

## The PhyloCode Is Fatally Flawed, and the “Linnaean” System Can Easily Be Fixed

KEVIN C. NIXON

*L. H. Bailey Hortorium  
Cornell University  
Ithaca, NY 14853, U.S.A.*

JAMES M. CARPENTER

*Division of Invertebrate Zoology  
American Museum of Natural History  
New York, NY 10024, U.S.A.*

AND

DENNIS W. STEVENSON

*New York Botanical Garden  
Bronx, NY 10458, U.S.A.*

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### I. Abstract

Promoters of the PhyloCode have mounted an intensive and deceptive publicity campaign. At the centerpiece of this campaign have been slogans such as that the Linnaean System will “goof you up,” that the PhyloCode is the “greatest thing since sliced bread,” and that systematists are “afraid” to propose new names because of “downstream consequences.” Aside from such subscientific spin and sloganeering, proponents of the PhyloCode have offered nothing real to back up claims of greater stability for their new system. They have also misled many into believing that the PhyloCode is the only truly phylogenetic system. The confusion that has been fostered involves several discrete arguments, concerning: a new “method” of “designat-

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ing” names, rank-free taxonomy, uninomial nomenclature, and issues of priority. Claims that the PhyloCode produces a more stable nomenclature are false, as shown with the example of “paleoherbs.” A rank-free system of naming requires an annotated reference tree for even the simplest exchanges of information. This would be confusing at best and would cripple our ability to teach, learn, and use taxonomic names in the field or in publications. We would be confronted by a mass of polynomial names, tied together only by a tree graphic, with no agreed name (except a uninomial, conveying no hierarchy) to use for any particular species. The separate issue of stability in reference to rules of priority and rank can be easily addressed within the current codes, by implementation of some simple changes, as we will propose in this article. Thus there is no need to “scrap” the current Linnaean codes for a poorly reasoned, logically inconsistent, and fatally flawed new code that will only bring chaos.

## II. Introduction

The battle between the PhyloCode <<http://www.ohiou.edu/phylocode/>> and the “Linnaean” codes has nothing to do with a belief that classifications should be based solely on monophyletic groups. Although proponents of the PhyloCode often allow this misconception to be printed in stories on the PhyloCode (e.g., Pennisi, 2001—after all, the reporters get the idea somewhere), the truth is that most modern systematists using the current codes believe in monophyletic classification. Contrary to the series of publications by de Queiroz and coauthors (e.g., de Queiroz, 1994), no modern taxonomists are really implicit essentialists. Instead, as the PhyloCode advocates have been forced to admit for species, a system of typification with single types is one of the best (we believe THE best) way to document names. Believing in a stable system of typification makes you neither an essentialist nor a typologist. Unfortunately, one of the techniques that the proponents of the PhyloCode have used very effectively is to promote the PhyloCode in the popular press. Indeed, cub reporters looking for a big story in biology are really excited to find out about the “gentle revolutionaries” (Withgott, 2000: 650) who promote themselves as overthrowing the old-fashioned, nonevolutionary Linnaean system of nomenclature. These stories (Pennisi, 1996, 2001; Chui, 1999; Milius, 1999; Fellman, 2000; Withgott, 2000) have been almost all biased toward the PhyloCode; there is no excitement in a story about retaining the “old” way.

## III. Rank Domains

One of the most interesting quotations to come out of the spin storm around the PhyloCode was the following: “People are scared to name something—they’re afraid of the nomenclatural consequences—it’s happened to me dozens of times, where I’ve discovered a major new clade of importance and [didn’t name it] because of bad downstream consequences” (Donoghue, quoted in Withgott, 2000: 650).

Let us consider the implications of that statement. First, what might those downstream consequences be, under both systems? When you name “something,” one possible bad consequence might be that what you named is not really a “good” group (i.e., it later turns out to be nonmonophyletic). This is independent of the system of naming but is actually what might create the opportunity for other “downstream” consequences. A group that is considered good at one point, under any phylogenetic system, would become “bad” only if there were a change in the accepted phylogeny such that the group is no longer monophyletic. Therefore, the downstream consequences alluded to in the preceding quotation must ultimately be due to changes in the topologies of accepted trees.

