

Introduction

As we enter the twenty-first century, the demand for taxonomy is greater than ever before. The global imperative for the conservation of biodiversity has brought into sharp focus both the need for and the needs of taxonomic research. Although commentators today frequently, and rightly, stress how comparatively little we know about the diversity of organisms with which we share our planet, we should not lose sight of the enormous progress that has been made in cataloguing, describing and understanding the Earth's plants, animals and microbes. This research programme was probably born among our hunter-gatherer ancestors, baptized by the Greeks, and then reached maturity in post-Enlightenment Europe with the Linnaean revolution. Its success has been due to the legion of naturalists and taxonomists who have explored every nook and cranny of the living world, and to a series of rules and protocols that have allowed this massive corpus of knowledge to be organized and arranged in an age of paper and post. Any student of biology in the nineteenth century, and for perhaps the first three-quarters of the twentieth century, would have spent a large fraction of his or her time learning systematic biology, and the tools and techniques needed to identify and describe various elements of the flora and fauna. Systematic biology and taxonomy was the fertile soil in which emerging sciences such as physiology, genetics, ecology and evolutionary biology had their roots and drew nourishment.

However, in the last quarter of the twentieth century, systematics and taxonomy lost its core role both in the biological curriculum and in the biologist's world-view. This surely occurred not because of a carefully laid Machiavellian plot to rob the field of its resources and respect, but because of circumstance—simply because biology got larger and expanded, and acquired whole new sub-disciplines, particularly towards the molecular end of the subject. There was just no more time for the leisurely amble through the natural world—‘today we have naming of nematodes’—that even those of us still in our forties remember with varying emotions. Taxonomy as a discipline also suffered reduced funding, even though at the time the total pot of money for biological research was getting larger. The problem was that the expansion never kept pace with the total increase in activity in the field of biology as a whole. In addition, taxonomy as then practised was essentially ‘cheap’ science—it costs much less to buy butterfly nets, glass jars and dissecting microscopes than to fund molecular biology laboratories, with DNA sequencers, centrifuges and thermal cyclers. Of course, we know that cheap does not mean low quality, but it perhaps led to a view that the subject did not need the same support as some of the newer biological disciplines. But in

addition to the problems associated with the burgeoning of biology, taxonomy and systematics did suffer from an image problem that contributed to its decline. It was a mature field that was not moving at the pace of molecular genetics, nor even at the speed with which ecology and evolution, also organismal biology, were being transformed in the 1960s and 1970s. Much of what taxonomists did was perceived as descriptive, at a time when every undergraduate had read a précis of a précis of Popper and equated ‘true science’ with falsifiability and experimentation. There also evolved an air of futility surrounding some of the classic problems of systematics. For example, every possible phylogenetic arrangement of the classes of the phylum Arthropoda had seemed to be championed by one authority or another at some time, with each taking its turn as the current favourite on a 40 year cycle; we exaggerate, but not much. To some outsiders, taxonomy appeared a victim of the narcissism of minor distinction.

Wounded by this relentless attrition, and in particular the accusation of being a descriptive enterprise, taxonomy responded with a philosophical makeover. The phylogenetic systematics pioneered most notably by Willi Hennig in the 1950s and 1960s provided a conceptual framework and set of workable tools to enable organisms to be classified in a consistent manner that explicitly took account of evolutionary relationships. For example, recognized taxa must be monophyletic and delimited by shared derived characters (synapomorphies). Critically, every taxonomic decision from a species definition to a system of higher classification was to be treated as a provisional hypothesis, potentially falsifiable by new data. Taxonomy was thereby rescued from purely descriptive natural history and brought into the fold of ‘hypothesis-driven science’. One cost of this progress was to make taxonomy harder work: phylogenetic systematics was hungry for characters, every species or taxon needed its own apomorphy, and derived characters often proved to be irritatingly non-independent. Reciprocal illumination Hennig-style meant going back and looking at decisions and characters again and again; the quick and dirty appeal to authority was no longer an option.

At the same time as the Hennigian juggernaut began to gain momentum, DNA sequencing escaped from the genetics laboratory and lodged itself in museums and herbaria, as well as potentially in any biology research group. Sequencing offered the prospect of unlimited characters and statistical approaches (including Hennig's own phylogenetic systematics) based on huge numbers of base pair differences that would allow competing taxonomic hypotheses to be distinguished. The incorporation of sequence data into taxonomy has not been a completely smooth ride, with several false dawns and blind alleys. A nice story, which we do not think is apocryphal, is of the first molecular phylogeny of three major groups of parasitoid wasps, which grouped the insects as predicted from

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long-established morphological arguments. Only later were the three sequences found to be cow, pig and human with the correct outgroup being obtained by chance. An anomalous mammal phylogeny that suggested the blue whale was a primate made more sense when it was realized that cut-and-paste errors extracting sequences from databases had led the whale to be confused with humans, whereas the true blue whale was labelled grey seal and the horse the harbour seal (resolved by Page & Charleston 1999).

Difficulties with the quantity of information in large sequence-based datasets, and the particular statistical problems associated with four-state characters (base pairs) with differential and perhaps variable transition probabilities, have sometimes appeared to be overwhelming and threatened to undermine the whole project. However, analytical techniques have largely kept pace with data generation, and for taxonomists working on living organisms there is no question but that molecular techniques will remain central to understanding evolutionary relationships. Perhaps the most impressive current example of the power of molecular techniques, especially when integrated with study of morphological character states, is the consensus phylogeny of seed plants masterminded by the Angiosperm Phylogeny Group (1998, 2003). Virtually all families of flowering plants (some modified somewhat to ensure monophyly) now have a well-supported phylogenetic position, and the community-wide project is now making firm progress towards full coverage at the genus level.

The phylogenetic revolution in taxonomy has brought major benefits, though there has also been a downside. Taxonomy is more than just phylogeny; it also involves the definition and description of species, and the organization of knowledge in a manner that can be used by the wider community. In the past 25 years this field of the subject has been perceived as less 'cutting edge' and therefore less fundable. It has disappeared from many universities whose hiring strategy faithfully follows research funding (though phylogenetic taxonomy also has not been immune to hard deans in grey suits), and even some major museums and herbaria who should know better, have rowed back on their commitment to this core part of taxonomy. A second downside has been the development of a certain brand of extremism that sees the whole field through a distorting prism of pure phylogenetics. This fundamentalist wing of phylogenetics advocates radical change in the way we perform taxonomy, which we think risks alienating both end-users and funders.

