

# Taxonomic triage and the poverty of phylogeny

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Revisionary taxonomy is frequently dismissed as merely descriptive, which belies its strong intellectual content and hypothesis-driven nature. Funding for taxonomy is inadequate and largely diverted to studies of phylogeny that neither improve classifications nor nomenclature. Phylogenetic classifications are optimal for storing and predicting information, but phylogeny divorced from taxonomy is ephemeral and erodes the accuracy and information content of the language of biology. Taxonomic revisions and monographs are efficient, high-throughput species hypothesis-testing devices that are ideal for the World Wide Web. Taxonomic knowledge remains essential to credible biological research and is made urgent by the biodiversity crisis. Theoretical and technological advances and threats of mass species extinctions indicate that this is the time for a renaissance in taxonomy. Clarity of vision and courage of purpose are needed from individual taxonomists and natural history museums to bring about this evolution of taxonomy into the information age.

**Keywords:** taxonomy; phylogeny; monography; cyber-infrastructure; nomenclature

## 1. INTRODUCTION

Biology enters the twenty-first century with a growing tension between 'phylogenetic biology' and taxonomy. Taxonomy, already weakened by decades of neglect, now suffers the loss of positions and funding to studies that reconstruct phylogeny that improve neither formal classifications nor the application of scientific names. Phylogenetic biology, capitalizing on the popularity of molecular genetics, advances at the expense of species discovery, description and hypothesis testing. Hennig (1966) understood that shared patterns of common ancestry were the only thread binding all species and introduced phylogenetic systematic theory as a means to improve the information content of classifications and names, making them the general reference system for biology. As phylogenies became available, experimental biologists quickly recognized their importance for evolutionary insights into comparative studies from behaviour to ecology to conservation (e.g. Coddington 1986, 1988; Wanntorp *et al.* 1990; Vane-Wright *et al.* 1991; Williams *et al.* 1991; Nixon & Wheeler 1992a; Wenzel 1992; Prance 1995; Daly *et al.* 2001). The increasing demand for phylogenetic patterns has resulted in a sharp rise in molecular phylogenetic analyses and concomitant reduction in traditional taxonomic works. Although studies of phylogeny are commonly cited as evidence of active taxonomic research, 'real' taxonomy has been decimated by almost every measure including doctoral degrees granted, research funds, faculty positions, upkeep and expansion of collections, biology curricula and prestige (Daly 1995; Schrock 1989; House of Lords 1992, 2002; Wheeler 1995a,b). Descriptive taxonomy is considered passé. Expertise on many taxa

is disappearing. What passes for morphology in phylogeny studies is sometimes little more than a literature review appended as a few lines in a predominantly molecular data matrix. Causes for the decimation of morphology and taxonomy include misunderstandings that stem from the non-experimental nature of taxonomy, preferential support for new technologies and a cynical equation of success with money. At root, the problems are more political and sociological than scientific.

Taxonomy has always been and shall remain essential for credible biology. Its countless contributions over the past 250 years have created so much taxonomic knowledge that the field can be neglected for decades before the disastrous consequences of too little taxonomy become felt. To the fundamental intellectual importance of taxonomy for biology we may now add urgency. The biodiversity crisis threatens to destroy much of the evidence of evolutionary history before it has been discovered or documented (Wilson 1985, 1992). In the face of this biodiversity crisis, the need to rebuild expertise and infrastructure for taxonomy is paramount (Wheeler & Cracraft 1996). This taxonomic imperative has theoretical, practical and even ethical implications.

Our generation is the first to fully appreciate the threats facing millions of species, and the last generation with the opportunity to explore, describe and classify life on Earth so completely. Species that are literally ours for the taking will soon be inaccessible to science at any cost. What we accomplish in taxonomic work in this century will be a priceless legacy to all the generations of scientists, natural historians and educated humans that follow. By accepting the challenge of completing an inventory of species through a taxonomic renaissance in the twenty-first century, we make an immediate and lasting contribution to our understanding of the diversity of life. We ennoble ourselves in the act by mitigating the intellectual losses otherwise associated with the loss of species. As humans, we

One contribution of 19 to a Theme Issue 'Taxonomy for the twenty-first century'.

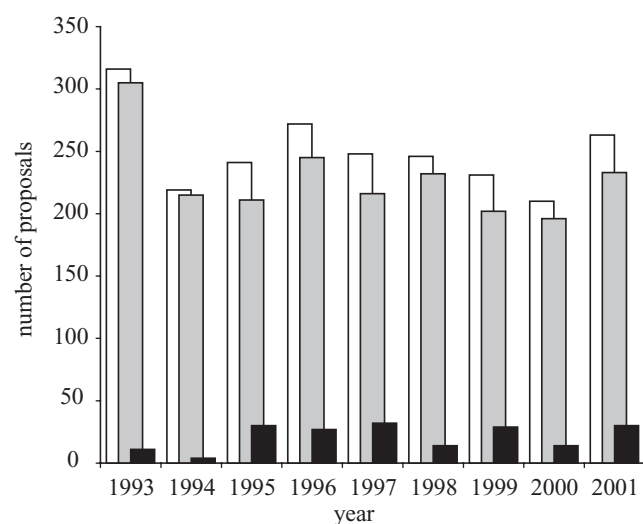


Figure 1. Number of proposals evaluated by the Systematic Biology Program of the US NSF for 1993–2001, categorized as ‘monographs’ (taxonomic monographs plus revisions, black bars) or ‘non-monographs’ (including phylogenetic analyses outside revisionary context, grey bars). White bars are totals.

are a part of the phylogenetic fabric of life on Earth and innately curious about our relatives near and far. A heavy investment in taxonomy now will help assure that we fulfil our intellectual manifest destiny to comprehend our place in the natural world.

Scientists are not immune to influences from the societal milieu in which they live. This is the only rational explanation for favouring newness over excellence or for trying to measure success purely in monetary terms. Technological sophistication does not assure better science. Those willing to sacrifice scientific principles can easily secure large sums of research funds. By constantly shifting one’s goals to match fashionable trends in science funding it is possible to become a skilled and highly productive follower. A better way to measure success in science is through the advance of knowledge. But this is much harder requiring instead vision, commitment and leadership at both the individual and institutional levels.

