
COMMENT AND OPINION

The editors welcome contributions to this new section, which will contain comments or critiques on previous papers and other contributions on matters of current taxonomic interest or controversy.

Money, Morphology and Molecules

Some comments on Wortley, Bennett and Scotland (2002), *Taxonomy and phylogeny reconstruction: two distinct research agendas in systematics* (see p. 335 of this issue)

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The state of systematics, for convenience here divided into taxonomy (the delimitation, description and inventory of species) and phylogeny reconstruction, is evaluated. Molecular systematics may seem overemphasized, but the resulting gains made in our understanding of relationships in a relatively short time are very considerable. Although morphological data currently play only a limited role in detecting large-scale phylogenetic pattern, the analysis by Wortley *et al.* of the role morphology has played in the past is not easily interpreted. At species level, it is unclear what effect molecular techniques will have on our understanding of species limits, but it is likely to be considerable. Although taxonomy is both essential and underfunded, there seems little point in asking for more money until we can justify the limits of the species we describe more clearly and until we have cleared up the impediments that so much slow the practice of taxonomy. Business *cannot* remain as usual if any of the grand inventory projects we have started are to be finished within a reasonable time, or even to be of much use when they are.

Keywords. Funding, inventory, molecules, morphology, phylogeny, taxonomy.

INTRODUCTION

Wortley, Bennett and Scotland (p. 335 of this issue) decry the current imbalance within systematics. They document an oft-made observation (e.g. Kruckeberg, 1997; Lammers, 1999) that phylogeny reconstruction is being emphasized at the expense of the description, delimitation and inventory of species, taxonomy in the strict sense, which is largely ignored. This is despite protestations that taxonomy is indeed an integral part of systematics (e.g. Anon., 1994; Donoghue, 2001). In a novel twist,

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they claim that morphological data are not only insufficient for phylogeny reconstruction, but are the proper preserve of taxonomy. Finally, they want (British) legislators, at whom their paper is presumably directed, to increase support for (morphology-based) taxonomy.

We are indeed in a period when phylogeny reconstruction at the level of genus and above, and its implications for our understanding of evolution, is being emphasized. As an undergraduate, I was taught by E.F. Warburg, Brian Styles and Frank White – a formidable and well-informed trio, yet sadly and very much to the general point raised by Wortley *et al.* all now dead – and I can only marvel at how far we have come since then, and in a relatively short time. To think that *Avicennia* may be part of the immediate clade that includes *Acanthus* and *Thunbergia*, that *Podostemaceae* may be in or near *Clusiaceae*, that *Tepuianthaceae* are in *Thymelaeaceae* (compare *Solmsia* with *Tepuianthus*) and that *Icacinaceae* may be in three quite separate places within the Asterids, to mention only a few developments in the last couple of years! (For references see Stevens, 2001.) Basic plant morphology takes on an entirely new light as we understand the phylogenetic context within which morphological change can be interpreted, and of course as we find out more about the developmental basis of form and the evolution of development. I can only say ‘thank-you’ to the likes of the ‘Soltii’ (P.S. & D.E. Soltis); they have earned their places in the Science Citation Index.

MORPHOLOGY IN PHYLOGENY RECONSTRUCTION

In morphology, I include disciplines such as anatomy, embryology, chemistry and cytology. Is morphology of much value? On balance, Wortley *et al.* seem to think not. They estimate that only about 5% of all informative nodes (those with two or more terminal taxa) have been retrieved by morphological observations. Yet morphology can be accurate. They quote a figure of 73% for confirmation of the monophyly of families previously circumscribed by morphological data when subsequently using molecular data (presumably taken from Appendices 2–4 in Källersjö *et al.*, 1998). But some familial circumscriptions used by Källersjö *et al.* have been affected by molecular data, so 73% seems to be a very low figure, except that for only 13% of the families were there suggestions that they were not monophyletic. The status of the other 14% was unclear.

