



3RD Young Systematics FORUM

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BIENNIAL 2003

Thursday, 30 November 2000
The Natural History Museum
London SW7 5BD

Studying historical relationships between living organisms and/or parts of their genomes (e.g. genes) represents arguably some of the most fascinating aspects of biology, investigations of interest on their own right but possibly even more interesting through creating fertile dialogs between diverse fields of biology. Never before so much data has been produced from so many diverse forms of life and new analytic methods developed allowing to further increase our knowledge of life's complex history, amazing diversity, and the subtleties of the evolutionary processes shaping this diversity. The *Young Systematists Forum* represents an informal setting for postgraduates to present their projects focusing either on the systematics of specific taxa and/or on methodological issues of phylogenetic inference and comparative biology. It will provide an opportunity for postgraduates to present their ideas to their peers in a relatively informal setting to promote discussion and support innovation.

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**The 2nd Young Systematics Forum, The Natural History
Museum, London
30 November 2000**

Thank you for participating in the Systematics Association's 2nd Young Systematics Forum. We shall have a great diversity of topics covered, which should represent an

excellent platform for exchange of ideas throughout the day. We hope that you will find the forum useful, stimulating and fun. The meeting is decidedly informal! There will be no "question time" after each talk but we strongly encourage everyone present to ask questions, offer constructive criticisms and discuss the presented projects during the breaks. Mark Wilkinson, the Associate Keeper of the Department of Zoology, will be chairing the sessions.

After the hard work we will have a "cheese and wine" session to thank all of the speakers and attendees for their contributions.

Good luck to all of you for your preparation and the talk!

Some suggestions for your presentations

You are encouraged to prepare your talks for a broad audience - for instance by giving a clear introduction of the aim(s) and the specific/general interest(s) of your study. Do not hesitate to present slides that illustrate the aesthetic of your organisms, their relevance for other fields of biology and/or every day life. For those working on theoretical and/or methodological developments you may want to illustrate with clear examples how they will be applied to address biological questions. Furthermore, arguably one of the important roles of Systematics is to increase the appreciation of life's diversity and beauty, do not hesitate to show this off!

!!!Please make sure that the timing of your talk is perfect so that we can respect the tight schedule!!!

Venue and how to get here

The meeting will be held in the Palaeontology demonstration room, on the ground floor of the Department of Palaeontology. Visitors will need to enter the Museum at the main entrance on Cromwell Road (leads to the Life Galleries) which is signposted from the South Kensington station, the nearest tube station (3 min walk) - *Circle, District* and *Piccadilly* lines direct from most mainline stations and Victoria coach station. There is a subway passage connecting the tube station to the Museum. The Museum opens to the public at 10h00 so you will have to state, by the main gate, that you are coming for the YSF. Report to the information desk where you will be given a visitor's badge and may be asked to sign in. Once in the main hall, turn right into gallery 30, the Waterhouse Way, situated just after the Diplodocus, and go straight up to the door by the end of that gallery which leads into the Palaeontology Building. The seminar room is on your left once through the door.

Timetable

09.00 Welcome by Mark Wilkinson

Session I

09.15 Trevor Cotton
09.30 Carlos Vaamonde
09.45 Elizabeth Moylan
10.00 Isabel K. Marshall
10.15 J Chris Pires

10.30 - 11.00 Break - coffee and discussions

Session II

11.00 Davide Pisane
11.15 Masato Nikaido
11.30 David Posada
11.45 Christopher Smejkal
12.00 Lucinda Evans

12.15 - 14.00 Lunch and discussions

Session III

14.00 Vanessa Pike - Funding opportunities for PhD and Post-Docs
14.15 Chris Creevey
14.30 Sophie Bentz
14.45 Max Coleman
15.00 James Cotton

15.15 - 16.00 Break - coffee and discussions

Session IV

16.00 Russ Seymour
16.15 Jovita Yesilyurt
16.30 Howsun Jow
16.45 Matthew Perry
17.00 Richard Grenyer

Session IV

Relaxing- cooling down session with cheese and wine, and more discussions...

