

The Systematist

Newsletter of the Systematics Association

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Editorial

25th Issue of *The Systematist*

Greetings and welcome to the Summer and 25th issue of *The Systematist: Newsletter of the Systematics Association*. The lead article in the Summer issue explores the revolutions in biogeography and their shaky past in relation to geology in *Biogeography and Scientific Revolutions* by Dennis McCarthy. McCarthy's 'thought provoking' exposé of biogeographical thinking over the last 150 years will be followed up by with a presentation for the Biogeography Symposium at the 5th Biennial Meeting of the Systematics Association in Cardiff during August 22 - 26. Also in this issue, we have a Systematics Association conference report of the *International Symposium on the Biology of the Palm Family* by Bill Baker as well as our *Spotlight* feature article on *Automated Object Recognition in Systematics* by Norm MacLeod, Stig Walsh and Mark O'Neill introducing their revolutionary new data recognition system called DAISY. MacLeod, Walsh and O'Neill will be hosting the *Algorithmic Approaches to the Identification Problem in Systematics Symposium* to be held at the *Natural History Museum* on August 19. We look forward to meeting you there!

Other articles in the Summer issue include a critique of systematics in Quentin Wheeler's review of the latest Systematics Association publication *Milestones in Systematics* edited by Williams and Forey followed by an in depth review of our other latest Systematics Association publication, *Organelles, Genomes and*

Eukaryote Phylogeny: an Evolutionary Synthesis by Hirt and Horner.



The book reviews start on Page 16

Last of all our *BackPage* lists all the events and contact details of the Systematics Association.

We thank our contributing authors for their views, reviews and thoughts. *The Systematist* is looking forward to receiving any responses or counter-views expressed in any recently published articles.

The editors look forward to your contributions and suggestions.

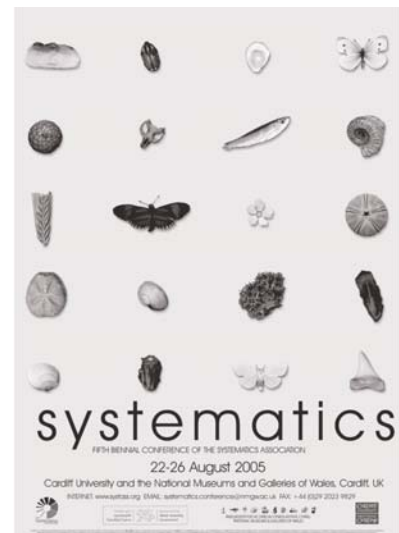
Change of Editorship

On a sad note, Paul Wilkin will be retiring as co-editor of *The Systematist*. Under Paul's editorship the Newsletter has seen a dramatic transformation. Now with a new title and an expansion to 24 glossy pages, *The Systematist* has already been cited in the *New York Times* (December 12, 2004) and reaches a wide audience of comparative biologists, journalists and geographers worldwide via our website (www.systass.org). In the new year the Systematics Association will assign a new co-editor to work with Malte Ebach. The new co-editor will be announced in the next issue of *The Systematist*. Malte will also be moving France, based at the

Université Pierre et Marie Curie in Paris. Please address all your correspondence to Malte Ebach (see address and email details on *BackPage*).

5th Biennial in Cardiff August 22 - 26

The 5th Biennial Meeting of the Systematics Association held in association with the *National Museum and Art Gallery of Wales* and the *University of Cardiff* will be held in Cardiff, Wales. The Meeting will have three invited symposia *The New Taxonomy* hosted by Quentin Wheeler, *What is Biogeography?* Hosted by Malte Ebach and Ray Tangney and *Compatibility Methods in Systematics* hosted by Mark Wilkinson. Contributing speakers will be holding parallel sessions during the duration of the conference. Interested parties wanting to attend for a day or for the whole symposium may pay their registration fees on the day. Please contact Ray Tangney (see www.systass.org) if you have any queries regarding the meeting.



Details of the 5th Biennial Meeting of the Systematics Association can be found at the Systematics Association website: www.systass.org

Malte C. Ebach and Paul Wilkin
Co - editors

Cover illustration : 'Dispersing Iguana' montage. Copyright 2005 Dennis McCarthy (published with permission). See page 3 for the lead article.

Biogeography and Scientific Revolutions

Dennis McCarthy

Buffalo Museum of Science, Buffalo, USA

As our past disputes over evolution and continental drift make clear: those who underestimate the probative value of distributional evidence are likely to end up on the wrong side of science history. It appears that biogeography, which has served as the focal point of two recent scientific revolutions, is about to usher in a third.

Currently, a significant number of distributional facts, particularly involving oceanic disjunctions of poor-dispersing taxa, are in direct conflict with conventional palaeomaps of the Mesozoic Pacific and Tethys. Many researchers have dealt with these inconsistencies by ignoring basic biogeographical realities and positing radical cross-ocean dispersal hypotheses to explain the problematic disjunctions.

The Revolutionaries

The five revolutionaries (see inset), a group which could also include T. H. Huxley (evolution), Alexander du Toit (continental drift), and Leon Croizat (vicariance), all helped raze conventional assumptions in geology, biology and psychology -- yet, as noted, each of them, like Huxley, du Toit, and Croizat, also happened to be biogeographers. The question is, 'Why would so many revolutionaries in so many disparate fields of thought all be specialists in the little known field of biogeography?'

One possible reason is that biogeography is the science of adventurers. During an interview about his book, *Consilience*, E.O. Wilson once told me he suspected that those who followed the consilient view of the sciences and the sociobiological view of human nature and culture

would be more likely, on average, to favor certain outdoorsy activities like rock climbing and kayaking. His implication, perhaps, was that a love of nature combined with a certain fearlessness or, at least, moxie might be helpful in rejecting religious and academic dogma for the

that time the longest crossing of an ice cap. The 'father of continental drift' would ultimately die on an expedition in Greenland in 1930. Alfred Russel Wallace spent a number of years along the Amazon and was one of the first Europeans to explore Rio Negro. In 1852, on his



Alfred Wegener
Continental Drift



Eduard Suess
Tethys and Gondwana



Alfred Russel Wallace
Evolution



Charles Darwin
Evolution



E. O. Wilson
Sociobiology

These five revolutionaries have led revolutions in three scientific fields ...

They have one thing in common... they are all biogeographers

steelier, realistic views of life. Adventurousness may also be a trait commonly shared by scientific revolutionaries. Wegener, while studying meteorology, took up hot air ballooning and in 1906 broke the world record for most time aloft, more than 52 hours. In 1912, while on an expedition in Greenland, he and his team barely survived what was at

trip back to England from South America, his ship caught fire and sank, stranding Wallace and his shipmates in cramped and leaky lifeboats until their rescue ten days later. Undaunted, Wallace would later travel to Indonesia and become one of the first Europeans to live in New Guinea for an extended period of time. Darwin's five year jaunt

around-the-world, with a stop in Galapagos is well known and needs little elaboration here. Du Toit, like Wallace and Darwin, studied extensively throughout South America. He also helped map the Cape of Good Hope and spent time in the other Gondwanan continents, India and Australia.

The writings of these revolutionaries, like their life histories, advertise their Magellanic nature.

Wallace's *On the Law Which Has Regulated the Introduction of New Species*, Darwin's *The Origin of Species*, Wegener's *The Origin of Continents and Oceans*, du Toit's *Our Wandering Continents*, do not smell of the class room; they smell of swamps, jungles, rivers, and beaches. Such risk-takers are not

tions to explain distributions; they used distributions to test orthodox assumptions.

In a letter to J.D. Hooker in 1845, Darwin described biogeography as the key to unlocking the mystery of speciation, referring to 'geographical distribution' as 'that grand subject, that almost keystone of the laws of creation.' Fourteen years later, he would publish *The Origin of Species* with two chapters devoted to 'Geographical Distribution.' In them, Darwin notes that frogs, toads, and newts are almost completely absent from oceanic islands - places where they would be expected to thrive. These distributions, as Darwin pointed out, are inconsistent with the 'theory of independent creation', that is, the idea that species

Verde Islands are related to those of Africa, like those of the Galapagos to America. I believe this grand fact can receive no sort of explanation on the ordinary view of independent creation; whereas on the view here maintained, it is obvious that the Galapagos Islands would be likely to receive colonists, whether by occasional means of transport or by formerly continuous land, from America; and the Cape de Verde Islands from Africa; and that such colonists would be liable to modifications; the principle of inheritance still betraying their original birth-place.'

Like Darwin, Wallace (1855) also used distributional patterns to help mould the theory of evolution and challenge conventional assumptions in biology. *On the Law Which Has Regulated the Introduction of New Species*, Wallace's rudimentary prologue to his evolutionary view, is first and foremost a biogeographical paper. In it, Wallace puts forth arguments that read much like the work of Croizat, anticipating Croizat's dictum that life and Earth evolve together:

'Of late years, however, a great light has been thrown upon the subject by geological investigations, which have shown that the present state of the earth, and the organisms now inhabiting it, are but the last stage of a long and uninterrupted series of changes which it has undergone, and consequently, that to endeavour to explain and account for its present condition without any reference to those changes (as has frequently been done) must lead to very imperfect and erroneous conclusions.

'The facts proved by geology are briefly these: -- That during an immense, but unknown period, the surface of the earth has undergone successive changes ... That all these operations have been more or less continuous, but unequal in their progress, and during the whole

The writings of these revolutionaries ... do not smell of the class room; they smell of swamps, jungles, rivers, and beaches.

likely to be awed by professors or cowed by textbooks. There is not a schoolmarm among them. But innovative and accurate theories require more than just chutzpah; they depend on an agile and unbiased mind encountering a store of telling facts that entail an often simple yet unconventional conclusion.

And this is what truly makes the study of biogeography so important. It is likely that, excepting the principle of material causality, no other known tenet or group of facts has proved more fruitful to the intellectual progress of the human race than the distributional patterns of plants and animals. Wegener, du Toit, Darwin, and Wallace were not simply biogeographers by hobby; they repeatedly used the implications of distributional facts to govern their earth-changing conclusions. Their method was so successful because it was so utterly biogeographical.