The familial circumscriptions of Cronquist (1981) did not draw on molecular data. Coincidentally, 72% of his families appear to be monophyletic when tested in subsequent molecular studies. I regard families such as *Gesneriaceae* as still monotypic, despite its possible acquisition of genera such as *Sanango*. Monotypic families were excluded from the comparison, and we should note that there are also 30 of these monophyletic families whose recognition makes other families paraphyletic. While the figure of 72% is solid (though not inspiring), the comparable figures for higher-level taxa are much lower. As an example, the system of Thorne (2000) takes into account some molecular findings. Among his subclasses, only one out of seven

is strictly monophyletic, as are 10/22 (45%) of his superorders, with another two including only small foreign elements. Of his orders, 27/49 (55%) are strictly monophyletic, with a further 20% including only a single family. (For references see Stevens, 2001.) However, about 67% of his suborders and about 85% of his families are monophyletic. Though he didn't define monophyly, Thorne recognized only monophyletic groups. As paraphyletic groups were to him the inevitable result of evolution, it is reasonable to assume that he would allow paraphyletic taxa and that his definition of monophyly is evolutionary monophyly (see Mayr & Ashlock, 1991). Of course, families have historically received rather more attention than higher and immediately lower levels (Davis, 1978; Angiosperm Phylogeny Group, 1998; Bremer *et al.*, 1999).

My understanding of generic limits is that they are likely to be little better than 70% confirmed by molecular data, but I have not done the calculations. We are in for an interesting time as work focuses more on this level and as Scotland's own work suggests. If there is increased work on species, then it will be very important to have our genera monophyletic as far as is possible so that undesirable name changes are kept to a minimum.

So is morphology really not very helpful? If it isn't, this may be because of the way we use morphology in phylogenetic work. Morphological character states produced by gap coding (the grouping of terminal taxa whose measurements for a particular feature overlap, measurements for the group as a whole being separated by gaps from those of other groups; see Stevens, 2000b, for a summary) may yield a strange understanding of evolution (Wiens, 2001), so when studying morphological evolution it may be best to fit morphology to a well-supported molecular tree. Yet we know surprisingly little about many morphological characters, as the simplest anatomical work carried out on *Martyniaceae*, *Pedaliaceae* and *Melastomataceae*, etc., during introductory classes on plant families classes makes abundantly clear. Our knowledge of morphology is also constrained by a typological approach (e.g. Carlquist, 1969; Floyd & Friedman, 2000; Herendeen & Miller, 2000). Indeed, although the major flowering plant groupings supported by molecular data may not have absolutely unique features, many can be characterized morphologically (Stevens, 2001). The full potential of morphology, however used, is still unclear, and the literature on the relative value of morphology and molecules in phylogeny reconstruction is replete with misinformation.

MORPHOLOGY AND TAXONOMY

Morphology has allowed us to recognize all the 200,000 or so species of land plants so far described, yet Wortley *et al.* rightly emphasize how little we really know about most of them. But will morphology always be sufficient? Wortley *et al.* appear, perhaps because of space constraints, too complacent about the value of morphology, implying that business will largely continue as usual. They quote the morphometricians Wiens and Servedio (2000) in support of the value of morphology in

species delimitation, and, as a first pass, it is generally adequate. However, integrating morphological and molecular findings may well lead to revisions of species limits (e.g. Baldwin, 2000; McGowen *et al.*, 2001; Chan *et al.*, 2002). This is an area where we can expect to see much progress, but it is one where botanists have not been as active as zoologists (Stevens, 2000a). In addition, much work is published under the heading of phylogeography and conservation or population genetics, and so we may not always see it.

