

The Systematist

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Editorial

You are reading the new, enhanced version of the SA Newsletter, with a better layout and much more content. We aim to provide our membership with interesting material to stimulate debate and discussion.

In this issue the hugely successful Dublin Biennial of the late summer is reviewed by both organisers and delegates, revisiting some of the key ideas for the future of Systematics. In particular, Quentin Wheeler's article is well worth a read. Do check out Chris Humphries' final 'Letter

Letter from the President

This is the last letter that I write for the newsletter before handing over at the AGM in December to my worthy successor, Dr Barrie Leadbeater. Naturally, my main task is to thank all of those people that have given their services to the Association over the last three years and who have helped me run the various projects that we have undertaken. When I became President I was simply amazed at how much

contributions I would particularly like to thank the officers, Donald Quicke, David Williams, Geraldine Reid, Zofia Lawrence and Gordon Curry for their tremendous combined expertise in helping run the formal side of the organisation. I would also like to thank Alan Warren, as Editor-in-Chief, Eileen Cox for the programme committee, Tim Littlewood for presiding over the Grants and Awards Committee, the webmaster, Rupert Wilson, and Messrs Robert Hirt, David Horner and Russell Seymour for so ably organising and running the young systematists forum.

It might seem to some that my most unenviable task was presiding over two biennial meetings. However, it has been a pleasure to work with all of the individuals who have given so much of their time to both enterprises. Although it is invidious to single out names because so many members and visitors contributed to the success of both meetings; the London meeting would have not have worked without Vilma Bharatan who did so much to make everyone feel at home. Also in Dublin during August 2003 Steve Waldren, Trevor Hodgkinson and John Parnell and their colleagues ran a wonderful 4th Biennial Conference at Trinity College, Dublin. For both meetings I would like especially to thank Tim Littlewood for his skill and sense of humour that he brought to the job of chairman of the judges, and my special thanks of course go to our Treasurer, Gordon Curry, who's

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from the President' and review of the Biennial, excellent reminders of the how Association has progressed and developed under Chris's presidency. This newsletter looks forward to reporting a continuation of such development in Barrie Leadbeater's coming term.

the Association had developed since I had previously been on council in its chosen role as a professional organisation helping its own professionals and encouraging and nurturing newcomers to the broad field of systematics. In addition to all of the councillors for their enthusiastic

undoubted monetary skills made both meetings profitable, troubleshoot currency exchanges and generally balance the books.

The quality of the work and the large number of students and young post-doctoral fellows that attend our biennial and other meetings is testimony to the fact that the Association is going some way in the direction



President: Christopher J. Humphries

that we all wish to go, and despite the obvious difficulties of finding ways of resourcing projects there is no lack of imagination amongst all of the players. The quality of research, talks and papers is outstandingly high amongst the participants and the students and young post-doctoral fellows particularly. During the last three years there has been copious output of empirical papers on all manner of groups in the literature. I am glad that the Association caters for a wide range of disciplines in zoology, protistology, botany, palaeontology and parasitology etc. despite rather biased interests towards higher plant systematics and catering for the exponential growth in molecular systematics. Undoubtedly amongst the considerable interests that I have seen develop it is rather illuminating that investigations have erred on the technological and algorithmic sides of achievement rather than in the epistemological and theoretical. I think it is worth noting that despite

the considerable wealth of curiosity and imagination too much analysis in the 'black box' rather than in the basics with pen and paper are apparent. There is so much to be achieved in general systematic theory, especially the underlying principles of systematic analysis, homology and biogeography, that I worry this is causing our students to losing grip on the basics of our subjects. Furthermore, it is worth noting that some of the fears of my predecessor, Peter Forey, about the *Phylocode* still appear in the literature, which means that it is quite apparent that many young turks are 'victims of ambition' to cite Løvtrup's colourful phrase rather than becoming well rounded systematists cogniscent in all of the necessary branches of the subject. The phylocodists have shown a rather dismaying trend that is beginning to appear in a number of fields that politics runs roughshod over science in the efforts to capture the middle ground rather than by reasoned debate and exposing populist myth.

The President's business has not only concentrated on the biennial symposia but also the various national initiatives that have taken place in the last three years. These

House of Lords transcripts can be found at www.systass.org/systass-lords-transcript.html

include attempts to raise awareness in the perceived decline of systematics in a shrinking scientific budget and the seemingly cavalier attitudes of funding bodies to the plight of systematics in the UK and elsewhere. To this end it was an interesting opportunity to participate in Baroness Walmesley's debate on the science underpinning research in biodiversity. Besides supplying written evidence, I also sat in front of the subcommittee with the President of the Linnean Society to give verbal evidence in February 2002. Subsequent presentations to the

House of Commons and replies were also made, but there was little in the way of genuine new interest recorded, but merely desultory support and very little increase in overall funding to systematics.

However, I am happy to report that one of the stated aims of the report was for the Linnean Society and the Systematics Association to work more closely. Its first achievement, through the efforts of Tim Littlewood and Richard Bateman, the two societies have produced a combined grants and awards scheme, of which more details will be given in the next round of calls later this year.

Finally, it is important to note that our publication procedures are changing as a result of Taylor and Francis buying up CRC publishing in the USA. In the future, book publication for Taylor and Francis, including the Association's publications will cease to be based in London but will be processed instead by CRC publishers in Florida. The Editor-in-Chief and the treasurer have been pursuing the ramifications of a shift in production across the pond and the Treasurer recently has received the revised instructions for editors of symposium volumes.

sium volumes.

All in all, I have spent a happy three years with the Association and the work has shown me that to run a successful organisation it is necessary to keep on top of the issues all of the time. I hope you feel that I have done my little bit towards this end, and like my predecessor I will be back to haunt you from time to time starting as of now, with the editing of the databases meeting.

Chris Humphries
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Transforming Taxonomy

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Using traditional methods, taxonomists have documented about 1.7 million species in 245 years. Assuming 8.3 million species remain to be described (an admitted guess) and a rate of progress equal to the average of the post-Linnaean period, we will need 1196 years to complete the job. If any of the gloomy prognostications about species extinction are even approximately true (e.g. Wilson 1992), we shall have missed many of the world's species, possibly including a large number of the most evolutionarily interesting ones. Many scientists have concluded that the task of a taxonomic inventory of life on earth is so impossibly large that we should simply give up. They assume, falsely, that taxonomists are limited by the methods and tools, and thereby tempo, of the past. This would be like denouncing plans to put a man on the moon in the 1960s because commercial aircraft did not fly fast or high enough. The urgency of the biodiversity crisis dictates that the taxonomic and museum communities can no longer accept business as usual. We need a revolution in how we conceive and solve taxonomic problems.

Ecologists have lamented that their work is constrained by the "taxonomic impediment." That is, any serious biological research in almost any biodiversity-rich country is limited by the ability to identify the species encountered accurately. The challenge to the taxonomic community is to determine the causes for this impediment and to clearly state what resources and tools are required to remove it. Clearly this will require funds for research and for collections, support for students and post-docs, and a new generation of efficient tools. What may be even

more difficult is a needed change in the taxonomic paradigm. We need to be international where we have been provincial. We need to act as a community where we have been fiercely independent individuals. We need to reinvent morphology-based taxonomy at a time when all forces are pushing the field increasingly toward the molecular. And we must embrace the molecular as an important tool for identifications and phylogeny reconstructions, but do so in a way that is intellectually balanced. Done well, we can enjoy the advantages of new data while maintaining the intellectual rigor developed in taxonomy over a long history. Such paradigm shifts are not simple or easy. Drastic changes are needed immediately by individual research scholars, taxonomic institutions, and the taxonomic community as a whole. We must begin at once to educate (not merely train) a new generation of taxonomists who think about their work very differently and who are effective ambassadors for this "new" taxonomy.

Although I would differ with regard to certain details, Godfray's (2002) contention that taxonomy and morphology are superbly positioned to take advantage of the Internet is true, and profoundly so. So-called "descriptive taxonomy," based largely on morphology, is perfectly positioned to take full advantage of the capabilities of the Internet. It is ironic that proponents of DNA barcoding seek to sideline morphology at the moment in history when technology has finally caught up with its demands for communicating visual data. While DNA barcodes are an exciting tool for species identification, they are a poor basis for making species hypotheses. They are eerily reminis-

cent of the arbitrary quantitative definitions of species proposed by pheneticists in the 1970s that proved evolutionarily impotent.

Morphology remains important for numerous reasons. It makes fossil and extant species comparable. It reveals patterns in need of evolutionary explanation. Its characters are efficient summaries of thousands of DNA base-pairs and the objects of natural selection. It makes Nature accessible to laypersons. It facilitates field identification of species. And it is intellectual fun to study. It is only because morphologists banked so many observations over the past few centuries that molecular phylogeneticists have had anything interesting to explain with their analyses, but such morphological descriptions exist for only a fraction of earth's species.

If taxonomists play their cards right, they can emerge from this period of Renaissance with a field stronger than it has ever been, capable of making research progress faster without sacrifice to rigor or quality. Miraculously, we could not have planned a better set of circumstances in which to lead this science revolution. The theoretical challenge following Darwin was to find a way to rigorously test phylogenetic hypotheses. It took a century to find such an approach, but thanks to Hennig (1966) this hardest-to-schedule advance has been made. What we need now is an equally impressive technological revolution. As luck would have it, both molecular and information technology advances seem tailor made for our needs.