They did not use orthodox assump-

could be independently created in two or more vastly separated regions. Instead, this biogeographical evidence supported the viewpoint of common descent. Frogs, toads, and newts are all descended from a mainland ancestor and have not been able to reach remote oceanic islands.

Likewise, all mammals, except bats, are absent from remote oceanic islands. As Darwin wrote:

'Why, it may be asked, has the supposed creative force produced bats and no other mammals on remote islands? On my view this question can easily be answered; for no terrestrial mammal can be transported across a wide space of sea, but bats can fly across.'

Darwin also pointed out that the endemic inhabitants from islands are nearly always most closely related to taxa from the nearest continental source:

'The inhabitants of the Cape de

series the organic life of the earth has undergone a corresponding alteration.'

After this passage, Wallace lists a series of observations from 'Organic Geography and Geology' such as the fact that families tend to be more widespread than genera, which in turn are more widespread than species, which are often limited to a particular geographic region. He also noted that the most closely related species are nearly always found in adjoining regions. These and other biogeographical and biogeological observations led Wallace to conclude that:

'Every species has come into existence coincident both in space and time with a pre-existing closely allied species'.

Three years later, in 1858, Wallace would pen his famous letter to Charles Darwin: *On the Tendency of Varieties to Depart Indefinitely From the Original Type*, where he clearly identifies the struggle for survival as a mechanism for evolutionary change. (Wallace disliked the phrase 'natural selection' because he believed it anthropomorphized Nature.) Wallace's intellectual progression is quite clear. His vast knowledge of biogeography led him directly to a biogeographical principle regarding speciation, which in turn, led him to the theory of evolution.

The recent rebellion in geology, which finally resulted in widespread acceptance of the pre-Jurassic closure of the Atlantic and Indian oceans, is no less indebted to biogeography. Suess named Gondwana after a region in India where the southern fossil flora *Glossopteris* is found, underscoring that Gondwana was, at bottom, a biogeographical concept. As with *The Origin of Species*, Wegener's *The Origin of Continents and Oceans* also contains a chapter on geographical distributions. Wegener's arguments need little elaboration here as they appear in most popular works and middle school text books on plate

tectonics. For example, a Google search shows that 832 webpages that refer to 'plate tectonics' also refer to '*Glossopteris*.' 485 webpages refer to both 'Plate tectonics' and '*Mesosaurus*'. The webpages are mostly educational primers on 'Geology Basics' or 'The Story of Plate Tectonics' and discuss the fact that the trans-oceanic disjunctions of these fossil taxa helped confirm that the oceans between the Gondwanan continents were closed because these taxa were unable to cross oceans.

In the middle of the twentieth century, those geologists and biogeographers like G.G. Simpson (1940, 1943) who fought to main-

objective. Historical lessons about the stabilist hypotheses of cross-ocean rafting or convenient fossil absences help underscore the rationalizations that scientists are willing to fashion in defense of orthodoxy. Yet, as will be shown, these same arguments are resurfacing today.

The return of radical dispersalism and the subordination of distributional evidence

In defending the view of continental stabilism, Dr. Rollin T. Chamberlin of the University of Chicago once wrote:

'Wegener's hypothesis in general

Wegener and du Toit, of course, have now been vindicated - and Simpson-like arguments often become the first examples in which young students learn that mainstream scientists are not always objective.

tain the orthodox view of continental stabilism put forth explanations for the disjunctions that included trans-oceanic rafting of vertebrates and a convenient pattern of fossil absences. In response, Alexander du Toit (1944) wrote the paper, Tertiary mammals and continental drift. A rejoinder to George G. Simpson, with quotes that remain relevant today:

'The notion of random, and sometimes two-way, 'rafting' across the wide oceans ... evinces, however, a weakening of the scientific outlook, if not a confession of doubt from the viewpoint of organic evolution...'

'To argue that such southern disjunctive distribution is due to colonisation from the north through forms not yet discovered in the Holarctic region, is neither scientific nor fair...'

Wegener and du Toit, of course, have now been vindicated - and Simpson-like arguments often become the first examples in which young students learn that mainstream scientists are not always

is of the footloose type, in that it takes considerable liberty with our globe, and is less bound by restrictions or tied down by awkward, ugly facts than most of its rival theories.'

What is ironic about Chamberlin's statement is that the exact opposite was the case. It was Chamberlin's views that were speculative while it was Wegener and du Toit who were confining themselves to facts. Chamberlin's assumption that continents were ever-stationary, no matter how firmly believed by experts of that time, was still an assumption. In contrast, we know precisely where certain taxa reside, and we know precisely how they move. We know that remote oceanic islands like Hawaii, Pitcairn, and Easter Island lack native terrestrial vertebrates. All these facts confirm that while terrestrial vertebrates may often cross narrow marine barriers to proximal islands, they clearly cannot cross the full extent of an ocean. The geological assumption that created an oceanic separation

between so many poor-dispersers was wrong.

Despite the efficacy of distributional analyses in past scientific revolutions, a number of researchers have abandoned this glorious tradition of biogeography and now use everything *except* distributional facts when fashioning distributional explanations. The result is a recent spate of hypotheses of cross-ocean rafting events of terrestrial vertebrates and patterns of convenient fossil absences - all of which are required to maintain fashionable geological and molecular-clock assumptions.

The biogeographical controversy today, mostly involving the question of vicariance across the Pacific, is between 1. researchers who agree that many distributions are the result of long distance, trans-marine colonization but who accept that certain distributional (and biophysical) facts provide compelling evidence for vicariance and, 2. radical dispersalists who, like their counterparts from the middle of the 20th century, believe that distributional facts should always be subordinate to geological (and now molecular) assumptions. The methodology of the latter mainly consists of looking at conventional paleomaps for the time period of diversification that has been inferred from fossil data and/or the most recent molecular analyses. If the paleomap places an ocean between the sister taxa, then the conclusion is an ancestor crossed it. This assumption is maintained regardless of the immobility of the taxon, its absence from all oceanic islands, the vastness of the alleged barrier, or the repetition and the precision of the distributional patterns. In other words, biogeographical facts, no matter how compelling or well known, are deemed irrelevant.

In one of the many recent papers that adopted this anti-distributional methodology, de Queiroz (2005) ended up advocating jump-dispersal of monkeys, cichlids, and geckos across the full extent of an ocean. De Queiroz dismissed concerns regarding the uncertainty in molecular dating techniques with the assurance that 'conservative choices can be made in such analyses'. But were all of the choices that he referenced really conservative?

De Queiroz supported the claim of trans-Atlantic rafting of New

of these times significantly post-dates the earliest fossils of these groups: ~48 mya, 50 mya, and more than 120 mya, respectively. Arnason *et al.* (1998, 2000) instead calculate that the Cercopithecoid-Hominoid divergence took place >45 mya and calculate the split between the New and Old World Monkeys at 60 - 70 mya. At this time, the oceanic barrier was merely a narrow seaway, and the Falkland plateau may have been particularly close.

Biogeography, despite what recent anti-vicariance papers attempt to imply, is by no means mute on this subject. Monkeys do not occur on any oceanic island (Mittermeier *et al.* 1999). So if they do have the ability to raft across oceans, it is apparently a talent they do not like to flaunt. Moreover, while a great number of primate species have colonized the continental islands of Indonesia (Borneo alone boasts 12 different species), they have been unable to cross the relatively narrow marine gap to New Guinea or

Australia (Brandon-Jones 1998). In fact, other than the macaques of Sulawesi and Lesser Sunda Islands and the leaf monkeys of Lombok (likely introduced by

humans), none of the Indonesian non-human primate species have been able to conquer the narrow Bali-Lombok strait (<40 km) of Wallace's Line (Brandon-Jones 1998).

Far from being the most 'conservative' option, the late date and trans-Atlantic rafting hypothesis of monkeys is actually the most fantastic. It is a deliberate theoretical preference, described as fact, that conflicts with the known distribution patterns of monkeys and would require one of the most extraordinary dispersal hypotheses in the his-



The banded iguana is only found on Tonga and the Fiji Islands. How did it get there?

World monkeys with a reference to the molecular analyses of Schrago and Russo (2003), who calibrate their molecular clock on an assumed Cercopithecoid-Hominoid split at 25 mya and calculate the divergence of New and Old World monkeys at 35 mya. Arnason *et al.* (1998, 2000) however note that even the traditionally assumed divergence at 30 mya for the Cercopithecoid-Hominoid lines is far too recent, for it suggests a diversification of Equidae and Rhinocerotidae at 28 mya, cetacean origin at 30 mya, and Eutheria origin at 80 mya. Each

tory of terrestrial mammals. Moreover, the assumption of this miraculous rafting event is then used as supporting evidence for dispersal miracles in general.

Another example of a 'conservative' assumption is that the vicariance hypothesis requires origin for freshwater cichlids prior to or during the Early Cretaceous while fossil and molecular clock evidence requires a Cenozoic origin. Each of these is disputable, if not dubious.

First, while the strip of Early-Cretaceous seafloor between Madagascar and Africa does require their separation at that time, the lack of similarly-aged Indian Ocean seafloor north of this strip *does not* suggest that *India* was also similarly

these Eocene fossil cichlids not only effectively doubled the age of the family (Murray 2000), indicating that 'as time goes on' the chance of such finds does not necessarily become 'less probable,' but also that these fossil cichlids represent derived African lineages (Murray 2001; Sparks 2004), suggesting a significantly older origin for the family'.

Third, the molecular clock analysis of Vences *et al.* (2001), which is at odds with the analysis of Kumazawa *et al.* (2000), has been challenged by Chakrabarty (2004) because it relies on cichlids of the East African Lakes for calibration. As Chakrabarty writes, '[The] wide estimates of ages for the lakes, and

hours (Riseng 1997).

2. Cichlids have been unable to reach any oceanic island and have a predominantly Gondwanan distribution, showing the precise sister relationships predicted by vicariance: Africa-South America and India-Madagascar. The dispersal hypothesis requires freshwater cichlids to have negotiated thousands of kilometers of open ocean between India and Madagascar without colonizing any other island or, for that matter, crossing the Mozambique Channel to Africa. Apparently, these taxa like to confine their oceanic jaunts between regions that were once connected.