Under either system, when phylogenetic changes affect the application of a name, there are three obvious negative consequences: 1) the name suddenly applies to a group that includes things other than what was intended—and the greater the net change in content, obviously, the worse the consequences; 2) even worse, the name might need to be applied to some other, larger or smaller clade, including some or all of the original group, and because of the rules of priority it must displace a more familiar name; and 3) the name turns into a synonym of another well-used name but does not displace it—this of course is the least consequential outcome. Consider some possible situations. Take, for example, some of the major important groups that the quoted proponent (Donoghue) of the PhyloCode discovered but (we assume) was afraid to name formally due to “bad” downstream consequences. We have already dealt with one of these, the “paleoherbs” (Nixon & Carpenter, 2000); with some additional observations, we will repeat that example here. Bryant and Cantino (2002) termed that example “misleading,” a characterization that is entirely false; revisiting the example highlights how the example refutes the PhyloCode’s claim for stability.

From various publications by Donoghue and Doyle (e.g., 1989a, 1989b), we have some informal names—for example, paleoherbs, winteroids, palmates, and anthophytes—never published but, in the case of paleoherbs and anthophytes, with an incredible amount of text devoted to them. If the PhyloCode had been available at that time, we might assume that there would have been no fear about formally proposing these as PhyloCode clade names. Thus we can compare what would have later happened as trees changed, both under the PhyloCode and under the Linnaean system, in the context of the possible bad downstream consequences listed above.

The paleoherbs in the original morphological analyses were based upon summary/exemplar terminals (or an undefined mix thereof) corresponding to the following taxa:

Lactoridaceae  
 Aristolochiaceae  
 Saururaceae  
 Piperaceae  
 Nympheaceae  
 Cabombaceae  
 Monocots (all)

Before we proceed, it should be noted that Donoghue and Doyle did not actually find all of the shortest trees for their matrix. If all of the shortest trees are found (a few seconds with the program NONA; Goloboff, 1999), it turns out that the paleoherb group was not actually monophyletic in all trees and thus does not appear in the (unpublished) strict consensus. This is not surprising, given the characters that “supported” the original group: “The other line, here called the ‘paleoherbs,’ is characterized by anomocytic stomata, two perianth cycles, and trimery in both the perianth and the androecium (except for loss of one or both perianth cycles in *Lactoris* and Piperales and secondary multiplication of parts in Nympheaceae)” (Donoghue & Doyle, 1989a: 28).

However, they thought highly of their new informally named group, even though they may have been afraid to name it formally: “An unexpected but apparently robust grouping is the paleoherb clade, including not only monocots and Nymphaeales but also Piperales, *Lactoris*, and Aristolochiaceae” (Donoghue & Doyle, 1989a: 37). Their enthusiasm for the paleoherbs was taken up by numerous authors and has been discussed many, many times. Often, the paleoherbs (give or take some taxa) are labeled as such on cladograms although they never, to our knowledge, form a monophyletic group in the original or subsequent analyses. There has

even been a paleoherb theory of the origin of angiosperms. We do not have space to map paleoherbs on all of the many published cladograms in which they fail to be monophyletic. Let us just examine one of the more widely accepted recent analyses, the 567 taxon, 3-gene tree (Soltis et al., 2000), for which Nixon found the shortest trees for the original publication (Soltis et al., 1999) using the ratchet (Nixon, 1999) with NONA (Fig. 1). Based on this widely accepted and well-supported tree, the downstream consequences of the paleoherbs would be very significant if they had been named under the PhyloCode. If Nymphaeaceae had been selected as one of the “specifiers,” then paleoherb would refer to all angiosperms with the exception of *Amborella*, based on this tree. This is a significant downstream consequence—in fact, a few hundred thousand species difference in content. Also, if Soltis et al. had named that node (something catchy like Euangiosperm), then later discovered the name “paleoherb,” they would not receive their deserved credit, and their proposed name would become a synonym of paleoherb. In fact, under the PhyloCode, the genera *Quercus*, *Platanus*, *Fraxinus*, *Acer*, *Eucalyptus*, *Dionaea*, *Aster*, *Orchis*, *Dianthus*, *Rhizophora*, *Nuphar*, and *Melocactus* would all be paleoherbs—although placed in other, non-paleoherb clades by Donoghue and Doyle. (Note that the list of generic names above provides a consistent and universal way to communicate clade information—they are all exclusive, nonoverlapping clades—something that will be lost if the PhyloCode succeeds.)

