

Points of view

Taxonomy: Myths and Misconceptions

by

Quentin D. Wheeler¹ & Antonio G. Valdecasas²

¹International Institute for Species Exploration, Arizona State University, Tempe, AZ 85287, USA
quentin.wheeler@asu.edu

²Departamento de Biodiversidad, Museo Nacional de Ciencias Naturales, José Gutiérrez Abascal 2, 28006 Madrid, Spain
valdeca@mncn.csic.es

Abstract

Wheeler, Q.D. & Valdecasas, A.G. 2007. Taxonomy: Myths and Misconceptions. *Anales Jard. Bot. Madrid* 64(2): 237-241.

Given the fundamental necessity of reliable taxonomy for biology, it is surprising that taxonomy is so frequently misunderstood. Even former disciplines of “natural history” with their roots in the taxonomic tradition frequently attack taxonomy on false grounds in spite of the dependence of such fields upon credible taxonomic information. We review and refute a number of such myths and misconceptions about taxonomy that seem to contribute to an indefensible lack of respect and support for taxonomists and their collections. We will discuss these myths and misconceptions in no particular order.

Taxonomy is “descriptive”. It is unclear why being descriptive is seen as negative by some experimental biologists; without accurate descriptive work all branches of natural history would be subjective and unreliable. Taxonomy is descriptive, of course, yet much of the substance of its descriptions—characters, species and clades—is based upon explicitly testable hypotheses about sameness and group membership. Because of the nature of evolution biologists deal to a very great extent with unique organisms, groups of organisms and attributes of organisms, making descriptive work inordinately important. That said, the hypotheses embedded in layers of taxonomic work and their rigorously testable nature make taxonomy both hypothesis-driven and scrupulously scientific. An in-

Resumen

Wheeler, Q.D. & Valdecasas, A.G. 2007. Taxonomía: Mitos y errores. *Anales Jard. Bot. Madrid* 64(2): 237-241 (en inglés).

nuendo implícito en such “it’s only descriptive” criticisms is that taxonomy is, therefore, somehow less scientific. That, however, is simply false (e.g., Gaffney, 1979; Nelson & Platnick, 1981).

Taxonomy is typological. Adherents to the New Systematics, and particularly Ernst Mayr (1942, 1969), perpetuated the myth that taxonomy is based upon typological thinking but this is neither historical nor contemporaneous fact. Perhaps because taxonomists use “type” specimens as standards for scientific names, the shared word root lent subconscious credence to Mayr’s claims. The claim was ludicrous in the first place given that taxonomists were among the first biologists to confront the problem of variability (Cracraft, 2000). The taxonomists’ “method of types” (called instead by historian of science Mary P. Winsor “method of exemplars”) is not essentialist as recently detailed (Winsor, 2003). Thus, neither Linnaeus nor any of his followers deserve the claim of Mayr that they were essentialists-typologists (Winsor, 2006).

Species of taxonomy are subjective. Several attempts have been made to replace explicit, testable species hypotheses in taxonomy with alternatives, often suggested by scientists in fields outside taxonomy only marginally engaged (if at all) in species discovery. Species exist. Were this not so and there were only one super-species on Earth, Darwin would have se-

lected a different title for his book and taxonomy would have outlived its utility by the turn of the 19th century. Let us be precise: species can be testable, rigorously scientific hypotheses. But DNA “barcodes” applied to species exploration and discovery (outside the context of corroborated species) are not (see Little & Stevenson, 2007). In spite of declarations to the contrary, “species” based on genetic distances are merely arbitrary constructs of convenience that only occasionally correspond to truly evolutionarily meaningful entities. Such crude species estimates are for the moment popular in bacteriology where evolutionary thinking has yet to arrive in regard to species (Goldenfeld & Woese, 2007). In a bizarre twist, some studying Eukaryotes where rigorous species applications exist are following suit with DNA-based estimates (Hebert & Gregory, 2005). The only conceivable explanation is the relative ease of securing funding for such inferior species discovery tools, for DNA barcodes indeed result in subjective species.