In both analyses involving monkeys and cichlids, the molecular and geological assumptions required for long distance dispersal have been independently challenged while the distributional evidence remains unambiguous. Thus, what was true in the middle of the 20th century is still true today, radical dispersalist hypotheses result from the elevation of disputed non-biogeographical assumptions and theory over uncontroversial biogeographical facts.

Pacific biogeography

Nowhere is the practice of subordination of biogeographical evidence more common than along the Pacific margins. As recently noted, a myriad of trans-Pacific disjunct taxa, both fossil and extant, link narrowly defined systems of sister areas on opposite sides of the Pacific, with each particular region from Tierra del Fuego to Canada showing a clear biological link to a corresponding Western Pacific region from Stewart Island to Japan (McCarthy 2003). A few examples of disjunct sister taxa from New Zealand and South Chile include: the flat oyster, *Ostrea chilensis*, which does not have an extended pelagic phase (O'Foighil *et al.* 1999), and the plant genus *Abrotanella*, which lacks the typical method of dispersal in the family,

In fact, as little to no ocean floor currently exists that could have separated India from Asia and Africa during the Late Cretaceous, there is no geological reason to assume significant Late Cretaceous separation of these regions at all.

separated from either Africa or South Asia. In fact, Briggs (2003a), who de Queiroz references for his conclusions about cichlids, has himself challenged this conventional view, concluding that Cretaceous Indo-Madagascar biogeography demands that 'the depiction of India in late Cretaceous as an isolated continent is in error'. Briggs instead shrinks the hypothetical Cretaceous Tethys gap by assuming a larger Indian continent that was greatly shortened during Himalayan orogenesis. In this way, 'India, during its northward journey, remained close to Africa and Madagascar even as it began to contact Eurasia'. In fact, as little to no ocean floor currently exists that could have separated India from Asia and Africa during the Late Cretaceous, there is no geological reason to assume significant Late Cretaceous separation of these regions at all.

Second, as Sparks and Smith (2005) argue: 'the discovery of

the fact that the lineages within the lakes may not be the same age as the lakes themselves (Meyer *et al.* 1991; Nishida 1991), make this molecular clock calibration suspect'. Chakrabarty concludes from his review of phylogenetic analyses that vicariance is 'the only explanation'.

Both the geological assumption of a wide Late Cretaceous Tethys and the molecular-clock and fossil-based assumptions of the late timing of the divergence would have to be true in order to necessitate a cross-ocean dispersal event of cichlids. But while each of these assumptions has been recently challenged (and in my view the notion of a wide Late Cretaceous Tethys has been all but refuted), the following distributional and biophysical facts about cichlids, all underscored by Sparks and Smith (2005), remain:

1. The only study done on saltwater tolerance of Malagasy cichlids confirmed that their exposure to saltwater was 100% fatal after 12

the pappus (Heads 1999). The most recent fossil relatives of the only living sphenodon, New Zealand's lizard-like, Tuatara are the Late Cretaceous sphenodontians of Patagonia (Apesteguia and Novas, 2003). Further north, the freshwater-restricted sisters, *Brachygalaxias* and *Galaxiella*, are limited to south-central Chile, Tasmania, and Southwestern Australia (Waters et al, 2000). The neotropical sun bittern (*Eurypyga helias*) is the closest relative of the flightless kagu of New Caledonia and two extinct flightless species (*Apterornis*) from New Zealand (Cracraft 2001). Fiji's banded iguana *Brachylophus* is sister to the Californian iguanid *Dipsosaurus* (Sites et al. 1996) and iguanas occur nowhere else in the Central or West Pacific. This is just a small sampling of hundreds of narrow-range, poor-dispersing trans-Pacific disjunctions that do not appear on any intervening oceanic island and strictly adhere to a common distributional pattern (McCarthy 2003).

To focus on a single example: the disjunction of the Fijian banded iguana and its Californian sister requires, according to conventional paleomaps, an 8000 - 12000 km rafting trip, mostly over hypothetical (i.e., currently non-existent) seafloor. This is more than three times longer than the now forsaken trans-Atlantic rafting trips put forth to save continental stabilism. This hypothetical trip would be the greatest oceanic jaunt of any taxon in the history of terrestrial vertebrates - and by far. Yet the banded iguana is restricted to Fiji-Tonga and appears on no other oceanic islands. Given that so many other taxa share the same tropical Western America - Western Pacific distribution, it is difficult to imagine a stronger biogeographical argument for vicariance. If a cross-Panthalassa rafting hypothesis does not strain credulity, then what dispersal hypothesis would?

Rafting vertebrates and distributional evidence

As stated earlier, many of the trans-Pacific disjunct taxa, like the banded iguana, the flat oyster *Ostrea chilensis*, the flightless kagu, the Tuatara, the plant genus *Abrotanella*, etc., are restricted to a very narrow Western Pacific range and absent from all other oceanic islands. Not only do the biophysical limitations of these taxa imply that they cannot cross the full extent of oceans, but their absence from all other purely oceanic islands confirms their difficulty with wide marine gaps. The importance of such evidence today is not simply ignored but openly challenged by those who support miraculous dis-

The points and counter-points of this debate have not changed much since the nineteenth century. The evolutionary assumption of common descent, like the hypothesis of vicariance, predicts that certain continental poor dispersing taxa will be absent from oceanic islands. Both theories require very clear distributional patterns, particularly involving poor-dispersers. Contrariwise, neither the theory of independent creation nor the theory that all these disjunct vertebrates are capable of oceanic jump-dispersal, offers a rational explanation for this pattern of island truancy. The aforementioned reviewer who rejected this argument claimed that absence is only partly due to dispersal ability and 'that all sorts of other factors

If a cross-Panthalassa rafting hypothesis does not strain credulity, then what dispersal hypothesis would?

persal events.

Recently, a paper submitted to a biogeographical journal noted the absence of a variety of alleged trans-oceanic dispersers from oceanic islands - and the reviewer, who suggested rejection, challenged the significance of such absences with the comment: 'Biogeography is not about things that haven't happened'. More than 140 years after Darwin first explained the theoretical significance of the absence of terrestrial mammals and amphibians from remote oceanic islands, modern 'biogeographers' are now contending that their subject is not concerned with such matters. Likewise, more than 60 years after du Toit challenged the hypothesis of cross-Atlantic rafting, which was used to rescue the hypothesis of a wide Mesozoic Atlantic, biogeographers are now positing rafting events across a gap nearly three times wider in order to rescue the hypothesis of a wide Mesozoic Pacific.

are involved, involving an amalgam of geology, climate, evolution, ecology, and history'. This is precisely the counter-argument Darwin anticipated from those favoring independent creation, which is why he was careful to note that such absences from oceanic islands 'cannot be accounted for by their physical conditions; indeed it seems that islands are peculiarly well fitted for these animals'. And Darwin is still correct. The most likely reason for the distributional pattern of monkeys and banded iguanas is *not* because of a conspiracy of local environmental circumstances that has somehow prevented long-term colonization of every other oceanic island in the world. The most reasonable explanation probably has to do with the fact that monkeys and banded iguanas drown -- so they cannot reasonably be expected to cross the full extent of an ocean. Analogous arguments hold for cichlids, *Ostrea chilensis*, *Abrotanella*, etc. Quite simply, the reason why all these

taxa appear both biophysically and distributionally to be isolated by wide marine gaps is because they are, in fact, isolated by wide marine gaps. It's not a coincidence.

Du Toit also seemed aware of the connection between the debate over vicariance and Darwin's past arguments against special creation, which is likely why he contended that the hypothesis of rafting across the wide oceans, i.e., the rejection of vicariance, 'evinces ... a weakening of the scientific outlook, if not a confession of doubt from the viewpoint of organic evolution.' In other words, supposing that the trans-Atlantic fossil sister taxa were always disjunct re-opens the door to theorists of special creation who had argued precisely the same thing.

McDowall (2004) challenged the seeming triviality that taxa that can cross the full extent of an ocean are likely to be wide ranging and found on other oceanic islands, by referencing a single counter-example: a diadromous fish that had merely crossed the Tasman Sea to New Zealand and had also colonized 'islands to the north.' This taxon, however, is not relevant to the claim that numerous taxa can traverse the full breadth of the ocean yet remain restricted to only two narrow regions.

This 'cross-Pacific dispersal/wide ranging' dispute need not foster endless debate amongst the litigants, for, in the end, empirical evidence raps the gavel. Kingston *et al.* (2003) have recently provided a comprehensive analysis of range data for each of the 114 species of flora on Pitcairn. Since Pitcairn is a juvenile oceanic island group that formed in the middle of the ocean, long-distance trans-marine dispersal is required for all inhabitants. According to Kingston *et al.* (2003): 'The flora of the Pitcairn Islands is derived from the flora of other island groups in the south-eastern Polynesian region, notably those of the Austral, Society and Cook Islands. Species with a Pacific-wide

distribution dominate the overall Pitcairn group flora'. They also note that Pitcairn, unlike New Zealand, *did not exclusively share any plant with South America*. Instead, all plants that had colonized both Pitcairn and South America had also managed to disperse across the full breadth of the Pacific. For example, *Asplenium obtusatum* G. Forst, found in both Pitcairn and South America, also occurs in Easter Island, Polynesia, New Zealand, and Australia. None of the 114 species were poor dispersers. None were

Pacific can annex nearer regions too. Often, the nearer regions are used as stepping stones. A handful of exceptions may exist, but one should not mingle exceptions with the overwhelming rule.

The following table comprises the terrestrial vertebrates and freshwater fish that are currently assumed to have crossed the full extent (more than 3000 km) of an ocean barrier. When different analyses have provided different dispersal dates, the most recent one was chosen (Table 1).