What about the Linnaean system? If paleoherbs had been named formally based on any one of the terminals as a type, it would never need to be applied to essentially all angiosperms, like the PhyloCode name “paleoherb.” Depending on the type, “paleoherb” could still be applied to a smaller but informative group that had some resemblance to the ill-conceived and poorly supported original paleoherb group (for example, it could be restricted to the Nymphaeales). Their other name, “Anthophyte,” would best become a synonym of Angiosperm, which actually reflects the change in hypothesis: No, the other groups originally included in “anthophyte” (e.g., gnetopsids, Bennettitales, Pentoxylon) are not closely related and do not have flowers or what can reasonably be interpreted as flower homologues.

Returning to the name “paleoherb,” there are two reasons why the name is more stable under the Linnaean system. The first is that a good taxonomist, a Linnaean one, has the option of restricting the name to a group in such a way as to maintain the least change in species to be included under that name. And indeed, this is how 99% of good Linnaean taxonomists both think and practice. The second reason why the name would not need to become the name for almost all angiosperms, as it must under the PhyloCode, is that, under the Linnaean system, it must be ranked. Thus, if Soltis et al. had named it “SUPERORDER Paleoherbosa” under the Linnaean system, the rank restricts where the name will have priority because the International Code of Botanical Nomenclature (ICBN) explicitly states that a name has no priority outside its own rank; not so with the PhyloCode name. Actually, priority is not applied above the rank of family, and in effect we can even ignore problematic changes at those levels. This positive feature of the Linnaean system we will refer to as the “domain of priority” for a given rank. It is lacking in the PhyloCode. Any clade can have priority over any other clade; thus the actual number of cases in which issues of priority will come into play is much higher under the PhyloCode than under the Linnaean system. This, combined with the more stable system of documentation (single types) and the flexibility allowed the author, makes the Linnaean system much more stable in the face of name changes due to priority. In cases in which priority still results in names being replaced, we still have the option of conservation under the current code.

This brings up the issue of the way in which the PhyloCode proponents proclaim their system to be more stable. It is impossible to comprehend exactly what they mean here, because

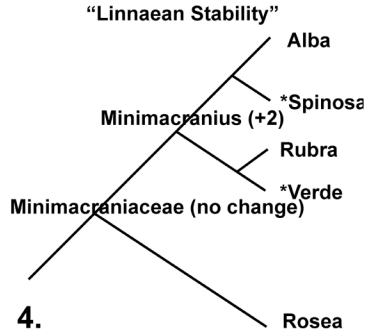
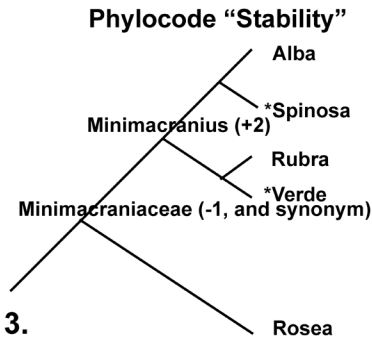
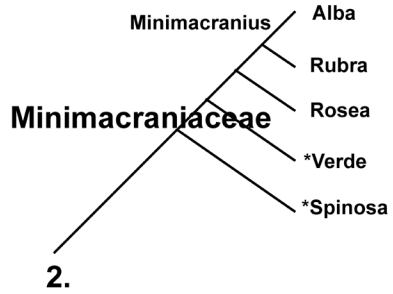
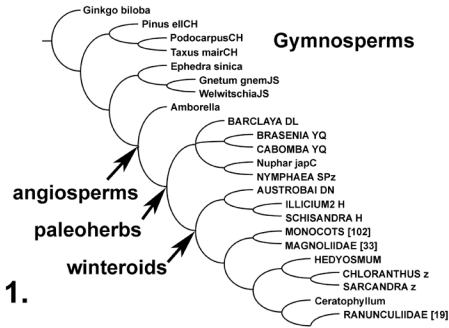


Fig. 1. Part of tree for Soltis et al. (2000); see text.

Fig. 2. Hypothetical cladogram, and classification. The asterisks indicate PhyloCode specifiers for Mimimacranaceae.

Fig. 3. Alternative cladogram, and resulting changes in PhyloCode classification.

Fig. 4. The same alternative cladogram, and resulting fewer changes in Linnaean classification.

they have failed to explain fully how massive changes in content could be more stable. They also have the advantage that there is no preexisting PhyloCode classification, so issues of priority, which affect the Linnaean system, cannot be revealed easily for the PhyloCode, which has no history (forcing the contrivance of examples such as those for the paleoherbs and anthophytes). That is why it is necessary to use examples of “what if” (e.g., cf. Figs. 2–4)—and in every case, it is easy to see that the Linnaean system is far superior.