The diversion of funds from taxonomy to phylogenetic biology is an international phenomenon. The recent House of Lords report (2002) states that funds allocated to taxonomy in the UK since the Lord Dainton report (House of Lords 1992) have primarily gone to support phylogenetic analyses rather than descriptive taxonomy. The same may be said of the USA where taxonomic revisions and monographs have been funded by the NSF’s Systematic Biology Program but at a consistently low level for years (figure 1). This trend has only further depressed an already established decline in taxonomic productivity since World War II (figure 2). On average, the sum of human knowledge (estimated by titles of books published) doubled every 33 years before the information age. The time was reduced to *ca.* 6 years in the 1970s, 1.5 years in 2000, and by some estimates will soon double several times per year. In sharp contrast, the doubling of taxonomic knowledge (measured in the number of new species described) has not kept pace. Before the Enlightenment our knowledge of species doubled about once every 400

years. By the late eighteenth century, in the time of Linnaeus, our taxonomic knowledge doubled every 50 years. By the mid-twentieth century, this had slowed to doubling every 100 years and now is closer to 200 years. This should be an unacceptable trend in the midst of the biodiversity crisis.

Even with most existing research money committed to phylogenetic studies, it is not nearly enough to keep pace with the growing demand for phylogenetic knowledge. The community, acknowledging this need for phylogenies and noting the rapid advances in information and molecular technologies, has suggested that the time has arrived to tackle phylogeny on a grand scale. As a result, the US NSF announced a new programme in the fiscal year 2002 called ATOL and provided *ca.* US\$8 million to support phylogenetic studies of several groups from bacteria to birds. A second competition was recently held for ATOL with funding increased to *ca.* US\$12 million for the fiscal year 2003. This programme is intended to expedite the growth of knowledge of phylogeny by engaging multidisciplinary teams (morphologists, palaeontologists, molecular phylogeneticists, etc.) in studies focused on major branches of the tree and supporting development of improved analytical tools.

With as many as 90% of the Earth’s species undescribed, the vision of a resolved phylogeny of life may be compromised unless there is a similarly ambitious effort to advance descriptive taxonomy. Further, the impact of phylogenetic knowledge will be limited if it is not translated into formal classifications. Although the precise impact of species excluded from an analysis varies from case to case, there is general agreement that such missing taxa are a serious concern to the recovery of phylogenetic patterns (e.g. Novacek 1992; Wheeler 1992; Graybeal 1998; Hillis 1998; Hillis *et al.* 2003). For all but a few relatively well-known small clades, this ignorance of species diversity will pose an impediment to resolving phylogenetic relationships. Biologists will be able to have little faith that such phylogenies are even approximately correct and phylogenies will be subject to frequent and major reorganizations.

Several programmes at the US NSF have begun to address the taxonomy crisis. The decline in taxonomic expertise has begun to be reversed by the PEET programme, which has trained an impressive number of young specialists (Rodman & Cody 2003). Recognizing that neither PEET alumni nor taxonomists in general were receiving substantial support for descriptive work outside the PEET programme, the NSF recently called for proposals for Revisionary Syntheses in Systematics, including strictly morphology-based revisions. As a result, nine out of 27 proposals recommended for funding in a recent systematic biology competition, fully one-third, were explicitly taxonomic revisions. In addition, the Biodiversity Surveys and Inventories programme—the programme specifically charged with supporting the discovery of new species—had an increase in its budget of 50% in the fiscal year 2003 to US\$9.1 million. Part of this increase came in the form of an innovative, large-scale experiment to dramatically speed the discovery and description of species. A Planetary Biodiversity Inventory competition offered up to US\$14 million to fund two to six awards that coordinated international teams of taxonomists and museums or

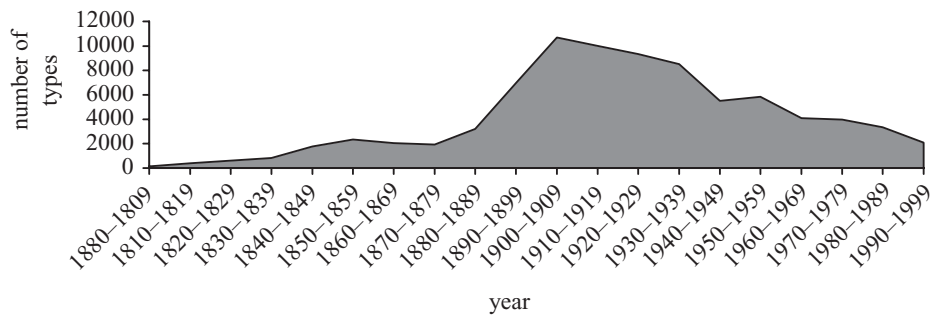


Figure 2. Rate of accumulation of type specimens in Kew Botanical Garden and United States National Herbarium (Smithsonian Institution) from 1880–1999 as an indirect measure of descriptive taxonomic activity. Data courtesy Dr W. J. Kress and Ms E. Farr.

herbaria to focus on intense species exploration and description for a target taxon across the entire world. This is the first such global-scale effort with a taxon focus that could dispel the myth that rapid growth in knowledge of species diversity of a group is impossible. Descriptions of these various programmes exist on the NSF Web site ([www.nsf.gov](http://www.nsf.gov)).

Considering what is at stake for human and environmental welfare in the biodiversity crisis, it is time to triage and move descriptive taxonomy to the forefront of science funding priorities. Phylogenetic studies do not have to be at odds with descriptive taxonomy and their goals were, until recently, coincident (Nelson & Platnick 1981; Wiley 1981; Schoch 1986). As explicitly stated in the Systematics Agenda 2000 initiative (Anon. 1994) these, along with dissemination of taxonomic knowledge, are the core missions of the field. Rather than pitting phylogenetic biology against descriptive taxonomy, it is time for the community to set clear priorities that assure coordinated and substantial progress on both fronts. The impact of phylogeny divorced from taxonomy is impoverished. Taxonomy divorced from phylogenetics suffers no less because phylogenetic classifications are optimally informative and predictive (Farris 1979; Nelson & Platnick 1981).

Another reason exists for immediately clarifying the vision, priorities and needs of the taxonomy community. Well-intentioned proposals for a DNA-based taxonomy present a new and growing threat to the advance of taxonomy. Although DNA barcoding is an exciting new identification tool for taxonomy, it lacks the theoretical base of traditional taxonomy and, unless handled rationally, could undermine the intellectual content of taxonomy making it a service industry providing an inferior service (Lipscomb *et al.* 2003). DNA is simply data.

We will soon witness the next generation of advances in cyber-infrastructure. Taxonomy, like academia in general, needs to prepare to take advantage of new information technology capabilities (Duderstadt *et al.* 2002). There is a fortunate conjunction of new theories, technological advances and urgent needs that make this the ideal time to revitalize comparative morphology and bring about a renaissance in taxonomy. No other activity in science holds certainty of such immediate and enduring growth of understanding and none is so clearly a challenge to our generation alone.