Taxon	Regions	Earliest assumed date of divergence	Reference
<i>Tarentola</i> geckos	Africa and Cuba	23 ma	de Quieroz (2005)
Monkeys (Platyrrhini)	Africa and South America	35 ma	de Quieroz (2005)
Caviomorph rodents	Africa and South America	35-31 ma	de Quieroz, (2005)
Cichlids	Africa and South America	41-58 ma	de Quieroz (2005); Vences <i>et al.</i> (2001)
Cichlids	India and Madagascar	25-29 ma	de Quieroz (2005); Vences <i>et al.</i> (2001)
Aplocheiloid killifishes	Africa and South America	Early to Mid Tertiary	Briggs (2003b)
Aplocheiloid killifishes	India and Madagascar	Early to Mid Tertiary	Briggs (2003b)
Boine snakes	South America and Madagascar and East Asia	Paleocene or earlier	Vences <i>et al.</i> (2001)
Iguanines	South America and Madagascar	Cenozoic	Vences <i>et al.</i> (2001)
Podocnemine turtles	South America and Madagascar (and perhaps Africa)	Cenozoic	Vences <i>et al.</i> (2001)
Agamid lizards	Australasia and South East Asia (across the Tethys)	30 ma	Hugall and Lee (2004)
Banded iguana	California and Fiji	Eocene (?)	Sites <i>et al.</i> (1995)

born of narrow range ancestors that appear in only one other distant continental region.

This empirically confirms that which had otherwise seemed self-evident: Taxa that are able to colonize the remoter regions of the

Table 1. Distribution ranges of taxa.

The preceding distributional hypotheses, as well as the evidence provided by oceanic islands, suggest a series of distributional patterns that require explanation:

Even accepting molecular clock

assumptions that provide the most recent dates of divergence, no terrestrial vertebrate has managed to cross an ocean (>3000 km) in the last 20 my - despite numerous alleged trans-oceanic dispersals prior to that.

No terrestrial vertebrate has managed to disperse to a juvenile (pre-Eocene) oceanic island more than 2000 km from a source (perhaps no more than 1500 km).

All of the seafloor barriers crossed by the taxa comprise crust that is almost all less than 83 my. The majority of the crust of these seafloor barriers is less than 40 my.

Every pair of regions (destination and source) are ancient regions that have recently been claimed to have been in proximity in the Late

got around to accepting continental drift, and our phylogeographic understanding was much distorted by this'. Yet even after the recent triumph of vicariance over the dominant stabilist paradigm in geology, some still tend to elevate geological speculation over basic distributional realities. Implicit in papers that indulge in extravagant dispersalism and a plethora of just-right fossil absences is the notion that the basic principles of biogeography are wispy and yielding while geophysical theories are made of sterner stuff. Such papers appear to extend the legend that planetary scientists work in a field devoid of speculation, the belief that when a biogeographer and geologist confront each other on a narrow path, the biogeog-

requiring drastic alterations to orthodox views. Recent paleomagnetic studies of the Detroit seamount have falsified the long-accepted view, taught to a generation of grammar school students, that the Emperor-Hawaii seamount trend was the result of Pacific plate motion over a stationary hotspot (Wilson 1963). The Detroit seamount was actually determined to have a paleolatitude nearly 20 degrees north of conventional expectations (Tarduno *et al.* 2003; Sager 2002), revealing that hot spots are not really 'fixed'. Palaeostratigraphic, Palaeomagnetic and palaeobiogeographical data have also refuted the view of an oceanic (Tethyan) separation of South Asia and East Asia from India and Australia, respectively, in the Palaeozoic. Instead, the classic plate tectonic view of Pangaea has now been abandoned - and all of southern Laurasia, including South and North China are now placed adjacent to the Eastern Gondwana continents India and Australia during that time. Likewise, the long standing view of India as an isolated micro-continent in the middle of the Tethys in the Late Cretaceous has been rejected by Briggs (2003a) because of the oceanic gap this would place between a variety of terrestrial vertebrates. Briggs instead adopts an inflated-India (narrower Tethys) hypothesis which allows Africa, Asia, India, and Madagascar to remain in proximity in the Late Cretaceous. Also, the extreme Tethys gap between Australia and Southeast Asia in the Late Cretaceous has also been recently challenged due to biogeographical and geological reasons (McCarthy 2005). Palaeomaps, it seems, are like the weather: If you don't like the alleged size or placement of a pre-Cenozoic ocean, just wait a while. It will change.

But while new discoveries continue to change our views on the formation of planets, continents and oceans, we can at least take comfort in the firmness of very basic biogeog-

Palaeomaps, it seems, are like the weather: If you don't like the alleged size or placement of a pre-Cenozoic ocean, just wait a while. It will change.

Cretaceous for geological reasons, including Africa-India-Madagascar (Briggs, 2003a), Fiji - Neotropics (McCarthy, 2003), Australasia - Southeast Asia (McCarthy, 2005).

The most likely explanation for these distributional facts is *not* that pre-Miocene vertebrates were better rafters and preferred to jump-disperse between ancient regions that were once in proximity. A more reasonable explanation is that the papers disputing the geological palaeomaps and molecular clock assumptions are, in fact, correct.

Geology, a speculative science

In a paper published posthumously, the Australian botanist L.A.S. Johnson (1998) introduced his historical analysis of Proteaceae biogeography with an interesting admission regarding his first views on the subject: 'Unfortunately, at the time we wrote this paper [on Proteaceae], we were misled by conservative geologists who had not

rapher must step aside. But the question Wegener and du Toit may well have asked half a century ago is still apropos today: Does any scientist, from any field, really believe that we know more about the formation and inner workings of planets than about the locations, habits, relationships, and biomechanics of plants and animals -- about taxa that we have watched and held and explored inside and out?

The fact of the matter is geology, geophysics, and planetary science are, by no means, settled subjects. Recently in the 125th Anniversary edition of journal *Science* (Vol. 309 [5731], 2005) a list of '125 Questions: What don't we know?' was put forth. Two of those questions were 'How do planets form?' and 'How does Earth's interior work?' Forty years ago the discovery of seafloor spreading revolutionized geological theory, revitalizing the long-rejected theory of continental drift. But even over the last decade, many long standing geological assumptions have been falsified,

graphical realities, like, for example, that terrestrial vertebrates drown and oceans are vast. This is why past scientific revolutionaries chose to focus on the 'grand subject' of distributions rather than remain faithful to the conventional assumptions of other fields of science.

Biogeography is really where the facts are - indeed the simplest facts of all. Wegener and du Toit faced ridicule for not accepting certain conventional geological assumptions, but no amount of authority can overcome the following elemental fact: Terrestrial vertebrates cannot cross oceans. That is why they do not appear on remote oceanic islands (>2000 km from a source). That is why we know they have not been able to cross an ocean in the last 20 million years. Their difficulty with wide marine gaps was obvious when Darwin used it as evidence for evolution; it was obvious when Wegener and du Toit used it as evidence for a closed Atlantic and Indian Oceans; and it is still obvious today. The 'grand subject' of geographical distributions is once again about to triumph over conventional assumptions in other fields of science.

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Dennis McCarthy will be presenting a talk at the SA Biennial Symposium in Cardiff, 2005.

Meeting Report

The Palms: an International Symposium on the Biology of the Palm Family

The Linnean Society, London and the Royal Botanic Gardens, Kew
April 6-8 2005

For an angiosperm family of relatively modest size (2361 species at the last count; Govaerts & Dransfield 2005), the palms appeal to a disproportionately large number of researchers in a plethora of different fields. Explanations for interest in the family are typically wrapped up in brave boasts such as 'palms are second only to the grasses in economic importance', though our legume colleagues might disagree, or the more romantic 'palms are emblematic of the tropics'. Regardless of the factual basis of such rhetoric, there is no doubt that palms have a special appeal that accounts for the impressive turnout at the recent international symposium on the biology of the family. More than 100 delegates from 22 different countries came to London in April this year for two days of talks at the Linnean Society and a day of workshops and tours at Kew.

In the opening lecture of the structural biology session, Barry Tomlinson (Harvard University) tackled 'the Uniqueness of Palms' head on from the perspective of functional morphology, exploring the opportunities and limitations of arborescent life within monocotyledonous constraints. He highlighted several record-breaking features of the family, some well known, such as the largest leaves and largest seed, and others less widely trumpeted. In particular, Barry detailed the astonishing corollary of a palm's

commitment to stem-building by primary growth alone: stem vasculature remains indefinitely functional over very extended periods. Given the exceptionally long life spans of some palm species, up to 720 years in *Livistona eastonii* (Hnatuik 1977) for example, this feature further underlines the record-breaking tendencies of this champion family.

The four talks that followed Tomlinson's further emphasised the remarkable structural properties of palms. Paula Rudall (Royal Botanic Gardens, Kew) approached palm floral morphology within the broader context of monocot flowers, focusing in particular on isolated taxa such as *Nypa* and *Eugeissona*. James Tregear (IRD, Montpellier) followed on with a report of his research group's activities in floral developmental genetics in palm oil; detailed work on MADS box genes suggests that some, but not all elements of the ABC model can be applied to palms. Still within the palm flower, Sophie Nadot (Université Paris-Sud) illustrated the surprising diversity of developmental patterns in monosulcate pollen types in palms. Sandrine Isnard (AMAP, Montpellier) concluded the session with a further ego boost to the palm community with her elegant examination of the outstanding biomechanical strategies of climbing palms, particularly in *Plectocomia*.

