

Systematics must Embrace Comparative Biology and Evolution, not Speed and Automation

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Abstract Systematists have come under a barrage of criticism because of the alleged inadequacy of the ‘traditional’ taxonomic paradigm to curb the ‘biodiversity crisis’ and expeditiously make available the products of systematic research—usually species names—to the professional biological ‘user’ community (including ecologists, physiologists, population geneticists, and conservationists). The accusations leveled on systematists range from being ‘slow’ to ‘incapable’ of furnishing these products at a rate considered (by users) appropriate, especially given that the professional systematic community is portrayed as being in stark decline while operating in a quickly deteriorating natural world. Some of the critics have proposed solutions to this ‘taxonomic impediment’ in the form of a triumvirate adjoining a unitary taxonomic cyberstructure + automated DNA barcoding + molecular phylogeny, which we consider to be nothing but a threefold miopia; one critic has even gone as far as to suggest that biologists who need systematists can circumvent this dependency by ‘doing systematics themselves’. The application of a quick-fix, ‘automated-pragmatist’ model is antithetical to a science endowed with a strong epistemological and theoretical foundation. We view

the current propaganda in favor of automation and pragmatism in systematics as a distraction from the real issues confronting systematists, who must do more to impede the current trend that has ‘marginalized’ organismal biology in general. Simply increasing the rate of species descriptions, as suggested by critics, will not ameliorate the ‘crisis’—taxa that correspond to incorrect hypotheses of biological entities (i.e. that are not monophyletic) will compromise the reliability of systematic information. Systematists must therefore provide more than ‘binomials’—they must strive to produce vigorous hypotheses of comparative biology that are historical and theory-rich in order to augment the general reference system that is so critical to research in other biological sciences and conservation.

Keywords Taxonomic impediment · Phylogenetic systematics · Taxonomy · Comparative biology · General reference system · Historical biology · Conservation

Introduction

... institutions and leaders [of descriptive taxonomy must] become more pluralistic in what they recognize and reward as excellence (Godfray and Knapp 2004, p. 568)

Taxonomy might indeed be threatened, but the greatest threats might be from those who would usurp the resources that it needs to grow and thrive (Lipscomb et al. 2003, p. 65)

In a recently published essay, Evenhuis (2007) discussed a facet of the ‘taxonomic impediment’ that he believes has

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been neglected by those concerned with the current ‘crisis’ affecting this branch of science—that many taxonomists are not delivering the goods because they are simply unproductive, and therefore apathetic about advancing the noble causes of taxonomy. In short, according to Evenhuis, some taxonomists are like junkies—they crave and seek the thrill of collecting and discovering new taxa, but that after this initial rush the tedious work of writing up their conclusions falls astray. To remedy this paralysis, Evenhuis proposed practical steps for taxonomists which he believes would solve this aspect of the ‘impediment’.

Evenhuis has undeniably exposed a difficulty impacting taxonomy, and one that may even be relatively common. However, even though his diagnosis may be partially correct, a proper analysis of its causes is lacking in his paper, which we believe may bring unwanted consequences for taxonomy. In our view, the lack of steady publication by some taxonomists is merely a *symptom* of the supposed ‘taxonomic impediment’ and not a major *cause* of it (like Evenhuis, by ‘impediment’ we mean the alleged slowdown in taxonomy; see also Crisci 2006a, p. 219).

We concede that there are taxonomists who fail to produce what is expected from them, and that their lack of publication constitutes a substantial barrier to progress. But, realistically, this is a predicament common to every branch of science and should not be offered solely as a sin of certain taxonomists; addressing the real reasons behind such cases would be, in effect, a more productive discussion. Furthermore, Evenhuis’ characterization of his particular example may be misconstrued as a general phenomenon, leading to a mistaken view of taxonomic science by policy-makers, conservationists, and other external readers. It is our belief that the reasons behind many such cases of unproductivity result from general shortcomings affecting taxonomic science in general, and not that taxonomy and society are at the mercy of idle and indisposed professionals.