It seems to me that taxonomy has been in steady decline since the field was intentionally commingled with population genetics by Mayr in

1942 (see Wheeler 1995). Just as Hennig reinvigorated the field by returning the focus to species and higher taxa, molecular phylogenetics diverted (wittingly or not) resources from taxonomy. As a result, most of the limited money earmarked for taxonomy supports only phylogenetic analyses that never follow through to improved classifications and names or provide descriptions of new species. Phylogenetics represents one of the most important theoretical advances since Darwin, but divorced from taxonomy poses a threat to biology (see Wheeler 2004).

Taxonomy must now be transformed into a large, coordinated, international science enterprise. This is not surprising. To the contrary, it is remarkable that it has not happened on its own. Like plate tectonics, oceanography, or astronomy, taxonomy requires worldwide data to reach credible conclusions. This has been done in the past mostly through an individual reviser or monographer examining all the necessary specimens from around the world by visiting, or borrowing specimens from, many museums.

Most explicit efforts to address the taxonomic impediment have come not from taxonomists but from ecologists. Well intended, such suggestions often fail to take account of the unique needs of taxonomic research. Some reasons for the impediment are obvious: too few taxonomists educated and employed, too few grants for basic taxonomic work, too low priority for taxonomy on university campuses and increasingly even within museums. Taxonomists now need to take a cold, hard look at their own science, determine where the bottlenecks exist, and devise a plan to open them up without sacrifice to the integrity of the research or quali-

ty of the scholarship.

Let's rethink how we do this. Take beetles as one example. The Natural History Museum in London alone has about 100,000 type specimens of beetles and makes a large number of loans each year, about 5000, to specialists who need to study them. This is slow, inefficient, and threatening to the physical well being of the specimens. Some number of such loans or visits to the museum will be needed regardless of changes made in practice. However, in a substantial number of instances, a skilled taxonomist can learn what he or she needs to know with a simple look at the specimen. Why not build a support laboratory at the Museum with digital microscopes accessible remotely online. A technician could place a type specimen under the

training a cadre of para-taxonomists, trained in the identification features of common species and best practices for collecting and preserving specimens, who are deployed around the world as needed. A research scientist at the museum could be shown the day's catch by the same kind of digital online microscopy and instantly decide whether the para-taxonomist should collect more specimens or not. This could expedite the pace of collecting by orders of magnitude. And even with a limited number of experts on an enigmatic taxon, expertise could be shared wherever it is needed.

What about education? Most universities either lack the experts or collections to offer advanced taxonomic courses, yet the demand for accurate identification work contin-

Taxonomy must now be transformed into a large, coordinated, international science enterprise.

microscope and, properly equipped, the facility could enable an investigator to manipulate, examine, and even digitally photograph the specimen remotely. I have often made trips to museums just to check one or two characters on a type specimen at considerable cost in money and time. Efficiency demands access to such a tool. An investigator could, in principle, examine a type specimen and confirm or eliminate an identification within minutes of a question arising, rather than using a curator's time and risking a specimen with damage by waiting days or weeks for a shipment. Similarly expeditious improvements are possible across the board.

Consider collecting specimens. An obvious constraint arises from physics: even the best scientist can only be in one place at one time. The field seasons come and go, and one can collect in a very finite number of places in one career. Imagine

ues to expand as well as the need for a new generation of taxonomists to discover and describe new species. With digital instruments and related online databases and resources, it is possible to conceive of online classes taught by world authorities and made available to students on many campuses and in many countries. At the same time that educating taxonomists becomes easier, automated on-line identification systems make identifications faster and more certain regardless of who makes them. This could be of immeasurable value to educators, inspectors at ports of entry, agricultural field agents, and countless others.

Literature access is another bottleneck. It is not unrealistic to think about searchable, full-text, digitized primary taxonomic literature. This would democratize science, with a student in a developing country suddenly having access to taxonomic

knowledge to the same degree as a professor associated with a research library at a major university.

Even if all retrospective literature were digitally accessible, there would remain a problem with new taxonomic publications. Good quality revisions and monographs frequently take years or even decades to complete and publish. These comprehensively comparative works are essential to taxonomy. They are the high-throughput, efficient, simultaneous testing of species hypotheses needed to keep nomen-

It is time for taxonomy to grow up.

clature informative and accurate, and databases in museums reliable. They need not be static documents published at fifty-year intervals given today's technology. Imagine instead virtual monographs that are online. New species, after peer review, are instantly "published" and available. Smart software incorporates them automatically into diagnostic keys, field guides, checklists and other derivative documents defined on demand by users. An eco-tourist headed to Costa Rica can generate a virtual field guide complete with picture keys including only those species occurring in that country or in a particular park... and inclusive of a new species "published" only hours previous, following peer review. The taxonomist's productivity is no longer measured by number of publications or a citation index, but rather by the number of times that users access this virtual monograph and either use the interactive key or generate a virtual publication. All data is kept current to the minute and the taxonomist's efforts are recognized and rewarded.

These are but a few examples of ways in which pieces of the taxonomic impediment can be chiseled away using new technologies. There are many others (the proposed *MorpoBank*, for example, and DNA barcodes tailored to particular-

ly problematic taxa and semaphoronts). And there are huge challenges, such as the kind of international government-level agreements needed to have a Linnaean primary description archive that is guaranteed in perpetuity and thereby capable of transforming taxonomy to e-publishing. There are no obstacles that cannot be overcome, but it will require huge investments in taxonomy and in museums. That, too, is very much within reach if, but only if, the taxonomic community can come together, identify their

needs, set clear priorities, and communicate these with a single voice. This means changing the culture of taxonomy. Taxonomists and their institutions must learn to act as an international community, and think very big and very far outside the box. The next generation will, I predict, come of scientific age accepting such circumstances and will be the leaders of the fruition of this Renaissance. Those of us in the field now, however, have a heavy responsibility to begin the revolution, to forget the limitations that our field has long accepted, and to forge community-wide partnerships for the betterment of the field as a whole.

Because of the biodiversity crisis, no generation of taxonomists has faced greater challenges. With the molecular and especially cyber tools that are rapidly evolving, no generation of taxonomists has had greater opportunities to advance the field. We have the theoretical context. We have the know-how and will. We have urgency on our side. What we need now is cooperation, a vision, and a plan. If we fail to seize this opportunity we will forever diminish taxonomy and human knowledge of biodiversity and evolution. We did not ask to be witness to the biodiversity crisis or challenged to adapt new technologies to solve these problems. Like it or not, we

have been chosen by history as the last generation with the ability to fully explore and document biodiversity on this planet. If we fail, we fail not only ourselves, but humanity and all generations of scientists to follow. If we succeed, we create a legacy of knowledge that will reduce the negative impacts of the biodiversity crisis, maximize conservation and knowledge gains, and ennoble our science as an agent for good in human and ecosystem welfare. Let's hope that we have the courage, vision and commitment to fight to victory.

It is time for taxonomy to grow up. Tentative steps have been taken, such as the recent Planetary Biodiversity Inventory projects funded by the U.S. National Science Foundation and collaborative efforts to reconstruct a framework phylogeny for life, but we have a very long way to go and little time to get there. There is no time to waste with missteps, like throwing out Linnaean nomenclature in mid-stream or replacing theory-informed species hypotheses with arbitrary DNA barcodes. Done well and done together, taxonomists, natural historians, museums, and herbaria can now have their finest hour after decades of neglect. I will meet you on the field of battle.

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The problem with biogeography

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Biogeography has an important place in biology. Biogeographic data was central to the formulation of Darwin's evolutionary ideas, and biogeography today has enormous potential to provide a site of synthesis for a wide range of biological data. However, its ability to fulfil this role is seriously compromised by its marginal position in evolutionary biology.

There are two notable aspects of current debate in biogeography. One surrounds the conception of biogeography; whether it is an independent discipline, with its own aims and methods, or whether it is merely an adjunct to other areas of study within biology. The other is the ambiguous role that spatial data, the distributions of taxa, have in biogeographic analysis.

As has been recently emphasised, biogeography is unusual as a discipline; there is a dearth of specialist biogeographers and most of those interested in the field are primarily systematists who write about the biogeography of their own groups. Consequently, biogeographic discussions often take place in a systematic context rather than in a strictly biogeographic one. Without a clear biogeographic focus, discussions are without reference to a core of agreed aims and principles that might facilitate conceptual progress. Yet, paradoxically, biogeography has a history of an elaboration of explanations and analytical methods. For example Cain (1943) detailed fourteen different criteria for determining the centre of origin,

a number that he considered excessive and which undermined the concept of centre of origin, and, currently, there are as many as nine approaches to biogeography incorporating more than thirty techniques (Crisci, 2001). Ebach and Humphries (2003) noted that the "... present plethora of techniques reflect a lack of debate and agreement as to what constitutes the ontology (specification of conceptualisation) of biogeography".

If biogeography is the study of the distributions of plants and animals, then for the conception of biogeography it is problematic that a critical point of discussion on its nature is the importance or status of spatial data, particularly in relation to data from other fields such as systematics and historical geology (Grehan, 2001). Is the data empirical, or is it susceptible to, or contingent upon, theoretical considerations (such as molecular clocks)?

If biogeography is one field, with one aim: to explain the distribution of taxa (space) with respect to time and form (Ebach and Humphries, 2003), it would seem that spatial data should be central to the field of biogeography, and the way in which spatial data were handled would define it as a discipline.

Interestingly, the general observation can be made that much of the biogeographic literature lacks distribution maps (Grehan, 2001), suggesting a reluctance to deal with the primary data.

