The imminent introduction of the draft PhyloCode (Cantino & de Queiroz, 2000) governing application of phylogenetic nomenclature (de Queiroz & Gauthier, 1990, 1992) has generated considerable discussion in this journal and elsewhere. Some contentious issues include the information content of Linnaean ranks, stability in meaning and content of taxon names, relative merits of node-, stem- and apomorphy-based definitions, restriction of widely-used names to crown-clades, and format of species names (e.g., see Brochu & Sumrall, 2001; de Queiroz & Cantino, 2001; Ereshefsky, 2001; Forey, 2001; Lee, 2001; Bryant & Cantino, 2002). However, one subject has not been sufficiently discussed: whether the PhyloCode should govern species names. This is a most important issue, since it will determine whether the PhyloCode will eventually affect the definitions and format of species binomials, which form the vast majority of existing taxon names.

Although the draft PhyloCode currently contains rules for naming only clades, there are plans to eventually extend it also to cover species (Cantino & de Queiroz, 2000), and various possible options for naming species in phylogenetic nomenclature have been presented (Cantino & al., 1999). These options all involve converting binomial species names defined under the current Linnaean codes into a different (either totally or functionally unimomial) format under PhyloCode. There are compelling reasons for such a change (see de Queiroz & Gauthier, 1990, 1992; Cantino & al., 1999; Ereshefsky, 2001; Pleijel & Rouse, in press; and references therein). The mandatory incorporation of the genus into a binomial species name creates instability in not just the genus name (e.g., new generic assignments due to splitting and lumping, or newly discovered phylogenetic relationships), but also destabilises the species epithet (e.g., secondary homonymy, or changes in gender of species epithet to match that of a new generic assignment). New species cannot be described until their generic assignments (i.e., phylogenetic relationships) are known precisely. Mandatory generic assignments for species produces redundant higher taxa (e.g., monotypic genera are identical conceptually to their sole species). Stem species of two sister genera cannot be assigned to either descendant genus, or placed in their own genus, without creating a paraphyletic genus. Finally, the genus rank does not exhibit any unique features distinguishing it from other Linnaean higher taxon ranks and is thus biologically meaningless. All these problems can be avoided by dropping the genus name from the names of species taxa. Species names would then be unaffected by generic reassignments, new species could be described without knowing their phylogenetic relationships, and monotypic (redundant) genera would never be created. In an ideal world, switching from binomial to unimomial species names would be easy and eliminate all the above problems. However, the real world contains substantial phylogenetic inertia. Converting the million-plus existing binomials into a different and (at least functionally) unimomial format represents a mammoth task. However, an even bigger obstacle is that binomial names are deeply entrenched throughout society, through their use in, for instance, popular books and field guides, faunal surveys, legislation (endangered species, animal ethics), and museum labels and catalogues. To expect all these institutions to smoothly adopt a new format for species names is overly optimistic, especially given the substantial effort required on their part, and the lack of appreciation by most non-scientists of the biological reasons for such a change. Thus, the question of whether the PhyloCode should be extended to species names requires careful consideration, and it is hoped this commentary will help generate relevant debate. I first discuss how PhyloCode can easily function without any reference to species at all, and then mention some problems that need to be addressed if species are to be included.

One possible reason why species names should be included in the PhyloCode is that species are commonly employed as reference (= specifier, "type") taxa employed in phylogenetic definitions (e.g., Cantino & al., 1997; Baum & al., 1998; Hárlín, 1999). For instance, the definition "the least inclusive clade containing Species X and Species Y" is affected by the stability of the names of the two reference species. If those species names are defined under the Linnaean system, these
Binomials will be unstable due to generic changes (caused by splitting and lumping of genera, and/or phylogenetic rearrangements). The phylogenetic definition of the clade will either become obsolete (names of reference species not valid) or will need to be regularly modified to accommodate any changes in the Linnaean binomials of the reference species. The need for stable species names to use as reference taxa in phylogenetic definitions of clade names is one of the justifications for including species in the PhyloCode, and consequently stabilising the names of reference species using uninomials.

