



Newsletter

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From the President

This is the last of my missives in this capacity, handing over as I do to Chris Humphries at the AGM. I would like to express all my thanks to the many people who have and continue to make the Association run so smoothly and make myself virtually redundant. Systematics is at one level a very synthetic field and at another a disparate field. Throughout the last few years I have met people who have expertise in many diverse taxonomic groups and they have certainly broadened my perspectives on what can be a very singular science, introducing me to problems I had not even thought of or dismissed as low priority. In other words I have learned a good deal. The Biennial meetings have been particularly enlightening both for the range of expertise displayed and the commonality of many problems we all face. To me the enthusiasm of the younger scientists who make up a large percentage of the attendees at these meetings and the high quality of their work is tremendous encouragement that the Association is fulfilling a unique role. I hope and expect that the 2001 Biennial will continue the success of the previous two. There are very good mini-symposia lined up and I hope all will take the time to visit the website and register.

During the last three years there have been many advances made in the practice of systematics, including new computer programs. These have brought new challenges. The growth of molecular systematics has been almost exponential and this has only alerted me to the fact that so much morphological work needs to be done to test the 'new phylogenies'. However, one particular area seems to me a retrograde step — the Phlyocode...

<http://www.ohiou.edu/phylocode>

...an attempt to name nodes and to stabilise the names in perpetuity. Others, of course, may have different views.

In stepping down as president I will of course continue to haunt you in some capacity or another. It has been an enjoyable three years and you have made it so.

Peter Forey

*Department of Palaeontology
Natural History Museum
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From the Editor

My apologies for the long interval between this issue of the *Systematics Association Newsletter* and the last. But if no-one sends anything in...

There has been much discussion in recent months about electronic versions of this newsletter, which Peter Forey puts to the membership in the Council News section below. Many of us already subscribe to at least one electronic mailing list, and there are already a number of on-line journals.

The other side of the argument involves cost and accessibility. When you log onto your e-mail or web account, it is the recipient who pays delivery charges, not the sender. For those of us working in large institutions this probably is not an issue, but it may be for small museums with dial-up modem accounts. Another problem is accessibility. Surprising as it may be to some, not everyone is *au fait* with the Internet. Some people rely on others to do their e-mail (secretaries, grand-children or even kindly post-docs!), while others do not even get that far.

Neale Monks

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The Systematics ASSOCIATION



Council News

Annual General Meeting

Please don't forget the AGM, December 6th in the rooms of The Linnean Society of London. AGM at 17.00, Annual Address at 18.00 – this year by Peter Forey and entitled "The data protection act". Some details have been circulated

Council Members

This AGM sees positions for 10 new Council Members. We would like to see active participants. If you would like to become such or know of a likely candidate then (with their permission) we need nominations and a seconder and details to be mailed to Dr Zofia Lawrence, International Mycological Institute, Bakeham Lane, Egham, Surrey TW20 9TY (e-mail z.lawrence@cabi.org) by 1st December.

Electronic Books

Taylor & Francis — our publishers — have recently approached us asking if they can put our books on the web in electronic form. This is a new venture for us and we are uncertain of the ramifications. E-books undoubtedly will become more available and they are used by the fiction world essentially as advertising. However, the Association depends for its existence on the royalties gathered through sales. We are meeting with T&F in December to discuss the vexed issue of if the royalties on sales will be affected by the availability of e-books. What is less certain is the issue of security. Given that one subscriber may pay for a book what safeguards are there that copy or chapters therein is not distributed free? Could we be entering the same mine-field as photocopying? Is there any member who has experience, direct or indirect with e-books who might give us some inside information? Information to Allen Warren (apw@nhm.ac.uk).

Electronic Newsletter

Still on the subject of electronic media, Council did consider the possibility of distributing the Newsletter electronically. Naturally this would not suit everyone and we would, of course, still mail to those who do not have e-mail or would prefer to receive hard copy. But, if the Newsletter were distributed by e-mail we would undoubtedly save money. The duplication charges would be (slightly) cheaper but the main savings would be made on postal charges. Sometimes the mailing contains nothing but the newsletter, and if this happened once per year we would save about £200. That would pay for two Young Scientists forums. Some feedback to Geraldine Reid, either by mail or e-mail (gr@nmh.ac.uk) would be useful to test the water.

