

The PhyloCode and the Distinction between Taxonomy and Nomenclature

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In a recent report on the First International Phylogenetic Nomenclature Meeting, Pickett (2005:81) concluded that the “architects of the PhyloCode have reversed their positions on the three main points of contention that they have articulated for some 15 years—namely that taxonomy must be a monophyletic, rankless, system that rejects the type concept.” Contrary to Pickett’s interpretation, advocates of the PhyloCode have not reversed their positions on any of these issues. The rejection of nomenclatural types (which should not be confused with typological or essentialist philosophies) was never a fundamental principle of phylogenetic nomenclature (see de Queiroz and Gauthier, 1992:459–460), and the reason that the PhyloCode does not prohibit the recognition of nonmonophyletic taxa or the use of categorical ranks is simply that it is a code of nomenclature rather than of taxonomy. In this paper, I highlight the distinction between taxonomy and nomenclature and use it to explain two of Pickett’s misunderstandings about the PhyloCode. My purpose is to call attention to this important but under-appreciated distinction using Pickett’s criticisms of the PhyloCode as examples; it is not intended to be a point-by-point rebuttal of his criticisms (for such a rebuttal, see Laurin et al., 2005).

NOMENCLATURE VERSUS TAXONOMY

Various criticisms of phylogenetic nomenclature and the PhyloCode, including the two just noted by Pickett, result from failing to distinguish between taxonomy and nomenclature. Taxonomy is concerned with the representation (and, in a broader sense, also the analysis) of relationships, including (under the common convention of representing relationships using groups) what kinds of groups are to be recognized as taxa. In contrast, nomenclature is concerned with naming taxa as well as with the application of existing taxon names in the context of subsequently proposed taxonomies. In short, taxonomy is concerned with taxa; nomenclature with their names. The two activities, and their corresponding disciplines, are closely related. In particular, taxonomies provide a context for coining new names and applying existing ones. Moreover, taxonomy can be considered to include nomenclature to the extent that part of the way in which relationships are represented is with named groups. Nevertheless, nomenclature is distinct from a number of exclusively taxonomic concerns, including the kinds of groups that are to be recognized as taxa (e.g.,

monophyletic, paraphyletic, polyphyletic) and how their hierarchical relationships are to be represented (e.g., with or without categorical ranks). This situation should be evident from the fact that a single approach to nomenclature, whether traditional or phylogenetic, can be adopted in the context of different approaches to taxonomy (e.g., gradistic versus cladistic).

THE PHYLOCODE AND THE RANK-BASED CODES

The PhyloCode (Cantino and de Queiroz, 2004) is set of principles, rules, and recommendations that describes a system of phylogenetic nomenclature (e.g., de Queiroz and Gauthier, 1990, 1992, 1994). It represents an alternative to the systems described in the traditional codes of rank-based nomenclature (e.g., International Union of Microbiological Societies, 1992; International Commission on Zoological Nomenclature, 1999; International Botanical Congress, 2000). The most fundamental difference between these alternative approaches concerns the methods used to specify the meanings or references of taxon names. Phylogenetic nomenclature uses explicit definitions that specify the references of taxon names in terms of clades and/or common ancestry; in contrast, rank-based nomenclature uses implicit definitions that specify the references of taxon names in terms of taxonomic (categorical) ranks (de Queiroz and Gauthier, 1994; de Queiroz, 1997; de Queiroz and Cantino, 2001; Cantino and de Queiroz, 2004). Despite this fundamental difference, the PhyloCode is otherwise similar to the traditional codes in a number of important respects (de Queiroz and Cantino, 2001; Cantino and de Queiroz, 2004; de Queiroz, 2005), one of the most basic of which is that it is a code of nomenclature rather than of taxonomy. Thus, like the traditional codes, the PhyloCode is designed only to govern the naming of taxa and the subsequent application of taxon names. It is not intended to govern taxonomic procedures or conventions, including the choice of analytical methods, the kinds of taxa that are considered valid, and how relationships are represented.

PARAPHYLETIC AND POLYPHYLETIC TAXA

The basic distinction between taxonomy and nomenclature accounts for positions that Pickett interprets as inconsistencies on the part of proponents of phylogenetic nomenclature (but which are not) concerning the names of paraphyletic and polyphyletic taxa and the use of

categorical ranks. The principle that only monophyletic groups (clades) are to be formally recognized as taxa is a fundamental principle of cladistic taxonomy (cladistic classification, phylogenetic taxonomy). Although this taxonomic principle is highly compatible with the principles of phylogenetic nomenclature, and vice versa, the two sets of principles (taxonomic and nomenclatural) are logically independent. This independence explains why it is possible to devise definitions that specify the references of the names of non-monophyletic taxa in terms of common ancestry relationships (though contrary to the impression given by Pickett, the PhyloCode neither endorses such taxa nor provides methods for defining their names). Moreover, contrary to Pickett's view, the developers of phylogenetic nomenclature have not reversed their position on this issue. Thus, the publication in which the three general classes of phylogenetic definitions were originally described (de Queiroz and Gauthier, 1990) discussed the possibility of defining the names of paraphyletic and polyphyletic taxa in terms of common ancestry relationships, pointing out that those definitions highlighted the incomplete nature of paraphyletic taxa and composite nature of polyphyletic ones (p. 311).