Abstracts - in alphabetic order of authors

Comparison of molecular evolutionary rates in the Amphibia / Polystomatidae association

S. Bentz and O. Verneau. Laboratoire de Biologie Animale, UMR 5555 du CNRS, Centre de Biologie et d'Ecologie Tropicale et Méditerranéenne, Systématique et Ecologie Evolutive des Parasites, Université de Perpignan, 66860 Perpignan, France.

The present study deals with the comparison of molecular evolutionary rates in the intimate aquatic tetrapods / Polystomatidae association. A molecular phylogeny of those platyhelminth parasites which are the unique monogeneans parasitizing freshwater tetrapods, namely chelonians and lissamphibians shows that chelonian and lissamphibian polystomatids are each monophyletic suggesting a very ancient origin of the family. Within the class Lissamphibia, we identify three major groups of parasites : the first associates all neobatrachian polystomatids, the second includes archaeobatrachian parasites and the third is composed by the species of the salamander. The bushlike relationships at the base of the three groups suggest that polystomatids have cospeciated with their anuran hosts at the time of the breakup of Pangaea 180 million years ago (MYA), and simultaneously diverged from caudatan parasites. We sequenced a homologous part of genome i.e. 400pb of Cytochrome Oxydase I (COXI) for representatives of anuran hosts and their parasites and compared the distance matrix obtained for the two types of organisms. The correlation observed for the amino acid comparisons validates cospeciation events between hosts and parasites. The different rates of evolution suggest that parasites evolve faster than their hosts and / or that COX1 is subjected to strong selective constraints in anurans.

Transatlantic disjunction of a desert Ragwort

M. Coleman and R. J. Abbott. Institute of Environmental & Evolutionary Biology, University of St Andrews, St Andrews, Fife KY16 9TH, Scotland.

The taxonomic and evolutionary relationships within a morphologically distinct group of three taxa placed in *Senecio* L. section *Senecio* (Compositae) has been examined using morphology, cytology, molecular markers and crossing experiments. *Senecio mohavensis* A. Gray occurs in the Mojave and Sonoran deserts of North America, and is very isolated from the two subspecies of *S. flavus* (Decne.) Sch. Bip. which have an east-west separation in the Saharo-Arabian desert. The only exception to this being the Sinai Peninsular where the western *S. flavus* subsp. *flavus* meets the eastern *S. flavus* subsp. *breviflorus* Kadereit. The type subspecies of *S. flavus* also occurs in the Namibian desert. Our chromosome counts of *Senecio flavus* subsp. *breviflorus* show it to be tetraploid ($2n = 40$), unlike the type subspecies which is diploid ($2n = 20$). *Senecio mohavensis* is also tetraploid. Close similarity of the tetraploids, despite their great disjunction, is also

provided by morphology and molecular markers. Controlled crosses have been achieved in these strongly self-compatible species. The tetraploids produce hybrid offspring, whilst crosses between the two subspecies of *S. flavus* have produced no hybrids. Taken together these results indicate that *S. flavus* subsp. *breviflorus* should be treated as a subspecies of *S. mohavensis*. Evidence for allo- versus autotetraploidy and possible causes of the disjunct distribution are discussed.

A phylogenetic approach to studying gene duplications, and what it tells us about vertebrate phylogeny

J. A. Cotton and R. D. M. Page. Division of Environmental and Evolutionary Biology, Institute of Biomedical and Life Sciences, Graham Kerr Building, The University of Glasgow, Glasgow. G12 8QQ.

Molecular biologists interested in the evolution of gene families and molecular systematists interested in the evolution of whole organisms are both concerned with the relationship between gene phylogenies and organism phylogenies. We present reconciled trees as a tool for exploring this relationship. Implementation of newly developed extensions to standard reconciled trees should allow rapid, automated analysis of large sets of gene families and even of whole genomes, producing well supported organism phylogenies and allowing us to quantitatively investigate patterns of gene family evolution. We have begun work using these techniques on Hovergen, a large database of vertebrate gene families, and present preliminary results from these analyses that largely support current ideas about vertebrate relationships.

