

On the Other “Phylogenetic Systematics”

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Accepted June 1, 2000

De Queiroz and Gauthier, in a serial paper, argue that biological taxonomy is in a sad state, because taxonomists harbor “widely held belief” systems that are archaic and insufficient for modern classification, and that the bulk of practicing taxonomists are essentialists. Their paper argues for the scrapping of the current system of nomenclature, but fails to provide specific rules for the new “Phylogenetic Systematics”—instead we have been presented with a vague and sketchy manifesto based upon the assertion that “clades are individuals” and therefore must be pointed at with proper names, rather than diagnosed by synapomorphies. They claim greater stability for “node pointing,” yet even their own examples show that the opposite is true, and their node pointing system is only more stable in a purely metaphysical sense detached from characters, evidence, usage of names, and composition of groups. We will show that the node pointing system is actually far LESS stable than the existing Linnaean System when stability is measured by the rational method of determining the net change in taxa (species) included in a particular group under different classifications. © 2000 The Willi Hennig Society

INTRODUCTION

De Queiroz and Gauthier (1990, 1992, 1994) as well as de Queiroz (1994) present a bleak view of the sad

state of biological taxonomy—arguing that the unannounced harbor “widespread belief” systems that are archaic and insufficient for modern taxonomy. Their basic complaint is that evolution retains a “superficial” rather than a “central role” in taxonomy. To ameliorate this, they propose discarding the current system of nomenclature and replacing it with a truly “phylogenetic taxonomy.” Unfortunately, as we shall show, their replacement is not carefully thought out and is replete with metaphysical presumptions of which they appear to be unaware.

THE NODE POINTING SYSTEM

Appropriately, we will assign the proper name “Node Pointing System” (NP System) to point at the “phylogenetic system” of de Queiroz and Gauthier, because the latter name already points to something else proposed by other authors (for instance, Hennig’s 1966 *Phylogenetic Systematics*). Using the same name for something entirely different would merely create confusion and instability in the nomenclature (de Queiroz and Gauthier, 1990, 1992, 1994). Although the NP System has not yet been *formally* proposed by de Queiroz and Gauthier, we hereby designate the Node Pointing System as the name that points to the concepts

in the descendant papers of de Queiroz and Gauthier (1990, 1992, 1994; de Queiroz, 1994) and whose most recent common ancestor is de Queiroz (1988). More distant ancestors are Griffiths (1973, 1974, 1976) and Ax (1987).

This Is the NP System

De Queiroz and Gauthier (1990, 1992, 1994) have discussed at least three possible methods by which to implement a phylogenetic taxonomy. These are, "node-based," "stem-based" and "apomorphy-based" methods. We will discuss in detail here only the node-based method, because that method has clearly been preferred by de Queiroz and Gauthier and most of their various disciples (e.g., Schander and Thollesson, 1995; but cf. Lee, 1999), at least for extant taxa. Moreover, both the node- and stem-based methods are implemented in the same fashion, with the only difference being whether a name is restricted to "crown clades" or includes taxa from the "stem clade" (and sometimes these are mixed; see Sundberg and Pleijel, 1994; Wyss and Meng, 1996; Sereno, 1999). The node-based method involves designating two (or more) descendants of a group and declaring that the name points to the common ancestor of the listed descendants and all other descendants of that ancestor. The stem-based method designates two (or more) descendants, one of which has the others more closely related to it than to some taxon outside the group. Thus, de Queiroz and Gauthier (1994, p. 30) and de Queiroz (1994) provided the example of fixing the name "Mammalia" as pointing to the common ancestor of "monotremes" and "therians" and all descendants of that common ancestor. Although they have illustrated the node-based method with reference to two members of a group, de Queiroz (1997, p. 68) used six members, and there has been no discussion of just when, exactly, only two or more (possibly all) members of a group should be the designated descendants that are used to "pinpoint" the ancestor of the group. As discussed below, whether two, or more descendants are selected has a major effect on the "stability" of the application of the name, as well as the logical consistency of the method, a fact that was not discussed in any of the versions of the de Queiroz and Gauthier paper (1990, 1992, 1994; de Queiroz, 1994).

Even though the NP System has been advocated

several times, the first more than 10 years ago, there are numerous omissions of obviously important points that need to be clarified before the system can actually be implemented (see also Moore, 1998). For example, de Queiroz and Gauthier (1990, 1992, 1994) and de Queiroz (1994) provided absolutely no discussion of documentation of the designations used in the node-based method; thus, the designated descendants are generally referred to by names that already have vague or controversial meaning, or must ultimately point to designated named descendants of lower and lower rank, until one reaches the level of species or below. Presumably (as discussed by us below under "Pseudo-classification and The Species Problem") species names must ultimately be fixed by pointing to two or more "individual" organisms (Lidén and Oxelman, 1996). The parallel situation in the outdated Linnaean system, of the need to fix (i.e., essentialistically typify) species names before higher names can be fixed, has been known for almost 200 years, so it is surprising that this aspect of the NP System has never been discussed by adherents (although Baum *et al.*, 1998, p. 322 did state: "the correct anchor is the type specimen of the species as determined under the traditional code"!). We are not sure what de Queiroz and Gauthier might some day propose, but for lack of a better term, or for that matter any term provided by de Queiroz and Gauthier, and pending the appearance of a "Phylocode" (Baum *et al.*, 1998; Cantino, 2000)¹ we will refer to the designated descendants that fix, and therefore document, a name under the node-based method as *pseudotypes*. By clearly indicating that such designated descendants are not equivalent to Linnaean types, this terminology divorces the concept from what de Queiroz and Gauthier view as essentialist typology. For this reason, the term pseudotype is better than the redundant "nominotypes" of Schander and Thollesson (1995). Of course, in order actually to implement a node-based system, one must first fix the names of at least two ultimate units ("species"?) within each group (node) pointed to

¹After this paper was in press, a "Phylocode" Web site appeared (<http://www.ohiou.edu/phylocode>). The self-appointed group of authors states that the "Phylocode" would be implemented independent of, and without consideration of, the governing bodies that promulgate current codes of nomenclature. Although the draft posted on the Web does not cover species, our criticisms with respect to higher taxa remain applicable. We will deal with specifics of the "Phylocode" elsewhere.

with a name. Thus, it would not be possible to “name” Mammalia under such a system as referring to the common ancestor of monotremes and therians until at least two species (pseudotypes) of each of those groups are first designated (pseudotypification). Otherwise, in the parlance of de Queiroz and Gauthier, the names point to nothing or at least to nothing that is certain.

To illustrate the nomenclatural stability of the NP System, de Queiroz and Gauthier (1992, p. 463, 1994, various boxes) have proffered the example of the lizard “families” Agamidae and Chamaeleonidae. Previously considered distinct families, new research establishes the paraphyly of Agamidae in terms of Chamaeleonidae. Elimination of the now-paraphyletic Agamidae by the usual procedures, entailing either use of the name Chamaeleonidae for the inclusive group (because of priority) or elevation of subgroups of Agamidae, is deemed to produce instability. The NP System resolves the situation, resulting in proclaimed stability, by retaining both names. Thus, Chamaeleonidae are a subgroup of Agamidae, without alteration of the form of the names. Both names are “maintained” despite one referring to a different group than it did originally, and Chamaeleonidae are nested within Agamidae. Because the endings of the names have not changed, stability in spelling has been achieved (Dominguez and Wheeler, 1997).

Condescension

Perhaps the most unsettling aspect of the papers advocating node pointing, actually beginning with a paper by de Queiroz (1988), is the condescending tone toward the vast bulk of taxonomists.

Taxonomists themselves have been largely unaware of their implicit adoption of the Aristotelian (methodologically essentialistic) perspective on definitions. They have also been largely unaware that they have recently begun toward an alternative philosophical perspective on definitions. (de Queiroz, 1994, p. 508)

De Queiroz is clearly more aware than taxonomists (“them”), who are practicing essentialists, but are unaware of this terrible fact.

This discovery is compelling them to coin new names, to redefine old ones, and— whether they realize it or not—to adopt a very different perspective on the nature and significance of taxonomic definitions. If I have interpreted this new perspective correctly, the changes associated with it should be welcomed.

They represent a move away from the constraining influence of essentialism toward an outlook that has been closely associated with progress in other scientific disciplines. (de Queiroz, 1994, p. 508)

The modern Prometheus (de Queiroz) has delivered fire to the essentialists, whether they realize it or not; but there remains doubt whether they (the ignorant essentialists, that is, the bulk of taxonomists) realize it and will be able to use it to improve their lot. In truth, modern taxonomists are rarely if ever essentialist in the real meaning of the term, as opposed to its use as a label of opprobrium. And most do know what it is they are doing, and why they are doing it, although there may be disagreement about the best way to accomplish their goals. Just as the arguments over paraphyly and monophyly have nothing to do with a belief in evolution, which is more or less given among modern taxonomists, the arguments about the best way to implement and document (e.g., by typification) a system of naming have nothing to do with essentialist beliefs. Indeed, the goal of the majority of modern taxonomists, namely, implementing a phylogenetic classification, may not be exactly the same goal aspired to by those who hurl the epithets of essentialist and “typologist.”

