

Abstract

To exploit the opportunities offered by our increased understanding of arbuscular mycorrhiza (AM) diversity and the potential to manage it requires greater knowledge of the indigenous AM fungi (AMF) involved in the symbiosis with target plants. Our ability to fully describe AMF diversity is still at early stage in terms of the taxonomic units present, despite recent developments in DNA sequencing capacity. The information required is the number of species or taxonomic groups present, the number of individuals that can be identified as belonging to the same group, and the level of variability there is within such a group in terms of their capability to enhance growth. With the techniques available it is possible to be precise over the molecular makeup of individuals but it is more difficult to be certain as to which species they may belong, particularly if that species has been mainly identified through its morphological characteristics, especially those of its spores, rather than from DNA sequencing. Consequently it is operational taxonomic units (OTUs) or virtual taxa that are used to describe taxonomic groups, which are identified solely through molecular techniques. Nevertheless variability exists in both species and OTUs. Effectiveness of a mycorrhizal symbiosis depends on environmental conditions, but is also influenced by the community of higher plants as well as the local soil biota. Establishing linkages between genetic and the functional diversity under field conditions with biotic and abiotic stresses is more challenging. Successful assemblages of AMF combine the ability to acquire P and to protect host plants against pathogens or abiotic stresses, consistent with greater diversity being associated with greater ecosystem functioning through enhanced trait richness. To capitalize on the potential benefits from managing AMF diversity, appropriate solutions are needed for different agroecosystems and applicable on a site-by-site basis. Identifying genetic and molecular markers that allows quantitative assessment of the potential to exploit indigenous AMF is crucial. Within AMF hyphae two markers have been identified in the ribosomal DNA that can be used to identify OTUs. Similarly mitochondrial large ribosomal subunit sequences have also been used. Short-term considerations suggest that more effort is needed to identify key markers in major crops for AMF assemblages that function effectively to offset major biotic and abiotic stresses.

Keywords: Biological diversity; functional diversity; genetic and molecular markers; small and large ribosomal subunits; operational taxonomic unit; AMF assemblages