It should be emphasized that making a family name a synonym of a genus name is not allowed under the Linnaean system; thus the domain of priority would prevent the kind of problem that is forced in the PhyloCode in this case, even if a reckless PhyloCodeer were trying to impose a PhyloCode-compatible classification under the Linnaean code.

Some things are certain beyond any doubt. Names such as “anthophyte” and “paleoherb” were best left informal or—better yet—unnamed. The downstream consequences of their informal coinage are obvious—the propagation of reams of discussion about a group that has no reality, even extending to it being the basis for one or more National Science Foundation-funded research projects. It should also be noted that the current code did not inhibit their use for the brief time that they were being pushed by their originators. They can now be ignored by

informed botanists. The downstream consequences, however, would have been far greater and much more insidious had these names been proposed under a PhyloCode. One would have probably been a synonym of all angiosperms, and the other a synonym of all seed plants—or worse, they would have become the accepted names, creating serious confusion due to the massive difference in application between the older and newer literature. If the PhyloCodeers had named angiosperms based on the *rbcL* tree (*Ceratophyllum* + *Aster*, say), then we could have actually ended up with a classification in which the name “angiosperm” applied to *Ceratophyllum* + tricolpates—even though the original group they wished to name (all angiosperms) was still monophyletic! Also, based on trees accepted now, *Amborella* would not be an angiosperm even though it has flowers! No such thing would happen with a Linnaean type and a reasonable application and adjustment of names as necessary to maintain stability.

This brings us to a final point about downstream consequences. Having downstream consequences is an important inhibitor of frivolous proposals for new names. The need to avoid such consequences is good, not bad. The current code makes the process precise enough and difficult enough that care and, above all, scholarship must be undertaken. The PhyloCode is a major relaxation of such care. In many ways, those who actually name species and genera form a special club, and entry into this club requires a reasonable amount of training, fieldwork, and, above all, experience with the taxa being named. Scholarship is forced by fear—fear of overlooking something. And anyone who has named taxa, as we have, has made some mistakes. Without such fear, frivolous names (such as “paleoherb”) would abound.

#### IV. The Species Problem

Dealing with the problems of naming species is doubtless the biggest issue that remains controversial (or perhaps more accurately, largely ignored) among proponents of the PhyloCode. A workshop on phylogenetic nomenclature was held at Harvard University in August 1998, organized by Donoghue, Cantino, and de Queiroz. The meeting was attended by a small group of people, including several of the most vocal proponents of the PhyloCode; e.g., Canatella, Gauthier, and Olmstead. An article by Cantino et al. (1999) was the result of this workshop. The need for dealing with this topic was apparent even to the most zealous: “[R]elatively little has been written about the naming of species in this system” (Cantino et al., 1999: 791).

Well, they changed that. They were finally able to agree on 13 different possible ways to name species under the PhyloCode. They also insisted that, although some of them end up looking like Linnaean binomials, every darn one of them is superior: “Although the authors of this paper do not agree upon which of the proposed methods for naming species is best, these methods ALL have advantages over Linnaean binomials. Linnaean binomials are logically inconsistent with phylogenetic nomenclature because they make the genus category mandatory” (Cantino et al., 1999: 806, emphasis added).

Because this article is so rigorous and intellectually complex, full understanding of the bold and brave new nomenclatural procedures that the authors are advocating requires a very careful reading. For instance, if one is not careful, one might conclude that they are just abolishing certain aspects of the Linnaean code and replacing them with the same thing under different names. Of course this could not possibly be true . . . or could it?

It appears that the message being promoted by Cantino et al. is that the binomial is unstable when species are moved from one genus to another: Because the binomial is, in essence, the species name and must change when the tree changes, binomials are “unstable.” The authors are really talking about spelling and pronunciation here; species content—i.e., which populations/individuals are recognized as belonging to the species—is not the issue. They “solve” the

problem of this “instability” of the binomial by making species names not reflective of phylogenetic position; thus every species name must be different from every other species name (no more *alba* or *virginiana* as epithet). They propose numerous alternatives to create these unique names (which the Linnaean binomial solved long ago, by combining genus and species). Some of their methods for creating new, unique, uninomial species names simply join together the Linnaean genus and species names: *Quercus rubra* would become *Quercus.rubra!* However, they realize a problem:

Although species names are not intended to convey phylogenetic information in any of the methods proposed here, names that consist of two parts may be misunderstood to imply relationship, when encountered by people who assume that they function like Linnaean binomials. In some cases, the relationships inferred will be correct, but in some cases they will not. . . . [T]hen *Potentilla-bifurca* would be more closely related to *Alchemilla-alpina* than to *Potentilla-norvegica*. . . . Moreover, the first part of the species name may be the established name of a clade to which the species does not belong. (Cantino et al., 1999: 800)

Even the novice field biologist should now begin to suspect that a switch to the PhyloCode may not provide all of the wonderful benefits that its proponents claim. No more learning of genera and families, and assuming certain things about what the names convey . . . PhyloCode names would convey nothing in terms of phylogeny, and now we must memorize unique species names, unique clade names, and the tree upon which to map them.