In this article, I address these concerns by reiterating that spatial data is central to the viability of biogeographic method, that biogeographic pattern is real and detectable, and that it is this pattern, derived from the comparative study of the distributions of plants and animals, that constitutes the context necessary for meaningful biogeographic discussion (Croizat, 1964; Craw et al., 1999). By way of example, I will outline the distributions in Australasia of the moss family

Lembophyllaceae. In examining the distributions in detail, I will show that the distributions of these mosses are congruent with a general pattern of distribution in the region.

In presenting the distributions of the Lembophyllaceae I am using panbiogeographic track analysis, as panbiogeography gives priority to analysing the distributions of organisms. Indeed, Grehan (2001) has argued that it is the only approach to do so.

The panbiogeographic method is to plot distribution records of taxa and join them to form tracks. Through the comparison of numerous taxa, composite or standard tracks are formed from the areas of agreement of tracks of individual taxa (Craw et al., 1999). In this way, panbiogeography first establishes a spatial pattern that is a biogeographic context in which other evidence, e.g. fossil and geological, can be considered and synthesised (Grehan, 2001).



Figure 1. The results of a track analysis of mosses in the Australasian region (Tangey, 1989).

Standard tracks in Australasia

Before details of the distribution of the Lembophyllaceae in Australasia are presented, the results of previous panbiogeographic studies in the area are outlined.

The results of a track analysis of mosses in the Australasian region (Tangey, 1989) yielded a series of intersecting standard, or general-

ized, distribution tracks as follows (Figure 1.): 1. a western track: Papua New Guinea to eastern Australia (Queensland to Tasmania), 2. an eastern track: Papua New Guinea-New Caledonia-New Zealand, and 3. a central Tasman transversal track, extending from the Queensland-New South Wales border in eastern Australia to the New Caledonia region (often via Lord Howe and Norfolk Is). The western and eastern tracks come together to the south of New Zealand, linking together Tasmania, mainland New Zealand and subantarctic Auckland and Campbell Is. The intersections of these tracks are recognised as nodes, areas characterised by species diversity and endemism (Heads, 1989).

The standard tracks highlighted by the analysis of mosses are also present in the results of track analyses of other plant and animal groups. Croizat's (1964; here figure 2.) analyses of different plant and animal groups in the region showed the same standard tracks. For example, he found that the track connecting eastern Australia at the Queensland-New South Wales border with the New Caledonia area was an important feature of the distributions of various groups in the region. He highlighted the eastern end of the Queensland-New South Wales border as an area of particular biogeographic significance. Recognised by Burbidge (1960; here figure 3.) as the MacPherson-



Figure 2. Croizat's (1964) analyses of different plant and animal groups in the region showed the same standard tracks.

Macleay overlap, Croizat considered this place to be one of the major global biogeographic features.

Distribution of the Lembophyllaceae

The Lembophyllaceae are a family of pleurocarpous mosses that are common on rocks and tree bases, and are often pendant epiphytes. The Australasian taxa form a monophyletic group of closely related



Figure 3. Croizat (1964) considered the MacPherson-Macleay overlap to be one of the major global biogeographic features.

species. Putative sister groups to this clade are the widespread north hemisphere *Isoetecium*, and the largely tropical *Pilotrichella*.

The Australasian Lembophyllaceae extend to Indonesia (Flores), Papua New Guinea and Fiji, and to southern South America (Figure 4.). Within Australasia, there are main massings (centres of diversity) in the north (Coral Sea), as shown by *Camptochaete* sect. *Thamniella*, and in the south (Tasman Sea), as shown by *Camptochaete* sect. *Camptochaete* (southeast Australia - New Zealand), and *Lembophyllum*, *Weymouthia* and *Fallaciella* (southeast Australia - New Zealand - southern South America). *Fifea* is endemic to New Zealand.

Distribution of *Camptochaete* *Camptochaete* occurs in Indonesia (Flores), Papua New Guinea, Vanuatu, New Caledonia, Fiji, eastern Australia (Queensland to Tasmania), New Zealand (Figure 5.). Sect. *Thamniella* is known from Flores, Papua New Guinea,

Vanuatu, New Caledonia, Fiji, eastern Australia (northern Queensland to Victoria and Lord Howe Is). Sect. *Camptochaete* is known from Vanuatu, eastern Australia (southern Queensland to Tasmania), New Zealand (including the Kermadec Ids, Chatham Is, Campbell Is and Auckland Is). There is also an unconfirmed record of this section from Hawaii.

The sections are geographically distinct for most of their range, with overlap between the two sections in Vanuatu and eastern Australia (southern Queensland, New South Wales and Victoria) (Figure 5.).

Distribution of the species

Sect. 1. *Camptochaete*

C. arbuscula. Eastern Australia: Victoria, Tasmania. New Zealand: North Is., South Is., Stewart Is., Chatham Is., Snares Is., Auckland Is., Campbell Is.

C. deflexa. Eastern Australia: Queensland, New South Wales, Australian Capital Territory, Victoria, Tasmania. New Zealand:



Figure 4. Extent of the Australasian Lembophyllaceae.

North Is., South Is., Chatham Is., Snares Is., Auckland Is., Campbell Id.

C. angustata. New Zealand: Kermadec Is., North Is., South Is. *C. pulvinata*. New Zealand: North Is., South Is. Hawaii.

C. leichhardtii. Vanuatu: Annatom. Eastern Australia; southern Queensland, New South Wales, Victoria.

Sect. 2. *Thamniella*.

C. excavata. Papua New Guinea;

Eastern Australia: Queensland, New South Wales, Victoria; Lord Howe Is.

C. curvata. Eastern Australia: Queensland, New South Wales.

C. porotrichoides. New Caledonia.

C. subporotrichoides. Indonesia (Flores), Papua New Guinea, Vanuatu, Fiji.

C. papuana. Papua New Guinea.

Distribution patterns within *Camptochaete*

Within the area encompassed by the sections, the species exhibit different distribution patterns. In sect. *Thamniella*, *C. excavata* occurs

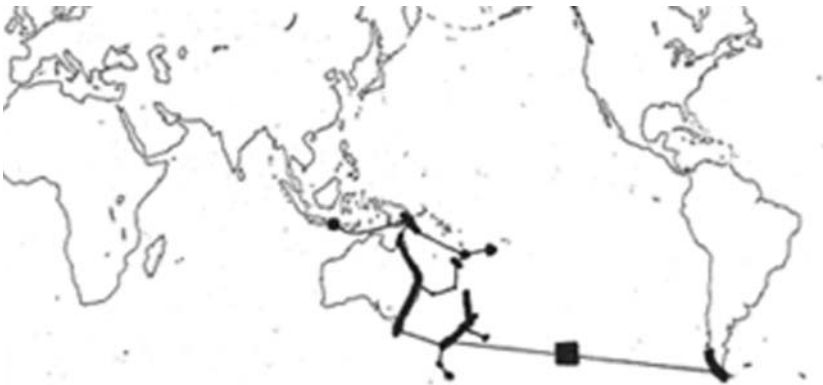


Figure 5. The sections are geographically distinct for most of their range, with overlap between the two sections in Vanuatu and eastern Australia (southern Queensland, New South Wales and Victoria)

from Papua New Guinea in the north, through eastern Australia to Victoria in the south. This contrasts with the distribution of *C. subporotrichoides* which occurs in Papua New Guinea, Vanuatu and Fiji. *C. papuana* is present Papua New Guinea. *C. curvata* is present in eastern Australia, at and around the Queensland - New South Wales border. *C. porotrichoides* is only in New Caledonia.

Sect. *Camptochaete* has a southern Tasman Sea distribution, with four of its five species present in mainland New Zealand, and two of these also in south eastern Australia. The distribution of the remaining species in sect. *Camptochaete*, *C. leichhardtii*, corresponds to the overlap between the two sections:

southeast Australia, southern Queensland to Victoria, and Vanuatu.

The distribution patterns shown by *Camptochaete* are in broad agreement with the results of the track analysis of moss distributions outlined above (see Figure 1), and may be interpreted in terms of these tracks. In sect. *Thamniella*, *C. excavata*, occurs along the western track, *C. curvata* is present at the Macpherson - Macleay overlap at the eastern end of the Queensland - New South Wales border. The distribution of *C. subporotrichoides* corresponds, in part, to the eastern track, with the occurrence in Fiji

providing an eastward extension, passing around New Caledonia where *C. porotrichoides* occurs. *C. papuana* is found at the New Guinea node.

Sect. *Camptochaete* occurs in the region of the southern junction of the eastern and western tracks, emphasising the links between southeastern Australia, New Zealand and subantarctic Auckland and Campbell Is. Sect. *Camptochaete* reaches its northern limit, in Australia, close to the Macpherson - Macleay overlap. The distribution of *C. leichhardtii* highlights the central Tasman transversal track. *C. excavata* (sect. *Thamniella*), which occurs on Lord Howe Is., also highlights this latter track in part.

There is no link between New

Caledonia and New Zealand in *Camptochaete* (corresponding to the southern section of the eastern track). *C. angustata* (sect. *Camptochaete*), endemic to New Zealand, occurs in the Kermadec Is. and therefore is a partial filling in of this latter track.

Biogeography of *Camptochaete* *Camptochaete* exhibits a pattern of distribution that is congruent with the standard tracks of a generalised distribution pattern in the Australasian region. The species distributions are largely vicariant, and this pattern of vicariance is common to different groups of plants and animals through congruence with standard tracks. The coincidence of vicariance and standard distributions is a fundamental feature of the distribution of life, and a central finding of panbiogeography. The significance of this observation is that the evolution of taxa is related to a generalised pattern of distribution.

