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MANAGEMENT OF THE BIOLOGICAL DIVERSITY OF AM FUNGI BY COMBINATION OF HOST PLANT SUCCESSION AND INTEGRITY OF EXTRARADICAL MYCELIUM

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Abstract text (max 250 words) :

Strategies are required for managing communities of indigenous arbuscular mycorrhizal fungi (AMF) associated with different host plants within agricultural cropping systems. In a non-sterilized soil, using 454 pyrosequencing of the LSU-D2 rDNA gene, host plant AMF diversity was assessed following successions of different plant species (*Ornithopus compressus* and *Trifolium subterraneum* as Fabaceae species and *Lolium rigidum* and *Triticum aestivum* as Poaceae species), grown with or without prior soil disturbance. When spores and colonised root fragments formed were the main propagules source (disturbed soil), the AMF communities present in the two legumes were clearly different from those of the two Poaceae members but were similar for plants within each family. Significantly wheat grown in undisturbed soil immediately after the legume *O. compressus* (extra radical mycelium (ERM) kept intact) acquired an AMF community closely related to that of the previous host plant, and different to that found when the soil was disturbed or not cropped prior to the growth of the wheat. Similar effects were seen in the succession from *L. rigidum* to *T. subterraneum*, indicating that these results are not unique to the legume-wheat sequence. These outcomes also suggest that, under no-till cropping, selected cover crops or crops in rotation could help building mycorrhizal communities that function throughout a sequence of several main crops. In a parallel experiment, symbiosis-related genes in wheat roots were differentially expressed according to the previous plant (*L. rigidum* or *O. compressus*) and the integrity of ERM, suggesting that the propagule type and composition of AMF communities affect the wheat response to AM symbioses.

References :

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