

The Systematist

Newsletter of the Systematics Association
Number 32 2010

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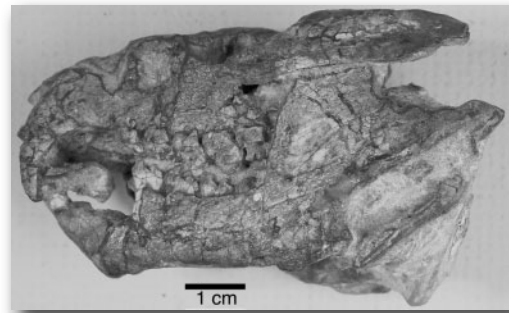
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Lead article

- The role of systematists in prioritizing conservation efforts

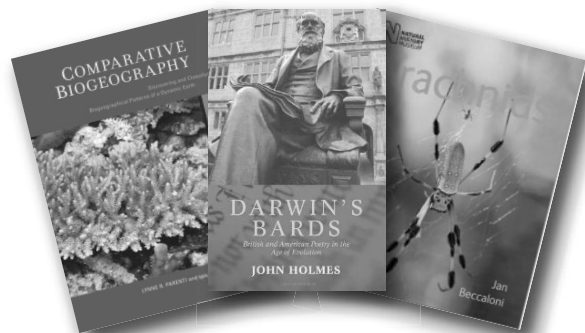
SRF Report

- Systematics of Tritylodontidae



Book reviews

- Darwin's bards
- Arachnids
- Comparative biogeography



Inspirations

- Sandra Knapp

And also...

- President's report
- New in Natural History: the Darwin Centre at the NHM
- Numerical taxonomy and the port of last resort



Editorial

A call to our members

Dear readers,

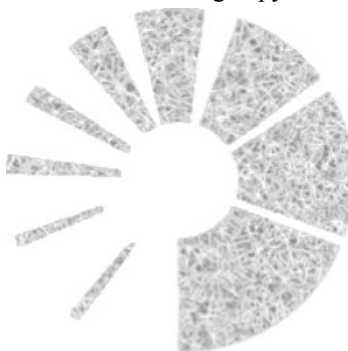
As the *International Year of Biodiversity* draws to a close, it is important that we do not let our enthusiasm and passion for the natural world flag. As a leading international association in systematic biology, we can't afford to lose our momentum in furthering the science of systematics in the various ways that the community has come to expect of us. Even though we saw our membership grow over the past year, that shouldn't be a reason for complacency. A larger membership means a greater responsibility, and more things to do and think about. For example, we continue to see an increasing interest in the various research funds that we administer. But a broader membership also means a broader support base that can help us to achieve our goals more effectively. Our charity exists, and has always existed, only by the grace of the time and effort invested by our dedicated volunteers. That was as true in the past, when luminaries such as Julian Huxley and John Gilmour were involved in the association, as it is today.

Accordingly, we would like to invite you, our members, to consider actively contributing to our association. There are various ways to do this. For those of you who would like to help to support our fascinating discipline, and who would like to help determine the future direction of systematics, why not become a council member of our association? If you would like to contribute, send your nomination -

for either yourself or someone else - to our president Juliet Brodie <j.brodie@nhm.av.uk>.

Nominations are open for all systematists, irrespective of specialty, and including PhD students and postdocs. Nominations should be in by 26 November.

If the newsletter didn't reach you on time, or you have missed this deadline for another reason, please don't hesitate to contact us anyway if you would like to contribute in some way. For example, if you'd like to write an essay or review a book for *The Systematist*, please contact the editor Ronald Jenner <r.jenner@nhm.ac.uk>. Similarly, if you'd like to comment on anything published in our newsletter, please let us know. We are always on the lookout for interesting copy.



**Details of the SA research grants, conference bursaries and funding for the organisation of meetings can be found at:
www.systass.org**

Cover illustrations: A tritylodontid skull (top photo, © Ian Corfe); a Hispaniolan solenodon, one the world's highly endangered species of mammal, © Eladio Fernandez, Zoological Society of London.

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 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.

For information on membership, contact the Membership Secretary, Dr Jon Bennett (membership@systass.org), St Pauls School, Lonsdale Road, London SW13 9JT, U.K.

The Systematist (ISSN 1744-5701) is the Newsletter of the Systematics Association.

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President's Report

By Juliet Brodie

As I write this, I am nearly a year into my Presidency, so I thought it would be a good idea to reflect on this period and also to look into the future. Although I have been a member of the Systematics Association for many years, my first experience serving on Council was in 2004, so taking on the Presidency six years later left me wondering whether my lack of a 'society memory' would be a handicap. Having thought about this for a while and knowing that I had a youthful and enthusiastic group of people to work with, I reckoned that this was an excellent time to become President and indeed that the lack of the society memory was possibly an advantage - few preconceived ideas to influence progress.

One of the first challenges in my role was to find a venue for the 8th Biennial meeting in 2011 (4-8th July). This is an important meeting, especially after the success of the 1st Biosyst meeting in Leiden in 2009, and I was delighted when Professor Christine Maggs at Queen's University Belfast agreed to host the meeting. This will be the first time that the Biennial has been held in Northern Ireland. There will be plenty of opportunity for people to present their work, and an exciting programme of symposia is coming together, including *Next Generation Systematics* - or how to study evolution and diversity in an era of ubiquitous genomics, *Arthropod Systematics*, which will explore higher-level arthropod phylogenetics from the perspectives of morphology, palaeontology and molecules, and *Algal Systematics* which will explore where to go next for this subject.

I am keen during my Presidency that the focus is primarily on the

science, and I aim to ensure that we can keep doing what we do well. The Systematics Association, which currently has members from 31 countries, provides excellent opportunities for scientific engagement: in addition to the Biennial meeting, we hold the annual Young Systematists' Forum - now in its 12th year - for people starting out in their careers. We also host the annual *Sir Julian Huxley Lecture* and the *President's Lecture*, where well-known scientists in the field of systematics are invited to speak, as well as the Policy Lecture which we hold jointly with the Linnean Society. The Systematics Association also administers two major funds in support of research in systematic biology: the *Systematics Research Fund* and

SynTax. We also have a long record of producing highly respected books, which frequently result from the many symposia that we support. These books typically have a lasting influence, and we currently have nine new titles in the pipeline with our new publisher Cambridge University Press, including a new textbook on phylogenetics. Finally, of course, there is this newsletter for which we are always glad to receive copy from our membership. All these activities happen because of the tremendous effort and dedication of the Council members and other members of the society.

My hope is that the Systematics Association will continue to be forward looking, to explore areas that need more attention, including wider outreach, to continue to develop relations with other societies, and to shape and inspire systematics and systematists for a long time to come.

President's Lecture 2010

Cichlid fish as a model for studying the microevolution to macroevolution continuum

Professor Ole Seehausen

University of Bern, Switzerland and EAWAG Swiss Federal Institute for Aquatic Science and Technology

Wednesday 8 December 2010, 6pm

The Linnean Society, Burlington House, Piccadilly, London
(Open to all interested, followed by wine reception)

Cichlid fish in African Great lakes have made spectacular radiations into hundreds of endemic species in very short time. Because they not only speciated rapidly, but built complex ecological communities with incredible alpha diversity in short time too, cichlid fish are fantastic systems to study various questions regarding the continuum from microevolution to macroevolution and from population ecology to macroecology. I will give a few examples from our work, starting where we try to reveal mechanisms during initiation and completion of speciation, through work about species persistence and coexistence, and ending with attempts to explain macropatterns in the distribution of cichlid diversity.

Can systematists help decide the relative worth of bits of biodiversity?

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Introduction

2010 is the United Nations' "International Year of Biodiversity" (www.cbd.int/2010/welcome/). Ostensibly, the year has been set aside for 'celebration', though this term is just the sugar-coating for the call to 'safeguard the variety of life on earth-' i.e. to do something. The United Nations knows that their member nations are in trouble, and a good deal of that trouble is due to the sad state of their biodiversity. The consensus view is that we are in the midst of a global biodiversity crisis.

Readers of this newsletter know well that the basic information on biodiversity (what bits are where) is generally produced by alpha taxonomists. As we venture ever deeper into the age of automated taxonomic identification (e.g. via various barcodes), this basic information will still be overseen by taxonomists, but no longer created by them. Will systematists and taxonomists become more peripheral? We argue here that, insofar as the Tree of Life is the true measure of first-order biodiversity (i.e. its moving parts), modern systematists must remain at the forefront of directed research on biodiversity and conservation. However, the argument we outline below is based on the premise that some bits of biodiversity are more worthy of our conservation efforts than others. This is contentious.