However, species do not have to be used as reference taxa. The current PhyloCode states that the reference taxa used in node-, stem-, and apomorphy-based definitions can be either species or specimens, with the strong recommendation that if specimens are used, they should be the type specimens of species. This recommendation ensures that if specimens are used as reference taxa, they will be appropriate specimens deposited in public institutions and freely and permanently available for study. It would also avoid the proliferation of types that would result if specimens other than species types were allowed to be used as reference taxa, e.g., one specimen of *Eucalyptus yumbarrana* could be the holotype of the species, but several other specimens could be reference taxa (“types”) for various named clades of gum trees. The permitted use of either species or specimens means that in a node-based definition (for example), two formats are possible: (1) “the least inclusive clade containing *Eucalyptus yumbarrana* and *Eucalyptus leucoxylon*”, or (2) “the least inclusive clade containing specimens AD97726343 and MEL1010317”, the types of *Eucalyptus yumbarrana* and *Eucalyptus leucoxylon*. However, because the taxa *Eucalyptus yumbarrana* and *Eucalyptus leucoxylon* are themselves defined using specimens AD97726343 and MEL1010317 as reference (type) specimens, definition (1) ultimately uses those type specimens as reference taxa, and is thus identical to definition (2). Thus, phylogenetic definitions are equivalent whether entire species or their type specimens are used as reference taxa: both versions refer ultimately to the type specimens. They merely differ in either referring to these specimens indirectly or directly. Restricting phylogenetic definitions to using only type specimens as reference taxa, and not species, will therefore not change their ultimate meaning in any way. There will be slightly less information if type specimens, rather than species, are employed in definitions without further discussion. However, this can be alleviated with the recommendation that the relevant species assignment under Linnaean codes is always cited as a descriptive phrase that is not part of the official definition: e.g., “The least inclusive clade containing specimens AD97726343 and MEL1010317; currently the types of *Eucalyptus yumbarrana* (Yumbarra mallee) and *E. leucoxylon* (Australian blue gum) respectively”. Subsequent changes to the species binomials can be accommodated by changing the names mentioned in the unofficial descriptive portion. This sort of definition can encounter problems if specimens AD97726343 and MEL1010317 subsequently are no longer types of valid species (e.g., if the species is synonymised, or if specimen is inadequate and a neotype designated). However, these problems can be greatly minimised by choice of reference specimens that are complete and the types of old species. If, despite these precautions, one of these specimens loses its status as type of a valid species, the definition can either be maintained unchanged (as an exception to the PhyloCode recommendation that reference specimens should be types of species), or might be changed so that a new individual representing a valid type is designated as a reference specimen (by petitioning the body governing the application of PhyloCode). However, if systematists take appropriate care in selecting reference specimens for phylogenetic definitions, such problems should be exceptionally rare.

If specimens are consistently used as reference taxa, as suggested above, stable species names are no longer prerequisites for stable phylogenetic definitions of clades (supraspecific taxa). This therefore negates one of the prime arguments for converting existing species binomials to a different (uninomial) format for phylogenetic nomenclature. The PhyloCode becomes a system governing naming of clades exclusively, and can function totally independently of species names, which are governed by existing Linnaean codes (Sneath, 1992; ICZN, 1999; Greuter & al., 2000).

Once the PhyloCode is widely adopted as the system for naming clades, then serious thoughts should be given to extending it to also embrace species. Current Linnaean definitions of species are very imprecise, and need to be made more rigorous. Like any Linnaean taxon, a species is defined using a rank and a type. For example, under the botanical code, *Eucalyptus yumbarrana* is “the species-level entity containing the holotype organism AD97726343”. This begs the question as to what constitutes a “species-level entity”, a question left totally unanswered by the current Linnaean codes. The nature and boundaries of any given species-level entity (and thus, the content of the species) can vary widely depending on which of the numerous species concepts is adopted. The codes are totally silent on this subject and thus implicitly allow all species concepts, including biologically unreasonable ones. In practice, the inclusiveness of a species can vary depending on whether widely-used concepts based on gene flow, cohesion, or diagnosability are employed. Thus, biologists can agree totally on a popu-
lation-level phylogeny but continue to argue over the number and boundaries of species present. These problems of undefinable ranks beset Linnaean higher taxa and have led to calls for their abandonment (see Ereshefsky, 2001, for review), but similar problems plague Linnaean species as well (Mishler, 1999; Pleijel & Rouse, 2000).

