most desirable mean of after-treatment of diesel exhausts.

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Is the PhyloCode better than Linnaean system?

——New development and debate on biological nomenclatural issues

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Abstract **The Linnaean system provides ultimate means governing biological nomenclature and classification. With series of modification, this system has admirably served biological sciences for some 250 years. The new PhyloCode, however, advocates the phylogenetic nomenclature that radically alternates the current nomenclatural rules. The new proposals upset many systematic biologists and have provoked hot debate on nomenclatural issues. Binomial nomenclature and hierarchical classification are the key components of the Linnaean system. Proposed abandonment of these in the PhyloCode is widely criticized for it would not help to promote systematics but create chaos. It is not the Linnaean system but the phylogenetic nomenclature that should be abandoned.**

Keywords: systematics, biological nomenclature, Linnaean system, PhyloCode.

The most impressive aspect of the living world is its magnificent diversity. There have been around two million species named and described, and there are probably 3—10 million more to be recognized today. In addition, an estimated half billion extinct species in the history of the Earth[1] are yet to be discovered from their fossils. The diversity of the living world has interested humans ever since the beginning of our history, and our knowledge of the variety of life accumulated through thousands of years laid the foundation of systematics——the science of the diversity and evolution of organisms.

To compile systematically the immense information of the living world we need an efficient system to govern the naming and classification of organisms. Such a system currently adopted by biologists is what is commonly called the International Codes or the Codes of Nomenclature. The currently operative Codes include: International Code of Zoological Nomenclature (ICZN), International Code of Botanical Nomenclature (ICBN), International Code of Nomenclature for Cultivated Plants (ICNCP), International Code of Nomenclature of Bacteria: Bacteriological Code (BC), and International Code of Virus Classification and Nomenclature (ICVCN). These are official sets of regulations governing taxonomic nomenclature and classification in different fields of biologi-

cal sciences.

Although having different starting dates, these Codes are more or less rooted in the work of the Swedish naturalist Carolus Linnaeus published as the *Systema Naturae* (10th edition in 1758), and hence, are commonly referred to as the Linnaean system. Under this system, a specific organism is denoted with a uniquely paired Latin name indicating its genus and species (e.g. *Homo sapiens*—— human). This is termed *binomial nomenclature*. Also under this system, all named organisms are classified with conventional categorical ranking such as species, genus, family, order, class, phylum, and kingdom. This categorical ranking is termed the *Linnaean hierarchy*. The Linnaean system of nomenclature has admirably served biological studies for some 250 years with a series of modification.

Over the past decade, the nomenclatural system has been further developed towards the formulation of a harmonized code for all organisms. This has led to the publication of the draft versions of what has been called the BioCode[2]. Parallel to this development, another set of rules has been proposed as the PhyloCode following a workshop at Harvard University in August 1998. In early 2000, just when the latest ICZN Code[3] (4th edition) and the ICBN Code[4] (St. Louis Code) came into force, a group of workers put on the Web (www.ohiou.edu/phylocode) a draft version of the PhyloCode, which advocates a methodology for tieing phylogeny to biological nomenclature. This has provoked hot debate on nomenclatural issues in several journals (e.g. Taxon, Systematic Biology, Cladistics, Biological Reviews). The publication of the PhyloCode on the Web upsets many systematists (cladists or non-cladists), as this new code is intended to replace the current nomenclatural system that has been working well for about two and half a centuries. A recent question on the popular The Dinosaur FAQ web page is: Is the PhyloCode a good thing?

1 A brief history of the PhyloCode

Phylogenetic nomenclature reflected in the PhyloCode is developed on the basis of what is called phylogenetic taxonomy or phylogenetic systematics, advocated in a series of papers by de Queiroz and Gauthier[5—7]. During the second half of 1990s, three symposia have focused on phylogenetic nomenclature. The first one, entitled "Translating Phylogenetic Analyses into Classification", was organized by Richard G. Olmstead at the 1995 annual meeting of the American Institute of Biological Sciences in San Diego, California. The second symposium, entitled "The Linnean Hierarchy: Past Present and Future", was organized by J. Mark Porter in 1996 at the 1996 Southwestern Botanical Systematics Symposium at the Rancho Santa Ana Botanic Garden in Claremont, California. The third and latest symposium, entitled "Overview and Practical Implications of Phylogenetic Nomenclature", was organized by Philip Cantino and Torsten Eriksson at the 1999 XVI International Botanical Congress in St. Louis, Missouri, USA.

