

Taxonomic Impediment or Impediment to Taxonomy? A Commentary on Systematics and the Cybertaxonomic-Automation Paradigm

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In the year in which we celebrate the 300th anniversary of the birth of the two greatest naturalists of the 18th century, Carolus Linnaeus and Georges-Louis Leclerc (Comte de Buffon), a statement expounding the significance of modern taxonomy is timely, especially given the current

demands stimulated by the 'biodiversity crisis' and by biologists and conservationists who require the availability of species names at an ever-increasing rate. Linnaeus and Buffon were arch-rivals who loathed each other but who have provided much of the foundation on which

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comparative biology subsequently flourished. But part of that foundation has increasingly been judged inadequate to meet the present challenge, undermining the success that taxonomy and systematics have had in general.

A case in point that highlights recent trends is yet another commentary on the current state of taxonomic science by H. C. J. Godfray (Godfray 2007). Godfray is a user of taxonomic end-products who has frequently been critical of the slowness with which modern taxonomy is furnishing these—especially species names—to ecologists, conservationists, ‘biodiversity scientists’, etc. (Godfray 2002; Godfray and Knapp 2004). Godfray’s criticism, echoed in other circles (Tautz et al. 2003; Gaston and O’Neill 2004; Blaxter 2004; Miller 2007), is cast in what he has termed the ‘second bioinformatics crisis’, viz. that the alleged lethargy of modern taxonomy is mostly due to the lack of an adequate cyberstructure to disseminate its much needed products. Godfray is convinced that cyber-initiatives, including his own (Godfray 2007), will ultimately rescue taxonomy from its ill-fated *status quo*, as if the real issues confronting taxonomists are simply those of informatics, i.e. the ‘administration’ of taxonomic names.

But what of the real ‘issues’ currently obstructing progress in taxonomy—the so-called ‘taxonomic impediment’ (Lipscomb et al. 2003; Scotland et al. 2003; Wheeler 2004; Carvalho et al. 2005; Crisci 2006)? Over the past few years the community of professional taxonomists has grown accustomed to being labeled not only as mere ‘service providers’ for the biological sciences, but ones that are becoming irrelevant due to obsolescence. In our defense we wish to underscore factual and cost-effective initiatives made by taxonomists addressing the most cited aspect of the ‘impediment’—the speed with which new species are described.

The National Science Foundation’s PEET and PBI programs are unique in the amount of funding allocated to basic taxonomy. For example, the All Catfish Species Inventory has funded dozens of students of catfish systematics world over which has increased catfish diversity, in just a few years, by roughly 10% (some 300 new species have been described since its inception; the program also funds field collecting and monography) (Sabaj

et al. 2003). Brazil’s ‘National Zoology Program’, created in the early 1980s at a relatively low cost, has led to the education of hundreds of new taxonomists. As a direct result the Brazilian zoological community continues to grow rapidly—more new Brazilian freshwater fish species have been described in the last five years than during any previous similar period (Buckup et al. 2007). The continuous support for taxonomy in the US and Brazil is reflected in the number of authors who have published in *Zootaxa* between 2001 and 2006: US 554, Brazil 496, Germany 118, France 95, UK 93 (<http://www.mapress.com/zootaxa/support/Statistics.htm>). Concurrently, natural history museums in the US and Europe continue to fund taxonomic research visits by students from abroad, including from regions with little financial support such as Africa, to examine specimens first-hand.

These and other comparable programs (see the NSF initiatives BSI and ATOL; www.nsf.gov) demonstrate that taxonomy is capable of substantial growth independent of the cyberstructures and automation touted as the immediate solutions to the ‘taxonomic impediment’. Note that we firmly believe that web-initiatives and technology are necessary so long as they aim to *enhance* the existing taxonomic enterprise, not aspire to *replace* it. We continue to stress, however, that taxonomy needs a greater investment in its foundation, namely in the education of future generations of taxonomic specialists and a greater allocation of funds for collections and basic research (Ebach and Holdrege 2005a, b). But genuine growth also depends on the establishment of faculty positions for taxonomists (Agnarsson and Kuntner 2007), requiring a reversal of the institutional ‘marginalization’ affecting organismal biology in general (Gropp 2004).

