

9TH YOUNG SYSTEMATISTS' FORUM

5th December 2007, Flett Theatre, Natural History Museum, London, UK

Programme

09.00	Registration	
09.35	Introduction	Juliet Brodie (NHM)
09.40	Welcome and introduction	Richard Bateman (President, Systematics Association)
09.50	OM Grace	<i>Leaf chemistry in the systematics of Aloe L. (Alooideae)</i>
10.10	Rob Lanfear	<i>Metabolic rate does not calibrate the molecular clock</i>
10.30	Rachel H Walker	<i>The taxonomy and biodiversity of articulated coralline algae in Britain and Ireland</i>
10.50	Isabel Blasco-Costa	<i>Morphological and molecular circumscription and phylogenetic affinities of the digenean (Platyhelminthes) families Haploporidae and Haplospalchnidae</i>
11.10	Coffee and posters	
11.40	Caroline Byrne	<i>Phylogenetic revision of Thai Clusiaceae and Hypericaceae</i>
12.00	Victoria Svinti	<i>Detecting reassortment in influenza viruses</i>
12.20	Peter Konstantinidis	<i>The monophyly of the Gymnodontes</i>
12.40	Jason Gibbs	<i>DNA barcoding phylogenies and the evolution of social parasitism in the bee subgenus Dialictus (Halictidae: Lasiglossum)</i>
13.00	Lunch and posters	
14.00	Mark T Young	<i>Feeding biomechanics and the evolution of sauropodomorph dinosaurs</i>
14.20	Neela Enke	<i>Molecular phylogeny vs. morphology: contributions towards a new generic and infrageneric delimitation of Crepis L. (Cichorieae, Compositae)</i>
14.40	Fergal Martin	<i>Investigating the phylogenetic relationships of 27 completed YESS group genomes</i>
15.00	Katy Morgan	<i>Molecular phylogenetics and biogeography of the forest dependent Leucospkyrus Anopheles mosquitoes within Southeast Asia</i>
15.20	Tea and Posters	
15.50	Farah Ishtiaq	<i>Tracking host colonization with their blood parasites in South Pacific islands</i>
16.10	Angela McCann	<i>The tree of genomes: an empirical comparison of genome phylogeny reconstruction methods</i>
16.30	Emma Sherratt	<i>A geometric morphometric approach to comparative evolution of the caecilian skull</i>
16.50	Magalena Zarowiecki	<i>Ecological and geographical drivers of speciation in the Anopheles sudaicus (Diptera: Culicidae) species complex</i>
17.10	Closing comments and presentation of prizes for best oral and poster presentations	
17.25	Reception	
19.00		

Organized by **Juliet Brodie** (Dept Botany, NHM) and **Peter Olson** (Dept Zoology, NHM)
with support from



ABSTRACTS

ORAL PRESENTATIONS

Leaf chemistry in the systematics of *Aloe* L. (Alooideae)

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The chemical composition of leaf exudate from *Aloe*, the source of a bitter natural product from certain species, has proved informative in systematic as well as pharmacological investigations of the genus. However, generic boundaries and species delimitation remain uncertain in *Aloe*, whereas considerable insight into the therapeutic properties of the group has been gained in recent decades. A survey is presently underway of leaf chemistry in the maculate complex in *Aloe*, a group that remains poorly resolved and for which few chemical data are available. Recent findings suggest that phytochemical compounds such as aloin and related flavonoids are widespread in the complex, whilst the presence of less common compounds in some species may coincide with geographical distinctions. Taken into consideration with additional leaf characters, it is possible that leaf chemistry may be of systematic significance to the maculate species complex in *Aloe*.

Metabolic Rate Does Not Calibrate the Molecular Clock

Rob Lanfear

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Rates of molecular evolution vary widely among lineages, but the causes of this variation remain poorly understood. It has been suggested that mass-specific metabolic rate may be one of the key factors determining the rate of molecular evolution, and that it can be used to derive "corrected" molecular clocks. However, previous studies have been hampered by a paucity of mass-specific metabolic rate data and have been largely limited to vertebrate taxa. Using mass-specific metabolic rate measurements and DNA sequence data for >300 metazoan species for 12 different genes, we find no evidence that mass-specific metabolic rate drives substitution rates. The mechanistic basis of the metabolic rate hypothesis is discussed in light of these findings.

