Advances in the Characterization of Soil and Root Arbuscular Mycorrhizal Communities and their Role in Sustainable Agriculture.

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Background:
Emerging knowledge on microbial communities associated with plants indicate that they define, to a significant extent, the life environment of the plant, affect growth and productivity parameters and are a key component to be considered in modern agriculture. Symbiotic associations between plants, microbes and fungi (especially Arbuscular Mycorrhizal Fungi, AMF) provide the plant partner with benefits ranging from enhanced access to nutrients and water, to enhanced protection against pathogens. As we are moving towards a more sustainable agriculture, based on the optimal use of resources, we need to identify the exact components of the microbial community of the soil and root and the mechanisms that contribute to the beneficial effects observed on the plants. What species and what functional features of microbial communities play a role in plant productivity and how can our practices select for these features in the field?

Project Overview:
We aim to characterize the AMF community associated with roots and soil both quantitatively (fungal biomass) and qualitatively (species composition) in space and time throughout the growing season and to identify correlations to crop productivity (wheat) in an agricultural setting in Saskatchewan. We have designed a molecular tool for the quantification of fungal biomass from as little as 200 mg of fresh soil or root material. The tool makes use of a conserved region present exclusively in the mitochondrial genome of many AMF species but absent in other fungal species. As such, the method is specific to this fungal group of interest. Total DNA is extracted from the sample and subjected to real-time PCR amplification and quantification. The amount of target DNA detected in the sample is proportional to the amount of fungal biomass present. We have established standard curves for biomass and amount of target DNA for several AMF species and have validated the tool on in vitro experiments on five different species of AMF as well as in colonization experiments in the greenhouse, on leek plants. We are also surveying AMF biomass and species diversity in wheat roots and soil from a field experiment composed of four distinct fertilization regimes.

Conclusions:
We have optimized procedures for DNA extraction and have designed molecular-based markers for the quantification of AMF biomass in the soil and roots. Our technique can detect down to 1 to 5 spores of AMF or less than 5 ng of DNA per 500 mg of soil or roots and provide estimates of fungal biomass in a sample within a week. The technique is sensitive to the viability and metabolic activity of the fungus and as such can provide essential information about the status of the symbiosis in a particular root sample and provides real-time information about fungal biomass in the soil. We propose that this tool in combination with AMF community characterization may be used to measure the extent of AMF contribution to plant growth in the context of precise soil physico-chemical properties and fertilization regimes and to derive prediction tools for further crop management.

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