We believe that taxonomy is once again about to enter a period of rapid change, similar to that of the phylogenetic revolution, but this time affecting the species-level descriptive side of the subject. There is currently a ferment of ideas and suggestions about how taxonomy should advance, and though it is far from clear how the science will emerge from this period, there seems little doubt that the taxonomy practised in 2050 will be different from that we see today. The engines for this change are twofold. First, there is a vocal, ever-increasing user community asking new things of taxonomy. It is not certain that taxonomy as practised today can completely fulfil these needs and continue to serve its own ends. Second, there are technical advances that offer new ways of presenting and

doing taxonomy. Perhaps the most significant of these are information technology and new applications of molecular techniques.

The collection of papers in this issue is an attempt to explore some of these issues. We have invited end-users to write about what they need from taxonomy, and commissioned articles on some of the new technologies that are likely to change the way taxonomy is performed. We have not covered every aspect of how taxonomy is done or might be done, and have had to leave out as much as we have included. Rather, we have tried to assemble some papers that will contribute to the debate on how taxonomy should emerge from the current maelstrom of ideas. The issue is not itself organized taxonomically; we do not have articles on how insect, echinoderm or angiosperm taxonomy may look in 50 years, but we have explored some of the particular issues facing microbial (Finlay 2004; Oren 2004) and fossil (Forey *et al.* 2004) systematics. Finally, in addition to the main articles, we have also included some shorter essays by leading figures who have been involved in debates on the subject over the past few decades (Crane 2004; Janzen 2004; May 2004; Wilson 2004; Raven 2004). In the remainder of this Introduction we explore a few of the key issues surrounding what we see as the engines for change in taxonomy.

1. WHAT PEOPLE WANT FROM TAXONOMY

Taxonomy is a proud and independent science whose achievements rank as some of the outstanding successes of modern science. It is not a technical support service for the rest of biology, but a science that advances through testing hypotheses about taxon status and phylogenetic relationships.

Yet taxonomy stands alone, divorced from the rest of biology, at its peril. Many areas of fundamental and applied biology rely on a firm taxonomic bedrock for their success, and these different fields can also assist the taxonomist in his or her work, either by providing new information or character states, or through the provision and adaptation of new analytical techniques.

But perhaps more importantly, taxonomy needs a strong and vocal constituency rooting for it in the increasingly cut-throat competition for research funds. It is not enough for taxonomy to show itself to be a modern hypothesis-based science, and to expect funding to follow. It has to show its relevance to other areas, not just its theoretical or assumed relevance, but also its actual uptake by other fields.

Three of the papers in this volume directly explore the relationship between taxonomy and its end-users, and others do so as secondary themes. Gotelli, a community ecologist, describes how different areas of ecology require extensive taxonomic input, and explores how ecologists and taxonomists might better work together for their mutual benefit (Gotelli 2004). This account is particularly informed by his recent research on North American ant communities, and by how, with the help of ant taxonomists, he mastered the intricacies of ant identification. Mace (2004) discusses taxonomy and conservation, and how correct identification and issues of phylogeny and taxonomic rank can influence conservation policies. This is a particularly complicated area as taxonomic decisions may

have legal ramifications for conservation obligations, and acting or not acting on these obligations can cost large amounts of money. The taxonomist may also find him or herself in the invidious position that a decision on whether a population is specifically or subspecifically distinct determines whether it is protected or left in the path of destruction. Samper (2004) examines the history and consequences of the Convention on Biological Diversity for taxonomists, particularly in light of the establishment of the Global Taxonomy Initiative.

Space precluded inviting further papers on the myriad other uses made of taxonomy. We have no papers on the role of systematics in human and animal health: how to distinguish among different pathogens and vectors, and how taxonomy contributes to understanding their biology in a way that might suggest new interventions. Similarly, taxonomy is important in identifying agricultural and forestry weeds and pests; and in their biological control, by assisting in the discovery of natural enemies that may help regulate the numbers of these 'unwanted' organisms. There are a series of celebrated cases of valuable drugs and other products that have emerged from taxonomic and ethnobotanical studies of floras, both tropical and temperate. There is, without doubt, further scope for this type of bioprospecting, though to the taxonomist, the prominence given to the likely economic benefits of biodiversity is a double-edged sword. True, it highlights the importance of good taxonomy, but it has made some governments very wary of allowing the export of specimens, whether on loan or recently collected, and this has seriously depressed taxonomic activity and international collaboration in some countries. We suspect that no taxonomist would quarrel with the idea that a country should enjoy a major share of the economic benefits of its own biodiversity, but a mechanism needs to be found to ensure that this occurs without harming the science that may actually be needed in the discovery of new products.

This section is entitled 'What people want from taxonomy'. If you pose this question to professional and amateur biologists, and to naturalists, the most likely response is accurate phylogenies and, of particular relevance to the issues discussed here, stable, informative and accessible classifications that enable easy identification. Turning the question on its head, we can also ask what people do not want from taxonomy, and surely the answer must be radical change for the sake of change. Here, we agree with points made by Wheeler (2004) in his wide-ranging essay exploring the dangers of taxonomy becoming purely an exercise in phylogenetics.

Wheeler, in particular, targets the proposal to do away with the Linnaean system of classification based on binomials and a hierarchy of ranked taxa, and replace it with a system of rank-free taxa based purely on phylogenetic principles, regulated by a new set of naming rules, termed the PhyloCode (<http://www.phylocode.org>). There are technical objections to the PhyloCode (see Forey 2002) concerned with the instability of nomenclature as evolutionary relationships are resolved or new taxa are discovered that render old ones paraphyletic, but here we highlight two more general issues.

First, the scientists behind PhyloCode and related ideas highlight the arbitrary nature of all taxa with the possible exception of species. They argue that there is no equivalency

between a genus of plants and a genus of insect (for example), and taxonomy is thus misleading the rest of biology by talking about ranks such as genera, families or orders. The only objective truth out there is the historical reality of phylogeny, and the job of the taxonomist is simply to obtain successively better hypotheses of the tree's topology. Names must reflect clades, and measures of morphological distinctiveness traditionally (but not universally) used to ascribe rank should be excluded because they are arbitrary and not amenable to formal hypothesis testing.