The taxonomy and biodiversity of articulated coralline algae in Britain and Ireland

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In the seaweed flora of Britain and Ireland there are five recognised taxa of geniculate coralline algae. The current taxonomy is based primarily on morphology but species are difficult to identify using these characters alone. An integrative study using the cytochrome *c* oxidase (*cox1*) gene, 18S rRNA gene and additional morphological characters revealed that the taxonomy of this group requires revision. The *cox1* and 18S rRNA gene phylogenies supported the division of the tribes Janieae and Corallineae. *Jania rubens* var. *rubens* (Linnaeus) Lamouroux and *Jania rubens* var. *corniculata* (Linnaeus) Yendo clustered together. This suggested that for the genes studied, there was no genetic basis for the morphological variation. The sequence difference between *Haliptilon squamatum* (Linnaeus) Johansen, Irvine & Webster and *Jania rubens* (Linnaeus) Lamouroux in the *cox1* phylogeny suggested that this was species level divergence. *Corallina officinalis* Linnaeus formed two genetically distinct clusters. *Corallina elongata* Ellis & Solander showed intraspecific variation between Atlantic, British and Irish regions.

Morphological and molecular circumscription and phylogenetic affinities of the digenean (Platyhelminthes) families Haploporidae and Haplospalchnidae

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The phylogenetic relationships and systematic position of the digenean families Haploporidae Nicoll, 1914 and Haplospalchnidae Poche, 1925 have always been controversial. Both groups are characterised by a very complex taxonomic history and the viewpoints of different authors have varied greatly as to their content and phylogenetic affinities. The objectives of our study were firstly to develop a modern taxonomic framework which places emphasis on the taxonomic consistency in the identification of these mullet parasites on a combination of morphological and molecular approaches using freshly-collected material. Secondly, we evaluated the genetic variation and phylogenetic affinities of the Haploporinae and Haplospalchnidae by the application of molecular methods aiming: (i) to test our hypothesis for the taxonomic boundaries and relationships within the Haploporidae, using partial LSU rDNA and ITS2 sequences; and (ii) to improve the resolution of higher level digenean phylogeny by a wider taxa sampling analysing SSU and partial LSU rDNA sequences. In the course of the study on the Haploporidae we have: (i) assessed intra-/inter-taxon variability of morphological characters within the constituent genera from the Mediterranean; (ii) refined the generic diagnoses and revised the allocation of their nominal species; (iii) described two new species, plus a number of additional forms; (iv) discovered two new genera and prepared a revised key to the genera of the Haploporinae. In addition, we built a new phylogenetic hypothesis for the relation of these families with the rest of digeneans.

Phylogenetic Revision of Thai Clusiaceae and Hypericaceae

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This project aims to produce a phylogenetic revision for the Thai Clusiaceae and Hypericaceae. Thailand is a severely under collected country and to present has experienced one of the fastest rates of deforestation in the world. For this reason a significant amount of biodiversity has been lost and therefore it is vital to maintain and document the remainder of Thailand's flora. The Clusiaceae and Hypericaceae of Thailand have never been studied before and therefore additional data is essential. This project aims to provide phylogenetic trees for key members of the two families using molecular and morphological data, descriptions and distribution maps, and an innovative web-based key to these families. To date all of the available material at worldwide herbaria has been examined (2468 specimens), along with fresh specimens. All formal descriptions have been completed. Distribution maps for all genera have been completed using ArcGIS desktop software. Descriptions completed to date have been uploaded to the Linnaeus II software and images and distribution maps are being prepared for uploading. Fieldwork was carried out for a 10 week period from February to May 2007. During the fieldtrip, fresh plant material was collected and examined. A five day computer-based training course (BRAHMS) was also completed during the trip to Thailand. All of the above will contribute to the on-going Flora of Thailand Project.

Detecting reassortment in influenza viruses

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The Influenza virus is a major cause of worldwide infections in the human population, having a dynamic history characterized by seasonal epidemics and occasional pandemics. The evolution of the virus is difficult to describe because it undergoes rapid evolution in order to evade the constantly adapting immune response of hosts. Its genome consists of eight individual segments of single stranded, negative sense RNA, each containing a single gene. This segmented nature of the genome allows for the exchange of entire genes between different viral strains when they co-infect the same cell through the process of reassortment. Identification of new reassortants is a crucial step in understanding viral evolution and in working towards preventing infections and the spread of fatal viruses. We present a method for detecting true reassortment that applies SPR branch moves on phylogenetic trees derived from each segment and uses a maximum likelihood test for the significance of difference in tree topologies. This test could identify real reassortment events and distinguish between these and simple limitations of phylogenetic analysis.