A 'big-hand' for the chelicerates?: The phylogeny of arachnomorph arthropods and the origins of the Chelicerata

T. J. Cotton. Department of Palaeontology, The Natural History Museum, Cromwell Road, London, SW7 5BD, UK and Palaeobiology Research Group, Department of Earth Sciences, University of Bristol, Wills Memorial Building, Queen's Road, Bristol, BS8 1RJ, UK.

The arthropod clade Arachnomorpha includes all taxa more closely related to chelicerates than to crustaceans. A new hypothesis of the relationships between arachnomorph arthropods is presented based on a cladistic analysis of 34 taxa and 53 characters. This study is considered to be superior to previous studies in providing detailed discussion of primary hypotheses of homology and by including a more complete range of terminal taxa. This analysis provides, for the first time, convincing synapomorphies for the Arachnomorpha and suggests that the marrellomorphs are not arachnomorphs. The assignment of Cambrian 'great appendage' (or megacheiran) arthropods to the Arachnomorpha is confirmed and potential synapomorphies uniting them and chelicerates are discussed and tested. Principal amongst these are the loss of the first cephalic appendages (the antennae/antennulae), loss of the exopods of the second cephalic appendages and modification of the endopods of these appendages into spinose grasping organs. The relationships of trilobites within a clade including naraoiids, helmetiids, tegopeltids and xandarellids are more fully resolved than in previous studies. This phylogenetic hypothesis is used to re-examine claims that unusual evolutionary processes were operating during the 'Cambrian explosion' of arthropods. A new phylogenetic classification of

the Arachnomorpha abandons the vast majority of previously erected higher taxa as superfluous.

Detection of adaptive evolution in protein coding sequences

C. J. Creevey and J. O. McInerney. Bioinformatics Laboratory, Biology Department, National University of Ireland Maynooth, Maynooth, Co. Kildare, Ireland.

The understanding of bacterial pathogenesis has been one of the most compelling reasons to sequence microbial genomes. Of the currently completed almost all of the organisms are implicated in causing human or animal disease. In each of these cases, the impetus has been to identify the genetic complement of the organism and perhaps from this information it might be possible to design suitable drug therapies. This study attempts to identify instances of adaptive evolution (positive Darwinian selection) in molecular data. There are many methods of detecting adaptive evolution in protein coding sequences, most of which use the ratio of replacement to silent changes at the nucleotide level (Ka/Ks) as an indicator. This detection method is of limited usefulness, silent substitutions are quickly saturated for change and an arbitrary ratio of 1 is generally used as the dividing line between positive and negative selection. In this study we have used detection methods based on a phylogenetic tree to identify adaptive evolution, with an emphasis placed on sensitivity (while keeping in mind the need for speed of execution and the ability to deal with large data sets). This talk will discuss the theory behind our methods, with reference to published data sets.

Development of microsatellite markers for the sheep scab mite, *Psoroptes* sp. (Acari: Psoroptidae).

L.M. Evans (1), D.A. Dawson (2), R. Wall (3), J.R. Stevens (1). (1) School of Biological Sciences, University of Exeter, Prince of Wales Road, Exeter, EX4 4PS. (2) Sheffield Molecular Genetics Facility, University of Sheffield, Western Bank, Sheffield, UK. (3) School of Biological Sciences, University of Bristol, Woodland Road, Bristol, UK.

One of the most economically important members of the astigmatid mites (Acari) is *Psoroptes* sp. This group of mites is most well documented for causing a severe skin disease in sheep, commonly known as scab. The taxonomic status of this genus has been called into question continually since its discovery in the 19th century, and it has yet to be resolved. A number of morphological studies and, more recently, sequencing analyses have found little variation between putative species. Hence, a novel approach, using a more sensitive marker system, has been attempted to clarify the species relationships within the Psoroptidae. A set of microsatellite markers are being isolated and characterised. These will be used to assess the variation between populations of mites from different hosts and varying geographical locations. This data will then be combined with sequencing analyses to provide a more thorough understanding of mite species relationships. It is anticipated that this research will contribute to a better understanding of astigmatid mite systematics and epidemiology. In turn this will lead to improved treatment and control of sheep scab, both in this country and abroad.