## 2. TAXONOMY AND PHYLOGENY

Darwin stated two reasons to study phylogeny.

The time will come I believe, though I shall not live to see it, when we shall have very fairly true genealogical trees of each great kingdom of nature.

(Burkhardt & Smith 1990, p. 456)

Our classifications will come to be, as far as they can be so made, genealogies.

(Darwin 1859, p. 486)

The first was to provide a conceptual context for biology, so that all facts and phenomena could be interpreted from an evolutionary–historical point of view. Another was so that our classifications could reflect the pattern of descent with modification that binds all species to a common history. Phylogenies remained highly speculative until Hennig (1966) distinguished apomorphies from plesiomorphies and made phylogenetic constructs open to rigorous testing (Gaffney 1979; Schuh 2000). In each case we study phylogeny so as to better understand and manage biological information. We do not study phylogeny for its own sake. Consider an extreme example illustrated in figure 3. We have six samples (numbered 1–6) and for each sample some sequence data. Given no more data, does anyone care whether sample 1 is more closely related to sample 2 than it is to sample 3? For what purpose? The reason that phylogeny matters is that it allows us to interpret the significance of the distribution of more complex and interesting features. Molecular data are helpful in reconstructing phylogeny but only in special circumstances is it inherently interesting and then in relation to another more complex character (e.g. the evolution of a protein, appearance of a regulatory gene, etc.).

Molecular phylogenies have retraced ground covered long ago by morphologists, ecologists and behaviourists. Without this historical background knowledge of interesting anatomical structures or behaviours, these molecular phylogenies would have little or no interest to science. Whiting *et al.* (2003) document the apparent loss and regain of flight in insects. This is of great interest because it calls into question long-standing hypotheses about the evolution of flight in insects as well as Dollo's 'law' and its prohibition of regained complex characters. Molecular phylogeneticists are in essence spending the intellectual

1	T-C	T--	---	ACT	ACC	CGG
2	T--	---	-CC	CAG	CAT	AAT
3	---	---	---	AAT	AAT	GGG
4	---	--G	---	GAT	AAT	AGG
5	---	--G	--G	AAG	AAC	AGG
6	---	--G	G-G	GAT	AAC	AGG

Figure 3. Sequence data viewed in isolation are interesting only in a trivial sense. A small portion of aligned mitochondrial (matR) sequence showing the INDEL (insertion/deletion) that distinguishes six taxa (1–6) from related ones. Known only as species 1–6, this series of aligned amino acids is of little interest. When names and known morphologies are revealed (*Gnetum*, *Welwitschia*, *Pinus*, *Ginkgo*, *Cycas*, *Zamia*) and the fact that these data are part of that hypothesized to distinguish these genera from one another and also basal angiosperms from gymnosperms, they become extremely interesting. Data from Qiu *et al.* (1999).

capital that has been banked by morphologists since the sixteenth century (Mayr 1982). Unless we begin to seriously reinvest in comparative morphology, ethology and ecology, we shall soon have little to explain with phylogenies. Molecular studies have been skimming the cream from such interesting and controversial stories, but would do well to recall that 90% of the evolutionary stories are yet to be told. It is time to reinvest in traditional sources of biodiversity exploration including morphology and all branches of 'natural history'. Ecologists and behaviourists stand to lose as many data as morphologists. There will not be sufficient time for in-depth, long-term or highly quantitative ecological studies before many unique ecosystems have been irrevocably degraded. Although the most visible products of alpha taxonomy are specimens, their associated data will be increasingly valuable as the biodiversity crisis progresses.

Once phylogenetic patterns are hypothesized, their translation into phylogenetic classifications allows us to store and retrieve information where it is known and predict its presence or absence where it is not. Scientific names, corresponding to hypotheses about species and monophyletic taxa, permit scientists to communicate with precision, clarity and with a minimum of words. The current funding of phylogeny divorced from classification and nomenclature short-changes biology in serious ways, even though it can take several iterations of phylogenetic analysis before the new understanding of relationships is so discordant with classifications and names that it poses a serious problem. We need to re-establish parity between morphological research and molecular; between phylogenetic analysis and classification. No one would suggest that we should not fund molecular phylogenies, but there are those profiting from this illogical and disproportionate allocation of research resources who are less altruistic about comparative morphology and taxonomy. Phylogenetic biology, rather than helping to remove the taxonomic impediment, is actually contributing to it by drastically retarding the pace at which basic taxonomy can be done.

### 3. WHY DESCRIPTIVE TAXONOMY IS NOT DESCRIPTIVE

It has been suggested that one reason for the lack of funds for taxonomy is that descriptive work simply cannot

compete against hypothesis-driven science. Two responses have merit, both mentioned in the House of Lords (2002) report. First, descriptive work enables other biological research and therefore should be supported to create necessary research resources. This is in no way different from the significant funding given to genomics and proteomics for work that is descriptive such as bacterial artificial chromosome libraries and the Human Genome Project. Second, as observed by Professor Boxshall, taxonomy is not merely descriptive. Taxonomy *is* hypothesis-driven science. That it is not generally recognized as such is more a measure of the failure of our education system than a comment about the science itself. Few students today, even among those pursuing a doctoral degree, have even a single formal course in the philosophy of science. Is it a wonder that so many biologists naively suppose experiments to be the demarcation between science and non-science?

How can non-experimental revisionary taxonomy be hypothesis-driven science? So-called descriptive taxonomy deals with hypothesis testing on multiple levels. Initial claims that two structures are the same (homologous) is a hypothesis. The conclusion that the distribution of a homologous attribute qualifies it as a character of a species or a synapomorphy of a higher taxon is a hypothesis. A species is a hypothesis. Every clade at every Linnaean rank is a hypothesis. Each and every one of these hypotheses represents a generalization from which specific future observations are predicted. When those observations are made, the hypothesis is either corroborated or refuted. Such testability demarcates science from metaphysics. Experiments are prized by experimental biology for precisely the same reason: they allow generalizations to be made that are open to critical testing. Linnaean names are more than arbitrary labels for subjective groupings of populations or species, although at times in history they have been such. A species name is an effective shorthand notation for an explicit hypothesis about the distribution of attributes among populations of organisms (Nixon & Wheeler 1992*b*; Wheeler & Platnick 2000). Higher taxon names refer to monophyletic groups that also predict the distribution of characters. Each time a new specimen is examined, particularly one from a previously unexamined population, species are tested. When new species and characters are added to a data matrix, higher taxa are opened to testing anew.

