

Integrating sequence-based environmental species into fungal taxonomy

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Fungal systematists face the daunting challenge of discovering, describing, and giving names to all of the species of Fungi on Earth. At present, about 100,000 species of Fungi have been named, with about 1200 species described annually for the last ten years. However, the actual diversity of Fungi has been estimated to be roughly 1.5 million species or more, suggesting that at current rates many centuries will be required to completely catalog the global mycota. At the same time, the rate of discovery of new fungal species based on environmental sequences has been increasing, and, with the advent of pyrosequencing methods, these data appear to be poised for explosive growth. Formal taxonomic recognition of sequence-based environmental species (and higher taxa) could help narrow the gap between the described and actual dimensions of fungal biodiversity. Unfortunately, sequence-based taxon description is not permissible under the International Code of Botanical Nomenclature, which requires a type specimen for establishment of a new taxon. Moreover, sequence-based species delimitation has multiple sources of error, including gene-tree species tree conflict (due to hybridization and incomplete lineage sorting, as well as rare cases of horizontal gene transfer) and intragenomic heterogeneity. Nonetheless, environmental sequences are enabling discovery of vast numbers of new taxa, which could have impacts our understanding of evolutionary and ecological processes, and inform conservation policy. To facilitate the inclusion of environmental fungal species in taxonomy, and to bring knowledge of these taxa to bear in all fields that make use of biodiversity information, a mechanism for formal naming of sequence-based taxa is needed. One option is to employ a “candidate species” category similar (but not identical) to the “candidatus” status adopted by prokaryotic taxonomists.