However, this congruence is not spatial homology. The concept of baseline is equivalent to spatial homology. Taxa with different baselines can exhibit the same pattern of vicariance in overlapping areas of their ranges. That is, they can have different main massings (centres of diversity) outside the region in which they share the same pattern of vicariance.

The Australasian *Lembophyllaceae* has a baseline that identifies it as a Pacific group. This shared baseline means that it is homologous with taxa such as the southern beeches (*Nothofagus*), and different from other taxa in the region, such as ratite birds (Craw et al, 1999). These groups exhibit a common pattern of vicariance on standard tracks in Australasia, but they have different baselines, i.e., different distributions outside the region, and it is this difference that marks out their different spatial homologies.

What is the centre of origin of *Camptochaete*?

By emphasising spatial data, pan-biogeography provides a pattern of distribution against which questions like 'what is the centre of origin?', or, 'when did *Camptochaete* evolve?' might be asked, and against which problems of distribution, e.g. mysterious, anomalous or 'unexplained' distributions, might be addressed. Similarly, it provides a context in which we might also ask 'what do we mean when we ask such questions?', or, 'what do we mean by mysterious or anomalous distributions?' That is, in the light of what we already know about distributions in general, what are the theoretical and empirical approaches appropriate to biogeography that would enable us to evaluate the relevance and meaningfulness of such questions? The present lack of consensus on approaches in biogeography is symptomatic of an absence of first principles in biogeography.

Biogeographic data needs to be treated empirically and to be given priority over theoretical considerations and over data from other fields. A devaluing of distribution data undermines biogeography itself, endangering its independence. Two ways in which this occurs are

dispersal, etc., then we undermine the value of the primary data. Not only does this undermine the value of spatial data, but it also makes explanation impossible; poor data, no pattern, no general explanation, no biogeography.

In synthesising biogeographic and geological data, geological data is often given priority (Grehan, 2001). "No evidence of land is taken to mean evidence of no land" (Heads, 2003), and geological evidence is used to deny biogeographic data. For example, the age of volcanic oceanic islands, often very recent, is interpreted to mean that they appeared *de novo* and were then colonised by long distance dispersal. Similarly, areas assumed to have been wiped clean of biota by geological processes of submergence, glacial activity etc., must have had their biota restored by recolonisation from outside the area. In both of these examples, it is possible that the biota has a long history in the area, surviving on a constantly renewing geology, and that it exhibits a pattern of distribution consistent with this latter view (Craw et al., 1999).

The way in which distribution data are treated will determine the ability of biogeography to synthesise biological data. The importance of panbiogeography in this synthesis

The methods detect and analyse biogeographic pattern and utilise a concept of spatial homology. In this way geography is central and pan-biogeography provides a powerful tool for synthesising biological and geological data. An excellent recent example of panbiogeographic analysis is the paper by Michael Heads on the biogeography of the Ericaceae in Melanesia (Heads, 2003), a wide-ranging paper synthesising geology, ecology, morphogeny etc., in a biogeographic framework.

The explanation of this common pattern of vicariance has yet to be adequately addressed and remains a challenge to biogeography. It is not just that the pattern requires explanation, this pattern provides the context within which discussions of phylogeny, morphogeny, area relationships, integration with geology, age of taxa, dispersal, areas of endemism, patterns of biodiversity etc., the how *and* why of biogeography (*c.f.* Ebach and Humphries, 2003), might take place. The geographic facts of biology are the key to not only what biogeography is, its conception (ontology), but also to what we know in biogeography, and how we go about it, its epistemology.

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The present lack of consensus on approaches in biogeography is symptomatic of an absence of first principles in biogeography.

noted here. Firstly, assumptions made about the data, and, secondly, subordinating distribution data to data in other disciplines.

If, for example, we assume that long-range dispersal is a major determinant of the distribution of plants and animals, or that the records of the distributions of taxa are, as a rule, too incomplete to be meaningful, or that any pattern that might be there has probably been obscured through chance events of

relates to its insights regarding biogeographic pattern. The pattern of vicariance is a central finding of panbiogeography, and the acceptance of panbiogeography (Humphries, 2000; Ebach and Humphries, 2003; Morrone, 2001; Crisci, 2001) recognises its importance to biogeography. It is a consequence of the way in which data is treated and analysed. In panbiogeography, spatial data is primary.

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News

Biennial Meeting - A Presidential Review

Our fourth Biennial Conference Of the Systematics Association was held at the Trinity Conference Centre in the Arts Building of Trinity College, Dublin between 18-22 August 2003. Attended by approximately 170 delegates it was a great pleasure again to see so many faces, old and new, particularly the many younger scientists and research students making their first appearance and presentations, and indeed, the talented mature students making their second and third out-

ings.

We continued in the spirit of the three previous Biennial conferences and fulfilled the main objectives of this, the European equivalent of AAAS, in bringing young researchers together to display their wares without being downtrodden or crushed by the old cognoscenti. Naturally there was quite a number of the older contingent (including myself) playing to the galleries especially in the thematic sessions. It was very good to see that the



Paul Cox with Barrie Leadbeater

meeting attracted several trans-Atlantic colleagues, particularly Diana Lipscomb and Quentin Wheeler, the providential funders of NSF who have been part of the recent large initiatives involving AtoL and PBI. As with all previous Biennial conferences there were many more botanists in both the presentations and on the delegates list. As I noted in my previous report it is difficult to know why this should be so, except perhaps that zoologists tend to organize their activities differently compared with botanists, but it was pleasing that there were one or two more zoology papers represented than at previous venues, and I hope that this trend will continue into future Biennial Conferences. Despite the subject imbalance it was encouraging to see at least 15 nationalities represented from countries in all of the major continents and as far apart as the USA and Australia. The Biennial is consolidating its position as a meet-

ing of truly international proportions, and the number of offered talks and posters from delegates grows on each occasion.

The talks were arranged into three different categories so as to give some interest and continuity to the proceedings during the week. There were three invited guest speakers, Dennis Stevenson, Vice President of the New York Botanical Garden, Paul Alan Cox, Director of National Tropical Garden in Hawaii, and Ole Seberg Professor of Botany at the

University of Copenhagen each invited to give their own perspectives of where we are at in systematics, where we are going in the future and what is in it for the next generation of biologists.

Dennis Stevenson presented work on his life-long interest in cycads to show the importance of understanding the biology, morphology, biochemistry and DNA to obtain as near a definitive classification that could be agreed upon by other cycad workers and what this all means to the systematics, phytochemistry, phylogenetics and biogeography. As the after-dinner speaker Paul Cox maintained the theme of cycads to show the importance of systematics to biology and medicine. By concentrating on a debilitating wasting disease in the islanders of Samoa he showed that the greater prevalence in middle-aged males was caused by the accu-

mulation and amplification of neurotoxins derived from cycad seeds in flying foxes which in turn caused the disease in the adult males who consumed them. This was a gripping detective story that underpinned the crucial need for systematics and was so rivetting that even the waitresses serving the dinner tables were moved by his presentation. The third invited speaker, Ole Seberg, closed the conference on the last day reflecting on the importance of systematics as the entire basis of biology and emphasizing the need for new alliances to undertake future projects. Taking his cue from the successes of AtoL and PBI in the NSF he suggested that large funded projects was one way forward to fund new systematics programmes in Europe, and there was a genuine need for co-operation to obtain future funding to undertake phylogenetic investigations.

The second category included the three special symposia convened (and hopefully three separate publications) showing the state of the art in phylogenetic analysis of large trees, systematic advances in human evolution and the developments in the creation and delivery of databases of systematic data.

The Systematics of large and species-rich taxa, organised by the local convenors Trevor Hodkinson and Steve Waldren, kicked off the proceedings. The purpose of this one-day symposium was to "to examine the problems and prospects of dealing with large and species-rich taxa" a topic clearly aimed at phylogeneticists and taxonomists.

The speakers were asked to address the contentious problems of analysing large trees from a series of perspectives from individual case studies through to the properties of handling enormous phyloinformatics systems. For me the most important thing to emerge was that systematists tended to be poor analysts and somewhat eclectic in their choices of technique. Concomitantly, as Miles Kingston

always says at moments like these "I could not reach any particular conclusion".

Sadly, the main breakthroughs during the post-Hennigian late 20th century had come from the development of black boxes - computerised algorithms that gave the ability to undertake the many millions of calculations required to produce trees of varying size and quality. Quentin Wheeler acted as the consummate politician that he has surely become, to show that terascale taxonomy will require a whole new shift in our



Quentin Wheeler

thinking. The inputs of phyloinformatics specialists are required to lift the rather desultory programme which we now find in post-Hennigian eclecticism into the general language of systematics that will tackle problems dealing with the whole of Life. The subsequent impact of cladistics on molecular analysis, monography, homology assessment and morphology has been far-reaching. However, it was clear that the world is not a happy place, as several studies found more questions than answers, exacerbated by the pot pourri of approaches ranging from the thorough analysis of raw data to the quick fixes of consensus and supertree analysis. Just comparing the papers of Geraldine Reid and Susanne Renner made one realise that agreement on method is far from accomplishment

and will need to be radically changed if we are ever going to solve the problem of comparing chalk with cheese.