Taxonomic revisions and monographs are regarded as the most extreme example of why taxonomy is descriptive. Each species description is a hypothesis about the discontinuous distribution of unique combinations of characters (Nixon & Wheeler 1990). All specimens of all populations of species cannot in practice (or knowingly) be studied, so that actual distributions of characters must be theorized. As additional specimens and populations are discovered or studied, these hypothesized boundaries are put to the test.

Species hypotheses are not efficiently tested in isolation. To critically test the distribution of attributes defining one species it is necessary to examine variation within that and all nearly related species. Given that many species have wide and complex ranges and that specimens for most species are scattered through museum collections in many countries, truly rigorous species testing is neither

automatic nor easy. To pull together tens of thousands of specimens of several species (and of unidentified congeneric specimens, too) from the world's collections to test a single species hypothesis can be done but is horribly time and cost inefficient. In fact, to do the full amount of comparative work appropriate to a first rate species hypothesis test one has in essence done the better part of a revision of at least some sub-clade of the higher taxon to which the species belongs. This is why taxonomists have relied upon revisions and monographs. Such comprehensive, broadly comparative studies are high-throughput, simultaneous tests for large numbers of related species. It is difficult to improve upon the logic of such an approach although emerging information technologies promise unprecedented advances in practice.

Some ascribe superficial meaning to the fact that formalized summaries of the characters of species are literally called descriptions. This is as specious an argument as the claim that type specimens have had anything to do with typological thinking for a very long time. Types are international standards for scientific names (see Knapp *et al.* 2004). As species hypotheses are tested and the idea of a species expanded or narrowed, the type specimen provides nomenclatural stability by assuring that the name reflects that species which includes within its range of variation that adopted standard. Typification, as practised today, is tied to sophisticated species hypotheses.

There are important practical consequences implicit in the recognition that revisionary taxonomy is hypothesis-driven science. For one, the description of a new species is not a one-time activity as intimated by Janzen (1993). The confidence one has in a species hypothesis is directly proportionate to the extent to which that hypothesis has been tested. Hypothesis testing is rarely done, even in the case of extinct species where new observations of related species have the potential to alter the hypothesis. Absent revisions and monographs, most species hypotheses are untested and, as new specimens accumulate in museums, the information content and reliability of identified material is slowly degraded. Meier & Dikow (2004) cite data from a recent revision of the robber fly genus *Euscelidia* that illustrates this erosion of information content in museums in the absence of revisionary studies (figure 4). In their study, they report an increase in the number of species known from 29 to 68 and predict that as many as 116 species await discovery. The majority of 1383 specimens in major collections had never been identified. Out of the 361 that had been determined, 83% were incorrectly identified owing to misidentification (73%) or synonymy (10%). Continuing emphasis on the mere computerization of label data from museums and herbaria is misguided, when eight out of 10 records may be mistaken. There is limited benefit in rapid electronic access to unreliable data. There are so few taxonomists that for many diverse taxa, such as insects, revisions are completed only once or twice per century. The challenge before us is thus not to computerize museum data but to have an efficient system and a sufficient number of taxonomists to support ongoing improvement and verification of data as well as making those data rapidly searchable.

Taxonomy, far from a merely descriptive science, is packed with intellectual content and societal relevance. Taxonomists synthesize and interpret billions of facts

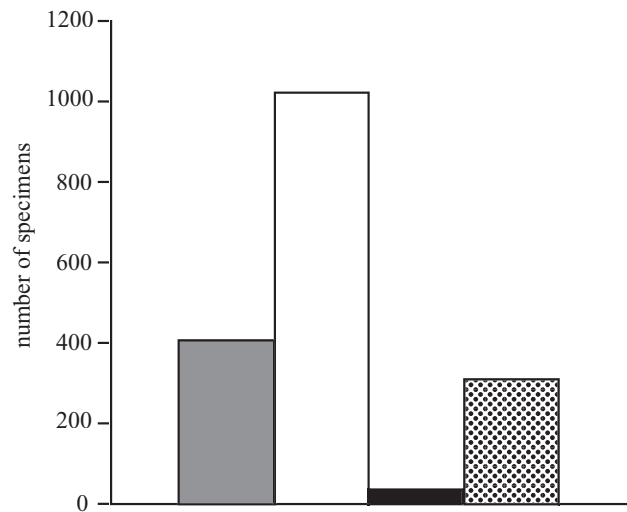


Figure 4. In the absence of taxonomic revisions and monographs, data in museums and herbaria become unreliable and their quality erodes over time. Data from a recent revision of the robber fly genus *Euscelidia* (Diptera: Asilidae) by Dikow. He examined 1383 specimens of which only 361 had been previously identified. Out of those, 83% were incorrectly identified owing either to misidentifications (73%) or synonymy (10%). Grey bar, identified; white bar, no identification; black bar, correct identification; dotted bar, misidentified. For details see Meier & Dikow (2004).

about millions of species, make those species identifiable, provide the vocabulary to talk about them, critically test the evolutionary units of biological diversity, and make accessible and predictable all that we know of life on Earth. It has a rich and proven epistemic basis that makes its hypotheses testable and its results as rigorously scientific as any.

#### 4. THE OLD PROBLEM OF THE NEW SYSTEMATICS

A decade after the Lord Dainton report, the state of taxonomy in the UK has not improved and has in fact worsened (House of Lords 2002) and limited funds for systematics, as in the USA, have mostly gone to phylogenetic biology. How has research so fundamental to modern biology been allowed to decline to such a great extent? What must be done to reverse this trend? Because these were not isolated events, it is important to understand the recent history of taxonomy to put this trend into place and to avoid its replication.

Taxonomy continues to suffer from a dynamic that was set in motion 60 years ago (Wheeler 1995c). No level of funding will reverse the fate of taxonomy unless and until certain prejudices and misconceptions, handed down to us from the New Systematics, are laid to rest. Taxonomy, already misunderstood and marginalized, suffers now also because of technophilia. We arrogate to molecular genetics a leading role in phylogeny reconstruction when the most fascinating and equally informative sources of data come instead from morphology, ontogeny and palaeontology. There are no credible theoretical reasons to favour one source of data over another. How the data are analysed is ultimately more important than its source (Hennig 1966). Undue technological influence is a problem of our time

and not unique to taxonomy. In the words of David Orr (2002, p. 63), 'unable to separate can do from should do, we suffer a kind of technological immune deficiency syndrome that renders us vulnerable to whatever can be done and too weak to question what it is that we should do.' In light of the biodiversity crisis, the should-do is clear and is the business of taxonomy.