However, people who use taxonomy want both accurate phylogenies and classifications that do not throw away all information except the topological arrangement of nodes in a tree. We think it unarguable that all taxa should be defined using phylogenetic (evolutionary) principles, for example that they should be monophyletic, but users look to taxonomists to provide classifications that reflect the fact that the morphological space occupied by plants and animals is lumpy rather than smooth. It is patronizing to non-taxonomists to say ranked higher taxa are arbitrary and thus they should not be allowed to use them. People know this, and yet when, say, a plant ecologist visits a new area whose flora is unfamiliar, he or she will frequently recognize genera or families without knowing anything about species. Recognizable groups help, even when they are not 100% perfect, and nested sets of taxa allow humans to organize their understanding within a logical framework. Indeed, with fossil taxa, as Forey *et al.* (2004) discuss, species concepts are so hard to apply that genera and higher taxa are of much greater value and indeed validity than species.

It might be countered that you could have all this with rank-free taxa, but this ignores an extremely important gift of taxonomy to the rest of biology. It provides a hierarchical series of partitions of biodiversity, however imperfect that might be. An ecologist can work with the generic and family diversity of insects in a field site, and compare this with other field sites. He or she knows that genera or family distinctions are arbitrary, but this matters less in comparative studies using the same taxa. Similarly, knowledge can be organized at different levels; keys exist to the families of flowering plants, and many major encyclopaedias of garden plants are organized as alphabetical lists of genera. Were taxonomists to retreat from ranked taxa, they would be re-invented by ecologists, naturalists and horticulturalists, and we believe that it would be better done by taxonomists.

The second point we want to make is as much political as scientific. There is intense competition for science funding today and any field seeking new or continuing monies is obliged both to point to its past history of success and list the enthusiastic end-users of its products. Taxonomy as currently practised can do both, yet the adoption of PhyloCode or similar proposals risks both. Reinventing nomenclature suggests that the Linnaean system of the past 250 years is not the success we claim, but rather a blind alley. It also risks severely alienating most people who use taxonomy. You need only look at how taxonomists are sometimes portrayed by their colleagues in other fields: as scientists who do a valuable job yet have the irritating habit of changing names for no apparent purpose. The wholesale abandonment of the Linnaean

naming system and its replacement by a new and untried method would destroy the support base for the field and imperil its survival. And it is not as if we cannot have our cake and eat it too. Especially today with modern Web technologies we can link Linnaean taxonomies with phylogenetic hierarchies and have the benefits of both.

2. TAXONOMY AS INFORMATION

Taxonomy was one of the first sciences compelled to organize a large body of data. The binomial system of nomenclature and the hierarchical system of higher taxa that were introduced by Linnaeus and his immediate disciples was a first attempt to do this, at a time when the diversity of life was underestimated by several orders of magnitude. Less than a century after the publication of the first edition of *Systema naturae* (Linnaeus 1735), the deluge of new species collected by the first heroic generation of tropical naturalists began to reveal quite how large the task confronting taxonomists was likely to be, while the problem of multiple descriptions of the same species began to be a real headache for systematists, especially those in Europe. It was to confront these problems that the International Code of Zoological Nomenclature (Zoological Code) and the International Code of Botanical Nomenclature (Botanical Code) were created and honed, a process that, as described by Knapp *et al.* (2004) has continued to the present day. No one would claim that the codes are perfect, but they have made an immensely important contribution to taxonomic order and stability. Today, molecular biologists are rediscovering the relevance of nomenclature and are designing 'codes' of their own for both gene and protein names. Although the rate of change of the organismal codes may seem glacial, perhaps this inertia is part of their success, rendering them largely immune from fads and fashions.

These problems, faced by eighteenth and nineteenth century taxonomists, might be called the first bioinformatics crisis, to use a phrase coined in the 1990s to describe the threat posed by the flood of data produced by high-throughput sequencing and genomic projects, and more recently by other industrial-scale molecular biology enterprises. This second bioinformatics crisis was averted by the widespread use of the Internet and all its associated technologies and capabilities. No subject that deals with the organization and dissemination of large amounts of information will remain unaffected by the Internet, least of all taxonomy—the Web changes everything. Already we can begin to see how taxonomy will change in the new information age, though as discussed by Scoble (2004), exactly how it will emerge from the current swirl of different ideas and initiatives is far from clear.

Two areas in which firm progress has been made are the compilation of species catalogues, and the digitization of museum and herbarium specimens. Species catalogues are the initial stage in any major taxonomic project and list available names, most usefully with authorities, references, synonyms and the location of types. Such catalogues exist for most groups in some form or another, though frequently as personal card indexes in the possession of particular experts or small groups of specialists. *The international plant names index* (<http://www.ipni.org/>; see Nic Lughadha 2004), a catalogue of all vascular plants, is

an example of a major resource that is now available on the Web, whereas the Species 2000 (<http://www.sp2000.org/>) project seeks to coordinate a myriad of Web-based catalogues and present them all to users in a uniform format. The current edition of the Catalogue of Life Programme of Species 2000 and ITIS (Integrated Taxonomic Information System; <http://www.itis.usda.gov/>) includes almost half a million names, though the rate at which it expands is critically dependent on groups outside the project finding funds to digitize or create catalogues.

Nearly all major museums and herbaria have developed programmes to automate retrieval of information about the most significant specimens in their collections. For example, many herbaria now have all, or a large proportion, of their specimen sheets barcoded and electronically archived, in some cases with the sheets photographed and stored digitally. Such a resource not only simplifies curation and physical care of the collection, but if mounted on the Web also allows anyone to know the extent of an institution's holding of any particular taxon. However, digitally archiving all collection specimens is unlikely to be cost-effective or even possible. For example, the major European and North American museums contain collections of insects running into many millions of specimens, and simply labelling each individual and transcribing the associated information would be enormously time consuming, even if no checks on the correctness of the identifications or rigour of the captured data were performed. It seems to us that digitizing collections will need to be prioritized, with emphasis placed on certain types of specimen (e.g. types or extremely fragile historical but still relevant specimens) and on taxa where this information is particularly useful. Soberón & Peterson (2004) show how specimens with accurate geographical data are an important yet largely untapped resource for many user groups in answering a wide range of biological questions, including critical issues in conservation biology such as those discussed by Mace (2004).