Let us dissect the motivations of the PhyloCode architects with regard to the naming of species. Most of this fear of species names being unstable derives from two situations: 1) A species is moved, so the genus part of the binomial changes (more on this later); and/or 2) When it is moved, there is already a species by the same name in the genus to which it is being transferred—a relatively rare and unimportant situation.

If one carefully reads the PhyloCode proposals for species naming, it is clear that much of what is proposed is merely a reinvention of the wheel. Take for example “Method L,” in which species names are terminated by a unique registration number (which is part of the name). As clearly stated:

The preexisting name *Sturnus vulgaris* becomes *vulgaris###* (or *vulgaris.###* or *vulgaris[###]*, depending on which convention is adopted). If the name *vulgaris###* by itself might be confusing to readers, it is recommended that *Sturnus* be cited as a taxonomic address. The taxonomic address plus species name would take the form *Sturnus vulgaris###* or *Sturnus/vulgaris###* or (*Sturnus*)*vulgaris###* or *vulgaris###* (*Sturnus*) or *Sturnus:vulgaris###*, depending on which convention is adopted. (Cantino et al., 1999: 795)

and “the information about genus membership that is lost if Linnaean binomials are abandoned is easily replaced by citing a clade address” (Cantino et al., 1999: 800).

The clade address—clearly a reinvention of the binomial or, even worse, the polynomial. Thus, when teaching a systematics course in the field, one can point to a tree and cite its clade address! Behold, my students, *Angiospermae Nymphaeopsida Chloranthoda Ranunculida Tricolpata Rosoidata Cucurbitalata Fagales Fagaceae Quercoideae Querc897 Querc893 Querc895 Erythrobalanus Qrubra-234*. (That is *Quercus rubra* for those of you with the old books!)

So, first we must banish the Linnaean taxonomic address (the binomial), because it is not metaphysically correct (and is “unstable”). Then the binomial (or polynomial) must be rein-

vented, as the PhyloCode taxonomic address, because, of course, no one is going to memorize unique species epithets for everything. The only accomplishment of all this diddling is to make nomenclature more confusing, more unwieldy, and, because the address one uses is arbitrary, less consistent. And exactly as unstable as the binomial, because the taxonomic address will change with new trees that change the position of species relative to broader groups.

The species article by Cantino et al. (1999) makes one thing absolutely clear. This is about an agenda driving their “logic” and “reasoning.” It is an abuse of phylogeny, based on a set of false and sophomoric premises—primarily that a ranked system is not phylogenetic. They have decided what they want before they have figured out whether it is feasible, much less useful. Thus, 10 years or more after a PhyloCode was first advocated, the efforts by the best minds in their camp result in a monumental “consensus” that at least 13 different approaches to species nomenclature might be valid. Upon inspection, most of these 13 methods can be characterized as simply absurd. This is just the tip of the iceberg—the whole PhyloCode “system” is replete with such poorly thought-out proclamations, driven by a desire to impose their own (rather quaint) philosophy on others. Although they admit the shortcomings of their whole theoretical framework for species, this does not deter them: “There is no reason why species names could not have phylogenetic definitions in phylogenetic nomenclature, as clade names do, but the theory underlying the application of such definitions to species names has not yet been developed” (Cantino et al., 1999: 791).

They have had more than 10 years, and they have failed. The truth is that any reasonable view of species precludes them from being treated as clades, as clearly stated by Hennig (1966) and as some authors have maintained for the last 10 years in the “species concept” debate (e.g., Nixon & Wheeler, 1990).