The threatened mammals of Madagascar: using the comparative method in conservation

Richard Grenver. Department of Pure and Applied Biology, Imperial College at Silwood Park, Ascot,

Berkshire. SL5 7PY.

Madagascar has the dubious distinction of being both an extraordinary centre of mammalian endemism and facing some of the most insoluble conservation challenges in the world today. As a result many of Madagascar's mammals are disproportionately threatened with extinction; my work examines how this threat is distributed across the Malagasy mammal fauna. Are there traits which predispose species to extinction? How do these traits function in concert? How much of the variance in threat can be explained by organismal biology, how much by ecological and geographic factors, and how much by human activity? As with any analysis across species, a comparative approach needs to be taken, and so in part the work presents a phylogeny of the endemic Madagascan mammals. The phylogeny has been used to create a statistically valid model of extinction correlates; a first for a complete group within a restricted range.

Structure Dependent Models of RNA molecular evolution

Howsun Jow. Department of Computer Science, The University of Manchester, Oxford Road, Manchester M13 9PL.

Models of sequence evolution have been used for some time now to construct phylogenetic trees. Most of these models treat each site on the nucleic acid sequence as a single unit of evolution, independent of all other units. However due to selective constraints not all sites can be considered to evolve independently. For example the secondary structure in RNA molecules is conserved. As a result the molecule evolves in such a way that it conserves base-pairing necessary to stabilise its secondary structure. This means that base-paired sites cannot be treated as statistically independent. The independence of sites is an important assumption that forms the basis of many statistical tests of phylogenetic trees. If traditional models of sequence evolution are used to construct phylogenetic trees from RNA molecular data we get misleading results. We will present more recent models of sequence evolution specific to RNA sequences and show how they differ from traditional models.

A MORPHOLOGICAL PHYLOGENY FOR THE BASAL AMBLYCERA (INSECTA: PHTHIRAPTERA)

Isabel K. Marshall. Division of Environmental and Evolutionary Biology, Graham Kerr Building, I.B.L.S.

University of Glasgow. Glasgow G12 8QQ.

Lice are obligate ectoparasites of most orders of birds and mammals. The suborder Amblycera (Insecta: Phthiraptera) comprises seven families three of

which (the Menoponidae, Laemobothriidae and Ricinidae) are distributed across a wide range of avian hosts. The four remaining families are confined to a small selection of mammals. The Boopidae are found on Australian and New Guinea marsupials and the Gyropidae, Trimenoponidae, and Abrocomophagidae on South and Central American rodents. Clay (1970) suggested that the Amblycera have undergone two major mammalian colonising events, with the boopid lineage resulting from an early divergence from the avian host and the remaining three mammal-infesting families stemming from a separate second event. This study examines the evolutionary relationships between the four most basal amblyceran families: the Menoponidae, Boopidae, Laemobothriidae, and Ricinidae. Each family is represented at the generic level (using the holotype for that genus) to make a total of 45 taxa in this study. 147 morphological characters were formulated and scored and the data analysed using parsimony to construct phylogenetic trees. 1000 random parsimony addition sequence replicates with TBR branch swapping found 6 equally parsimonious trees (1 island) of length 650 steps (CI: 0.326; RI: 0.585; HI: 0.683). Character state distributions were viewed using MacClade. Support analysis (bootstrap, jack-knife; and Bremer support) all showed strong support for the deep branch relationship between the families and in many instances for supra-generic groupings within the families. The clades common to the strict consensus tree will be discussed in relation to: i) within family relationships; ii) character choice and the problems of homoplasy within the Amblycera and iii) host distribution.

Systematics of *Hemigraphis* Nees (Acanthaceae)

Elizabeth Moylan. Department of Plant Sciences, Oxford University, South Parks Road, Oxford, OX1 3RB, UK.

Hemigraphis Nees is widespread across peninsula India, south-east Asia, Malesia, Australia and New Caledonia and comprises annual/perennial species that vary from erect shrubs to small creeping herbs. Two unresolved problems of *Hemigraphis* systematics are: (i) species delimitation and (ii) generic circumscription. Current research is addressing species delimitation in the Philippines through investigation of macromorphological and micromorphological characters.