CATEGORICAL RANKS

The distinction between taxonomy and nomenclature also explains why the PhyloCode does not prohibit the use of categorical ranks. The principle that the relationships among taxa are to be represented without the use of categorical ranks is a fundamental principle of rank-free taxonomy. Although this taxonomic principle is highly compatible with the principles of phylogenetic nomenclature, and vice versa, once again, the two sets of principles (taxonomic and nomenclatural) are logically independent. Consequently, phylogenetic nomenclature can be used in the context of either ranked or rank-free taxonomies. Moreover, contrary to Pickett's view, the architects of the PhyloCode have not reversed their position on this issue any more than on the previous one. Although advocates of phylogenetic nomenclature have argued repeatedly that categorical ranks should have no influence on the application of taxon names, and even that it might be best to abandon such ranks entirely, they have also presented examples in which phylogenetic definitions are applied in the context of categorical ranks (de Queiroz, 1997: figs. 3, 4; see also de Queiroz, 2005), thus demonstrating the logical independence of phylogenetic nomenclature from rank-free taxonomy. Moreover, they have explicitly stated that the nomenclatural problems solved by phylogenetic definitions do not require elimination of the categorical ranks from taxonomy but only their replacement as the basis of the current nomenclatural systems (de Queiroz, 1997:141–142; de Queiroz and Cantino, 2001:259–260).

CODES OF NOMENCLATURE, NOT TAXONOMY

Virtually all of the developers of the PhyloCode are advocates of the principle of monophyly (at least for

supraspecific taxa), and some are also advocates of rank-free taxonomy. Nevertheless, we made a conscious decision to restrict the rules in that document to those governing the naming of clades and the subsequent application of names—that is, to rules of nomenclature and not of taxonomy. In this respect, we chose to follow the precedent set by the rank-based codes in maintaining as great a separation as possible between nomenclature and taxonomy so that the PhyloCode would infringe as little as possible on taxonomic practices. Although neither rank-based nor phylogenetic approaches to nomenclature are able to maintain complete separation between nomenclature and taxonomy, both the rank-based codes and the PhyloCode avoid placing restrictions on taxonomic practices that are not fundamental to the functioning of their respective nomenclatural systems. Thus, although the rank-based approach requires the use of ranks, and although the phylogenetic approach requires a general evolutionary conceptualization of taxa, neither the rank-based codes nor the PhyloCode regulate what kinds of entities are to be recognized as taxa (e.g., monophyletic, paraphyletic, polyphyletic), what kinds of evidence or methods are to be used to recognize those taxa (e.g., morphological, behavioral, genetic; distances, parsimony, likelihood), or, in the case of the PhyloCode, how the relationships among taxa are to be represented (e.g., ranks, sequencing, indentation).

CONCLUSION

The distinction between taxonomy and nomenclature, though fundamental, is commonly overlooked. In fact, I accept part of the responsibility for Pickett's confusion, because this fundamental distinction was not made in two of my own (early) publications outlining the basic principles of phylogenetic nomenclature (de Queiroz and Gauthier, 1990, 1992). On the other hand, the relevant distinction has been pointed out explicitly in more than one subsequent publication (de Queiroz, 1997:126; de Queiroz and Cantino, 2001:260–261). But regardless of whether Pickett should have been aware of this distinction, his conclusion that the PhyloCode has "abandoned its philosophical foundation" (p. 82) is incorrect. This conclusion results from confusing the principles of cladistic classification and rank-free taxonomy with those of phylogenetic nomenclature. When the relevant distinctions are kept in mind, there is a simple answer to the question posed by Pickett (p. 82) at the end of his report: "If the PhyloCode no longer embodies the allegedly important principles that gave it birth . . . what principles remain?" The simple answer is this: The PhyloCode still embodies the only principle that was ever fundamental to distinguishing phylogenetic nomenclature from the traditional alternative, namely, the principle that the application of taxon names is to be based on methods that specify the references of taxon names in terms of common ancestry rather than categorical ranks.

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Statistical Approaches for DNA Barcoding

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The use of DNA as a tool for species identification has become known as “DNA barcoding” (Floyd et al., 2002; Hebert et al., 2003; Remigio and Hebert, 2003). The basic idea is straightforward: a small amount of DNA is extracted from the specimen, amplified and sequenced. The gene region sequenced is chosen so that it is nearly identical among individuals of the same species, but different between species, and therefore its sequence, can serve as an identification tag for the species (“DNA barcode”). By matching the sequence obtained from an unidentified specimen (“query” sequence) to the database of sequences from known species, one can thus determine the species affiliation of the specimen. Importantly, the specimen may represent any developmental stage or be just a small fragment of the whole organism, displaying no morphological traits required for standard identification. Although this technique will by no means eliminate the need for the traditional descriptive taxonomy (Dunn, 2003; Lipscomb et al., 2003; Seberg et al., 2003), it is nevertheless envisioned as a key element of future taxonomy research (Stoockle, 2003; Tautz et al., 2003). The

idea of DNA barcoding, although perhaps not surprisingly being a matter of heated debate among dedicated taxonomists (see *Trends in Ecology and Evolution*, volume 18, no. 2, 2003; Will and Rubinoff, 2004), gained rapid acceptance among biologists from other fields. According to the news report in the April 2004 issue of *Nature*, the Barcode of Life Initiative—an international consortium of museums with the secretariat at the National Museum of Natural History in Washington DC—is being established with the goal of creating a database of DNA barcodes from known animal species based on mitochondrial gene cytochrome *c* oxidase subunit I. The DNA barcoding protocol has been already adopted by the Census of Marine Life, a growing global network of researchers in more than 50 countries engaged in a 10-year initiative to assess and explain the diversity, distribution, and abundance of life in the ocean (O’Dor, 2004).

The weakest spot of DNA barcoding is the obvious fact that no gene can serve as an ideal barcode, i.e., be always invariant within species but different among species. It has been pointed out by several authors that