The phylogeny and evolution sessions commenced with a review of the palm fossil record by Madeline Harley (Royal Botanic Gardens, Kew). The palms have the richest fossil record in the monocots (sorry, another superlative), but as Madeline showed, this should not be interpreted as evidence for great age. The palms, in fact, do not appear unequivocally until the Santonian/Coniacian boundary in the late Cretaceous, some 40 million years later than the earliest monocot fossil, *Mayoa* attributed to Araceae (Friis *et al.* 2004). Aaron Pan (Southern Methodist University,

Dallas) looked in detail at the African fossil record. The modern African palm flora (excluding Madagascar) stands out as it is relatively depauperate, but the fossil record indicates that a much richer palm flora may have once occurred there. Aaron's analysis strongly suggests that the decline in African palms occurred through the Palaeogene, not, as is widely thought, through extinctions during dry periods in the much more recent

his collaborators. Finn Borchsenius presented some of the cutting edge activities developing in the University of Aarhus on delivering taxonomic information to a wide range of users through the web. Andrew Henderson (New York Botanical Garden) provided a controversial view of palm taxonomy based on his recent experiences of applying morphometric techniques, all of which have resulted in substantial increases in numbers of

first three by Edwino Fernando (University of the Philippines, Los Baños), Saw Leng Guan (Forest Research Institute, Malaysia) and Rodrigo Bernal (Universidad Nacional de Colombia, Bogota) demonstrated that for those regions in which palm expertise resides, there is reason to be optimistic about the future of palms and palm habitats. All three detailed their strong grasp of patterns of diversity and threat, and are actively participating in national conservation policy making. It seems unlikely, however, that the same can be said for many other palm diversity hotspots that lack such expertise and interest. Terry Sunderland (WCS, Limbe Botanical Garden) closed the session with his presentation of problems and opportunities in African palm resource management, and concluded with a fitting link back to sound taxonomy as the key to effective sustainable management of threatened forest products.

The day of workshops and tours at Kew was sandwiched between the two days of talks. Four workshops were held, paralleling the main themes of the formal programme of lectures. We saw a high degree of participation in all workshops, with some debates becoming heated, though thankfully without acrimony. Participants were given the opportunity to relax in the afternoon while Kew staff showcased the rich living palm collections in the two great Victorian conservatories, the Palm House and the Temperate House. During a boozy reception in the Palm House, we found an opportunity to embarrass John Dransfield, the World authority on palm taxonomy, recent Linnean medallist and former head of palm research at Kew in whose honour the meeting was held. A surprise planting of a new genus of palm soon to be named after John was captured by a BBC film crew for the 'Year at Kew' series. At the conference dinner later that night, the guest speaker, Sir Ghilleen Prance, paid further

Aaron's analysis strongly suggests that the decline in African palms occurred through the Palaeogene, not, as is widely thought, through extinctions during dry periods in the much more recent Pleistocene.

Pleistocene. Three talks by Conny Asmussen (Royal Veterinary and Agricultural University, Copenhagen), Bill Baker (Royal Botanic Gardens, Kew) and Carl Lewis (Fairchild Tropical Botanic Garden, Miami) addressed matters systematic and biogeographic within phylogenetic frameworks. Conny presented a very thorough phylogeny that forms the basis of a new classification of the palms into five subfamilies, one fewer than the current arrangement. Bill used supertree and supermatrix methods to arbitrate between competing published datasets, generating a complete phylogeny of all palm genera that, when dated, supported the idea advanced by the fossil record, that the palms diverged from other monocots in the late Cretaceous. Carl Lewis brought us down the taxonomic scale to look at genus delimitation and phylogeny in Caribbean palms and this was followed by an exhilarating tour of the biogeographic history of the coconut by Hugh Harries (Royal Botanic Gardens, Kew).

The second day of talks maintained the systematic theme, firstly with a presentation of the forthcoming phylogenetic classification of the palm family by John Dransfield (Royal Botanic Gardens, Kew) and

species recognised.

Turning to palm ecology, Stine BJORHOLM (University of Aarhus) and Rommel MONTUFAR (IRD, Montpellier) provided insights into patterns of diversity in neotropical palm floras at different scales. With an added phylogenetic systematic component, Stine provided compelling evidence for the diverse biogeographical origins of the clades that make up the American palm flora. Marie-Charlotte ANSTETT (CNRS, Montpellier) gave an overview of palm pollination, including some of her exciting work on the European fan palm, *Chamaerops humilis*, which has been found to attract pollinators not by scent emitted from the flowers, but from the leaves instead. Mauro GALETTI (Universidade Estadual Paulista, Sao Paulo) provided a perfect transition to the conservation focus of the final session by exploring the impact of fragmentation and loss of seed dispersers on palms in Brazil. His work reached the alarming, but inevitable conclusion that palms that depend on scatterhoarding rodents for seed dispersal may become regionally extinct if forest fragmentation and hunting pressures persist.

Of the four talks in the conservation and sustainable use session, the

tribute to John as an outstanding botanist and fieldworker and an inspiration to colleagues and generations of students, many of whom have become leaders in plant diversity research in tropical countries.

This conference proved that research on palm biology is global, youthful and in very good shape. A large proportion of the participants were either students or from developing countries (or both!) Thanks to the generous support of the Systematics Association, the Annals of Botany, the Linnean Society and the Royal Botanic Gardens, Kew, we were able to provide low registration rates for students and nine bursaries for participants from developing countries. In addition to the programme of oral presentations, more than 40 posters were presented on a host of subjects. This meeting was partly born out of an established network of European palm specialists (EUNOPS - the European Network of Palm Scientists), now approaching its sixth annual meeting. The relaxed and friendly ethos of EUNOPS infiltrated this larger meeting and has created a precedent for open, international meetings on palms in the future. A second meeting, in Brazil, has already been proposed. I'm packing my suitcase already...

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Bill Baker,
Royal Botanic Gardens,
Kew

Spotlight

Automated Object Recognition in Systematics

Norman MacLeod and Stig A. Walsh Natural History Museum, London, UK and Mark O'Neill University of Newcastle upon Tyne, Newcastle, UK

The automated identification of biological objects (individuals) and/or groups (e.g., species, guilds, characters) has been a dream among systematists for centuries. The goal of some of the first multivariate biometric methods was to address the perennial problem of group discrimination and inter-group characterization. Despite much preliminary work in the 1950s and 60s, progress in designing and implementing practical systems for fully automated object identification has proven frustratingly slow. As recently as 2004 Dan Janzen updated the dream for a new audience.

'The spaceship lands. He steps out. He points it around. It says

ple.' However, recent developments in computer architectures, as well as innovations in software design have finally placed the tools needed to realize Janzen's vision in the hands of the systematics community not in several years hence, but now; and not just for DNA barcodes, but for digital images of organisms too. A recent survey of accuracy results for small-scale trials (<50 taxa) obtained by such systems (Gaston and O'Neill 2004) shows an average reproducible accuracy of over 85 percent with no significant correlation between accuracy and the number of included taxa or the type of group being assessed (e.g., butterflies, moths, bees, pollen, spores,

As all readers of this newsletter know, the world is running out of specialists who can identify the very biodiversity whose preservation has become a global concern.

'friendly-unfriendly-edible-poisonous-safe- dangerous-living-inanimate'. On the next sweep it says '*Quercus oleoides* - *Homo sapiens* - *Spondias mombin* - *Solanum nigrum* - *Crotalus durissus* - *Morpho peleiades* - serpentine'. This has been in my head since reading science fiction in ninth grade half a century ago' (Janzen 2004: 731).

Janzen's preferred solution to this classic problem involved building machines to identify species from their DNA. His predicted budget and proposed research team is 'US\$1 million and five bright peo-

foraminifera, dinoflagellates, vertebrates). Moreover, these identifications-often involving thousands of individual specimens-can be made in a fraction of the time required by human experts and can be done on site, on demand, anywhere in the world.

These developments could not have come at a better time. As all readers of this newsletter know, the world is running out of specialists who can identify the very biodiversity whose preservation has become a global concern. In commenting on this problem in palaeontology as

long ago as 1993, Roger Kaesler recognized ...

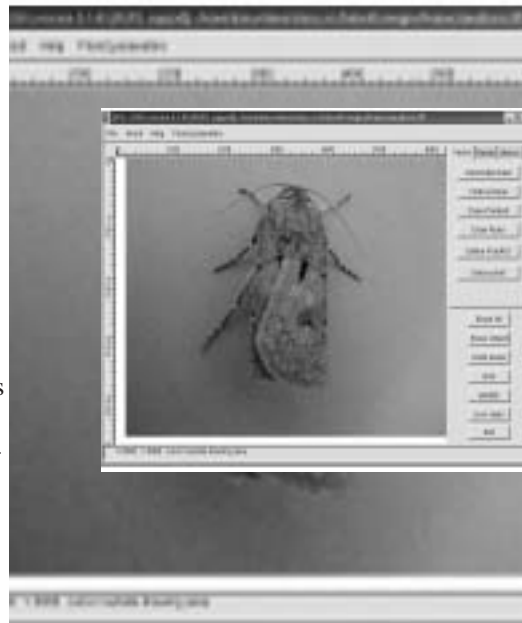
'... we are running out of systematic paleontologists who have anything approaching synoptic knowledge of a major group of organisms ... Paleontologists of the next century are unlikely to have the luxury of dealing at length with taxonomic problems ... [palaeontology] will have to sustain its level of excitement without the aid of systematists, who have contributed so much to its success' (Kassler 1993: 329-330).

This expertise deficiency cuts as deeply into those commercial industries that rely on accurate identifications (e.g., agriculture, biostratigraphy) as it does into a wide range of pure and applied research programmes (e.g., conservation, biological oceanography, climatology, ecology). It is also commonly, though informally, acknowledged that the technical, taxonomic literature of all organismal groups is littered with examples of inconsistent and incorrect identifications.

This is due to a variety of factors, including taxonomists being insufficiently trained and skilled in making identifications (e.g., using different rules-of-thumb in recognizing the boundaries between similar groups), insufficiently detailed original group descriptions and/or illustrations, inadequate access to current monographs and well-curated collections and, of course, taxonomists having different opinions regarding group concepts. Peer review only weeds out the most obvious errors of commission or omission in this area, and then only when an author provides adequate representations (e.g., illustrations, recordings, gene sequences) of the specimens in question.

Systematics too has much to gain, both practically and theoretically, from the further development and use of automated identification systems.