Hemigraphis has been distinguished from other closely related genera in the subtribe Strobilanthinae (tribe Ruellieae - Acanthaceae) on the basis of ovule number: *Hemigraphis* has more than four ovules in the ovary whilst *Strobilanthes*, the largest genus of the subtribe, has fewer than four. However, use of ovule number is not only highly artificial and arbitrary, but is also inconsistent: other genera of Strobilanthinae also have more than four ovules. Molecular sequence data from the internal transcribed spacer (ITS) regions of nuclear ribosomal DNA and the chloroplast *trnL-F* region have been used to test the monophyly of *Hemigraphis* and investigate relationships with other genera. The results presented have implications for the recognition of *Hemigraphis* and for the future classification of the Strobilanthinae.

Retroposon analysis of major cetacean lineages: the monophyly of toothed whales and the paraphyly of river dolphins

Masato Nikaido and Norihiro Okada. Faculty of Bioscience and Biotechnology, Tokyo Institute of Technology. 4259 Nagatsuta-cho, Midori-ku, Yokohama 226, Japan

The monophyly and the paraphyly of toothed whales, and of river dolphins have been highly contentious issue in evolutionary biology of mammals. SINE (Short interspersed element) insertion analysis is now emerging as a powerful new method for inferring the ambiguous common ancestry of eukaryotic taxa. In this study, we characterize 25 informative SINEs inserted into unique genomic loci during evolution of toothed whales to construct a cladogram. We demonstrate that (1) Odontocetes form a monophyletic group; (2) Ganges river dolphins, beaked whales, and ocean dolphins diverged after sperm whales, in this order; (3) ocean dolphins and the three river dolphin taxa, namely Amazon River, La Plata, and Yangtze River dolphins, form a monophyletic group. We also determine a total of 2.8 kb of the flanking sequences of these SINE loci per taxon to estimate the divergence times among lineages. Thus, the branching orders, as well as the time estimation of their divergences, of the six major cetacean lineages are presented, providing comprehensive solutions to a number of long-standing problems regarding cetacean evolution.

Chocolate and a spot of TLC

Matthew D. Perry. John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, U.K.

Theobroma cocoa (L.) is widely cultivated throughout the tropics and is the sole source of cocoa butter, liquor and powder for the confectionery and pharmaceutical industries. Current market value is in excess of £3.5 billion, yet despite increasing demand, world production is in decline. Disease is a major cause of the market deficit and has reduced the production of one of the world's largest cocoa growers, Brazil, by almost half. Cocoa breeding programmes are limited and, outside of Cameroon, Ivory Coast and Malaysia, have had little impact. Initial breeding strategies were focused primarily on yield, however, the emphasis must now be directed towards disease tolerance/resistance. Unfortunately, the development of superior varieties is severely constrained by the lack of information concerning the identification and characterisation of cocoa at both a phenotypic and genotypic level.

Thin-layer chromatography (TLC) has previously been utilised to identify taxonomic markers in both temperate and tropical species and may be utilised in conjunction with more complex molecular techniques. In an attempt to improve the identification and characterisation of cocoa planting material, a number of commercially significant varieties were screened for their component flavonoids.

Biosystematics and molecular phylogenetics of Brodiaea(Themidaceae) and related lilioid monocots

J. C. Pires. Department of Botany, University of Wisconsin-Madison. Jodrell Laboratory, Royal Botanic Gardens, Kew. Richmond, Surrey TW9 3DS.