The Monophyly of the Gymnodontes

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Cuvier and all subsequent researchers have been recognized the tetraodontiform families Triodontidae, Tetraodontidae, Diodontidae, and Molidae as a monophyletic group the Gymnodontes. This is mostly based on the conspicuous beak-like jaws and the fixation of the ethmopalatine articulation. We describe and compare the formation of the beak and the fixation of the ethmopalatine articulation of nine of ten tetraodontiform families. Our results shed some doubt on the assumption that the formation of the beak and the fixation of the palatine to the ethmoid region of the skull are a single event during the evolution of the Tetraodontiformes and thus are not valid as synapomorphies of the gymnodonts.

DNA barcode phylogenies and the evolution of social parasitism in the bee subgenus *Dialictus* (Halictidae: Lasioglossum)

Jason Gibbs

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DNA barcoding projects are currently generating large numbers of sequences that may provide valuable data for phylogenetics. In particular, DNA barcodes may allow for dense taxon sampling formerly only feasible with morphological datasets. While more robust phylogenetic approaches are necessary to resolve major branches of the “tree of life”, DNA barcodes may be useful for aiding in resolution of the leaves of the tree. Phylogenies based solely on DNA barcodes could provide rapid testing of standing evolutionary hypotheses and could aid in the formulation of new ones. The bee subgenus *Dialictus* displays an incredible array of social systems and is an ideal group for studying the evolution of social behaviour. Solitary, communal, primitively eusocial and parasitic *Dialictus* species have been identified. Parasitic *Dialictus* are social parasites of other *Dialictus* species. A DNA barcode phylogeny of North American *Dialictus* shows for the first time that parasitic *Dialictus* are polyphyletic.

Feeding biomechanics and the evolution of sauropodomorph dinosaurs

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Sauropodomorph dinosaurs include some of the most bizarre and biomechanically unfeasible animals ever to have existed. How they fuelled their multi-tonne bodies on an apparently nutrient poor diet of fibrous plant matter challenges our understanding of both extinct and extant biological systems. Previous studies focused on the shape of the skull and teeth, and characteristic tooth wear patterns produced by tooth-tooth or tooth-food contact. Although immensely valuable, until now no attempt has been made to quantify the biomechanics of the sauropodomorph skull. Utilising the biomechanical technique finite-element analysis upon CT scan data of various skulls this will be addressed techniques in order to characterise the craniofacial evolution and diversity of feeding behaviours within this fascinating group of dinosaurs. Here results taken from quantitatively testing between competing feeding behaviour hypotheses of *Diplodocus* will be show that it stripped soft leaves from branches via propaliny of the mandible.

Molecular phylogeny vs. morphology: Contributions towards a new generic and infrageneric delimitation of *Crepis* L. (Cichorieae, Compositae)

Neela Enke and Bridgit Gemeinholzer

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Babcock (1947) revised the approximately 200 species of *Crepis* L. (Compositae) arranging them into 27 sections based on morphological and karyological traits. To reinvestigate his sectional arrangement a molecular phylogeny based on ITS and *matK* was reconstructed. The results revealed *Crepis* L. to be polyphyletic. A monophyletic clade including Central Asian and North American species of *Crepis* section *Ixeridopsis* is clearly isolated from *Crepis* sensu stricto and, as also supported by morphology, needs to be transferred to the genus *Askellia* Weber (1984). A second clade comprising the genera *Lapsana* L. and *Rhagadiolus* Juss. as well as a statistically strongly supported clade of several *Crepis* species is sister to a third clade: the monophyletic *Crepis* s.s.. Within *Crepis* s.s. there is a clear discrepancy between taxonomic groups recognized by Babcock and those resulting from molecular analysis. To establish a new infrageneric delimitation from molecular and morphological evidence several characters were screened, among them karyological traits, pollen structure and floral features.

Investigating the phylogenetic relationships of 27 completed YESS group genomes

Fergal Martin

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The group formed by *Yersinia*, *Escherichia*, *Shigella* and *Salmonella*, sometimes termed the YESS group, are of particular interest as many members are human pathogens. Diseases such as dysentery, plague and salmonellosis are caused by the YESS group, resulting in several million deaths worldwide each year. In this study we investigate the phylogenetic relationships of 27 published YESS group genomes under a number of different scenarios, including a 16s rRNA tree, data concatenation and supertree construction. In particular we examine how these relationships vary based on the method of tree construction and examine the reasons for disagreement between methods.

