

The Systematist

Newsletter of the Systematics Association

Number 27 2006

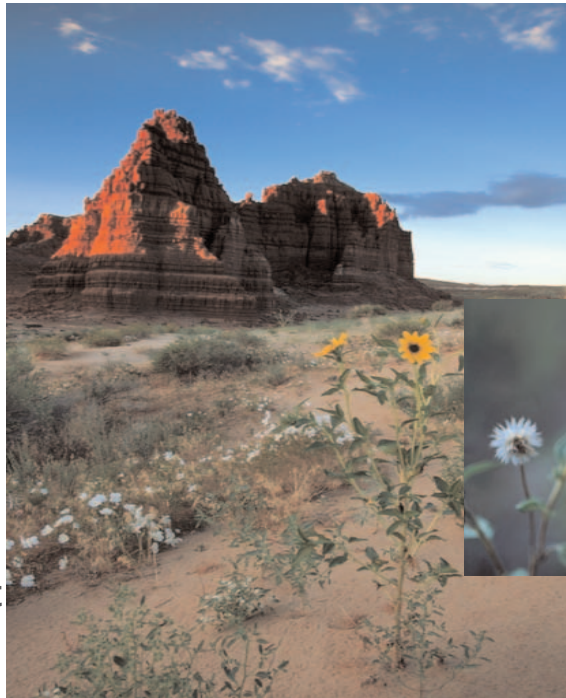
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Inspirations

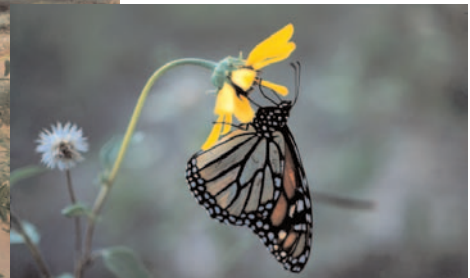
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Reality or Fantasy?

Editorial

27th Issue of *The Systematist*

Enjoy the new issue!

Systematics Association Biennial Conference 2007

The 2007 Biennial Conference of the Systematics Association will be held at the Royal Botanic Garden, Edinburgh on the 28st - 31st August 2007. The conference will consist of a mix of an open programme of contributed talks and posters, along with two thematic symposia. The two planned thematic symposia are 'Speciation' and 'Floras and Faunas serving Biodiversity Research'.

To encourage student participation there is a bursary scheme. Bursaries will contribute towards the cost of registration, accommodation, and subsistence for students (and recently graduated students) giving a paper on their own research work. Current research students and those who graduate after August 2006 are eligible to apply. Allocation of bursaries is competitive, based on assessment of an abstract that must be submitted by 31st December 2006, for decisions in January 2007.

Further details of the meeting, registration details, and the procedures for applying for student bursaries will be posted on the Systematics Association web page in early November 2006.

The Choanoflagellates - Serendipity or Fate? - An appetizer for the Annual Lecture at the AGM -

The major research topic of my professional life, and the subject of my

forthcoming Presidential address on December 6th, came about unexpectedly and resisted all attempts to discard it no matter how much I tried. My early research was as a botanist working on dinoflagellates and marine phytoplankton. In 1970, I visited Norway with the aim of isolating coccolithophorids (calcifying phytoplankton) from a region normally rich in these cells. Alas, 1970 turned out to be a 'fallow' year for coccolithophorids and so instead I collected whatever I could lay my hands on and came up with a strange entanglement of silica threads, which I soon learned was a choanoflagellate. That might have been the end of the story except that a choanoflagellate subsequently turned up as a contaminant in an algal culture. This was followed in 1976 by the 'inadvertent' isolation of another species whilst taking a student field course in France. In 1996, I visited Melbourne, Australia and on a trip to the Great Ocean Road I collected and isolated two further species of significance. Eventually, in 2000, I succumbed to what I can only describe as the hand of fate and decided that what had until then been a hobby pursued on the side should become the major object of my attention. Thankfully, a generation of dedicated Birmingham students has helped me discover the magical lives of these tiny but fascinating cells that live in baskets. The moral of this story must surely be, that no matter how much we try to direct and manage science, there must always be a place for the unexpected.

Barry Leadbeater
President of The SA

Cover illustrations : Different species of sunflower (Copyright 2006 Loren Rieseberg)

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 Associations newsletter, *The Systematist* and mailings of information.

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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Plant Species Evolution

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*Dr. Loren Rieseberg presented this year's Sir Julian Huxley Lecture

Since the colonization of land some 400 million years ago, there has been an explosion in plant diversity, with approximately 300,000 forms of land plants extant today. An important question is whether there is a phenotypic continuum connecting these forms or do discontinuities exist that can be used to partition diversity into groups? The success of the taxonomic enterprise implies that discontinuities do exist in at least some plant groups, although this is contested.

In this brief essay, we ask whether plant diversity is partitioned into discrete clusters (separated by discontinuities) and, if so, whether these clusters are comparable across groups that vary in mode of reproduction, life history, and levels of gene flow. We also ask whether these clusters (when they exist) correspond closely to reproductively independent lineages or "units of evolution," and then discuss the likely mechanism (selective sweeps) that holds species together.

Are discrete phenotypic clusters common in plants?

Botanists disagree as to whether plants occur in discrete phenotypic clusters that are called species by taxonomists or whether these species taxa represent arbitrary divisions in more or less continuous "morphospace" (Box I). These disagreements stem in part from philosophical differences among authors about the nature of species, but also from variation in the degree of distinctness of species taxa in the different genera or families studied by

the disputants. A belief in special creation, for example, pre-disposed early taxonomists such as John Ray (1627-1705) and Carolus Linnaeus (1707-1778) to assume that species were discrete and immutable entities. The job of the naturalist was to discover them. Likewise, the neo-Darwinian view of species as evolutionary units is prejudiced toward the existence of discrete clusters (Ereshefsky 1999). On the other hand, if species are viewed primarily as products of evolution, then there is no reason they should be discrete or at least any more discrete than higher taxa (e.g., Darwin 1859; Raven 1975; Mishler and Donoghue 1982; Mallet 2001). Indeed, it was variation that occurred within species that led Darwin to doubt the immutability of species. Note that both expectations are equally consistent with evolutionary theory: species may be both products and units of evolution. Thus, this is an empirical question that must be answered by analyzing patterns of phenotypic diversity across many plant groups as opposed to verbal arguments based on dated and qualitative caricatures of the literature.

Evidence from floras and monographs

Although legions of biologists and philosophers have contributed to discussions of the nature of species, it is taxonomists who are most familiar with patterns of phenotypic variation at or below the species level. Thus, it seems prudent to ask whether taxonomists often have difficulties in delimiting species in local floras and botanical mono-

graphs.

The most relevant analysis of a local flora was by Mayr (1992), who investigated the species status of 838 indigenous species of vascular plants of Concord township in eastern Massachusetts, USA. He found that 697 of 838 named species (83.1%) were "morphologically well-defined, relatively uniform, and sharply set off against all other species" (p. 236), but no statistical assessment of morphological discreteness was made (Whittemore 1993). However, analyses of local floras may underestimate the proportion of problematic species because sister taxa often overlap minimally or not at all in geographic distribution (Lynch 1989; Cozzolino et al. 2001). As a consequence, morphological intergradation may only become evident when phenotypic variation within and among closely related species is analyzed across their ranges.

Problems with species delimitation also appear to be infrequent in botanical monographs, which, unlike floras, do include all close relatives and consider species-wide variation. McDade (1995) surveyed 104 monographs from three journals to assess the difficulties faced by practicing taxonomists in defining and delimiting species. Surprisingly, only 120 of 1,790 species surveyed (7%) were reported as problematic by botanical monographers. Intraspecific taxa were recognized for an additional 192 species (10%), which may indicate that complex patterns of phenotypic variation sometimes exist within a species even if the author did not state this explicitly. Nonetheless, these results

imply that most plant species are distinct and contradict an earlier more limited study of 11 genera, which reported only 57% good species (Grant 1957).

The biological processes responsible for generating problematic pat-

terns of variation are less clear. While hybridization was reported for approximately 12% of the species in McDade's (1995) survey, in only 1% of species did the hybridization create problems in species delimitation. Likewise, asexual reproduction contributed to species uncertainty in only 2 of the 104 studies (~2%).

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The most straightforward interpretation of these data is that the majority of plant species are indeed discrete and that too much has been made of a small number of botanical "horror stories" (Fisher 1954; Diamond 1992). An alternative interpretation, which cannot be refuted from these kinds of monographic and floristic studies, is that the apparent discreteness of species taxa stems more from our adeptness at recognizing and classifying organisms than from the presence of real discontinuities (Hey 2001). A frequently cited example is the propensity of humans to subdivide the continuous spectrum of light into discrete colors (Coyne and Orr 2004).

Comparisons of folk and Western taxonomies

The distinctiveness of species taxa has also been evaluated by comparing the taxonomies of indigenous peoples with those developed by Western taxonomists. Strong correspondence between folk and Western species would imply that species taxa represent objective and discrete groupings of organisms; humans with different cultural backgrounds and education seem unlike-

ly to partition continuous phenotypic variation in the same way. Weak correspondence, on the other hand, would lend credence to arguments that species taxa are arbitrary constructs - a consequence of our predilection to categorize objects,

even when variation is mostly continuous or when discontinuities do not correspond across traits. Correspondence of folk and Western taxonomies is surprisingly strong for animal groups such as birds (70-90%; Mayr 1963; Diamond, 1966; Majnep and

Bulmer 1977), frogs (80%; Bulmer and Tyler 1968), and reptiles (95%; Bulmer et al. 1975). The situation for plants is more heterogeneous, but the match between folk and Linnaean species can be striking.

The first study of this sort in plants involved the Tzeltal people of Southern Mexico (Berlin et al. 1966). Only 68 (34%) of 200 Tzeltal plant names were reported to correspond one-to-one with Linnaean species. This result was taken as evidence that plant species are theoretical constructs of the human mind rather than objective, natural groupings of organisms. However, this early report was invalidated by a more comprehen-

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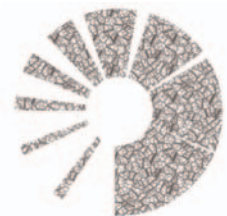
Following the acquisition of CRC Press by Taylor & Francis, Systematics Association book production operations have been transferred to the CRC Press offices in Florida. Members of the Systematics Association receive a 25% discount of all Systematics Association volumes published by Taylor & Francis.