The argument

In an idiosyncratic but provocative essay, Brian Bowen and Joe Ramon suggested the "Orlog model" for characterizing biodiversity (Bowen & Ramon, 2005). In this Norse Mythological story, Urd, Verdandi, and Skuld are three sisters who tend the tree of life, and their names evoke the past, present and future. Bowen and Ramon suggested biodiversity could be viewed from a similar temporal set of perspectives. In this framework, phylogeny is the study of the past history, ecology is the study of present interactions, and evolution is the study of the future potential of some subset of biodiversity. According to the authors, all three perspectives should be considered when measuring the worth of any particular subset in the context of conservation.

Researchers working in systematics are ideally placed to inform the historically-minded handmaiden Urd's choices. Simply put, we can aid the process of making conservation decisions by providing additional information about species derived from the process of evolution. Vane-Wright et al. (1991) of the Natural History Museum (London) were perhaps the first to explicitly consider using phylogenies to establish the conservation priority of sets of taxa and this important concept has been quantified and continually refined by Faith (1992 and onwards). Importantly, Faith introduced the quantity "phylogenetic diversity" to mean the sum of branch lengths of the phylogenetic tree that connects

together all the taxa in a set.

We cannot predict the future course of evolution, and, therefore, betting on evolutionary winners and losers is likely to be nonsensical over relevant timescales (Bowen & Ramon, 2005; Barraclough & Davies, 2005). Instead, using Faith's phylogenetic diversity measure we can choose to conserve sets of species that maximise phylogenetic diversity, thereby maximising the past routes of evolution, and so carrying forward a varied portfolio of species into an uncertain future (Faith, 1992). But here lies the contention: By looking to maximise phylogenetic diversity, we are implicitly changing the mindset of conservation from one where a species' need for conservation attention is dictated by its probability of its extinction (e.g. the Red List; www.redlist.org), to one where we value species based on their ability to conserve past evolutionary history, and therefore, deciding instead, which species we cannot afford to lose.

Given this previous body of work, we appear to have a fledgling basis for using evolutionary history to make conservation decisions, and this might appear to be the end of the story for systematists in the realms of conservation decision making. Interestingly, however, there is some evidence of an agreement between the three sisters' points-of-view. The first hint of such an agreement comes from Faith's assertion that, in theory, 'phylogenetic diversity' is a robust index of the combined 'feature

diversity' of the set. By looking to maximise phylogenetic diversity we could, therefore, also maximize the 'features' contained by the species we are choosing to save.

Reconciling phylogeny and ecology

The precise nature of the 'feature diversity' assigned to the branches of a phylogeny by Faith (1992) can be interpreted in several different ways. One interpretation is any measurable heritable difference between species. Ignoring for a moment biases in phylogenetic construction, if branch lengths within a 'true' phylogeny are to accurately represent the number of physical differences between species, phenotypic changes would need to occur at the same rate(s) as DNA substitutions - or, if we assume a molecular clock, at a constant rate through time. Furthermore, for this relationship to be useful across taxonomies, this consistent relationship between genetic and phenotypic change would also need to be on the same scale across the tree of life. We know of no systematic test of these ideas, but it is a lot to ask of Nature.

Instead, we could look beyond the basic phenotypic differences between species. We could consider 'feature diversity' as measuring those evolutionary changes that affect a species' ecological role (i.e. 'features' are considered to be changes that are non-synonymous in terms of ecology). Here we may be on safer theoretical ground, since ongoing, continual evolution by natural selection may indeed allow for accumulation of ecologically-relevant change at some average rate, at least over long time periods. Again, in order to compare across taxa, this rate would have to be similar across very different biologies.

At the limit, we already know that rates of ecological change vary among groups. George Gaylord

Simpson, in his 1944 book *The Tempo and Mode of Evolution* coined the term 'bradytelic', which he used to describe those taxonomic groups who appear to have remained almost static in their measurable appearance, during their known fossil record. In this respect, Cyanobacteria are perhaps the organisms most unchanged by the process of evolution, as fossil Cyanobacteria dating from ~3.8 billion years ago appear to show similar biochemical patterns to those left by today's extant taxa. Other lineages are more readily modified; for example, the major phenotypic radiations of Angiosperms, birds and mammals have occurred within the last 100 million years. So, we know that the amount of evolutionary change is unlikely to be consistently correlated to time-based branch lengths, throughout the entire tree of life.

Setting aside these extreme examples, let us assume that within more restricted taxonomic groups (e.g. within the mammals) branch lengths might, on average, correlate with the build-up of ecologically-relevant traits. Then, by selecting the subset of species which contain the maximum possible 'phylogenetic diversity' value, we might suppose to reach some agreement between two of the Orlog handmaidens: by conserving the widest set of possible historical phylogenetic paths we also capture a wide array of ecological diversity. This way, we would not only look to maximise our historical portfolio but also our present day ecological one. This would be a property worthy of investigation, and, if proved correct, worthy of greater public attention.

What does previous work tell us? Forest and colleagues (Forest et al., 2007) considered phylogenetic diversity in a large scale conservation planning exercise in the South African fynbos. As part of their study, they found that a greater number of economically-relevant

species are conserved when phylogenetic diversity was used to choose sets of species than when species were chosen at random. This was because different types of economically-relevant traits were clustered in different parts of the tree. Devictor et al. (2010) show that, for birds, there is a general correlation between the amount of 'functional trait' diversity and phylogenetic diversity across grid cells in France ($R^2 = 0.26$), with areas of both surprising congruence and incongruence. Work by Suzanne Fritz & Andy Purvis (2010) may also be relevant: they present evidence that the variation in mammal body size for an ecoregion (a surrogate measure of total ecological diversity of mammals) is predicted to drop much more than both phylogenetic diversity and species richness if IUCN-listed mammals are lost. This is because at-risk mammals tend to be large. Whether overall phylogenetic diversity and body-size variation in mammals is correlated at various geographic scales is still an open (and simple-to-test) question, though we do know that related mammals do have similar body-sizes.

Marc Cadotte goes one step further in linking phylogeny to ecology, by testing whether greater phylogenetic diversity can lead to greater ecosystem productivity. Working with data from David Tillman's long-term community ecology plots in Minnesota, he and colleagues found that phylogenetic diversity measured in inferred substitutions was a better predictor of productivity (above-ground biomass) in these plots than species richness, and better than 12 other biodiversity measures (Cadotte et al., 2008, 2009). Phylogenetic diversity even outperformed total functional diversity. In other words, the total number of inferred DNA substitutions linking species sown into an experimental plot (or a rate-smoothed version of this that

produces a clock-like tree) was a better predictor of ecological function than compound measures of ecological differences measured from traits of the species themselves. As the authors state, their phylogenies may reflect integrated phenotypic differences among taxa and so be a more encapsulating measure than sets of singular, discretely measured traits. This is precisely Dan Faith's original argument in his seminal 1992 paper.

This tantalizing finding has the potential to bring past evolutionary history and the present, ecological, dimension of biodiversity closer together. The mechanism at work here could be that species from the least related (and most phenotypically different) evolutionary routes represent more complementary ecologies, providing a more efficient use of resources. This is a tempting idea but remains unproven. Furthermore, if we also consider that maximising past routes of evolution and wide sets of ecological characteristics puts us in good stead for riding out unknown future changes, this approach might also take into account the views of our final, forward-thinking handmaiden.

Urd as the standard bearer

But why do we suggest that Urd, the historically-minded handmaiden lead the other sisters into battle against biodiversity loss? We would not expect evolutionary information to ever perfectly predict evolutionary potential or the ecological or functional attributes of species. Any conservation importance index based on evolutionary information, therefore, will, to some degree, discount the importance of the other two biodiversity axes.

One good reason to use evolutionary information is that we appear to know more about our past than about either our present or

future. Large scale phylogenies for many mega-fauna groups have been around for several years; large scale databases containing information about the morphology and ecology of entire species groups are only slowly becoming available in a digital format; each museum or wild-caught specimen has to be painstakingly measured. Sequencing machines have, to some degree, mechanised molecular data collection; although molecular phylogenetics requires expert knowledge, it is not often taxon-specific.

We know even less about the future evolutionary or future functional roles of species. The young science of functional ecology, whose remit it is to establish the role of species on the productivity, resilience or biodiversity of its habitat (which one could call a species' 'keystone-ness') is yet to reach consensus on anything more than a handful of species. Furthermore, so little is known about many of the vast number of invertebrates groups that it seems reasonable to think that it would take decades to produce a meaningful measure of ecological importance for even a sizable fraction.