Species and specimen catalogues are what might be called the raw data of taxonomy; this is then integrated to produce taxon revisions and identification keys. Traditionally taxon revisions are published in the paper literature—journals and books—which are made available in libraries and as reprints. To what extent will this primary, processed taxonomic information move to the Web? The rate will be determined both by processes extrinsic and intrinsic to the subject. To consider the external forces first, the death of specialized journals in paper form has been predicted for over a decade, yet they stubbornly cling to life. There are strong economic forces at work here. Publishers are often unwilling to risk the guaranteed income stream from low-circulation, expensive journals that will always be bought by at least a few specialized libraries by mounting material in open-access sites on the Web. Similarly, many learned societies are kept afloat by income from their journals. There is thus a tension between authors who typically get no financial reward from publication and who want their work to be circulated as widely and appropriately as possible, and publishers (and sometimes authors in a different role as society officers) who are seeking a different goal of maximizing or at least stabilizing income stream. There is an alternative financial model in which authors rather than readers pay

for the publication, which to a certain extent exists already with page charges. This model is now being experimented with in the biomedical sciences, but has not reached taxonomy in any serious way. The picture is complicated by tremendous inertia in the system. Money currently invested in journal purchase is not easily re-routed to pay-as-you-go publication, and the prestige and reward system throughout the sciences emphasizes publication in a rather narrow suite of established journals rather than in new journals or innovative media. It is ironic that for scientists one of the most valuable products of the new information age is the publication and citation database maintained by the Institute of Scientific Information, but that the journal impact factors calculated from this resource are a major disincentive to publish in new places. Taxonomic papers are long, require many illustrations, and typically have a very specialized audience that lasts for many years—the half-life of a taxonomic monograph can be calculated in decades or even centuries rather than years or months. Taxonomy is clearly one of the fields that will gain most from a changing culture in scientific publishing.

There are also intrinsic factors within taxonomy that act as a break to Web publication. At present the Zoological Code and Botanical Code do not allow Web-only descriptions. However, the 1999 edition of the Zoological Code allows electronic publication, provided a limited number of copies are deposited in at least five major libraries of record, so at least for animals the code is not a real barrier to electronic publication. A few electronic journals are beginning to be used for taxonomy, for example the journal *ZooTaxa* (<http://www.mapress.com/zootaxa>) which is published online, with hard copies lodged in public libraries to satisfy the requirements of the Zoological Code. The speed with which new taxa are rigorously peer-reviewed and published in this journal is astonishing; market forces will surely stimulate more such efforts in the very near future. The real barrier seems to us to be part cultural—‘that’s not how taxonomy is done’—and part a concern for the permanence of material on the Web. The latter we see as a real but far from insurmountable problem: there is not a paper copy of the human genome or of some of the other molecular databases of enormous economic value. But neither are these data stored in single sites or in single institutions. The innovative journals archiving service JSTOR (Schonfeld 2003) similarly stores identical information in several places; a guarantee against disaster or server failure. We need a recognized and trusted means of archiving Web taxonomy in a manner that will guarantee its continued access. Perhaps our great museums and herbaria should embrace this task as an adjunct to maintaining their permanent physical collections (including their major libraries).

But simply switching taxonomy as it is done now on paper to the Web does not make use of the full potential of the Internet and associated technologies, nor will it necessarily speed up the actual doing of taxonomy (the scientific part of it). How much further should one go now, and is there not a danger of kicking over the traces, of putting at risk the whole taxonomic enterprise that we argue is a jewel in science’s crown? Not only is the answer not clear but we also at least partly disagree on the best way forward (Godfray 2002a,b; Knapp *et al.* 2002). We

shall first describe what we see as a relatively uncontroversial next step, and then one of us (C.G.) will briefly describe a more radical transformation of taxonomy that will then be criticized by his co-author (S.K.).

The taxonomy of a group currently consists of the sum of the species descriptions and revisions in the paper literature, possibly supplemented in the future by the same material in electronic format, backed up by type and other material in museums and herbaria. The taxonomy is thus distributed across several sources, and not concentrated in any one location. The taxonomist will know intimately the contours of this information landscape for his or her particular group, and in fact this is as much a part of ‘knowing’ a group as being able to identify specimens. But this distributed taxonomy is of only limited use to the more general biologist, to the end-users of taxonomy. What they require is the information in a more digested form that is suitable for their particular uses, for example, species identifications and relationships, series of images of organisms or natural history information on different groups.

Currently user needs are met (where they are met) by monographs, floras, field guides and handbooks, all almost exclusively in paper format. We believe that there is widespread agreement that electronic media, including the Web, could provide extremely valuable taxonomic tools that would supplement existing resources. Perhaps the main advantage of the Web for this ‘processed taxonomy’ is that far more information can be provided than is feasible in printed formats. Many floras and handbooks are famously challenging to use, employing a recondite if not abstruse vocabulary, and often requiring substantial experience with the group before even simple identifications can be effected. Some taxonomists delight in these hermetic arcana, but these are the minority, especially today. Taxonomic works are hard to use because distinctions between species are often subtle, and because the economics of publishing in print normally require terse descriptions with relatively few illustrations. The Web gives taxonomists the space they need to be understood, and also the room to include as much information as required on topics such as structure, biochemistry, ecology, biogeography and natural history. One can see taxonomists becoming curators of the sum of information about their chosen group. The Web also allows innovative use of techniques not possible in paper publishing—of interactive keys and three-dimensional images and even sound and film. Although these can be published on CD, the Web allows the resource to be updated and linked to other sites in a manner that is unique to the Internet. The multi-dimensionality of the Web makes taxonomy even more relevant as it is connected to new data emerging in genomics and other rapidly moving fields of molecular biology. For example, there are plans to sequence the complete genomes of a wide range of *Drosophila* species and it will be imperative that information on the taxonomy, biology and natural history of these insects is organized in an accessible manner. We suspect that some laboratory-based biologists are not fully aware of what can be achieved by comparing their model organism with their many relatives, something that might change if information on the richness of data about the natural world was easier to access.

With today's technology the transfer of this type of information to the Web would provide an invaluable tool for the biologist or naturalist's desk. With a modest advance in technology it would accompany him or her into the field, replacing and improving field guides and excursion floras. The critical breakthrough is probably the invention of so-called electronic paper, a computer display that presents texts and images with the same resolution and look of real paper. Large amounts of money are being invested in electronic paper, and it will surely become a mainstream medium within a decade if not sooner. Taxonomy should and can be ready.

Some exciting initiatives that will result in rich taxonomic information on the Web have recently been announced. In September 2003 the National Science Foundation (USA), in cooperation with the ALL Species Foundation, announced the financing of four projects under the Planetary Biodiversity Inventories programme (run by NSF; www.nsf.gov/pbi). The results of these projects will be Web-available taxonomies of four major groups on a global scale—more than just lists of names, the taxonomies are intended to be information and content rich and include descriptions and links to other relevant sites.