Mayr (1942, p. 7) belittled traditional taxonomy: 'the trend which I have tried to express by comparing the characteristics of the old and new systematics is, however, unmistakable. It is primarily characterized by the fact that the new systematist tends to approach his material more as a biologist and less as a museum cataloguer.' Although the good systematist mimics the geneticist, the 'enormous time which the thorough genetic analysis of a species requires ... makes it impossible for the geneticist to study more than a very small proportion of the known organisms' (Mayr 1942, p. 10), leaving the vast majority for the less-than-thorough taxonomists to study. Since that time, the goals of taxonomy have been confounded with those of related areas of science whether population biology, tropical biology or molecular biology and few individual or institutional voices have made unapologetic assertions of the importance and credibility of taxonomy for its own sake.

Although Hennig (1966) returned respectability to studies at and above the species level, taxonomy has never fully recovered from being thus tainted as non-scientific (even non-biological!). This view was further codified by Mayr (1969) in characterizing taxonomy as a subset of systematics concerned with classification. Systematics in this scheme was conceptually broader, in the words of Simpson (1961) encompassing 'any and all relationships' among species. The fate of taxonomy might have been different had an alternative view been adopted. As Crowson (1970) advocated, there is merit in regarding systematics as a subset of taxonomy. The former studies phylogeny to provide a pattern that can be translated into the classification and names of the more inclusive field of taxonomy. This is a commendable suggestion, but is a battle for another day.

Darwin (1859) convincingly argued for the importance of mechanisms of inheritance for natural selection and for the reconstruction of phylogeny to provide the big picture of evolutionary history. In Darwin's time the genetic mechanisms of inheritance were unknown and no rigorous method of phylogeny reconstruction was available. Theoretical advances were needed in each case, and they came first to the geneticists. A century would pass before necessary theories were developed for phylogenetics (Hennig 1966). Great strides in genetics in the 1920s and 1930s led to the New Synthesis and authors like Mayr (1942) tried to recast systematics in the image of modern genetics. It is fair to say that important foundations for the field of population biology grew out of (and at the expense of) taxonomy through what Mayr described as 'population thinking'. This trend culminated in the 1970s when good population thinkers in systematics called themselves 'bio-systematists' to distinguish themselves from traditional taxonomists. Today, 'tree thinking' has led to a segregated study of phylogeny that may, according to O'Hara (1997), be the beginning of another new splinter science. Once again a new name, phylogenetic biologist, distances these

tree thinkers from taxonomy. It is informative that Hennig (1966), the father of phylogenetics, devoted about two-thirds of his book to issues related to classification, and that resistance to his ideas centred on questions of classification (e.g. Mayr 1974). Hennig's theory was one of phylogenetic *systematics*.

It is difficult enough that the infrastructure of taxonomy must be rebuilt rapidly to respond to the biodiversity crisis—and to meet the needs of basic and applied biology, to reincorporate taxonomy into the fabric of biology, and to literally re-conceive taxonomy in the electronic age—without unnecessary and unwarranted attacks on Linnaean taxonomic practices. Two recent proposals, if adopted, could jeopardize the revival of taxonomy and drastically delay or derail its work. One proposal is for DNA-based taxonomy. The other proposes what is described as PC and rankless classifications (i.e. the so-called PhyloCode). Viewed uncritically these proposals could appear to have merit, but in each case they are misguided, based on false assumptions, and dangerous to the progress of taxonomy.

DNA evidence has been incorporated into taxonomy in various ways almost from its first availability. So a rejection of recent proposals is in no way a rejection of DNA data that are and will remain extremely important to taxonomy. However, the incorporation of new technologies into taxonomy should be used to improve rather than replace taxonomy. Hebert *et al.* (2003, p. 313) and also Blaxter (2003), Blaxter & Floyd (2003) and Blaxter (2004) discuss biological identifications through DNA barcodes and imply that supporting many taxonomists is an inherently bad thing: 'whereas physicists deal with a cosmos assembled from 12 fundamental particles, biologists confront a planet populated by millions of species. Their discrimination is no easy task. In fact, since few taxonomists can critically identify more than 0.01% of the estimated 10–15 million species (Hammond 1992; Hawksworth & Kalin-Arroyo 1995), *a community of 15 000 taxonomists will be required, in perpetuity, to identify life if our reliance on morphological diagnosis is to be sustained.*' (emphasis added). The fact that knowing all of Earth's species requires a large number of scholars is a reason to educate and employ taxonomists, not an argument to abandon scholarship in favour of theoretically vacuous technology.

DNA barcoding is an extremely exciting and potent tool for making species identifications but is a poor approach to species discovery and description. Even in some taxa readily identified in one life stage by morphology, DNA barcodes can enable associations with other life stages (Hebert *et al.* 2003). There is an enormous difference, however, between using such DNA benchmarks to help recognize species already hypothesized to exist based on complex characters, and throwing out the theoretical content of species hypotheses for such technology (Mayr 1963; Wheeler & Meier 2000).

Thus, Hebert *et al.* (2003, p. 319) are mistaken when they suggest replacing taxon scholars with technicians: 'moreover, the generation of COI [cytochrome oxidase I gene] profiles will provide a partial solution to the problem of the thinning ranks of morphological taxonomists by enabling a crystallization of their knowledge before they leave the field. Also, since COI sequences can be obtained

from museum specimens without their destruction, it will be possible to regain taxonomic capability, albeit in a novel format, for groups that currently lack an authority'.

Tautz *et al.* (2003, p. 70) admit the primarily morphology-based system of recent centuries 'with its main anchor in publicly funded collections, has produced a reliable and steadily updated taxonomy'. They continue, 'however, the system depends heavily on specialists whose knowledge is frequently lost when they retire' ... and 'the respective literature is often difficult to access'. Once again, compelling reasons to educate and hire young taxonomists and to adopt information technologies, not to destroy a previously unbroken chain of taxon-based scholarship spanning centuries. Such proposals miss the point of taxonomy (Seberg *et al.* 2003) and threaten 'to relegate taxonomy, rich in theory and knowledge, to a high-tech service industry would be a decided step backward for science'. (Lipscomb *et al.* 2003, p. 66).

Rather than abandon taxonomic theory and practice, this is the time to adapt information and molecular technologies to carry out taxonomy better and faster than ever before. Morphologists and curators are on the threshold of transforming taxonomy in the world of cyber infrastructure making possible identifications of obscure species routine and easy, access to the world's total knowledge of species openly accessible, and sharing the wonders of biological diversity with the general public through user-friendly interfaces. We are on the brink of the most exciting leap forward in morphology-based taxonomy since Linnaeus (1758), making this an inopportune time to give up.