Two New Books

A couple of new books have appeared that may be of general interest:

Wiens, J.J. (ed.) 2000. Phylogenetic analysis of morphological data. 220 pp. Smithsonian Series in Comparative Evolutionary Biology, Washington: Smithsonian Institution Press. paperback. ISBN 1-

56098-816-9. £17.95/US\$ 26.95 (Pbk) £32.95/\$49.95 (Hbk).

Schuh, R.T. 2000. Biological Systematics: Principles and Applications. 236 pp. Comstock Publishing Associates: Ithaca and London. Hardback. ISBN 0-8014-3675-3. £29.50/US\$ 45.00 (Hbk).

Reviews will appear in the next Newsletter.

Peter Forey

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Website News (www.systematics.org)

Rupert Wilson (Rupert Wilson school of Plant Sciences, University of Reading) has kindly taken on managing the Systematics Association website (Division of Environmental and Evolutionary Biology, University of Glasgow). All of us on the Council pass on our thanks.

One of his first changes has been to up-load electronic versions of the *Systematics Association Newsletter*, going back as far as the April 1998 issue. These are archived as Acrobat files. To read these files you will need either Adobe Acrobat or the free version of that application, Adobe Acrobat Reader which can be downloaded from the Adobe site:

www.adobe.com

Acrobat files retain the format of the paper version, and are platform independent, which means they look equally good on Macintosh or Windows machines. Any queries, ideas or comments should be forwarded on to him. His e-mail is r.g.wilson@reading.ac.uk.

Neale Monks

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SA Grant Scheme

Information and application forms for the 2000/2001 round of the Systematics Association Grant Scheme are enclosed in the current mailing. Further copies of the forms can be obtained from the Systematics Association's web page, or from me directly. The closing date for the 2000/2001 grants is 31st December 2000.

Peter Hollingsworth

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Award Recipients

David Fewer, Disjunct populations of the marine red alga Rhodochorton purpureum

Rhodochorton purpureum is a filamentous turf-forming marine red seaweed with a world-wide distribution. It is absent from equatorial regions where water



temperatures do not permit growth. This disjunction between southern and northern hemisphere populations was first identified by F.W. Knaggs over three decades ago. The aims of this study were to reconstruct the historical biogeography of *R. purpureum* and to test competing hypotheses regarding the origin and timing of this conspicuous bipolar disjunction. The Systematic Association kindly funded the collection and sequencing of additional individuals from the southern hemisphere. This enabled us to test whether this disjunction is recent as proposed by Knaggs or ancient as expected under vicariance models. Our results indicate that the disjunction between the northern and southern hemispheres is indeed recent and suggests that this marine seaweed has undergone a range expansion. These results are important because it is generally anticipated that the distribution patterns of sessile marine seaweeds are best explained by vicariance. My masters degree has been accepted and a manuscript is in preparation. The Systematics Association research grant was very useful and I would like to thank the Systematics Association for the chance to further this study.

David Fewer

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Quick Notices

**Affiliated Societies Forum, Institute of Biology
16th November, 2000**

*Institute of Biology, 20 Queensberry Place, South Kensington,
London*

A one-day forum .Principal speaker Dr. Michael Clark MP, chairman of the Commons Science and Technology Committee.

For details see the Institute of Biology website:

www.iob.org

Or contact Jonathan Cowie, Institute of Biology, 20-22 Queensberry Place, London; e-mail j.cowie@iob.org.

**Royal Geographical Society Explore 2000 meeting
18th & 19th November, 2000**

Royal Geographical Society, 1 Kensington Gore London

Explore 2000 is the expedition planning seminar of the Royal Geographical Society (with the Institute of British Geographers). It is of relevance to any biologists planning to make expeditions a little further than the spirit collections of the Natural History Museum!

Download a working programme or a booking form from the Explore 2000 website:

www.rgs.org/Explore2000

Alternatively, contact Anna McCormack at the Expedition Advisory Centre, Royal Geographical Society (with the Institute of British Geographers), 1 Kensington Gore London SW7 2AR; telephone +44.(0)20 7591 3032.