We have discussed electronic as opposed to paper publication, and of presenting taxonomic syntheses on the Web. But this does not alter the basic distributed nature of taxonomy, the fact that the raw details of the subject are scattered over many different publications, some of which may be quite obscure. In the modern information age, should we be moving from a distributed to a unitary model for taxonomy, with the treatment of particular taxa curated and policed by a central authority? Or is it possible to achieve the same ends without central authority, purely through community-wide consensus, the model behind projects such as the International Plant Name Index, the ICTVdb (database of the International Committee on Taxonomy of Viruses), or the Global Plant Species Checklist (see below)? Can bottom-up initiatives succeed or must there be rules dictated from top-down?

Often seen as the least controversial move in this direction is the creation of name directories, central registers for particular taxa, with the voluntary or compulsory requirement that the details of any new species name proposed are entered onto a single database. Models for such registers already exist, for example all new names in prokaryotes must be published in the *International Journal of Systematic and Evolutionary Microbiology*, or if published elsewhere, cited in a validation list; however, valid publication of a name is no guarantee of its legitimacy or its priority of publication (see Tindall 1999). The lists of all validly published bacterial names are available on the Web (see <http://www.bacterio.cict.fr/>) and are not a compulsory central registry. A perhaps more surprising model comes from botanical horticulture; international cultivar registers, largely maintained by volunteers, exist for many of the well-known groups of garden flowers—roses, daffodils and clematis for example—and these have brought a degree of order to what was before a rather chaotic system of cultivar naming.

Registers work most effectively when the number of names is few or where community-wide consensus drives the process. Nic Lughadha (2004) proposes a model for

the creation of a voluntary register—something that will come about as a by-product of achieving a globally agreed goal—a 'widely accessible list of known plant species'. This is Target 1 of the Global Strategy for Plant Conservation (GPSC) as adopted by the sixth Conference of the Parties (decision VI/9 of COP VI in 2002) of the Convention on Biological Diversity (see www.biodiv.org). However, both the botanical and zoological communities emphatically rejected attempts to impose central name registration at their last congresses, partly because of disagreements over policing, management and centralization of control. To some, the creation of registers is an unalloyed good, long overdue and their absence an indication of the immaturity of the science of taxonomy. Others point to the financial implications, and the risk of centralization and control by cliques. These issues need to be urgently addressed.

However, should one go further and shift the entire higher taxon's classification from its present distributed model in the literature to a 'unitary' model, a one-stop-shop on the Web? One of us (C.G.) believes this is the way forward. A first Web revision would list and describe a series of accepted and unaccepted taxa, explicitly linked as previously to type specimens, and these would become the set of names available for the group. Nomenclature would essentially begin again for that group, as happened for the prokaryotes in 1980. Henceforth there would no requirement to delve into the paper literature, except for historical interest. The Web-based treatment would form the foundation upon which higher-level, more general user-orientated material would be built. An end-user might start to use the site like a field guide or popular monograph, but then be able to delve as deeply as required into the technical information such as types or details of fine morphology. Such a site would need careful and continuous curation and organization, and this raises two possible problems. First, the natural organizations to act as hosts for unitary taxonomies are our great museums and herbaria, but this could only occur if they were resourced appropriately. The idea needs substantial new money. Second, unitary taxonomies pose a potential threat to the independence of taxonomists, especially if the 'legal' status of accepted names were to change substantially. Currently, anyone can publish anything about a group as long as they can find someone to publish it (or, as has several times happened, they can set up their own journal to avoid traditional scrutiny). Adherence to the rules of nomenclature or to good taxonomic practice is purely voluntary. If a unitary taxonomy were to be 'legally' enforced, might not a narrow clique dictate whose ideas make the unitary taxonomy? For some groups a unified and largely agreed-upon taxonomy would be an easy and workable model, whereas for others, for example orchids or cycads, the number of conflicting taxonomies can be quite enormous (though one could argue that this makes the need for a unitary taxonomy even more pressing). Issues of authoritarianism could be mitigated by insisting that unitary taxonomies be moderated by international review panels akin to the system of peer review, and that hypotheses not included in the current Web revision are nevertheless lodged on the same site for future research. One can simultaneously have a current consensus taxonomy for the end-user and a host of competing hypotheses for

workers in the field. But if a unitary taxonomy were to be adopted it is unquestionably true there would be less of a free-for-all than exists at present. Might this be a price worth paying for a more efficient way of doing taxonomy, and one that provides a product that is more attractive to fund and easier to use?

As stated previously, one of the editors of this issue is a proponent of unitary taxonomies whereas the other (S.K.) is less keen, and would prefer a similar unified, but less authoritarian, approach. We both agree that bringing together the scattered taxonomic information about any given group is important and useful, and synthesis is definitely a priority. The degree to which taxonomy is hampered by legacy information differs radically between taxonomic groups, and can even differ geographically. For example, obscure names are rarely resurrected for mammals, most name changes occur because of changes in species concepts or taxonomic opinion; in many groups of insects, however, the weight of the past is perceived as a definite hindrance to progress. Botanists working in Europe are faced with much historical confusion to untangle, whereas those working in the tropics are faced with what has been termed an excess of novelty. Systems that accommodate all variations in how taxonomy has been done need to have broad 'buy-in', both by users and taxonomists themselves, to be successful. In general, bottom-up, community-led initiatives have had more long-lasting success than top-down, authoritarian systems (see Nic Lughadha 2004). If any single taxonomy, be it on the Web or otherwise, is legislated, will people contribute and buy into the system? Will it attract the best in our science? Only if taxonomy is the best possible will the broad community accept it; what we really need is excellent work that will then be taken up by market forces, just as the Linnaean binomial system won the day in the eighteenth century. Good taxonomy will win and become universal by being the best. What is urgently needed is for the community, taxonomists and users alike, to pull together to create these best taxonomies, authoritative, without being authoritarian. Consensus and synthesis are difficult to achieve (see Vane-Wright 2003), but worth striving for. That the presentation of taxonomic information on the Web in a single place would represent a great step forward is without doubt; how this is managed and policed is where we disagree.

Perhaps the way forward is to explore both ideas and see which works best. The paper by Scoble (2004) explores further the pros and cons of unitary taxonomies and other similar ideas.