Morphologists deal with visual knowledge of complex structures. The advent of digital imaging is a technological breakthrough for morphology. Digital images are to morphological knowledge what the Gutenberg Press was to the written word, and morphology is about to explode into the twenty-first century. Digital libraries of morphology will make structural knowledge as readily searchable and accessible as GenBank has for molecular sequence data. Taxonomic publications that interpret and explain morphology may be supplemented by online access to such digital libraries of unlimited size. Teachers, children and naturalists will have images of nearly every known species at their fingertips. Inspectors on borders will submit digital images of intercepted specimens to smart systems that will show possible matches with known morphological structures and suggest probable identifications, much as fingerprints are screened for matches by law enforcement today. Field biologists carrying hand-held wireless computers will have access to such visual identification systems for countless applications.

The PhyloCode rests on arguments that range from the misguided (e.g. that names should be immutable for hypotheses that change; Dominguez & Wheeler 1997) to the false (e.g. that the PhyloCode is more stable than the Linnaean system; Nixon & Carpenter 2000; Nixon *et al.* 2003) to the absurd (e.g. that the Linnaean system cannot convey evolutionary schemes because it predates Darwin!). The PhyloCode has been rebutted on many levels (Benton 2000; Keller *et al.* 2003; Carpenter 2003; Kojima 2003; Janovec *et al.* 2003; Moore 2003; Schuh 2003). From such critiques it may be fairly concluded that what the PhyloCode seeks to do does not need to be done and what

it claims to do it does not. Taxonomy faces important and exciting intellectual and scientific challenges and should waste no more effort on what Carpenter (2003) aptly describes as 'pure folly'. The community should, in my view, boycott the proposed international meeting on the PhyloCode in France in 2004 with deafening unity. There are many good reasons to go to Paris. This is not one of them.

PC (which conveniently denotes both PhyloCode and political correctness) is flawed in principle and practice, but we need not look to PC's failure but rather Linnaean nomenclature's success to predict its continued contributions in the twenty-first century. Why has Linnaean nomenclature remained in continuous use for nearly 250 years? Linnaean categories and names are nested providing an ideal means to communicate the hierarchical structure of phylogeny. Binomials allow common descriptive adjectival words to be used repeatedly as an aid to communication and to memory. Stability of taxon 'intent' is achieved through getting taxa approximately right. For example, controversies over new fossils do not prohibit clarity of discussion about 'mammals'. Typification ties species hypotheses to observable evidence (characters). Linnaean nomenclature is not perfect, but as luck would have it, neither is our knowledge of phylogeny. By getting it approximately right and by using a system that is flexible enough to adjust to the growth of knowledge, Linnaean nomenclature provides an effective, efficient language for biologists. This simplicity and practicality has sustained Linnaean nomenclature and made it nearly equally useful to Creationists, Quinarians, Evolutionary Taxonomists, Pheneticists, Cladists and New-New Systematists. We are even able to understand the grievous examples of PC when its proponents use Linnaean names. This flexibility will make Linnaean nomenclature useful to twenty-first century taxonomists, too, through the ebb and flow of the theoretical landscape. Even within phylogenetics there are disagreements about classification, such as whether paraphyletic taxa should be recognized (e.g. Brummitt 1997; Brummitt & Sosef 1998). Although I do not find it useful to recognize paraphyletic taxa, I would not want a nomenclatural system that prohibited the freedom of thought and expression allowed by the Linnaean rules.

What of other PC positions? Were taxonomists in the late nineteenth and twentieth centuries just recalcitrant, clinging to archaic practices? Were they truly too dull-witted to grasp the implications of Darwin? On the contrary, great minds have weighed the options and chosen Linnaean nomenclature with deliberation. Much effort was expended to purge unnecessary evolutionary process assumptions from *phylogenetic systematics* (Eldredge & Cracraft 1980, Schoch 1986). What about the brilliant observation that Linnaean nomenclature is non-evolutionary because it predates the *Origin*? Adherence to similar logic would deny the monophyly of Coleoptera because it was named before Hennig's precise definition of that word. This is silly.

Linnaean nomenclature is stable enough to say what we know, flexible enough to accommodate what we learn; independent of specific theory, yet reflective of known empirical data; compatible with phylogenetic theory, but not a slave to it; particular enough for precise communication, general enough to reflect refuted hypoth-

eses. Linnaean nomenclature is an effective international, inter-generational and trans-theoretical system of classification that was forged and tested by those describing the Earth's biota, not touting political slogans. It has weathered more worthy adversaries than the PC and will be in wide use long after the PC is a curious footnote to the history of taxonomy.

## 5. THE NATURAL HISTORY OF MUSEUMS

Natural history museums were traditionally the place where the best and most extensive descriptive taxonomy was completed. Even after a 'publish or perish' culture characterized many university campuses, museums continued to support comprehensive taxonomic revisions and monographs (Crowson 1970). Although museums are important as repositories for voucher specimens associated with many kinds of biological research, they also play an essential role in documenting biological diversity through specimens associated with taxonomic research and their attendant supporting natural history information. Museums are the first and foremost institutions for taxonomy. It follows that a renaissance in taxonomy is impossible without visionary and courageous leadership in the museum community. Regardless of how much information in museums is databased or how many specimens are scanned and high-resolution images posted to the World Wide Web, the ultimate value of collections resides in specimens. They will remain the ultimate arbiters in questions of identification or character expression for the researcher and they will remain the unique draw for children and adult visitors alike. There is a reason that tourists who have seen pictures of the Eiffel Tower or the great pyramids on a Web site still spend money to travel to France and Egypt. There is something deeply significant about being in the presence of the actual object. Ask any child standing agape before a dinosaur skeleton and he or she will explain the difference.

As natural ecosystems are altered or destroyed it will be increasingly true that all that we know of many species is the information associated with museum specimens. There will never be time or money to carry out rigorous ecological studies on more than a tiny fraction of the species living today. This does not suggest that there is no value to simple, qualitative, natural history observations. To the contrary, there is enormous intellectual benefit to documenting even simple information such as latitude and longitude, seasonal appearance, host associations and similar information for species that may be extinct in a few years. In our technological arrogance we have forgotten how much enjoyment people derive from such simple observations in nature. Field guides still outsell automated sequencers in the general public.

The museum of the twenty-first century will be a centre of cutting edge technology with molecular laboratories as well as nodes in the most sophisticated information technology networks. However, the focus will return as it should to taxonomy and natural history. Many kinds of laboratory can be created almost overnight on any college campus. The comparative work of taxonomists requires access to worldwide synoptic collections of specimens that can be amassed only over centuries.