The relevance, or lack thereof, of current taxonomic methods for the challenges of the 21st Century has been a topic of much recent debate in the scientific literature (e.g. Tautz et al. 2002; Godfray 2002, 2007; Thiele and Yeates 2002; Knapp et al. 2002; Seberg et al. 2003; Lipscomb et al. 2003; Scotland et al. 2003; Godfray and Knapp 2004; Wheeler 2004; Wheeler et al. 2004; Carvalho et al. 2005; Crisci 2006a; Carvalho et al. 2007), as well as in the sociopolitical arena (see AMNAT 2006). In our view, Evenhuis’ (2007) critique cannot be divorced from this greater context. We approach this issue from the perspective of professional taxonomists who see their science as the frequent target of criticism by conservationists, ecologists, population geneticists, and other professionals who all too frequently fail to understand the true scientific and epistemological nature of taxonomy and systematics (terms for

which we hold the same implicit meaning; see also Wheeler 2007). The comments presented below are not meant to be a reply to Evenhuis, but instead deal with broader issues (and some slogans) that are commonly laid bare in the multifarious and growing forum on the so-called ‘taxonomic impediment’.

A Dearth of Resources?

The first factor to consider as a possible cause of the supposed publication deceleration in taxonomy is funding. Taxonomy as a worthy scientific endeavor is undeniably at risk when universities do not hire taxonomists and university collections are threatened with dissolution. Many non-molecular systematists in particular have experienced difficulty in obtaining funding for their research. These are indications that organismal biology is presently going through a phase of ‘marginalization’ (Cotterill 1995; Dalton 2003; Gropp 2003, 2004; Suarez and Tsutsui 2004; Raven 2004; Schmidly 2005; Flowers 2007a), even though we are deeply embedded in a ‘biodiversity crisis’ (Wilson 2003a). This paradox has resulted in a palpable sense of isolation affecting many taxonomists nested in university departments wherein the majority of faculty are biochemists, physiologists, molecular biologists, and other ‘big lab’ professionals who usually have greater amounts of funding and frequently work (and publish) in teams. These taxonomists have been referred to as the ‘invisible poor of taxonomy’, who often only ‘exist outside the the inner circle of large institutions and grants’ (Flowers 2007b, p. 5), and who may even form a substantial part of the working taxonomic force (Löbl and Leschen 2005).

We agree with Evenhuis (2007) that taxonomists need to do more to overturn this scenario, and increasing publication output is clearly a step in the right direction. But significant results have been obtained when proper funding for taxonomy has been made available (e.g. Rodman and Cody 2003; Sabaj et al. 2003), corroborating that the ‘impediment’ is really a *result* of the lack of initiative, and not a *cause* of it. So why have not such positive funding initiatives been repeated *ad nauseum* in order to ebb the ‘biodiversity crisis’, especially in countries in which considerable funding is available (cf. Landrum 2001; Flowers 2007a)? An affirmative and relatively inexpensive example was set in Brazil, wherein increased funding for student and post-doc fellowships, field collecting, and other crucial aspects of the taxonomic enterprise, coupled with the *hiring of taxonomists by universities*, has enormously increased publication rates in taxonomy (just the program ‘Taxonomic Capacitation’ launched in 2006 by the federal granting agency CAPES has already benefitted more than 125 researchers; <http://www.capes.gov.br>). This publication increase

concerns not only the description of new species, but also in the generation of general hypotheses related to biodiversity research, such as the elucidation of evolutionary history, delimitation of areas of endemism, and detection of zones of maximal diversity. This demonstrates that not only a fair amount of funding is needed, but also an appropriate policy for the long-term development of systematics (see also Cotterill 1995; McNeely 2002; Schmidly 2005; Flowers 2007a). This policy must also take into account the maintenance and augmentation of scientific collections, as well as the re-identification of their included specimens to guarantee their currency and avoid the propagation of misidentifications (Meier and Dikow 2004; Wheeler 2004).

Critics of the traditional taxonomic paradigm may be portentous competitors for the limited financing available in the modern scientific world (Lipscomb et al. 2003; Flowers 2007b). Are resources that should be destined to taxonomists being usurped by those who need the products of taxonomic research? This viewpoint is still somewhat controversial, but is apparent at least in the skewed division of funding in some biodiversity mega-projects, wherein only a small fraction of the funds, if any, are dedicated to ‘real’ taxonomy (i.e. for the production of primary taxonomic information, such as species descriptions), while most of the money goes to ‘secondary’ aspects (such as databasing and internet availability; the Global Biodiversity Information Facility [GBIF] is one such example). One worker even concluded that web-based taxonomy and database initiatives that simply apply ‘new technology to existing data rather than generating new data [have] mopped up a not inconsiderable fraction of the available money during the Biodiversity Decade’ (Flowers 2007b, p. 5). In the same vein, systematists are constantly being instructed on how to become more relevant to other biologists in order to obtain greater funding (Godfray and Knapp 2004; Gotelli 2004; Godfray 2007), as if somehow our long-term survival should depend on the degree to which we satisfy the needs of researchers in other biological subdisciplines.