All volumes published by Taylor & Francis/CRC Press should now be ordered via either the CRC Press offices or the CRC press office in London (details below). The 25% SA members' discount is claimed by using a promotion code, for details of this code please contact Alan Warren, Systematics Association Editor-in-Chief.

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sive study by the same authors, in which 291 of 471 (61%) of Tzeltal species were shown to have a Linnaean equivalent (Berlin et al., 1974). Most of the remaining Tzeltal taxa (35%) were under-differentiated relative to Linnaean species, whereas only a handful (4%) were over-differentiated.

An even greater correspondence (87.7%) has been reported between Linnaean names and folk names of the Dai people of Yunnan China based on a survey of more than 1,000 plant species (Wang et al. 2004). However, in contrast to the survey of Tzeltal names, Dai taxa were more likely to be over-differentiated (8.8%) than under-differentiated (3.5%). Generally, species of considerable cultural or economic significance tend to be over-differentiated by indigenous peoples, while less important species may be under-differentiated.

In contrast, only 12-22% of local, vernacular names were congruent with Linnaean species in an inventory of primary forest in Central Kalimantan, Indonesia (Wilkie and Saridan 1999). In this latter study, however, the indigenous population relied less heavily on the local flora that either the Tzeltal or Dai peoples, and it may be that some indigenous knowledge has been lost.

As pointed out by Coyne and Orr

species and the rarity of folk over-differentiation provides strong support for the discrete and objective nature of species taxa in plants.

While correspondence between folk and Western taxonomies can be remarkable, critics of this approach correctly point out that this is not a truly independent test given that different human cultures likely share similar neurological processes (Mishler and Donoghue 1982; Ridley 1996). Indeed it is reasonable to suggest that regardless of culture, humans may emphasize the same traits when recognizing and classifying organisms. If discontinuities do exist, but show little correspondence across traits as some botanists have argued (e.g., Mishler and Donoghue 1982; Donoghue 1985; Raven 1986), then it would be conceivable for folk and Western taxonomists to identify similar, but arbitrary groupings. Nonetheless, the weight of the evidence does favor the conclusion that discrete morphological entities do exist at the species level in plants.

Statistical approaches

A more rigorous approach derives from the application of statistical procedures to taxonomy (Sokal and Sneath 1963). To bring objectivity into taxonomic practices, statistical

not be found by these statistical methods if there is not substantial correspondence in discontinuities across traits.

As far as we are aware, the only quantitative analysis of the phenetic literature was one that we conducted recently (Rieseberg et al. 2006). Briefly, we analyzed 218 phenetic studies of plants and animals, covering over 400 genera, for correspondence between species taxa and phenetic clusters, based on the most recent taxonomic treatment prior to the phenetic analyses. In the majority of taxa studied, phenotypic variation was partitioned into discrete clusters (83% for plants and 88% for animals). Thus, real phenotypic discontinuities do exist in most taxonomic groups. However, the correspondence of these clusters to previously recognized species taxa was low (52.8% for plants and 52.1% for animals), and similar to Grant's (1957) earlier, subjective estimate of the proportion of good plant species of 57%. Lack of correspondence was mostly due to over-differentiation by taxonomists (87.4%) rather than under-differentiation (13.6%).

A finer-scale analysis of these data revealed that correspondence between species taxa and phenotypic clusters was significantly reduced by polyploidy and asexual reproduction. This finding makes sense because both phenomena provide a means for stabilizing hybrid reproduction, thereby filling the phenotypic space between diploid progenitor species. Indeed, agamic complexes, which contain sexual species and taxa that reproduce asexually through seeds (apomixis), are notorious for instability of classification, with the number of species recognized by different authorities often varying by orders of magnitude (Camp 1951; Richards 1973; Sinnott and Phipps 1983; Weber 1996; although see Mishler 1990). A more surprising observation was that contemporary hybridization among species of the same ploidal level failed to cause taxonomic

We analyzed 218 phenetic studies of plants and animals, covering over 400 genera, for correspondence between species taxa and phenetic clusters... In the majority of taxa phenotypic variation was partitioned into discrete clusters

(2004), under-differentiation of folk species should not be viewed as evidence against the objectiveness or discreteness of species taxa because taxonomists have been trained to identify cryptic differences that might not be useful to indigenous peoples. On the other hand, over-differentiation does constitute evidence against the discreteness of species taxa. Given this interpretation, which seems reasonable to us, the congruence of folk and Western

or "numerical taxonomy" advocated a classification based on the quantitative analyses of as many characters as possible, with each character given equal weighting. This approach largely obviates concerns about biases inherent to human neurological processes, which cannot be fully eliminated from the analysis of species discreteness in floras and monographs or from comparisons of folk and Western taxonomies (above). Also, discrete clusters will

problems, despite its frequent mention as the primary cause of fuzzy species boundaries in plants (Grant 1957). However, McDade (1995) also reported that hybridization was rarely associated with problematic taxa. It may be that diploid hybrids rarely cause taxonomic problems because they tend to be pulled back into the orbit of the parental species by backcrossing. Alternatively, the lack of association between contemporary hybridization and taxonomic difficulties may be an artifact of the difficulty of recognizing hybrids in groups where taxa are not distinct to begin with.

While congruence between species taxa and phenotypic clusters is low, this does not necessarily mean that taxonomists are doing a poor job of recognizing reproductive communities or evolutionary units. Because taxonomists rely on evidence from geographic distribution, chromosome number, as well as patterns of morphological variation, it might be that their classifications more accurately reflect patterns of gene flow/ancestry in natural populations than do groupings derived from standard phenetic analyses. It is equally reasonable to argue, however, that phenetic clusters are likely to correspond more closely to real biological entities since they represent more objective groupings and are based on the assessment of a larger number of phenotypic traits than most species diagnoses. To distinguish between these alternatives, it is necessary to explore the relationship between phenetic and taxonomic groups and reproductive communities.

Correspondence between species taxa, phenetic clusters, and reproductively independent lineages

In the previous section we showed that phenotypic space within most genera is discontinuous and that these discontinuities often correspond to boundaries between taxo-

nomic species. However, this result does not necessarily demonstrate that species taxa and/or phenotypic clusters represent fundamental evolutionary units. For example, it might be that neither correspond closely to reproductive communities or evolutionarily independent lineages.

One method for addressing this question is to analyze the fertility and viability of intra- and interspecific crosses among closely related species. If hybrids from intraspecific (or intra-cluster) crosses are fertile and viable, but crosses with closely related congeners are significantly less successful (i.e., have reduced crossability), then the species (or phenetic cluster) likely represents a reproductive community that is evolving independently from other such communities. These data are often reported as a crossability index (CI), which is calculated by dividing the mean interspecific (or inter-cluster) crossability by the average intraspecific (or intra-cluster) crossability (McDade and Lundberg 1982). CIs range from 0, which indicates complete sterility and/or inviability of interspecific hybrids, to 1 (or slightly above), in which hybrid crossability and/or fitness is equivalent to that of intraspecific crosses. In general, CIs ~0.8 or lower indicate the presence of sig-

nificant postmating reproductive isolation.

We applied this approach to the analysis of 37 plant genera having both phenetic and crossability data (Rieseberg et al. 2006) and found that CIs were generally consistent with both species taxa ($71.2 \pm 7.1\%$) and phenetic clusters ($75.2 \pm 6.8\%$). However, further analyses showed that phenetic clustering approaches tend to outperform taxonomists in groups lacking polyploidy, but a trend in the opposite direction was observed when polyploids were present. This result makes sense because phenetic clustering fails to take into account variation in ploidy, which often generates strong reproductive isolation.

These results imply that many plant species do correspond to reproductively independent lineages (~70%) and thus appear to represent biologically real entities. However, the CI is a fairly crude measure of reproductive independence because only postmating reproductive barriers were assayed. Species in some groups may be isolated entirely by premating barriers, which would lead to an underestimate of congruence between species taxa and reproductive communities.

How are species held together?

Box I. Species denial.

In the 1960s (Ehrlich and Holm 1960; Ehrlich and Raven 1969) a self-proclaimed scientific revolution emerged, taking aim at fundamental concepts ensconced in the literature of evolutionary biology during the Modern Synthesis. The targets of this critique spanned the disciplines of evolution and ecology - concepts such as "niche," "competition," "community" and "species" were brought under the deconstructive lens - but a key focus was the species problem. The nominalist view espoused by Ehrlich and colleagues, i.e. that individuals and populations are real but taxonomic groups artificial, has proved very influential on biologists working at the species level and lower, especially in botanical circles (e.g. Levin 1979, Mishler and Donoghue 1982; Bachmann 1998). The nominalist argument has gained particular traction with botanists because hybridization, genomic doubling and diverse reproductive modes that are characteristic of many plant groups can yield complex patterns of variation, and consequently, challenging taxonomic problems. Interestingly, botanists have been blamed for fouling Darwin's mind on the nature of species, convincing him that species in general are artificial.

The fact that intraspecific hybrids are fully fertile does not necessarily mean that conspecific populations represent a reproductive community. Indeed, botanists have frequently questioned whether there is sufficient gene flow among conspecific plant populations for them to evolve as an evolutionary unit (Levin 1979; Mishler and Donoghue 1982; Raven 1986). These arguments assume that gene flow is a homogenizing force that acts mostly to ensure that populations retain shared, ancestral characteristics that define the species--an assumption that does require gene migration rates exceeding those reported for many plant and animal species (Morjan and Rieseberg 2004).

However, gene flow may also act as a creative evolutionary force by enabling the spread of advantageous alleles (i.e., selective sweeps). Only very low migration rates are required for selective sweeps (Morjan and Rieseberg 2004), and molecular population genetic data indicate that species-wide sweeps are frequent: one every 16-80 years for sunflowers (N. Kane and L. Rieseberg, unpublished), one every 45-80 years for flies (Bierne and Eyrewalker 2004), and one every 200 years for primates (Fay et al. 2001). Thus, it appears that selective sweeps hold even low gene flow species (such as annual sunflowers) together. Also, because the rate of adaptation appears to be remarkably high (evolution is not such a slow process after all), there will be many diagnostic differences between even very closely related populations or species. Reliance on single diagnostic characters for species delimitation will therefore inevitably lead to taxonomic over-differentiation, as appears to have occurred in many plant taxa (above).