The Revisionist View of the History of Taxonomy

De Queiroz and Gauthier deny the influence of evolutionary thought on modern taxonomy:

During the century following the publication of Darwin's . . . *Origin of Species*, biological taxonomy waited for the revolution that should have followed upon acceptance of an evolutionary world view. Although the principle of common descent gained wide acceptance early in that era, it assumed a largely superficial role in taxonomy . . . (de Queiroz and Gauthier, 1992, p. 449)

They take this stance despite acknowledging various of the intellectual movements in systematics:

During the same time, biological taxonomy has also experienced the birth, or at least the codification, of various schools, or approaches, from the new systematics of the evolutionary synthesis . . . to phenetics . . . and cladistics . . . The influence of some of these approaches notwithstanding, acceptance of Darwin's proposition that ‘community of descent is the hidden bond which naturalists have been unconsciously seeking’ . . . has thus far had little effect on biological taxonomies or the underlying principles governing their construction. (de Queiroz, 1988, p. 239)

The influence of evolution on taxonomy is limited to after-the-fact rationalization:

Modern biology requires a taxonomic system based on evolutionary concepts and principles. The New Systematics . . . and Phylogenetic Systematics . . . initiated the development of such a system by granting the tenet of evolution a central role in concepts of species and higher taxa . . . respectively. (de Queiroz and Gauthier, 1994, p. 30)

It is only the adoption of phylogenetic taxonomy that will “evolutionize” taxonomy:

Now, more than 130 years after the publication of Darwin’s (1859) *Origin of Species*, taxonomists are finally freeing themselves from the bonds of ancient traditions and bringing about a reorganization of the very core of biological taxonomy (e.g., de Queiroz and Gauthier, 1991). (de Queiroz, 1992b, p. 309)

In fact, of course, from the time of Haeckel (1866) evolutionary ideas have infused taxonomic practice—not always with happy consequences. For example, the New Systematics inadvertently played a major role in the decline of systematics as a field during the second half of this century (Wheeler, 1995), reorienting several generations of taxonomists from pursuit of phylogenetic research to serving a supporting role to population genetics. Hennig did not invent the concept of monophyly, nor was he the first to advance criteria for the recognition of synapomorphy, as he discussed in detail in *Phylogenetic Systematics*. The extensive bibliography of that book documents a welter of evolutionary thought in taxonomy prior to 1966. Somehow, in revisionist history, this had no influence on “modern” taxonomy.

Political Appeals

Donoghue also argues that ‘using the Linnaean hierarchy can goof you up² if you’re trying to study the process of evolution.’ (Michael Donoghue, as quoted by Pennisi, 1996, p. 181)

In his outgoing presidential address at the systematics and evolution meeting, he [Donoghue] lobbied forcefully for scrapping the classification system that has been the bedrock of biology for the past 2 centuries—and he called on systematists to do the dismantling. (Michael Donoghue, as quoted by Pennisi, 1996, p. 181)

²For those not familiar with American slang, Goof up: To blunder (American Heritage Dictionary of the American Language, 1979).

An adoption of this nomenclature would promote instability, not stability. I think it’s going to be ignored by working taxonomists. (James Carpenter, as quoted by Pennisi, 1996, p. 181)

An audience of ecologists, behaviorists, and so forth, might indeed be receptive to the notion of scrapping Linnaean nomenclature. After all, and understandably, most biologists hate taxonomic instability, insofar as it affects the name of their study taxon (usually incorrectly referred to as “organism”). Of course, systematists hate instability too, and therefore the codes of nomenclature are designed to promote stability. In addition, cladists have often pointed out that Linnaean categories are not necessarily natural nor comparable in evolutionary studies. That is the reason for elimination of paraphyletic groups and for proposals to add conventions to the Linnaean system to incorporate cladistic information with as little disturbance of existing nomenclature as possible (e.g., Wiley, 1979): the intent is that both stability and monophyly be attained. Such proposals, unfortunately, are receiving little press. After all, adding conventions to the codes entails retaining the codes, and it is far easier to advocate scrapping the Linnaean system entirely, without providing specific details of what is to replace it nor examples of the drastic effects such a system would have on stability.

WHICH SYSTEM IS GOOFIER?

It is important at this point to clarify what we mean by stability versus what de Queiroz and Gauthier mean by stability. We would measure stability in terms of all taxa included in a group referred to by a name; i.e., stability is measured by the number of terminals that do not occur in each application of a particular name. Thus, a classification in which a name “X” refers to (A B C D E), versus a later one in which X refers to (C D F), is unstable in that B, E, and F are not members of one or the other groups designated by X in both cases. However, under de Queiroz and Gauthier’s definition of stability, X is always stable, because it always refers to the “same” “clade” and could be applied to the two groups in question only if its pseudotypes were exactly C and D, and not A, B, or E. Astonishingly, the example provided by de Queiroz and Gauthier and mentioned

above, in which the composition of the group pointed to by the name “Agamidae” changed dramatically in composition (from lacking the entire “Chamaeleonidae” to including it) was used as an example of “nomenclatural stability under phylogenetic definitions” (de Queiroz and Gauthier 1994, p. 30, Box 5). As Lee (1996, p. 188) put it [approvingly!]: “it is not the names of clades that change, but the contents of those named clades” (see also Bryant, 1996, and Cantino *et al.*, 1997). We will discuss this unusual view of stability in more detail below, but it should be apparent to most readers that the de Queiroz and Gauthier version of stability is not the same view of stability that has persisted in taxonomy since its earliest beginnings. Since they have deliberately defined instability in classification out of existence in the NP System, de Queiroz and Gauthier can then make very bold claims about having solved age-old problems that have been traditionally viewed as contributing to instability:

An explicitly phylogenetic approach to nomenclature eliminates the problems caused by splitting and lumping. It also provides a context for developing rules³ aimed at converting traditional taxonomies into phylogenetic ones in a way that maximizes continuity in the evolutionary connotations of taxon names. (de Queiroz and Gauthier, 1995, p. 108)

Here they use the term “continuity” interchangeably with stability. The claim for increased continuity here has two aspects, the first of which is really a claim for metaphysical stability (ignoring traditional stability, and see below). The other component of stability claimed for the “phylogenetic system,” which might be measured in a traditional manner, is fully a consequence of changing rules of priority to apply outside of rank (by eliminating ranks entirely). Because the same stability could be achieved (if sanctioned by the community) also in the Linnaean type system, the stability of expanded priority is neither a unique nor a necessary attribute of a so-called phylogenetic system. Such problems of name changing of widely used names are addressed in the Linnaean system by the *conservation* and *rejection* of names, the rules for which have been liberalized over the years. Of course, conservation and rejection of names are metaphysically incorrect by the standards of de Queiroz and Gauthier and actually

³While the “context” for developing rules has persisted through many versions of their paper, no explicit rules have yet been proposed.

create metaphysical instability by changing the meanings of names.

The Mammal Example

It is appropriate here to provide examples of what might happen if some form of the node-based method was implemented. We begin with the example of fixing the name Mammalia as pointing to the common ancestor of monotremes and therians and all descendants of that common ancestor (de Queiroz and Gauthier, 1994, p. 30; de Queiroz, 1994). Of this simple example, one disciple stated:

If Mammalia is attached to ‘the least inclusive clade containing monotremes and eutherians,’ then there is no reason why the clade has to be renamed if the position of monotremes and eutherians with respect to certain taxa (e.g. multituberculates) changes. Rather, one can retain the taxon name Mammalia for ‘the least inclusive clade containing monotremes and eutherians’—multituberculates simply might or might not be part of Mammalia. (Lee, 1996, p. 188)

However, if the intention is to include multituberculates within Mammalia, and new “research” shows that they are, say, not more closely related to eutherians than to monotremes (Fig. 1, top), but are rather the sister-group of monotremes + eutherians (Fig. 1, bottom), they are no longer part of Mammalia—although there has merely been an internal rearrangement within a clade, now the name must be applied to a different (sub-)clade. The name Mammalia has thus gone from referring to three taxa (in Fig. 1, top) to two (in Fig. 1, bottom). In contrast, in the current Linnaean

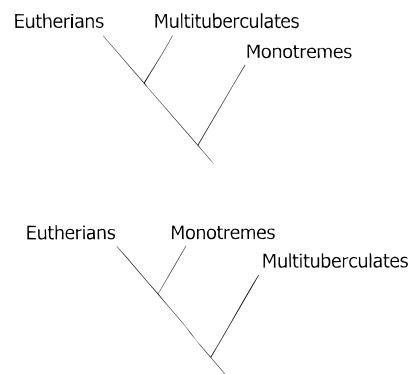


FIG. 1. Alternative phylogenetic arrangements of some mammals.