The resurrected plant family Themidaceae Salisb. contains 12 genera and 61 species of perennial geophytes from western North America. These

genera, formerly recognized as tribe Brodiaeae in the Alliaceae, have been previously divided into two complexes: the underdescribed Milla complex centered in Mexico and the Brodiaea complex centered in the western United States which includes genera that are classic examples of evolutionary radiation. Phylogenetic analyses of plastid DNA sequences of *rndhF*, *trnL-F*, and *rpl16* are presented. The Milla complex of Mexico is supported as monophyletic within a paraphyletic Brodiaea complex of western North America. Within Themidaceae, four major clades are identified: 1) the Milla complex containing *Bessera*, *Dandya*, *Milla*, *Jaimehintonia*, and *Petronymphe*; 2) *Brodiaea*, *Dichelostemma*, and a monotypic *Triteleiopsis*; 3) *Triteleia*, *Bloomeria*, and *Muillaclevelandii*; and 4) the other species of *Muilla* and *Androstephium*. These well-defined clades strongly suggest that the morphological characters (e.g., an extended perianth tube) that have been traditionally used to circumscribe the genera within Brodiaea complex have evolved independently at least twice. In addition, common biogeographic distribution patterns (e.g., Brodiaea and *Triteleia* having centers of diversity in northern California and the Pacific Northwest) appear to be the result of separate evolutionary radiations.

The Squamate Supertree and what it can tell us about MRP

Davide Pisani, Department of Earth Sciences, University of Bristol, Wills Memorial Building, Queens Road, Bristol BS8 1RJ, UK.

A Squamate supertree obtained combining 39 partially overlapping phylogenetic trees representing the cladogenetic relationships among all extant Squamate families and some of the most important fossil forms will be presented. The relationships inferred from this Supertree, obtained using the matrix representation using parsimony (MRP) approach, will be discussed. Furthermore, the same tree will be used to discuss some of the problems posed by the presence of biases in the MRP approach and, in general, to evaluate if it is possible to test the validity and the quality of an MRP-Supertree estimate.

The effect of recombination on phylogeny estimation

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Typical phylogenetic studies based on DNA sequences ignore the potential occurrence of recombination, which produces different gene regions with different evolutionary histories (mosaic genes). Traditional phylogenetic methods assume that a single history underlies a set of aligned sequences. If mosaicism is present, is the inferred phylogeny reliable? We examined this question by applying traditional phylogenetic reconstruction methods to computer-generated mosaic DNA data sets. Here we show that the effect of recombination on phylogeny estimation depends on the location of the recombinational breakpoint along the sequences and on the relatedness of the sequences involved in the recombinational event. If the recombinational breakpoint does not divide the sequences in two regions of similar length, if the recombinational event is ancient, or if recombination has occurred among closely related taxa, the evolutionary history corresponding to the majority of

the positions in the alignment is generally recovered. However, when recombination has occurred recently among divergent taxa and the recombinational breakpoint divides the alignment in two halves, very different trees are inferred.

Morphology, Phylogeography and the Subspecies of the Giraffe, *Giraffa camelopardalis*.

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University(3).

Intraspecific variation is a logical corollary of Darwinian evolution and is well documented in the majority of widely distributed animal species studied. The question for subspecific taxonomy is whether any such differences are structured geographically enabling discrete taxa to be diagnosed below the species level. An acceptable, functional determination of subspecies may have implications for our views of mammalian biodiversity and may have an effect on mammalian conservation efforts. Delineation of taxa can be dependent upon the type of data and on the method of analysis used. This study uses genetic, morphometric and pelage pattern analysis techniques to investigate subspecific groupings in the giraffe. Results from each type of data will be presented. The usefulness of each data set and analytical procedure in elucidating subspecific variation will be discussed. Conflicts and congruence between the results will also be discussed.

Substrate specificity of chlorophenoxyalkanoic acid degrading bacteria is not dependent upon phylogenetically related *tfdA* gene types

Christopher W. Smeikal (1), Tatiana Vallaey (2), Sara K. Burton1 and Hilary M. Lappin-Scott (1). (1) School of Biological Sciences, University of Exeter, Hatherly Laboratories, Prince of Wales Road, Exeter, Devon, EX4 4PS, UK; (2) Lab.Microbiology, Radioactive Waste & Clean-up Division, SCK/CEN, Boeretang 200, B-2400-MOL-Belgium

