

**POINTS OF VIEW****Taxon names, not taxa, are defined**Kevin de Queiroz<sup>1</sup> & Philip D. Cantino<sup>2</sup>

In commenting on the draft *Phylogenetic Code of Biological Nomenclature* or *PhyloCode* (Cantino & de Queiroz, 2000), Stuessy (2000) argued that, contrary to the wording in that document, taxon names are not defined. Although one of us presented a counter-argument including evidence that taxon names are indeed defined (de Queiroz, 2000), Stuessy (2001) has reiterated and elaborated on his earlier proposition, asserting as well that the *PhyloCode* is not purely a system of nomenclature but rather a combined taxonomic and nomenclatural system and that it is two-ranked. Here we argue that Stuessy's proposition that taxon names are not defined is still incorrect and results from his both failing to recognize different kinds of definitions and confusing different meanings of the term "definition". We also argue, countering Stuessy's other assertions, that the *PhyloCode* separates nomenclature from taxonomy more successfully than do the codes of rank-based nomenclature, such as the *International Code of Botanical Nomenclature* (ICBN; Greuter & al., 2000), and that the categories "clade" and "species" of the *PhyloCode* are not ranks.

Stuessy begins his paper with a discussion of organisms (individuals) and their names. According to Stuessy, "Individuals can be described, or if you like defined (my preference would be 'characterized'), but *not* their names" (p. 185). On the contrary, individuals can be described or characterized but *not* defined; only their names can be defined (e.g., Ghiselin, 1966a, b, 1984). The reason is that "Definitions apply only to words, not to the things to which the words correspond" (Ghiselin, 1966a: 127). Stuessy states that names differ from other words in that they are "solely labels for purposes of communication" and that they are bestowed by "christening" (p. 185). These statements suggest that his objection has to do with the propositions that the names of individuals are proper names and that the proper names of individuals cannot be defined *intensionally*—that is, in terms of necessary and sufficient (defining) properties (e.g., Ghiselin, 1984; but see Kripke, 1980: 112–115). These propositions do not, however, rule out the possibility of defining proper names. The reason is that names can be defined by other means than necessary and sufficient properties; in particular, they can be defined *ostensively*—that is, by pointing (e.g., Ghiselin, 1984). The act of pointing constitutes a definition in that it specifies the meaning or reference of a word.

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In biological nomenclature, the names in question are those of taxa rather than organisms, but the same considerations apply. Just as in the case of organisms and their names, taxa can be described or characterized but *not* defined; only their names can be defined. Moreover, some authors have argued that the names of biological taxa are proper names and cannot be defined intensionally (e.g., Ghiselin, 1984, 1995; but see de Queiroz, 1992, 1995). These same authors, like Stuessy, have likened the manner in which taxon names are bestowed to christening, but unlike Stuessy, they consider the proper names of taxa to be defined using ostensive definitions. Thus, according to Ghiselin (1984: 106), “taxa ... do not and cannot, in principle, possess defining properties. Their names can be defined, but not in terms of defining properties. They are defined ostensively, connecting the name with the thing as at a christening”. Indeed, Ghiselin (1995) has explicitly interpreted the statements (phylogenetic definitions) that Stuessy objects to calling definitions as ostensive definitions. They point verbally to particular clades.

For these reasons, Stuessy is incorrect in saying that the name “*Asteraceae*” cannot be defined. Under the traditional system, it is defined as “the family containing the genus *Aster*”; under a phylogenetic system, it might be defined as “the least inclusive clade containing *Barnadesia spinosa* and *Aster amellus*”. These statements are definitions in that they specify the meanings or references of words, in this case, taxon names. They specify the taxa to which the names refer. Moreover, their interpretation as definitions is in no way contradicted by Stuessy’s propositions that taxon names are merely labels to facilitate communication or that they are bestowed on taxa through a process similar to christening.