There is no single necessary or sufficient species concept. Today we have several dozens of species concepts and, in several cases, an interesting distinction between concept and criteria. Paraphrasing Galileo, despite this species Babel, taxonomy remains alive and very active describing between ten and twenty thousand new animal species (and a lesser number of plant species) every year. A recent synthesis of the origin of species (Coyne & Orr, 2004) has been praised as if of comparable merit to Darwin’s *Origin* (Meyer, 2004) but at the same time declared “simply dogmatic” (Hollacher, 2006). Taxonomists know better. What is important is the empirical world, the observable attributes of species that are inherited in their original or some modified form (Platnick, 1979).

It remains important that we achieve a universally applicable species concept if possible in order to compare species richness of areas and ecosystems as well as various modes of evolution. Those who would simply give up and say that life is so diverse that a pluralistic approach to species is necessary are invariably focused on micro-evolutionary processes rather than historical patterns. The many traits that vary within populations and species create a fog of irrelevant, uninformative and misleading information. When “characters” (in the strict sense of Nixon & Wheeler 1992) are teased apart from such traits and when the vast range of processes that contribute to speciation (e.g., allopatry, sexual selection, etc.) are set aside from the interpretation of patterns of character distribution, it is possible to recognize species as the end results of any or all micro-evolutionary causes. Such a species concept based only on patterns has been pro-

posed in the form of the Phylogenetic Species Concept (Wheeler & Platnick, 2000 and references therein). Much of the current confusion results from each taxon expert emphasizing the processes evident (or assumed) for those organisms; this ignores the important lesson from cladistics to distinguish pattern from unnecessary assumptions of process (Eldredge & Cracraft, 1980; Nelson & Platnick, 1981).

Taxonomy as a mindless, mechanistic procedure. Periodically, attempts are made to replace taxonomists with a mechanical system that matches shapes and sizes, as if the activity of identifying species were nothing more than matching morphometrics or arbitrarily chosen distances (e.g., Sokal & Rohlf, 1966; Rohlf & Sokal, 1967). Certainly taxonomy could be reduced to nothing more than arbitrary image-matching, but why should that be considered an advance? The lesson of the 1970s that such “objective” uses of overall similarity does not mirror evolutionary history has seemingly been forgotten by some. For example, some proponents of DNA barcoding adopt the same bankrupt assumptions using instead mere genetic distances.

Taxonomy is quantitatively challenged. Because taxonomy is an historical science, the usual statistical assumptions simply do not apply: what kind of “universe” exists for a historical question? There is, by definition, precisely one sequence of events that is the past. Without a universe of equally possible histories, standard statistics are powerless. Because of the nature of evolutionary novelties and their inheritance by descendant species (Platnick, 1979; Nelson & Platnick, 1981), however, precise predictions about character distributions make taxonomic assertions both scientific and testable. Still, because taxonomy is not experimental many biologists falsely hold it in suspicion.

Taxonomy is old. Because taxonomy has been practised for centuries and because Linnaeus got some things “right” such that they are equally useful today (e.g., binomial nomenclature, hierarchical groupings, etc.), it is seen by many as out-dated (Valdecasas & al., 2007). As a result, every new wave of technology is accompanied by calls to replace the “old” taxonomy with this or that new technology. Taxonomy has been incredibly adept at integrating new technologies, particularly those that led to discovery of new characters or improved testing of existing ones. Taxonomy will continue to incorporate and adapt new tools as they come along. However, we are well advised to not underestimate the incredibly potent eye-brain dyad in discerning meaningful patterns among characters and species and the fact that high-tech solutions are not needed for every problem. Taxonomy is constantly

reinventing itself through new tools and improved theories and methods. To denounce it as “old” is as silly as abandoning physics or chemistry or medicine for the same reason.

Taxonomy is inefficient. This is a variant on “taxonomy is old”, but is difficult to quantify. As we have said, taxonomists are quick to apply new technologies and therefore constantly improve upon efficiency. It is true that virtually every step of taxonomic research, from field collecting and specimen preparation to publication, could and should be improved upon. It is also true that the next generation of cyber-infrastructure promises to open numerous bottlenecks that have held back more rapid taxonomy in the past (Page & al., 2005). Some aspects of science are more labor intensive than others. As we assess new tools for improved efficiency, we need to be careful that we not sacrifice excellence for nothing more worthy than speed. Thoughtful implementation of new ways and means can be done to enhance, not diminish, excellence.