3. NEW TECHNIQUES

A common caricature is of the traditional taxonomist with his or her plant press or butterfly net being dragged reluctantly into the scientific mainstream by a molecular Young Turk who uses modern techniques to establish new species boundaries or erect a revolutionary new phylogeny. This caricature is unfair on several grounds. First, taxonomists have a long history of embracing new techniques from outside their field to help resolve species identities and relationships. A good example of this is the use to which scanning electron microscopes and plant secondary compounds have been put in plant taxonomy.

Second, only occasionally do molecular techniques overthrow existing taxonomies, they are far more likely to confirm morphologically based analyses, or help resolve contentious issues; and frequently the most progress is made by comparing and then combining morphological and molecular data.

Yet the enormous importance of molecular techniques, and in particular DNA sequencing, to modern taxonomy is clear, though its greatest impact so far has been in the reconstruction of phylogenies. The past few years have seen some bold suggestions about how the molecular revolution may influence species-level taxonomy, as well as the relentless advance of new methodologies in molecular biology that will influence other fields in the near future.

Some of the impetus for the incorporation of molecular tools at the species level has come from prokaryote taxonomy, for long a Cinderella subject, hamstrung by the relatively few morphological character states available for analysis. As Oren (2004) describes in this issue, the lack of characters for traditional taxonomy (and perhaps also the much greater familiarity with molecular techniques by prokaryote taxonomists in comparison with their eukaryote colleagues) led to a rapid adoption of the at least partial molecular characterization of bacterial taxa. However, the degree to which this experience has lessons for eukaryote taxonomy is perhaps restricted by unique aspects of prokaryote biology. In particular, the lack of traditional sex in prokaryotes means that many of the species concepts used for eukaryotes cannot be applied successfully (see Oren (2004) for a discussion of this problem). Also, the sex that bacteria do have, swapping genes using plasmid or phage vectors, or vacuuming up DNA from the environment (having sex with the dead as John Maynard Smith memorably put in), can lead to curious reticulate patterns of evolutionary relationships, very different from the predominantly tree-like dichotomous structures of eukaryote gene phylogenies.

Many of the issues discussed in prokaryote taxonomy also apply to attempts to classify viruses, a subject not represented in this issue. Here, sex (recombination) can occur, though its effects are even more varied and capricious than with bacteria. Viruses are also odd in that their genomes are so small that although close relationships can be identified, their ultimate origin is usually obscure and often unknowable. At least some viruses are probably renegade genes, derived from their hosts, and this poses an interesting conundrum for some strictly phylogenetic definitions of higher taxa. Does a virus derived from, say, a dog, render *Canis familiaris* paraphyletic; and should the virus itself be classified as a new species of mammal? Dogs do suffer from an infectious disease derived from the dog genome, not a virus but a sexually transmitted, cellular cancer. Leroi *et al.* (2003) recently discussed its evolution and, tongue-in-cheek, suggested it was a new species of mammal.

Finlay (2004) describes advances in the taxonomy of unicellular eukaryotes, the groups that until relatively recently were conveniently amalgamated in the phylum Protozoa but which we now know, again thanks to molecular studies, are more phylogenetically diverse than the rest of the eukaryotes put together. With protists, molecular techniques have had less influence at the species level than is the case for prokaryotes, at least for free-living

species. Indeed Finlay and his colleagues' own work, which is changing completely our view of protist biogeography, has almost completely relied on morphologically defined species, thanks to the rich variety of characters displayed by protists such as ciliates and diatoms. It is still not clear whether protist systematics will follow a prokaryote or a 'higher' eukaryote route, partly because we do not yet know for more than a relatively small group of taxa whether sex plays a dominant role in maintaining species integrity. Finlay discusses the genetic and ecological factors that may determine protist species boundaries, and the fascinating recent discoveries of profligate and varied endosymbiosis in these groups.

There are some groups of eukaryotes that seem as barren in characters as prokaryotes and where traditional taxonomy has always had great problems in defining species and sometimes even higher taxa. Nematodes are one such group and Blaxter (2004), who works on these animals, writes about how the routine adoption of molecular sequencing may provide a workable means of identifying nematode species that just does not exist at the moment. But his argument is broader than this and he suggests that as DNA sequencing becomes cheaper and simpler this might become the easiest way of distinguishing among large groups of species, even those for which good morphological characters are available for use by specialist taxonomists. The promise is held out of simple unambiguous means of species characterization, of a molecular barcode that will reveal a species identity as faultlessly as the barcode on a product in a supermarket checkout. Hebert and colleagues have also been forcibly arguing for this idea, and have gone further and explored one particular gene that might act as the barcode, or more realistically for large groups of species, as part of the barcode. They have shown that sequencing the mitochondrial CO1 gene can distinguish correctly among groups of moths, though, as critics point out, the species used do not pose any particular problems for systematists. Janzen (2004), however, in a characteristically provocative essay, takes up the cudgels for molecular barcoding, and mentions work with Hebert on Lepidoptera that has led to new insights: distinguishing among a group of skipper butterflies (*Hesperiidae*) that have different biologies but which were inseparable using traditional morphological characters.

Molecular barcoding is one of the major emerging ideas in species-level taxonomy, and the next decade will bring much more stringent tests of its utility. We mention here a couple of issues that will need to be addressed over this period.

The first issue is the mechanics of providing the sequencing information. Today it is relatively straightforward to sequence any particular gene in any particular organism, providing you have a basic molecular laboratory, access to a PCR machine and a sequencer, the requisite primers, and the computing and Web facilities necessary to analyse the results and compare them with previously collected data. But it is still expensive to set up such a laboratory, and still relatively expensive to sequence any particular specimen. Remember, a taxonomically savvy ecologist might routinely identify several thousand specimens (of a restricted suite of species) in a survey or experiment by eye, to do this by sequencing would be prohibitively expensive and essentially a waste of time. At the moment

molecular barcoding is a niche activity and probably only cost-effective when traditional morphology fails.

