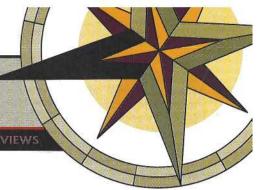
COMPASS

LETTERS SCIENCE & SOCIETY POLICY FORUM BOOKS ET AL. PERSPECTIVES REVIEWS



Taxing Debate for Taxonomists

As EDITOR-IN-CHIEF OF *THE AMERICAN* Journal of Botany, which regularly publishes articles dealing with plant molecular and morphological systematics, I found Elizabeth Pennisi's News Focus article "Linnaeus's last stand?" (23 Mar., p. 2304) as cogent and well balanced as the logic of the proposed PhyloCode is ill conceived and worrisome.

The PhyloCode system of taxonomic classification rests on the proposition that cladistically based phylogenetic relationships are sufficiently stable such that formal taxonomic designations can be ascribed to critical cladogram nodes or node clusters. My experience as an editor indicates that nothing

could be farther from reality. In the scramble to publish—and publish often—it is not uncommon to find some authors submitting for review new cladograms overturning the systematic relationships they've published in a preceding issue of the same journal. Until the phylogenetic relationships among

plant and animal taxa become reasonably well stabilized in the literature, the use of the PhyloCode could thus lead to endless (almost monthly) revision of plant and animal names.

Equally worrisome is that fact that a small, albeit vociferous, group of PhyloCode advocates appear eager to bypass the protocols established internationally by generations of scientists who have been duly appointed by the scientific community to modify as well as

codify the Linnaean system. This premature usurpation of well-established and time-tested scientific protocols is probably doomed to failure, but not before it may cause irreparable harm and confusion.

The Linnaean system is anything but antiquated or inadequate. It provides stability, flexibility, and a high degree of structure that facilitates communication, information retrieval, and editorial sanity. In contrast, the precepts of the PhyloCode appear to rest on the currently unstable bifurcate hierarchies of seemingly endlessly revised cladograms, whose nodes may have nothing to say about the hierarchy of taxonomic ranks or their biology.

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SOME OF THE COMMENTS MADE IN PENNISI'S News Focus article by detractors of the PhyloCode, the project to develop a phylogenetic code of biological nomenclature, are misleading.

First, contrary to Kevin Nixon's complaint that PhyloCode proponents "have the ear of the large funding agencies" and

Jerrold Davis's comment that the project is "starting to consume resources," the PhyloCode project has never re-



The stability of names is of primary concern to taxonomists, a problem illustrated by the name changes of the groups to which these plants belong.* The Linnaean and PhyloCode systems have different sources of name instability.

* See Pennisi's article for details.

ceived support from any source outside the home institutions of the authors and members of the advisory group.

To date, this has been a low-budget operation that has in no way competed for the funds available for systematic biology research.

Second, contrary to Nixon's concern that we "are going to erect a shadow government and [set up] a coup," proponents of the PhyloCode do not wish, nor do we have the power, to force the community of systematic biologists to adopt our proposals. As stated in the Preface of the PhyloCode (www.ohio.edu/phylocode), "[t]he PhyloCode is designed so that it can be used concurrently with the preexisting codes or (after rules governing species names are added) as the sole code governing the names of taxa, if the scientific community ultimately decides that it should." If this new code of nomenclature is eventually adopted by a substantial number of systematic biologists, adherence to its rules will only be enforced by the members of the community themselves.

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PLANTS AND ANIMALS ARE NOT THE ONLY

groups facing renaming problems that would be introduced by the proposed PhyloCode classification scheme. Similar difficulties have afflicted the world of microbes, especially bacteria. Rampant renaming of bacteria, based on an assumed "Rosetta Stone"—namely, a single molecular property (16S RNA sequence)—is causing confusion in literature searches and also has the potential to interfere with prompt identification of bacteria important in medicine and public health.

One such example, the proposed reclassification of *Chlamydia*, has been challenged by Schacter *et al.* (1). They note that creation of an excessive nomen-

Letters to the Editor

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