Meeting Reports

Millennium Brachiopod Congress, 10th-14th July, 2000

The fourth five-yearly international congress on brachiopods, whose previous venues were France, New Zealand and Canada, was held at The Natural History Museum, London and was sponsored by The Systematics Association, The Geological Society and The Palaeontological Association. 146 delegates from 31 different countries attended and over 70 papers and 30 posters were presented over the four day period which was preceded by an excursion to the Palaeozoic of Wales and the Welsh Borderland and continued on into a week-long field excursion to the Mesozoic of south-eastern England. The conference was organised by Robin Cocks, Howard Brunton and Sarah Long of the NHM and Alwyn Williams of Glasgow University. All the manuscripts for publication have now been received and are undergoing peer review and author revision before being sent to press in April for publication later in 2001 by Taylor and Francis on behalf of the Systematics Association.

Robin Cocks

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The NERC Taxonomy Today Conference, 3rd-5th July 2000

Hosted by The University of Reading and organised by a team from The Universities of Reading, Glasgow and London (Imperial College), the NERC-sponsored conference "Taxonomy Today" lived up to its name with papers covering much of the range of current research in taxonomy and systematics. More than 140 delegates attended the conference, which took place over three days and comprised three thematic sessions. The first, organised by Donald Quicke (Imperial College), examined Key Innovations: past and present. Paul Goldstein (Field Museum, Chicago), the keynote speaker, grappled with slippery concepts (radiation, adaptive radiation and key innovation) which have been variously defined to the point of definition gridlock, but managed to flag some of the exciting biology behind the terminology. The second session (organiser Alastair Culham, University of Reading) addressed issues of Rate and Time in Phylogenetics. Speakers included Mark Pagel, (University of Reading, UK; Inferring the historical patterns of biological evolution), and Alastair Culham (Three genomes, one clock: relative rates of change in DNA sequence data). A third session, The Catalogue of Life: discovery, classification and information systems, was organised by Frank Bisby. This diverse session ranged from the discovery of new taxa from marine and anchialine environments (Geof Boxshall, Natural History Museum, London), to "How many trees would it take to build the tree of life?" (Bill Piel, Leiden University); the former was a visual treat, the latter a chance to catch up



on the Hollywood Small World Network. More insight into the range of current taxonomic and systematic activity was provided by opening and closing speakers. Elizabeth Kellogg, a defender of the Christmas Tree approach to morphology, called for a return to morphological systematics with a twist: sequence data describe relationships, molecular genetics uncovers the relationships between morphological structures. Our closing speaker, Peter Bridgewater (UNESCO, Paris) spoke about the Global Taxonomy Initiative - 2001: a species odyssey.

The conference was funded as part of NERC's 5 year Taxonomy Initiative. A policy forum was conceived as an opportunity to address national research priorities and their facilitation, as the Taxonomy Initiative draws to a close. The Forum was chaired by Bill Chaloner; NERC was represented by John Lawton, and BBSRC by Alf Game. Six speakers were allotted 5-10 minutes to describe research priorities in the taxonomy of neglected groups, intelligent systems in taxonomy, phylogeny and evolutionary developmental biology, and Flora and Fauna writing. A lively debate followed Lawton's down-beat overview of NERC's position. NERC clearly does not have any plans to fund another initiative specifically for taxonomy. However, question-driven "Blue Sky" research, which may be underpinned by taxonomic or systematic research, will be supported by both NERC and BBSRC - so pack away your wet weather gear. The possibility of "ring-fenced" NERC PhD studentships to ensure continuing taxonomic expertise was raised by John Lawton.

Those who missed the meeting may be interested to read the abstracts, available online:

www.systematics.reading.ac.uk/taxonomy_today

Julie A. Hawkins,

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Forthcoming Meetings

Young Systematists Forum, 30th November 2000

Abstracts — in alphabetic order of authors

Comparison of molecular evolutionary rates in the Amphibia / Polystomatidae association
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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 archaebatrachian parasites and the third is composed by the species of the salamander. The bush-like 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 Oxidase 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

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University of St Andrews, St Andrews, Fife, UK

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 Peninsula 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, UK

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, UK and Palaeobiology Research Group, Department of Earth Sciences, University of Bristol, Wills Memorial Building, Queen's Road, Bristol, 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 naraoidids, 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 (K_a/K_s) 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. Evans¹, D.A. Dawson², R. Wall³, and J.R. Stevens¹

1—School of Biological Sciences, University of Exeter, Prince of Wales Road, Exeter, UK

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 Grenyer

Department of Pure and Applied Biology, Imperial College at Silwood Park, Ascot, Berkshire, UK.