In 1998, the backbone group of the PhyloCode (Donoghue, Cantino and de Queiroz) organized a workshop at the Harvard University Herbaria, Cambridge, Massachusetts. Aimed at promoting the preparation of the PhyloCode, the workshop was attended by 27 people from five countries (USA, Canada, Australia, United Kingdom, and Sweden). Following this workshop, a draft PhyloCode was put on the Web with a starting date on January 1, 2000.

2 PhyloCode vs. ICZN Code

Under the PhyloCode, monophyletic clades are the only taxonomic groups to be recognized. This is the cladistic principle that has been widely accepted today. However, naming such groups under the PhyloCode requires phylogenetic hypotheses in hand for systematists. In other words, no phylogenetic hypotheses, no classifications. To many other systematists, classification and phylogeny are "two special subjects within the broader scope of systematics…. The fundamental difference is that phylogeny is something that happened and classification is an arrangement of its results"[8].

The PhyloCode conflicts the Linnaean system in several aspects. First, the PhyloCode is rank free; namely, conventional categories (Kingdom, Phylum, Class, Order, Family, Genus and Species) and their logical extensions (e.g. superfamily and subfamily) are not allowed in this new system. In its Article 3 on hierarchy and rank, the PhyloCode states: "Although clades are hierarchically related, assignment of a categorical rank (e.g. genus, family, etc.) is not part of the formal naming process and has no bearing on the spelling or application of taxon names." Using birds as an example, the Phylum Chordata becomes just Chordata, the Subphylum Vertebrata becomes just Vertebrata, the Class Aves just Aves. Using dogs as another example, the Order Carnivera would be only Carnivera, Family Canidae would be Canidae, and Genus *Canis* would be simply *Canis*.

Second, to validate a taxon name under the Linnaean system requires a type designation (for familial and lower level taxa) and a character diagnosis, which can be used to differentiate such taxa from other similar or closely related taxa. In contrast, to establish a taxon name under the PhyloCode one must provide a phylogenetic definition of the name, whether it is a node-based, stem-based definition, or apomorphy-based definition (see Fig. 1). Such a definition refers to a part of a phylogenetic tree and applies to whatever clade fits that definition. The models that the PhyloCode (Note 9.4.1) provided for each of these are: (1) A node-based definition takes the form such as "the clade stemming from the most recent common ancestor of A and B" or "the least inclusive clade containing A and B"; (2) a stem-based definition takes the form such as "the

clade consisting of Y and all organisms that share a more recent common ancestor with Y than with W" or "the most inclusive clade containing Y but not W"; (3) an apomorphy-based definition takes the form such as "the clade stemming from the first species to possess character M synapomorphic with that in H". For example, a node-based definition of the clade name Lepidosauria would be "the clade stemming from the most recent common ancestor of Rhynchocephalia and Squamata" or "the most inclusive clade containing Rhynchocephalia and Squamata" (Fig. 1(a)). Similarly, a node-based definition of the clade name Mammalia would be "the clade stemming from the most recent common ancestor of monotremes and placentals" or "the least inclusive clade containing monotremes and placentals" (Fig. 1(b)). Such definitions of taxon names are the sources for much of the recent debate[9—14].