In addition to solving an old problem of how species evolve together, studies of the boundaries of selective sweeps offer an objective means for identifying evolutionary units and determining the causes of

speciation. That is, once we have identified where many (most?) sweeps end in a given taxon, we can ask why. Is there a change in a geographic barrier, or a change in habitat, or a change in genetic background? Because sweeps occur in asexual taxa as well, the same approach can be applied to both asexual and sexual lineages.

Conclusions

The quantitative analyses of floras, monographs, folk taxonomies, phenetic studies, and crossability data reviewed above indicate that, contrary to repeated claims in the botanical literature, plant species often form discrete phenotypic clusters in nature and these clusters frequently correspond to reproductively independent lineages. The fact that good species predominate in many plant genera does not necessarily mean that there is a single kind of natural group at the specific level in plants. It has long been known, for example, that agamic groups such as hawthorns, blackberries, and dandelions may consist of hundreds or thousands of "microspecies" that do not correspond closely to sexual species (Stebbins 1950; Grant 1981). Species that predominately self and those that hybridize frequently in nature are also considered to represent "deviations from the standard of good biological species" (Grant 1981, p. 75). Selfers are believed to form locally distinct microspecies akin to those found in agamic complexes, whereas frequent hybridizers such as oaks and irises are thought to form "syngameons" (Grant 1981), in which the reproductive community is expanded to include two or more closely related species taxa (Lotsy 1925). As a consequence, botanists have frequently recognized the existence of multiple kinds of species (Camp and Gilly 1943; Davis and Heywood 1963; Grant 1981) and have championed a pluralist species concept (Mishler

and Donoghue 1982).

While there is strong statistical support for the view that phenotypic variation in agamic complexes is partitioned differently than in sexual species, only marginally significant differences have been documented between selfers and outcrossers and no differences have been found between groups that vary in the presence or absence of contemporary hybridization (Rieseberg et al. 2006). Thus, while it may make sense to recognize two different kinds of species-level taxa in plants (i.e., agamic lineages versus sexual species), there is little statistical justification at the present time for recognition of other kinds of species, such as the 12 such categories listed by Camp and Gilly (1943). Of course, this conclusion may be temporary as we await results from sweep-based identification of the most inclusive units of plant evolution.

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Meeting Reports

Unraveling the algae: The past, present and future of algal molecular systematics

On the 11th and 12th March 2006, some 85 people from at least 15 countries from around the world came together at the Natural History Museum in London to participate in a symposium to review the impact of molecular techniques on algal systematics. This symposium, run under the auspices of the Systematics Association, was also supported by the British Phycological Society, The Linnaean Society and the Natural History Museum. In addition to the 16 invited oral presentations, there were 27 posters which covered almost all the algal groups.

After welcoming comments by Johannes Vogel, the Keeper of Botany at the Natural History Museum, the first day opened with a presentation by Chuck Delwiche (University of Maryland) who gave an engaging overview of the algae through the evolution of their plastid acquisition. Chuck regards the algae as being monophyletic through their possession of plastids, a concept he illustrated with the picture of a bonsai tree as the ultimate alga. Paul Hayes (University of Bristol) navigated us through the immensely confusing field of cyanobacterial taxonomy where it appears that there is very little congruence between morphological and molecular results. Paul demonstrated that genetic approaches could reveal unknown diversity in some groups but might lead to over classification in others, hence he advocated a polyphasic approach, i.e. a taxonomic approach that makes use of both stable phenotypic characters and molecular markers, to the investigation of cyanobacteria. Chris

Maggs (Queen's University Belfast) and Olivier de Clerck (Ghent University) covered the red algae, following the development of our understanding of this class over the last century. Their intriguing and insightful analysis based on studies of which genes, parts of genes or spacer regions had been deployed in red algal taxonomy, demonstrated not only that particular genes were potentially helpful at different levels of classification but that over the years since molecular tools had become available that there had been a shift in the level of taxonomy that was being addressed going from trying to understand higher-level classification in the early days to an increase in species-level approaches today.

An extended lunch break enabled people to spend time discussing the excellent posters that had been provided for the meeting and a chance to engage with the students, who made up almost a half of the participants and whose work was very much in evidence. Poster topics were wide-ranging from the general to the specific, covering macroalgae to ultraplankton and from phylogenies to the development of identification tools using molecular techniques. The afternoon session started by Thomas Pröschold (Dunstaffnage Marine Laboratory) demonstrating, using green algae, how useful molecular approaches can be in combination with traditional morphological approaches. Then, John Hall (University of Maryland) brought us to the charophytes, a group that is relatively poorly known and patchily sampled and equally patchily studied. John explored the difficulties in interpretation this can bring but offered future hope for this group in the guise of genomic data. Following on, an even more obscure group that was only discovered in the 1980s, the chlorarachniophytes, was brought visibly to life by the startling videos presented by Ken-

Tsukuba). Ken also showed that these marine amoeboid unicellular algae, whilst presenting a fascinating plastid acquisition history, are much more diverse with several resolved lineages than hitherto expected. The final presentations of the day covered the haptophytes, given by Bente Edvardsen (University of Oslo) and the cryptophytes, presented by Federica Cerino (Stazione Zoologica, Naples). Both speakers spoke of the challenge of taxonomic revision that these two groups presented in the light of molecular data and that there was much to do to achieve taxonomic resolution. A wine reception followed to round off the day's events.

The second day began with a review of algal evolution by Tom Cavalier-Smith (University of Oxford). Rarely can so much information have been packed into such a short space of time! Progress in this field has been breathtaking with the advent of molecular techniques allowing the testing of detailed hypotheses to drive reconstructions of the past forward. This field has clearly benefited by the information that can be provided through molecular approaches. Returning to a specific group of Øjvind Moestrup (University of Copenhagen), as with Chuck, used a tree to make a point, not this time a bonsai, but the famous dinoflagellates tree presented to us upside down to illustrate the impact of molecular data on the taxonomy of the dinoflagellates, a group that surely displays profligacy in the number of postulated past symbioses. Jane's maxim that it never pays to generalise about dinoflagellates is true! David Mann (Botanic Garden, Edinburgh), using diatoms, reiterated the overarching theme that more than one type of information is required to do meaningful phylogeny. He went on to show how progress is confounded by the lack of high-grade information available for most taxa even in this comparatively well-studied

group. The classification of brown algae was covered by Bruno de Reviers (Muséum national d'histoire naturelle), and as with many other classes, molecular information has led to a major upheaval in phylogenetic thinking for this group leading to new hypotheses and the movement of many taxa to new orders and families. Robert Andersen (Bigelow Laboratory, Maine) finished the morning by covering the rest of the heterokont algae, in particular the chrysophytes and some related groups, and proposed that 'within class' resolution may be possible using appropriate molecular sequence data.

After another extended lunch, with more posters read and the museum explored, we returned to consider the development of whole genome sequencing. Chris Bowler (Stazione Zoologica, Naples and ENS, Paris) gave an erudite exposition on the potential developments that arise from this type of information and the opportunities this provides us with. He reported that six eukaryotic algae have been completely sequenced, including green, red and brown algal lineages, with more underway with all the implications for new information, such as the evolution of different groups of photosynthetic eukaryotes with respect to each other and with respect to other eukaryotes. David Williams (Natural History Museum, London) discussed the principles of classification in a passionate presentation, illustrated using examples from the diatoms. The symposium finished with a review of molecular techniques with emphasis on the future. This was illustrated with examples from the microalgal field by Linda Medlin (Alfred-Wegener Institute for Polar and Marine Research, Bremerhaven) and macroalgal field by Jeanine Olsen (University of Groningen), who both set new challenges and food for thought.

From the presentations it was clear how rapidly our understanding

of algal systematics has moved in the last twenty years. It was also overwhelming clear that it was inappropriate to focus on a single technique to further our understanding in the future, rather, a range of traditional and molecular approaches are required. A number of speakers also highlighted the need for transmission electron microscopy in order to support interpretation. Discussion sessions on both days were animated and allowed participants to debate issues as they arose and to speculate on the shape of the future. Arising from these debates it was clear that there is concern around the appropriate use and interpretation of 'DNA barcoding' and its use in taxonomy and that there is a need for proper long term vouchering of analysed material to sit alongside any electronic record (e.g. genbank) allowing further investigation if required in the future.

All in all this was a successful meeting which demonstrated to us the power of having a focussed subject and the value of bringing people together from a wide range of backgrounds to discuss the material. We believe that the book that will result from the symposium (of the same title) will be a valuable legacy of this noteworthy and timely event in the development algal systematics.

Juliet Brodie and Jane Lewis

Palaeogeography and Palaeobiogeography: Biodiversity in Space and Time

During the Third International Biogeography Society meeting in 2005, Claire Slater put forward a proposal to hold a biogeography-themed meeting in the UK in 2006. The proposed meeting took place in the Centre for Mathematical Sciences at the University of Cambridge between 10-13th of April 2006, attracting around 70 delegates. An explicit objective of the meeting was to attempt to bring

together palaeogeographers and palaeobiogeographers, who tend to have earth sciences backgrounds, with ecologists and biologists working on the modern biota who tend to have life sciences backgrounds. We were successful in attracting a fairly cosmopolitan selection of delegates from over a dozen countries, and from a wide range of research fields.

The four days of the meeting were divided into two days of talks and two days of workshops. Throughout the conference posters were on display. The afternoon of the first day was taken up with three keynote speeches. Brett Riddle (University of Nevada, Las Vegas and current President of IBS) set the tone of the meeting by discussing biogeographic patterns among a range of plants and animals that had no clear geological cause in Baja, California, and threw the matter open to the geologists in the audience. Brett was overwhelmed with suggestions for possible geological processes that might have generated the observed north-south split. Paul Upchurch (University College London, and a co-organizer of the meeting) followed on with a talk with the crowd-baiting title "What's wrong with palaeobiogeography?" which focused on the problems of the multiplicity of methods available for palaeobiogeographic reconstruction. Alan Smith (University of Cambridge) concluded the session with a talk explaining the problems of generating global palaeogeographic reconstructions.

After the keynote session we were able to retire to the Sedgwick Museum for an evening reception and a chance to view the exhibits and socialize. Dave Norman gave a talk introducing the museum, and thanks go to him and Dan Pemberton. The people who were still thirsty at the end of the reception were able to explore Cambridge's many hostelries at their leisure afterwards.