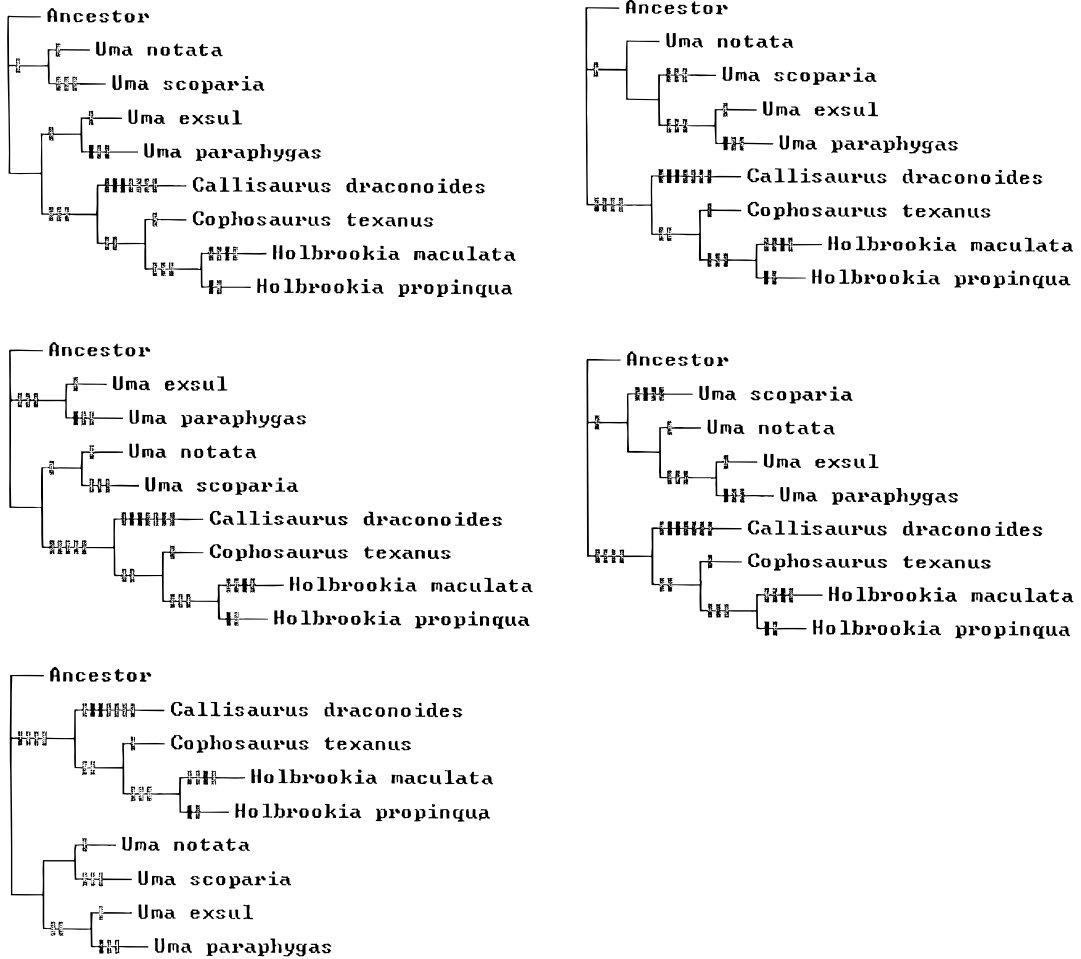


FIG. 2. Alternative cladograms for sand lizards.

system,⁴ no change whatsoever in the content of the name need occur.

The Sand Lizard Example

The second example is taken from de Queiroz (1992a). He presented an analysis of 28 electrophoretic characters for eight species of sand lizards, reporting five cladograms, redrawn here in Fig. 2. The cladograms, calculated with Paup (Swofford, 1989), are not all strictly supported (that is, included branches that had a minimum length of zero; see Nixon and Carpenter, 1996b), as pointed out by de Queiroz (1992a, p. 342),

⁴Strangely, Lee repeatedly wondered how the "current system" differed from the NP System.

and the consensus does not support the monophyly of the genus *Uma*, as is readily apparent from inspection of Fig. 2. Nevertheless, de Queiroz (1992a, p. 342) stated that the monophyly of *Uma* "should not be considered in doubt," alluding to support by eight morphological characters in another study (which should of course have been included in a simultaneous analysis; see Nixon and Carpenter, 1996a).

Choice of any of the five cladograms as a basis for classification would therefore be questionable, but that very fact enhances their utility for the purposes of illustration. What if de Queiroz had "phylogenetically" named the (rankless) genus *Uma* in accordance with the NP System (remember, we should not doubt the monophyly of this group)? First, he would have been faced with the decision as to which of the four species

included in *Uma* to select as pseudotypes. A minimum of two being required, supposing he had, not doubting the monophyly of *Uma*, ignored the first two cladograms in Fig. 2 and just considered the last three. What if he had selected, for example, *U. paraphygas* and *U. notata* (which are respectively apical and basal in the fourth cladogram of Fig. 2), but then later new research shows that *U. exsul* + *U. paraphygas* really are more closely related to the other four species of sand lizards (first cladogram of Fig. 2)? These other four species are now nested within *Uma*, and the name goes from referring to four species to referring to eight, including three other genera! In this situation, of course, there would be instability in the Linnaean system as well—but it would be less. With a single type, the name *Uma* need only be restricted to whatever sister-group pair contained the type, and the name need only change from referring to four species to two.

The Paleoherb Example

Our third example will be a botanical one, which has been provided by a vocal proponent of the Node Pointing System. Donoghue and Doyle (1989a, b) presented numerous cladograms showing various hypothetical phylogenetic patterns within the angiosperms. In some of these cladograms there appeared a monophyletic group of seven terminals [Lactoridaceae (1 sp.), Aristolochiaceae (400 spp.), Piperaceae (2000 spp.), Saururaceae (7 spp.), Nymphaeaceae (excluding *Nelumbo*; 75 spp.), Cabombaceae (7 spp.), and Liliopsida (representing all of the monocots, with 65,000 spp.)], which they designated informally as the “paleoherbs” (Donoghue and Doyle, 1989a, p. 28; repeated in Donoghue and Doyle, 1989b). While they also informally named some other groups (e.g., “palmates” and “winteroids”), none have had the persistence and widespread attention that the paleoherbs have enjoyed. Not only have the relationships of the paleoherbs been discussed in several papers (e.g., as recently as Soltis *et al.*, 1997; it was also mentioned by de Queiroz, 1997, p. 67), but discussion of the “group” is *de rigueur* for any grant proposal for large-scale phylogenetic analyses of plants. The importance of the paleoherbs as a group to be discussed in almost every subsequent angiosperm analysis seems far to outweigh the paltry characters that supported its monophyly in the original:

The other line, here called the ‘paleoherbs’, is characterized by anomocytic stomata,⁵ two perianth cycles,⁶ and trimery⁷ 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 Nymphaeaceae). (Donoghue and Doyle, 1989a, p. 28)

Even with relatively few and weak characters, Donoghue and Doyle apparently felt rather strongly about the paleoherbs:

An unexpected but apparently robust grouping is the paleoherb clade, including not only monocots and Nymphaeales but also Piperales, *Lactoris*, and Aristolochiaceae. (Donoghue and Doyle, 1989a, p. 37)

In fact, the “consensus” tree presented by Donoghue and Doyle (1989a, Fig. 3.2), aside from being modified by excluding the collapse of one node caused by Canelaceae, was based on a subset of the actual set of shortest trees. The actual consensus for the original data set (Fig. 3) does not even include the “robust” group that was designated as the paleoherbs (see also Crepet and Nixon, 1998). Thus, it is not surprising that the original paleoherb group has failed to appear as a clade in any subsequent analysis, of either morphological or molecular data. Yet, it still seems to have been a favorite topic of discussion in the botanical literature for the past 10 years.

What if Donoghue and Doyle (1989a) had “formally proposed” the (rankless) name *paleoherbs* for their robust clade in accordance with the NP System of de Queiroz and Gauthier? First, they would have been faced with the decision as to which of the included taxa to select as pseudotypes. Based on their preferred cladogram in Fig. 3.1, redrawn here as Fig. 4, they would have had to select at least one pseudotype from the group (LAC, ARI) and a second pseudotype from the group (PIP, SAU, LIL, CAB, NYM) in order to designate the ancestor of the entire group. We will refer to the two-pseudotype method as *dipseudotypic*. Alternatively, they could designate all seven terminals as pseudotypes (*omnipseudotypification*, or NP-complete). Of course, some intermediate choice could be made, such

⁵Found throughout the seed plants and common in nonpaleoherb angiosperms.

⁶The most common state throughout flowering plants.

⁷Occurring in several magnoliid angiosperms outside of the paleoherbs. Note also the extent of the exceptions.