Depending on findings over the coming decade, information taken from molecular phylogenies may offer a cheap and dirty surrogate for precious information about the evolutionary and ecological importance of species. One potentially interesting but untested route here is the role of DNA barcoding. Work is ongoing to establish to what extent CO1 barcode data (in concert with taxonomic information) can provide a good approximation of phylogenetic diversity for birds and mammals, even if they produce fairly poor phylogenetic trees. Depending on the results, barcodes may offer a surrogate of a surrogate for informing conservation of taxa with limited phylogenetic

information.

Phylogenetic information and conservation policy

If we were eventually to conclude that by maximising 'phylogenetic diversity' we select a useful set of species in terms of ecological traits and even functional traits, there are still significant practical problems regarding current conservation policy. This is because most legally-binding conservation programmes assess the need for conservation attention on a species-by-species basis (Possingham et al. 2002). Problems arise because phylogenetic diversity is intrinsically a measure of group information content and not a characteristic that is easily attributable to a single species.

There have been several attempts to calculate a species-specific phylogenetic importance measure (stretching back at least to Vane-Wright et al., 1991). All work on the principle that species with fewer close relatives contain less redundant evolutionary information. The platypus, the ostrich, and the tuatara are examples of such species. And, indeed, those species with fewest close relatives are the ones most likely to complement any other random subset of species, and so sets of species chosen using importance values do capture more than random amounts of phylogenetic diversity (Redding et al., 2008). We note, however, there is no published importance score that has this as its goal.

There are some species-specific measures of phylogenetic importance that stand out from the rest as being, at least, partially interpretable in an evolutionary biology context: 'Species Age' – the amount of time since a species split from its most closely related, usually extant, sister species; and 'Evolutionary Distinctiveness' (see Isaac et al., 2007) – which, by pure chance, approximates the potential

contribution of species to future evolutionary trees (K. Hartmann, PhD thesis, 2008). Most other phylogenetic importance measures remain simply statistical approximations of tree topology and branch length. Though there is limited evidence that species chosen using importance scores span a wider than expected range of ecologies (Magnuson-Ford et al., 2009; Redding et al., 2010), most of the proposed phylogenetic conservation importance measures (there are approximately 10 published) have lost the clear objectives set out by Faith, that is, to maximize the 'feature diversity' of taxa being conserved. Therefore, if one of these measures were widely adopted, instead of choosing one representative from every branch on the tree of life (as we would under Faith's conservation approach), the over-arching aim of conservation becomes, instead, an attempt to conserve, in an evolutionary sense, the loneliest species on the planet.

The lack of a coherent conservation objective behind species-specific phylogenetic importance measures has not prevented the adoption of 'Evolutionary Distinctiveness' into one global conservation approach. The 'Evolutionary Distinct, Globally Endangered' (EDGE) project (www.edgeofexistence.org) has received significant media attention and successfully promoted the use of evolutionary information in conservation decision making.

Phylogeny on the landscape

Conservation does not operate solely at the species level either. Perhaps the principal agent of conservation mitigation is the nature reserve, and this was also the framework for the initial discussion of phylogenetic diversity (Vane-Wright et al., 1991; Faith, 1992). Under at least some models, choosing to maximise species

richness does a good job of conserving phylogenetic diversity (Rodrigues et al., 2005); given that so few new reserves are being created, maximizing total PD during reserve design might not often be practical.

A different approach was recently introduced by Dan Rosauer from the University of New South Wales. His "phylogenetic endemism" approach is a methodology that distributes the total phylogenetic diversity of a candidate clade over the landscape as a function of each member species' phylogenetic isolation and its range size (Rosauer et al., 2009). Overlapping small-range endemics that have few close relatives would represent the densest possible sample of phylogenetic history and the areas where they are found would have high phylogenetic endemism scores. It is even possible to include the probability of extinction of branches of the tree into these calculations, in order to identify areas where the long and threatened branches of the tree of life are concentrated. This is ongoing work in our labs.

There is also ongoing work mapping the location, or hotspots, of species with few close relatives, i.e. those species that score highly using the phylogenetic importance measures outlined above. Perhaps unsurprisingly, the species richness of an area is a good predictor of where the most distinctive ones are found: there are more species with few close relatives in the mega-diverse tropical rainforests than in the polar-regions, for instance. Given this, an approach to maximize species richness, such as Conservation International's Hotspots programme, should also adequately protect those species with the fewest close relatives. While this finding should be taken seriously in policy-making decisions, there are geographical discrepancies, where some areas have much higher numbers of evolutionary isolated species than

expected. For birds and mammals, for instance, these areas may include the sub-tropical mountains of sub-Saharan Africa, Eastern Madagascar, and coastal Papua New Guinea - all good candidates for a geographically-centric EDGE-style programme.

Conclusion

The science we have sketched out above is one at heart of triage. The handmaidens tend to the Tree of Life, but it is a tree that is being rapidly pruned back. It is important that the research in the area of phylogenetic conservation is robust enough to support the expanding and popular strategy of considering the path of evolution that every species has travelled along when making hard decisions about which species, and which geographical areas, we cannot afford to lose. It is heartening to note that one major UN-sponsored international biodiversity initiative, DIVERSITAS (www.diversitas-international.org) has recently set up a separate subprogramme called bioGENESIS, whose first core goal is to facilitate the creation and testing of new phyloinformatics tools and data to help produce the phylogenies needed to do this work.

More work is required to test the idea that some (sets of) species are more evolutionarily and ecologically important to conserve than others, and that phylogenies can help predict which. If they can, then readers of this newsletter, as the producers and interpreters of phylogenies, can indeed help decide which bits of biodiversity are most worthy of conservation. This might be a task with a moral dimension, and one that might carry some significant responsibility.

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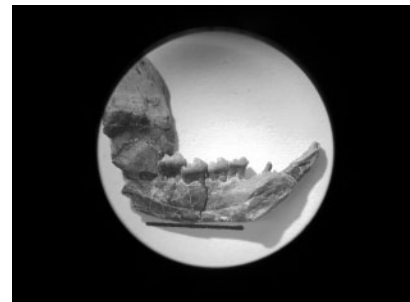
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research trip! I was in the USA to visit the University of California Museum of Paleontology (UCMP) in Berkeley, and the Museum of North Arizona (MNA), Flagstaff, in order to carry out research into a relatively obscure group of extinct animals, the Tritylodontidae. These are non-mammalian synapsids (previously mammal-like reptiles) that lived from the latest Triassic through to the Early Cretaceous, beneath the feet of the dinosaurs,



Tritylodontid jaw © Ian Corfe

alongside their close relatives the earliest mammals. This close relationship has seen them proposed as the sister group to Mammalia (Kemp 1982, 1983; Lucas & Luo 1993, Ji et al. 2002). This, in addition to the increasing number of genera and species described in recent years, and the extension to their 'traditional' Triassic-Jurassic presence provided by Lower Cretaceous taxa from Japan (Setoguchi et al. 1999, Manabe et al. 2000; Matsuoka & Setoguchi 2000) and Russia (Tatarinov & Matchenko 1999, Lopatin & Averianov 2006) has led to an increasing interest in the group. Given the large number of Mesozoic localities, it is surprising that the Americas were about 100 years behind the rest of the world in reporting the presence of tritylodontids. However, discoveries and publications in the last 25 years or so have allowed the naming of four new genera in addition to the identification of a possible new species of the genus *Oligokyphus*, previously known from Late Triassic and Early Jurassic deposits in Germany, England, Wales and

SRF Report

Flying into San Francisco at sunset with the Golden Gate Bridge visible out of the left window of the plane was a pretty spectacular start to a

China. The four are *Kayentatherium* (Kermack 1982), *Bocatherium* (Clark & Hopson 1985), *Dinnebitodon* (Sues 1986), and *Nearctylodon* (Lewis 1986) – though the latter is probably a junior synonym of *Kayentatherium*. All but *Bocatherium* (which is from Mexico) are from Arizona. Further undescribed or unnamed specimens may represent new genera, species, or simply show ontogenetic and population level phenotypic variance (Sues 1985, Winkler 1991).