The second day of the meeting

consisted of the invited speakers talks. A brief summary of the main points is given below.

Terrane recognition through the Phanerozoic - Dr Robin Cocks (Natural History Museum, London) explained that prior to 170 million years ago paleomagnetic data yields accurate paleolatitudes but is unable to provide paleolongitudes. This makes the positioning of terranes unreliable. Robin outlined the use of climate-sensitive sediments and benthic invertebrate fossils to better resolve the position of terranes.

The systematics of biogeography - Dr Malte Ebach (Université Pierre et Marie Curie, Paris) presented a talk that was a mixture of history and philosophy of biogeography. He traced the history of the idea of areas of endemism from 1805 to the present day, and urged a more systematic, or evolutionary, approach to biogeography, rather than a classification-based system, echoing the between ranking and relatedness-based criteria among organisms.

Combining GIS and Phylogenetics in Paleobiogeography: Assessing the role of Invasion events during Mass Extinctions - Prof. Alycia Stigall (Ohio University). Alycia focused on combining phylogenetic and range data in Geographical Information System environments. Then she gave the example of GIS analyses of species ranges coupled with phylogenetic analyses used to examine faunal dynamics of brachiopods and bivalves during the Late Devonian mass extinction. Alycia noted that if Late Devonian species invasions and range expansions contribute to reduced vicariance, then modern invasive species may depress speciation rates in the modern biota as well.

Geographic Range and extinction risk: lessons from ancient marine benthic organisms - Dr Wolfgang Kiessling (Humboldt-Universität zu Berlin). The question of whether geographic range is a significant factor in predicting extinction risk

during mass extinctions remains equivocal despite the strong predictive power range it has in the modern biota. Wolfgang used data on Middle Triassic to Late Jurassic benthic taxa to analyse correlations between taxon longevity and geographic range. He found that extinction trajectories of widespread versus geographically-restricted taxa show similar patterns as the trajectories of common versus rare taxa. However, narrowly distributed and rare taxa have significantly higher extinction rate per stage than widely distributed and common taxa.

Mesozoic Paleogeography: Methods, Limits and Uncertainties - Dr Roy Livermore (British Antarctic Survey). Roy discussed developments in computer-based reconstructions of the continents over the past 30 years. He described the progression from simple models of land and ocean distributions through to the latest advances made possible by GIS, which has allowed the integration of information on climate-sensitive sediments, ancient drainage patterns, and fossil plant data to provide much more detailed reconstructions of the earth through time.

Southern Hemisphere biogeography: perspectives from the fossil record of Antarctica - Dr David Cantrill. This talk fitted well with the aim of the meeting to demonstrate the links between modern and ancient biogeographic processes. Dave mentioned the role of the Ethiopian Rift in generating vicariance, even in the absence of ocean opening in the area as yet. He used this as an example of genuine vicariance that would not yet have a geological signature. He then moved on to discuss angiosperm palaeobiogeography during the Mesozoic, and made a strong case for the need for detailed palaeogeographic maps to better understand the observed distributions and generate testable hypotheses about the processes governing the spread of angiosperms.

Towards a specimen-based biotic history of Indo-West Pacific

Cenozoic corals: (1) the story so far - Dr Brian Rosen (Natural History Museum, London). Towards a specimen-based biotic history of Indo-West Pacific Cenozoic corals: (2) the future - Dr Kenneth Johnson (Natural History Museum, London) Brian and Ken started the afternoon with back-to-back talks on Indo-West Pacific (IWP) corals. Brian underlined the importance of understanding the patterns of extinction and recovery of coral reefs through time because of the current threats to reef systems. One of the continuing arguments about coral distribution is why IWP corals are so diverse, and whether the diversity evolved in situ, or is the result of shifting biogeographic distributions. Brian presented results that support a Neogene age for the onset of the current high IWP diversity. During most of the Palaeogene coral diversity was much higher in the Atlantic. Brian also noted a poor fit between climate and coral diversity curves. Ken presented work with Dutch colleagues on the distribution of scleractinian coral diversity. A specimen-based databasing approach was used in Ken's analysis, with age assignment based on planktonic and large benthic foraminifera biostratigraphy at each locality. This work found that coral diversity peaked during the Pliocene.

New approaches to historical biogeographic analysis - Prof. Isabel Sanmartín (Uppsala University, Sweden) stressed the importance of vicariance and dispersal for biogeographical processes, in generating the current distribution patterns for historical biogeography. She also underlined the challenges facing those of us who are involved in simulating these processes, particularly the problem of computational time when using fixed geographic models with predetermined geographic connectivity.

The geological, oceanographic and climatic controls on the Wallace Line - Prof. Robert Hall (Royal

Holloway). This line, which is most probably the most well-known biogeographic boundary, is located between Borneo and Sulawesi. As early as 1858 Wallace recognised the biogeographic significance of the differences in the fauna and flora. The current geology in the area is governed by a convergent tectonic regime that has driven major change in topography and oceanography in the area over the last 55 million years. Such changes in ocean circulation may have regional impacts on connections among different areas of the Indonesian archipelago.

Morphological disparity as a biodiversity metric to explore biogeographical patterns: Recent cuttlefishes as a case study. - Dr Pascal Neige (CNRS, Université de Bourgogne). Pascal is a fellow ammonoid worker who also works on extant cephalopods. In this talk Pascal compared and contrasted taxonomic diversity and morphological disparity across the range of modern cuttlefish. His results showed that along the western African coast there is a morphological disparity peak without a taxonomic diversity peak whereas in the Indo-Pacific species richness is higher, but disparity is lower.

Phylogenetic Methods in Palaeobiogeography: Closing the Gap between "Is" and "Ought" - Dr Daniel Brooks (University of Toronto). Dan is a great speaker who gives wonderful overviews of the subject of biogeography, and seeks links between disparate areas of science in the same way as the late Steve Gould. Despite the Kantian overtones of the title, this was more Daniel Dennett. Dan discussed the limitations of the human mind, particularly our need to generalize solutions. He encouraged us to embrace the inherent complexity of biogeographic patterns, and come to terms with the reticulate nature of area relationships.

Bat Biogeography Revealed by Molecular Phylogenetics - Dr

Emma Teeling (University College Dublin). Emma presented the first well-resolved molecular phylogeny, which supported the hypothesis that that megabats are nested within microbats. Divergence time estimates indicate that the four major microbat lineages began to diversify during the early Eocene. As global temperatures rose during the Eocene insect and land plant diversity rose. A southern origin for bats was not supported. Based on these data, bats originated in Laurasia possibly in North America.

Circulation in ancient epi-continental seas: the use of finite-element modeling to understand non-uniformitarian systems - Prof. Peter A. Allison (Imperial College). Most of the record of marine rocks in the geological record is from epi-continental seas (such as the North Sea to the east of Great Britain). Tidal range is likely to have been of key importance to the hydraulic behaviour of these seas. Stratification in these systems is of particular interest. The Imperial College Ocean Model (ICOM) has been used to simulate these epi-con-

tinental seas. Tides in the Mediterranean have been successfully simulated, and Peter showed results for the Late Carboniferous. Tidal range may be an unrecognised but important factor influencing the fossil record of epi-continental seas. The 'adaptive mesh' routines used in the model may also have many applications outside of fluid dynamics.

The two final days of the meeting were in workshop format, rather than talks. One of the advantages of the CMS site was access to a computer lab, which allowed a "hands-on" component to some of the workshops, which was a success.

The morning workshop on day

three focused upon palaeogeography, with a demonstration of TimeTrek by Alan Smith and his colleagues Colin Reeves and Lawrence Rush. During the first hour of their session they showed some of TimeTrek's capabilities. The animations were particularly impressive. You can examine the range of palaeogeographic mapping tools the group has developed at www.the-conference.com/CPSL/

Allister Rees (University of Arizona) ran the afternoon session dealing with various on-line data bases. Allister and the TimeTrek group were able to integrate data sets and display various palaeontological and climate-sensitive sediment data sets on the animations. Allister's work and links to data sets can be found at www.geo.arizona.edu/~rees/.

The second day of workshops concentrated on analytical tools. Malte Ebach (Université Pierre et Marie Curie, Paris) took to the chalk boards for some "chalk and talk" about his program "3Item" which is a consensus-based methodology for phylogenetic reconstruction that he

Daniel Brooks is a great speaker who gives wonderful overviews of the subject of biogeography, and seeks links between disparate areas of science in the same way as the late Steve Gould

is working on extending to biogeographic problems.

Trying to keep things going through the final afternoon, Paul Upchurch and Al McGowan presented the (almost) finished version of Simulation Program for Area-Taxon Analysis (SPARTA). We have been able to start using simulated data from SPARTA to begin to assess the ability of various biogeographic methods to recover a signal from known data. We have also developed some additional software tools for processing biogeographic data.

The workshop days also gave people the opportunity to explore Cambridge. One botanist managed

to fit in a pleasant trip to the Cambridge Botanic Gardens. Other people took the opportunity to have more extended discussions about topics they were particularly interested in. CMS is an excellent facility for this purpose, as the building has many subdivided areas for small group discussion, as well as a large canteen area.

We must thank the National Institute for Environmental e-Science (NIEeS), who helped with a great deal of the logistical and computing support for the meeting, as well as hosting it. Quantifying and Understanding the Earth System (QUEST) provided substantial funding to help support the meeting. The Geologists' Association, International Paleontological Association, Cambridge University Press, Blackwells and Taylor & Francis all made contributions that helped to make the meeting possible.

The Systematics Association, another major sponsor of the meeting, will be handling the publication of a special volume based on the meeting through CRC Press. A special issue of the journal 'Historical Biology' will be coming out in 2007 with some papers from poster presenters. To whet your appetite until then, the meeting abstracts are available on the website www.tethys.org.uk/biogeography as a PDF.

We will be migrating the meeting website to a permanent on-line archive soon, and will make as many of the speakers presentations available as possible. Anyone who is interested in copies of the software and resources that were distributed at the meeting should contact Al McGowan by email (a.mcgowan@nhm.ac.uk).

