

APPROPRIATELY SIZED GENERA AND APPROPRIATELY RANKED HIGHER TAXA

There are some truly pressing problems for systematic mycology, for example, “What should be done about fungi known only from environmental DNA sequences (Hibbett *et al.* 2011, Hibbett & Taylor, 2013)?” or, “Is a population any different from a species when both are genetically differentiated in nature and each possesses unique adaptive phenotypes (Ellison *et al.* 2011, Neafsey *et al.* 2010)?” These are problems that can be solved by objective research, so I am not going to say any more about them. Instead, I want to explore the current buzz about naming taxa above the species level, which is a problem of a more subjective nature and which was the topic of the recent 2014 CBS Spring Symposium on “Genera and Genomes” (<http://www.cbs.knaw.nl/index.php/meetings/396-2014-cbs-spring-symposium-the-genera-of-fungi>).

Two taxonomic issues bother me – those of inappropriately large genera and that of taxa of inappropriately elevated rank. Beginning with genera, one might ask, “Is there an appropriate size for a genus and, if so, what should it be?” The taxonomic study that helped precipitate the one-fungus-one-name revolution began with a large sexual (teleomorph-typified) genus, *Botryosphaeria*, and used DNA variation along with sexual and asexual (anamorph) reproductive characters to sort it into 12 genus-level clades, one of which retained the original name (Crous *et al.* 2006). Subsequently, similar work was done using fungi with *Fusarium* asexual morphs, this time using DNA variation to identify multiple clades and then examining sexual characters to sort them into species, while retaining *Fusarium* for the clade that harboured the type specimen (Grafenhan *et al.* 2011, Schroers *et al.* 2011). Not many

fusariologists were happy with this outcome, and a counter proposal was published arguing that the genus *Fusarium* should be kept large to acknowledge, among other things, its social importance (Geiser *et al.* 2013). Another large, long-established genus, *Penicillium*, was also examined and found to be too large because *Aspergillus* and other genera lay between its two large clades, one having and one lacking *Talaromyces* sexual morphs. Here, the authors neatly restored monophyly, without argument, by applying *Penicillium* to one group and *Talaromyces* to the other (Houbraken & Samson 2011). However, in their *Penicillium* study, those authors also argued that *Aspergillus* should be kept as a large genus. This suggestion has been contested by a recent study showing that fungi with *Aspergillus* asexual morphs can be sorted into several smaller genera, each embracing phylogenetic diversity similar to that of the recently narrowed *Penicillium*, and each congruent with genera based on sexual morphs that were previously described to accommodate their distinct morphologies and physiologies (Pitt & Taylor 2014). If a trend can be drawn from these few examples, it might be that there is sentiment to keep large genera when they are socially important and share an easily recognized, ancestral, asexual morph. Admittedly, there are benefits to larger genera, but there are also drawbacks. As noted by Grafenhan *et al.* (2011), when speaking of two large clades of fungi with *Fusarium* anamorphs, “. . . the amount of morphological diversity incorporated in both of these large clades was huge, rendering the resulting taxonomy meaningless from a practical point of view.” The task for mycologists is to define genera that are scientifically meaningful and, at the same time, politically useful. Where that task seems impossible, should we err



on the side of scientific meaning? As these debates play out, it is calming to remember that nomenclature follows taxonomy, and if today’s inappropriately large genus is divided tomorrow, the names for the smaller genera will still be available for each of them.

I am reminded of the second issue, that of appropriate taxonomic rank, each time I teach mycology. It’s a problem that is nicely illustrated by observing Fig. 1 taken from the current, “Classification of Fungi” (Hibbett *et al.* 2007). Here, all fungal phyla and even some subphyla radiate directly from the base of the *Fungi*, with one exception. That exception is the phylum of rumen fungi, *Neocallimastigomycota*, which emerges from a branch that it shares with *Chytridiomycota*. Why, students ask, is *Neocallimastigomycota* a phylum when it might better be a subphylum or class of *Chytridiomycota*? To answer, I tell them about the unusual niche and exceptional phenotypes of rumen fungi. But, as I do so, I know that we mycologists have let phenotype wrongly dictate taxonomic level. By the time the class reaches *Basidiomycota*, those same students raise the same question

