

Phylogenetic nomenclature: the end of binominal nomenclature?

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In phylogenetic nomenclature the name of a clade is defined ostensibly by specifying an ancestor and all of its descendants in a hypothesised phylogeny. This new system of nomenclature was proposed and elaborated in a seminal series of papers by DE QUEIROZ & GAUTHIER (1, 2, 3), and has received a positive reception from many systematists (references in 4), though a few authors have rejected it (5, 6). The rules for this new system are now worked out in a new code, the PhyloCode, still in preparation. The draft version can be found on <http://www.ohio.edu/phylocode>. However, no consensus has yet been reached on the format for species names. The draft version of the code only governs the rules for naming supraspecific taxa (i.e. clade names), and not species names as yet.

CANTINO et al. (4) proposed and discussed 13 different ways for naming species, all fundamentally different from the Linnean binomen. The drawbacks of the Linnean binomina have been thoroughly discussed (references above, 7, 8). Even though CANTINO and his co-authors (4) did not reach agreement on the form of a species name, all seven authors of this paper agreed that the old Linnean binomen should not be used in phylogenetic nomenclature. A “converted name” should replace the “old” binominal Linnean species name.

CANTINO et al. (4) divided the 13 methods into two major groups: (1) the converted name to be based only on the species epithet of the Linnean binomen. These epithet-based methods seem to be favoured by the majority of the people directly involved in the making of the PhyloCode (see 4, p.804); (2) the converted name to be based on the entire Linnean binomen (distinguishable or not from the original). A thorough discussion on the advantages and disadvantages of the various methods has been made (4), including some of the issues considered further on. The authors of that paper thus deserve full credit for the original ideas. All I want to do here is take a firm position in favour of the binomial-based (or binomen-based) conversion and make a choice from the methods proposed.

One of the most important properties of a name is its uniqueness (for the sake of simplicity I use the terms unambiguous and unique interchangeably, as uniqueness

is the easiest way to make a name unambiguous). Non-unique names can lead to confusion and ambiguity, and are therefore less useful in scientific communication. If a code of biological nomenclature is to provide a universal language to speak unambiguously about organisms, it should avoid non-unique names. Universal uniqueness should be inherent to the name of a species so that just by mentioning the name and only the name, one can speak about one and only one species of all the living organisms. Such universal uniqueness would be inherent to binomial-based converted names, since the pre-existing codes have ensured the uniqueness of the correct Linnean binomina, e.g. by the rules of priority in cases of homonymy. There may be some overlap between the different existing codes as to genus names (e.g. animals and plants can have the same genus names), but organisms with exactly the same Linnean binomen are rare. In contrast, epithet-based converted names without a numeric portion (see further) would lead to numerous cases of ambiguity. A quick look through lists of the Belgian flora and fauna reveals that *arvensis* is a specific epithet for at least 24 plants and two animals (a bird and a beetle). This would mean that already in the Belgian flora and fauna alone, at least 26 species would be called *Arvensis*. To keep these epithet-based names unique, it was proposed that a unique number be added to the name (e.g. *Arvensis1*, *Arvensis2*, etc.). Although in theory a good solution, in practice the use of such names would be very difficult, if only because numbers are much harder to remember than are names. Only within a small field of specialists could numbers be practical. For someone working on Lamiaceae phylogeny, it would not be too difficult to remember that e.g. *Arvensis26* is the old *Stachys arvensis*, *Arvensis33* is the old *Acinos arvensis* and *Arvensis69* is the old *Mentha arvensis*, and thus know to which species the name refers. However, for an ecologist or a biology student, or an amateur biologist for that matter, lists of names would become an entangling collection of numbers. To diminish this problem, the addition of a “taxonomic address” was proposed, and in cases such as the *Arvensis* example, *Stachys* (for example) could be added to the numbered name as a “taxonomic address”. However, is it not much simpler to choose a method that precludes ambiguity, such as a binomial-based conversion method?