## V. Proposals

A salient difficulty with the current ICBN (Greuter et al., 2000) and International Code of Zoological Nomenclature (ICZN, 1999) is the “automatic” erection of subtaxa based on the type of the primary rank, when new subtaxa are named. This is referred to as the “Principle of Coordination” in the ICZN. Take, for example, genus X. If we name subgenus Y of genus X, then we are implicitly erecting the type subgenus, subgenus X, to include the type of the genus and any species not placed in other subgenera. Thus, if we want to recognize subgenus *Cyclobalanopsis* of genus *Quercus*, we must also recognize subgenus *Quercus*, with at a minimum *Quercus robur* (the type of *Quercus*). If the “leftover” species do not form a monophyletic group, then we have created a paraphyletic or polyphyletic subgenus. We could actually solve that problem by restricting subgenus *Quercus* to only the type species and placing the remainder of species as *incertae sedis*. However, this is cumbersome.

### A. PROPOSAL 1

We therefore propose to eliminate the rule that type subtaxa are automatically erected when a subtaxon is named. For example, the type species of a genus is also placed in a subgenus of the same name only if explicitly stated in the classification. We do not have to recognize *Quercus* subg. *Quercus* if we want to recognize *Quercus* subgenus *Cyclobalanopsis*.

### B. PROPOSAL 2

We also propose to allow unranked taxa to be intercalated between ranks. This is already implicitly allowed (remember “anthophyte” and “paleoherb”?). However, if formalized it would



improve the scholarship of such names, and rules of priority could be applied, within some domain.

## VI. Conclusions

We are being asked to accept a system that has yet to be worked out in theory, much less in practice. The plan for the PhyloCode is to run this system in parallel, without making any effort to modify the existing Linnaean codes, and then fully replace the Linnaean codes at a later date. This is arrogant and will only invite chaos.

Ranks actually restrict the domains of names, such that ranks limit their effect in questions of synonymy. Thus, a generic name under the Linnaean system will never displace a younger family name, and vice versa. This is not true under the PhyloCode, where synonymy will have universal domain and any name can replace any other name. Thus, combined with the fact that Linnaean classifications are more stable to rearrangements in phylogeny than are PhyloCode ones, the limited domain of synonymy due to ranks means that Linnaean names are less likely to result in synonymized names at higher ranks when taxa are moved. Of course, conservation is available for cases in which newly imposed synonymy is unpalatable. Conservation can actually take care of most of the real issues that arise due to changing phylogenies under the Linnaean system.

Under the PhyloCode, one needs merely a mailbox to receive some material, extract some DNA, and run PAUP\* to start naming all of the myriad unnamed clades one can find in a tree. One need not even be able to identify any of the species in the named clade. Perhaps this is the real goal of the PhyloCode.

One must assume that claims that clades were not named because of fear of consequences under the Linnaean system but that fear would be removed under the PhyloCode are simply propaganda. The fear was well founded—because the groups were not. It had nothing to do with the Linnaean system, which would have treated these silly hypotheses with more flexibility. So the following example is simply illogical: “Example 1: If it is questionable whether the type species of *Magnolia* belongs to a clade that is to be named, this species should not be used as a specifier, and the clade should not be named *Magnolia*, *Magnoliales*, or any other name based on the stem name of *Magnolia*” (Article 11, draft PhyloCode). When someone names a “clade” under the PhyloCode, it is determined by what specifiers are used. Because there is no guarantee that any other taxa except the specifiers will remain in the clade following a phylogenetic rearrangement, the idea that the inclusion of *Magnolia* is “questionable” is silly. Either the namer wishes to name the clade that is the common ancestor of *Magnolia* and, say, *Piper* and descendants or he/she does not want to name that clade. By definition, any taxon not a specifier is “questionable” because it may or may not end up under that name in the future. By making *Magnolia* a specifier, the “question” is removed! In other words, the only way to insure that *Magnolia* is in the clade is to use it as a specifier!! The PhotoCodeers have actually stated here that if you are not sure whether *Magnolia* belongs in the clade *Magnoliales*, do not name it *Magnoliales* and do not use the type of *Magnolia* as a specifier. This is the kind of reasoning one can find throughout the PhyloCode, because it is a vain attempt to encode a logically flawed system.

The most important conclusion is that we need community involvement in this. A small group of people who have very significant resources, and thus influence, are overthrowing your government—the ICBN and the ICZN. If the community does not become actively involved in fighting the PhyloCode, they will succeed, and in so doing, demolish much of the hard work that our predecessors have built into the current codes. We do not need a parallel

system. The phylogenetically disposed scientists who use the ICBN and ICZN need to propose a few rules that will “fix” an imperfect, but very useful, system—one that is far superior to an unranked PhyloCode.

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