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Spotlight

A Taxonomy of Taxonomy and Taxonomists

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On 1st March, 2006, a Network of Excellence, "Towards the European Distributed Institute of Taxonomy" (EDIT; www.e-taxonomy.eu), with the purpose of integrating European taxonomic research and funded by a grant from the European Commission's 6th framework programme came into existence. In addition to 23 institutions representing 11 European countries (Belgium, Denmark, France, Germany, Hungary, the Netherlands, Poland, Slovakia, Spain, Sweden, and United Kingdom), EDIT includes four institutions (two Russian, two American) and two network organisations, Species2000 and Society for the Management of European Biodiversity Data, which constitute an extra-European and a non-governmental component in the network, respectively.

With such a large-scale approach to taxonomy, it is crucial that a consensus of the meaning of the concept "taxonomy" is reached, or at least approached. We here offer our view of what taxonomy is, and of what taxonomists are. Being ourselves taxonomists, our approach is rather classificatory.

One aspect of taxonomy which is not open to discussion is that despite it European roots taxonomy is not a special European discipline. For political and funding reasons EDIT is from the outset focused on Europe. But taxonomy cannot survive and thrive if a global view is not adopted. We therefore invite anybody to comment on our ideas.

What is taxonomy?

Taxonomy is often considered a purely descriptive science, basically because it has its historic roots in the age of the Enlightenment (~1690-1780) when essentialism was prevalent, epitomised in Linnaeus' attempt to unravel the Creator's plan at Genesis. Additionally, its vocabulary points in the same direction as we describe species, make species diagnoses etc. Like the Human Genome Project taxonomy is not experimental, but not being experimental is not equivalent to not being hypothesis-driven. Today's species descriptions are based on a synthesis of a broad range of different data - including DNA data - making it possible to create interesting hypotheses about the distribution of attributes among organisms. It must be realised by our fellow biologists that taxonomy is not only a service to other biological disciplines but is an integral part of evolutionary biology, which makes it possible to test evolutionary hypotheses at all levels from the evolution of characters, over the evolution of species, to the evolution of clades. Species concepts, species delimitations, phylogenetic reconstructions, homology statements, character polarizations, and ultimately classifications are not static, but are scientific hypotheses which change as science progresses. The drawers and cupboards of any major collection are literally filled with a nearly endless number of untested hypotheses.

"The task of inventorying is sometimes mistaken for "stamp col-

lecting” by thoughtless colleagues in the physical sciences [sadly one might add and among ecologists and microbiologists]. But such information is a prerequisite to the proper formulation of evolutionary and ecological questions, and essential for rational assignment of priorities in conservation biology. Lacking basic knowledge about the underlying taxonomic facts, we are impeded in our efforts to understand the structure and dynamics of food webs, patterns in the relative abundance of species, or, ultimately, the causes and consequences of biological diversity.” (May 1999: 43).

Recognising and describing the living species on Earth and unravelling their relationships ("assembling the tree of life") is Big Science and its planetary scope makes it mandatory that all countries realise their responsibility for adding to this endeavour. The international taxonomic community is faced with a tremendous task as only 1.75 millions of the estimated 10+ millions species have currently been described. Meeting this challenge will require a fundamental restructuring of the way we do science. This amounts to more than a simple cry for more money and manpower. It necessitates fundamental changes in the manner taxonomists work, from one man projects in splendid isolation into team-works, and moving into cyber-space, doing cyber-taxonomy, e.g. online revisions and development of morphobanks (repositories of images etc.) that are searchable and can be manipulated online, etc. It is an effort that in magnitude by far surpasses the effort that went into sequencing the human genome.

For the purpose of the EDIT project, taxonomy is understood in a very broad sense similar to the one adopted by the work program for the Global Taxonomy Initiative (Decision VI/8 of the 6th Conference of Parties to the Convention on Biological Diversity, e.g. www.gti-kontaktstelle.de/toolk-

[it/workshop/GTI_Program_COP06.pdf](http://www.gti-kontaktstelle.de/workshop/GTI_Program_COP06.pdf)):

“Broadly understood, taxonomy is the classification of life, though it is most often focused on describing species, their genetic variability, and their relationships to one another. For the purposes of the Convention taxonomy is taken in its broadest sense and is inclusive of systematics and biosystematics at the genetic, species and ecosystem levels.“

In this broad sense, taxonomy includes various types of often tightly interlinked activities:

1. Recognition, description and naming of taxa (species, genera, families etc., also revision of older description, synonymisations, etc.) (\approx alpha-taxonomy).
2. Comparison of taxa, including studies of relationship (phylogeny) (\approx part of beta-taxonomy).
3. Classification of taxa (preferably based on phylogenetic analyses) (\approx part of beta-taxonomy).
4. Study of (genetic) variation within species (\approx gamma-taxonomy)* ,
5. Construction of tools for identification (keys, DNA barcodes).
6. Identification of specimens (referring them to taxa, using the tools)
7. Inventories of taxa in specific areas or ecosystems (using the tools for identification)

What is a taxonomist?

All practitioners of any of the above listed activities are per definition taxonomists. It may, however, be useful to classify taxonomists:

1. *alpha-taxonomists*: describe, name, revise and synonymise taxa
2. *beta-taxonomists*: compare and classify taxa, make phylogenies
3. *gamma-taxonomists*: study intraspecific variation
4. *tool-makers*: construct keys and other identification tools
5. *tool-users*: identify specimens, make inventories

Any taxonomist may belong to more than one category, and most probably do. More generally, a taxonomist should in the future be a scientist who feels equally at home in the field, in the collections, in the lab, and in front of a computer.

Taxonomy and collections

Taxonomy has been described as a low-cost science. That taxonomy is 'cheap' is not true, and has never been true, although relatively expensive sequencing facilities, etc. are a recent addition to the taxonomic toolbox. The singularly most important resource for taxonomists are the natural history collections in museums, botanical gardens, etc. Without these collections, including the type-specimens which play a key role in stabilizing the use of species names most high level taxonomic research cannot be conducted. **Taxonomy is a collections-based science.**

There is a positive feed-back between (taxonomic) research and collections: the better the collections, the better the collections-based research, and the more and better this research is, the more useful and better the collections are for future research. Collections are an irreplaceable resource assembled over the last 250 years, which are not used up, but gain in value by being used.

Non-considered aspects

We have deliberately avoided entering the rather futile discussion of systematics versus taxonomy (cf. the Global Taxonomy Initiative definition we have used) and we have also not provided an extensive list of references either, although a very large number of authors have written about taxonomy as a discipline. For those interested, Wheeler (2004) is a good starting point.

*However, this does not encompass population genetics and population biology per se.

References

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Prizes for best poster and talk at the 7th Young Systematists' Forum, Natural History Museum, London, December 2005

The winners of the poster and talk prizes the last YSF are Ruth Eastwood for best poster, and Simon Loader for best talk. Congratulations! Here follow brief biographic sketches of our winners.

Best talk Simon Loader

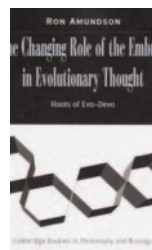
Simon Loader has eight years of field and lab experience with the herpetofauna of East Africa. Initially this was as a volunteer in 1997 and then as an Assistant Research Coordinator with Frontier Tanzania in 2000, following the completion of an MSc in Advanced methods in Taxonomy and Biodiversity at Imperial College and the Natural History Museum in 1998. He completed his PhD studies on the biogeography of Eastern Arc amphibians in 2005, based at the University of Glasgow and the Natural History Museum London. As a post-doctoral researcher his work continues to focus on African amphibians, especially caecilians and microhylid frogs of East Africa.

Best poster Ruth Eastwood

Ruth Eastwood is just completing her D.Phil at the University of Oxford. She has been investigating the systematics of Andean lupins and the origin of a domesticated species, *Lupinus mutabilis*. This project involved traditional taxonomy, fieldwork in the Andes and molecular systematics. Ruth has strong interest in botany, natural history and gardening which has been cultivated from an early age. She is also a keen photographer, specialising in close-ups of plants and animals.

Book Reviews

Embryos and Evolution



A review of Amundson R, 2005. *The changing role of the embryo in evolutionary thought. Roots of evo-devo*. Cambridge University Press, Cambridge.

Ron Amundson's book *The Changing Role of the Embryo in Evolutionary Thought* is the 26th in the *Cambridge Studies in Philosophy and Biology* series. He sets out to explore the relationship between development and evolution, the subtitle reflecting a modern pre-occupation: *Roots of Evo-Devo*. As Amundson writes in his introduction, "At the annual meeting of the Society for Integrative and Comparative Biology in January of the year 2000, a new division was formed: the Division of Evolutionary Development Biology". "In the minds of many of its practitioners", Amundson continues, "evo-devo was new... Nevertheless, the subject is more than 150 years old" (p. 1). Why, then, in 2000 would it be

regarded as a new field? Amundson explores the idea that "only a minority of biologists believed that ontogenetic development had *any relevance at all* to evolution" (p. 1, his italics). His book is a history of evolutionary biology – a different history.

When summarising the book's contents, Amundson offers, if perhaps just a little too cutely, that he will "write his revisionist history of evolutionary theory, offering an alternative to SH..." (p. 27). Here SH is Synthesis Historiography, the traditional narrative designed to explain the rise of the synthetic theory of evolution (the modern synthesis), associated with the claim that essentialism (and typology and by extension morphology) haunted and retarded studies in evolution, systematics and taxonomy for 2000 years, succinctly captured by the title of David Hull's contribution to the subject: "The effect of essentialism on taxonomy: 2000 years of stasis" (Hull 1965a, b). The 'typology-essentialism-morphology' story, created in 1959 and solidified in the mid-1960s, was primarily the creation of Ernst Mayr, Arthur J. Cain and David Hull (Winsor 2003). In the late 1960s it was promoted by Michael Ghiselin, reaching its climax in the new century providing philosophical justification for the application of the *Phylocode* to the naming of organisms (Ereshefsky 2001, another volume in the *Cambridge Studies in Philosophy and Biology* series), the whole forming a "miserable history of depreciatory comment without a particle of truth" (Nelson 2004). Revision of this history began with Polly Winsor's study (2003) but earlier, as noted by Amundson, (p. 208) the anthropologist Scott Atran, for example, captured the spirit of critique in his 1990 book *Cognitive Foundations of Natural History*, ably summed up in this paragraph: "For my part, I have so far failed to find any natural historian of significance who ever adhered to the strict

version of essentialism so often attributed to Aristotle. Nor is any weaker version of the doctrine that has indiscriminately been imputed to Caesalpino, Ray, Tournefort, Linnaeus, A.-L. Jussieu and Cuvier likely to bear up under closer analysis...to reduce all this to 'two thousand years of stasis' is to nullify a monumental movement in human thought – a movement which, by the eighteenth century, was at least able to offer up the whole of the living world, including man, as an object of study and insight" (Atran 1990, p. 84).