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, UK.

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, UK

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 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, UK

Hemigraphis Nees is widespread across peninsula India, south-east Asia, Malaysia, 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

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The monophyly and the paraphyly of toothed whales, and of river dolphins have been highly contentious issues 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, UK

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

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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 *Triteleioopsis*; 3) *Triteleia*, *Bloomeria*, and *Muilla levelandii*; 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

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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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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

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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 phenoxyalkanoic acids 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

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The phylogenetic relationships of 75 *Phyllonorycter* leaf-mining moth 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
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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.

Molecular and Morphological Phylogenetics of King Crabs (Crustacea, Anomura, Paguroidea, Lithodidae)

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Members of the king crab family are amongst the world's largest arthropods; they are morphologically diverse, spectacularly ordained, and possess considerable economic importance (e.g., *Paralithodes camtschaticus*, the Alaskan king crab). However, relatively little is known about them. How and why this group of crabs evolved has been debated since the mid 1800's. Early morphologists suspected close genealogical ties to hermit crabs (Paguridae, Anomura), and recent molecular evidence supports a basal hermit crab hypothesis. However, several recent morphological descriptions disagree with this prognosis and suggest that the Lithodids are instead the basal lineage. Herein, I will discuss evolutionary relationships between the hermit and king crabs, and also discuss relationships within the king crab family, based on both molecular and morphological characters analyzed using recent cladistic analyses.

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Student Conference on Conservation Science 28th - 30th March 2001

Building links among young conservation scientists and practitioners.

We are pleased to announce the second in a series of student-oriented conferences on conservation science, hosted by the Department of Zoology, University of Cambridge. The conferences are aimed at people actively engaged in research in conservation science in biological, environmental and geography departments of universities as well as in conservation and resource management agencies. Conservation practitioners from leading international and national conservation bodies attend and contribute to discussions. The first conference of the series in March 2000 was attended by 130 postgraduate students from 28 countries and staff from 14 conservation agencies and NGOs.

Your contribution

The most important part of the three-day programme will be poster sessions and 35 fifteen minute talks by students on any aspect of conservation science. Presentations of work in progress, from a broad range of countries, and from economic and social as well as biological aspects of conservation, will all be welcome. Besides the posters and talks, there will also be workshops, presentations by conservation NGOs and agencies and social events designed to give participants the opportunity to make new contacts in their own and related disciplines. Prizes are awarded to posters and talks of outstanding quality and relevance to conservation.

Plenary lectures

There will be plenary lectures by leading figures in the field. The speakers will be:
Professor Madhav Gadgil (Indian Institute of Science)
The Rt. Hon. John Gummer MP (House of Commons)
Dr Georgina Mace OBE (Institute of Zoology,

Zoological Society of London)
Jeffrey A. McNeely (Chief Scientist, IUCN)

Costs and benefits

The conference fee, including registration, tea and coffee and three evening events, is £30. Accommodation from the night of 27th March onwards is available at St Catharine's College at the highly subsidised rate of £10 per person per night, including breakfast. However, if you can stay elsewhere, this will help us to keep the prices low. Lunchtime sandwiches can be bought in the Zoology Department, while reasonably priced evening meals are available nearby.

Registration

Places are limited so please complete the application form, available at:

www.zoo.cam.ac.uk/sccs/index.html

Application forms are also available directly from the Conservation Biology Group, Department of Zoology, Downing Street, Cambridge CB2 3EJ, UK/e-mail: sccs@zoo.cam.ac.uk. Return this form by 1 November 2000 at the latest. Allocation of places will be made shortly afterwards. Note that it is not essential to present a talk or poster in order to attend.

Andrew Balmford & Rhys Green

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Details can also be obtained directly from Mrs Grace Barter, Molecular Systematics Short Course, Plant Sciences Laboratories, University of Reading, Reading RG6 6AS; email: g.barter@reading.ac.uk.