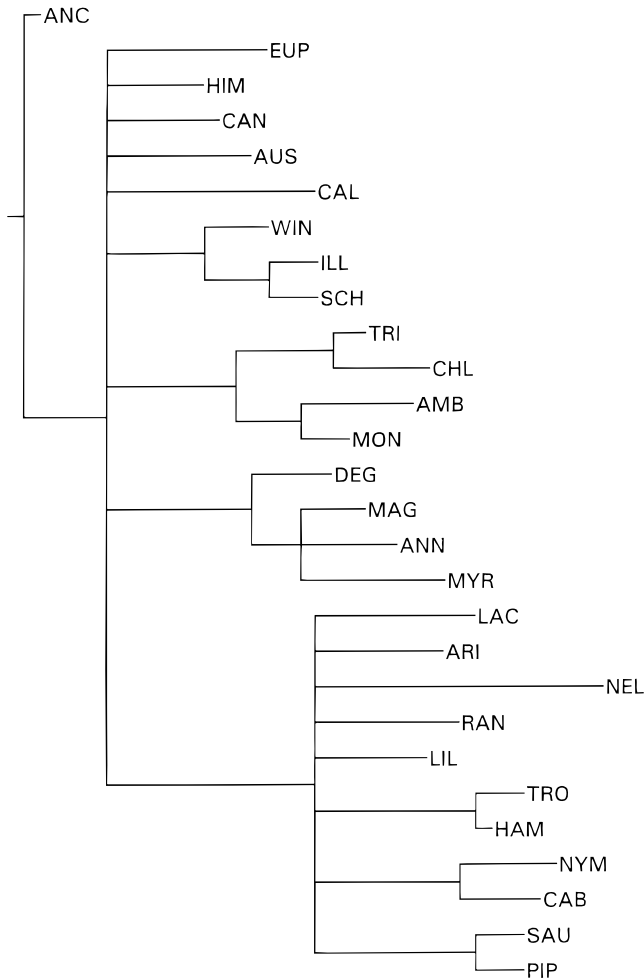


FIG. 3. Consensus of cladograms of length 178 as calculated with a variety of search routines using the program Nona (Goloboff, 1998) for the data of Donoghue and Doyle (1989a). With the default setting “amb-” there are 27 cladograms; with “amb=” (i.e., ambiguously supported branches included), there are 49 cladograms. Donoghue and Doyle (1989a, p. 25) found “over 30” cladograms of length 178; that this was a subset of the number reported by Nona is demonstrated by the more resolved consensus tree presented by those authors.

as designating four or five pseudotypes; such a designation would be *polypseudotypic*. It is important to note here that de Queiroz and Gauthier have taken no position on which method is better⁸—although in most of

⁸An exchange at AIBS (1995, San Diego):

DE QUEIROZ had presented his system and only provided an example of designating two taxa to “point” to a group; e.g., the group that is the common ancestor of *Bernadesia* and *Aster* and all descendants of that ancestor = Asteraceae.

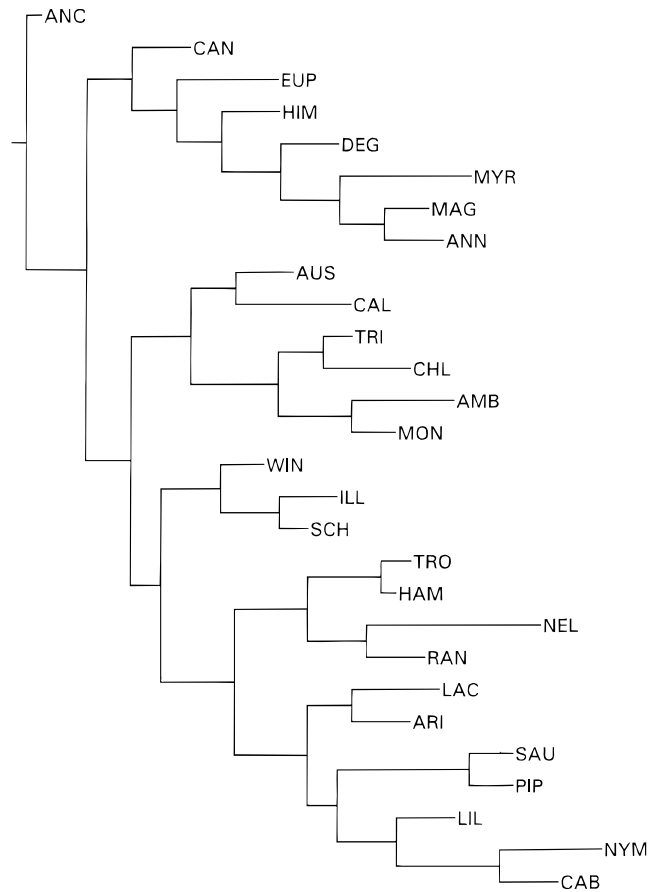


FIG. 4. Cladogram redrawn from Donoghue and Doyle (1989a, Fig. 3.1).

their papers they have provided examples of designating only two pseudotypes, de Queiroz (1997) used six pseudotypes. Other adherents have used (implied) *omnipseudotypification* outside of the constraints of any current code of nomenclature:

Thus, Malvaceae is redefined to refer to the most recent common

Paraphrased exchange:

NIXON: what about the case where one of the two “types” becomes nested higher within group, e.g., *Bernadesia* is found not to be the sister-taxon of the remainder of Asteraceae?

DE QUEIROZ: It might be better to designate ALL members, not just two. Then it would be stable even if *Bernadesia* moved within the group.

NIXON: How is that more stable? Then, the repositioning of any member to a position outside the group will create instability; e.g., if one species of Asteraceae is moved to Rubiaceae or Calyceraceae, then those families and everything in between would be subsumed in Asteraceae.

ancestor of plants previously considered to be 'Tiliaceae,' 'Sterculiaceae,' 'Bombaceae,' and Malvaceae, and all the descendants of that ancestor. (Judd and Manchester, 1995, p. 138)

Note that in the Malvaceae example, because the pseudotypes (Tiliaceae, Sterculiaceae, Bombaceae and Malvaceae) have not themselves been pseudotyped, we are left with uncertainty as to which clade the newly defined "Malvaceae" is actually pointing at.

Because of this confusion, disagreement, or lack of concern about which way to pseudotypify NP names, we will consider both extremes (dipseudotypification and ominipseudotypification) in our example.

We can now follow the fate of the pseudotypic taxa for *paleoherbs* in subsequent cladistic analyses that have been published, with a view toward evaluating taxonomic stability in the traditional sense, not the NP sense. Several analyses have included one or more of the original *paleoherbs* since the name was coined in 1989, and some of these are considered below. The intent here is not to determine whether the *paleoherbs* are worth recognizing or discussing, which was never a serious question based on the list of "synapomorphies" presented (a question, of course, that has been defined out of existence in the NP System). The *paleoherbs* have been selected because they are an enlightening example of the contrast between metaphysical stability and real stability and of how implementation of the NP System would result in unstable classifications.

For comparisons of stability among different approaches, the following three methods of applying the name *paleoherbs* to subsequent cladograms were selected:

(1) Dipseudotypification: The name refers to the common ancestor and all of its descendants of two pseudotypes selected from the clade to be pointed at.

(2) Ominipseudotypification: The name refers to the common ancestor and all of its descendants of all taxa (pseudotypes) belonging to the clade to be pointed at.

(3) Good Linnaean taxonomist: The name is applied in such a way that it includes the type and maintains the highest correspondence in taxa with previous usage or intent, based on the diagnosis of the group. This is equivalent to a formal phylogenetic definition based on diagnosis, i.e., the largest inclusive group bearing the designated homologies.

Stability is measured here as the net change in terms of terminals originally included in a group compared to the group as defined on a new tree. Species are used

here to avoid the severe effects and fluctuations in this value that would be caused by sampling and taxon definition if higher level terminals were used. Thus, we must substitute the estimated number of species for the groups under consideration. We have used the most recent species estimates for angiosperm families and genera by Takhtajan (1997) for our evaluations. Net changes in species composition are denoted by "Δ."

Doyle *et al.* (1994, combined morphology and rRNA tree presented in their Fig. 16):

Dipseudotypification:

With pseudotypes ARI, NYM: Δ 195,000 (including ALL dicots)

ARI, SAU: Δ 260,000 (excluding monocots, including ALL dicots)

ARI, PIP: Δ 260,000 (excluding monocots, including ALL dicots)

ARI, LIL: Δ 195,000 ARI, NYM: Δ 195,000 (including ALL dicots)

ARI, CAB: NA (not applicable, because CAB was not included in Doyle *et al.*, 1994)

LAC, NYM: NA

LAC, SAU: NA

LAC, PIP: NA

LAC, LIL: NA

LAC, CAB: NA

Ominipseudotypification:

Δ 195,000

Good Linnaean taxonomist:

with type in NYM: Δ 67,425

LIL: Δ 2,500

PIP: Δ 65,500

SAU: Δ 65,500

ARI: Δ 67,100

Soltis *et al.* (1997: 18S ribosomal DNA tree presented in their Figs. 1A–1D):

Dipseudotypification:

ARI, NYM: Δ 195,000 (including ALL dicots)

ARI, SAU: Δ 195,000 (including ALL dicots).