Molecular phylogenetics and biogeography of the forest dependent *Leucosphyrus Anopheles* mosquitoes within Southeast Asia

Katy Morgan

University of Manchester

Southeast Asia is unique amongst tropical regions with regard to the dramatic influence of Pliocene and Pleistocene sea level fluctuations on its biogeography, specifically its landmass configuration, aridity and tropical forest cover. The impact of such changes on the speciation and dispersal history of the *Leucosphyrus* group of *Anopheles* mosquitoes, a group of forest dependent taxa distributed across Southeast Asia, is investigated through the construction of a molecular phylogeny. Analysis of mitochondrial and nuclear markers suggests a southern

origin for the group, in the island region of Indonesia and Borneo, with subsequent northwards dispersal through the Thai-Malay peninsula to the mainland. This scenario supports the survival of tropical forest habitat in Indonesia, Borneo and peninsula Malaysia throughout the Pleistocene glaciations, which has implications for the conservation of other forest taxa. The evolution of anthropophilic feeding behaviour, of interest in malaria control, is thought to have occurred twice in this group.

Tracking host colonization with their blood parasites in South Pacific Islands

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We tested the hypothesis that malarial parasites of silvereyes (*Zosterops lateralis*) provide sufficient geographic signal to track colonization on two South Pacific islands. We recovered 32 genetically distinct avian malaria parasite lineages. Our results from 944 silvereyes sampled across mainland Australia towards recently colonized island populations in the South Pacific indicate that parasite lineages show geographical structuring and provide site-specific information. This could suggest that silvereyes have most likely colonized Vanuatu and New Caledonia from mainland Australia whereas the Tasmanian ancestral population provides enough signatures of colonization in New Zealand and its surrounding islands.

The tree of genomes: an empirical comparison of genome phylogeny reconstruction methods

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The emphasis for reconstructing species phylogenies has moved from single gene analysis to multiple genes and completed genome analysis. However, gene duplications and losses, along with lateral gene transfer (LGT) can lead to situations where there is only an indirect relationship between gene and genome phylogenies. There is a perception, sometimes explicitly stated, that many of the genome trees are practically the same as one another, and phylogenetic trees derived from the SSU RNA (1). In this study we examine five widely-used approaches to see if indeed they are more-or-less saying the same thing. In particular we focus on Conditioned Reconstruction (2), a method designed to work well even if LGT is present. We confirm a previous suggestion that this method has a systematic bias. We show that no two methods produce the same results and conclude that genome phylogenies need to be interpreted differently, depending on the method used to construct them.

(1). Choi, I. G., and S. H. Kim. 2007. Global extent of horizontal gene transfer. *Proc Natl Acad Sci U S A* 104:4489-94.

(2). Lake, J. A., and M. C. Rivera. 2004. Deriving the genomic tree of life in the presence of horizontal gene transfer: conditioned reconstruction. *Mol Biol Evol* 21:681-90.

A geometric morphometric approach to comparative evolution of the caecilian skull

Emma Sherratt

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Research into caecilian skull morphology has historically been limited to qualitative descriptions or traditional morphometrics on relatively few species. These limbless amphibians, exhibiting adaptations to terrestrial, subterranean or aquatic lifestyles, are excellent models for investigating convergent evolution of skull shape. Using landmark-based geometric morphometrics, the skulls of thirty species were analysed to quantify morphological variation across the order, which was then examined within a phylogenetic framework, indicating that significant historical associations are apparent in skull variation. Canonical variates analysis of morphometric data explored disparity between explicit species groupings: Morphological traits are influenced by geography since species from

the same continents form distinct groups, with some overlap of African and South American species furthermore supporting a Gondwanan origin. Similarly, species from the same family tend to cluster, despite current taxonomic ambiguity. Finally, species with similar ecological backgrounds cluster together, suggesting that habitat-niche constraints have played an important role in caecilian radiation.