The phenoxyalkanoic acid herbicides constitute a group of chemically related molecules that have been widely used for over fifty years. A range of bacteria have been selected from various locations for their ability to degrade these compounds. Previously reported strains able to utilise 2,4-D include, *R. eutropha* JMP134, *Burkholderia* sp. RASC and *V. paradoxus* TV1 and *Sphingomonas* sp. AW5 able to utilise 2,4,5-T. In addition a novel set of mecoprop degrading strains including *Alcaligenes denitrificans*, *Alcaligenes* sp. CS1 and *Ralstonia* sp. CS2 are here described. It has been reported recently that TfdA enzymes, initially reported to have a role in 2,4-D catabolism are also involved in the first step cleavage of related phenoxyalkanoate herbicides. However, a diversity of *tfdA* gene sequences have been reported. We relate the *tfdA* gene type to the metabolic ability of these strains. The *tfdA*-like genes were investigated by PCR amplification using a set of specific *tfdA* primers. Degradation ability was observed via phenol production from a range of unsubstituted and substituted phenoxyalkanoics including, 2,4-D (2,4-dichlorophenoxyacetic acid), MCPA (2-methyl 4-chlorophenoxyacetic acid), racemic mecoprop, (R)-mecoprop, racemic 2,4-DP

(2-(2,4-dichlorophenoxy) propionic acid), 2,4,5-T (2,4,5-trichlorophenoxyacetic acid), 2,4-DB (2,4-dichlorophenoxybutyric acid), MCPB (4-chloro-2-methylphenoxybutyric acid) and phenoxyacetate. Mecoprop degrading strains showed partial *tfdA* sequences identical to the one described for *V. paradoxus* TV1 (a strain isolated on 2,4-D). However, substrate specificity was not identical as *V. paradoxus* exhibited greatest activity to 2,4-D and MCPA only, whereas the mecoprop degrading strains showed intense activity towards 2,4-D, MCPA, racemic mecoprop and (R)-mecoprop as substrates. However, *Sphingomonas* sp. AW5 which has been shown to carry a very different *tfdA*-like gene was the only strain to utilise the phenoxybutyric acid MCPB as a sole carbon source. In this study, we thus demonstrate that sequence diversity is not related to substrate specificity within the *tfdA*-like gene family. However, phylogenetically unrelated sequences may govern substrate specific activity.

Evolution of host plant utilisation in Phyllonorycter (Lepidoptera, Gracillariidae) leaf-mining moths based on nuclear and mitochondrial DNA sequence data.

Carlos Lopez Vaamonde. NERC Centre for Population Biology & Department of Biology Imperial College at Silwood Park, Buckhurst Road, Ascot, Berkshire SL5 7PY, UK

The phylogenetic relationships of 75 Phyllonorycter leaf-miningmoth species were determined based on the partial nucleotide sequence of the nuclear 28S rDNA. The molecular phylogeny is used to (1) establish the frequency of host shifts among Phyllonorycter species; (2) investigate directions of host shifts and identify the ancestral host plant; (3) provide a preliminary assessment of the sequence of host plant colonisation and speciation. The results provide unambiguous evidence for phylogenetic conservatism - closely related Phyllonorycter species feed on closely related plants. No statistically significant evidence of parallel cladogenesis between Phyllonorycter moths and their host plants was found. It is likely that this host plant colonisation scenario proposed here might apply to other endophytic Lepidoptera lineages.

Species concepts in *Doryopteris* from Brazil

J. Cisilinski Yesilvurt. Botany Department, Natural History Museum. Cromwell Road, London SW7 5BD

The delimitation of a "species" can be very complex. Delimiting species on the basis of morphology may be more problematic than species delimitation based on other species concepts. An example taken from a preliminary hypothesis of the evolutionary relationships among *Doryopteris* taxa, is used to illustrate this. There is no intention, however, to advocate the use of one concept over the others. The aim of better resolution of taxonomy is separated from the study of the phylogeny of the genus. The example discussed displays large morphological variations (in the leaf shape and lamina dissection). This situation has misled systematists as the extent of phenotypic variability is unknown. Some individuals involved in this group have been identified as hybrids. However, they do not express any obvious morphological hybrid characteristics. They will be investigated using techniques such as cytology, palinology, molecular analysis, alloenzyme electrophoresis, anatomical

dissection and biogeographical analysis.

List of speakers

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