The aim of this research visit was to collect data on the specimens housed in institutions in the USA in order to produce a phylogeny of the group. This will then be used to address such evolutionary questions as the nature of faunal transition over the Jurassic-Triassic boundary; the origin of mammals and the identification of their sister group; phylogenetic relationships of the advanced non-mammalian synapsids; and the identification of attributes that promote generic/familial longevity. The holotype of the first officially



Tritylodontid skull © Ian Corfe

described American tritylodontid, *Kayentatherium*, resides in the UCMP in Berkeley, so that was my first destination. In addition to this material, there were further *Kayentatherium* fossils plus specimens and casts of other tritylodontids from around the world to examine (including some recovered from the Welsh fissures just over the border from Bristol where I was based at the time – I had to fly half way around the world to set eyes on them!), ensuring a busy but productive week. I was



Chicken coop lodgings © Ian Corfe made to feel very welcome by staff and students, attending seminars, being taken for lunch, and continuing discussions on weighty matters such as avian origins, and the cosmopolitan nature of Early Jurassic terrestrial vertebrate faunas to the accompaniment of live music at the local after hours haunt!

Moving from the bustling cradle of the counter culture movement to the deserts and mountain plateaus of Arizona was a slight shock, but one necessitated by moving on to the Museum of North Arizona, Flagstaff. Here were housed numerous remains collected from the Lower Jurassic Kayenta Formation, covering parts of Northern Arizona in addition to Colorado, Utah and Nevada. The tetrapod fauna represented is broadly similar to that of the Welsh fissure deposits mentioned above, as well as the Chinese Lufeng formation, all thought to be approximately contemporaneous. As far as tritylodontids go, the holotype of *Dinnebitodon* plus additional remains of *Kayentatherium* and *Oligokyphus* are found in the MNA. While the fossils themselves are kept in a temperature and humidity controlled purpose built repository, visitors and summer excavation volunteers are housed in chicken coops across the road. Yes you did read that correctly! The chicken coops are, however, quite tastefully refurbished, and show no signs of their former occupants ever having lived there. Welcoming hosts and a large number of geologically interesting features in the area (the Grand Canyon, Meteor Crater etc)

made this half of the visit both an enjoyable and, workwise, fruitful one.

The purpose of the trip, to collect data and generate new phylogenetic characters, was successfully accomplished. To date, no phylogenetically informative characters for the postcranial skeleton of tritylodontids have been suggested, but examination of material in the UCMP and MNA and comparison with literature and specimen-based observations of other tritylodontid genera and species has allowed a significant proportion of the data matrix currently under construction to be composed of postcranial characters. It also allowed missing data points in the matrix for American specimens to be filled. The predicted output will be a primary paper detailing tritylodontid phylogeny at the species level and a number of secondary papers using this phylogeny to address the questions above.

I wish to thank Pat Holroyd, Kevin Padian, Bill Clemens and the staff and students of the UCMP; Dave and Janet Gillette at the MNA; and the Systematics Research Fund for allowing this research visit to happen.

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New in Natural History



The Cocoon in the Darwin Centre. © Natural History Museum

The Darwin Centre Cocoon is a state-of-the-art science and collections facility. This extension of the Natural History Museum opened in September 2009 and currently holds the entomology and botanical collections. As well as providing more space for the specimens and the scientists working on them, the new building aims to reveal the Museum's scientific work and part of the hidden collections to the public. The Cocoon's architecture is contemporary and elegant, as awe-inspiring to my eyes as the main Museum building would have been

to the Victorians. Inside, they have made the visitor experience change according to our times, using audiovisual and interactive technology.

At the entrance the visitor can pick up a NaturePlus card to collect information from the screens at the displays. This interactive tool during the visit to the galleries also serves to extend the museum experience at home by logging into the NaturePlus website with the card to retrieve information and to participate in the blogs with Museum scientists. Inside the Cocoon and welcoming the visitor are the wall projections introducing the Museum guides: scientists and curators of the collections. The "virtual" presence of the experts talking about aspects of their research or how to prepare specimens for collections makes the visit more engaging. The displays are beautiful and didactic; some of them invite the visitor to touch as well as to observe. The information panels not only describe the exhibit but also explain scientific concepts and terms, such as *tree of life* and *specimen*, making the specialist jargon more accessible to the public.

During the visit along the corridors, the visitor is taken through the process of how science is done in the Museum, in particular taxonomy: collecting specimens, classifying, using DNA techniques, analysing data and writing publications for peer-review. One activity, that allows the public to design and prepare a collection trip, aims to convey the excitement of going to exotic places to find specimens and the thrill of discovering a new species. Presenting the "process" of making science, besides displaying the collections, gives the visitor an insight into the day-to-day work and challenges of scientists. The glass-fronted laboratories open to the galleries offer another point of contact between the public and the scientists working in the Museum.

The visit to the Cocoon ends with interactive screens where the public can provide feedback and express their opinions about biodiversity and conservation issues.

Besides building an impressive extension to harbour more than 3 kilometres of cabinets and provide more laboratories for scientists, the Natural History Museum has made an enormous effort to open up to the public through the Cocoon. From a science communication viewpoint they have made the museum experience more engaging, with all the interactive exhibits, and more appealing to a broader public with interests ranging from biodiversity and conservation to entomology and botany. They have made the science relevant to people's lives by highlighting the impact of the Museum's scientific work on society and the environment, and by inviting us to reflect on the implications. Most important of all, they have brought scientists and the public closer with the open laboratories, the opportunities to chat to the researchers through the website, and the seasonal lunchtime talks to meet the scientists face to face in the adjacent Attenborough studio. This initiative makes the Museum a meeting place for dialogue where visitors have the opportunity to discuss and be inspired.

The Cocoon is the modern face of a historical institution and part of one of the top 12 "coolest" museums in the world (Newsom and Crump, 2009).

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Numerical Taxonomy and the Port of Last Resort

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What's the connection between musician John Zorn and numerical taxonomist Robert Sokal? You'll forgive me for assuming that most readers of this newsletter know a thing or two about Robert Sokal but probably nothing about John Zorn. So that's where I'll begin, with Zorn. Zorn is a highly prolific and eclectic musician and composer, promoter and owner of the record label Tzadik (<http://www.tzadik.com>). In 2006 he was awarded a MacArthur Fellowship. It's almost impossible to categorise his music. Here's a piece written for a short biography when Zorn gained his MacArthur award:

"In his eclectic orchestrations, including solo works, chamber ensemble pieces, and compositions for complete orchestra, Zorn dismantles, reconstructs, merges, and refines disparate musical idioms. His experimentation with rhythm, harmony, symphony, and instrumentation creates highly original musical landscapes."

In other words: unusual. Anyway, among his wide range of musical interests, in 1992 Zorn began to explore his Jewish roots by examining different forms of Jewish music. The exploration blossomed into the Masada music books, a series of 200 or so Jazz—Klezmer compositions played by a variety of different line-ups: quartets, quintets, string quartets and so on. These 200 compositions were to be book one. A second book of compositions, *The Book of Angels*, which began in 2004, draws on another 300 compositions. Well, I did say he is prolific. Another project of Zorn's is

a series of film soundtracks. His 'Filmworks VIII: 1997' recording includes two very different soundtracks, one for a film called *The Port of Last Resort* (1998), a documentary concerning the lives of Jewish refugees who escaped from Nazi Europe between 1938 and 1945, fleeing to Shanghai (the other soundtrack is for a film called *Latin Boys Go to Hell* – I think I already mentioned eclectic). *The Port of Last Resort* soundtrack features new 11 Masada compositions. I have yet to see the film but I do have the soundtrack and have seen some of the haunting black and white photographs that appear in the film (some can be viewed at the Winter & Winter website, the distributors of the film,

<http://www.winterandwinter.com>).

Every now and then I search the web to see if a copy of the film becomes available to buy at a reasonable price. So, when searching, you'll understand my surprise when I came across the "Emeritus Faculty Association newsletter #104 December 2004" for Stony Brook University, Department of Computer Science, New York, announcing an up and coming event:

"As previously announced, Bob Sokal will show *Port of Last Resort*, a video on the Shanghai Ghetto in World War II, at 10:30 a.m. Friday, January 7 in the Wang Center, Lecture Room 1. Follow the signs inside the building." (<http://www.cs.sunysb.edu/~drs/newsletter104.htm>)

I wondered if it could possibly be the same Robert Sokal, author of *Principles of numerical taxonomy* (with Peter Sneath, 1963),

Numerical taxonomy : the principles and practice of numerical classification (also with Peter Sneath, 1973) and *Biometry: the principles and practice of statistics in biological research* (with James Rohlf, the 3rd edition published in 1995). The newsletter noted an event from the previous meeting:

“Mel Simpson introduced Distinguished Professor Emeritus Robert Sokal. He described Bob's exemplary scholarly record and argued that Bob would have won a Nobel Prize if that prize was offered in the field of numerical taxonomy.”