Ecological and geographical drivers of speciation in the *Anopheles sundaicus* (Diptera: Culicidae) species complex

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The relative roles of ecology and geography in generating biodiversity, both within and between species, are still controversial. For the mosquitoes in the *Anopheles sundaicus* species complex, two competing hypothesis exist: Polytene chromosomal forms and allozyme data indicate that there are several sympatric species which occupy different ecological niches. But mitochondrial molecular data indicates that most diversity has been created by allopatric vicariance. Our research aims to reconcile and tests both hypotheses. The evidence for ecological speciation is tested by sequencing of a candidate allozyme marker, and looking for associations with larval habitat, signs of reproductive isolation, and balancing selection. The hypothesis of allopatric speciation is addressed by reconstruction of the biogeographical history of the species complex using one mitochondrial and two nuclear markers. We find no support for either hypothesis of speciation, and conclude that *A. sundaicus* is best regarded as one species.

POSTER ABSTRACTS

Character evolution in Callitrichids: variable rates and punctuated change

Jack Lighten

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Understanding the pattern and mode of character evolution has remained at the forefront of evolutionary biology for the past 60 years. How do characters change along a lineage? Does the rate of change remain constant within and between lineages? What factors govern changes in character evolution? Using morphometric data and phylogenetics I identify the mode and correlates of character evolution within an extremely interesting group of New World monkeys – the callitrichids. Variation in evolutionary rates between and within clades, and the biological implications imposed, is investigated by means of phylogenetic comparative - and morphometric methods. There is minimal correlation between traits and environmental conditions. Morphometric variation is believed to be idiosyncratic of callitrichids and in the most part non-adaptive. Differential rates of evolution between genera and within, entices speculation of causes of such phenomena with illumination of further avenues of investigation. I also demonstrate how character change in callitrichids has undergone punctuated evolution associated with speciation events. However, character evolution is not purely punctuational and is coupled with a less significant amount of phyletic change. I thus argue that the long term belief in the dichotomy between micro- and macroevolution is largely non-existent in callitrichids.

Eco-morphological Convergence in Dung Beetles

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The dung beetles of the subfamily Scarabaeinae display a diverse array of morphologies and nesting behaviours. It is thought that this variation has arisen due to adaptations enabling the efficient exploitation of their main resource

(dung) in a highly competitive environment. A number of behavioural, ecological and morphological groups within the Scarabaeinae have been hypothesised in the past. The “rollers” and “tunnellers” were long believed to form monophyletic groups, with the “dwelling” Aphodiinae as their sister group. However, molecular phylogenetic studies have severely questioned the monophyly of these behavioural groupings, suggesting that the behaviours have evolved independently, multiple times. The present study used eigenshape morphometric techniques and a recent molecular phylogenetic tree to investigate the relationships between morphological characteristics and dung beetle ecology, observing that convergence in behaviour has been matched with strong convergence in some aspects of morphology.

Using Oceanic Islands as a Yardstick to Measure the Spatial Scale of Speciation

Yael Kisel

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The theory of allopatric speciation holds that populations must be geographically isolated in order to diverge and develop reproductive isolation. This suggests that there should be a minimum area required for speciation to occur, below which populations will not be sufficiently isolated from one another. A survey of speciation rates on oceanic islands finds clear evidence for minimum areas for speciation for lizards, angiosperms, and macrolepidoptera, but not for snails, ferns or bats. Snails appear to have a minimum area smaller than the scale of the study, and bats a larger, while island ferns seem to speciate largely through polyploidy. Furthermore, there is a significant correlation between the minimum areas for speciation for the groups and average gene flow values estimated from the literature. These results imply that there is large taxonomic variation in the spatial scale of speciation and that it is controlled by variation in population genetic processes.

Protozoan and helminth parasites of British bats

Jennifer Lord, Geoff Hide and Darren Brooks

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Chiroptera is one of the most successful and diverse of mammalian orders, with an estimated 1100 species worldwide. Bats act as hosts to a range of infectious agents, including rabies, SARS, and ebola viruses, and they also harbour a plethora of parasites. Within the UK, extensive analysis of blood smears¹ has shown that bats are naturally infected with trypanosomes, *Polychromophilus murinus* and *Babesia vesperuginis*. Other studies, primarily conducted outside the UK, have shown that bats are hosts to a range of helminth species. The protected species designation of chiroptera however makes such studies challenging and hence there are many fundamental questions about bats and their parasites that remain unanswered. To begin to address some of these issues, during 2006/2007 we collected 90 bat specimens. These specimens are currently being analysed using microscopy and PCR-based techniques to assist identification of both protozoan and helminth species and progress will be reported.