However, we can be reasonably certain that DNA sequencing will become both cheaper and more straightforward in the future. The celebrated Moore's law of computing states that processor power doubles every 18 months and something akin to this probably applies to sequencing power. Current sequencer technologies based on gel and capillary separation may be reaching their limits, but there are new technologies on the horizon where individual DNA molecules are sucked quickly through microscopic holes in membranes and their base sequence determined by measuring microscopic changes in electric fields. These and similar technologies are still some way from the laboratory bench, but they are attracting serious venture capital, and people like Craig Venter are talking of US\$1000 to sequence a whole genome (in September 2003 the Craig Venter Foundation offered a prize of US\$500 000 to 'an individual or group of researchers whose technology significantly enhances the field of high throughput DNA sequencing by enabling a human genome to be sequenced for US\$1000 or less'; <http://www.venterscience.org>). At the very least, taxonomists need to consider what the effect on their subject might be of a world where large amounts of sequence data can be collected quickly and cheaply, at a fraction of the cost and time it would require a human to explore the specimen's morphology.

Many of these consequences are explored by Blaxter (2004), whereas Janzen (2004) in messianic mode considers the 'Star Trek Scenario', when all we need do is point a machine at a leaf or an insect, and like Mister Spock's tricorder it returns its identity and a host of other potentially useful information. This sounds like science fiction, but we believe it will happen, though we suspect not as quickly as Janzen suggests. In the nearer future our greatest concern is that a quantum leap in sequencer power might lead to traditional taxonomy becoming separated from a new molecular taxonomy based on some type of clustering algorithm. Were issues of species definitions (discussed below) to be solved would it matter if traditional taxonomy were replaced by a new way of classifying and possibly naming species? Our reply is an emphatic 'yes', at least for most higher taxa. We have learned a massive amount about the Earth's flora and fauna since the time of Linnaeus and, like it or not, this information is indexed by Linnaean binomials. We think it essential that if, or more likely when, industrial-scale sequencing becomes commonplace in taxonomy it does so in conjunction and not in opposition with systematics as currently practised. This is a strong argument for developing unified, Web-based taxonomies, though there are undoubtedly other ways that this highly desirable marriage can be achieved. The important thing is not to risk throwing away 250 years of accumulated knowledge, much of which would then need to be rediscovered. A subsidiary argument against molecular taxonomy going it alone is that a major and increasing group of end-users and even generators of taxonomy are amateur scientists and naturalists who have contributed a huge amount to our understanding of many groups of organisms, especially the popular groups such as vertebrates, flowering plants and the more charismatic insects. Short of

tricorders becoming as cheap and available as fridges or butterfly nets, it is unlikely that amateurs will be able, or even want, to convert to a pure molecularly based taxonomy; it would be a shame if this immense and increasingly important workforce was alienated or disenfranchised. Much the same applies to the very many expert taxonomists in developing countries, many of whom will not have access to large-scale molecular facilities in the foreseeable future.

But will molecular barcoding work? This is largely a testable hypothesis as we have excellent morphological taxonomies for many groups of plants and animals, and these can be used to test different molecular approaches. As mentioned above, people have begun to do this already, and the tests can be made progressively more challenging. This calibration will reveal whether there is sufficient—but not too much—variation in the genes chosen for barcoding to separate recognized species, and whether the clustering algorithms work sufficiently well. It should throw up challenges to traditional schemes that can then be investigated by using independent studies, both of molecules and morphology. It will also tell us whether possible problems such as non-congruence of species and gene phylogenies, and heterogeneity among gene phylogenies, are fatal, and whether they can be circumvented by using more genes or other DNA sequences, or whether a total evidence approach is the best.

What is certain is that barcoding and related techniques will make us reassess exactly how best we should define species. Species concepts will continue to be controversial, and we have already touched upon some of the difficulties likely to occur if radically new species concepts are introduced out of what we see as misplaced notions of philosophical purity. Here, we make a couple of further points. First, for most plants and animals, species boundaries based on the extended family of ‘biological’ species concepts are relatively straightforward and uncontroversial, and provide species delineations that are usable by the consumers of taxonomy, whether they are an ecologist or evolutionist, or a hunter-gatherer in the highlands of New Guinea or the forests of Paraguay. We know that this approach fails for swarms of asexual species such as dandelions and brambles, but to adopt any particular species concept just because it is universally applicable seems to us counter-productive and tantamount to throwing the baby out with the bathwater.

Applications of information technology and molecular ecology will also lessen the problems of uncertain species boundaries. Consider birds: with the exception of the occasional Andean endemic we essentially know the diversity and structure of the ‘avisphere’, yet the number of species fluctuates as different species concepts are applied, and allopatric populations are raised to, or lowered from, species status. Such activities should matter little to end-users (with the possible exception of the dedicated ‘twitcher’). Essentially, what people need is full information about geographical variation, biology and increasingly genetic structure; they will then be in a position to decide whether the populations should be enumerated separately for the purpose in hand. Similarly, with closely related sibling, incipient and hybridizing species, questions of whether there are one or two or more species will increasingly become irrelevant as high-throughput

sequencing allows us to understand patterns of gene flow and introgression, and the varying rates at which different parts of the genome differentiate during the process of speciation. This is already happening for the model organisms of pure and applied biology. For example, 50 years of mosquito genetics has given us exquisite insights into the structure of malaria-transmitting *Anopheles* populations, and has added a great deal to our understanding of their biology as well profoundly affecting disease control strategies. The rank at which we recognize these biologically important groups, however, is not as important as recognizing their differences. Botanists have dissected an intricate pattern of hybridization and ploidy changes in plants such as wild *Senecio* (ragworts) and wild and cultivated *Brassica* and this knowledge, to a certain extent, transcends the strict naming of biological species. We stress that our argument in no way diminishes the importance of taxonomy, and that traditional ways of delimiting species work much of the time. But taxonomists in the future, increasingly supported by the routine use of large-scale sequencing and related data-gathering techniques, will co-opt approaches such as these that are currently the preserve of ecological genetic and evolutionary laboratories.

We have concentrated almost wholly in this section on sequencing as the molecular technique most likely to revolutionize species-level taxonomy. However, other technological advances, both molecular and non-molecular, are likely to make a difference to the way taxonomy is conducted. Again, work with prokaryotes provides examples. A very efficient way of separating and identifying different bacterial taxa is through studying their phospholipid and fatty acid profiles (PLFA analysis), which can be done automatically, and with high throughput. At the present time such methods are simpler and cheaper than sequencing, though undoubtedly this will change. Possibly molecular separation using other families of molecules might prove useful in eukaryote groups, perhaps for fossils or subfossils where nucleic acids have degraded but other groups of organic chemicals are more stable. It is also possible that more recent molecular advances based on RNA profiling or proteomics may prove useful, though exactly how is not yet clear, at least to us.

