Response to Comment on “Global assessment of arbuscular mycorrhizal fungus diversity reveals very low endemism”

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Bruns and Taylor argue that our finding of widespread distribution among Glomeromycota “virtual taxa” is undermined by the species definition applied. Although identifying appropriate species concepts and accessing taxonomically informative traits are challenges for microorganism biogeography, the virtual taxa represent a pragmatic classification that corresponds approximately to the species rank of classical Glomeromycota taxonomy, yet is applicable to environmental DNA.

which uses multiple genomic loci to assess limits on recombination (4). In practice, morphological and phylogenetic species concepts are applied in specimen-based classification of the apparently asexual Glomeromycota. About 300 species of Glomeromycota have been described on the basis of morphology (mostly, but not exclusively, of spores) and DNA sequences [internal transcribed spacer (ITS) region or large subunit (LSU, also called 28S) rRNA gene, both widely used markers in the taxonomy of Fungi]. Although this number is low in the context of some microorganism groups, it is consistent with species number estimates in other early-diverging fungal clades (2). Furthermore, evidence for cryptic species among Glomeromycota is limited; rather, merging of described species has been proposed (6). Although we see no compelling evidence to suggest massive underestimation of Glomeromycota species numbers in the current taxonomy, Bruns and Taylor are right to point out that reliance on conserved or limited traits for taxonomic assignment is a potential stumbling block for microorganism taxonomy. It is notable that, irrespective of species boundaries, widespread AM fungal taxa are known to harbor globally distributed genotypes (7, 6). Nonetheless, we trust that progress in officially describing new fungal species on the basis of DNA data, including population genetics approaches, will improve estimates of global fungal species numbers (9) and prove to be a catalyst for advancing Glomeromycota taxonomy and understanding species-level distribution patterns.

DNA-based taxonomies incorporating both specimen-derived and environmental records have identified approximately 350 SSU rDNA-based VT (at ≥97% similarity threshold) (10) and more than 2000 ITS-based species hypotheses (SH) (at 98.5% similarity threshold) (11) among Glomeromycota. Application of other, nonribosomal markers has revealed similar classification and species number estimates (12, 13). Both VT and SH are pragmatic species classifications, validation of which is ongoing. VT are known to be slightly higher in taxonomic rank than (morpho-)species of Glomeromycota and may be equivalent to groups of closely related species in some genera. However, the species-discriminatory power of the SSU rDNA marker is only slightly lower than that of the markers widely used by taxonomists (14), and VT are clearly finer in taxonomic rank than the families or genera of classical Glomeromycota taxonomy (15). Thus, given the best available taxonomic information, the VT approach provides an effective means to survey approximately species-level diversity in the group.

We contend that the biogeographies of different organism groups are comparable but that taxonomic assignments must be made using appropriate traits, and these differ from group to group. For example, species-discriminating morphological traits for plants are frequently those of flowers; for animals, those of bones. The quest for DNA-level traits for species discrimination has not yet identified a universally suitable marker region. Plastid markers are used for plants, mitochondrial cytochrome oxidase I for animals, and nuclear ribosomal ITS for fungi. These markers are rarely optimal for all species within organism groups, and the ITS region is known to be too conserved or too variable in some fungal groups (15). We argue that the central fragment of the SSU rRNA gene distinguishes approximately species-level taxa among Glomeromycota and is therefore practical for research on the diversity patterns of these fungi. However, we recognize that use of this marker region for species identification of other fungi, let alone of plants or animals, would be as inappropriate and fruitless as an attempt to identify plants using bones, or animals using flowers.

REFERENCES AND NOTES


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