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The Poverty of the Phylocode: A Reply to de Queiroz and Donoghue

NORMAN I. PLATNICK

Division of Invertebrate Zoology, American Museum of Natural History, New York, NY 10024, USA; E-mail: platnick@amnh.org.

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To understand the issues raised by de Queiroz and Donoghue (2011), in their critique of my arguments against the Phylocode (Platnick 2009), one needs to grasp only a single elementary idea. The Linnean hierarchy works superbly because it can pack vast amounts of information into single names by using a system of coordinate, mutually exclusive taxa that are recognizable, as such, simply by the standardized endings of their names. Thus, one needs to know only that an organism is a member of the spider family Oonopidae to know also that it is not a member of any other family of animals (or plants, for that matter), and that no member of any other family is also a member of the Oonopidae. Moreover, one can make all those inferences without having available a complete classification of the species included, either in the Oonopidae or in any other family.

That the system championed by the phylocoders (here termed the NB system, referring to one of its methods, the Node-Based approach) allows the use of such ranks is irrelevant; what matters is that it does not require them, so that the mutual exclusivity of names with standardized endings is no longer certain. Under the NB system, one can no longer deduce, from their names, anything about the mutual relationships of taxa in coordinate groups. The NB Salticidae, the NB Carabidae, or even the NB Hominidae might all be subgroups of the NB Oonopidae, or vice versa, for all that those names could ever tell you. The NB system is therefore decidedly inferior to the Linnean hierarchy because the names it uses convey less information (“Linnean” refers here to those names conforming to the International Code of Zoological Nomenclature, not the Phylocode, i.e., those having rank-signifying endings and typography). By themselves, NB names of family-group taxa prohibit no species at all from being members of the group in question, whereas Linnean names at those ranks exclude all species belonging to any other group of coordinate rank. Linnean names are therefore vastly stronger, more testable hypotheses. By losing such restrictions, all NB names are reduced to having exactly the same minuscule amount of information content, which is actually the minimal achievable in any classification restricted to monophyletic groups: just that some unknown assemblage of species has been hypothesized to be monophyletic, includes a type taxon, and has been named.

So yes, of course, given (literally) complete formal classifications that list every single species included in

each higher taxon, or in which all coordinate higher taxa are identifiable as such by the amount of indentation (i.e., on an extremely wide screen!) or by some technique other than standard suffixes, one could make the appropriate deductions, even in an NB system. But then again, I never argued that NB classifications cannot accurately represent a cladogram; I merely pointed out that “no NB system can possibly produce a more predictive classification than would a fully informative Linnean hierarchy based on the same cladogram . . . [and therefore that] there is no possible potential gain in predictive power to be achieved by switching to an NB system, and many possible potential losses of that power” (Platnick 2009, p. 181).

The point, though, is that formal classifications are not the primary way in which taxon names are actually used, by anyone; names do not normally come with built-in recognizable indentations or with parenthetical lists of all their included taxa. In the real world, names are always presented in a context involving at most an incomplete listing of all the other known taxa on the planet, and they are usually presented in a context that does not involve even a complete listing of their own members. For many groups of organisms, no such complete listing of all their members even exists, anywhere. One should not need to access a complete classification of the world’s Oonopidae just to deduce that no member of the Hominidae is an oonopid. Depriving those taxon names that are recognizably coordinate—such as all the family names currently in use in biology—of their mutual exclusivity (and therefore of much of their practical utility) would be a tremendous step backward, particularly as abandoning that exclusivity achieves nothing more than trivial stability in spelling (i.e., avoids occasional changes in rank-related endings).

Indeed, if this approach were to be carried to its logical conclusion, would one even be able to assume that the members of the NB genus *Oonops* are not actually just a subgroup of the NB genus *Homo*, or vice versa? Should not the phylocoders be equally happy to abandon the built-in mutual exclusivity of generic names, so that we could prevent the shocking and intolerable instability introduced by generic-level synonymies and transfers that might actually be required to maintain the monophyly and predictive power of generic names? After all, those changes are far more dif-

difficult to detect and manage than trivial changes in the suffix of a higher taxon!

In other words, those readers of [Platnick \(2009\)](#) who surmise that the stability in spelling sought by the phylcoders is simply not worth its cost in the decreased information content of names currently at the various family-group levels are entirely correct. They would also be correct in surmising that extending the system of coordinated ranks with readily identifiable suffixes to other higher taxa (such as the orders, classes, and phyla of animals) would significantly increase the utility of those names as well. Thus, I advocate exactly the opposite approach from that promoted by the phylcoders; the systematic zoology community

should extend, rather than abandon, the use of mutually exclusive taxon rank endings. We should seek to increase, not decrease, the information content of the taxon names we use, and we should certainly not settle for a system that purposefully limits the information content of taxon names to the minimal amount possible.

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