To the Editor:

“If you subvert the basis of the revolution, if you dispense with principles and substitute expedients, you will extinguish that enthusiasm and energy which have hitherto been the life and soul of the revolution; and you will substitute in its place nothing but a cold indifference and self-interest, which will again degenerate into intrigue, cunning and effeminacy.”

Thomas Paine (Conway, 1893)

After decades of neglect, taxonomy is on the threshold of a renaissance (House of Lords, 2002; Wheeler, 2004). The “big questions” of taxonomy seemed insurmountably large, until now (Cracraft, 2002; Page et al., 2005). Theoretical advances in taxonomy have made classifications predictive, hypotheses of species and characters testable, and names highly informative (Hennig, 1966; Nelson and Platnick, 1981; Wiley, 1981; Schoch, 1986; Schuh, 2000; Wheeler and Meier, 2000). Impediments to the growth of taxonomic knowledge are rapidly disappearing. Four “Planetary Biodiversity Inventory” (PBI) projects funded by the NSF are describing or re-describing more than 5000 species in just five years and forging a collaborative paradigm. This is just the beginning. New cyber-infrastructures promise further increases by orders of magnitude (Page et al., 2005; Atkins et al., 2003). Other NSF programs are educating a new generation of taxonomists (Rodman and Cody, 2003), challenging monographers to apply innovative tools (RevSys), and capitalizing on abundant molecular data to complete an inclusive phylogeny (AToL). Because of the biodiversity crisis (Wilson, 1985, 1992), we have but a fleeting chance to explore and document species diversity. Tragically, molecular data useful for species identification is being hijacked (as “DNA barcoding”). This threatens theoretical and practical advances of decades (Ebach and Holdrege, 2005) and loses sight of the science goals of taxonomy (Nelson and Platnick, 1981; Cracraft, 2002; Lipscomb et al., 2003; Wheeler, 2004). Costly lessons learned from the failed “phenetics” paradigm are forgotten and DNA “barcoding” would repeat its mistakes (Prendini, 2005).

Taxonomy does not exist to answer the question “What species is this?” We can answer it because taxonomic research explores Earth’s species, their distributions, relationships, complex characters and classification (Hennig, 1966; Nelson and Platnick, 1981; Cracraft, 2002) producing knowledge transferable to identification systems. Barcoding, like any identification tool, merely applies knowledge derived from tested hypotheses on many levels from homology to synapomorphy, species and monophyly. In the absence of testing, “species” become less informative about the world as new characters and specimens become known. This is the reason for traditional revisions and monographs.

An impressive number of species concepts exist, their relative merits debated (Mayden, 1997; Claridge et al., 1997; Wheeler and Meier, 2000). Why are species concepts of such perennial interest? Because species are the elements of phylogeny, ecosystems, and classifications, essential for comparative biology, and occupy the unique boundary between micro- and macro-evolution (Nixon and Wheeler, 1992; Wheeler, 1999). Hebert et al. (2005) conclude they have found new species yet mention no criteria for nor cite any literature on species concepts. They demonstrate genetic bottlenecks and variation, but what does that mean evolutionarily? Nothing when species are reduced to arbitrary genetic distances. Barrett and Hebert (2005) criticize spider taxonomists for “overwhelming reliance on genitalia for the determination of species boundaries” then proceed to overwhelmingly rely on COI instead. Phenetics of morphology metrics did not reflect evolutionary patterns and neither can DNA-based phenetics (Farris, 1979; Ridley, 1986; De Queiroz and Good, 1997). Good lessons from phenetics, such as using many characters, have been forgotten by barcoders too.

Schindel and Miller (2005) say that barcoders do not intend to replace morphology, but consider Tautz et al. (2003) and the following: “A COI-based identification system will undoubtedly provide taxonomic resolution that exceeds that which can be achieved through

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morphological studies. Moreover, the generation of COI 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” (Hebert et al., 2003) and “We also emphasize the need for the acceleration of species discovery... DNA barcoding is a powerful approach for the discovery of new species” (Hebert and Barrett, 2005). Further, “If taxonomists fail to embrace molecular technology, Hebert is clear about the consequences: ‘There is no more likely death of a discipline than the failure to innovate’” (Nicholls, 2003). But morphologists are innovating. Molecular evidence has been accepted for decades in identification, phylogenetics and studies of the development of characters. Moreover, morphologists refine an ever expanding number of digital tools from SEMs to remotely operable digital microscopy, computer assisted tomography, and confocal laser microscopy. Barcoding would reduce taxonomy to a mere technical service (Lipscomb et al., 2003).

“What is new about Dr Hebert’s approach is his proposal to standardize this process by using the same gene for all animal species” (Wade, 2004). But, having abandoned the idea of a single universally applicable DNA short-segment as a species identifier, it is disingenuous to persist in describing DNA barcoding as a “uniform, practical method” (Barrett and Hebert, 2005; Savolainen, 2005). There is no “uniform” but rather diverse genes to solve diverse problems in diverse taxa, including innovative ways to speed access to new morphology characters (Miller et al., 2005). Taxonomists understand the difference between identification and classification and therefore the place of DNA data (Bello et al., 1995; Prendini, 2005). It is telling that the abandonment of the core tenet of barcoding did not distract proponents from their quest for funding.

Taxonomists have long preferred a multi-character integrative approach gathering together, synthesizing, interpreting and summarizing all useful sources of information in their classifications (Simpson, 1961; Seberg et al., 2003; Will and Rubinoff, 2004; Will et al., 2005). Thus, the logical way forward is not a return to the failed paradigm of phenetics and single-character typology but instead what Will et al. (2005) call integrative taxonomy. Since the 1940s taxonomy has suffered almost uninterrupted confusion with other disciplines (Wheeler, 1995) and must not be undermined by barcoding just as it is about to blossom. Taxonomy does not exist to identify species for ecologists and conservation biologists; it is a necessary complement to general biology, an independent science exploring, describing, analyzing and classifying Earth’s species (Nelson and Platnick, 1981). Identification (applied taxonomy) is important, but it is not a research program and relies upon the fact that credible taxonomy is done.

Accepting the DNA barcode proposal we lose more than the plot. As the last generation with the opportunity to explore and classify Earth’s species, we must not put short-term profits over a permanent legacy of knowledge. Museum specimens, observations of complex characters, and our best estimates of species are a far richer bequest to future generations than a crude and arbitrary sampling of diversity. Artificially delimiting molecular operational taxonomic units at the expense of testable species hypotheses can only be justified by technological self-indulgence and abandonment of most of what we have learned from taxonomy, comparative morphology, and evolutionary biology. Digital environments are the ideal medium for communicating complex structural knowledge and are only beginning to realize their potential (Bisby et al., 2002; Godfray, 2002; Atkins, 2003; Wheeler, 2003, 2004; Scoble, 2004; Wheeler et al., 2004). Molecular profiteering at the expense of continuing the grand biological project enjoined in 1758 will leave but an ignoble record for a rapidly changing planet. My conclusion about the DNA barcoding proposal is the same as that reached by Ross (1964) more than 40 years ago when the same phenetic methods were first proposed for taxonomy: it is “an excursion into futility”.

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References


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