ARI, PIP: Δ 195,000 (including ALL dicots except

AMB, Illiciales, *Austrobaileya*)

ARI, LIL: Δ 195,000

ARI, NYM: Δ 195,000

ARI, CAB: NA

LAC, NYM: Δ 195,000

LAC, SAU: Δ 195,000

LAC, PIP: Δ 195,000

LAC, LIL: Δ 195,000

LAC, CAB: NA

Omnipseudotypification:

Δ 195,000

Good Linnaean taxonomist:

NYM: Δ 65,000

SAU: Δ 65,000

PIP: Δ 65,000

LIL: Δ 2,500

ARI: Δ 67,000

LAC: Δ 67,000

A related example also provides insight into the NP claim for stability. Because Donoghue and Doyle (1989a, b) evidently failed to find all most parsimonious trees, it is interesting to check the stability of their group under the NP System on one of the trees that was not reported in which the paleoherb clade did not occur, given here in Fig. 5:

Dipseudotypification:

NYM, PIP: Δ 2

NYM, SAU: Δ 2

NYM, ARI: Δ 2

NYM, LAC: Δ 2

CAB, PIP: Δ 2

CAB, SAU: Δ 2

CAB, ARI: Δ 2

CAB, LAC: Δ 2

LIL, SAU: Δ 85

LIL, ARI: Δ 2,092

LIL, LAC: Δ 2,092

LAC, ARI: Δ 2,092

SAU, ARI: Δ 85

SAU, LAC: Δ 85

PIP, ARI: Δ 85

Omnipseudotypification:

Δ 2 (*Nelumbo* added)

Good Linnaean taxonomist: If one accepts the tree in Fig. 5, the best solution is merely to include *Nelumbo* in the paleoherbs.

NYM: Δ 2

CAB: Δ 2

SAU: Δ 2

PIP: Δ 2

LIL: Δ 2

ARI: Δ 2

LAC: Δ 2

Bremer *et al.* (1998): Based on the "tree" presented

in their Fig. 1, the original paleoherbs are distributed in at least two basal groups such that paleoherbs under the omnipseudotypification method would include all angiosperms (and thus all of the original paleoherbs). Depending on which two pseudotypes were selected for dipseudotypification, most, all, or only a small clade of angiosperms would be included in the paleoherbs, and anywhere from only two to all of the original paleoherbs would be included in the group. The good Linnaean taxonomist would be able to restrict the application of the name to be a subset of the original group, without including anything originally excluded from the group.

It is obvious from the examples above that a good Linnaean taxonomist outperforms or matches the stability of the NP System in all cases. In fact, if a Linnaean

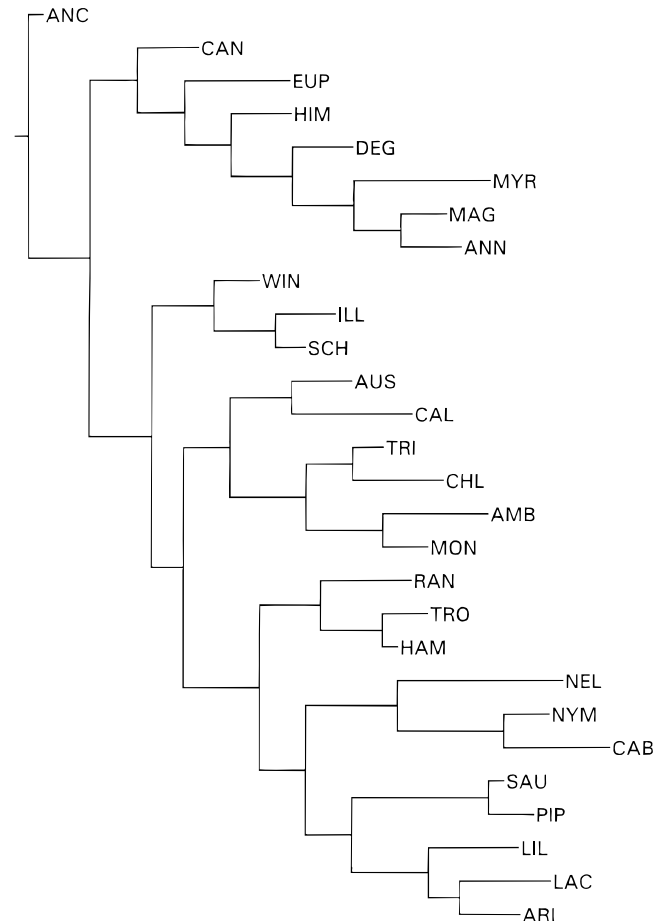


FIG. 5. One of the 27 cladograms for the data of Donoghue and Doyle (1989a). Unlike Fig. 3, this cladogram is strictly supported; that is, it has no branch of zero minimum length (=ambiguous support).

classification is based on a type that is one of the pseudotypes of an NP classification, it is *always* possible to maintain a classification at least as stable as, and usually more stable than, the NP classification. In the paleoherb example, most subsequent trees result in a paleoherb grouping that includes either all “eudicots” or most or all angiosperms. An adherent of the NP system would have no choice in this matter, whereas a good taxonomist would be able to maintain a small group that resembled the original intent of paleoherbs. Because of the “revised” hypothetical ancestor for NP paleoherbs in later trees, if we diagnose the characters of the “original” paleoherb ancestor, it differs dramatically from the “all angiosperm” NP-paleoherb ancestor of, for example, the Doyle *et al.* (1994) combined trees. Thus, there exists proof that the “ancestor” pointed to in the original tree is not the same ancestor pointed to in later trees—it is diagnosed by conflicting characters. In fact, it is merely a hypothesis, and pointing to a hypothesis cannot be taken seriously as equivalent to pointing at something “real”. This conundrum apparently has escaped the attention of NP proponents.

As a final note on the stability of the NP system with respect to seed plant and angiosperm classification, it is worth evaluating recent phylogenies of seed plants. Based on the rbcL trees (Nixon, 1999) available until recently, naming the angiosperms under the NP System would have required selecting *Ceratophyllum* as a one pseudotype and at least one other angiosperm as the other pseudotype. Based on more recent analyses (Soltis *et al.*, in press) with more taxa and data, *Ceratophyllum* is now a sister-group of just the tricolpate clade, and all magnoliids and all monocots would be excluded from the angiosperms. This is shocking, considering that the intent was to name *exactly the same clade* (all angiosperms) and the proponents of NP claim it has greater stability. Of course, under the Linnaean system, the angiosperms would remain the exactly the same with either tree. Another telling example is the group called the “anthophytes,” which was originally proposed to include the gnetophytes, bennetitales, and angiosperms. With recent molecular analyses that support a monophyletic gymnosperm clade with gnetopsids well nested with gymnosperms, the term anthophyte (coined for the presence of “flowers”) would now have to become a synonym of whatever name is applied to all seed plants. Thus, the stability claimed

for the NP System is merely stability in spelling, not what species are included.

METAPHYSICAL STABILITY

The examples presented above establish that the avowed goals of the NP System, namely, stability and continuity in the application of names to clades, are met only in a purely metaphysical (or perhaps typographical) sense. On average, for any nonstatic set of relationships, as new evidence changes our view of relationships, names in an NP System will deviate much more from previous usage than will Linnaean names determined by a reasonable, working taxonomist. The disparity between the two systems will be greatest when names in the Linnaean system are associated with character distributions, as they generally are in modern taxonomy in the form of diagnoses. This fact seems to be lost on (or never considered by?) the proponents of NP. Proponents of the NP System believe that basing names on characters is old-fashioned:

The use of phylogenetic definitions liberates biological taxonomy from a 2,000-year-old tradition of basing the definitions of taxon names on characters. (de Queiroz and Gauthier, 1990, p. 310)

Of course, another benefit of the NP System is that an understanding of characters is not necessary for “naming” taxa. Thus, the required “diagnosis” or “description” of the Linnaean codes would be jettisoned, even for new names not previously described. In fact, it would not be necessary for those naming taxa ever to look at specimens (eliminating the need for collections) or bother to read about their characters in the older literature.

When considered as a whole, the series of papers by de Queiroz and de Queiroz and Gauthier constitutes an effort to impose a form of metaphysical correctness on the field of systematics. This is part of a broader movement for metaphysical correctness that also permeates the controversy on species concepts (e.g., Frost and Kluge, 1994, de Queiroz and Donoghue, 1988; Baum and Donoghue, 1995; Baum, 1998). Part of this effort is implemented through name-calling and pseudophilosophical jargon; thus, de Queiroz labels all those who disagree with his particular metaphysics as

essentialist and typologist . . . terms that have been used repeatedly to attack taxonomists, whether phylogenetic or not (e.g., Hull, 1965; Mayr, 1969; Ghiselin, 1984a). The papers of de Queiroz, de Queiroz and Gauthier, Frost and Kluge, de Queiroz and Donoghue, Baum and Donoghue, Baum, and Ax (1987) ultimately point to inspiration from the earlier papers of Ghiselin (1966, 1969, 1974, 1984b, 1987) and Hull (1978) and the concept of "individuality" as a requirement of correctness in systematic thinking. Of course, as pointed out by Davis (1997), such name-calling, while effectively distracting the reader from the real issues, does not serve to further the scientific enterprise. Thus, those who do not agree with the concept of individuality are "pattern cladists," "operationalists," and may even be "pheneticists" in addition to being essentialists and typologists.

