Teleostei: Siluriformes: Anchariidae): Diversity, Systematics and Historical Biogeography

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The Anchariidae is a group of catfishes endemic to the island of Madagascar, off the Southeast coast of Africa. This group

consists of a single genus, *Ancharius* (Steindachner;1880), whose diversity has been poorly studied due to their rarity in museum collections. The phylogenetic relationships of *Ancharius* in relation to other catfishes is also unclear. They have previously been considered a sister group to either the marine catfish family Ariidae or the African catfish family Mochokidae. Based on materials from recent collections, this talk will outline the diversity of *Ancharius*, as well as test current hypotheses of phylogenetic relationships of the Anchariidae to other catfishes using both morphological and molecular data. The implications for the historical biogeography of the group from the results of the phylogenetic analysis will also be discussed.

Annonaceae: Phylogeny reconstruction in the 'short branch' clade

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Projects at the National Herbarium of the Netherlands are contributing to the building of a molecular phylogeny of the family Annonaceae. Results so far divide the family into a number of basal lineages plus two major derived clades with contrasting apparent rates of molecular evolution. The consequences for reconstructing phylogeny in taxa of the 'short branch' clade is a far greater demand for character sampling. Supporting monophyly of genera and their closest sister groups for use in species level phylogeny remains challenging. This is the particular aim of my PhD project, with respect to the Neotropical genera *Crematosperma*, *Malmea*, *Mosannonna* and *Klarobelia*. With the markers *rbcL* and *trnL-F* these genera fall within three separate clades, the relationships between which are unresolved in a basal polytomy also including a contrastingly well supported large clade of almost exclusively Asian distribution. Relationships at this level could thus be key to the understanding of biogeographical relationships within the clade as a whole. Preliminary results of analyses using a range of chloroplast markers at species level in *Crematosperma* and at generic level will be presented, and biogeographic implications discussed.

A recent radiation of Neotropical fern genera in páramo ecosystems

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A rigorously studied case of adaptive radiation in a group of Andean ferns in páramo ecosystems is presented. A phylogeny of *Jamesonia* and *Eriosorus* was reconstructed based on the plastid *rps4* gene and the External Transcribed Spacer (ETS) of 18s-26S rDNA. Specimens of *Pterozonium cyclosorum* and *Pterozonium reniforme* were included as outgroups. All analyses supported the monophyly of *Jamesonia* and *Eriosorus* together, however, neither genus is itself monophyletic; *Jamesonia* is polyphyletic and *Eriosorus* is paraphyletic. Character evolution studies indicate a sharp ecological shift significantly correlated with the evolution of jamesonia-morphotype; there is a repeated trend towards pinnae reduction and indeterminate growth, apparently related to the extreme environmental factors prevailing in neotropical páramo ecosystems. A potential increase in morphological disparity was evaluated by analyses of variance indicating that the number of leaflets per leaf is significantly greater among species with the jamesonia-phenotype across the global phylogenetic analyses. The three radiations of jamesonia-morphotype appear to have happened within 0.35 and 2.93 million years ago.

Molecular phylogeny, ecological adaptation and species boundaries in a problematic group of Indomalayan pitvipers

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We analyse molecular and phenotypic evolution in a group of taxonomically problematic Indomalayan pitvipers, the *Trimeresurus sumatranus* group. Mitochondrial DNA sequencing provides a well-resolved phylogeny, with each species representing a distinct lineage. Multivariate morphological analysis reveals a high level of phenotypic differentiation, which is congruent between the sexes but does not reflect phylogenetic history. An adaptive explanation for the observed pattern of differentiation is supported by independent contrasts analysis, which shows significant correlations between current environmental conditions and the characters that most account for the variation between taxa, including those that are presently used to identify the species. These characters relate mainly to scale counts on the head and colour pattern. Scale counts increase in hotter, drier environments and by partially determining the surface area of exposed interstitial skin, may play an important role in heat and water exchange in these animals. Colour pattern variation is hypothesised to reflect selection pressures involving camouflage and thermoregulation.

A molecular and morphological investigation into the diploid *Fragaria* (poster)

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My topic of research is the morphological and molecular diversity of the diploid *Fragaria* (wild strawberries). I have spent the first year of my PhD characterising the morphological diversity within the genus and producing a phylogeny from molecular sequence data. I am intending to continue the project by looking at the genetics of key morphological traits, using a map-based approach that will study interspecific F2 populations that are segregating for key morphological traits of interest.

Patterns of Change in the *Cycloidea* Gene During Angiosperm Floral Evolution (poster)

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The *Cycloidea* gene family is being studied in seven genera that possess interesting variations of the medial zygomorphy found in flowers of *Antirrhinum majus*. The aim of this research is to find correlations between changes in the gene and changes in morphology. Stage one of the research is almost complete; copies of the *Cycloidea* gene have been sequenced for four of the seven genera under study, and possible copies have been amplified from the remaining three. Developmental studies using Scanning Electron Microscopy are underway for comparing the different stages of floral development in each genus. The genetic control of morphological development is a key area of research in evolutionary biology. Understanding the patterns of change during the evolution of the *Cycloidea* gene family will aid in establishing a general model for patterns of floral symmetry evolution

Rooting the eukaryotic tree: the phylogenetic position of diplomonads and parabasalids. (poster)

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Diplomonads and Parabasalids have traditionally been considered to be the most primitive eukaryotes, on the basis of ultrastructural features, and analyses of small subunit rRNA and

protein sequences. Data previously used to infer their basal status are re-analysed here using more complex and computationally intensive methods, and conclusions drawn about the evidence for the basal status for diplomonads and trichomonads.

Systematics of *Thomandersia* Baill.: Approaches to Phylogeny Reconstruction

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Thomandersia (T. Anders. ex Benth.) Baill. is a distinctive, monophyletic genus comprising six species of trees and shrubs from west and central Africa. It is a member of Lamiales, an order containing some traditional families (e.g. Acanthaceae) that are well-supported and others (e.g. Scrophulariaceae) now known to be polyphyletic. In most previous classifications *Thomandersia* has been placed in Acanthaceae, with which it shares the morphological character retinacula (hardened projections of the funicle in mature fruits).

Extensive anatomical studies demonstrate a high degree of topological correspondence between the retinacula of *Thomandersia* and Acanthaceae. However no other morphological characters support this relationship, and analyses of molecular sequence data for the chloroplast genes *rbcL* and *ndhF* place *Thomandersia* outside a monophyletic Acanthaceae.

I will outline the different, morphological and molecular, approaches I have employed to resolve this apparent conflict, and the potential of different types of data to reconstruct the phylogenetic position of *Thomandersia* within Lamiales.

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