No doubt. But it was the same person – and it was a surprise. Details of Sokal's early years can be found briefly summarised in David Hull's book, *Science as a Process*. It goes a bit like this: the Sokal family fled Vienna from the Nazi's; they ended up in Shanghai, China, where their son, Robert, gained a degree and married “the daughter of a well placed Chinese family” (Hull 1990, p. 119); after the war, the couple eventually moved to Chicago, USA and numerical taxonomy was born. I was to learn that the story was a bit more complex.

In Austria, the film *The Port of Last Resort* is known as *Zuflucht* in Shanghai. I used that as a search item in Google and came across a book by Stefan Schomann, *Letzte Zuflucht Schanghai: Die Liebesgeschichte von Robert Reuven Sokal und Julie Chenchu Yang*, which roughly translates as *Last Refuge in Shanghai: The Love Story of Robert Reuven Sokal and Julie Chenchu Yang*. Stefan Schomann, a German journalist who divides his time between Berlin and Beijing, was introduced to Sokal by a former refugee. Here's a small extract from the prologue of *Letzte Zuflucht Schanghai*:

“Whenever the residents of Ningpo encounter something extremely unusual and precious, a singular occurrence,

they refer to it as a ‘big yellow fish’. This means it is a prized and valuable example of the croaker family of fishes. Fishermen regularly catch ordinary specimens of these fish, but a “giant” yellow fish rarely thrashes about in their nets.

The love story between Julie Chenchu Yang, daughter of an esteemed family from Ningpo, and Robert Reuven Sokal, a young Jewish refugee from Vienna, is such a big yellow fish, a fascinating singularity. An improbable romance against the norms of time and place, it is not surprising that it occurred in the middle of the twentieth century, in a decade dominated by the unimaginable, in a distant city, where exceptions are the rule – in Shanghai” (text kindly provided by Stefan Schomann; the paperback is called *Der große gelbe Fisch*).

A more detailed English account of Schomann's story can be found on a podcast derived from the 2009 Shanghai International Literary Festival (<http://www.cityweekend.com.cn/shanghai/articles/blogs-shanghai/silf/silf-podcast-stefan-schomanns-last-refuge-in-shanghai-of-love-and-war-and-troubled-times/>).

Schomann's book tells this much fuller story of the relationship between Robert Sokal and Julie Yang, against the wartime background of emigrant life in Shanghai. You won't learn much about the birth, development and growth of Numerical Taxonomy but you will gain an insight into one of its creators. The book, written in German, has yet to have an English translation (a Chinese translation is due soon, Schomann, pers. comm.). Unless, of course, some general interest in getting one done is shown. Let Stefan know.

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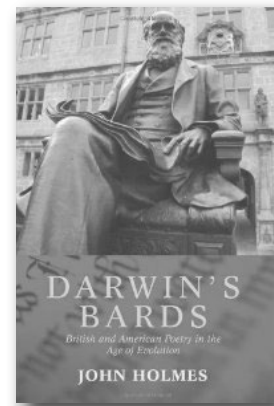
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Book Reviews

Darwin's bards. British and American Poetry in the Age of Evolution



Holmes J. 2009. Edinburgh University Press. Hardback ISBN 978 0 7486 39403, £60.

For those acquainted with natural sciences, art, philosophy and literature, the so-called humanities appear as a strange garden of otherworldly delights somehow still imbued with metaphysics. Nevertheless the impact of Darwin's dangerous idea has been the alkahest of culture, its universal acid, rapidly corroding the last remnants of platonic ideas, vitalism and dualism down to their own roots. For some, this cultural reaction led to a deeper separation between natural sciences and humanities but for others, more willing to accept the new world depicted by the theory of evolution, it opened a whole universe of new insights on human nature, nature and existence itself. It is therefore possible to study the Darwinian revolution even from the observation point of humanists.

The book *Darwin's Bards* explores the insights of this new worldview in British and American poetry. The author, Dr. John Holmes, is a senior lecturer in the Department of English & American Literature at the University of Reading. He set himself the goal of marching through the last hundred-and-fifty years of literary history in search of meaning after Darwin, arriving at the conclusion that not only Darwin changed poetry, but also poetry can change our views on Darwin. The overture of the book (*Poetry in the Age of Darwin*) consists of a preamble summing up the history of darwinism, the major differences among different thinkers throughout history as well as a bullet-point description of the actual consensus on the theory of evolution. This introduction will be welcomed especially by readers not versed in the subject. The last part of the introduction is dedicated to the reaction of literature to Darwin.

In fact, when the Darwinian worldview was mixed with the humanistic one, it opened up more questions than it answered; in a fashion that was the exact opposite of the scientific worldview. Paradoxically, until the Enlightenment, there was no clear distinction among natural and human areas of knowledge: it was all anthropocentric and anthropomorphic. By that time, literature already reached some of its highest achievements, while science was quietly waddling its way from the backstage to the center of scene itself. The Eighteenth century, with the birth and blooming of Romanticism, also marked the apex of a full-fledged Positivism. Backed-up by scientific discoveries, the anti-metaphysic movement became a metaphysic movement itself imbued with faith in the advance of society. It is in that time, in the Victorian Era of Britain, that Darwin gave birth to his descent with modification by means of natural selection: a theory

so elegant and simple, yet so counter-intuitive, that it took at least one hundred years to fully understand and metabolize its consequences, some of them still lingering outside of our everyday comprehension.

The book is then divided into thematic areas that cover almost every existential question produced by the encounter of darwinism and poetry: God, death, humanity's place in nature, humans and other animals, love and sex. After Darwin almost all of this changed. Time drifted far away from human history: the shallow time of religion was replaced by an increasingly deep, geological time. The common ancestry of all living beings drew the animal kingdom closer to the half-divine kingdom of humans. Where before began a ladder of unlimited progress, from mud to God, now there was a branching tree with infinite possible endings (the adaptations) and no final solution, either survival or death, evolution or extinction. Therefore, nature had been left bare of her goal, and ceased to be a servant of the gods, a mere created creature, and became a feral beast, suited for the struggle of existence, blind to any reason, charged of animistic character. The logic of the multitudes, the natural populations, became the *ultima ratio* of existence (so-called population thinking), while pure ideas and essences became abstractions rather than absolute realities (Plato's ideas). Love became a complex of chemical pathways that inexorably lead to sex and sex became the only way (at least for us humans) to fulfill the now biological imperative "Be fruitful and multiply". Faith and religion, more than anything, began to actively question the role of a God in a Darwinian world: is he good? Is he evil? Or, worse, totally uninterested in his creatures? Does he exist at all? Is he male, female or none? Is Nature God? Is man the creator? Is death the end? But

nevertheless, the more the classical world of adamantine certainties faded in the collective unconscious, the more a need to establish new connections with nature and the universe arose. It is at this stage that new Darwinian lineages of art, literature and philosophies were born. Darwinian poetry is an answer to those new questions, a powerful means of immediate representation of and empathy for nature, connecting the distant Darwinian time and world to the ever present human world of here and now.

It's beyond the scope of this brief review to cite the poetry contained in the book but, to give readers some at least idea, the book contains entire poems and their detailed analyses. The variety of poets represented is vast, such as: Alfred Tennyson, Robert Browning, Thomas Hardy, Robert Frost, Ted Hughes, Thom Gunn, Amy Clampitt, Edwin Morgan. The scholarly nature and rather formal register deployed in the book is definitely not something all general readers would enjoy reading. Nevertheless, the collection of poems itself is a continuous surprise, page after page, and even a general reader, bold enough to fight with complex words and concepts, can discover new, subtle ways to deal with evolution, which usually go unnoticed. For sure, it is a book principally designed to interest connoisseurs of either natural sciences (especially biologists) or humanities (especially scholars), both seeking reciprocal understanding of each other's themes and tropes. It inevitably follows that the dual nature of the readers will be mirrored in the book: it will superficially appear as a Janus Bifrons, the mythical god with two faces fronting opposing directions. On the contrary, the book clearly shows how human culture is an inevitable mixture of natural and supernatural, empiricism and mysticism, facts and emotions. It's the human phenomenon itself that

holds all of this together, or better his world of ideas, words and poems, that strives for survival and adapts to an ever changing cultural landscape.

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Arachnids



Beccaloni J. 2009. *Natural History Museum, London*. Hardback ISBN 978 0 565 09220 7, £30.