One of the advantages of epithet-based names is that they would automatically be stable after conversion. The

name would never change, which would be a boon to people working with or interested in nature, but not specifically in taxonomy or phylogeny. However, this stability can also easily be achieved by using binomial-based names. In fact, most of the binomial-based methods proposed in (4) result in stable converted names (as illustrated in 4, Table 3, column three). Even though a binominal name would be based on the entire Linnean binomen, this does not mean that it would have the same properties as a Linnean binomen (7). In Linnean binomina, the first name is the genus name, expressing relationships with other species having the same genus name (and thus variable with our progressing views on relationships). In binomial-based converted names, the first name should not imply any relationship. It would not be a genus name, it would just be a forename (or praenomen) (8), and therefore it would not need to change with changing hypotheses of relationships. Opponents of binomial-based methods fear that people would not be able to distinguish between the “old” Linnean binomen and the “new” binomial-based name, and would still think of the praenomen as referring to some kind of relationship (9). Solutions can be found to that problem. First: the binomial-based name should be clearly different in form from the Linnean binomen. The Linnean way of writing a name is so well established after 250 years, that any change would immediately be noticed. Dropping the capital and replacing the space between genus name and species epithet by a hyphen or dot (e.g. *stachys.arvensis* or *stachys-arvensis*) would immediately make it clear to everyone that the new name is not a Linnean binomen. It would also be possible to drop the capital **and** the space (*stachysarvensis*) but this could lead to almost unpronounceably long names. Second: the use of praenomina as clade names could be prohibited (as in method C in 4). In this case, if there is a species called *stachys-arvensis*, there should be no clade with the name *Stachys*. This, however, would lead to the replacement of all the old genus names, and thus the abandonment of many names we are familiar with. For practising taxonomists this might be an argument to reject phylogenetic nomenclature completely, and from this viewpoint it seems better not to adopt this convention. But even then, by introducing a few conventions, binomial-based names and epithet-based names could have the same properties after conversion: stability and ease of recognition from the Linnean binomen from which they were derived. Binomial-based names would then be equivalent to uninomina in practice. The converted name would not be a binomen in the Linnean sense, but just a hyphenated unimon (7).

An obvious advantage of the binomial-based conversion system is that it would change the “old” names only in the way of writing them, hence ensuring continuity with the presently existing names. This would certainly also ease the acceptance of the new code by the scientific

community not involved in systematics, and by amateur biologists. On the other hand, as long as the present codes of nomenclature remain valid (and the different codes will co-exist for a good while), species names governed by the present codes can be altered because of generic changes (example in 4, p. 804). The stable binomial-based name then would become different from the Linnean binomen, and this is seen as a disadvantage by those in favour of epithet-based names. This divergence is of minor importance however, since the binomial-based name would retain the old epithet. Moreover, if the generic realignment also included a change of the epithet (because of secondary homonymy), the binomial-based name would differ completely from the Linnean binomen, but also the epithet-based converted unimon would differ from the new epithet of the Linnean binomen. However, because of the common practice of indicating the older synonyms when a new species name is proposed, the once converted name could easily be located.

From all the above, it should be clear that converted names would be best as binomial-based. Such a conversion method would ensure uniqueness of the name, cause minimal disruption with the old nomenclature, and enhance the acceptance of the new method by the scientific community. To reduce the risk that one might think of the praenomen as implying relationships, the converted species name should be clearly distinguishable from the Linnean binomen, but remain easy to read and pronounce. For the sake of simplicity, all names in a nomenclature system should have the same form, converted names as well as new names. Of the methods proposed by CANTINO et al. (4), only two meet the requirements discussed above, namely methods B & C (and F to a lesser extent). The methods differ in that praenomina can (method B) or cannot (method C) be used as clade names. Method C is preferable from a theoretical point of view since it reduces the risk of misunderstanding the praenomen as implying relationships. However, method B is preferable from a practical point of view, as many familiar names can be retained. A very common concern of practising taxonomists about phylogenetic taxonomy is that it would replace many old names by new ones, at the moment based on a misconception (10). However, adoption of method C would legitimise this concern.

To conclude: for these reasons, the best conversion method to adopt in the future is method B of CANTINO et al. (4), although with a slight adaptation. I would suggest conversion of the name by dropping the capital (even when starting a sentence) **and** adding a dot or hyphen (*stachys-arvensis*), instead of choosing between one of both as was suggested (*stachys arvensis* or *Stachys-arvensis*). This would serve to make the distinction between the converted name and the Linnean binomen more obvious.

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