Systematic Advances in the Study of Human Evolution was a parallel symposium and another plenary session (as in the third biennial conference) organised jointly between the Palaeontological and Systematics Associations. Una Strand Vidarsdottir designed the symposium to discuss the important new ventures in human evolution today and to bring the star players together under one roof. It was so much a display of modern methods in systematics, as rather a series of reviews and detailed narratives and I was amazed at the range of material that masquerades under the rubric of human evolution. The theme of the meeting was to compare "ground-breaking" innovative work on ancient DNA, with phylogenetics, molecular studies, ontogeny, morphometrics and behavioural studies. Although most of the research seems to be based on the most minuscule samples of data there were several presentations that were truly imaginative and interesting from a comparative perspective. However, in the same meeting some of the more outlandish work ever undertaken on cultural evolution was presented. Although I only managed the briefest look in on the meeting it did seem to be of great interest to participants presenters alike. I guess there is nothing like a good old narrative to put the bums on seats as some of my friends from the ICA might say.

The third plenary symposium, *Biodiversity Databases: from Cottage Industry to Industrial Networks*, organised by Gordon Curry and me, provided a panoramic view of database research. As a response to the call for improved data management and delivery systems we tried to give a feeling for the changes that are being undertaken across every conceivable aspect, from the underlying politics of the

major NGOs and government agencies to the database and web developers, and to the dedicated souls who populate the databases for disseminating taxonomic information to an ever more varied audience. Important representatives in all areas were invited to the meeting to try and convey the challenges and needs of the information age. For



Ray Tangey (left) will be co-organising the next Biennial in Cardiff

me this was an extremely successful meeting that will, I hope, produce a new kind of publication for the Systematics Association.

Recognising the speed of change brought about by information studies means that any book will be short-lived. We intend to try and link together a paperback book of the meeting with web-based or CD ROM technology to keep readers up to date and to reopen a series of symposia into the future. Database workshops have always been of interest to the Association since the early days of Frank Bisby's ILDIS. Now that the topic has come of age the time is ripe to resurrect investment into the field and to be cogniscent of the need to get up to terascale phyloinformatics systems as envisioned by Quentin Wheeler, but from everything from names and descriptions of taxa as well as molecular barcodes.

For the Contributed Papers the whole of Thursday and Friday morning was devoted to three parallel contributed paper sessions, and involved the student competition for best speaker and best poster presentations. It was a great pleasure that out of 28 original applications for

student bursaries we managed in the end to fund fourteen students and young scientists. The quality of their presentations was remarkably good and I was pleased to be able to meet with so many new and able people.

As at the second Biennial Conference there was still a predominance of botanical papers on molecular sequence analysis but

there was thankfully a wider range of interests covered. Of the 58 contributed botanical papers, it seemed that new ideas were emerging around the problems of congruence between different data sets, whether they were solely molecular or a combination of morphology and molecular characters. The Chase lab was well represented with a strong display of papers on orchids, Liliales and other monocots, but, it was good to see that this was counterbalanced by some very interesting contributions from South Africa on speciation in the Cape, Australia, tropical trees from South America and the classification of Pipers, poppies, lupins and composites. I suppose if I was going to be critical I would ask what goes for science in systematics these days? I must say I did get tired of hearing and reading about phylogenies when the authors meant cladograms and the evolution of this and that when in fact the information was about classification. Hopefully, this band-wagon approach and consensus as to what is normal science will subside and eventually begin to break down and we might witness some stronger ideas on comparative biology rather

than using all point data merely as characters. In some ways it is comforting to know that here and there a mature view is emerging: the idea that we might need to understand all aspects of the life cycle and not just base sequences or morphological characters in the dreaded black box matrix.

What was of great interest to me was the range of presentations in terms of choices of study groups. Although few of the papers were theoretical in content, most were extremely interesting new empirical investigations. Amongst the plants at least 24 families of flowering plants were considered (from Acanthaceae to Asteraceae), ranging from systematic studies of genera (e.g. *Androsace*, *Bulbophyllum*, *Dioscorea*, *Trema* and *Leucaena*) to consideration of pollen morphology in monocots and floral development in basal angiosperms. The application of cladistic information, although significantly used for generating phylogenies, showed some novel applications. These included repetitive formation of polyploids in



Timothy Waters and Alex Wortley

Dactylorhiza (Orchidaceae), genetic differentiation in *Ophrys* (Orchidaceae) and most bizarrely, reconstructing ancestral habitats in the Cape flora.

It was comforting to see that there was a couple of papers on diatoms, mosses and various biogeographical and one philosophy paper. Also there were 12 contributed papers on zoological or protist genera ranging from the copulatory apparatus of platyhelminth parasites of butterfly

fish to the origins of sand gobies, worms and nematodes. I was particularly intrigued to hear about the phylogeny of spangatoids (echinoderms) and Matthew Craig's continuing studies of the serranid fish genus *Epinephelus*. The latter talk showed that biogeography can be profitable but dispersal scenarios are pretty useless in this day and age. As all the talks showed, whether botanical or zoological, systematics has sadly become synonymous with phylogenetics. However, what was demonstrated quite forcefully at this meeting, as I noted earlier, was the plurality of methods. The idea that phylogenetics has become somewhat uncritical in its black box collection of nifty algorithms and craftily designed computer programs, means that we will have to draw more upon the basics to actually determine and engage in using the appropriate methods for analysis. Why some of the key literature of the 1980s and the early 1990s is not read for what it is worth remains a mystery to me.

It simply is not good enough any more to say that I will undertake a study in a particular way simply



Steve Waldren

because the methods are out there. He who uses Mr Bayes, Maximum Likelihood or Maximum parsimony, or a particular means of optimising a character or a particular molecular

character will have to be clearer for why they did it. This point was brought home in the interesting paper by David Williams on the last day of the proceedings and it gave me much to think on as to how science and philosophy should be taught as in the old universities rather than the modern polyvarsities.



Tim Littlewood and friends

Nevertheless, the standard of presentation of nearly all of the talks was truly outstanding. This is at one level was due to the fact that people have virtually gone 100% for Powerpoint and encapsulated postscript presentations using the sophisticated graphics and pictures obtainable with modern digital cameras. Also, it was remarkably clear that an immense amount of thought had gone into material content. It was obvious that there had been many hours of practice to capitalise on the relatively short amount of time that each talk was given. The messages and how effectively we convey them is the ultimate measure of any contribution.

Presentation was just one of the criteria used to decide the student prizes. These included the breadth, depth and relevance of the science beyond the immediate area of investigation, the take home messages, and the way in which the talks were structured and kept to time. This provided the criteria for judging both the talks and the posters. Many congratulations to all of the eligible students for the high standard of presentation. The judges, under the chairmanship of Tim Littlewood, finally agreed that the student pre-

sentation prize should be awarded to Gillian Brown from CSIRO in Australia for her beautiful talk on the Phylogeny of *Rhododendron* section *Vireya*: subsectinal collapse, geography a closer match. The runner up was the last Biennial winner, Alexandra Wortley from the Department of Plant Sciences,

University of Oxford, UK.) for her talk on Reconstructing the Phylogenetic Position of *Thomandersia* Baill.; she, as before, demonstrated a rare talent in one so young of being a great communicator of difficult information.

There were thirty seven posters on display during the week of which sixteen were up for the student prize. As with the majority of the talks the posters showed considerable skill and ingenuity of effort that made the choice of the student very hard to pick out. In the final analysis Pavel Nikolov of the Bulgarian Academy of Sciences, with his poster, Taxonomy and phylogenetic relationships within the subfamily Progynotaeniinae, was the clear-cut outright winner. Congratulations to both he and Gillian and commiserations to the runners up.

Trinity College provided an excellent venue for the conference and I extend my thanks to Steve Waldren, Trevor Hodgkinson and John Parnell for their help and organisation. I should also like all of their wonderful helpers for giving up so much time and for making the formal and social events work so well. I would

also like to single out Janet Ashdown of the Linnean Society of London for freely giving her time behind the registration desk throughout the week.

The lecture theatres were modern, close to one another for parallel sessions, comfortable and well-equipped with all mod. cons. including data-projection facilities. Accommodation in the student rooms on Trinity's grounds was truly excellent and within a stones throw of the breakfast lounge, local pubs and lecture theatres. I would also like to give many thanks to the Linnean Society for sponsorship of the conference and especially the database meeting. I would also like to thank the Council of the Palaeontological Association for their sponsorship and for organising the "Human Evolution" symposium and Taylor and Francis for their generosity for providing the student prizes. Thursday evening was a fine Banquet in the Gandon Suite south of the Davenport Hotel, and I thank the after dinner speaker, Paul Cox for flying in especially to spoil his dinner by providing the excellent detective story that made one pleased that we did not have fruit bat on the menu.

In all, I very much enjoyed the meeting and hope that everyone shared this feeling. The size of the meeting, plus the range of taxonomic expertise, meant there were many opportunities to make new contacts and share common systematic problems. The organisation went remarkably smoothly, from everyone's point of view and for this I must thank my colleague Steve Waldren for all of his excellent cool efforts in making things run smoothly. Finally,

I should also mention Gordon Curry, as treasurer, for holding the folding and although we have yet to finalise the books it looks as if the 4th Biennial Conference will be a great financial and scientific success.

Chris Humphries
NHM, London

Quo Vadis?

Who were our ancestors?

Evolution has been moulding life for over three and half billion years and in that last couple of million years, humans have evolved from small, hairy ape-like descendants. It is tempting to want to retrace our evolutionary ancestry from the trees to the London underground tube, but will we ever find our evolutionary Adam and Eve?

... future palaeontologists would probably never be able to see that there was indeed a city inhabited by millions of balding apes going to places like Ronnie Scott's clubs or shopping at Harrods.