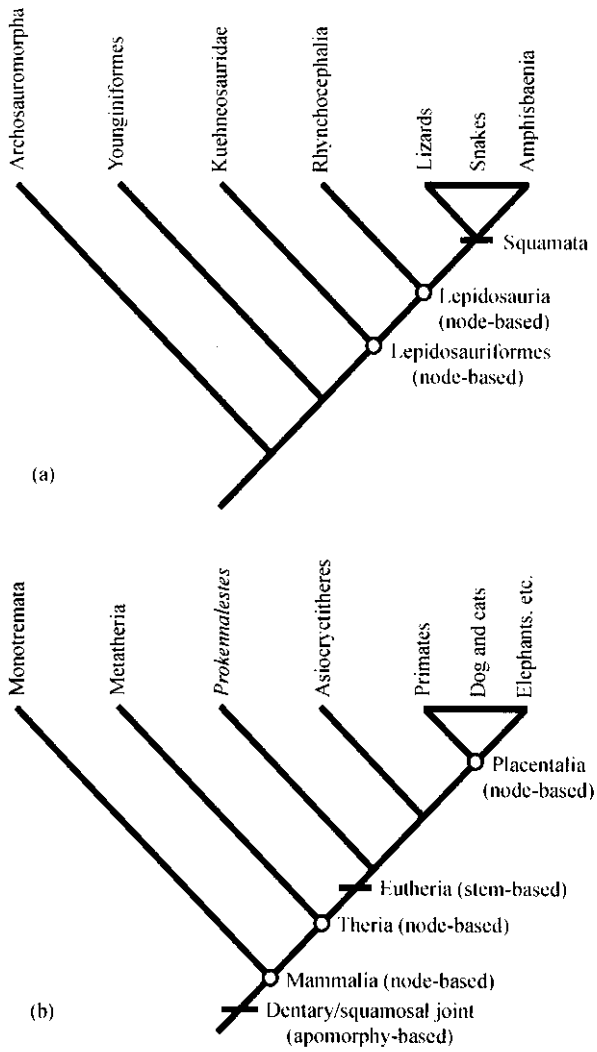


Fig. 1. Cladograms showing node-based, stem-based, and apomorphy-based definitions of Lepidosauria and Mammalia. (a) Both Lepidosauriformes and the less inclusive Lepidosauria are node-based clades; (b) three taxa (Mammalia, Theria, and Placentalia) are node-based clades, whereas Eutheria is a stem-based clade. The stem-based definition of Eutheria can be phrased as: the clade consisting of Placentalia and any other taxa that share a more recent ancestor with Placentalia than with Metatheria. Apomorphy-based definition of Mammalia can be phrased as: the clade stemming from the first species to posses a dentary/squamosal joint as a synapomorphy with Theria.

Third, the PhyloCode uses specifiers "as reference points that serve to specify the clade to which the name applies" (Article 11.1). This is somewhat different from the "type method" of the ICZN Code, in which a designated type provides the standard reference to tie the taxonomic name to that taxon (or Simpson's: the name-bearer of a taxon)[15]. Under the ICZN Code, a type could refer to the actual organism or part of it in the case of the type specimen of a particular species (holotype, syntype, lectotype, neotype); also, it could refer to a category concept in the case of the type species of a genus or the type genus of a family. Under the PhyloCode, however, specifiers can be species (concept), specimens (organisms), or synapomorphies (characters) that in the ICZN Code are regarded as the diagnosis of the taxon. Also under the PhyloCode, the taxon name of the specifier group does not necessarily influence the formation of the name of the clade with which the specifier is associated. For example, the familial name Canidae under the Linnaean system is rooted from the name of the type genus *Canis* with a standard ending -idae (other standard endings include -oidea for superfamily, -inae for subfamily, and -ini for tribe). The new PhyloCode regards these standard endings are unnecessary; all that is needed for a clade name is a single word with a capital letter. The PhyloCode (Article 6.1A) also recommends to have "all names established under this code" to "be italicized when they appear in print". Under the ICZN Code, only those generic and species names are italicized, while suprageneric names are not.

3 Is the PhyloCode better than the Linnaean system?

The Linnaean system has served biological research and the public domain well for about two and a half centuries, and the Codes with improvements will continue to work well. To many systematists (cladists or non-cladists), there is no need indeed to replace such a long-lasting system. Since the Web publication of the PhyloCode, there have been floods of papers rebutting phylogenetic nomenclature. Much of the criticisms have focussed on the following areas.

(i) Binomial nomenclature. Regarding binomial nomenclature, the PhyloCode states: "This draft of the PhyloCode governs only the naming of clades. Rules governing species names will be added to a later version,

but it is not clear at this time whether this will be done before or after the rules for clade names are implemented. Some parts of the current draft may be modified as a result of future decisions regarding the naming of species. Because the code does not currently cover species names, the examples in the present draft use Linnaean binomials when species names are cited in the phylogenetic definitions of clade names. This is a temporary situation and should not be interpreted as implying acceptance of Linnaean binomial nomenclature."

Obviously, the PhyloCode shows a strong intention to drop binomial nomenclature. The reason for this goal is more philosophical than practical: PhyloCode advocators[16] argue that Linnaean binomial nomenclature is logically incompatible with phylogenetic nomenclature. The same argument can be made against phylogenetic nomenclature, as one can say that phylogenetic nomenclature is logically incompatible with binomial nomenclature. In fact, binomial nomenclature is the principle that has long been "established" (not in the sense of the PhyloCode), while phylogenetic nomenclature is not. Binomial nomenclature must be discarded only if it becomes useless, but it is not. If it had to be discarded, what would be the best to replace it? The PhyloCode group authors have no idea for now, though they have 13—15 proposed schemes to be discussed. Criticizing the motion to drop binomial nomenclature, Benton[13] considers abandonment of Linnaean binomen "the most scary consequence of phylogenetic nomenclature." "Which ever of the 13 (or 15) proposed systems is finally incorporated into the PhyloCode, systematists will have to redefine all species so far named, and register them with a central committee. This opens up endless vistas of fruitless timewasting and bickering, and for no benefit whatsoever." Benton[13] concluded: "The legislative side of phylogenetic nomenclature… opens up a nightmare scenario for the future of systematics."