It is now widely recognized that the days of systematics as the field of eccentric individuals, pursuing knowledge in splendid isolation from funding priorities and economic imperatives are rapidly drawing to a close. In order to attract both personnel and resources, systematics



Example of the DAISY System interface with a region of interest located on the moth wing. For this group, wing colouration pattern is the primary taxonomic character complex.

must transform itself into a 'large, coordinated, international scientific enterprise' (Wheeler 2003: 4). Many have identified use of the internet—especially via the world-wide web—as the medium through which this transformation can be made. While establishment of a virtual, GenBank-like system for accessing morphological data, audio clips, video files and so forth would be a significant step in the right direction, improved access to observational information and/or text-based descriptions alone will not address either the taxonomic impediment or low identification reproducibility issues successfully. Instead, the inevitable subjectivity associated with making critical decisions on the basis of qualitative criteria must be reduced or, at the very least, embedded within a more formally analytic context. Properly designed,

flexible, and robust, automated identification systems, organized around distributed computing architectures and referenced to authoritatively identified collections of training set data (e.g., images, gene sequences) can, in principal, provide all systematists with access to the electronic data archives and the necessary analytic tools to handle routine identifications of common taxa. Properly designed systems can also recognize when their algorithms cannot make a reliable identification and refer that image to a specialist (whose address can be accessed from another database). Such systems can also include elements of artificial intelligence and so improve their performance the more they are used. Most tantalizingly, once morphological (or molecular) models of a species have been developed and demonstrated to be accurate, these models can be queried to determine

which aspects of the observed patterns of variation and variation limits are being used to achieve the identification, thus opening the way for the discovery of new and (potentially) more reliable taxonomic characters.

In order to summarize the current state-of-the-art in automated group-recognition systems and assess their potential to make practical contributions to systematics and taxonomy both now and into the future, the Systematics Association and The Natural History Museum (London) have agreed to jointly sponsor a free, one-day symposium entitled *Algorithmic Approaches to the Identification Problem in Systematics*, to be held in the Flett Theatre of The Natural History Museum, London on August 19 2005. The purpose of this symposium—which is part of The

Systematics Associations Biennial Meeting-is to provide leaders of research groups, researchers, and students working or studying in any area of systematics with an opportunity to 1. learn about current trends in quantitative approaches to the group-recognition problem, 2. become familiar with the capabilities of various software systems currently available for identifying systematic objects/groups and, 3. evaluate various applications of this technology to present and future systematic problems. Special attention will be paid to showing how different approaches to automated identification can be applied to various organismal groups and in various applied research contexts (e.g., biodiversity studies, biostratigraphy, conservation, agriculture, curation). A book in The Systematics Association's Special Volume Series will also be produced from the edited proceedings. Details of the symposium, along with a complete programme of the presentations, are available on the website: http://www.nhm.ac.uk/hosted_sites/paleonet/aaips_symposium/. All are invited to attend.

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For information about please visit the Systematics Association website www.systass.org

Book Reviews

Millstones on Systematics

A review of Williams DM. and Forey PL. (eds.) 2004. *Millstones in Systematics*. Systematics Association Special Volume Series 67. CRC Press, Florida

Millstones is based on an interesting premise to 'invite contributors who had first-hand experience of the changes in systematic practice that were taking place in the last third of the twentieth century' to record and reflect upon the meaning of that period of history. The eleven chapters are remarkably diverse in perspective. Mary Winsor suggests that scientists writing history usually 'hope to foretell or even influence the future, a motive uncongenial to historians.' She makes her point vividly with two uncongenial examples based on work by Ernst Mayr on Charles Darwin and by Peter Sneath on Michel Adanson; in each

nometic crisis' might have been mitigated if some of his message had been heard. The wholesale support and promotion of molecular phylogenies at the expense of Linnaean classifications and formal nomenclature might have been avoided with some common sense, forethought, and respect for that which came before. I was left feeling that Blackwelder may have been somewhat short-changed by Cain, too. His reading of Blackwelder's biased views in the context of the SSZ are well documented and seemingly irrefutable; however, had Cain put this formative episode in its broader historical context, I wonder whether Blackwelder might have fared better. In particular, it now seems clear in retrospect that Mayr and the 'New Systematics' succeeded in undermining the core goals of systematics, not to mention taxonomy (Wheeler 1995). Perhaps Blackwelder's fear and loathing were better founded than a look at 1947 in isolation suggests.

Two chapters present some heavy philosophical arguments. The first, by Bock, contrasts nomological-

... it now seems clear in retrospect that Mayr and the 'New Systematics' succeeded in undermining the core goals of systematics, not to mention taxonomy.

case they get history wrong but succeed, at least momentarily, in advocating a particular position. I have found Winsor's works in the past to be very scholarly and thought provoking; this chapter was no exception.

Joseph Cain's account of the formation of the *Society of Systematic Zoology* (SSZ) in 1947 was a story of biased conflict and intrigue. At the height of the battles among cladists, evolutionary taxonomists and pheneticists, Blackwelder's lone voice for traditional taxonomy seemed anachronistic at the time and was wholly muted by the din of war. In retrospect, the current 'taxo-

deductive explanations (N-DEs) with historical-narrative explanations (H-NEs) and concludes that of five primary areas of evolutionary theory, four are N-DEs while the one central to systematic biology -- i.e., the one dealing with classification, Haeckelian phylogenies, Hennigian cladograms, evolutionary histories of characters and clades, and historical biogeography -- is historical. The point Bock makes with H-NEs is that most of systematic biology is concerned with descriptions of singular historical events and that testability may not apply in the way that many systematists have suggested. I was uncon-

vinced by Bock's distinction and conclusions. Virtually every aspect of evolution is pieced together from patterns or sequences of events (or observations) and many of his N-DEs represent an accepted ontological view rather than a realistic account of how evolution is actually pieced together (e.g., Nelson and Platnick 1981). His claim that the 'phylogeny of groups of organisms deal with singular events' is not so; many species and nearly all clades

because of the elegant simplicity of the all-or-nothing statements made by cladists about characters (Nixon and Wheeler 1992).

For me, the most important message in the book emerged from a surprising combination of seemingly unrelated chapters. With apologies for marginalizing other important aspects of each chapter, it was striking that Rieppel, Wägele and Nelson all draw attention to the importance and centrality of charac-

William Diller Matthew's writings of the 1920s. Matthew was convinced that phylogeny could be read simply and confidently from the fossil record; a claim that resonates loudly, and with similarly indefensible authority, in more recent claims about molecular sequence data by, for example, Avise (2000). When the fervour of political correctness subsides and the history of the 21st century is written, this observation by Nelson shall be seen in retrospect as prophetic.

From all these authors we are reminded just how little attention has been paid to characters for several decades. The shift from a *a priori* character polarity hypotheses to global character analysis and *post hoc* polarity inferences (see Wägele) paved the way for the arrival of abundant molecular data and the demise of comparative morphology. The entire emphasis shifted to: 'How are trees generated from the matrix?' and 'How is one tree chosen from a sea of nearly equally parsimonious ones?' As a result, we lost the plot. The complex characters of evolution that we set out to explain and understand are no longer studied in detail and are sidelined for more rapidly analyzable data that lacks such inherent interest and distracts from that which is most intellectually exciting. As Nelson suggests, we have much yet to learn from a returned emphasis on character analysis and a cladistic revolution to complete. It is worth noting, too, that one of the most promising interfaces for character analysis is with developmental biology, quite possibly an intellectually richer place to focus molecular work so as to bridge the continued gap between our understanding of genotype and phenotype. Ultimately, our understanding of and appreciation for evolutionary history will depend upon continued high-quality comparative morphology, revising and testing existing homology hypotheses and exploring the complex structural diversity of the 75% or more

I do note that some philosophers make compelling arguments that the dichotomy between falsification and verification is a false one and that these merely describe two sides of the same coin.

are characterized by an accumulated set of character transformations most of which occurred as separate evolutionary events, not as one. At least a loose analogy can be drawn to experimental biology where repetitive experiments are also merely a series of singular recorded events. The second, by Rieppel, argues that Popperian falsificationism is not applicable in the context of cladistics. Rieppel argues that a necessary link between phylogenetic hypotheses and the distribution of characters on trees does not exist, with a resulting absence of the necessary asymmetry between falsification and verification. Without that asymmetry, the justification for disconfirmation does not obtain. I confess that I have not spent the time that Rieppel has teasing this logic apart and will reserve judgment on Rieppel's central conclusion. I do note that some philosophers make compelling arguments that the dichotomy between falsification and verification is a false one and that these merely describe two sides of the same coin. Without taking sides (no pun intended), I merely add that if the kind of Popperian arguments so deeply engrained in 20th century cladistic literature do apply (see, e.g., Gaffney 1979) then it is

ter analysis in systematics and its widespread neglect. Rieppel admonishes us to 'Assume homology in the absence of contrary evidence, but contrary evidence is to be derived from a critical discussion of character hypotheses in themselves, not merely from the reciprocal relationships among all characters.' (p. 89). In an age characterized by global character analyses of a deluge of molecular base pair data, Wägele boldly asserts that 'Complexity of characters is the most significant criterion of homology' (p. 116). Nelson's chapter makes the point in an even stronger, if decidedly more sarcastic, way. Nelson's chapter is short but remarkably insightful; this is good stuff and well worth the multiple readings required to appreciate its full implications, not easily gleaned in one pass. For the critical thinker, his simple observation that 'evidence, not revelation, is the relevant concern' should be grounds enough to dismiss with any further consideration of the 'Vile-o-Code' (i.e., De Queiroz & Gauthier 1994) that persists in spite of thorough refutation (e.g., Carpenter 2003; Nixon et al, 2003). A light came on in my head when Nelson compared molecular phylogenies to palaeontologist



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of eukaryotic species that remain unknown to science.

Palaeontology appropriately retains a very special place in systematic thought. Early attempts to explain fossil remains were pivotal to the rise of modern systematic thinking. Countless examples exist where fossil taxa add uniquely to our understanding of systematics, character phylogeny and biogeography, making palaeontology of enduring importance. Palaeontology has had as tortuous a history as any field in the 20th century; changes in systematic theory being just one major force along with developments in geology and stratigraphy. Just as the genetics revolution of the 1930s sidelined taxonomy, so it detracted from the logical and critically important place of palaeontology. Forey points out the increasing importance of temporal arguments in cladistics, systematics and evolutionary biology and the continued conceptual issues surrounding the precise role of palaeontology.