Confrontation and Science

Confrontation of ideas is central and necessary for the advance of science. Taxonomy has a well-deserved reputation as a particularly confrontational branch of science, as indeed it has been. Taxonomy was the foundation of the evolution and recapitulation debates of the 19th century; it was the framework from which modern population biology emerged in the early 20th century; and Hennig’s theories have returned a historical context to nearly every biological sub-discipline. Perhaps the most ferocious examples, however, were in the 1970s, when evolutionary taxonomy, phenetics, cladistics and traditional taxonomy clashed again and again as, for example, in the pages of journals such as *Systematic Zoology* (Hull, 1988).

Debates are most effective when they consist of a clash of ideas rather than of personalities. Once arguments become truly personal, they descend rapidly into unproductive *ad hominem* attacks. We are concerned that attacks are leveled on taxonomy with little concern for hearing alternative points of view or a clear desire to seek the truth. There exists a cynical milieu in which well-funded science is assumed to be “good” science and alternative views that might endanger funding are quieted.

We are concerned that there are not louder and more debates at the moment over the assumptions routinely made by molecular phylogeneticists, that seem to be phenetic at best and to contravene some of the most basic theoretical advances made by Hennig (1966). Similarly, there should be much greater outcry

over proposals for the PhyloCode and for DNA barcoding and DNA taxonomy, all of which violate fundamental assumptions of “good” taxonomy. As long as lucrative grants exist to fund molecular work it seems that ignoring two centuries of theoretical advances and empirical lessons is acceptable.

Ironically, the same phylogenetic reconstructions that were to assure that taxonomy produced a “general reference system” are now done divorced from the character considerations central to Hennigian reasoning (e.g., special similarity). Cladograms are no longer a means toward that reference system but rather an end produced in service to other branches of biology. That is, this aspect of taxonomy has ceased to be a research paradigm of its own and only a means to a framework for the interpretation of other people’s data. We seem poised now, thanks to DNA barcoding, to also abandon good science surrounding species discovery in order to “better serve” those same other branches of biology. This is ironic, of course, in that the best taxonomy comes from taxonomy done to its own highest standards. Users seem content with inferior products; molecular “taxonomists” with providing them. We need to question current assumptions, adhere to defensible theories, and adapt the right tools for particular jobs.

Species and Rhetoric

When an idea is relentlessly repeated it can come to be seen as a virtual absolute truth. Such has happened with the concept of species within zoology with the Biological Species Concept relentlessly promoted by Mayr (1942, 1963, 1969, 2000).

A long-standing implicit approach to species within the taxonomic community involves recognizing groups of organisms that share a unique combination of characters. Mayr tried to minimize the credibility of the concept by referring to it as the “morphological” species concept, as though it took no notice of genetics. And by describing it, falsely, as being typological (see above). This traditional species concept has been formalized as the Phylogenetic Species Concept (PSC, see Cracraft, 1983; Nelson & Platnick, 1981; Nixon & Wheeler, 1990; Wheeler & Platnick, 2000), not to be confused with the “phylogenetic” concept advocated by Mishler and Theriot (2000) among others. That concept might better be called the Autapomorphic Species Concept as it insists that each species be “monophyletic” (see Wheeler & Platnick, 2000).

Modes of speciation are nearly as diverse as life itself (e.g., Mayr, 1963; Otte & Endler, 1989). Thus, when biologists have attempted to impose their particular views of the speciation causation in their fa-

vorite taxon upon the recognition of species it has resulted in a proliferation of species concepts, each limited in its applicability. From our perspective this is an unfortunate development. It means that it is impossible to compare numbers of species across taxa, ecosystems or modes of speciation. It is important that we be able to assess such differences in order to address fundamental questions about evolution. For example, is there greater species diversity in comparable areas of tropical as opposed to temperate habitat? Do non-sexual lineages evolve (measured in number of distinct species) faster than sexual ones? Why are there vastly more species of insects than of birds?