Stuessy’s incorrect conclusion also seems related to his failure to consider different meanings of the terms “define” and “definition”. In the *PhyloCode*, these terms are used in the sense described above—that is, “to state or set forth the meaning or reference of a word”. These same terms, however, are also used in a different sense—namely, “to determine or fix the boundaries or extent of”. This alternative definition approximates one of the meanings of the term “circumscribe” (i.e., “to mark off or delimit”), and Stuessy equates “definition” with “circumscription.” For example, he says: “The taxon...*Asteraceae* does have defining characteristics (i.e., it can be circumscribed)” (p. 185). Stuessy’s statements—that taxa can be defined but that their names cannot—make sense if “define” is used to mean “to determine the boundaries or extent of,” but that fact does not validate his criticism of the term “definition” as it is used in the *PhyloCode*, which is correct if “define” is used to mean “to state or set forth the meaning or reference of a word”.

The crux of our disagreement with Stuessy, then, seems to be whether phylogenetic definitions specify the references of taxon names or, as he proposes, they circumscribe taxa. Definitions, whether traditional or phylogenetic, function in the following manner: first, as the result of a systematic analysis, a taxon (group) is circumscribed; that is, its limits and composition are proposed or hypothesized. Next, a name is given to the taxon. Under the traditional approach, naming is accomplished by ranking the taxon (e.g., as a family), which determines the ending of its name (e.g., *-aceae*), and selecting a type (e.g., *Aster*), which determines the root or stem of the name (e.g., *Aster-*). This procedure has the effect of implicitly defining the name according to rank and type (e.g., *Asteraceae* = the family

containing the genus *Aster*). Under the phylogenetic approach, naming is more flexible in that the name of a taxon need not be based on the name of one of its subordinate taxa (though it can be), and any ending can be used (since ranks play no role in naming). In any case, the name is connected to the taxon to which it refers by explicitly defining the name according to the phylogenetic relationships of selected reference points (e.g., *Asteraceae* = the least inclusive clade containing *Barnadesia spinosa* and *Aster amellus*). Finally, if a new taxonomic arrangement is proposed—that is, a new set of ranked groups or a new phylogenetic hypothesis—the definition (whether traditional or phylogenetic) determines the taxon to which the name is to be applied. Thus, a definition specifies the reference of a name in that it determines how the name is to be applied in the context of a new taxonomic arrangement or hypothesis.

Traditional and phylogenetic nomenclature differ in how existing names are applied in a new taxonomic context. Under traditional nomenclature, the group to which a particular name applies is identified (i.e., selected) prior to applying the name to it. The reason is that the group must be identified before it can be ranked, and ranking is integral to the application of names. In contrast, ranks are irrelevant under phylogenetic nomenclature, and the group to which a particular name applies is identified simultaneously with applying a name to it. The reason is that the group designated by a particular name is identified by applying (i.e., invoking) the definition of that name. Thus, in traditional nomenclature, ranking (in conjunction with types) effectively determines the application of names and separates that process from the process of identifying the group to which the name applies. In contrast, in phylogenetic nomenclature, ranking plays no role in the application of names, and the group to which a particular name applies is determined simultaneously with (and as a result of) applying the name through its definition. Nevertheless, in both cases, the limits and composition of the candidate groups for designation by a particular name are determined by prior systematic analysis. Consequently, those groups are circumscribed prior to, as well as independent of, applying names (or ranks) to them. Ranking or invoking phylogenetic definitions only determines which of the previously circumscribed groups are referred to by particular names. Thus, although phylogenetic definitions associate particular names with particular groups, this is not the same thing as circumscribing taxa. Instead, it is a simple consequence of the de-emphasis on ranking that characterizes phylogenetic nomenclature and removes a superfluous step in the process of applying taxon names. The function of phylogenetic definitions is to determine how taxon names are to be applied, and Stuessy's suggestion (p. 186) that the word "circumscribe" should be substituted for "define" throughout the *PhyloCode* is therefore misguided.

Stuessy is also wrong when he states: "Whether taxa should be circumscribed by stem-based, node-based, or apomorphic criteria (definitions) is a legitimate concern of cladistic methodology and plant systematics in general, but it is not a nomenclatural matter" (p. 186). Under the *PhyloCode*, the application of a name is determined by its phylogenetic definition, and the kind of definition that is most appropriate is determined by the kind of clade that one wishes to name. For example, if one wants to name a "crown" clade (terminology of Jefferies, 1979), a node-based definition must be used; to name a "total" clade, a stem-based definition



must be used. The issue here is selecting a definition that accurately points to the clade to which the name is intended to refer. Contrary to Stuessy's assertion, this is definitely a nomenclatural matter.