I once heard a gentleman interviewed on a radio programme who had grown up in what is now Arizona at the beginning of the 20th century who quipped that 'The older I get, the better I was.' I will leave it to historians to determine whether Edwards had indeed identified and solved so many of the core issues of the field as he recalls and the extent to which this actually influenced the course of events over ensuing decades. This would not be the history I would write, nor would I conclude with Edwards that maximum likelihood is the 'optimum procedure' for systematic biology; such advice can only throw us back into the kind of slippery *ad hoc* hypotheses that prevailed among the evolutionary taxonomists into the 1970s. If you don't like the answer, you merely have to improvise with more 'realistic models of evolutionary divergence' to assure the desired outcome. To paraphrase Winston Churchill, this is a modest little chapter with much to be modest

about.

Returning to the challenge of making character analysis (and a focus on what goes into a matrix rather than merely deriving trees from it), a central part of systematics again, Williams' essay on homologues and homology is central to the way forward. Next to species concepts, the literature on homology must be among the most expansive and perennially important bodies of work in biology. Williams draws our attention to a distinction between homologue (as part) and homology (as relation) that dates from the time of Sir Richard Owen but that has been commonly muddled with the passage of time. This is one of the

Systematic biology seems to be at a crucial crossroads in its history. Rapid developments in digital technologies and cyber-infrastructure have opened a window of opportunity for revitalizing comparative morphology and descriptive taxonomy

better treatments of the history of this idea so central to systematic biology, an anchor of the volume, and yet another reminder of the undeniable importance of thinking about individual characters.

The chapter by Christopher Humphries on cladistic biogeography is another superb piece of history by one of the leading architects of modern biogeographic theory. Humphries details how the dispersalist paradigm, begun at the time of Linnaeus, has persisted to the present coexisting with subsequent cladistic perspectives. Humphries' chapter is an important retrospective of the 20th century developments in analytical approaches to biogeography, particularly those advances since Croizat's 1964 *Space, Time, Form: The Biological Synthesis*. Holland gives an historical analysis of the rise of evolutionary developmental biology, perhaps proving the point that some perspective is helpful in writing history; it may be that we are still too close to most of these developments to see them in

any challenging context. I would give much more credit to the closeness of developmental biology and evolution than Holland grants. Little reference is made to the great recapitulation controversies of the 19th century nor some important retrospectives on ontogeny and phylogeny in the 20th century (e.g., Gould 1977). The same arrogance about molecular techniques ridiculed by Nelson in the context of phylogeography surfaces again here; it might seem to the uncharitable reader that until a molecular biologist has rediscovered an idea it simply does not exist. How can you write a chapter on this subject in a book directed at systematic biologists and

not even mention Gareth Nelson's (1978) reformulation of the biogenetic law? I feel compelled to point out that the 'discovery' (p. 270) that there are ancient genes and not 'mouse genes' and '*Drosophila* genes' was pre-empted by Darwin, Hennig, and many others (arguably beginning with Linnaeus, if not Aristotle). If I may paraphrase Norman Platnick (1979) who said it best: all genes are inherited from an ancestral species in their original or some subsequently modified form. That is, all genes are 'ancestral genes', modified or not. Sadly, having been discovered through comparative morphology, this evolutionary history insight had to await molecular validation.

Systematic biology seems to be at a crucial crossroads in its history. Rapid developments in digital technologies and cyber-infrastructure (Atkins *et al.* 2003) have opened a window of opportunity for revitalizing comparative morphology and descriptive taxonomy (Wheeler 2004; Page *et al.* 2005) and for shed-

ding the weights that have held the field back for decades. This is a perfect chance to restore complex characters to centre stage where, as several authors in this volume suggest, they rightfully belong -- and an opportunity to identify and eliminate the impediments to necessary progress. Unless we understand how and why mistakes were made in the 20th century that arrested the logical development of systematics, how can we hope to avoid similar mistakes now or in the future? This book is far from a complete history of even the latter part of the 20th century with which it is explicitly concerned. Because no adequate history has been written of the enormously negative impacts of the 'New Systematics' from which the field is yet to fully recover, it is hard to do justice to subsequent historical developments. That said, this book is an important contribution to the history of systematics that has much to teach us about how we have arrived at where we are and the questions we must ask ourselves to plot the best course for the future.

The production values of the book are not as impressive as the contents but don't judge the book by its cheap feeling glossy cover or by its aesthetically offensive page layouts that have barely 9 mm at the bottom of many pages. Students and scholars alike will miss any marginal spaces for note taking. This unattractive printing is particularly unfortunate for a book about history that, more than many other titles, promises to have a very long shelf life.

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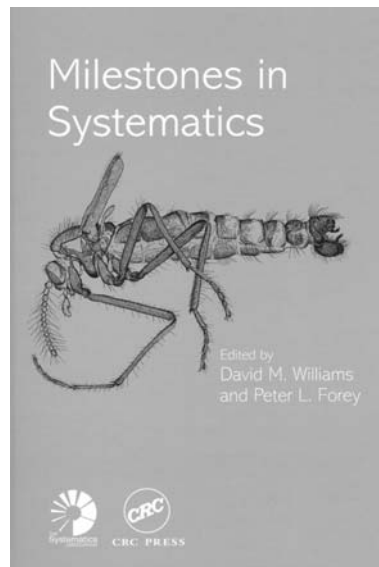
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A review of Hirt RP, Horner DS. (eds.) 2004. *Organelles, Genomes and Eukaryote Phylogeny: An Evolutionary Synthesis in the Age of Genomics*. CRC Press, Florida

This book of 16 chapters and 29 authors is number 68 in the Systematics Association series of Special Volumes. It might have been but is not the result of a particular meeting of the International Society for Evolutionary Protistology (ISEP), but is rather of continuing attempts to resolve the basal evolutionary branching of unicellular eukaryotic organisms (protists) and to improve the taxonomy of their kingdoms, phyla and classes. Its authors are mainly from the UK, Canada, Germany and France with one each from Australia, Croatia, Italy and the United States, all from universities with one exception

(Hirt) from the Natural History Museum, London. It features two chapters by Thomas Cavalier-Smith (Oxford), coincidentally the recipient of the International Prize for Biology 2004 (Japan Society for the Promotion of Science), awarded among other achievements for newly describing 'over eighty classes and almost twenty phyla' (www.jsps.go.jp).

As explained in the Overview (chapter 1, Horner & Hirt) protists are problematic. Some of their interrelationships prove to be different than originally proposed on the

diplomonads, parabasalids and other flagellates). 'Cavalier-Smith (1983, 1987) formulated the explicit hypothesis that these ... diverged before the acquisition of the mitochondrial symbiont. He united these groups as a taxon Archezoa' (subkingdom of Protozoa, p. 29). The hypothesis was subsequently supported by findings for SSUrRNA. The hypothesis soon unravelled when mitochondrial genes were found within the nucleus, implying transfer from the genome of previously existing mitochondria, and when enigmatic organelles, double-

informative title, 'Origin and evolution of animals, fungi and their unicellular allies (Opisthokonta).' They consider that the animal-fungi grouping is well established, but note molecular phylogeneticists who favor plant-fungi and plant-animal perspectives. They consider recent proposals to include within the clade (p. 110) 'a diverse collection of protistan taxa, also known as the Choanozoa (Cavalier-Smith, 1998b)', a subphylum within kingdom Protozoa. They also note that (p. 114) 'a single basal flagellum on reproductive cells is one of the few morphological disagnostics for Opisthokonta.' They consider other C-S protozoan phyla, Amoebozoa and Apusozoa, as likely sister groups, and a basal branching of eukaryotes into opisthokonts, on the one hand, and on the other 'the modern Amoebozoa, Apusozoa and the rest of the eukaryotes.' Their concluding vision is that 'if animals and fungi are indeed as old as the new rooting of the eukaryote tree suggests, then it is also to be expected that many taxa have branched off these lines before multicellularity evolved, some of which should still be extant and awaiting discovery' (p. 122).

'Pitfalls in tree reconstruction' is the thoughtful theme of chapter 6 (Gribaldo and Philippe), who observe a troubling finding: 'with the completion of genome sequences from representatives of the three domains [Archaea, Bacteria, Eucarya], it has become evident that trees based on alternative markers are largely in contradiction with the SSUrRNA phylogeny as well as with each other, weakening the general consensus.' They locate the troublesome causes both in biology (lateral gene transfer, hidden paralogy) and in 'tree-reconstruction artefacts,' particularly highlighting the sobering fact that 'all the markers used to infer universal trees appear to be saturated mutationally' (p. 135). They spell out the consequences: 'this leads to

Conceptually, this volume stems from the situation of the 1980s, when some thousand nucleated species were thought primitive in lacking mitochondria (pelobionts, entamebas, microsporidians, diplomonads, parabasalids and other flagellates)

basis of sequences derived for the small subunit of ribosomal RNA (SSUrRNA) -- the basis for the 'universal tree of life' that germinated in the 1980s and that has been growing ever since its early incubation by Carl Woese. Accordingly,

'Many workers who have previously concentrated on resolving phylogenies are now devoting a considerable amount of their efforts to underlining and illustrating the potential weaknesses of those very conclusions and the methodologies used to infer them' (p. 8).

By way of background they explain:

'...light microscopic techniques and ... the electron microscope allowed extensive anatomical characterization of many groups of protists; systematic analysis...resulted ... [in] phylogenetically coherent taxa.... [whose] interrelationships ... continued to pose problems....'

Conceptually, this volume stems from the situation of the 1980s, when some thousand nucleated species were thought primitive in lacking mitochondria (pelobionts, entamebas, microsporidians,

membrane-bounded, were recognised as mitochondria -- still in existence, apparently, albeit in modified form. Again in the classificatory suggestions of Cavalier-Smith most archezoans are now in an infrakingdom, Excavata (of Protozoa), so named because of a conspicuous feeding groove in the cell surface; they are reviewed in chapter 2 (Simpson and Roger), which details possible relationships between forms with and without functional mitochondria and argues for the monophyly of the whole. And microsporidians are in the kingdom Fungi, grouped with kingdom Animalia in the clade Opisthokonta, a grouping deemed 'far too phenotypically diverse to be useful as a major unit of eukaryote classification' (Cavalier-Smith, 1998. *Biol. Rev.* 73:213). The question naturally arises how useful, then, is the (p. 208) 'Empire or Superkingdom 2. Eukaryota,' a grouping even more phenotypically diverse.