If you are an ‘arachnastic’, such as myself, this book is as good a place as any to shake hands with spiders, scorpions, mites, and their close phylogenetic kin. *Arachnids* is a handsome book made visually striking by the many beautiful color photos that adorn all 12 chapters. Each of the 11 major living groups of arachnids is featured in their own chapter. These follow the same basic layout, discussing the group’s classification and diversity, external and internal anatomy, distribution and habitats, general biology, behavior, and life history. Both arachnophiles and arachnostics will certainly find much of interest in this book, and its many stunning illustrations make it an attractive purchase for beginners and aficionados alike.

Yet, the book hasn’t been designed to completely satisfy the wishes of either of these groups of readers. The title of the book’s first chapter, *Spiders aren’t the only*

arachnids, makes clear the book’s laudable aim to reach a broader audience. Yet, in some instances basic concepts aren’t always introduced in an unambiguous manner, which can lead to misunderstanding or confusion. For example, sexual dimorphism is simplistically defined as “differences in size or shape between males and females of a particular species” when clearly many more organismic traits can be dimorphic. The section on phylogeny is particularly problematic. Cladograms are introduced as “dichotomously...branching tree diagrams,” which may leave some readers guessing as to whether a depicted trichotomous tree is in fact a cladogram or not. Cladograms are said to be produced “using cladistic techniques,” without explaining in the text what cladistics, or cladistic techniques are. The glossary just offers the following ambiguous definition: “method of inferring evolutionary relationships based on features inherited from a shared common ancestor.” A “clade” is defined as “a group of organisms descended from a common ancestor,” which doesn’t disambiguate it from para- or even polyphyletic groups. One also reads that cladogram nodes can be considered “ancestors,” but that in

with the author’s admission that she did “cheat a little” because the order of the chapters in the book doesn’t strictly follow the pattern of the phylogenetic relationships of the major groups. How and why one would want to linearize a branching diagram in the first place may not be obvious to most readers, myself included. This, however, may not really matter because the author does not make it clear to the readers why she chose the specific cladogram according to which the chapters were arranged; it is neither the most recent, nor the most comprehensive analysis published.

Perhaps not many readers will stumble over these phylogenetic niceties – not everyone is a phylogenetic hairsplitter. But the one subject that is surely of universal interest to potential readers of this book suffers from similar vagueness. Many arachnids are venomous, and some of their bites and stings can be lethal to humans. Several pages in different chapters of the book deal with venom, but I found precious little about the composition and physiological effects of venoms. We learn that venom may contain such ingredients as “small amino acids,” (the author presumably means small peptides), salts, neurotoxins, cytotoxins, and proteolytic enzymes. We don’t learn a lot, however, about

Both arachnophiles and arachnostics will certainly find much of interest in this book, and its many stunning illustrations make it an attractive purchase for beginners and aficionados alike

“modern ‘transformed’ cladistics” such nodes “have no actual taxa on them.” Novices are unlikely to know what the author is on about here. It is also stated that molecular cladograms may not include extinct species “because of the great difficulty in doing molecular work on fossils,” a rather surprising statement in the age of the Neanderthal genome. The very brief introduction to phylogenetics ends

how these components act on a victim’s body. We read not much more than that proteolytic enzymes may help pre-digest the prey’s tissues, that “neurotoxic venom” “affects the nervous system”, and that “cytotoxic venom” “affects the tissues” and can cause necrosis. I think it is a missed opportunity that the author did not delve somewhat deeper into the available corpus of knowledge about the composition

and fascinating physiological effects of the various venom components. This would have been well worth the extra pages.

Yet, my greatest hang-up about the book is that a lot of detailed information is presented in the text without sufficient illustrative backup. This is particularly true for the pages describing the internal anatomy of the various groups, and most annoyingly so for the internal anatomy of the genitalia. For example, we learn that in schizomids the “genital atrium opens into the spermathecae. These are very interesting structures, and unlike those of other arachnids. Instead of being paired, they may have many branches or lobes, looking like chilli peppers or small growths of mushrooms! They may have distinct stalks and bulbs. These are secretory glands that surround the spermathecae. These probably discharge secretions into the spermathecae via small ducts.” This is only part of the lengthy description that is offered on internal genital anatomy in schizomids, without so much as a single picture as illustration. For some groups, such as Opiliones and Amblypygi, the space devoted to describing internal genitalia rivals or exceeds that dedicated to the internal anatomy of the central nervous system, circulatory system, digestive system, and excretory system combined! Only four of the chapters on the different groups (those on scorpions, spiders, ricinuleids, and opilionids) present a single, broad-brush schematic drawing on internal anatomy, showing just the most basic outlines of some of the internal structures. The descriptions of the internal anatomy of the remaining seven groups remain unadorned by any illustrations. Without some well-chosen illustrations only the most masochistic readers could be expected to maintain their interest in the text. It should not be too difficult to free up a few extra pages

for illustrations in future editions of the book. Firstly, much of the material on anatomy in the first chapter is redundant because each of the subsequent chapters discusses the same topic in more, taxon-specific, detail. Secondly, some redundancy is caused by strictly separating the discussions of the external and internal anatomy of single organ systems, such as respiratory systems and genitalia. I think that a tighter organization can be achieved by the judicious integration of these separate sections.

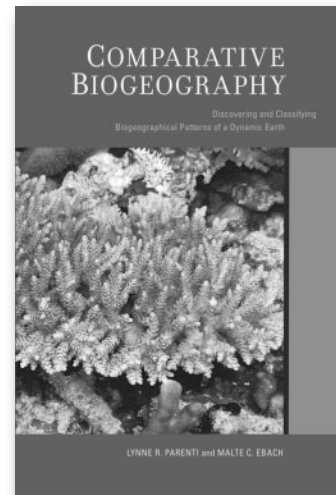
A future edition of the book can similarly benefit from some form of integration of the references and the text. As is usual for a book intended for a popular audience, the information presented in the text is not supported by specific citations. Yet, a reference section at the end of the book offers a miscellany of references for each chapter, without, however, organizing these according to their subject matter or referring to the text. This means that the reference list is likely to be of little use to the average lay reader. This situation is not helped by only providing abbreviated journal titles for articles from the primary research literature. Although readers can be expected to hobble over the occasional typo without problems, they may, however, have greater trouble locating the journals CLADEC, NATRA, TOXIA, and LANCA, which should instead refer to *Cladistics*, *Nature*, *Toxicon*, and *The Lancet*, respectively.

All in all, and despite the problems noted above, *Arachnids* remains a desirable book. It contains a wealth of information on the biology of arachnids, and the many beautiful illustrations make it a delight to browse. There is certainly no shame in having it on your bookshelf, rubbing covers with David Attenborough’s *Life in the undergrowth*.

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Comparative biogeography. Discovering and Classifying Biogeographical Patterns of a Dynamic Earth



Parenti LR, Ebach MC. 2009. University of California Press. Hardback ISBN 978 0 520 25945 4, £27.95.

‘To do science is to search for repeated patterns, not simply to accumulate facts, and to do the science of geographical ecology is to search for patterns of plant and animal life that can be put on a map.’ MacArthur (1972)

The epigraph for this review comes from the well known opening lines of Robert MacArthur’s last book – Geographical Ecology – published in 1972, just before his early death from cancer. Some 13 years later this book was highly influential in the development of my own thinking when I read it, repeatedly, as a Masters student. However, this epigraph raises an obvious question – how does one analyze the results of all this mappery? Parenti and Ebach’s (2009) new book sets out one approach to this question, firmly based on cladistic methodology. This approach (and therefore this book) appears to me

to be deeply unsatisfactory. Whilst I am not in sympathy with the approach taken in the book I found my time reading it very valuable – if only because it helped crystallize my own problems with this approach.

This review is ‘critical’ in several meanings of the word and because of this it may be a useful warning to readers to point out that there are several reasons why I am likely to be biased against the authors approach. I have written extensively on dispersal biogeography (sometimes on plants and fungi, but mainly on eukaryotic microbes) and indeed one of the authors of the book has in the past cited my work as a good example of what he thinks is wrong with biogeography (Ebach & Humphries 2003) - for my reply, which contains arguments which overlap with this review see Wilkinson (2003). I am also an ecologist, rather than a systematist, which has implications for the questions I tend to focus on. Like all (?) biologists, classifications are crucial to what I do, but they are to me just a tool which allows me to address the questions I find most interesting. These questions tend to be more ecological, hence my admiration for MacArthur’s book (I was also extremely impressed by his fruitful marriage of natural history and mathematics). In addition I have some sympathy with the view that a useful biological classification scheme should be based on more information than just cladogenesis (e.g. Margulis & Chapman 2009). As such I am not a strict cladists – even for the classification of organisms, never mind biogeographical areas! It is also apparent that Parenti and Ebach have a very different view of science to myself. I fail to see anything other than the most arbitrary divisions between the ‘different’ sciences and indeed I see some areas of science grading almost seamlessly into parts of the arts and humanities (e.g. Kemp

2007 or Wallace 2003). Parenti and Ebach are much keener on demarcating particular areas of science and argue that one of the advantages of their cladistic approach is that it would help unify biogeography into a tightly defined science. So a reviewer with a different background may have had a very different take on this book.