Stuessy (2001) goes on to argue that the *PhyloCode* is not solely a nomenclatural code but also has a taxonomic component. He bases this conclusion on his belief that "the *PhyloCode* system makes it impossible to name paraphyletic groups" (p. 186), while in contrast, "The modern *Codes* of nomenclature have no such taxonomic requirement—one can name groups circumscribed through any system of biological classification" (p. 186). First, it should be noted that although the *PhyloCode* is designed to name clades, it does not expressly prohibit the naming of paraphyletic groups. Moreover, phylogenetic nomenclature has no more and arguably less of a taxonomic component than the traditional system. Although both the *PhyloCode* and the *ICBN* attempt to separate nomenclature from taxonomy, the *ICBN* contains at least two taxonomic elements that are not present in the *PhyloCode*: (1) Before a group can be named, it must be assigned a rank—a taxonomic decision that affects the spelling and priority of its name. Rank-assignment is not necessary under the *PhyloCode*, and even if used, it does not affect the spelling or priority of names. (2) In Linnaean binomial nomenclature, the names of species have a taxonomic component—the assignment of species to genera. Species names are not yet covered by the *PhyloCode*, but none of the methods under serious consideration for naming species (Cantino & al., 1999) incorporate information about relationships into the name (though such information can be conveyed by other means).

Stuessy's conclusion that the *PhyloCode* is "a taxonomic and nomenclatural system combined" (p. 186) is related to a fundamental difference in what traditional and phylogenetic nomenclature are designed to do, which is in turn related to the broader contexts of traditional and phylogenetic taxonomy in which these approaches were formulated. The goal of traditional taxonomy is to group organisms into taxa, which may or may not be monophyletic, and to rank those taxa into a hierarchy of categories such as genera and families; traditional nomenclature (as represented by the *ICBN*) is designed to govern the names of these ranked taxa. In contrast, the goal of phylogenetic systematics is to discover and infer the limits of species and clades; phylogenetic nomenclature (as represented by the *PhyloCode*) is designed to govern the names of these clades, and eventually species. Thus, neither traditional nor phylogenetic nomenclature is entirely independent of taxonomy. Stuessy interprets the fact that the *PhyloCode* is designed to name clades as a taxonomic constraint because of his traditional views on the nature of taxa; i.e., taxonomists erect or construct taxa, which may or may not be monophyletic depending on one's taxonomic philosophy. In contrast, the *PhyloCode* is consistent with an alternative view on the nature of taxa—namely, that clades exist as complete systems of ancestry and descent that are discovered or inferred rather than constructed by systematists. The job of systematists is to discover and name clades and species, and the purpose of the *PhyloCode* is to standardize certain aspects of the latter process. If some taxonomists wish to continue naming taxa that are not clades or species, the traditional system will still be available to them, but this is not the purpose of the *PhyloCode* (see Cantino, 2000 for discussion of the relationship between the *PhyloCode* and *ICBN*).

Finally, Stuessy questions whether the *PhyloCode* is truly rankless, noting that it ultimately will deal with the names of both clades and species. Because species are included within clades, he considers clades and species to be ranks and thus the system to be two-ranked. While it is true that the terms “clade” and “species”, like the traditional ranks (kingdom, division, class, etc.), refer to taxonomic categories, there are important differences between the two sets of categories (see de Queiroz, 1997 for a review of the relationship between the categories “clade” and “species” and the categories of the traditional taxonomic hierarchy). In the *PhyloCode*, “clade” and “species”, rather than simply referring to different levels in a hierarchy of successively more inclusive groups, refer to fundamentally different kinds of biological entities. Species are metapopulations or metapopulation lineages (see de Queiroz, 1998, 1999), and clades are monophyletic groups of species. The relationship between clades and species is thus more closely analogous to the relationship between a cell clone and its component cells (which are different kinds of entities) than to the relationship between a family and its subordinate genera. Therefore, although species are “included within” clades, the two categories, unlike those of the traditional taxonomic hierarchy, are not merely ranks applied to entities of the same basic kind, and for this reason, it is misleading to refer to the *PhyloCode* system as “two-ranked”.

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