If phylogenetic definitions are to be extended to species, numerous methodological and pragmatic problems arise. Methodological problems include constructing appropriate phylogenetic definitions for species. Node-, stem- and apomorphy-based definitions were designed to apply to entities exhibiting hierarchical relationships, and cannot be applied readily to reticulating populations (a necessary context if one wants to define species using such phylogenetic definitions). The concept of monophyly might be extendable from species (Hennig, 1966) to entities such as populations and organisms, provided they exhibit hierarchical relationships (de Queiroz & Donoghue, 1988). However, populations and organisms of sexual species exhibit widespread reticulation. “The least inclusive clade containing specimens X and Y” is difficult to delineate if the populations containing X and Y are themselves polyphyletic, and reticulate with each other and other populations. Also, even if it is possible to delineate phylogenetic entities using current phylogenetic definitions and call them “species”, they are unlikely to coincide with the species delineated under many of the most widely used species concepts. For example, most of the current species concepts employ as criteria cohesion, reproductive isolation, or diagnosability through a unique combination of character states (see Wheeler & Meier, 2000; Ereshefsky, 2001; Hey, 2001); but node-, stem- and apomorphy-based definitions cannot be readily phrased to delineate species corresponding to these criteria. Many if not most workers accept that species are conceptually different from clades. Indeed, this distinction is essential if the species category (rank) is to be formally recognised, otherwise one need only recognise populations and clades. If species are fundamentally different from clades, it might be futile to attempt to define species using phylogenetic definitions designed for naming clades. Current debate has focused on the format of species names in phylogenetic nomenclature (Cantino & al., 1999); the issue of how species are to be defined in phylogenetic nomenclature (and indeed, in Linnaean codes) also needs to be addressed.

In addition, if Linnaean binomials are converted to PhyloCode uninomials, problems will arise if the original Linnaean binomial name is changed, e.g., due to synonymy or secondary homonymy. A Linnaean binomial can always change but once converted to a Phylocode uninomial, that Phylocode uninomial will remain fixed forever (Cantino et al. 1999). For instance, *Eucalyptus yumbarrana* might be converted to *yumbarrana*, but might subsequently change to *Eucalyptus citriodora*: in which case the Linnaean binomial *Eucalyptus citriodora* would now correspond to the PhyloCode uninomial *yumbarrana*. Such instances will lead to a gradual divergence in the species names under the two codes (Cantino & al., 1999), with potential communication and information retrieval problems. This problem will not be great if the Linnaean codes are rapidly abandoned and replaced by the PhyloCode. Very few instances will arise before the Linnaean codes are abandoned, after which those instances will no longer be of any consequence anyway. However, it is almost certain that the two systems will co-exist for an extended period, in which case “intercode mismatch” will cause difficulties.

The PhyloCode represents one of the greatest advances in biological taxonomy since Linnaeus, and deserves to be considered seriously by all scientists. However, it arose as a system for naming clades, and extending it to species without modification might lead to numerous taxonomic and pragmatic problems. Restricting it to clades and making it totally independent of species will avoid such problems, and can be done easily by stating that specimens only, rather than species or specimens, must be used as reference taxa. This arrangement will further allow the PhyloCode to coexist smoothly with existing codes, the PhyloCode governing the names of clades, and existing codes governing the names of species (and for those who wish to recognise them, the names of higher Linnaean ranks). There will be cases in which certain small clades (named as uninomials under PhyloCode) will correspond to species (named as binomials under Linnaean codes). This simply means that each such entity is both a clade and a species, and thus can be named using both systems. Problems of synonymy will therefore not arise: both names are valid. The uninomial PhyloCode name reflects the entity’s status as a clade, whereas the binomial Linnaean name reflects its status as a species. These names, being governed by different systems, can change independently. For instance, changes of an entity’s species name under the Linnaean codes have no effect on the entity’s clade name under the PhyloCode, and vice versa. As an analogy, the entity Sting is also known as Gordon Sumner (Welch, 1996). This is because he is both a recording act and a person, and can be named under two systems. The name Sting refers to the entity in the system of names for recording acts, the name Gordon Sumner refers to the entity in the system of names for people. These names, being governed by different systems, are free to change independently. For instance, if the entity changes his stage name from Sting to something else, his personal name can still remain Gordon Sumner.
The pragmatic advantages of excluding species from the PhyloCode (at least initially) are substantial. The PhyloCode becomes a “pure” system for naming only one type of entity: the clade. It would thus fill the gaping hole left by current Linnaean codes, which do not explicitly attach names to clades. The PhyloCode can be introduced immediately with little disruption, without the need for conversion of the million-plus species binomials, and without clashing with existing codes governing those binomials. Species names can therefore retain the familiar binomial format used throughout society. If appropriate phylogenetic definitions for species are later devised, evaluated and shown to be effective, species might be incorporated into the PhyloCode at some future date.

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LITERATURE CITED