The following quotation from Parenti and Ebach’s introduction highlights, for me, the main philosophical difficulties with their approach. ‘The problem with particular explanatory distributional mechanisms – such as individual episodes of long distance dispersal – is not that they fail to explain distributions and biodiversity, but that these explanations cannot be refuted empirically. Such explanatory hypotheses lack empirical rigour and are untestable. Only with a natural classification of taxa and biotic areas are we able to compare distributions and discover historical biogeographical patterns. This is what this book is about’ (Parenti & Ebach 2009, page 7). A good example of a disputed case of long distance dispersal has been the colonization of Madagascar by mammals. Contrary to the argument in this book such theories can be tested. Seventy years ago G.G. Simpson used the restricted nature of Madagascar’s current mammal fauna to argue for a strong role of chance (hence dispersal rather than vicariance) in the colonization of Madagascar. More recently the modelling of palaeo-ocean currents and, most crucially, data from molecular systematics have strongly suggested that Simpson was correct (Krause 2010). As this example makes clear, even in the absence of a good fossil record such ideas are testable by a mix of molecular methods and an understanding of past geological history (e.g. Madagascar was still attached to Africa in the late Jurassic when many mammal lineages were evolving and so, in theory, a

vicariant explanation is possible). In the face of examples like this, based on molecular/fossil and geological dating evidence, Parenti and Ebach argue that ‘These comparative ages are not evidence, as they represent no more than estimates of the time of one event compared with estimates of the time of another’ (Parenti & Ebach 2009 page 109). However such an argument effectively makes all science impossible as scientific data are always potentially mistaken – a fact which many philosophers now understand greatly weakens Poppers well known falsification criteria for a good scientific theory. This is particularly relevant for historical sciences such as biogeography and palaeontology (Cleland 2001). In this respect the ‘estimates’ that Parenti and Ebach object to are nothing special; they are typical of most scientific data. Indeed there is a maxim, that I have heard attributed to Francis Crick, which states that any scientific theory that explains all the empirical data must be wrong – as you can be certain that at least some of the observational and experimental data will be found to be mistaken!

The book doesn’t just overlay the difficulties with rival approaches but fails to fully critically assess the many confounding problems with the cladistic approach. Many of these problems are well known and even described in undergraduate textbooks (Cox & Moore 2005). For example if a vicariant event is not followed by speciation then cladistic analysis will not be able to identify it. Alternatively extinction may greatly complicate the signal. The cladistic approach also effectively assumes allopatric speciation (following a vicariant event). However there is now a growing feeling that we were too quick to write off sympatric speciation in the second half of the 20th century. There is increasing evidence for sympatric speciation in many taxa – although it is not yet clear how

common this is (Sherratt & Wilkinson 2009). Even Ernst Mayr, the arch evangelist for allopatric speciation, conceded in his last book that the occurrence of sympatric speciation was no longer in any doubt (Mayr 2004). Obviously widespread sympatric speciation would greatly complicate cladistic approaches to biogeography.

So far this review has largely discussed Parenti and Ebach's ideas on their own chosen ground; namely the history of higher taxa on long geological time scales. Their book aims to 'unite the many aspects of biogeography under one banner: *Comparative Biogeography*. [This] uses the naturally hierarchical phylogenetic relationships of clades to discover the biotic area relationships amongst local and biogeographic regions'. (Parenti & Ebach 2009, page 9). This narrow definition rules out much of biogeography as defined by textbooks (e.g. Cox & Moore 2005) or leading journals in the field, such as *The Journal of Biogeography*. As I have previously argued (Wilkinson 2003) much of biogeography focuses on Quaternary, or shorter, time scales. At these scales dispersal and extinction are usually more important than vicariance, and cladistic based methods are likely to be relatively uninformative. For example as I write this review, in North West England, there are Collared Doves *Streptopelia decaocto* feeding on my bird table. This bird was only recorded breeding in Britain for the first time in 1955; following a huge European range expansion of this species – starting from the area around Turkey in the 1930's (Evans 1993). The time scale of this example is probably more typical of most biogeographical studies; unless we follow Parenti and Ebach in their highly restrictive definition of this area of science which, if I understand them correctly, would redefine this example as ecology – not biogeography.

Does this above discussion imply that this book is without any value? The answer to this is probably no. Although its underlying philosophy appears deeply suspect it does set out in some detail cladistic approaches to a subset of biogeographical questions which may well prove useful in some situations. This is especially so for people interested in long term patterns in groups of higher taxa. In this sense these approaches are perhaps similar to phytosociological classifications of plant communities in ecology. Although the underlying theory (that plant communities have a real existence analogous to organisms) is now considered wrong by most plant ecologists, these classification techniques are still useful in some situations and can be defended on pragmatic grounds (e.g. that nature reserve managers and others find them useful). I would also draw comparisons with conventional taxonomy; although I am not a strict cladist this doesn't prevent me from agreeing that cladistic approaches can often be very informative.

Finally it is worth saying something about the book as a material object. The publishers should be congratulated on its production. It is a well made hardback, with colour illustrations and a pleasure to handle – and sold for under £30! This is very unusual in modern academic publishing. The clue to how this has been achieved is probably in the acknowledgments to the Smithsonian Institution for their 'generous contributions to this book'. At such a price you can always read it for yourself – rather than relying on my rather negative judgement.

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Inspirations

An Interview with Sandra Knapp

Sandra Knapp is Merit Researcher in the Department of Botany of The Natural History Museum in London.

How would you summarize yourself in the form of a title of a scientific paper?

“Botanist tries to combine all forms of evidence to study the species level taxonomy of a HUGE genus”
Or maybe
“Monographing a monster”

Summarize the when and where of your academic career

BA – Pomona College, Claremont, California (1978)
PhD – Cornell University (1986)
Resident collector in Panama (Missouri Botanical Garden) – 1981
Resident collector in Peru (Missouri Botanical Garden) – 1986-1987
NATO post doc (NHM, London) – 1987-1988
Research Associate, Institute for Botanical exploration, Starkville Mississippi – 1988-1991
NHM, London – 1992- present... A long time!!

When did you decide to follow the career path you are on now?

Totally serendipitous – I was at Pomona thinking in my freshman year that I might major in French, and had to take a science class – marine biology was full so I took botany. We went in the desert every weekend with microscopes to identify plants and I have never looked back.... Had to change my major pretty smartly though to enable graduation!

What are the main goals of your research, and what is your future ambition?

I began all this to understand the origin of species, and am still trying! In a way, my ambitions have become more realistic, I will be happy if I can understand why there are so many (ca. 1500) species of the genus *Solanum*, but this has led to so many other things that limiting it to just that would be unrealistic. Maybe origin of species is not a bad goal!

What organisms have you worked on, and which are your favourite organisms and why?

I work on the members of the nightshade family, the Solanaceae, and more specifically on the mega-diverse genus *Solanum*, which contains some very important agricultural species like the potato, tomato and aubergine. With 1500 species *Solanum* is one of only about 10 flowering plant genera with more than a thousand species – why? I have also worked on a



Sandy Knapp in the field

number of other plant families in my floristic projects; for Flora Mesoamericana I have done treatments of families for which there is no expert (or the expert doesn't want to contribute) – these taxonomic treatments are fun and teach me a lot about characters and how to examine them critically. You can get in a rut if you stick too much to one thing. I think taxonomy involves the ultimate transferable skill, careful examination and comparison of characters – although we all tend to stick to a single group

of organisms for our entire career, we could switch; it might take a little while to learn the new characters, but it certainly would be possible.

How many hours per week do you work?

Too many or not enough, depending on how you look at it. I love what I do, so it never seems too much to me.

What percentage of time do you spend on each of your different responsibilities?

