

## Getting to the Root of Mycorrhizal Symbioses: Impact of Fungal Genomics on Mycorrhizal Research

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Within the plant microbiota, mycorrhizal fungi are striking examples of microorganisms playing crucial roles in nutrient acquisition. They have coevolved with their hosts since the raise of land plants and the recent development of calibrated phylogenies, linked with the growing understanding of fungal genomes, provides remarkable insights into the evolutionary histories of mycorrhizal symbioses. The comparison of 100+ genomes from mycorrhizal fungi, wood decayers, soil decomposers has revealed several independent lifestyle transitions from saprotrophism to mutualism in fungal lineages. In addition to reconstructing the evolution of mycorrhizal symbioses, our growing ability to use reference genomes for profiling differentially-expressed transcripts, for instance, is helping us to identify hundreds of symbiosis-related genes. Mycorrhizal genomics has thus chalked up some sweet victories. But when it comes to how genes shape the traits that matter most to us — from host specificity and nutrient efficiency to plant fitness and plant adaptation — the Age of Genomics underdelivers on actionable knowledge. We have an idea as to some of the genetic underpinnings in plants that render them susceptible to mutualistic fungi, but the molecular mechanisms that underlie the development and physiology of mycorrhizal symbioses have yet to be elucidated. Indeed, a molecular definition of the mycorrhizal symbioses remains a major challenge for the field. We now know what mycorrhizal fungi are present in a specific environment, we have 100+ of ecologically-relevant mycorrhizal reference genomes at our disposal, but are these data useful in furthering our goal of understanding how the mycorrhizal fungal community as a whole contributes toward ecosystem function?

The challenges facing our community include determining the mechanisms that regulate nutrient trade dynamics, as well as characterizing how perturbations of the recognition and accommodation systems influence plant responses, how metabolic responses are regulated in multiple symbiotic interactions and how the signaling pathways triggered by multiple microbial interactions are integrated by host cells. Using synthetic ecosystems constructed using specifically chosen plant and microbial combinations that are easily manipulated and for which we have genomic and molecular data is likely a promising avenue. We must work together as a community to set new research priorities to make meaningful advances in the coming years taking benefit from the Age of Genomics.

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