¹Studies on the Haematozoa of British Bats. Gardner, R.A. (1986), PhD Thesis, University of Salford.

MOTU_define.pl: Turning Sequences into Taxa

Jenna Mann and Mark Blaxter

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The number of meiofaunal 'species' is unknown, but likely to be in the millions. In the absence of time and manpower, how can these organisms be identified, taxonomised and analysed? We can acquire DNA barcodes from individuals, but in most instances we do not have exemplar specimens identified to species, nor do we expect to get sequence from type specimens. So how can we identify taxa independent of external reference samples? Here we investigate behaviour of clustering, based on divergence in sequence data, for three different genes (one

mitochondrial and two nuclear) and the molecular operational taxonomic units (MOTU) defined by the computer program MOTU_define.pl.

Estimating heterotachy without inference

Douglas Chester, Donald Quicke and Alfried Vogler

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There is compelling evidence that the presence of heterotachy (site-specific variation in rate) can mislead the inference of phylogenetic trees. A number of methods exist for detecting heterotachy, typically using site rates inferred from subclades of the group under study. These methods can be lengthy, particularly when the dataset is large (as will increasingly become the case). This represents barrier for wide-scale adoption of heterotachy testing in standard phylogenetic procedures. The availability of a simple procedure for estimating the extent of heterotachy would be beneficial, as it could be utilised where thorough analyses are unfeasible. Here, I assess a number of inference-free methods for their potential in predicting the level of heterotachy. Using simulated sequences, procedures using inter-clade differences in nucleotide variability are not significantly different to those based on inferred rates, over much of the parameter space. A convenient permutation-based statistical measure of heterotachy (which partially accounts for heteroscedasticity) is also introduced here.

Phenotypic variation of three-spined sticklebacks (*Gasterosteus aculeatus*) on North Uist, Outer Hebrides

Sonia Chapman and Andrew MacColl

University of Nottingham, UK

A central question in evolutionary studies is whether morphological variation between taxa results from adaptation or phylogenetic history. Populations of three-spined sticklebacks in lochs on North Uist have very different morphologies. Past research states that variation in boney external armour may be the result of differing calcium concentrations of the lochs across a steep environmental gradient. Machair lochs in the west of the island are calcium rich as a result of shell rich sand blown in from the sea, while in the east lochs are on peat and tend to be acidic. However glacial history also suggests that stickleback populations on either side of the island were probably established by different ancestral marine populations. We will explore whether variation in external boney morphology among lochs is more consistent with adaptation to calcium concentration or phylogenetic constraint, using geographical location as a proxy for likely phylogenetic history.

Systematics and Biogeography of Sulawesi *Begonia* L.: Dispersal across Wallace's Line?

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The Indonesian island of Sulawesi is located at the western border of Wallacea, an interface region where Asian and Australian biotas meet. Sulawesi's *Begonia* flora, in common with much of the island's biota, is of enigmatic origin. Phylogenetic relationships of 70 SE Asian *Begonia* species with focus on taxa from Sulawesi were investigated with parsimony analyses of ITS sequence data. The results indicate the presence of three lineages on Sulawesi: I) Most species are retained in a *Begonia* section *Petermannia* clade. II) Three species form a monophyletic group in the "*Begonia longifolia* complex" in section *Sphenanthera*. III) One species forms a strongly supported clade with *B. taiwaniana* and *B. halconensis* in section *Sphenanthera* s.lat. (incl. section *Platycentrum*). Multiple but infrequent long-distance dispersal events from Borneo and Java across Wallace's Line to Sulawesi and subsequent autochthonous speciation seem to have played the major roles in the formation of Sulawesi's *Begonia* flora.

Phyloclimatic modelling can estimate ancestral areas

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Ancestral area selection is traditionally based on geographic patterns analyzed alongside phylogenetic data. The approach assumes consistent climate and will only select areas from within present day distributions. However, by modelling a species' climatic niche we can estimate its potential distribution of species for the past, present and future. Assuming niche heritability, we can reconstruct ancestral niches using phylogenetic techniques and so estimate ancestral areas. Ancestral area selection via climatic niche differs from traditional methods, as areas outside the observed distribution can be selected. We present an example using *Drosera* (Droseraceae). We reconstruct the climatic preferences of lineages to model ancestral niches. These models are explored to determine the limits of distribution within contemporaneous palaeoclimate scenarios suggested by a temporally calibrated phylogeny. Our findings support a restricted Southern Australian distribution for the ancestral *Drosera* that offers a plausible explanation of the current centre of diversity in South-Western Australia.