I try (and probably fail) to do too many things at the same time so it probably adds up to more than 100%. In the early part of my career I spent a lot of time in the field, but once I had children I spent more time in the herbarium and near home; I don't regret this a bit, and now they are all gone I can do more field work again I hope! I seem to spend a lot of time in meetings and organizing things at the moment, but that ebbs and flows. It is a luxury working at the Natural History Museum where I can take the odd half hour to work in the herbarium; in recent years though the whole days one needs to really get to grips with a problem requiring examination of lots of specimens are few and far between. That said, I did spend a week a month or so ago sorting out a real tangle with thousands of specimens on loan. In my job I nominally spend 80% of my time on research – for me that is the reading, writing, field work and herbarium work – I am very lucky to have so much of my time to do the things I really enjoy.

Working in the Natural History Museum, we do not teach per se, but our version of teaching is being involved in public programmes offered by the NHM. I do a lot of speaking in Nature Live [a program at the NHM where curators and researchers provide public outreach, ed.]; I love it, for me, sharing my

passion for my job with others who aren't like me is a real buzz.

How many undergraduate, PhD students, postdocs, and technicians are in your lab?

I don't like to think of my workspace or team as "my" lab – I work with great people on various projects, currently about 5 people, but it is at a bit of a low point in numerical terms – it will pick up again in the New Year as new members join the team.

What gives you the most satisfaction and frustration in your job?

I love looking at plants and interacting with people; it is frustrating when I can't do either of those things.

Could you say something about the importance of international collaborations for your research?

Crucial!!! I could not do the work I do without my fantastic network of international colleagues. In my view the best science is collaborative, and for me, the opportunity to work with a wide range of interesting people is part of what drew me in, and keeps me in, taxonomy.

What kind of field work do you do and where has it taken you so far?

Sixty four thousand dollar question – I have had the incredible good fortune to have been an amazing number of wonderful places with wonderful people! I do field work to collect plant specimens in their native habitats; I was lucky enough during my PhD to be hired by the Missouri Botanical Garden to be their resident collector in Panama – I was given a place to live, a truck (Ford F150) and a quota of plants to collect – it was a blast! Over the course of my peripatetic career I have been to lots of countries in South America (Peru and Paraguay stand out for the length of time I was there, but it would be

impossible to say which was best) and Central America (because of being the editor of *Flora Mesoamericana* I do a lot of field work in Central America and southern Mexico); I have also had the chance to go to Uganda to teach on a TBA (Tropical Biology Association) course, which was a great experience, and more recently have been working in South China with colleagues from Beijing studying aubergines. I have also done collecting in Europe and North America.... *Solanum* is everywhere!

Did any memorable incidents happen during field collecting?

Um er.... Over a beer maybe. One great incident was the discovery of a passion flower floating in a river in eastern Panama, I saw it and KNEW it was new, so thought to myself the only way to find this is to walk upstream in the river until I find it.... So I did. Up to my chest in water I only had to walk about a kilometer (or maybe less) until I saw the plant high up in a tree. Now, I am totally rubbish at climbing trees, so I found someone with an ax to chop the branch off, it fell in the river and I collected every flowering thing..... the new *Passiflora*, a couple of new epiphytes and a new record for the region of the tree... all in all a pretty good haul. We named the passion flower liana for a friend John MacDougal – *Passiflora macdougaliana*. Another time I nearly jumped out of a tree onto a bushmaster (large rather poisonous snake) but fortunately looked before I leaped! I could tell field work stories all day.....

Is there any paper or book that has been very influential for your thinking?

As an undergraduate I read the series of papers by Clausen, Keck and Heisey in the 1940s (Carnegie Institute of Washington Publications) examining the degree

to which genetic and environmental differences contributed to phenotypic variation they observed in various species of California plants. Their elegant experiments and detailed observations made me start to think about variation and origins of diversity in new ways.

How was the most important mentor in your career?

Three people in botany stand out for me – first was Michael Whalen, my PhD supervisor who gave me freedom and just said "great, go for it" when I suggested new directions. He tragically died of brain cancer at the age of 36 just after I defended my PhD. Tim Plowman (Field Museum, Chicago) was another, he locked me in a room in Chicago to write my thesis when I was having trouble because Mike was so ill.... he too sadly passed away. The third person has been the constant - Peter Raven, the President (now Emeritus) of the Missouri Botanical Garden has always been there for me since I was a grad student; he is truly amazing. When I worked for Missouri in Panama the unwritten rule was, if a scientist wants a particular plant collected get it if you can, if a Missouri staff member wants it, plan a trip soon, but if Peter wants it, drop everything and go! So plants were sent off, often to deafening silence – but Peter was different; one always got a letter for thanks, and several years after I had collected material of the rare epiphyte *Alzatea* for him he sent me the symposium volume in which the studies using that material appeared! That was amazing, not necessary and one of the many reasons Peter is a true leader that people will follow.

Last in my set of mentors, but definitely not least, was my father. A particle physicist, he always talked science with me and all my siblings; no topic was too esoteric, and he taught us all to explore ideas fully, rather than just accept what was the going opinion. He died last year, and I miss his conversation

and advice about things scientific. He also taught me the “physics is the only true science” – something that has made me think creatively about why taxonomy is important ever since!

What is the best advice you have ever received?

Never look back. This is not to say ignore learning from your mistakes, but is about not dwelling on the past and instead, moving on.

How many scientific publications do you have at the moment?

I have written or co-authored 18 books, been responsible for 3 websites, written about 160 peer-reviewed papers or book chapters and have written about 100+ popular articles and book reviews.

Could you nominate any of your discoveries or papers as the most important one, or the one (or several) that you personally like best? Why should people not working on your organisms care about your work?

For me, my monographs of groups of *Solanum* or other genera in the Solanaceae are the publications I am most proud of. They will last a long time (I hope) and are useful for so many things beyond the scientific realm. They are unfashionable at the minute, but fashions are just fashions, usefulness lasts.

You have a lot of papers with co-authors. Is there a particular contribution you generally bring to these papers?

I like to work with teams of people with diverse expertise and to these teams I bring my knowledge of the plants themselves and their “habits”. I have a great deal of field experience, and it really helps. I also like to write, and am a ferocious editor!

What skills do you think a successful researcher in your discipline must

possess?

Patience, good humour and the ability to laugh at yourself are key to success in life in general, but in a field biologist are absolutely critical. I would have long ago given up if I had been angry when things didn't go quite right, like when buses just don't arrive, or plane flights get cancelled or it rains for a week solid, or a hurricane arrives – just staying cheerful and positive has an absolutely amazing propensity to make things happen!

Taxonomy today requires an enormously broad range of skills – to do it all one needs to be able to drive a Land Rover and program a PERL script (not that I can do either of those things particularly well!). This means collaboration and teamwork are key to doing good taxonomic science today; each person can contribute something a bit different to make an outstanding whole.

Do you have any tips for students aspiring to a career like yours? Be flexible, ready for change and don't take no for an answer. Seriously though, flexibility is really important these days – it may be that as a taxonomist you end up working on several different groups, or doing something you didn't expect, but I can guarantee you will learn something new, and you might even like it!

What do you think are currently the greatest impediments to achieving a successful career in your field, and how could you go about dealing with these?

Contrary to popular belief there are more taxonomists describing new species now than ever before (see Joppa et al. Proc. Roy. Soc., B; <http://rspb.royalsocietypublishing.org/content/early/2010/07/07/rspb.2010.1004.full.pdf>); this almost certainly means that the action is not all in places like the UK or USA. So I think the biggest impediment to success is inflexibility or a desire to have it all one's own way. It may be necessary to go somewhere new and

different, to move or to change taxonomic groups. Dealing with these impediments requires one to follow my top tips above, but there are no guarantees in life or in a career, it is what you make it.

Calendar

**1 December 2010
12th Young Systematist Forum**

The Natural History Museum, Flett Lecture Theatre
See www.systass.org/ysf/

**8 December 2010
AGM and The President's Lecture**

The Linnean Society, Burlington House, London, 5pm (AGM), 6pm (lecture)
Speaker: Prof. Ole Seehausen
See advertisement on page 2.

**21-27 February 2011
BioSystematics Berlin 2011**

Berlin, Germany
See www.biosyst-berlin-2011.de/

**4-8 July 2011
8th Biennial Meeting**

Queens University, Belfast
See www.systass.org/biennial2011/

**23-30 July 2011
XVIII International Botanical Congress**

Melbourne, Australia
See www.ibc2011.com/

**5 October 2011
Sir Julian Huxley Lecture**

The Linnean Society, Burlington House, London
Speaker to be announced.

**7 December 2011
AGM and President's Lecture**

The Linnean Society, Burlington House, London
Details to be announced.