To understand our ancestry we need to unravel the deeper meanings of life. Palaeontologists talk about it, biologists study it and Hollywood makes films about it, but what exactly is evolution? Charles Darwin's controversial idea was that every living species that has ever existed on Earth evolved from one common ancestor. We believe this to be true because all species on Earth, including ourselves, share common characteristic forms. The similarity of form shows that human forearms may be modified bats wings and, our legs, transformed whale tails. These structural similarities are the basis for understanding evolutionary relationships, and how one species is related to another. Systematic analysis of body parts shows us for instance that humans are more closely related to chimpanzees than to gorillas. The evidence is that they share similar bone and DNA structures. However, can we ever really know that apes evolved into low browed humans? We were not there to see such events, and the fossil record upon which we base our

ideas is very patchy.

Why are there not more fossils? The answer lies in the fact that they rarely form in the first place. Take for example the cities and towns in which we live and work. They are constantly overturned like ploughed country fields. Occasionally we find remains, such as evidence of Roman civilization in London, but the Roman conquest occurred in a geological blink of an eye. Now imagine London in 20 millions years time. How much would we find of Roman civilization then? Not a denarius. The fossil record is made

up almost entirely of marine organisms that lived on reefs, warm lagoons and seas or in muddy estuaries or peat bogs. Humans today live on land, but those lucky enough to die and be buried on reefs and in estuaries may survive to be discovered by future palaeontologists. The 21st century British fossils that would survive the erosion of millions of years would most likely include coral, a couple of water rats and the odd scuba diver. From this limited information future palaeontologists would probably never be able to see that there was indeed a city inhabited by millions of balding apes going to places like Ronnie Scott's clubs or shopping at Harrods. With this in mind it is not surprising that we have found fewer fossilized species than living ones. Palaeontologists have dug up less than 1% what has ever walked, crawled, and swam on Earth. What seems so surprising is that we still expect to find fossils of our ancestors.

Just as we may not recognize our great, great, great grandparents if

they walked down the street, in the same way we may not recognize our direct ancestors in the fossil record. We can at best make well-educated guesses at relationships based on similarities. Studying the relationships of phenotypic (physical) features and DNA structures, and the means of classifying them is called systematics - a subject vitally important to understanding evolutionary relationships. Yet even with the tools of systematics, there are snags. We know that when we look back far enough in our own family genealogy we find that we are distantly related to many other people, most of whom we do not know, and yet are alive today. The same complex layering of relationship is magnified a million fold over time in the case of seeking our evolutionary ancestors

Systematics can be revealing, for example it shows us that birds are more closely related to dinosaurs than they are to any other known group of organisms. The science of systematics can also link us to our nearest relatives, our hairy, slightly stooping cousins, but the task of finding our 'Adam and Eve' is impossible.

Malte C. Ebach

Book Review

Evolutionary Déjà Vu

A review of *Life's Solution. Inevitable Humans in a Lonely Universe*, by Simon Conway Morris. Cambridge University Press. pp. xxi + 464. Hardback, ISBN 0 521 82704 3.

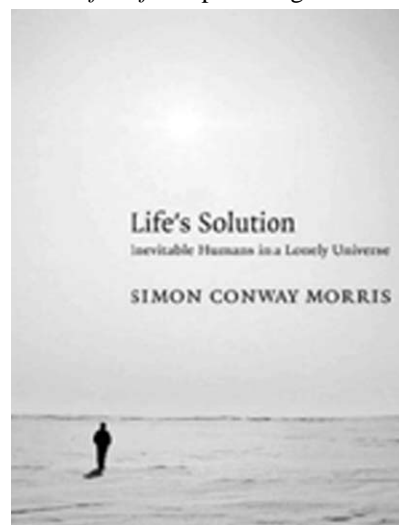
"Do you hear that, Mr. Anderson? That is the sound of inevitability." Agent Smith in *The Matrix* (1999) by A. Wachowski and L. Wachowski.

Two qualities make this book well

worth reading. First, Simon Conway Morris doesn't loathe stirring up a bit of controversy. In January 2001 I attended the yearly meeting of the Society for Integrative and Comparative Biology in Anaheim, California to take part in a symposium on the Cambrian explosion of animal body plans. Conway Morris discussed this topic at length in his interesting hour-long seminar. However, amidst a multitude of slides of fossils and phylogenies he had inserted a rather graphic slide of the majestic Two Towers in New York, with in the foreground two armed FBI agents. Conway Morris may have carefully selected the slide to illustrate a pertinent point about the deep history of the Metazoa, although I cannot recall what that could have been. However, the chief effect of this slide was certainly not scientific enlightenment, as the audience was once again confronted with the unspeakable horror of an act of absolute evil unparalleled in the history of the United States that unfolded just four months prior to the meeting. Second, Conway Morris doesn't particularly eschew polemics either, which on an earlier occasion led one reviewer of his previous book *The crucible of creation. The Burgess Shale and the rise of animals* (1998) to write that "the way Conway Morris goes about biting the hand that once fed him would make a shoal of piranha seem decorous." Of course, the nourishing hand in this instance belonged to Stephen Jay Gould, who exalted Conway Morris as a scientific hero in his best-selling book *Wonderful life. The Burgess Shale and the nature of history* (1989). Conway Morris' extensive work on the Burgess Shale fauna has considerably revised our understanding of early animal evolution, and the views championed by Gould in *Wonderful life* are based on these initial ideas of Conway Morris. However, since his major work on the Burgess Shale was published in

the 1970s and 1980s, Conway Morris has changed his mind considerably. Combine this with his substantial disagreement with Gould's general view of evolution, and you have the major motivation for writing *The crucible of creation*, which is effectively one long argument against Gould's view of life. In *Life's solution* Gould is less visible, but he nevertheless appears at some crucial junctures throughout the book.

In fact, Conway Morris' *The crucible of creation and Life's solution* are interestingly convergent on Gould's *Wonderful life* and *Full House: The Spread of excellence from Plato to Darwin* (1996). Gould wrote his two books in sequence to "present an integrated and unconventional view of life's history and meaning" (*Full house*, p. 4) with *Wonderful life* emphasizing the



unpredictability and contingency of evolution based on an analysis of the Burgess Shale, and with *Full house* denying that progress defines the history of life, and promoting a reconceptualization of evolutionary trends as expansions in variation. Conway Morris' two books relate to each other in much the same way as Gould's, and they present a different "integrated and unconventional view of life's history." *The crucible of creation* uses the Burgess Shale to argue that evolution is not so haphazard as Gould portrays, and *Life's*

solution elaborates this argument into a general theory of evolution that downplays the role of historical contingency, and instead emphasizes that evolution is much more constrained and predictable, and will therefore inevitably lead to the emergence of certain biological properties. Not surprisingly, it is the importance of evolutionary convergence that is the main theme of *Life's solution*.

The subtitle of *Life's solution* is the shortest possible summary of the book's main message, which is that although the evolution of life on a lifeless planet is almost shockingly improbable, after this most crucial initial step is taken, the large evolutionary strides towards certain end-

inevitability" (p. xii) I am less convinced.

Conway Morris argues "that we are interested only in the emergence of particular biological properties" (p. 271), especially human intelligence. Yet, is the argument really just about certain biological properties? I think not. For example, Conway Morris considers "mammal-ness" and "ape-ness" to also be just biological properties (p. 308). However, when he writes that "we, in a sense, are evolutionarily inevitable" (p. xiii), it becomes clear that he is not strictly concerned with the inevitability of just certain biological properties, but really with the inevitability of all the various biological attributes that together

ground for concluding the inevitability of mankind? I don't think so for a rather simple reason. The emergence of humanoids requires the combined probability of all the more or less probable steps that lead to mankind. The evolution of a proportionally large brain in elephant fishes, and the independent invention of agriculture in several groups of insects exemplify steps in the evolution towards mankind, but considered in isolation this doesn't tell us much. To be human depends upon possessing a complex combination of different traits, the combined evolution of which is vastly less likely than that of the individual traits. This is consistent with our uniqueness (at least so far) on this planet. Conway Morris writes "what is at issue is not the precise pathway by which we evolved, but the various and successive likelihoods of the evolutionary steps that culminated in our humanness" (p. 284).

However, we cannot simply add up the potentially high probabilities of the evolution of individual traits, and then conclude that this makes the complex end product inevitable. How likely is it that the large-brained octopus and elephant fish develop agriculture? How likely will the farming leaf-cutter ants evolve large brains and complex cognition? Although the evolution of these individual features may be likely when considered in isolation, it is quite another matter to witness their coming together in the form of a socially advanced naked ape, or other human-like sentient being. In the end the difference between the inevitability and the contingent emergence of humans on Earth may be reduced to the relatively uninteresting issue of whether there is time enough. When evolution can wield the chisel of natural selection for a leisurely 50 or 100 billion years, then a humanoid form may eventually be sculpted from what was initially a luke-warm pool of prokaryotes, but the history of our planet is not so unconstrained. In a few bil-

... we cannot simply add up the potentially high probabilities of the evolution of individual traits, and then conclude that this makes the complex end product inevitable.

points are virtually inevitable and therefore predictable. More precisely, Conway Morris emphasizes the inevitable emergence of "particular biological properties," such as human intelligence, because of evolutionary constraints and the fact that there are only a limited number of 'solutions' to certain 'needs.' In order to do this Conway Morris presents a wonderfully rich collection of tales about evolutionary convergence and parallelism (unfortunately the important distinction between convergence and parallelism is only touched upon ever so briefly in a footnote), ranging from animal agriculture to echolocation, and from lens crystallines to human culture. In showing the prevalence of convergence throughout the animal kingdom across all levels of biological organization, Conway Morris has succeeded wonderfully. However, as for his main goal, which is "to argue that, contrary to received wisdom, the emergence of human intelligence is a near-

make us human. After his impressive documentation of the convergence of many organismic traits, many readers may be willing to entertain the possibility that, once a given level of organismic complexity is attained, the evolution of certain properties becomes rather likely. The evolution of multicellularity may be a good case in point. However, Conway Morris evidently goes beyond considering isolated biological properties. This is most strikingly illustrated by his repeated claims that aliens visiting the Earth would look and function remarkably like us.