The critique is not new, as many working scientists (as opposed to historians) had already detected flaws in the story (see Winsor 2003, p. 389, for examples). Thus the use of 'essentialism' by taxonomists before Darwin and the idea that Darwin ushered in a revolution forcing taxonomists to switch from typological thinking to population thinking has no basis at all. If anything, "Darwin's theory provided an explanation for the hierarchical shape of nature that taxonomists had discovered" (Winsor 2003, p. 387 but see below) and had nothing whatsoever to do with 'population thinking'. By implication, of course, the entire Synthesis Historiography is "without a particle of truth".

Amundson situates his account within this revisionist history. He gives a full explanation of the 'population thinking versus typological thinking' conundrum, detailing the evidence for the essentialist position – or lack thereof: "...it is embarrassing how very slim the historical evidence was for the Essentialism Story...Quotations that merely demonstrated an author's commitment to species fixism were taken as proof of the essentialist underpinnings of this belief" (pp. 204–209). Amundson explains how and why he came to write this book: "...many histories of evolutionary biology had been written by people who considered the Evolutionary Synthesis to be essentially correct

about evolutionary biology, including its modern alternative theories that involve development" (p. 10). Thus, or so it seems, the stage was set for revising this history, now capturing development as a major factor in evolutionary studies – a

Amundson offers, if perhaps just a little too cutely, that he will "write this revisionist history of evolutionary theory to SH..." Here SH is Synthesis Historiography, the traditional narrative designed to explain the rise of the synthetic theory of evolution

factor assumed neglected – thereby enhancing evolutionary biology making it a richer subject altogether, and placing the 'new' science of evo-devo at its centre, or at least near its heart.

The book is divided into two parts of roughly equal size: "Darwin's Century: Beyond the Essentialism Story" and "Neo-Darwin's Century: Explaining the Absence and the Reappearance of Development in Evolutionary Thought". The first part, 'Darwin's Century', explores the Natural System, its form, discovery, meaning and interpretation, beginning with Linnaeus (Chapter 2), dovetailing into a chapter on the origins of morphology, beginning with Goethe (Chapter 3). Halfway through Part 1 of Chapter 4 the general concept of evolution is introduced, contrasting Richard Owen with Charles Darwin, archetypes with ancestors, followed by a brief review of the first evolutionary morphologists, primarily Carl Gustav Gegenbaur and Ernst Haeckel, both of whom saw development as an essential ingredient for evolutionary biology (Chapter 5). Of significance is the discussion of the biogenetic law – or at least Haeckel's version of it, via the work of Fritz Müller – and the early explorations of phylogeny with respect to ontogeny. Haeckel is indeed significant, but in a sense I believe Amundson misses, a topic I return to below.

Chapter 6, while still within Part

I of the book, is an Interlude and it is here I believe Amundson misses a beat and possibly creates another history. In this chapter he describes "Darwin's Other Primary Achievement – The Tree of Life": "Darwin's *Origin* was designed not

merely to prove that species can change, but also to prove that *the shape of the Natural System can be explained by common descent*...Darwin showed how to reinterpret the *real* Natural System as a genealogy" (p. 133). Haeckel is indeed relevant – as is relates to Amundson's theme of species fixity versus species transformation. It was Haeckel, of course, who published the first 'proper' phylogenetic trees. After all, phylogeny was his word (Haeckel 1866). But to find the right form to represent phylogeny, Haeckel's influences were somewhat eclectic and are worth dwelling on a little. Alongside Darwin, Haeckel absorbed the work of palaeontologist Heinrich Georg Bronn and the linguist August Schleicher (Williams In Press).

Haeckel read the German translation of Darwin's *Origin* between 1860 and 1861. The book had a significant impact on him. The German translation was prepared by Bronn, who added his own 15th chapter outlining some of the difficulties he had with Darwin's views. Interestingly, and relevant to Amundson's more general thesis on species fixity versus species transformation, Bronn noted that distinguishing between the two was beyond empirical resolution and amounted to a commitment of belief (Bronn, 1860). For while Bronn states his enthusiasm for Darwin's general thesis, he suggests that it

remains simply a hypothesis, one “possible scenario of life’s history”. Haeckel realised that he could assist Darwin’s cause by marrying the systematic arrangement of organisms, as revealed by the hierarchical ‘natural system’ (their classification), with a graphic representation of genealogy, a pedigree of species. He found one way to represent a pedigree in Bronn’s work, with a branching diagram relating various groups of animals to each other (Bronn, 1858, p. 481, reproduced on the dust jacket of Bowler, 1976).

He found another way in the work of August Schleicher, with whom he became good friends, “...the historical significance of their friendship is enormous” (Alter, 1999, p. 117). Haeckel convinced Schleicher to read Darwin’s *Origin*. Schleicher did so and was immensely impressed as he was able to argue that contemporary languages have also undergone a process of change, not too dissimilar from the one Darwin suggested for organisms: evolutionary theory thus *confirmed* language descent, rather than suggesting it: “these assumptions [the origins of an Indo-European language family], deduced logically from the results of previous research, can best be depicted by the image of a branching tree” (Schleicher, 1853, p. 787, translation from Koerner, 1987, p. 112). “...Schleicher’s greatest and lasting contribution to evolutionary understanding may simply be the use of a *Stammbaum* to illustrate the descent of languages...Haeckel quite obviously took his inspiration from his good friend Schleicher. And Haeckel’s *Stammbäume* have become models for the representation of descent ever since” (Richards, 2002). Schleicher was convinced that the evolution of languages provided definitive evidence for the evolution of man and a way of tracing their development. His arguments for linguistic superiority are remarkably similar to those offered today for DNA sequence

data – a universal ‘higher criterion’ and the source of data that made contemporary evo-devo possible, reducing morphology to a series of developmental processes rather than additional, independent evidence for the relationships among organisms. In any case, Haeckel’s genealogies set about representing the transformationist view, graphically and literally.

Haeckel invented the word phylogeny for the “tribal history, or ‘palaeontological history of evolution’”, “Phylogeny includes palaeontology and genealogy” (Haeckel, 1874, p. 710). With palaeontology firmly in mind as the prime source of evidence for genealogy, Haeckel delved into ontogeny and its potential relevance: “This palaeontological history of the development of organisms, which we may term *Phylogeny*, stands in the most important and remarkable relation to the other branches of organic history or development, I mean that of individuals, or Ontogeny. On the whole, the one runs parallel to the other. In fact, the history of individual development, or Ontogeny, is a short and quick recapitulation of palaeontological development, or Phylogeny, dependent on the laws of Inheritance and Adaptation” (Haeckel, 1876). In a round about way, Haeckel was alluding to the three-fold parallelism, a subject he returned to periodically: “The first rough drafts of pedigrees that were published in the *Generelle Morphologie* have been improved time after time in the ten editions of my *Naturalische Schopfungsgeschichte* (1868—1902)...A sounder basis for my phyletic hypotheses, derived from a discriminating combination of the three great records – morphology, ontogeny, and palaeontology – was provided in the three volumes of my *Systematische Phylogenie* (Berlin, 1894-96)” (Haeckel, 1909). Yet this version of the threefold parallelism was from Louis Agassiz, who remained an opponent of Darwin’s

throughout his life.

I mention this summary ‘additional’ history, as it represents not the development of evolutionary biology, which as Amundson documents in the second part of his book is intimately connected with the study of the mechanisms of inheritance (pp. 139—168). It represents the history of systematics, the study of the Natural System *after* Darwin. In Part II of Amundson’s book, he proceeds as if systematics had little, if anything, to offer after Darwin ‘explained’ the “groups within groups”. Indeed, in the second part of his book, *Systematics* and *Phylogeny* receive two short chapters summarising the effects of the synthesis on these endeavours, together these passages contributing roughly a page. Amundson does note that “Higher taxa regained their importance only after cladist methods placed their determination on sounder footing in the 1970s and thereafter” (p. 167) – and he footnotes a comment that “Some [cladists] are resentful of the period of new systematics”. Resentful is an emotional reaction. That the core is a “miserable history of depreciatory comment without a particle of truth” is open to historical investigation.

In this connection, developments in European morphology and systematics are of interest – if not for the shameful neglect they have received as a topic of historical enquiry. For example, Amundson mentions in passing (p. 126) the remarkable Swiss biologist, Adolf Naef, who, in Amundson’s opinion, was a “flawed idealist phylogenist”. That characterisation – almost self-contradictory – requires exploration but impression gained from reading just a sample of Naef’s work indicates his perceptive critique of evolutionary morphology after Darwin – or more appropriately, after Haeckel. Naef was among the first serious critics of Haeckel, stripping away his excesses and fanciful ‘ancestor worship’, proposing a coherent ‘*systematic morphology*’, a

way of studying the *Natural System* in the knowledge that organisms are related through descent but not relying on that fact. Development (ontogeny) was important to Naef, who proposed a formulation that became known as ‘Naef’s theorem’, “Morphogenetic processes of an

‘form’, the *Natural System*. Quite what role is played by molecular systematics in any reformulation is of obvious interest.

It is a pity the history of systematics *after* Darwin is not perceived as relevant to progress in evolutionary biology, absent entirely from

It is a pity the history of systematics *after* Darwin is not perceived as relevant to progress in evolutionary biology, absent entirely from many accounts

ontogenetic stage through whose modification a following stage arises are to be looked upon as phylogenetically older than those which grew out of them”.

In turn, Naef was to be an influence on the brilliant palaeo-ichthyologist Erik Stensiö, who created the Stockholm school of palaeozoology. This school became the spiritual home for another generation of palaeo-ichthyologists (Gareth Nelson, Colin Patterson, Nils Bonde, Roger Miles and Philippe Janvier, among others), who forged the cladistic revolution of the 1960s, demolishing the second wave of ‘ancestor worship’. These morphologists understood the decisive nature and relevance of ontogeny in determining the relationships of organisms (Williams & Ebach, Submitted). Now, alas, we happen to be amidst a third wave.