There is really no doubt that taxonomists may indeed benefit from a more inclusive mindset, especially in terms of obtaining funding through collaborative research projects which include a strong systematic component. But theoretical and epistemological progress must ultimately be driven from within—in order to be truly useful to other biological sciences, and society in general, systematics cannot compromise its much-earned theoretical identity and overall independence. Systematists, however, must bear in mind that this can be accomplished while simultaneously making our results amenable to the general scientific community. The use of highly structured phylogenetic information in studies of comparative physiology, for example, is a strong example of how systematics can be pivotal in the development of other branches of science (Garland et al. 2005).

‘Taxonomy Needs Evolution, not Revolution’ (Knapp et al. 2002)

Many critics of taxonomy simply do not understand the real dimensions of biodiversity, even though they pay considerable lip-service to it. Biodiversity knowledge encompasses not only an extraordinary number of ‘taxonomic names’, but also an extraordinary amount of variation—morphological, behavioral, and molecular—embodied by the natural entities represented by those names. An appropriate depiction of taxonomic complexity is a matrix with hundreds of thousands of characters on one axis and thousands of organisms on the other, with millions of data points filling in the spaces (eventually optimized as relationships, i.e. taxa). How much of this colossal amount of information should be at the hands of any single taxonomist? And how many taxonomists are working on the evolution of hyper-diverse groups, such as fungi, beetles, bacteria, flowering plants, fishes, nematodes, mollusks, flies, birds, etc.? The discrepancy between the amount of unknown taxa and those that need revision (the ‘staggering number of specifics’ of Vane-Wright 1996), on one side, and the overall lack of professional taxonomists in universities and even in museums, on the other, may contribute to the sense of isolation felt by professional taxonomists (Wilson 2003a).

Evenhuis’ (2007) quick-step list of procedures was provided to facilitate the description of new species and thereby overcome at least this aspect of the taxonomic impediment. To Evenhuis, therefore, it seems that what needs to be presently optimized in taxonomic science is a greater availability of species names, a viewpoint also held by critics of modern taxonomy (see Tautz et al. 2002; Godfray 2002; Tautz et al. 2003; Hebert et al. 2003; Gaston and O’Neill 2004; Janzen 2004; Godfray 2007). In particular, Evenhuis’ (2007) Step 6 (‘enjoyment of describing’, p. 10) shows how to expedite the descriptive process: species descriptions in diverse taxa could simply follow an automated style based on a template description which is changed according to the taxon being described. If even this proves to be too much, Evenhuis states that it is possible to describe new species solely on the basis of the *minimal* amount of taxonomic information needed to be accepted by current biological codes, although he does not sanction this approach himself: ‘in zoology, one only needs to describe characters that differentiate one taxon from another. At a minimum, one could theoretically say “Yellow, 20 mm long” and that would validate the description and naming of a new taxon’ (pp. 10–11).

It is true that such a terse account is acceptable according to the zoological code of nomenclature, but is it *desirable*, especially for a branch of science endowed with a strong epistemological commitment? Taken to the letter,

this minimalist approach may further promote superficiality and lack of professionalism in taxonomy, although clearly leading to faster species descriptions. But quickly describing alleged ‘species’ without the proper systematic foundation will result in nothing more than a hodgepodge of names that may not refer to any real units in nature. These names are therefore not only useless for taxonomy itself but also for inferences about character and taxic evolution, historical biogeography, and conservation (Vane-Wright 1996; Wheeler and Platnick 2000; Wheeler 2004; Santos and Amorim 2007). In other words, even though ‘quantity’ is presently needed from taxonomy, it cannot come at the expense of ‘quality’, as taxonomic names corresponding to flawed hypotheses of biological entities will compromise the reliability of systematic information for society. The current nomenclatural codes should take direct steps to eradicate, and not endorse, minimalism and amateurism from taxonomy.

