

March 14th, 2006. **Classification V - phylogenetic taxonomy**

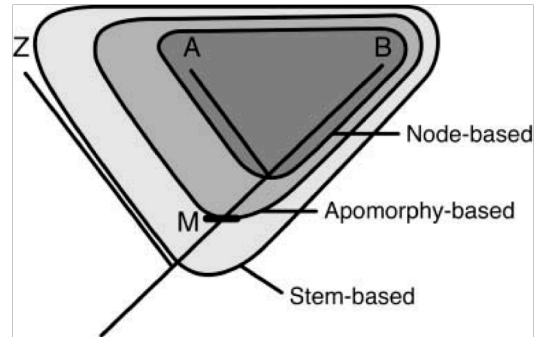
A number of recent calls have been made for the reformation of the Linnaean hierarchy (e.g., De Queiroz & Gauthier, 1992). These authors have emphasized that the existing system is based in a non-evolutionary world-view; the roots of the Linnaean hierarchy are a specially-created world-view. Perhaps the idea of fixed ranks made some sense under that view, but under an evolutionary world view they don't make sense. There are several problems with the current nomenclatorial system:

1. The current system, with its single type for a name, cannot be used to precisely name a clade. E.g., you may name a family based on a certain type specimen, and even if you were clear about what node you meant to name in your original publication, the exact phylogenetic application of your name would not be clear subsequently, after new clades are added to the tree.
2. There are not nearly enough ranks to name the thousands of levels of monophyletic groups in the tree of life. Therefore people are increasingly using informal rank-free names for higher-level nodes, but without any clear, formal specification of what clade is meant.
3. Most aspects of the current code, including priority, revolve around the ranks, which leads to instability of usage. For example, when a change in relationships is discovered, several names often need to be changed to adjust, including those of groups whose circumscription has not changed. E.g., when it was detected that the Cactaceae is nested inside of the Portulacaceae, one of these well-known family names has to be abandoned. Frivolous changes in names often occur when authors merely change the rank of a group without any change in postulated relationships.
4. While practicing systematists know that groups given the same rank across biology are not comparable in any way (i.e., in age, size, amount of divergence, diversity within, etc.), many users do not know this. For example, ecologists and macroevolutionists often count numbers of taxa at a particular rank as an erroneous measure of "biodiversity." The non-equivalence of ranks means that at best (to those who are knowledgeable) they are a meaningless formality and perhaps not more than a hindrance. At worst, in the hands of a user of classifications who naively assumes groups at the same rank are comparable in some way, formal ranks lead to bad science -- removing the ranks would serve the same purpose as child-proof door locks for the back seat of your car!

It is not completely clear at this point how exactly a new phylogenetic code of nomenclature should be written (see draft of the Phylocode and other materials at: <http://www.ohiou.edu/phylocode/index.html>), but the basics are clear. Such a new code should maintain the principle of priority (the first name for a lineage should be followed) and other aspects of the current code that promote effective communication of new names to the community. However, two major changes would be made:

1. The Linnaean ranks would be abandoned, Instead, names of clades would be hierarchically nested uninomials regarded as proper names. A clade would retain its name regardless of where new knowledge might change its phylogenetic position, thus increasing nomenclatorial stability. Furthermore, since clade names would be presented to the community without attached ranks, users would be encouraged to look at the actual attributes of the clades they compare, thus improving research in comparative biology.

2. Two or more types (called "specifiers") would be used, for efficient and accurate representation of phylogenetic relationships. There are two types of specifiers, internal and external. Two or more of the former are used to name node-based groups. two or more of the former and one of the latter are used to name stem-based groups. Apomorphy-based names are controversial, and really shouldn't be used.



It is important to emphasize that, despite misrepresentations to the contrary that have appeared, those who advocate getting rid of ranks don't at all advocate getting rid of the hierarchy in biological classification. Nesting of groups within groups is essential because of the tree-like nature of phylogenetic organization. Think of a non-systematic example -- a grocer might classify table salt as a spice and group spices together under the category "food items." This simple hierarchy is clear, but requires no ranks to be understood. In fact, all human thought is organized into hierarchies, and becoming educated in a field is essentially learning the hierarchical arrangement of concepts in that field. Taxonomy is unusual in the assigning of named ranks to its hierarchies -- there are at best superfluous to true understanding and at worst misleading.

How could rank-free classification be applied to terminal taxa? At the moment, the species rank is the most controversial topic among Phylocode advocates. Some (primarily zoologists) want to retain it as one fundamental rank in an otherwise rank-free system, others (primarily botanists) want to get rid of it and

1. Names of clades (including the terminal level), could be regarded be hierarchically-nested uninomials regarded as proper names (as at all levels in the Phylocode, current usage should be followed as much as possible to retain links to the literature, databases, and collections).
2. As at all taxonomic levels, recommended to use node-based names with two or more internal type specimens.
3. To deal with the rampant homonyms that will result from treating current species eiphtets as uninomials, several proposals have been made. My preference would be to regard all the higher clades to which a taxon belongs as part of its complete name. Thereby each clade would have a uninomial given name, but also a set of more and more inclusive "family names, " thus homonyms could be told apart by higher-level clade names.