We see only two solutions to the “species problem”. It would be possible to simply acknowledge this diversity of processes and to accept a plurality of species concepts as advocated by Mishler & Donoghue (1982) among others. Because this so constrains our ability to assess patterns broadly (as stated above), such an admission of hopeless plurality should be a last resort. The other solution is to avoid direct reference or inference of mechanisms of speciation and to focus instead on patterns of character distributions. Stated another way, adhere to the traditional approach of taxonomists.

A primary reason to seek to recognize species is to acknowledge the “end products” of evolutionary history. Just as having a cladogram provides a chronological framework in which to assess various evolutionary processes, having species reflect patterns of characters that are the evidence of evolutionary history provides a similar starting point to compare processes.

What can be done and what ought to be done

“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”. David Orr, 2002

The estimation of what is useful and important should not rest only or even primarily on criteria of novelty. In science, there is an understandable premium on innovation but there are many useful concepts that are not new. No one would suggest exclusion of anatomy from medicine, the periodic table from chemistry, or the laws of thermodynamics from physics, yet in biology, taxonomy is often seen as anachronistic only because it got fundamentals of the field correct long ago.

What should be done? In the midst of a biodiversity crisis (Wilson, 1992) we should make species exploration, discovery and description an extremely high priority. We should make the growth and devel-

opment of natural history collections to serve as comprehensive evidence of species and clade diversity a high priority. And we should make the practice of taxonomy according to its very best theories and methods a mandate, since we have only one chance to chart the biosphere.

Instead funds flow to the latest molecular techniques that we seem to do only because we now can, not because they offer improved estimates of species or reference systems.

What makes “good” taxonomy good?

A good species description is a standard in perpetuity. High quality descriptive taxonomy publications are cited and studied and referenced for centuries. Taxa new to science are, of course, not frequently cited by biologists in general, severely constraining the citation impact of taxonomic papers. The minimization of taxonomic publication impact is also driven by users of such publications and names without citation by non-taxonomists and the fact that citation impact measures limit themselves to a few years. The fact that taxonomic publications are not adequately evaluated by existing systems of citation tracking was first pointed out by Valdecasas & al. (2000). A specialist might only be cited by half a dozen colleagues, yet the quality of his work may be extremely high. Further, the gold standard publications of taxonomy, monographs, are not even included in such indexes (Wheeler & Valdecasas, 2005).

It would be interesting were there an index of taxonomic performance (ITP) adopted that could help scale on numerical grounds the value of taxonomic works. It should not be difficult to take account of variables within taxonomy such as the number of species studied (comprehensiveness), the inclusion of diagnostic and identification sections (utility), etc. In this way the relative merit of the paper could be indicated as well as its citation by other authors. Comprehensive monographs would rank very highly on such a scale, while isolated species descriptions would be much lower. It has also been suggested that with the advent of electronic publishing it would be possible to link names from such monographs through ZooBank to electronic journals and to track the use of names from a monograph in any biological publication, whether or not its author was cited (Wheeler, 2007).

Conclusion

In conclusion, taxonomy is not a minor discipline of biological science but rather a fundamental and ab-

solutely necessary discipline. Many of its theories and methods are not new or perceived to be spectacular, yet when done to high standards it underpins credible biological research and is rigorously scientific. Given the urgency of advancing taxonomic knowledge and exploring Earth's species, it is intolerable that numerous myths and misconceptions continue to serve as excuses to not elevate the stature and funding for taxonomy and collections. Taxonomists have an obligation to promote and defend good taxonomy, to adopt and adapt new tools of course, but in a way that extends rather than undermines existing excellence. Newcomers to taxonomy or related fields need to learn the theory and traditions and unique requirements of taxonomy and accord to taxonomy the same considerations due to any other discipline.

Acknowledgements

A.G. Valdecasas worked under grant CGL2005-02217.

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Received: 7-VI-2007
Accepted: 13-VI-2007