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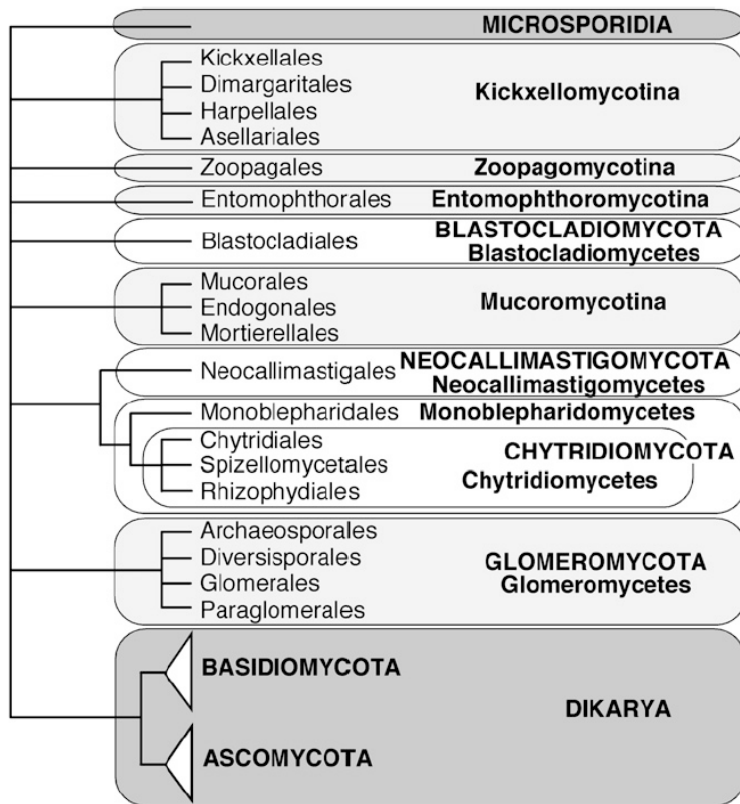


Fig. 1. Position of *Neocallimastigomycota*. Reproduced from Hibbett *et al.* (2007).

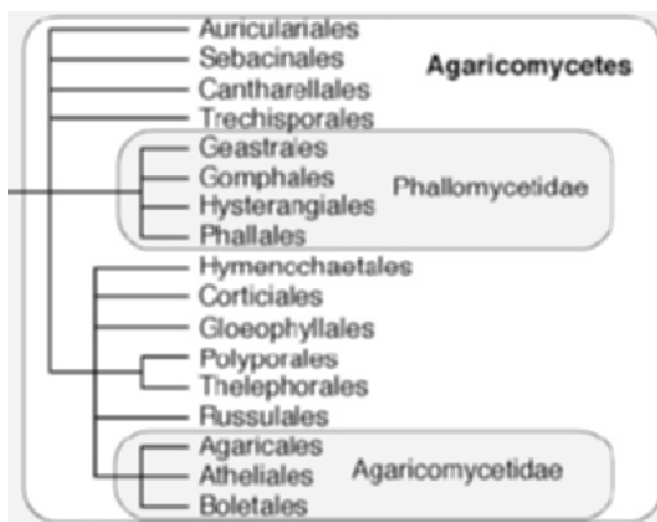


Fig. 2. Position of *Phallomycetidae*. Reproduced from Hibbett *et al.* (2007).

about the *Phallomycetidae*, seen in Fig. 2 taken from the “Classification of Fungi” (Hibbett *et al.* 2007, fig. 2). Now that it is late in the semester (and now that I have tired of defending these lapses in mycological logic), I generally admit that this subclass ought to be an order, and that its elevation stems, again, from its remarkable phenotypes, evolved this time through dispersal by animals. In these cases of wrongly elevated rank, it seems that

one distinctive phenotype has trumped the phylogenetic signal of thousands of genetic differences. The next time that the classification of fungi is revised, those of us who teach mycology ask that taxa are assigned to their appropriate rank, at least where possible.

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