The ‘cybertaxonomic solution’ (e.g. Godfray 2007) reveals a traditional misunderstanding that regularly emanates from the more ‘applied’ side of biology—that the only significant data taxonomists provide are the species name, diagnosis, and distribution for the purposes of identification by non-taxonomic end-users. This ‘end-user’ attitude reflects a lack of appreciation that taxonomy, systematics and phylogeny are interwoven, hypothesis-driven sciences with a vigorous theoretical base (Lipscomb et al. 2003; Wheeler 2004; Carvalho et al. 2005; Crisci 2006). Taxa, including species names, are *not* mere end-products—they are hypotheses of relationships (i.e. of evolution) that require corroboration and which may change with ongoing testing as further data becomes available. As hypotheses, taxa are essential to phylogenetic and biogeographic studies which themselves underlie any real understanding of biodiversity, evolution, and their causes. It is such integrative knowledge that is indispensable to other areas of biology as well as for conservation (Purvis et al. 2005; Mooers 2007; Forest et al. 2007). Poor

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systematic hypotheses, after all, will lead to erroneous conservation priorities, and paraphyly may lead astray even the most well-intentioned ecologist. A substantial contribution from taxonomy to science and society in general will not come from huge numbers of species names destitute of biological meaning, but rather from reliable evolutionary hypotheses regarding natural entities—the expected outcome of thorough research by professional systematists.

So it is to our great concern that we read in Godfray's (2007, p. 259) recent essay comments that appear to represent the mind-set of many DNA barcoders and other advocates of automation and pragmatism in systematics: 'tasks that were once the unique preserve of the taxonomist can now be done by most biologists', or that, in reference to species limits and their phylogenetic relationships, '[taxonomists] often forget that many of the traditional user communities of taxonomy can now investigate these questions themselves', or even that 'biologists who might have previously looked to taxonomists to provide a phylogeny of a group are finding it increasingly *easy* to do it themselves as sequencing becomes cheaper and more widely available' (emphasis added). Concerning species identification, Godfray views as a *problem* that the relevant literature or the taxonomist is frequently needed. And, finally, the upshot: 'Ten years ago the only solution to [species identification in biodiversity hotspots] would have been more investment in traditional taxonomy. Today there is an alternative: molecular identification methods, DNA barcodes or related technologies...' (Godfray 2007, p. 260). Indeed, why invest in the training of taxonomists if machines can do the job for us?

The bottom-line of this reductionist approach to systematics, of which Godfray appears as a leading campaigner, is crystal-clear—we must accelerate progress in taxonomy by automating species identification, since research in phylogenetics, according to many reductionists, is already a simple matter of plugging sequences into a computer program. But advocates of 'cake-recipe' systematics ignore empirical data that have demonstrated that 'DNA barcoding is much less effective for identification in taxa where taxonomic scrutiny has not been thorough' and that the 'promise of barcoding will be realized only if based on solid taxonomic foundations' (Meyer and Paulay 2005, p. 2229; see also DeSalle et al. 2005; DeSalle 2006). In other words, the arguments against 'traditional' taxonomy in favor of molecular identification methods are illusory even for proponents of barcoding. Phylogenies produced by 'point-and-click' biologists who lack a theoretical background in phylogenetic inference and a solid empirical knowledge of the organisms under study will simply not withstand scrutiny (Grant et al. 2003). Moreover, by so casually dismissing 'traditional' taxonomy as a means of

independently testing molecular hypotheses, we *constrain* our ability to identify artifacts and errors in sampling, voucher identification, and sequencing. Will not such errors propagate unchecked? (Users of GenBank, beware!). As part of this perfunctory taxonomic New World, Godfray (2007) even advocates a web-only taxonomy that will include 'cybertypes' (images of type specimens), the examination of which he considers often superior to that of real type specimens.

Therein lies the true 'taxonomic impediment'—one that is doctrinal, mechanical, and delivered by end-users of taxonomy apparently not familiar with the complexity of its hypotheses and identity as a real, successful, and independent science. The collective opera of Linnaeus and Buffon need not be relegated to the wastebins just yet.

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