A molecular phylogenetic analysis of *Platymiscium* (Leguminosae: Dalbergieae) using plastid (*trnL*, *trnL-F* and *matK*) and nuclear (ITS) DNA regions: taxonomy, biogeography and divergence times

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Platymiscium is a legume genus of forest trees endemic to the Neotropics. It comprises 19 species (29 taxa) and is distributed from Mexico to Bolivia and South Brazil. It is popular with the timber industry and several species are endangered to various extents. This study uses the plastid regions *trnL*, *trnL-F* and *matK* and the nuclear region ITS for a molecular phylogenetic analysis of the genus, using parsimony and Bayesian methods. Divergence times are estimated using a Bayesian method assuming a relaxed molecular clock. The results support monophyly of the genus, which is separated in three clades, with more or less distinct geographic ranges. *Platymiscium* invaded Amazonia twice and Central America was invaded three times, two of which before the closure of the Isthmus of Panama. Divergence times of the *P. pubescens* complex, restricted to the seasonally dry tropical forests (SDTF) of South America, provide possible ages of splits of the SDTF.

A molecular phylogeny of the hawkmoths (Sphingidae) of Madagascar and correlates of endemism

Hauke Koch

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Hawkmoths are a diverse cosmopolitan family of Lepidoptera known for their adaptation to rapid, sustained flight, rendering them good dispersers. In spite of this, the hawkmoth fauna of Madagascar has a high proportion of endemic species. A phylogenetic tree for 50 of the 60 Malagasy hawkmoth species using one mitochondrial (COI) and two nuclear genes (EF1-alpha, wingless) is presented. The phylogeny is used in a phylogenetically corrected correlation analysis looking for morphological traits predicting endemism and range size. These traits are also reconstructed on the phylogeny. Endemism can be predicted by small size and short, broad forewings, probably reflecting limited long distance dispersal ability of the endemic taxa. A trend towards these features occurs several times on the phylogeny.

Systematics of Arabian Peninsula Burseraceae

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Taxonomically the flora of the Arabian Peninsula is poorly known, especially with reference to Burseraceae species. Arabian species of the Burseraceae are poorly represented in published phylogenetic studies of the family. The aim of this study is to determine the extent of distribution of the Burseraceae in the Arabian Peninsula and its Islands, to determine the relationships of the species, to test the monophyly of Arabian groups and to treat and clarify the ambiguities within the family. The approach was to make a morphological revision of the species in the Peninsula and to reconstruct a molecular phylogeny of *Boswellia* and *Commiphora* based on an external transcribed spacer nuclear region ETS sequences and two chloroplast regions (*psbA-trnH* and *rps16*). The preliminary molecular analyses are presented here. They include *Commiphora* samples collected from 24 different locations in Saudi Arabia analysed along with published data. Arabian species were placed in different sections and do not comprise a monophyletic group, with some African *Commiphora* species were found closely related to Arabian species. In some *Commiphora* species there is a need to carry out cloning of ETS products to test the possibility of hybrids.

Ecdysozoa versus Celomata: the effect of outgroup selection and taxon sampling in phylogenomic studies

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Ten years ago a complete rearrangement of the phylogeny of animals, termed the “new animal phylogeny”, was proposed from the analysis of 18S rRNA sequences. Most Protostomia were re-arranged into two major clades: the Ecdysozoa and the Lophotrochozoa. Although many zoologists have accepted the new phylogeny some issues remain. Central to the current debate is the placement of the nematodes within the Ecdysozoa. Traditionally, the nematodes were considered pseudocoelomates, and were grouped toward the base of the animal tree, a view that is generally referred to as the Celomata hypothesis. Thus far phylogenomic studies (i.e. phylogenetic analyses of complete genomes) have failed to lend support to the new animal phylogeny favouring instead the Coelomata hypothesis. Detractors of the new animal phylogeny defend the results of whole-genome analyses on the grounds that they use all the available evidence. On the contrary poor taxon sampling and long-branch attraction have been suggested as reasons for the failure of whole-genome data to converge with rRNA analyses. Here we investigate the effects of outgroup choice and taxon sampling in a whole-genome based phylogenetic analysis of Metazoa.

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