Never mind what happened in evolutionary biology, in systematics ontogeny neither vanished nor retreated but remained of central significance. In truth, it may just not be possible to answer or even investigate Amundson’s pivotal issue: the struggle to find a “...conceptual connection between the development of an individual (ontogeny) and the evolution of a lineage (phylogeny)...” (p. 1). That problem may very well have been solved some years ago when Nelson (1978) reformulated the threefold parallelism, noting that morphology, palaeontology and ontogeny are but evidence for the regularity of

many accounts (e.g. Love 2006). Amundson may have captured the common perception, through the lens of Peter Bowler’s book (1996) and the catchphrase of William Diller Matthew, that “phylogenetic history was *Life’s Splendid Drama*, an interesting narrative that served no important theoretical purpose” (p. 167). That statement is almost unequivocally false – and is detrimental to progress in evolutionary studies. Rather than dwell on this point, one might turn to the discussion of homology, treated by Amundson as a problem of cause, of origin, when in reality it is a problem of systematics, of how to discover the “groups within groups” (pp. 238–244).

Amundson notes David Hull’s claim that the historical work he undertook in the 1960s and 1970s was “history done in a good cause”. Thus, as Amundson notes, “His [Hull’s] good cause was won (with his able help), and my good cause is a different cause” (p. 10). Hull has recently written that “...Cain, Mayr, and Hull used history in their promotion of ‘the’ synthetic theory of evolution, several in Winsor’s group are using it to further their own EvoDevo ends” (Hull 2006, p. 19). So be it. But such actions are sociological not historical, about promotion and ‘good causes’, as Hull would readily admit. In any case, it might be problematic to identify universally accepted good causes anywhere, never mind in science. Nevertheless, it will not escape the

notice of other systematists that Hull was responsible for writing a ‘history’ of cladistics (Hull 1988), which now one might well regard as “history done in a good cause” rather than objectively, regardless of what that particular ‘good cause’ might have been. History suggests many things but “...by its nature [it is] an act of hindsight, of understanding, or understanding better, what was understood less well at the time, or of *understanding again what has been temporarily forgotten*” (Barnes 2002, p. 9, my italics).

Amundson has written an interesting book, one worth reading. As a systematist with a concern for history rather than ‘good causes’, it still leaves me feeling much of interest is neglected (Williams & Ebach Submitted). Until that time comes, “those who cannot remember the past are condemned to repeat it”, and those who invent it should simply be condemned.

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Why taxonomy is fundamental to conserving the plants of this world



A review of E. Leadley and S. Jury (eds.), *Taxonomy and plant conservation*. Cambridge University Press, Cambridge.

(inset: Vernon Heywood, to whom the book is a tribute)

This book is a great concept, pulling together the fields of taxonomy and plant conservation in one place to emphasise the important basis that taxonomy provides for many different aspects of conservation. It is something that many taxonomists talk about in the abstract but the compilation of concrete examples of successes and problems has the potential to be a valuable resource.

The book is also a celebration of the career, body of work and influence of Vernon Heywood and the first chapter begins with an apt quote from him, setting the tone: “taxonomy...the lonely voice speaking on behalf of an interest in diversity”. The layout is in four parts, part one covering a general introduction. Chapter one (Crane and Pleasants) discusses taxonomy and the future of plant diversity science and is a good opening for a selling document for taxonomy. In the brief history there is perhaps a bit of a simplistic linear sweep from folk taxonomies to molecular techniques and phylogenetic analysis with less emphasis on the continued importance of all of the tools in a taxonomist's kit. There is a useful history lesson, including more recent history and introduction to many recent important acronyms such as the CBD (Convention on Biological Diversity), the GTI (Global Taxonomy Initiative), GSPC (Global Strategy for Plant

Conservation) and MSB (Millennium Seed Bank). Many of these recur throughout the book and if they aren't familiar, I recommend this as useful background reading for anyone involved in taxonomy or plant conservation. As a taxonomist it was nice to have this summary of many pieces of legislation and organisations that I knew of but not in detail.

Chapter two (Paton, Williams and Davis) introduces other important acronyms such as GBIF (Global Biodiversity Information Facility) and CONABIO (Comisión nacional para conocimiento y uso de la biodiversidad). I especially appreciated the clear inclusion of targets and guidelines from some of the most important documents such as the CBD. This chapter makes a very good point that those countries that need the most taxonomic work have few overstretched taxonomists and are the exact people who do not have time to write detailed applications for funding.

The second section covers the practise of taxonomy starting with a very clear and vibrant chapter (Stuessy) leaving the acronyms behind and going on a brief historical romp from the Ancient Greeks to the APG (Angiosperm Phylogeny Group - so not entirely acronym free). There are some nice principles and diagrams and a very clear description of the taxonomic process. Although again the story of data types is given as a progression from morphology through cytology and SEM (Scanning Electron Microscopy) to DNA (Deoxyribonucleic acid), without referral to the continuous use of multiple evidence types. For those who like controversy, there is even a brief allusion to web publication and registration of names.

Chapter four (Cullen and Walters) discusses the recent proliferation of plant families, linking the topic into the book using reference to Vernon Heywood again, giving a cohesiveness and personal touch. There is an

interesting discussion of the practicalities and usefulness of classifications and taxonomies derived from different theoretical standpoints.

And then there is a very impressive table documenting 662 published family names. I found this initially confusing as the table referred to in the latter part of the text is after the references, but understandable due to the sheer size of the table which is there to make a simple point that there is a lot of splitting going on at the family level (apparently cladists are to blame, particularly molecular ones). What is important is that this creates instability and leads to potential confusion for users.

There is a concise case study of the Flora Iberica work (Castroviejo) which clearly exemplifies the importance of detailed taxonomic

work for conservation status and priorities followed by an even more detailed chapter on nomenclature (Brummitt). This includes possibly too much detail for the general scope of this book and seemed slightly out of place, but then again it is important information for those who are interested. Despite being one of those interested in this topic the density and detail did get a bit much and I would have appreciated a bit more effort to explicitly draw the link between nomenclature, taxonomy and conservation (something the previous chapter did clearly in one line). Chapter seven (Prance) is another concise contribution looking at ways of making taxonomic research more accessible and more useful to those unfortunate enough not to be taxonomists themselves (my bias added).

Part three investigates the issues of establishing priorities in conservation. The first chapter (Humphries) has a very dense writing style and seems the least tailored to this book, using a lot of jargon and a preponderance of animal

examples. Despite this it covers very interesting ideas and I think the concepts of trying to measure the representativeness of evolutionary lineages as a priority system for conservation is a very important topic, however it is not as easily accessible or readable as other chapters. The following chapter (Richard and Evans) deals with another approach, that of conservation areas, with a focus on Europe. This is a clear broad introduction to conservation and might have been a better starting chapter for this section. It contains wonderful real examples of incorrect use of taxonomy and nomenclature inhibiting conservation progress.

One of the highlights for me was the chapter on the Medusa project (Skoula and Johnson), covering

The book is also a celebration of the career, body of work and influence of Vernon Heywood

Mediterranean plants that are used by humans for multiple purposes. It was very clearly tied into the book's theme and showed another viewpoint of taxonomy end users. Chapter eleven (Grayer) is a good flow on, giving more in-depth information about chemotaxonomy. Despite the use of chemical compounds in taxonomy having been alluded to in the introductory chapters on the way to DNA supremacy, chapters ten and eleven give a compelling argument for their continued inclusion in taxonomic treatments. An interesting point is that one reason given for plant conservation is the potential usefulness of plants for humans but that sometimes the usefulness of a plant leads to its need for conservation due to overuse.

The last ten chapters constitute part four and cover conservation strategies. In discussing the conservation of island floras using pithy quotes as subheadings the first chapter (Bramwell) is an interesting addition as it exposes the soft vulnerable underbelly of taxonomy - the timeless debate of what is a species. The

chapter uses a great analogy of waves in the ocean for species, but in a world demanding certainty - eg lists of species known by 2010, admitting the in-built trials and tribulations of species delimitation seems somewhat dangerous if applaudably honest. The following chapter (Rich) continues in the vein of why taxonomy fails us in some difficult to identify groups. This is a clear pragmatic view from someone

currency of biodiversity” goes to show just how important it is for systematists to spread their understanding to a wider audience. This chapter was another high point in the book for me.

Another clear and thoughtful contribution (Blackmore and Paterson) covers botanic gardens using gardening analogies. A discussion of the downsides of hotspot protected area choice is included, along with

Overall I think this book fulfils its potential as a very valuable resource that is relevant to a wide audience

who is obviously on the ground doing conservation work. I particularly like the phrase “...the taxonomist can be usefully applied...”, like a salve or a computer algorithm.

There are then chapters covering conservation strategies involving in and ex situ reintroductions, emphasising the need to identify local variants (Akeroyd). A rattan case study (Dransfield) gives clear evidence of the necessity of good taxonomic knowledge based on binomials, not common names, as well as taxonomic assessments that cross country borders. The importance of user friendly outputs from taxonomic work such as interactive keys based on serious science cannot be stressed enough. Molecular systematics is covered in a chapter (Culham) where it is interesting that, in a book concerned with correct application of taxonomy and names, the text refers to *Olea europaea* subsp. *laperrinei* but the caption for the picture says only *Olea europaea*.

Legislation is discussed (McGough) using CITES as an example, highlighting the important role of scientific experts on committees. This is a nice case of taxonomic expertise being valued in significant decision making processes. The idea of police and custom officials being enthralled by “their introduction to taxonomy as the international

the management of protected areas. There is more on the importance of botanic gardens in habitat restoration as living repositories of information and the fundamental question of what moment in time to preserve. The last three chapters come back to the beginning again, as all good story arcs do. There is a brief recap of the book so far (Leadley, Willison and Wyse Jackson) and more detail about botanic gardens and the importance of collaboration, another issue close to Vernon Heywood’s heart. My favourite image of the book is a group of proud traditional healers in Mexico holding up their herbarium specimens during a basic plant taxonomy course. The penultimate chapter (Smith) covers wild seed banks and the point is made again that taxonomists often write for a specialist audience and apparently there is a 13 point strategy for how to remedy that situation for Floras, which unfortunately was not included. The very last article (Jury) is a quick ride through some very impressive collaborations, hopefully something there will be more of in this continually globalising world.