This fundamental ignorance of the systematic *praxis* by users of taxonomic products (i.e., in over-emphasizing species names and their distributions as the primary units to guide conservation efforts and environmental policy), further ignores two primary aspects of systematics: (1) that only monophyletic units, independent of their rank, must be understood as ‘natural entities’ (and therefore *real*, subject to conservation); and (2) that the organismal collectives which are described as species, and that receive formal binomials, do not necessarily correspond to natural, monophyletic units. Species names are intuitive resources indispensable for purposes of communication and organization of information at the species level, but in themselves do not *necessarily* contain any real scientific value since many species are simply not corroborated as monophyletic (and there is still disagreement concerning the issue of whether species *must* be monophyletic; e.g. Wheeler and Meier 2000). Conservation efforts should be aimed at monophyletic units, not at binomials devoid of real existence.

Moreover, taxa (of all levels) are hypotheses of relationships which may change with further analysis, reinforcing the true scientific nature of systematics. The incorporation of phylogenetic hypotheses to revisionary studies has, in fact, added an extra dimension to the labor of taxonomists. In recognizing that real entities are what systematists need to provide to conservationists and other biologists, ‘biodiversity’ takes on a new meaning—one associated with monophyletic groups (historical hypotheses), reinforcing that taxonomic revisions need to be even more inclusive in terms of data and theoretical underpinning. The revision of the neotropical freshwater fish genus *Steindachnerina* serves as an example (Vari 1991). Twenty-one species were recognized as valid, of which two were described as new. But the number of hypotheses erected that are relevant to comparative biology in general

is much greater, including the hypothesis of monophyly of the genus and eight of its species (13 species could not be corroborated as monophyletic), in addition to 12 other hypotheses of monophyly related to groups of species. For users of taxonomic end-products, then, this revision indicated that many previously recognized ‘units’ should not, perhaps, be taken into account due to their non-monophyly, and that others, previously undetected, must also be considered. A thorough revision, therefore, provides a sound and scientifically testable guide to conservation.

Original work on a new species should, consequently, include at least a detailed characterization of its morphology or molecular design, as well as insights concerning its phylogenetic relationships. It is just such knowledge that may prove essential to ecologists or conservationists (Stiassny 1992; Stiassny and de Pinna 1994; Purvis et al. 2005; Ennos et al. 2005; Forest et al. 2007). This may account for at least some of the perceived apathy in publishing new species as some taxonomists strive to do more inclusive work. In other words, we should not be so preoccupied about *expediting* the descriptive process, but rather in making it more meticulous and evolutionarily relevant. Is it better to have huge numbers of nominal species available but devoid of this relevant information, or fewer numbers of natural (monophyletic) entities, independent of rank, that are better characterized morphologically, molecularly, and evolutionarily, and which therefore are more reliable guides to conservation? Indeed, the usefulness of taxonomic information after its publication is strictly dependent on the robustness of its holomorphological (including behavioral and molecular) and evolutionary characterization. Users of taxonomic end-products, such as other biologists and conservationists, need to understand these points in order to move beyond the misconception that taxonomic science is simply about making species names available (see also Lipscomb et al. 2003; Wheeler 2004, 2005; Prendini 2005; Carvalho et al. 2005; Crisci 2006a; Carvalho et al. 2007). After all, these same users will certainly feel cheated if the taxonomic information supplied to them proves to be unreliable.

‘Historical Amnesia’ and the Flawed Appraisal of Taxonomy

The above considerations bring us to perhaps an unexpected situation—that there has been, at least for certain groups, an *increase* in the number of taxonomic papers, in the number of described species, in the quality of those descriptions, in the number of pages in those papers, and in the heuristic value of the hypotheses proposed—and all within a general environment, world over, of *reduced* funding. After some 250 years of formal taxonomic work, the rate in which new species are described has indeed

increased for many groups (but not for all, of course), indicating that the perceived slowdown in productivity by taxonomists is partly fallacious even if we employ this criterion—mistaken in our view—as a yard-stick.