This brings us to the topic of individuality.

On Individuality

Certain camps have decided that the concept of species and clade individuality is a necessary requirement for correct "evolutionary" thinking. Of course, those labeled pattern cladists have generally thought otherwise:

Several workers . . . portray species-as-individuals as crucial to evolutionary biology, although they have been slow to produce cases in which biological problems might be solved better by applying this concept than by ignoring it. (Farris, 1985)

See also Carpenter (1987), Nixon and Wheeler (1990), and Luckow (1995).

It is not within the scope of this paper to explore the morass of convoluted argumentation that has been presented on the topic of individuality (e.g., Frost and Kluge, 1994). We intend here to make a few main points: (1) Clades-as-individuals is a necessary belief system that underlies the NP System. (2) Individuality is a particular metaphysics that has no place in science. (3) Whether or not one believes in species-as-individuals, clades cannot be individuals because of a logical conundrum. Point 1 has been thoroughly expounded upon by de Queiroz and Gauthier (*ad infinitum*). We add here the observation that only under such a metaphysical view of clades can the *instability* of the NP System to changes in understanding of phylogenetic relationships be, by reverse logic, considered stable . . .

on the basis that a name points to some immutable invisible ancestor, no matter how the composition of the group may change. Point 2 speaks for itself, although some might contest the point. Point 3 is much more interesting, indeed.

The division of objects into types is necessitated by the vicious-circle fallacies which otherwise arise. . . These fallacies show that there must be no totalities which, if legitimate, would contain members defined in terms of themselves. Hence any expression containing an apparent variable must not be in the range of that variable, *i.e.*, must belong to a different type. Thus the apparent variables contained or presupposed in an expression are what determines its type. This is the guiding principle in what follows. (Whitehead and Russell, 1962, p. 161)

Various of the authors cited have argued that not only species but also clades have individuality and listed the attributes of individuality as, among other things, having a unique beginning and a unique end. It requires very little thought to realize that clades cannot meet the requirement of individuality . . . because they have neither unique beginnings nor unique ends. This may also be expressed in terms of the theory of types, which merely states that no individual, or element, can be composed in part or whole by other individuals or elements *of like kind*. Thus, a clade cannot be made up of subparts that are clades, or it is not an individual clade. The end of a clade is not unique if it is also the end of other clades to which it "belongs." Individual humans are not made up of parts that are individual humans, individual beach balls are not made up of other individual beach balls, and so on (a point Baum, 1998, probably unaware of the theory of types, appears to have failed to grasp). Yet, the proponents of clade individuality have overlooked the fact that individual clades are made up of individual clades, which can be arbitrarily designated on the basis of "cladogenesis" or character distributions. Thus, clades are arbitrary divisions of the "tree of life." By definition, clades are nested one within another; this is not so, for instance, in "replicating" individuals, such as the species of many species concepts and, for instance, reproducing higher organisms. Thus, even if one adheres to the concept of individuality for species and organisms, it cannot be applied to clades and the whole metaphysics that underlies the NP System is found to be logically inconsistent. Under the view that clades are individuals, every complex clade is at one and the same time one individual and more than one

individual—a logical conundrum that has yet to be considered by the proponents of clade individuality. If one believes in individuality, then species can be individuals, and the tree of life is an individual, but clades are certainly not individuals.

Aside from the logical conundrums of applying the concept of individuality to subclades of life, other attributes of individuality that have been expounded by its proponents are difficult or impossible to apply to clades. These include “cohesion” and “continuity,” which are easily visualized in individual organisms and can be seen in species if one really squints (the acrobatic explanations of how species are “cohesive” and have continuity or are “connected” even when they occur as disjunct populations make amusing reading; cf. Mishler, 1985; de Queiroz and Donoghue, 1988; Baum, 1998). However, even the most gullible reader would have difficulty accepting the idea that aphids and blue whales show continuity and cohesion relative to their ultimate relationship in some broad clade emanating from their common ancestral worm. Argumentation along these lines merely amounts to redefinition of terms, hence obfuscation.

Interestingly, Hennig, who was an adherent of the idea of individuality, held a species concept (termed the “internodal” concept by Nixon and Wheeler, 1990) that actually is consistent with individuality at least in the sense of a unique beginning and end. So, in fact, is the phylogenetic species concept of Nixon and Wheeler (1990), in which species also have a unique beginning and end, although those authors concur with us that this is irrelevant. Alas, the species concept that fails to the greatest degree to fulfill the attributes of individuality is the “monophyletic” or “autapomorphic” concept, for the very reasons outlined for clades above . . . because it is merely a concept that the ultimate clade is the species. This failure to identify an entity with a unique beginning and history leads to the need to coin new terms, such as “metaspecies” for the nonmonophyletic detritus left behind following cladogenesis, and explains how something is a species one day, and not the next, merely because it has given rise to a new species.

Metaphysical questions do not belong in science. Bad (inconsistent) metaphysics does not belong in academics. And the individuality of clades is just logically inconsistent metaphysics.

Accuracy in Pointing

De Queiroz and Gauthier argue that by listing descendants they are pointing to a real ancestor and that this differs from the essentialist, typological, old-fashioned type system of fixing the application of names. There are several aspects of these claims that bear further comment. First, of course, it is only by declaration that they have affirmed that listing descendant terminals (taxa? specimens?) really points to something that listing specimens does not. This is reminiscent of the distinction between history and characters that is claimed by proponents of certain species concepts, who claim that finding evidence of a species on the basis of characters is somehow different from finding evidence of a species on the basis of characters. It is easy to see that it is not possible to point to anything without listing its attributes, whether they are geographic coordinates or some other unique attributes (e.g., descendants, component parts, or synapomorphies). Distinctions here are merely sleight of hand, again, and have no basis in science. However, we must request that our readers suspend their disbelief in pointing for a moment and consider the implications of pointing using lists of descendants, assuming that one really is pointing at something. The simple example of the case (e.g., the Mammals) in which an internal rearrangement within a clade results in the necessity for the name to be applied to a different (sub-)clade shows that this method of pointing, is, simply put, inaccurate. It is inaccurate because the intended ancestor that was supposedly being pointed to (the common ancestor of all mammals listed in the cladogram) was in fact not being pointed to, since subsequently the same pseudotypes point to a more recent ancestor within the mammals and excludes some of the mammals originally listed. It is interesting that the method passed over by de Queiroz and Gauthier, namely, to list all included taxa, is, apparently, the only accurate method of pointing. But, of course, as seen in the paleoherb example, it is also the most unstable convention for assigning names of the available possibilities, because removal of any member to another clade will require the inclusion of the other clade in the group designated by the new name. Such a convention, of course, would paralyze taxonomy quickly, especially given the vast differences among cladograms being generated on the basis of new data (see paleoherb example).

Interestingly, the other convention for naming that was largely passed over by de Queiroz and Gauthier, and dismissed by Schander and Tholleson (1995) and Baum *et al.* (1998), namely, the convention of using characters (synapomorphies), is by far the most accurate of the methods proposed thus far (see also Moore, 1998). Diagnoses are not sensitive to internal rearrangements (e.g., no matter how the relationships within angiosperms change, we still apply the name to things with double fertilization, carpels, etc.). Given an effort to maintain the original meaning of the name, diagnostic taxon definitions are also more stable to new data, as shown in the paleoherb example above. In addition, because the current codes of nomenclature require diagnoses or descriptions (which of course would change in the new system), the current system seems to be both more accurate and more stable than anything proposed by de Queiroz and Gauthier (contrary to claims by Lee, 1999). This is no surprise, because modifications to the codes for the past century have focused on increased accuracy (documentation through types, diagnoses) and increased stability (documentation, diagnoses, and modifications to allow conservation and rejection of names). Unfortunately, in the minds of de Queiroz and Gauthier, these modifications have neglected metaphysical stability at the expense of a system that has the greatest stability for its users.