(ii) Definition of taxon names. Much of the debate on the PhyloCode is on the definition of taxon names. PhyloCode advocators[17] criticize the Linnaean nomenclature as being non-evolutionary and its method of definition (diagnosis) being implicit rather than explicit. Requiring a phylogenetic definition to establish a taxon name, the PhyloCode departs from Linnaean system by attempting to unconditionally tie the taxon names to phylogenetic hypotheses. A node-based definition is preferred. For this reason, Nixon and Carpenter[18] labeled the phylogenetic nomenclature a "node-pointing system." As shown by the above-mentioned examples on Lepidosauria and Mammalia, the taxon names are defined according to the relationships of the taxa included in the clades. It is said that "nomenclatural clarity is achieved" by providing such phylogenetic definitions. PhyloCode opponent Stuessy[9,10], however, argued that taxon names serve as labels for the taxa and are not defined, while character-based diagnoses are the "definitions" for the taxa to which those names apply. Another opponent Schuh[14] concluded that "the taxa must remain nameless, otherwise their names would be character based" as indicated by the diagnoses of the taxa under Linnaean system. In taxonomic practice, recognition of a taxon is done by referring to its diagnostic characters, while homology of such shared derived characters owing to a common ancestor is interpreted not observed. Moreover, how realistic to have all the taxa known so far (some 2 million species) redefined following the PhyloCode, and what is the benefit for this?

(iii) Linnaean hierarchy. Hierarchical classification is a key component of the Linnaean system. Binomial nomenclature only applies to species level, but hierarchy applies to different categories of all named organisms. In biological classification, Linnaean hierarchy provides us an indispensable tool for placing the immense variety of living things in good order. In comparison, the PhyloCode without a hierarchical system is merely a nomenclatural but not a classification system.

The PhyloCode promoters argued that categorical ranks are redundant and meaningless in terms of phylogeny; therefore, Linnaean categories are abandoned under the PhyloCode. While most systematists now agree that classifications should stick close to current knowledge of phylogeny, they also realize that phylogenies are real and classifications are not. This goes back to Simpson's argument on the same subject: "phylogeny and classification are two things, not only separate but also different in kind… The fundamental difference is that phylogeny is something that happened and classification is an arrangement of its results. Although phylogeny cannot be observed as such over periods long enough to be really significant, it existed as a sequence of factual events among real things (organisms) and in a philosophical or logical sense it is objective or realistic in nature. Classification is not. It is an artifice with no objective reality. It arises and existed only in the minds of its devisers, learner, and users. There is an aspect of classification as an art and of the taxonomist as an artisan, which does not mean that classification is not, or at least that it cannot be, also a science and the taxonomist a scientist"[8].

As Mayr and Ashlock[1] have pointed out, "hierarchical arrangements are used in many classifications, not only those of organisms. The classification of the language families is hierarchical, and even most artificial classifications, such as those of books in a library, are hierarchical". While higher taxa may have no reality in the biological world, hierarchical classification provides the ultimate means for communication. In this aspect,

Mayr and Ashlock[1] gave an example as: "Once we know that a given organism is a cardinal, we know that it also has the attributes of song-birds, vertebrates, chordates, and animals." Under the PhyloCode, however, "no information on inclusion/exclusion relationships will be found in the names themselves"[14]. This will directly affect not only the public domain but also biological scientists. For example, it is the common practice in biodiversity studies to count and record the existence of a representative of a family or genus; without rank counts are abandoned[19]. For more than two million species have been named and more will be recovered, for the classification of higher taxonomic groups needs collaboration of specialists in the same field, one wonder how biological researchers can effectively communicate without the means of the Linnaean hierarchy. Furthermore, we must say that Linnaean hierarchy indeed has evolutionary meanings, because this system "indicates degree of similarity and recency of common origin. The lower the rank of a taxon, the more similar the included species usually are and the more recent their nearest common ancestor is"[1].

4 Conclusions

The Linnaean system (binomial nomenclature and categorical hierarchy) has been standing for the last two and half centuries in the history of biological sciences. Now the new PhyloCode, purportedly better than Linnaean system, is proposed to entirely replace the currently operative international codes. Many systematists (cladists or noncladists) worry about the negative influence of the PhyloCode. Since the Linnaean system has worked fine for 250 years, to introduce an entirely new system (the PhyloCode) with drastic changes would bring the biological nomenclature into chaos. Also, even if a wholesale replacement of the current Linnaean system is indeed necessary and the PhyloCode will do good for the development of biological nomenclature, practice such a untested new system in real research seems to be too early to do. To many researchers including those in theory support the PhyloCode, it is a wait and see business. As debate on nomenclatural issues goes on, the question remains: Is the PhyloCode a better system than Linnaean?

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