Taxon or not, animals and their kin and their recent molecular literature, are reviewed in chapter 5 (Steenkamp and Baldauf), with the

a paradox -- an abundance of information blurs the authentic signal', in this apparently entropic system of human endeavour. They consider the underlying causes as compositional biases, long-branch attraction, and heterotachy (variable rate of substitution at a particular position), and indicate corrective procedural possibilities. As an alternative approach they consider 'rare genomic events' (indels), which they term 'Hennigian markers' (synapomorphies), concluding that such 'changes can be helpful in reconstructing organismal phylogenies only when they are used to complement sequence data ..., but their use as per se kinship indicators ... should be treated with great caution' (p. 140). This naturally raises the questions, *great* relative to what, and why? They nevertheless favour multigene approaches over single-gene, and believe that 'molecular phylogeneticists can now look at the future with optimism, thanks to the high throughput of sequences... and to progresses in the implementation of tree reconstruction methods (e.g., by accounting for heterotachy). This will ultimately lead to the inference of a well-resolved universal tree' with many benefits ensuing. This naturally raises a question about the possibly enlarging pitfalls of the future, when perspectives change from genes to genomes, as considered also in the thoughtful chapter 8 (see below).

Five chapters stress genomics: in relation to natural selection and evolutionary biology generally (chapter 7, Charlesworth); as complicated functional systems, at the genomic level, unlikely due to convergence (chapter 8, Stiller); 87 genome phylogenies (mostly bacterial) that mainly agree with SSUrRNA results (chapter 9, Charlebois et al); characteristics of the sequenced genome of the microsporidean *Encephalitozoon*, compared with other 'minimal' eukaryotes (chapter 10, Méténier and Vivarès); cyanobacterial genes in nuclei and

their proteomic repercussions (chapter 11, Leister and Schneider). Other interesting chapters review TOM & TIM and TOC & TIC complexes of mitochondria and chloroplasts, respectively, and intraorganelle protein transport (chapter 12, Fulgosi et al); transformation of mitochondria into mitosomes and hydrogenosomes (chapter 13, van der Giezen and Tovar). If these chapters have a common theme it is the eukaryotic cell and the relations, both functional and phylogenetic, between genes

and morphology.

There are two illuminating chapters on membranes. Dacks and Field (chapter 14) review the membrane system, how it works and how evolutionary perspectives arise through 'bottom up' and 'top down' constructions. There is an example of search methods for sequence homologs, helpful to the uninitiated, using the BLAST protocols of the National Center for Biotechnology (NCBI) of the National Institutes of Health (NIH) of the US. Cavalier-Smith (chapter 15) provides an elegant overview of the system of '18 kinds of genetic membranes' (p. 340) -- *genetic* because 'membranes, like genes and chromosomes, never form *de novo*, but always arise from pre-existing structures of a related kind. Like chromosomes, they carry genetic information in their preexisting structure' (p. 337). From his viewpoint, 'Changes in the number of genetic membranes in the membranome are among the most important megevolutionary changes in the history of life, as they have been responsible for much of its structural diversity' (p. 342). The message here is easily grasped through Figure 15.1 (pp. 338-339), which shows the 'Major changes to the membranome from the origin of cells to the origin of eukaryotes.'

Again, the theme here is structure relevant to the phylogenetic history of molecular workings of the cell -- more, indeed an abundance of, Hennigian markers.

The volume terminates with a chapter on epigenetic inheritance and its possible basis for evolutionary adaptation (chapter 16, Pál and Hurst). Here epigenesis is exemplified (p. 354) by 'genetically identical cells of an embryo [that] come to have, and stably maintain, different fates.' Its further meaning is

Views conflict over the number of secondary endosymbiotic events necessary to explain the occurrence of the various types of plastids.

sought in gene regulating networks of *E. coli* and baker's yeast, cytoskeletal variation in ciliates, flagellar position in trypanosomes, membranes and their marvels, prions infecting yeast, and so on. The upshot (p. 366): 'We can then be sure that spigenetics is of importance, but it is unclear whether when uncoupled from DNA-based inheritance ... it will be of importance in the process of adaptation.'

Aside from the Overview (chapter 1, above), there is no summary of the volume, which I see perhaps best exemplified in two of the four chapters of Section 1, Eukaryote Diversity and Phylogeny.

Plastids, and their tortured still not completely understood history, are reviewed in chapter 3 (Archibald and Keeling). The story begins in 1883 with AFW Schimper, continuing with Konstantin Mereschkowsky's endosymbiotic theory of 1905, and the modern evidence relating to primary (cyanobacterial) and secondary (red and green algal eukaryotic) endosymbionts as evidenced by their membranes and sometimes, in the latter case, their remnant nuclei complete with DNA. Views conflict over the number of secondary endosymbiotic events necessary to explain the occurrence of the vari-

ous types of plastids. The authors favor two secondary green events (euglenids and chlorarachniophytes) and one red one (p. 65): 'All algae containing secondary plastids of red algal origin thus appear to comprise a eukaryotic supergroup dubbed as the chromalveolates (Cavalier-Smith, 1999).' They consider that certain dinoflagellates exhibit possibly tertiary endosymbiosis, replacing their original symbionts with others stolen from 'three of the five red secondary-plastid-containing lineages' (p. 67). One implication in that 'Loss of photosynthesis -- which should be distinguished from outright plastid loss -- now appears to be far more common than previously appreciated.'

Finally, comprising another non-taxon, chromalveolates are the subject of the 34 pages of chapter 4 (Cavalier-Smith). As the longest chapter it bristles with important, even startling, facts, generalities, and conjectures relating to the overall theme that 'Chromalveolates are a major branch of the eukaryote tree' (p. 75). Indeed 'chromalveolates embrace a major fraction of eukaryotic biodiversity, ranging from minute intracellular parasites of bacterial dimensions to brown seaweeds (giant kelps) longer than a blue whale' (p. 76), (and what of 'empire or superkingdom 2,' which includes the blue whale?). In the author's classification they combine the seven phyla of the entire kingdom Chromista and the entire infrakingdom Alveolata (of Protozoa). 'Phylogenetically, chromalveolates can be defined as the chromophyte algae (those ancestrally having chloroplasts with chlorophyll c...) and all their disparate nonphotosynthetic descendants.' Grouped in 47 classes, 'there are 123,000 or more described species..., more than half of all protists and perhaps as many undescribed ones.' The chapter reviews their major innovations: 'the origin of novel genetic membranes..., of cortical alveoli, feeding and defen-

sive organelles, macronuclei and ciliary hairs....' Noted also are many losses. The author concludes that 'The status of chromalveolates as a major holophyletic branch of the eukaryotic tree is clear. Their unity was formerly obscured by the high frequency of differential organelle loss....'

Perhaps appropriate here is a comment on the classificatory views of Cavalier-Smith, who advocates paraphyletic taxa such as 'Protozoa, the basal eukaryotic kingdom.' This taxon is creatively defined so as to include relatives of kingdoms Animalia, Fungi, Chromista and Plantae, such that the one (Protozoa) may be said to be ancestral to the others. Again the question naturally

arises as to whether evidence of paraphyly is also evidence of ancestry? -- as if the two (paraphyly, ancestry) really were the same -- as if creatively defining the one also conjures the other.

Overall, this is a fine volume of wide interest, in which the editors, authors, and publishers may take justifiable pride. It is a worthy addition to the uniquely valuable 'special volumes' series of the Systematics Association, which began with Julian Huxley's *The New Systematics*, published in 1940 (reprinted 1971).

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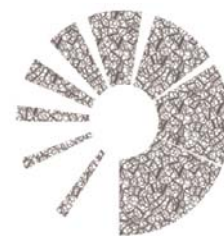
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August 19, 2005

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Contact: Dr. Norman MacLeod, Natural History Museum, London, UK.

Conference Details at:

www.systass.org. (See article on page 22).

August 22-26, 2005

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National Museum and Gallery of Wales, Cardiff, UK.

Contact: Dr. Ray Tangney, National Museum of Wales, Cardiff, UK.

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Biennial Symposia

The New Taxonomy

Contact: Dr. Quentin Wheeler, Natural History Museum, London, UK.

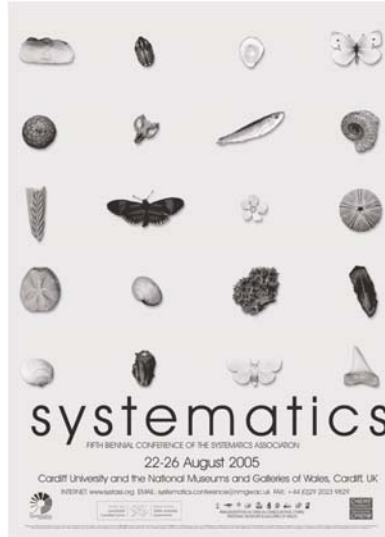
What is biogeography?

Contact: Dr. Malte Ebach, Natural History Museum, London, UK.

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Compatibility Methods in Systematics

Contact: Dr. Mark Wilkinson, Natural History Museum, London, UK.



December 6, 2005

Systematics Association Young Systematists' Forum

Flett Theatre, Natural History Museum, London, UK.

Contact: Dr. Mark Carine, Natural History Museum, London, UK.

Forum details at: www.systass.org

December 7, 2005

Systematics Association AGM and Lecture

Linnean Society, London, UK.

AGM Starts at 5pm

Guest Speaker: Prof. Rod Page

Lecture starts at 6pm.

Contact: Bill Baker.

2006

April 11-12 2006

Symposium on the State of Molecular Systematics in Algae

Natural History Museum, London

Contact: Juliet Brodie and Jane Lewis.

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, Natural History Museum, Cromwell Road, London, SW7 5BD, U.K.

The Systematist Newsletter of the Systematics Association.

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