Invisible Ancestors

The metaphysical inconsistencies of the NP pointing convention actually go much deeper than we have indicated thus far. As shown above, the dipseudotypic method of pointing is inaccurate. There is the first appearance that the omnipseudotypic method is accurate, but is this really so? It is easily seen that this also presents a logical conundrum. If the only accurate method of pointing to an ancestor is listing all included terminals, then what of the case when one names group "Q" and lists all descendants, ABCE, for the tree (A (B (C E))), and then a subsequent analysis gives the tree (A (B (C (D E))))? We have already established that in order to be accurate, the pointing method must list all descendants. Should we now emend the list of pseudotypes for group Q also to include descendant D, in order to ensure accuracy? While this may seem like a

reasonable kludge,⁹ it in fact presents another conundrum. For, if we look back at the original cladogram on which the name Q was based, we see that the emended list of pseudotypes actually designates a different clade than what we intended to name as Q. While this seems absurd on the surface, it is easily explained by the fact that we are not, in either case, looking at "true trees,"¹⁰ but instead, each cladogram is merely a hypothesis of relationship. Thus, it should come as no surprise (at least to pattern cladists) that each tree points to nothing real, but only a nest of "hypothetical ancestors" . . . ancestors that are not, in fact, metaphysical entities in the sense of de Queiroz and Gauthier. And, if one tree is wrong (e.g., presumably the tree in which Agamidae and Chamaeleonidae are both monophyletic), then the common ancestor of a monophyletic Agamidae excluding Chamaeleonidae simply does not exist, anytime, anywhere, anyhow. It was simply an error based on a wrong hypothesis (a wrong tree), and using it to point at anything was just a "pointless exercise". It is interesting that those who claim to be able to distinguish between real entities (e.g., real species vs. character-based species) fail to realize that nothing concrete can be claimed for a hypothesis . . . the changing nature of which proves its inadequacy to point at real things. Apparently, the proponents of NP believe that clades can be "seen" or "perceived" in the way that one can see or perceive an individual person:

Until somebody can show that clades are abstractions or have instances, the individuality thesis will be the only known way to make sense out of them. (Ghiselin, 1995, p. 222)

This silliness is necessary if one is to reject the notion that characters must be used to see clades. And, of course, if anything can be seen, and is concrete, it is observed characters. Clades are not observed; characters, as distributed on semaphoronts, are observed. If clades could be seen, and pointed to, we would not need character data to do so . . . which, of course, is what the NP proponents are proposing. But perhaps we should not let all of these messy details dissuade us from proclaiming that we are pointing to the real

⁹Kludge: quick fix of bad computer code.

¹⁰True trees: whether simulated (e.g., Hillis, 1996) or merely assumed (e.g., Cunningham, 1997), these elusive/illusory commodities loom large in certain circles as arbiters of goodness for phylogenetic methodology.

ancestor, thus claiming to have solved the problems of instability in nomenclature (e.g., Donoghue in Pennisi, 1996).

Pseudoclassification and the Species Problem

Species names would change under the Node Pointing System:

... a phylogenetic system of taxonomy cannot retain the Linnaean method of forming binomials [sic]; specifically, the names of genera cannot be parts of species names. . . . (de Queiroz and Gauthier, 1992, p. 459)

Even if binominal nomenclature is retained:

The first name of a binomial [sic] species name would not be the name of a genus or a clade of any rank . . . Instead, the first name would simply be one part of a two part species name; Griffiths . . . suggested calling it a forename or praenomen. Consequently, a given species would not necessarily be more closely related to other species having the same praenomen than to those with a different praenomen, and this would be a potential source of confusion as long as the names continued to carry connotations about genera. (de Queiroz and Gauthier, 1992, p. 459)

Confusion or not, the effect of this would be salutary:

A taxonomic system in which the names of species are independent of the names of higher taxa, whether uninomials [sic] or non-Linnaean binomials [sic], would also contribute to stabilizing the names of species. (de Queiroz and Gauthier, 1992, p. 459)

Thus,

Modification of the Linnaean approach to forming species names is not only necessary for phylogenetic taxonomy, it would also promote nomenclatural stability, one of the primary functions of the current codes. (de Queiroz and Gauthier, 1992, p. 459)

Whether rankless taxonomy would indeed promote stability is something we will take up below. First, we will delve into the matter of designation of the species.

De Queiroz is a well-known proponent of the monophyletic species concept (e.g., de Queiroz and Donoghue, 1988; see also Nixon and Wheeler, 1990). Given this belief, and their disdain for essentialist-type specimens, one might assume that de Queiroz and Gauthier would propose the same form of pseudotypification for species as for clades above the species level. This, of course, would require designation of two or more descendant populations or individual organisms to point to the common ancestral population or individual organism that would be the ancestor of the species.

This is what we might surmise, but De Queiroz and Gauthier have been silent on this point—and in fact have not dealt with the issue of documentation at any rank other than in the context of cladograms and have never discussed species documentation. This issue continues to be completely ignored in more recent discussions of formation of species names in the Node Pointing System (Cantino *et al.*, 1999; Pleijel, 1999). Baum *et al.* (1998), however, in a recent paper by NP proponents, apparently believe that the old-fashioned Linnaean-type system would necessarily be retained for the species level within the NP System.

And perhaps Baum *et al.* are right on this one. The nightmare of NP pointing within species, i.e., using individual organisms or populations, should be painfully obvious. What if a gene tree showed some individuals to be outside the clade pointed to by the pseudotypes? We would be confronted with a situation in which the name previously intended to point at the whole species now points only to a part of the species; then, of course, the species that had already been named would need to be named again. Not unlike what happens at higher levels with the NP system, one can only ask again, how is this more stable?

REAL STABILITY

Since their inception, the codes of nomenclature have been repeatedly modified in order to ensure stability. De Queiroz and Gauthier ignore or downplay this, citing only proposed revisions, without discussion. When a type is moved to another clade, the Linnaean system exhibits its greatest instability and may even approach the instability of the Node Pointing System of de Queiroz and Gauthier. In such situations, if the community deems the instability too great, *names are simply conserved*. Of course, conservation of names would be anathema to de Queiroz and Gauthier, because the most important aspect of a name is the invisible ancestor at which it points, and this ancestor is immutable in their minds (this eternal coupling of name and ancestor being the source of their claim of stability). By not allowing conservation of names, de Queiroz and Gauthier have disallowed another means of maintaining stability in classification, but have saved themselves from metaphysical incorrectness.

On Ranks

Hierarchies are inherently ranked, whether or not each level is given a categorical designation or formal "rank" (e.g., family, genus). In fact, a system that is not ranked, i.e., nested, is not hierarchic. Aside from the hierarchy of the Linnaean system, the other vertebrae of the modern codes of zoological and botanical nomenclature are *priority* and *documentation* (as typification). De Queiroz and Gauthier dismiss the latter as merely essentialist/typologist and trivially suggest without methodological detail that a similar form of priority should be implemented for a "phylogenetic-based" system (de Queiroz and Gauthier 1994, p. 29). In reality, priority is meaningless without a system of documentation (such as typification) by which the synonymy of two names can be determined. And no system of documentation has been proposed in any of the papers thus far published on the matter by the major proponents.

The idea that ranks should be abandoned has reached the level of slogan, as evidenced by T-shirts available from graduate students at Harvard University that read "Phyla Schmyla: support rankless classification" (Nixon T-shirt archive). Naturally, these T-shirts do not suggest why one should abandon ranks, but then vacuous slogans are not absent from the literature either:

The names Valerianaceae and Dipsacaceae could be retained for clades within the newly defined Caprifoliaceae, although this would mean that taxa with family names (having the traditional ending -aceae) would be nested within a taxon with such a name. This suggestion reflects the view that categorical ranks are best abandoned. (Donoghue, 1995)

Although Donoghue actually did not commit to a definite position here, the reader is left with a vague feeling that he might be in favor of abandoning ranks. Later, slogans are interspersed with buzzwords:

we need to free ourselves of taxonomic ranks and find tree-based¹¹ ways of talking about diversity through time and space. (Donoghue, as quoted by Pennisi, 1996, p. 181)

We are still left with considerable doubt as to whether "talking about" diversity implies actually proposing formal classifications or explicit methods by which to produce them.

¹¹As opposed to character-based or evidence-based ways of thinking.

De Queiroz and Gauthier have also suggested the elimination of ranks (and see Gauthier *et al.*, 1988), although not always of Linnaean binominals. One argument for this is that one will be misled by trying to compare taxa of the same rank, when they are not equivalent. Of course, we cannot protect our ecologist and evolutionary biologist friends from such obvious mistakes, and changing our whole system for such a reason is not only ridiculous but has very serious downsides. Our natural form of communication (even as evidenced by the common human binominal system of naming ourselves) is clarified by the use of ranks and binominals. The use of ranks conveys very broad information about set exclusivity in conversation and writing (see Moore, 1998). De Queiroz and Gauthier (and before them Ax, 1987) fail to understand this and would rather discard this shorthand information about relationship between two names and instead always refer to cladograms. Generally, these proponents have not even acknowledged this necessary consequence, although some NP adherents face the prospect with equanimity (Schander and Tholleson, 1995; Graybeal, 1995; Lee, 1996, 1999).