Throughout the book I wondered exactly who the target audience was. If it is aimed at taxonomists, much of it is preaching to the converted while other sections are aimed squarely at teaching taxonomists to play better with others

(eg nice interactive keys etc). On the other hand, some of the chapters assume a lower level of taxonomic expertise and seem aimed at those who use taxonomy as a window into the specialised world we inhabit and a prospectus for why funding should be given to such work. The difference in voices and intent do not make a dissonant whole, but make the book accessible and useful for multiple audiences. Few people will read the entire book from cover to cover, but dip into the chapters that interest them or are of relevance to their research or question. To this end I think the diversity of approaches offers a flexible read with something for everyone: nomenclature specialists, morphology based alpha taxonomists, genetic systematists, cladists, phylogeneticists, chemotaxonomists, natural medicine practitioners, agricultural users, ecologists, planners, government agencies and the list goes on.

Overall I think this book fulfils its potential as a very valuable resource that is relevant to a wide audience. It links the globally significant worlds of taxonomy and plant conservation, and I hope it graces the shelves of many, enthusing them about these vitally important fields.

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**Details of the SA
research grants, con-
ference bursaries and
funding for the organi-
sation of meetings can
be found at:
www.systass.org**

Inspirations

For many systematists the mainspring of their work chiefly resides in the intellectual arena, as the interminable hours behind the microscope or with pipette in hand offer little in the way of visceral excitement. Some of us, however, go significantly beyond the practical drudgery of handling dried and pressed corpses of plants and the decolorized and shriveled remains of liquid preserved animals. Bryan Grieg Fry is emblematic of those rare systematists whose work combines equal parts Indiana Jones and Q. Spending many months every year in the field, Bryan hunts some of the world's most venomous animals, mostly snakes, which he then milks for what he is most interested in: their venom. In a series of remarkable papers Bryan has created unexpected insights into the origin and evolution of snake venoms, the echoes of which reverberated even as far as the pet trade. He revealed that even archetypal non-venomous pet snakes, such as the Asian ratsnake, produce potent neurotoxins. For this and other work Bryan was awarded the 2004 Zuckerkandl Prize for that year's most significant contribution to molecular evolution in the *Journal of Molecular Evolution*.

This issue's *Inspirations* features Bryan Fry. Born in 1970 Bryan has already made significant contributions to our understanding of the evolution and pharmacological effects of snake venoms, some by unfortunate first hand experience. Early during his PhD studies Bryan hunted down his first Stephen's banded snake. As far as anybody knew at the time, these snakes were not dangerous. "I clearly discounted this as my body hit the ground seconds after the bite" recalls Bryan.

Visit Bryan's webpage www.venom-doc.com to find out how this painful accident ended, and how it unexpectedly led him to a central focus for his PhD studies.

Introduction

Can you provide a capsule review of your career to date?

I did a dual honours degree (molecular biology and scientific philosophy) at Portland State University in the USA, then a Ph.D. (awarded in 2002) in Biochemistry at the Institute for Molecular Biosciences at the University of Queensland. I am currently the Deputy Director of the Australian Venom Research Unit at the University of Melbourne.

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

Ever since I was a small child, all I have ever wanted to do is work with venomous snakes for a living. I consider myself to be absolutely blessed to be doing for a career what was my childhood dream.

What are the main goals of your research?

My research has several parallel goals: understanding the intricate relationships between venom evolution and the ecology/evolution of the animals themselves; the mechanisms by which venom evolved; and how to harness the incredible molecular diversity of venom proteins as lead compounds for use in drug design and development. The best place to find a novel toxin is from a novel venom and the most novel venoms are likely to be found where significant evolutionary changes have

occurred in the snakes. So it all ties nicely together.

How is information from systematic biology important to your work?

A proper systematic framework of the animals is absolutely essential for all aspects of my research. It is quite simply the essential skeleton of my entire research program. Without a robust phylogeny the variations observed between different taxa would be meaningless and a phylogenetic framework is essential as well for clarifying my work's theoretical and practical implications. Without an understanding of the animals themselves, the forces driving changes of venom would remain obscure. Without understanding the forces driving the changes in venom, the search for novel toxins would rely upon random sampling, hardly an efficient mode of investigation. So at the end of the day, it is absolutely imperative that I have a reasonable understanding of animals themselves. To this end, I have a very active collaboration with Blair Hedges from Penn State University, USA and Nicolas Vidal, Muséum National d'Histoire Naturelle in France [Hedges and Vidal apply molecular data to high-level snake phylogeny (ed).].

What are your favourite organisms and why?

Snakes are my personal favorites but anything venomous is fun to work with.

Work and responsibilities

How much do you work?

I work every day, whether at home working on the computer analyzing data, in the lab creating new data, or caring for the animals that are the ultimate source of all the data.

What percentage of your time do you spend on each of your differ-

ent responsibilities?

I travel extensively. At least four months a year overseas and at least three months out in the field in Australia. Lab work is done in intensive bursts, accounting for about 3 months of the year. The rest of the available time is taken up writing grants, papers and doing generic papershuffling.

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

Due to the extreme travel of the last couple years, I have been spending more time in collaborators' laboratories than in my own and consequently haven't been taking many students or staff on. I will start expanding my laboratory again next year to have it back up to a half dozen Ph.D. students, two postdocs and a technician.

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

The most satisfaction is discovering something new and interesting about the animals that I have such fascination for. The most frustrating is that there are so many snakes, so little time.

Do you have any international collaborations?

Extensive. For example, in the recent *Nature* paper [2006, vol. 439, 584], there were fourteen authors, from twelve laboratories based in six countries. During the course of that study, I visited every single one of those laboratories. This was absolutely essential for the success of the project.

Fieldwork

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

My field work is very extensive. It has taken me high up in the rainfor-

est canopy, fifty meters below the ocean and everywhere in between. I prefer to collect all the animals I work on myself. This is what gives me my competitive advantage. If I work on venom that can be purchased from Sigma, then I could be working on the same project as anyone from here to India. Hardly a key to success. By collecting animals no one has ever worked on before, I can have a monopoly on the area. Much more efficient. And of course, much

We can't predict the future, but we can prepare for it. Every member of the field team has to have a current first aid certificate and their own personal first aid kit that is kept on them at all times when away from base station. We also travel with a satellite phone when in the field. If we are going really remote or out to sea, we bring our own antivenom and an emergency physician.

Influences



A stand-off between Bryan and a monitor lizard.

more fun that way.

What kinds of organisms have you collected?

Everything from centipedes to cobras to stingrays to scorpions.

Did any memorable incidents happen during field collecting?

Fieldwork is always full of incidents, whether it be having a giant termite mound collapse while I was at the top of it trying to get a lizard out, sending me free falling four meters flat on to my back (it was OK, the ground broke my fall), the usual bumps, scapes and cuts, the occasional broken bone or, of course, an envenomation. That is why we always prepare for any contingency.

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

Snakes: The Evolution of Mystery in Nature (Harry Greene) and *Australian Snakes : A Natural History* (Richard Shine) are two books that have profoundly influenced my philosophical outlook.

Who was the most important mentor in your career?

Elazar Kochva has had the biggest impact upon my career. Elazar has been working on the evolution of venom since before I was born. His insights are truly humbling. I firmly believe that if the molecular tools we have today were available to him,

much of what I am doing would have been done many decades ago. It is the classic case of standing on the shoulders of giants.

What is the best advice you have ever received?

To use my passion as fuel.

Output

How many scientific publications do you have at the moment?

29

On how many toxins and with how many species have you approximately worked so far?

I have sequenced several thousand toxins and have worked with several hundred reptiles and a few hundred other venomous organisms (stingrays, centipedes, scorpions and others).

Which of your papers do you personally find most important or do you like best?

The recent paper in *Nature* on the single, early evolution of venom in reptiles was the most important and one that was a huge amount of fun to collect the animals for, the laboratory work was a huge mountain to climb and as a result reaching the summit of this study was the sweetest feeling of my life. Second of course only to the day I married my best friend (Alexia).

You have an elaborate website dedicated to your work. Why did you decide to do this, and do you think it is important?

I think scientific communication is tremendously important. If for no other reason that my work is publicly funded and therefore I have an obligation to disseminate the knowledge

gained. Many scientists complain that the general public doesn't 'get' their research, but they do nothing themselves to help them get it. An unexpected side effect of doing the scientific communication is that I think it has made me a better scientist. To explain my work in a five minute talk that any one can understand is much more difficult than writing a journal article. It requires absolute clarity of thought. Before I started doing lots of scientific communication, I would get comments back on grant proposals such as 'diffuse and difficult to penetrate'. Now the comments are more along the lines of 'clear, easy to understand and well-organised'.

Is there a particular contribution you generally bring to papers with multiple authors?

What I bring to the papers is the discovery itself. However, discovery is not enough. Every aspect of it has to be elucidated in a rapid but high quality manner. So I bring specialists on-board to do a particular task as needed. In the current studies, my personal laboratory contributions range from collecting the animals, milking them for the venoms, isolating the toxins, constructing and sequencing the cDNA libraries and undertaking the molecular phylogenetic analyses. Depending on what is needed, I may bring in a specialist in peptide synthesis, pharmacological analyses, molecular modeling, histology, etc. Whatever is needed to obtain the complete picture.

Advice

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

The same as in any discipline: passion and a high tolerance for mental pain. The race for quality has no finish line, technically it's more like a

death march. The greater the success, the greater the investment of hard work it took to get there.

Do you have any tips for students aspiring to a career like yours?

Find an area your are passionate about, obtain a unique suite of skills and carve out your own unique niche.

Calendar

December 6, 2006
SA AGM and Annual Lecture
Lecture by Barry Leadbeater:
Simple but Smart: How our closest Protozoan Relatives (the Choanoflagellates) Conquered the World. The lecture will be in the Lecture Theatre of the Linnean Society, Burlington House, London.

December 7, 2006
Young Systematist Forum
Flett Theatre, The Natural History Museum, Cromwell Road, London
Contact: Jonathan Bennett (j.bennett@nhm.ac.uk), Juliet Brodie (j.brodie@nhm.ac.uk)

December 31, 2006
Deadline SA Research Funds
See SA website for details and application forms.

June 2007
A Linnean Tercentenary Celebration: The Evolution of the Animal Phyla
The Royal Society, London
Contact: Max Telford (m.telford@ucl.ac.uk), Tim Littlewood (dtl@nhm.ac.uk)

August 28-31, 2007
Systematics Association Biennial Conference
Royal Botanic Garden, Edinburgh
Competitive student bursaries available based on abstracts that need to be submitted by 31 December 2006. See the Association's website for further information.

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