Consequently, Conway Morris addresses the convergent evolution of many features that combine to make us human, including complex image-forming camera eyes, colour vision, bipedality, viviparity, warm-bloodedness, agriculture, tool use, sophisticated vocalizations, consciousness, and complex culture. But is this really, as Conway Morris tries to convince us, sufficient

lion years the sun will explode, terminating life on Earth, debarring any natural experiment to take place.

Life's solution is the most recent argument in a fascinating, old, but irresolvable debate. There exists a broad range of viewpoints about the relative unpredictability or inevitability of evolutionary change. Conway Morris presents his case in a highly readable format. The central part of the book treats the reader to many bits of fascinating biology, and is highly worth reading.

However, my judgement is more reserved about the parts that explicitly deal with the inevitability of humans in a lonely universe, and the penultimate chapter on a "theology of evolution." In this respect, Life's solution distinctly reminded me of Edward O. Wilson's book *Sociobiology. The new synthesis* (1975). This book was enthusiastically received by the scientific community, with the exception of the last chapter, in which Wilson attempted to apply the explanatory apparatus that he had built up in the rest of the book to explain the evolution of social behaviour in the human species. This chapter stirred up an incredible amount of scientific and popular controversy about the genetic underpinnings of human nature. I doubt whether Life's solution will evoke the same emotion, but the book is definitely worth reading and pondering. My overall impression of Life's solution is best captured in Conway Morris' own words, written in appreciation of E. O. Wilson's book *Consilience*: "Wilson expresses himself with fervour and conviction, but a more dispassionate reading of *Consilience* leaves me more impressed by Wilson's faith in the argument, accompanied by leaps in logic, unwarranted assumptions, and oversimplification" (p. 324).

Ronald Jenner
University of Cambridge

Student Report

Vireya *rhododendrons*

Gillian Brown

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I have been told several times that I am extremely lucky to work on a group of plants with 'big pretty flowers' that grow in amazing places. But I did not know just how lucky until we went on a fieldtrip to Sulawesi, Indonesia, mid last year. My Ph.D project is on the phylogeny and biogeography of vireya rhododendrons. I presented my molecular findings at the recent Systematics Association Meeting in Dublin, so I thought I would briefly summarize my project and results before I fill you in on some of the trials, tribulations and joys of our search for vireyas in Sulawesi.

Unveiling the vireyas

Vireya rhododendrons are classified as section Vireya. It is the largest section of *Rhododendron*, consisting of around 300 species, about a third of the genus. Vireyas predominantly grow in the Malesian island archipelago as both epiphytes and terrestrial plants and can be found from sea level to the alpine zone, although they more commonly grow above 1500m. Only a few non-vireya species of *Rhododendron* are found growing in this region, with the rest of the genus distributed throughout mainland Asia, Europe and North America. The key morphological characters that distinguish section Vireya are seeds with tailed appendages at both ends, the

twisting of capsule valves after opening, and placentas that separate as thread-like structures from the central axis as the capsule opens (Cullen, 1980; Sleumer, 1980). Recently leaf anatomical investigations have uncovered another potentially defining character, the presence of idioblasts in or just below the epidermis (Nilsen, 2003). The last major treatment of the section was by Sleumer (1966) for Flora Malesiana, where he recognised seven subsections on the basis of corolla shape and leaf scale type: *Albovireya*, *Euvireya*, *Malayovireya*, *Phaeovireya*, *Pseudovireya*, *Siphonovireya* and *Solenovireya*.



Since then, a number of new species have been described and insights into the biology of vireyas have provided information that may be useful for understanding the evolutionary relationships of the group. However, to date no studies have concentrated on elucidating the evolutionary history of the section. This is where my study fits. The main aim of my research is to investigate the monophyly of section Vireya and its seven subsections. We plan to use this phylogeny to investigate biogeographic hypotheses about the Malesian archipelago region, although this has not been done as yet.

Above: *Rhododendron eymae*

Phylogenies were produced using sequences from two chloroplast DNA regions, the *trnT-trnL* intergenic spacer and the *psbA-trnH* intergenic spacer, and also the internal transcribed spacer (ITS) region. The analyses suggest that section *Vireya* is not monophyletic and six of the seven subsections appear to be polyphyletic. Not surprisingly most of the traditional morphological characters used to delineate the subgroups appear to be homoplasious. The morphology is congruent with the molecular data in segments however, with some of the taxa in smaller, strongly supported clades sharing a number of morphological similarities.

Subsection *Pseudovireya*, while not monophyletic, is strongly supported as sister to the remainder of

middle Malesia).

My results lead me to believe that the *vireya* rhododendrons have radiated into Malesia several times, and these radiations were probably followed by mass speciation resulting in a large morphologically diverse group of closely related taxa. The dating of phylogenetic nodes and a cladistic biogeographic analysis of the group should help to further test these hypotheses.

Rhododendrons in the Clouds, Riding on Cow Carts and Dodging Rattans: fieldwork in Sulawesi
In July of 2002, my supervisor Lyn Craven and I went on a collecting trip to Sulawesi, Indonesia. We chose Sulawesi as a destination as this was a major hole in my data set and it also represents an important biogeographic link in the region,



the section; it is divided into two clades: a mainland Asian clade and a Malesian clade. Geographic divisions are found throughout the phylogeny, with many of the supported clades correlating more strongly with geographic areas, than with the subsections identified in the current classification. The remainder of section *Vireya* is divided into two main clades, one including all representative taxa from Australia, New Guinea and the Solomon Islands (eastern Malesia), and the other made up of species from Borneo, the Moluccas, the Philippines, Sulawesi and Sumatra (western and

being situated between the larger islands of Borneo and New Guinea, which both possess rich rhododendron floras.

After two years of planning we were finally on our way. We were met by Lina Juswara, our Indonesian counterpart from Herbarium Bogoriense, at Jakarta airport and travelled to Bogor where we based ourselves for our time on Java. Our first week was spent visiting numerous government, police and forestry offices to obtain the appropriate letters and permits for our fieldwork, which meant several trips to Jakarta and back. Once we

had all of the necessary paperwork complete we flew to Makassar (Ujung Pandang), the provincial capital of South Sulawesi. There we took the letters from Jakarta to their respective government and forestry offices, and they wrote us letters to give to their kabupaten (next administrative level) offices where we would be conducting our fieldwork. Once we had obtained all the letters in Makassar and finalised our supplies we drove north to Rantepao, getting ever closer to our first mountain, Gunung (Mount) Rantemario.

Gunung Rantemario is in the Kabupaten Enrekang. Unfortunately we arrived at their government office at 1.45pm, fifteen minutes after the office had closed for the day. So the next day we had to return from Rantepao, a three hour drive along winding roads, to get our letter from them. Although this did not go as smoothly as planned. The officials in Enrekang thought we were going to the village Rantemario not the mountain for which they had a slightly different name, and hence addressed the letter to the wrong kecamatan (next administrative level) for the mountain. So when we took it to Baraka, the kecamatan for Mount Rantemario, they would not open the letter let alone issue the one we needed from them. So the following day we went back to Enrekang again to sort out the misunderstanding; finally we were heading to the mountains!

We hired a 4WD truck that slogged and slipped its way up to the end of the road, a village called Pasongken, where we stayed the night. In the morning we hired horses to ride and carry our gear to the last village before the forest of Gunung Rantemario, Karang (c.1500m). The people of Karang were extremely friendly and welcoming and the surroundings were absolutely spectacular. We stayed the night in the Kepala's (headman's) house where we arranged for

porters to lead us and carry our things up the mountain; the kepala even decided to come along as one of our porters. After a good night's sleep we started our ascent of Gunung Rantemario, a well known location of rhododendrons on the island.

We crossed the river three times by log bridges before we began our trek up through the oak forest on a narrow but well defined path. This is the highest mountain in Sulawesi and is very popular with trekkers. As a result it has been divided into eight signed Pos's, relatively flat, open areas that you can rest or camp at. We aimed to camp at Pos 2 (c.1850m) on our first night as it would be our last access to water before 2500m and then we could maximise our collecting along the way. We collected a range of plants from the lower montane rainforest; some of the common families were Gesneriaceae, Rubiaceae and Moraceae but we also found an interesting climbing bamboo and climbing daisy. No rhododendrons yet! That night we slept on an overhang just deep enough for us to lie down without our feet hanging over the edge. Needless to say the constant hum of the fast flowing river and the fear of slipping off the edge was enough to keep us all awake for a good part of the night.

The next day we had a hard walk, or should I say climb, from Pos 2 to Pos 7 (3100m), but it was all worth it because I got to see my first rhododendron in the wild. We found at least five different species of rhododendron today, two of which dominated the vegetation at different times forming mini rhododendron forests with plants in flower, bud and fruit. From about 2200m to 2500m we were walking through a *Rhododendron malayanum* forest, then this species petered out and shortly after another rhododendron species took over, so now we were walking through a *Rhododendron laguncularipum* forest to about 2800m. Gorgeous!

