

Rhizosphere and Mycorrhizosphere Interactions

– Selection, Detection, Selectivity and Function

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ABSTRACT

Soil microorganisms (symbionts, saprotrophs & pathogens) are key determinants of soil fertility and plant health. Better understanding of the interactions of these microorganisms with each other and with plants is a prerequisite for the efficient, sustainable management of soil fertility and crop production. Although bacteria, pathogenic, saprotrophic and symbiotic fungi may exist in intimate association with each other and interact directly, they have traditionally been studied separately by separate groups of scientists, working within different research traditions.

The rhizosphere has been studied intensively since the term was first used by Hiltner in 1904 but the study of the mycorrhizosphere is still in its infancy. Symbiotic mycorrhizal hyphae provide the main direct route for carbon flow from plant roots to the soil microbial community, accounting for between 10 and 20 % of the total plant photosynthate in natural and semi-natural ecosystems. The surface area of these hyphae is the ultimate plant-soil interface, typically exceeding that of the roots by 1-3 orders of magnitude. These hyphae provide the main pathway for nutrient uptake from soils by plants. In conventional, intensive agriculture the biomass and functional importance of mycorrhizal associations is reduced by high fertiliser inputs, disturbance and agro-chemicals. However in low input, sustainable systems symbiotic mycorrhizal mycelia may play a crucial role in maintaining productivity by improving plant access to nutrients and water, reducing the negative impact of pathogens, and providing an important niche for plant growth promoting or other beneficial bacteria.

Different examples of rhizosphere and mycorrhizosphere interactions in both forest and agricultural systems will be examined. Many systems are characterised by high overall diversity and appropriate methods are sometimes required to enrich the relevant microbial populations and to examine the selective effects of different plants or mycorrhizal symbionts. New high throughput sequencing methods provide novel opportunities to examine the metagenomes or transcriptomes of different systems but relevant questions and appropriate temporal and spatial levels of sampling must be identified.

KEYWORDS: bacteria, carbon flow, fungi, mycorrhiza, mycorrhizosphere, rhizosphere