As an example, we highlight the description of new species of fishes, which has seen a substantial increase in the last few decades (Eschmeyer and Froese 1999; Nelson 2006). This is made quite clear when comparing the four editions of Nelson's *Fishes of the World*, the standard textbook treating fish diversity (published in 1976, 1984, 1994 and 2006). In particular, neotropical fishes have been the subject of much revisional research and new species descriptions (see Reis et al. 2003; Buckup et al. 2007). Amphibians represent another such case; almost half of the known species inhabiting Brazil, which detains the most diverse amphibian fauna, have been described in the last 40 years (Pimenta et al. 2005). Many other examples could be listed here (e.g. neotropical ants; Wilson 2003b). So why does the 'taxonomic witch-hunt' of late persist (e.g. Godfray 2007) if taxonomists are capable of demonstrating substantial growth on their own?

There seem to be two causes for this mistaken evaluation of taxonomy. The first is that complaints against taxonomy really have nothing to do with taxonomic work per se, but rather correspond to the earnest desire of having all of earth's biodiversity described in face of the ongoing environmental onslaught. Of course, species extinction is not in any way the particular responsibility of the taxonomist—our ability to save species or environments is not immediately jeopardized by the lack of taxonomic names. The other factor is that there appear to be undeclared interests behind the 'speeding up' of the availability of taxonomic products. Recent criticisms of taxonomy appear to be self-serving, concealing an agenda—the promotion of 'quicker', mechanized methods for taxonomic research. This is by no means the case of Evenhuis' (2007) comments, but of the recent reductionist approach of automated molecular taxonomy such as DNA barcoding (Hebert et al. 2003; Blaxter 2004; Barrett and Hebert 2005; Godfray 2007; Miller 2007).

Perhaps it has already been forgotten that phenetic taxonomy tried a very similar approach not too long ago. With the availability of calculators and computers in the late 1950s and early 1960s, there was great optimism concerning the development of an operational, quicker, and 'non-subjective' taxonomy, strongly propagated by non-evolutionary taxonomists. Twenty-five years later, the founders of this approach had to abandon its principles because they realized that the taxa they proposed, both at the species level and above it, had no real connection with nature (Farris 1977, 1979, 1983).

In some measure we are now experiencing a 'molecular-operational' remake of this movie, even though we are already familiar with how it ends (previous remakes starred electrophoresis, cytogenetics, and DNA hybridization).

Incongruent molecular hypotheses for the same taxa published in the last two decades has led to the realization that there is also much conflict in molecular data, not to mention the outstanding methodological issues related to gene choice, sequence alignment, and tree construction (e.g. DeSalle et al. 2002; Naylor et al. 2005; Prendini 2005). Even proponents of barcoding have concluded that without a strong taxonomic foundation the method is ineffective (Meyer and Paulay 2005; see also the cogent remarks of Will and Rubinoff 2004; Ebach and Holdrege 2005; Wheeler 2005; Prendini 2005; DeSalle et al. 2005). As stated by a leading molecular systematist, '[i]n a taxonomic context DNA sequence information in the absence of other corroborating evidence can never be used by itself as an indicator of species delimitation' (DeSalle 2006, p. 1545).

This fundamental discussion about the nature and acquisition of molecular data should be an integral part of the debate concerning the lack of greater speed in describing new species, given the 'one minute-one sequence-one name' (Janzen 2004, p. 732) frenzy of the quick-fix strategists. We strongly adhere to the maxim (Ebach and Holdrege 2005, p. 697) that 'DNA barcoding generates information, not knowledge'—if not a taxonomic specialist, who, then, will *define* the species in question? Therefore, does the implementation of this method not require, beforehand, a robust taxonomy? Paraphrasing these same authors, it is pertinent to inquire '[h]ow long will it be until even the specimen is no longer necessary to understand the organism?' Within the current mood beckoning the 'Big Machine of DNA automation' to the rescue, the organism is, little by little, being relegated to the trash-heap. Meanwhile, proponents of automation continue to conflate species delimitation with species identification (e.g. Barrett and Hebert 2005; Godfray 2007), demonstrating their fundamental ignorance concerning taxonomic science (Lipscomb et al. 2003; Prendini 2005; Wheeler 2005). It seems that a form of 'historical amnesia' reappears in systematics from time to time as old tendencies creep back into vogue, albeit usually under a new guise (Nelson 2004). In the current automation paradigm, we may have, indeed, the erection (or resurrection) of a *nouveau* phenetics—one employing DNA barcodes.