Beyond supporting species inventories and ongoing

taxonomic research, museums must be centres also of public and formal education from preschool to post-doctoral research. The fact that taxonomy is misunderstood by many professional biologists suggests that it is virtually invisible to the public. This is a challenge and opportunity to museums to educate the public about taxonomy, share its intellectual excitement and demonstrate its importance to science and society.

Building support for taxonomy and natural history studies among the public is an easy sell compared with explaining nuclear physics or molecular mechanisms at a cell membrane. Humans have a close, literally congenital, connection with nature and an innate curiosity about other species (Wilson 1984). Take anyone for a walk through the woods and their first question upon seeing an unfamiliar plant or insect will be 'what is it?' Given an answer, the next question will be an ecological one, 'what does it do?' On a planet where nine out of 10 species are new to science and many of them face imminent extinction, there is no shortage of work for the museum in collecting and preserving evidence of that biodiversity and making that knowledge accessible to the public.

Information and digital technologies have only begun to show their impact in collections. The simplest application is capturing data associated with specimens, itself a difficult and costly endeavour (Smith *et al.* 2003), and one best done in association with active taxonomic research (see above).

Although the origins of the world's great natural history museums, herbaria and botanical gardens are varied and tied to motives as diverse as their creator naturalists and nations, it may be said that the periods of great growth in collections including the Victorian age were tied to taxonomy. Vast collections were compiled for and by taxonomists and natural historians. Access to such synoptic worldwide samples for particular taxa are prerequisites to good taxonomy. Access to such wondrous assemblages of specimens contributed directly to an appreciation for genetic variation, structural homology, adaptation, developmental genetics, ecological assemblages, theories of evolution and other trends in biological thought but were nonetheless the fruits of taxonomy.

Natural history museums in the USA are being crippled by current budgetary problems (Dalton 2003; Gropp 2003). Given a general downturn in the economy, the fact that museums should suffer a disproportionate share of the cuts should not come as a surprise. I believe that a major reason that museums are not doing well today is that they have increasingly distanced themselves from their taxonomic roots. As museums have lost sight of their unique role in science and have increasingly emulated other kinds of institution, they have only compounded the problem. Museums that try to 'info-tain' like biological theme parks or pursue every kind of popular biology like bush-league universities invariably end up being also-ran institutions. Those that promote their unique and essential contributions to documenting biological diversity can create their own opportunities.

## 6. TAXONOMY AS BIG SCIENCE

To meet the biodiversity crisis, taxonomy must rapidly transform to become big science. Its guiding agenda, after



all, is to fully discover and describe the species of an entire planet. If it is worth billions to determine whether there is or ever was life on Mars, it is surely worth more to document the results of thousands of millions of years of evolution on Earth. In all probability, this is the first and last opportunity to study the patterns of diversification of life on a spectacularly biologically diverse world. Taxonomy not only deserves support, it deserves massive support to meet this last ditch effort to document species.

Challenges facing taxonomy are too immense to be solved by the approaches of the past. It is essential that taxonomists approach their work on a scale commensurate to these challenges. This will necessitate research tools and projects on new scales and a cultural change among taxonomists who need now to function as a community. Although there will always be room for individuals to pursue the intellectual rewards of taxonomy and natural history studies, it is imperative that large-scale approaches be adopted that can advance knowledge in very efficient ways. The taxonomic community needs research tools that integrate individual taxonomists, museum collections and cutting edge technology into a seamless research platform that is comprehensive and resilient.

Rapid advances in cyber infrastructure, bioinformatics, digital imaging and related information technologies suggest that the taxonomy and museum community set high goals for research that tests and makes accessible existing information, generates new information on a scale appropriate to meet the decline in biodiversity, and does so in a way that creates and maintains in perpetuity an archive of crucial taxonomic information. Some of the immediate information technology opportunities for the community include the following:

- (i) cyber taxonomy research and education platform;
- (ii) virtual monography tools;
- (iii) a visual data Morphobank analogous to GenBank;
- (iv) high-resolution images of type specimens;
- (v) online open library with all published species descriptions;
- (vi) image recognition software with applications for species identifications and search engines for a morphology image data bank; and
- (vii) sophisticated interactive identification keys.

Cyber infrastructure is on the threshold of revolutionizing science (Atkins *et al.* 2003). Taxonomy is poised to take full advantage of this revolution and to completely reinvent itself for the twenty-first century. Most of the constraints that made taxonomic research slow and laborious are about to be lifted and it is entirely reasonable to envisage taxonomy in the twenty-first century melding the theoretical advances of the twentieth century with the emerging technologies of the twenty-first century to maintain the excellence of scholarship that has marked taxonomy, while expanding and expediting its work in ways unimagined a generation ago.

Cyber infrastructure has the potential to unite the world's museums and taxonomists into a seamless virtual biodiversity observatory. This observatory, like a telescope, would allow scientists to see biodiversity from new taxonomic perspectives. Palaeontological collections permit observations of biodiversity in the geological past

whereas hundreds of millions of specimens allow observations of biodiversity through more recent historic time. The most powerful use for the observatory, however, is to establish a clear image of the *status quo* as a basis against which to observe changes in biodiversity in the future. Such an observatory would complement other efforts to use sensors to monitor environmental change and be an incredible resource for all biologists. This taxonomic platform would be much more than a virtual biodiversity observatory, however, and constitute the most powerful instrument ever conceived for taxonomic research and education.

Imagine museums and universities as nodes in this cyber network. State-of-the-art research facilities, collections, taxon experts and students connected in a vast interactive system. Taxonomists are unique in their need for access to worldwide collections of specimens to compare species of a taxon throughout their geographical and ecological ranges. In the past, this necessitated a combination of travel to and borrowing specimens from scores of museums to complete a revision or monograph and many special trips to examine type specimens. Although such travel and shipment of material will always be necessary at some level, there are thousands of routine observations and identifications of specimens that could be accomplished remotely using such a distributed research tool. Many observations could be accomplished by examination of libraries of digital images. In other cases, a specimen could be mounted in a remote microscope and manipulated and studied virtually. Research assistants involved in field inventory work can similarly be in touch with the taxonomist leading a project through the system. Taxonomists can also make identifications and be accessible for consultation to other scientists, border inspectors and students through this facility.

Another traditional limitation on taxonomic productivity involved access to the millions of published species descriptions (Agosti & Johnson 2002; Anon. 2002). A part of this network would involve access to full text and illustrations associated with every species description. A taxonomist working at a remote field site could download a description as well as a taxonomist in a small institution in a developing nation. Such efforts are already well underway (Agosti 2003).