Our porters had realized that we were collecting plants in flower, and looked on with quizzical interest whenever we pressed them. By that afternoon when the porters found something they thought we might like they would pick a bit and bring it to us. They even prepared a surprise for us at Pos 6. They all got to the Pos before we did (as usual), then collected and arranged a huge posy in the ground, mostly of rhododendrons and *Amyema* (Loranthaceae). It was beautiful, and also really helpful because we had not been able to reach the Loranthaceae creeping through the branches. Exhausted, we arrived at Pos 7 around 5pm and processed the last of the afternoon collections while the porters set up the tarps,

... while we were stopped at the checkpoint we heard that a bomb had gone off in a bus the day before, killing five people.

got fires started and water boiling for tea.

After a cold night at c.3000m we woke to a beautiful day and an amazing view back across the rest of the Latimojong Range. We spent the whole day collecting around camp and up to the puncak (peak). On the way to the peak (3433m) the vegetation changed to an open montane heathland that was extremely rocky and exposed in parts. Here we found four more species of rhododendron, including *Rhododendron eymae*, which is endemic to Gunung Rantemario and probably one of my favourite vireya species. We found it growing in exposed rocky crevices; it is a gorgeous little dwarfed shrub with small yellow corollas dotted with brown scales, the scales are also densely covering the pedicels and young leaves turning them completely brown. The following day we walked back down the steep and often slippery path to Karangan where we again stayed in the headman's house before saying our

thank-yous and goodbyes, and hopping onto our horses to start the long journey back to Rantepao.

We had a day to recover and then went on a day trip in search of *Rhododendron rhodopus*, which has beautifully scented white trumpet shaped corollas. We knew it grew on Gunung Sesean, north of Rantepao, so we headed in that direction and found it in flower and fruit on the roadside in the village of Batutumonga (1359m), near the base of the mountain. Later that day on our way back into town, Lina spotted the bright salmon-orange corollas of *Rhododendron vanvurenii* growing on a steep roadside embankment. It was our first collection of this attractive species, and the only one we found in flower.

The next day we headed north, via the east coast, with the intention of driving through Poso to Palu, the provincial capital of Central Sulawesi. We crossed into Central Sulawesi late in the afternoon and came across our first police checkpoint in a little town near Lake Poso. The Poso region has had a lot of civil unrest in recent times, but we had been told by several people that it was now safe to drive through. Although, while we were stopped at the checkpoint we heard that a bomb had gone off in a bus the day before, killing five people. After hearing this, we decided to spend the night in Pendolo, still two hours south of Poso, and then turn around and try to fly to Palu instead. The next day we drove for 13 hours back to Makassar, where we organised our flights and arrived in Palu only a day and a half later than originally planned, and safely. At Palu airport we were met by Ramadhanil, the curator of herbarium Celebense. Because we were

now in the province of Central Sulawesi we had to visit the provincial government and forestry offices to obtain the appropriate letters for this leg of our fieldwork. The forestry officials requested we take one of their junior officers with us, so Samuel joined our travelling group, along with Ramadhanil. Once all the paperwork and field supplies were restocked we piled the five of us and our gear into a minivan for a hot, uncomfortable seven hour journey north to the village of Sibolang, near our next mountain Gunung Sojol. The closest village to the forest of Gunung Sojol was kampung Sipatoh, and they told us the best way to get us and all our gear there from Sibolang was by a gerobak dan sapi, a cow and cart! We bumped along the uneven road for about two hours getting many a wave or 'hello mister/missus' from the locals, and then walked the final half hour to the village. Once again we were warmly welcomed by the locals and about half of them joined us in the headman's house to watch while plans were made for hiring of porters and last minute food provisions for our next few days on the mountain.

The following day the 12 of us set off - seven porters, Ramadhanil, Samuel, Lina, Lyn and myself - from Sipatoh (c.190m) for five days of hiking and collecting. Most of the way we followed a path worn in by local rattan collectors but the walking was undulating and hard going, especially when we lost the path and went bush bashing for over an hour. We eventually made it back to the path a little scratched and bruised after what seemed like an eternity of slipping, tripping and climbing up and down rattan and smilax filled slopes. Needless to say I will never forget the Indonesian words for 'be careful' and 'slippery'!

There was not as much in flower here as on Gunung Rantemario and unfortunately we did not find as many rhododendrons as we would have liked, partly because our time

limitations prevented us from reaching more than 1500m. But we still collected three *Rhododendron* species and also found some other interesting plants. Rubiaceae and Gesneriaceae species were again common, and we also found a number of different gingers, some of them with huge, apparently edible, fruits. The porters again helped us to collect, climbing trees at the drop of a hat, digging up the ginger fruits or chopping off a branch with flowers or fruits that we could not reach. One time they were a little over eager, or perhaps it was just communication difficulties that resulted in a whole tree being chopped down



We found seven species in flower that day including our first collection of the endemic *Rhododendron celebicum*

so we could collect more fruits from it, oopps! The five days on the mountain went by so fast and we were back in Sipatoh in no time, preparing for our return journey to Palu.

Back in Palu we spent the morning looking at the collection of the Herbarium Celebense, the only herbarium on the island. Then we were back in the field the following day in search of vireyas one last time. Ramadhanil and Christian, a German scientist working with the STORMA (Indonesian-German Research) project, took us to several places in Lore Lindu National Park about an hour or so south of Palu

where they has seen three species of *Rhododendron*. We were able to drive to about 2100m where vireyas should be more abundant, and they were. We found seven species in flower that day including our first collection of the island endemic *Rhododendron celebicum*. As we started to drive off the mountain I spotted a vireya in fruit that we had not seen before and asked the driver to stop so we could collect it. When we got out Lyn said that he thought he had seen one in flower on the embankment back up the road a little, and he was right. It turned out to be a spectacular form of *Rhododendron rhodopus*, with 23 fragrant white flowers in the truss. Without hesitation Lyn was off up the embankment, in the rain, while Christian and I directed him from the road. We heard a few crashes and then he emerged, successfully negotiated his way around a big spiky rattan and collected the plant without too much damage to himself or the specimen. What an end to a fabulous day!

Unfortunately our time in the field, and Sulawesi, had come to an end. We had an extremely successful trip, collecting 14 species of *Rhododendron* for herbarium and molecular studies and about 12 species for living collections, unfortunately about half of these did not survive the methyl bromide treatment required by Australian quarantine.

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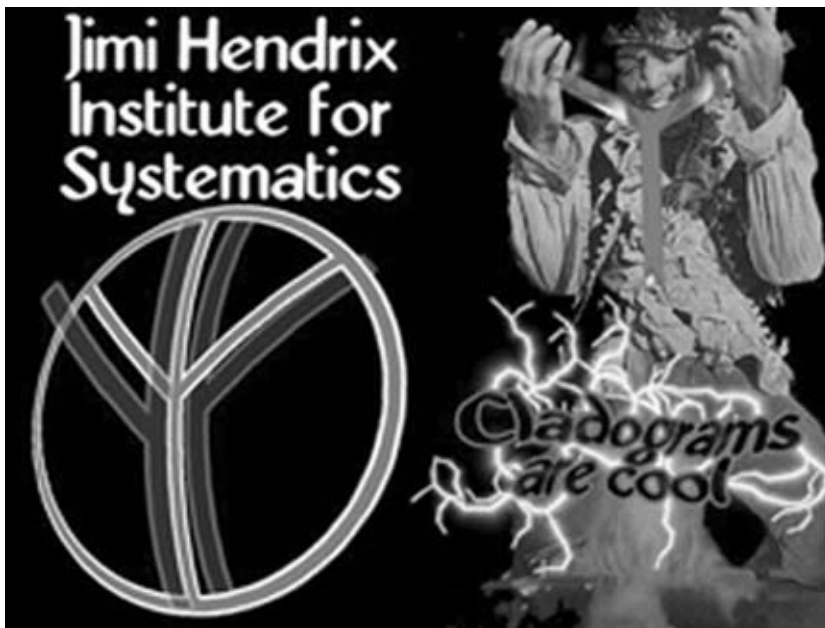
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Gillian Brown won the prize for the best oral presentation at the Biennial Conference of the Systematics Association in Dublin.

BackPage



The new way forward for systematics? Montage by René Zaragüeta Bagils.

SA Business

Council Meetings for 2004

The council meetings and AGM will be held at the Linnean Society, Burlington House, Piccadilly, London, W1J 0BF, U. K. on Wednesdays at 1pm on these dates:
January 14th
March 24th
July 7th
October 6th

The AGM will be held on December 8th. All members welcome.

Do you want to contribute an article, letter or notice to *The Systematist* ? Please contact the editors.

Deadline for contributions: 28th May 2004.

The Systematics

Association is committed to furthering all aspects of Systematic biology. It organises a vigorous programme of international conferences on key themes in Systematics, including a series of major biennial conferences to be launched in 1997. The association also supports a variety of training courses in systematics and awards grants in support of systematics research.

Membership is open to amateurs and professionals with interests in any branch of biology, including microbiology and palaeontology. Members are generally entitled to attend the conferences at a reduced registration rate, to apply for grants from the Association and to receive the Association's newsletter, 'The Systematist' and mailings of information. Please visit our website for more information:
www.systass.org

For information on membership, contact the Membership Secretary, Dr G. Reid (membership@systass.org), Department of Botany, The Natural History Museum, Cromwell Road, London, SW7 5BD, U.K.

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