

# Arbuscular mycorrhizal fungal communities exposed with new DNA sequencing approach

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One of the two study sites -- the Nic-Te-Ha cenote in a dry seasonal tropical forest in the Yucatán Peninsula, Mexico. Credit: Louise Egerton-Warburton

The roots of most land plants are colonized by arbuscular mycorrhizal fungi, which help their plant partners to grow while also influencing the wider environment. Their hidden nature has meant these fungi are poorly understood, but researchers from the Chicago Botanic Garden and Northwestern University have developed a new approach to detect and identify the many species involved in these ecologically vital communities.

Arbuscular mycorrhizal [fungi](#) partner with around 65-75% of [land plants](#) to provide them with nutrients from the soil in return for sugars made during photosynthesis. These fungal communities have a big impact on the types of plants that can grow in a particular location, and scientists are keen to learn more about their diversity and their ecological effects. However, the nature of arbuscular mycorrhizae means that the fungi grow within the plant tissues, so it can be tricky to tell which [species](#) are present in a particular environment.

Although DNA sequencing has been used to identify around 350 of the most abundant arbuscular mycorrhizal fungi in certain regions, these approaches are unlikely to give a full picture of the species in a particular environment. To better characterize the diversity of the arbuscular mycorrhizal fungi, PhD candidate Benjamin Morgan and his supervisor Dr. Louise Egerton-Warburton developed a new technique capable of detecting the rarer fungal species in a community, paving the way for future insights into how they might vary in response to environmental changes. Their results are published in a recent issue of *Applications in Plant Sciences*.

Morgan and Egerton-Warburton built on recent advances in the characterization of arbuscular mycorrhizal communities by adapting proven fungus-specific DNA sequencing tools for use with state-of-the-art technologies. They added a "barcode" tag to the primers, molecules that bind to the DNA, to allow them to be used with extremely sensitive

high-throughput DNA sequencing equipment to detect rarer species.

The researchers used this new approach to analyze soil and root samples from two forests in the Yucatán Peninsula, Mexico, revealing one of the highest levels of species richness recorded to date. They identified 2,213 "operational taxonomic units" (OTUs), which represent either separate species or genetically variable individuals from a smaller set of species. The arbuscular mycorrhizal fungal communities were dominated by a small number of very common fungi; just 22 OTUs accounted for 89% of the DNA sequences identified in the study. Morgan elaborates, "The large number of well-supported OTUs was surprising, and likely reflects the increased sensitivity of this approach and its ability to capture rare taxa that would be easily overlooked in spore-based community assays and other sequencing approaches."

The researchers were also intrigued by the differences they detected between the fungal communities of the two study sites, which have very similar plant communities and are only 50 miles apart. Soil alkalinity and the levels of nitrogen and phosphorus in the soil resulted in certain groups of species being more common at one site or the other, with the differences being most pronounced in the rarer OTUs. Future studies are likely to reveal many more environmental interactions, explains Morgan: "This is really just a snapshot of two arbuscular mycorrhizal fungi communities. Given the tremendous importance of the wet/dry seasonality to the ecology of these systems, much more extensive seasonal resampling has been a primary goal of our follow-up to the currently published work".

Arbuscular mycorrhizal fungal systems play crucial roles in their environment, affecting the [plants](#) that can grow there and the nutrients that are stored and released from the soils. This study is a promising start to the expansion of our knowledge of these systems. Morgan continues, "It is very likely that global arbuscular molecular fungal diversity is

much higher than current estimates. Given their importance in shaping ecosystems, we're interested in learning more about these species and their possible functions, especially in communities that are likely to undergo significant change as a result of anthropogenic disturbances and climate change in the coming decades."

**More information:** Benjamin S. T. Morgan et al, Barcoded NS31/AML2 Primers for Sequencing of Arbuscular Mycorrhizal Communities in Environmental Samples, *Applications in Plant Sciences* (2017). [DOI: 10.3732/apps.1700017](https://doi.org/10.3732/apps.1700017)

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