Once such an archive becomes permanent (that is, there exists an international commitment to its backup on emerging media types in perpetuity and with unrestricted access), it will have a very liberating influence on taxonomic research. With mechanisms for peer review and quality control in place, electronic publication will allow entirely new kinds of taxonomic publication. Monographs, rather than large, static, episodic works, can become interactive ongoing enterprises. Consider a virtual monograph in which species (peer reviewed and accepted) are instantly accessible in diagnostic keys and checklists. Virtual monographs with exhaustive information on each species form a knowledge-base from which the user may access a full and up-to-date monograph or design a virtual publication to meet specific needs, such as a key to the species that occur in a particular country.

One component of this virtual research instrument would be a digital image library, a bank of morphology images to function much like GenBank as a way to

document observations. Publications linked to this image database would offer to morphologists potentially unlimited space to convey information about structure. Intelligent species identification software could search this database much as police forces currently match images of fingerprints. Another component would be DNA barcodes for species identifications.

## 7. VISION FOR TWENTY-FIRST CENTURY TAXONOMY

There is a conjunction of factors that indicates that this is the time for a renaissance in taxonomy. Theoretical advances in phylogenetics, realigned with the goals of taxonomy, make possible the best classifications in history. There is a heightened appreciation for the urgent need to pursue an inventory of the planet's species before it is too late to do so. Advances in information technology, including digital imaging, provide a foundation for a new vision of how traditional taxonomic goals can be achieved. Cyber infrastructure, in its next generation, will make a multi-institutional, multinational taxonomic research and education platform with the potential to totally transform taxonomy. There is a growing awareness of the importance for governments to invest more heavily in science infrastructure. Decision makers are asking for objective science on which to develop policy that derives from environmental observatories; linked museums are the best option for a virtual biodiversity observatory. A unique opportunity is open to us to create a legacy of knowledge of biological diversity and to open up human knowledge of all species to the people of the world. Although I disagree with details in Godfray's (2002) proposal, I agree completely that taxonomy must be reinvented for the digital age and that morphology-based taxonomy is ideally suited to electronic communications (Bisby *et al.* 2002).

Taxonomy is an exciting science, not an identification service for other scientists, although the need for reliable species identifications is a major justification for supporting this science. The immediately needed renaissance in taxonomy must be guided by taxonomic theories and needs rather than those of related fields. Taxonomy must adapt appropriate technologies to achieve its research agenda and not be distracted by technologies themselves, achieving evolutionary change into the information age (Knapp *et al.* 2002; Mallet & Willmott 2003).

For 60 years, taxonomy has been moulded by priorities set by other communities. This tactic has consistently weakened taxonomy and diverted attention and resources from its goals. The single most important thing that the taxonomy and museum community can do today is to come together, set an explicit set of goals for the next decade, articulate what tools and resources are needed to meet those goals, and speak to the world univocally about its self vision.

Because phylogenetic biologists are concerned with 'tree thinking', their top priority is reconstructing trees. Taxonomists are concerned with exploring and understanding biological diversity at and above the species level (i.e. with species and clades) and hence are concerned about homology, character analysis, classification and nomenclature in addition to phylogenetics, the last critical to excellence in the other goals. When the goal is merely reconstructing

a tree, it makes sense to use DNA data extensively (if not exclusively) because it offers rapid access to a large amount of data. However, when the goal is to understand species, homologies and apomorphies, then related fields acquire immense importance including comparative morphology, geography, natural history, etc.

A major goal of every biologist concerned with species extinctions must be to make nature accessible to the general public so that they may know, enjoy and value wild places. Although some may become starry eyed at the prospect of an automated sequencer in every living room, there will always be those (professional and amateur) who appreciate aesthetic beauty in nature and who will want to go into wild places with a field guide (or palm computer) and be able to identify species based on observable morphology. It is intellectually stimulating, visually exciting and just plain fun to know and appreciate morphology. Were every species on Earth identical in morphology but conveniently segregated into discrete kinds differing by 5% of the base pairs in an arbitrarily chosen DNA segment, I doubt that there would be all that much interest in DNA taxonomy after 'describing' the first few thousand species. Humans have marvelled and puzzled over morphological diversity for thousands of years. We now have the opportunity to put centuries of scholarship on morphology into perspective and share it with the world. Why forego all that is intellectually engaging and aesthetically beautiful to settle for that which is clinically efficient? The visual data of morphology could never be efficiently communicated in the past. We have now the technology for a golden age of comparative morphology if we can overcome pressures to conform to 'technological correctness'.

Securing the research tools and support for museum growth that are essential to the taxonomic enterprise, the community must immediately become politically savvy. Were the world's museums and herbaria to combine their voices with those of every taxon-focused professional society and individual taxonomist, an agenda could enjoy the backing of tens of thousands of scientists. No one could be naive enough to believe that a roomful of taxonomists, much less several tens of thousands, could possibly agree on a shortlist of priorities. However, this does not preclude the community from coming together and fighting out a shortlist of near-term priorities. That list must then be promoted as the needs of the community. Over time, all factions could identify one or more priorities on such a community short list. The *status quo*, a cacophony of discordant voices, results in negligible support for taxonomy. Surely it would be an improvement to have half a dozen major goals funded rather than none. The community should set forth a bold decadal vision for taxonomy as well as a 5 year set of attainable goals. This 5 year plan should be revisited with fanfare annually, with successes highlighted and a rolling set of goals.

Taxonomy, the sleeping giant, has awakened. Armed with the latest information technologies and a renewed sense of purpose, driven by the now or never urgency of the biodiversity crisis, the community has the opportunity to lead a big science project that could define our generation. Had Linnaeus had the kinds of digital tools available today to visually describe and share morphological and species knowledge, it is doubtful that taxonomy would

have lost ground in funding or prestige. The time is at hand for taxonomy to take its rightful place among big sciences and to lead society in a meaningful response to the biodiversity crisis. There are no actions in science with the practical, intellectual, societal or ethical benefits that will accrue to this taxonomic renaissance. Will our generation of taxonomists do the right thing and create an enduring legacy of knowledge of Earth's species diversity? Or will we continue to go for the easy money and let our priorities be dictated by other fields and technology? Will we explore and document life on this little-known planet? Or will we sell out centuries of scholarship for short-term technical self-aggrandizement? These choices are uniquely ours because no future generation will have the opportunity available to us to create this legacy of taxonomic understanding. The community's response must be decisive and visionary and as a purpose common to scientists and natural history institutions alike. Given the immensity of the challenge ahead, we are exceedingly fortunate to have the scientific perspective, theoretical framework and technological tools to succeed.

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#### GLOSSARY

ATOL: assembling the Tree of Life

NSF: National Science Foundation

PC: PhyloCode

PEET: Partnerships to Enhance Expertise in Taxonomy