But taxonomy is a rather strange bird, and to compare the Human Genome Project (HGP) with taxonomy points out some important differences between the two. The HGP, and institutions such as GenBank, store basic data, i.e. sequences (ideally linked to vouchers), in the public domain. The data accumulate as new sequences are added, and the more comparisons that can be made, the greater the value of the data. Indeed, progress in our understanding of phylogeny has been so fast partly because information has accumulated, and that is one reason why funding agencies have been willing to support the endeavour. Taxonomy does not accumulate nearly as much as one might think or hope. Taxonomists rarely store their comparable basic data, such as measurements and images linked to specimens, anywhere. Even databanks such as TreeBase are far removed from basic observations (Stevens, 1996). If the limits of a species have to be checked, a commonplace activity in poorly understood floras, then there are no data to reanalyse and they have to be reassembled. This hardly seems efficient.

Not all groups give us major headaches, but there will be some in any sizeable genus. Are there 14 species of *Fagraea* in Borneo, with 3 endemic, or 42 and 25 respectively (Stevens, 2000a)? Is there only one species of *Allophylus* throughout the tropics and one species of *Drimys* in Malesia? These are cases where the way in which we assemble and compare specimens can affect the limits of the taxa we recognize, a problem similar to that we encounter in coding morphological characters for phylogenetic analysis (Gift & Stevens, 1997).

DISCUSSION

Yes, there are too few taxonomists – but would we say otherwise? Yes, we must attract new funding and good students working at the species level. But money alone will not be the cure. The way in which taxonomy has been institutionalized, formalized and taught over the centuries seems almost designed to make us inefficient and appear obscurantist. Wortley *et al.* highlight a dangerous and growing shortfall in taxonomy: we do need to know much more about plant species if we are to understand evolution, diversity and ecology, but our patrons will not wish to support ‘business as usual’. We need to re-evaluate what we do as morphological taxonomists, and why and for whom we are doing it.

Every monographer or Flora-writer checks all relevant names. Even with the growing electronic availability of botanical literature and types this is a substantial task. Why do we not consign synonymized names to oblivion once a group has been

monographed? And what about the plethora of editorial conventions for citing types and specimens, descriptions in which the same parts are described in different orders, the lists of specimens sometimes pages long accompanying species descriptions, and the shifting nomenclatural codes? Why do we continue to rely on dichotomous keys that emphasize reproductive features? We spend an inordinate amount of time – and money – on nomenclatural matters alone. Even in 1994 an estimate of \$22,000,000 was offered as to the cost of biological nomenclature world-wide (Hawksworth, 1994). We have also sunk a great deal of money into museum databasing and collections management, yet with relatively poor returns (Australia perhaps excepted) because of our failure to adopt common approaches.

We don't often talk about concepts in the context of how we actually analyse variation, i.e. how we use the criteria needed for putting any concepts we have into action (McDade, 1995). Concepts and criteria matter (Mishler, 1999; Peterson & Navarro-Sigüenza, 1999), since the very entities in need of conservation may change depending on the concepts applied. It is partly because we have difficulty in providing answers to questions such as these that morphology-based data gathering, and its products (species descriptions and monographs), is seen as being 'unfocused, imprecise, and therefore unfundable' (Wortley *et al.*, p. 344). For targeted groups, morphology and molecules must be integrated at the species level. For others that are being surveyed for preliminary assessments of diversity, we must find a way of being far more efficient and focused, not on the past, but on the future, and in particular on those who will access the information we provide. Business *cannot* remain as usual if any of the grand and laudable inventory projects we have started, and that Wortley *et al.* mention, are to be finished within a reasonable time, or to be of much use when they are.

There is a larger issue. Kirschner (1994) remarked almost casually in *Nature* to the effect that arbitrary classifications (in his case, the spectral classification of supernovae) have 'the distasteful aura of botany'; similar dismissive comments about botany, plant taxonomy and natural history have occurred in other prominent journals (Hudson, 1995; Goodstein, 1998). Taxonomy in particular has a stereotype – hard names, amateurism, and mindless classification are all linked with it – that is over 200 years old. We have to be careful how we present ourselves. Perhaps we should put our house in order before we cry poverty.

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