Trivializing Taxonomy—the 'Do it Yourself' Dictum

Another source of renewed criticism to taxonomy has come from proponents of web-based initiatives that aim to become repositories of taxonomic information. Some have even declared that the triumvirate 'unitary taxonomic cyberstructure + automated DNA barcoding + molecular phylogeny' will save taxonomy from its downfall and modernize management of the biodiversity crisis. The

same proponents of this sheer pragmatism have characterized taxonomy as a ‘do it yourself’ science, especially given available technology and its constantly reducing costs. In other words, according to these critics, with the right equipment and software, and making full use of one-stop, web-based taxonomic shopping, ecologists or other non-taxonomists can simply (and finally!) do away with the dusty, sluggish, and idiosyncratic systematist and deal directly with species identification and phylogeny—technology, after all, has rendered these complex issues a simple matter of ‘cooking’ (see Grant et al. 2003 for a critique of ‘point-and-click’ systematics).

The most declared advocate of the ‘do it yourself’ school is Godfray (2007). In light of the rebuttals published by taxonomists addressing previous commentary on these issues (Thiele and Yeates 2002; Knapp et al. 2002; Seberg et al. 2003; Lipscomb et al. 2003; Scotland et al. 2003), including a detailed one in a recent colloquium co-organized by Godfray himself (Wheeler 2004), we are left wondering why his fanfare was repackaged and delivered anew. Perhaps Godfray’s (2007) essay was calculated to further his own database initiative, a unitary, web-based taxonomic repository that will ‘be self-contained and require reference to no other sources’ (Godfray 2002, p. 17). According to Godfray (2007), even Linnaeus would have supported it, for he would have been a ‘techie’—a revisionist strategy employed to recruit that great luminary in support of Godfray’s own cause. Our contention here, of course, has nothing to do with web-based tools or technology itself, but with a concerted directive to discredit ‘traditional’ or ‘established’ systematics—using our founders against us is just straws in the wind.

The ‘do it yourself’ catchphrase can never represent, by any standard, a healthy prescription for a scientific endeavor. If ecologists, population geneticists, and other biologists prefer to have quick species names and even quicker phylogenetic trees at their disposal—and without a deeper appreciation for their essential qualities as hypotheses—then, perhaps, they should simply not rely on systematic information at all. These biologists clearly do not wish to embrace an ‘ahistorical’ paradigm, which would be overly anachronistic, but in some way that is the effect of the ‘do it yourself’ mindset. What can be more important in science than an unreserved concern for data (characters) and methods of analysis (optimality criteria)?

An Overture for Taxonomy

Research oriented, professional taxonomists must take the bull by the horns and raise their voice against the many criticisms that have diverted the discussion from how to increase the successful, ongoing taxonomic undertaking, to

an attempt to substitute the current paradigm for a reductionist-pragmatist one. Balance in employing different sources of data and methods that are in fact constructive are essential to maintain steady progress in systematics (Crisci 2006b). But systematists must bear some blame here as well—*qui tacet consentire videtur* (‘he who keeps silent is assumed to consent’). Evenhuis (2007) is correct in partially blaming taxonomists for at least some of the supposed taxonomic slowdown, but not necessarily for the reasons he advocates. In our view, the coherent remarks of Crisci (2006a, p. 219), in describing the intellectual climate surrounding systematics, are more to the point: ‘... the climate of opinion depends on who speaks and who keeps quiet, [which is described by social scientists] as a “spiral of silence” ...’. And, as a consequence, ‘[e]ditors, peers, administrators, and [some] policy-makers become enforcers of a *vox populi-vox dei* [in support of] molecular systematics’, leading to a ‘new kind of superficiality ... where technological advance is equated with conceptual progress’. Conceptual progress is achieved only when tied to a strong epistemological basis, and not by the mere application of technical innovations—science is ultimately much more about the meaning of information than about information in and of itself.

For taxonomy to be effective for science and useful for society in general what is needed is more than species names or undemanding ‘taxon-tags’—taxonomy needs in-depth studies of evolution. We must move beyond the slogan that a faster, minimally informative, two-dimensional and algorithmic approach to species descriptions will save taxonomy from irrelevance—superficiality will not advance taxonomic science. Taxonomists must provide robust hypotheses about real (monophyletic), natural entities, and about the relationships of the areas they inhabit. In other words, taxonomists must do more—they must embrace the integrative strength of comparative biology (Hennig 1966; Nelson and Platnick 1981; Rieppel 1988) and remain focused on substantiating the ‘general reference system’, which is by no means an outcry for quicker publication.

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