It would seem that such a system would not really gain widespread support, if those promoting it understood the implications. A very simple example follows. Given our present system, and assuming a phylogenetic classification but using Linnaean ranked nomenclature, you know without further information that no species of the genus *Quercus* is nested within the genus *Betula*. Based on this, if one says *Quercus rubra* and *Quercus alba* and *Betula alba*, you the reader will immediately know that two of these are more closely related to each other—the two *Quercus* species—because genera are at the same rank in the Linnaean system. However, under the NP System, you would not know if *Q. alba* is more closely related to *B. alba*, or *Q. rubra* to *B. alba*, without having explicit reference to a cladogram. Lee (1999) misconstrues this property of a ranked classification, in his claim that the ranked endings (suffixes) of Linnaean names do not convey inclusion, when the point is that ranks indicate *exclusion* (i.e., Fagaceae cannot be nested within Betulaceae, since they are both at the rank of family). Under the de Queiroz and Gauthier system, we are left without any indication of the relative relationships of the three species above without reference to a cladogram. Moreover, the NP System discards information for nothing; we

sacrifice the information conveyed by ranks in order to save our colleagues from themselves (so that they do not try to compare taxa inappropriately). A better solution is to maintain the flexibility and information inherent in a ranked system and educate the users of the system as to the meaning and limitations of ranks.

Monophyly

Consequently, the concepts of paraphyly and polyphyly will become superfluous and interesting primarily in a historical context. (de Queiroz and Gauthier, 1990, p. 312)

The fact that the Node Pointing System is both unnatural for normal communication and not feasible is evidenced by the fact that even proponents adhere to discussion of groups as essentialist constructs . . . such as discussing whether paleoherbs or eudicots or anthophytes are monophyletic, paraphyletic, or polyphyletic even though under the NP System they are forever monophyletic, no matter what any evidence shows about the original circumscription. Of course, the alternative, to exclaim, “Look! Paleoherb is still monophyletic but includes all angiosperms and is therefore a synonym of angiosperm!” or “conifers are anthophytes” is not only unwieldy, but also confusing.

On Paleontological Classifications

A major driving force in the promotion of the NP System is the belief that paleontological classification is more difficult with the current Linnaean system. Typically, this involves a distinction between “crown” groups and “stem” groups (see Jefferies, 1979). While these concepts seem to convey great import to distinctions in classification between fossil and extant taxa, in truth the problems in classification are identical and involve the placement of terminals (extant or fossil “taxa”) into a hierarchy. Theoretically, fossil terminals are no different than extant terminals in this context (Ax, 1987), and thus, the problems inherent in the NP System are identical in paleontological or neontological classification. However, it should also be noted that the problem of instability in paleontological classifications is, on average, much greater than the instability of extant classifications (Nixon, 1996). This is merely the obvious consequence of a lack of complete and comparable information for fossils—which has been

accentuated in recent years with the plethora of molecular data sets (often with seemingly random results—see Soltis, *et al.*, 1997). What is apparent is that the NP System, which requires two (or more) terminals to be designated as pseudotypes, will be particularly unstable when one or more of these pseudotypes is a fossil with incomplete information and, thus, relatively uncertain phylogenetic affinity. Character-based definitions within the context of the Linnaean system, of course, will be much more stable to changes in the positions of fossils and allow classifications that retain the original intent of names to a much higher degree than the NP System.

On Naming

One inspiration of the NP System is that there are not enough ranks available to provide formal names for all of the clades that need to be named:

More importantly, if we consider the proliferation of taxonomic categories problematical, this implies that maintaining the traditional, limited number of categories supersedes the goal of representing phylogeny . . . However, given that the primary task is to represent phylogeny—and acknowledging that there are already more taxon names than anyone can remember—then naming clades seems preferable to leaving them unnamed. . . (de Queiroz and Gauthier, 1992, p. 457)

Our response to this is simple: names are a tool for communication, and as such every node from a cladogram need not be named. Even some proponents of the NP System realize this (Schander and Thollessen, 1995; Lee, 1996). Significant unnamed clades can be discussed by reference to a tree diagram or list of taxa included in a clade. We do not see how it follows that if there are already too many names to remember, it is preferable to produce more . . . perhaps de Queiroz and Gauthier really meant it is no worse to have a plethora of useless names, not preferable. If there are, say, 10 million species on earth, then naming every node in the tree of life would result in an additional 9,999,999 names (and synonyms, not counting subspecific names, and assuming that the whole tree gets a name). Probably the vast majority of such names would never be used by anyone except the original authors or those wishing to dispute their claims of priority under an NP System.

CONCLUSIONS

De Queiroz and Gauthier and colleagues are promoting the dismantling of the Linnaean system, without providing specifics of how to implement the new phylogenetic system. This promotion includes suggestions that ranks should be discarded and that we should move to uninominal names (discard binominal nomenclature).

Claims of increased stability for the new, undescribed code are well received by those who do not practice taxonomy. Many who do practice taxonomy have assumed that these proposals will wither and thus have not responded (see Lidén *et al.*, 1997). This lack of response has even led one proponent of the NP System to conclude that it "has mostly been politely accepted by the systematic community" (Schander, 1999, p. 401)!

The claims of greater stability in the phylogenetic system are unfounded and refer to a kind of metaphysical stability that is best avoided.

But biological taxonomy must eventually outgrow the Linnaean system, for that system derives from an inappropriate theoretical context. Modern comparative biology requires a taxonomic system based on evolutionary principles. (de Queiroz and Gauthier, 1992, p. 472)

What de Queiroz and Gauthier actually object to in the Linnaean system is not a theoretical context or basis, but a context and basis not clouded by metaphysical suppositions (e.g., the individuality of clades). And what they wish to replace it with is a system based on principles of metaphysical correctness that have nothing to do with science or putative "evolutionary principles."

Classifications are in truth only a means of retrieving information (Farris, 1979), a point well understood by both ancient and modern taxonomists. The attempts by de Queiroz and Gauthier (*et al.*) to corrupt the system to be instead a vehicle for metaphysical correctness are clearly a step backward. Names are not proper names, except in the sense that they are handles for unique classes of living things, which bear characters.

Nothing is falsifiable in the NP System. Predictivity is not tested. Particular clades, once named (created), are always true; these clades henceforth always exist. This is trivial: every higher level taxon name that has

ever been proposed is verified in this sense. The paleohorbs provide a perfect example of trivial verification, in which they are monophyletic no matter what.

The "new" system, if formally implemented in some way consistent with the current sketchy proposals, would create widespread instability in nomenclature, as measured by changes in the correspondence between the composition of groups and the names applied.

The Linnaean system, as codified in a system of rules that have been developed over the past 200 years, and earlier, has moved toward increased taxonomic stability. This is stability in terms of composition of groups and correspondence of names.

In nomenclature, it is apparent that stability is a trade-off between rigidity and flexibility. If the system is too rigid, without any flexibility or remedy, then stability suffers, unless the system is static. The proposals of Wiley (1979) are a step in the right direction. We will now extend positive proposals as well.

ACTUAL PROPOSALS

- Maintain the current type system.
- Maintain ranks for ease of communication.
- If the community agrees on the need to "standardize" the application of names, do so with an accurate method. The best (most stable) method of documentation of names would be to tie a single type to a diagnosis (see Moore, 1998). A name would then be applied to the most inclusive clade that included the type and bore the designated homologies in the diagnosis [the distinction between homology and character proposed by Lee (1999) as a criticism of Moore (1998) can be safely ignored if the term homology is used]. This is independent of any tree and can be applied even to older names that are not based on explicit phylogenetic hypotheses, merely by rediagnosing the listed taxa.

Such a method might tie characters to types, such that they clearly identify clades, by combining a type specimen (or name) with one or more synapomorphies (homologies; again, see Moore, 1998). The combination of a type + synapomorphy would actually designate the group (clade) that is intended. For example, Angiospermae could be designated as the clade that includes the type of angiosperms (e.g., *Magnolia virginiana* L.)

and which begins with the unique origin of double fertilization, or the carpel, or some other synapomorphy. This would provide a means to classify fossils unambiguously as well.

Although de Queiroz and Gauthier cited only themselves for the alternative concept of tying classifications to characters, this is in fact the traditional approach to taxonomic classification . . . to tie a name to a diagnosis, which, if the classification is phylogenetic, is most efficiently presented as a list of synapomorphies for each level in the classification. Indeed, Farris (1979, p. 489) referred to such diagnoses as being integral to the definition of names: "The names of taxa form a system that refers to diagnoses and descriptions of those taxa." All that remains is to codify this aspect of common taxonomic practice.

- Allow (informal or specifically indicated) unranked names that are typified and tied to characters just as formal names are.

- Allow emended character (synapomorphy) diagnoses in order to maintain the highest level of stability relative to previous classifications.

- If approved by the taxonomic community, allow priority of names independent of rank.

- In all cases, evaluate repercussions prior to changing the code and prior to propagating new names and "parallel" classifications. Any new system must be approved by the systematic community through the normal (legal) channels for changes in the codes of nomenclature. Any effort to create an independent parallel system (see Cantino, 2000) will create only chaos, not stability.

ACKNOWLEDGMENTS

We are grateful for the encouragement by countless working taxonomists for our presentation and are somewhat less grateful for the arguments by perpetrators of the NP System. We "thank" John Wenzel and Jyrki Muona for trying to save us from ourselves.

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