Finally, there are non-molecular advances that will help taxonomy. Progress in image analysis provides two examples. Gaston & O'Neill (2004) explain how it is possible to digitize images of specimens and then train sophisticated software to distinguish among different known species. Currently, the techniques work best with two-dimensional structures such as wing patterns and venation in insects, but in principle they could use three-dimensional images. Three-dimensional imaging has recently been applied with considerable success in palaeontology. Some important fossils are three-dimensional but embedded in a matrix that effectively conceals most of the critical structure. However, three-dimensional structure can be reconstructed by taking photographs of successive polished sections, and then using image-manipulation software to reconstruct the organism (see, for example, Sutton *et al.* 2001). The disadvantage of the technique is that the specimen is destroyed—it is erased, layer by layer—but the resultant detailed structure can at the moment be obtained in no other way. Three-dimensional

photography is also increasingly being used for archival purposes in certain groups such as nematodes (see De Ley & Bert 2004; <http://faculty.ucr.edu/~pdeley/vce.html>) and fossils (Forey *et al.* 2004).

4. CONCLUSIONS

How can taxonomy survive and flourish in the twenty-first century? Many of the authors in this volume address this question explicitly or implicitly, and not all arrive at the same conclusion. The truth is, no one knows, but that will not stop us listing what we think are a series of key factors. In doing this we have not tried to summarize the papers in this issue, though we have certainly been influenced by them. We are also aware that as neontologists, working with living organisms, we have paid insufficient attention to issues in palaeontological taxonomy.

(a) *Taxonomy is not just phylogeny*

We start with what seems a negative point. Phylogenetic systematics has completely changed the way comparative biology is performed, and has enabled biologists to ask more relevant, targeted questions in evolution, ecology and development, to name just a few fields. However, to arrive at a useful phylogeny, and to use phylogenies to ask interesting questions about nature, one needs taxa—the tips of the phylogenies—that are described and identifiable. For that one needs descriptive taxonomy. Phylogeny, description and identification are the three facets of taxonomy, and should be seen to compliment rather than compete with each other.

There is a belief among some taxonomists, which has some basis in fact, that more status accrues from phylogenetic rather than descriptive work. This is perhaps natural considering the advances made in phylogenetics in the last 40 years; rapidly moving fields are understandably fashionable. As phylogenetics matures, however, and the immense need for descriptive taxonomy becomes ever more pressing, we think it essential for a balance to be restored, and for proper credit to be given to the best taxonomy of whatever type. For this to happen there must be changes both within and outside taxonomy. Descriptive taxonomy must modernize, the whole field become less factional, and its institutions and leaders become more pluralistic in what they recognize and reward as excellence. Outside the field, other biologists and scientific administrators need to realize that taxonomy is ill fitted to many modern metrics of scientific achievement (especially citation indices as currently calculated), and develop new means of identifying the best in systematics.

(b) *Pay great attention to the end-user*

Taxonomy has a multitude of end-users, from scientists engaged in blue skies research through applied biologists and geologists, to amateur naturalists, and ultimately to the general public. Few other sciences have such a broad potential audience. To reverse the attrition of funds going into the subject it is imperative that all these communities are more closely engaged with what taxonomists do. Taxonomists must manufacture better products that are used by all these groups, as this will initiate a virtuous circle in which the quality of the output leads to calls for greater quantity. Disinterested appeals for more resources

for taxonomy carry greater weight when they come from outside the field than from within, whereas engaging the general public may lead to novel sources of funding.

We stress that we are not calling for taxonomy to become purely a service industry, just that by paying greater attention to the users of taxonomy the whole field is likely to grow. We also acknowledge there are potential conflicts, spending more time producing taxonomic work that can be used by a broad audience takes time away from basic revisionary work that is of immediate use to a specialist and of use to everyone in the future. One of us (S.K.) has to confront this tension on a daily basis. And finally we note that information flow is not one way; increasingly significant contributions to taxonomy are being made by non-taxonomic biologists and increasingly by amateur naturalists. With better access to taxonomic information these last groups would be empowered to make an even greater contribution.

(c) *Agree on important and achievable targets*

In the current science-funding climate generalized appeals for more funding are unlikely to be successful. What are needed are concrete goals, the taxonomic equivalent of ‘complete the human genome sequence’ (of course having defined completion such that it is achievable) or ‘survey all the stars in the sky’ (again defining completion carefully). The taxonomic community historically has not been good at agreeing concerted targets, though this is beginning to change.

The GPSC (Crane 2004; Nic Lughadha 2004) has as one of its goals the creation of a global plant species checklist by the year 2010. Already the plant taxonomy community is pulling together to achieve this ambitious goal; similar types of product could be proposed for other key taxonomic groups. One agreed goal of the World Summit on Sustainable Development in Johannesburg (September 2002) was to achieve a ‘significant reduction in the current rate of biodiversity loss by 2010’. How can we even begin to assess this without a baseline against which to measure this loss? Only taxonomy, and by extension the taxonomic community, can provide the high-quality species-level information to construct this baseline—ignore the clarion call and risk less qualified groups stepping in to take up the job.

Beyond species lists, the greater goal is to describe the world’s biota. In September 2000 the ALL Species Foundation was initiated and set itself the target of describing all the world’s plants and animals within 25 years—a human generation. This was a fabulous vision, and has done much to stimulate debate on how such large projects might operate and financed. But we worry that it might be a taxonomic bridge too far, at least at present. Global treatments of key groups such as those financed by the Planetary Biodiversity Inventories programme in the United States (see above, with which the ALL Species Foundation is associated) may be a more realistic and achievable goal; but we need far more projects than the four currently supported.

(d) *Prepare for new technology*

Finally, the subject needs to adapt itself to existing recent technologies, and prepare itself for new developments. We have devoted most space here to novel

techniques in the information and molecular sciences which are already changing the way taxonomy is practised, and where it is possible to predict at least some of the innovations likely to influence taxonomy in the next decade or so. However, it would be foolish to pretend the subject can anticipate all eventualities. What we do think important is that the subject should be prepared to adapt itself to and partly adopt these and potentially other new techniques. For example, taxonomists should continue to embrace the use of the Internet and related media to enhance taxonomy, and fuse modern molecular approaches with traditional morphology. This is what Linnaeus and the great polymaths of the eighteenth century would have done if alive today. Syncretism, in the sense of advancing by picking the best out of different philosophies and observances, should be the field's watchword, for the alternative is revolution, schism and chaos.

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