Abundance and diversity of AM fungal communities associated with agricultural factors

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Introduction

AM fungal communities live in a dynamic equilibrium set by host plants and the soil environment over time. Agricultural activities such as tillage, soil input, monoculture and annual plant could strongly affect indigenous AM fungi communities in many ways. For instance, regular tillage disturbs soil and destroyes AM fungal mycelium; P fertilization rates are negatively correlated with AM root colonization. In addition, monoculture could affects AM fungal diversity and composition and degrade the mycorrhizal potential of soils. In order to reveal the changes in AM fungal communities induced by agricultural management, we compared the AM fungal diversity in rhizosphere soil of fields planted with wheat and in that of adjacent stable plant communities of the roadside.

Method and material

We took 153 soil samples from wheat fields located across Saskatchewan and in part of southeast Alberta at the beginning of July 2009 or 2010. Each sample site locations was recorded by GPS. Rhizosphere soil in wheat fields and corresponding roadsides were taken and sieved through 2 mm and stored at -20°C until DNA extraction. Roadside vegetation was normally highly dominated by bromegrass (Bromus inermis Leyss.), but was diverse at some locations.

Total DNA were extracted with UltraClean® Soil DNA Isolation kit following the protocol of manufacturer. Primer pair AMV4.5/AMDGR with fusion adaptors and MIDs were used to amplify 18S rDNA. Target fragments (~300 bp) were analyzed on agarose gel.

PCR amplicons were submitted to Plant Biotechnology Institute (PBI, in Saskatoon, Saskatchewan, Canada) for 454 pyrosequencing after purification by ChargeSwitch® PCR Clean-Up kit.

Results

214,801 good AM fungal reads were generated from pyrosequencing (excluding reads shorter than 230 bp, longer than 300 bp, and rare sequences). Of these, 81,663 reads came from field soil

and 133,138 reads were from roadsides (Figure 1). Reads number in wheat field was only 61% that of roadsides.

A total of 169 operational taxonomic units (OTU) were calculated by Mothur (v.1.15.0). The taxonomic classification of a representative sequence of each OTU obtained by BLAST against GenBank is shown in Fig. 2. Seven OTUs where dominant in wheat fields; they accounted for 49.9% of all reads. Roadsides were more diverse. Some AM fungal OTUs were specific to roadsides, but others were quite specific to wheat fields; and there were also generalists. AM fungi resembling *Claroideoglomus lamellosum* and *Funneliformis mosseae* were by far the most represented OTUs in both field and roadside soils (Figure 2). OTU149 (94% similar to *Glomus iranicum*), OTU160 (99% similar to *Glomus hoi*), OTU41 (95% similar to *C. lamellosum*), OTU90 (99% similar to *Rhizophagus vesiculiferus*), OTU95 (97% similar to *Glomus constrictum*), and OTU162 (97% similar to *Glomus macrocarpum*) were uncommon in field soil but abundant in roadsides. OUT 131, an uncultured Glomus, was specialized in cultivated fields (Figure 2).

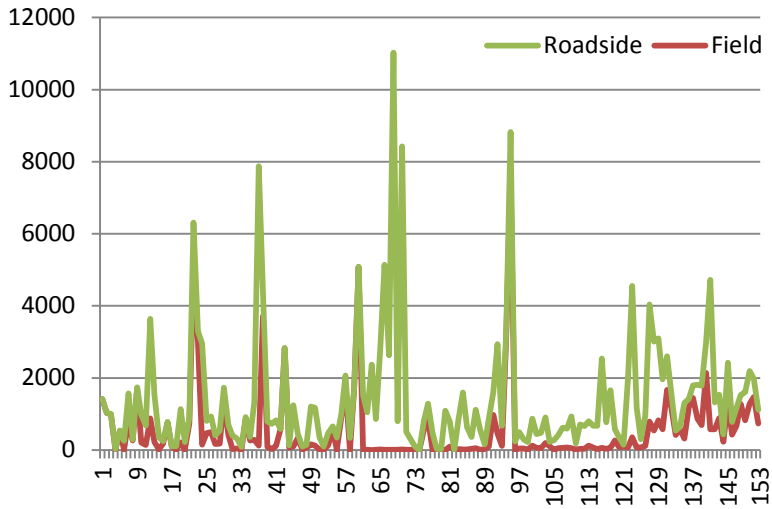

Figure 1. Relative abundance of AM fungi in the wheat fields surveyed and corresponding roadsides, as indicated by the number of 454 pyrosequencing reads.

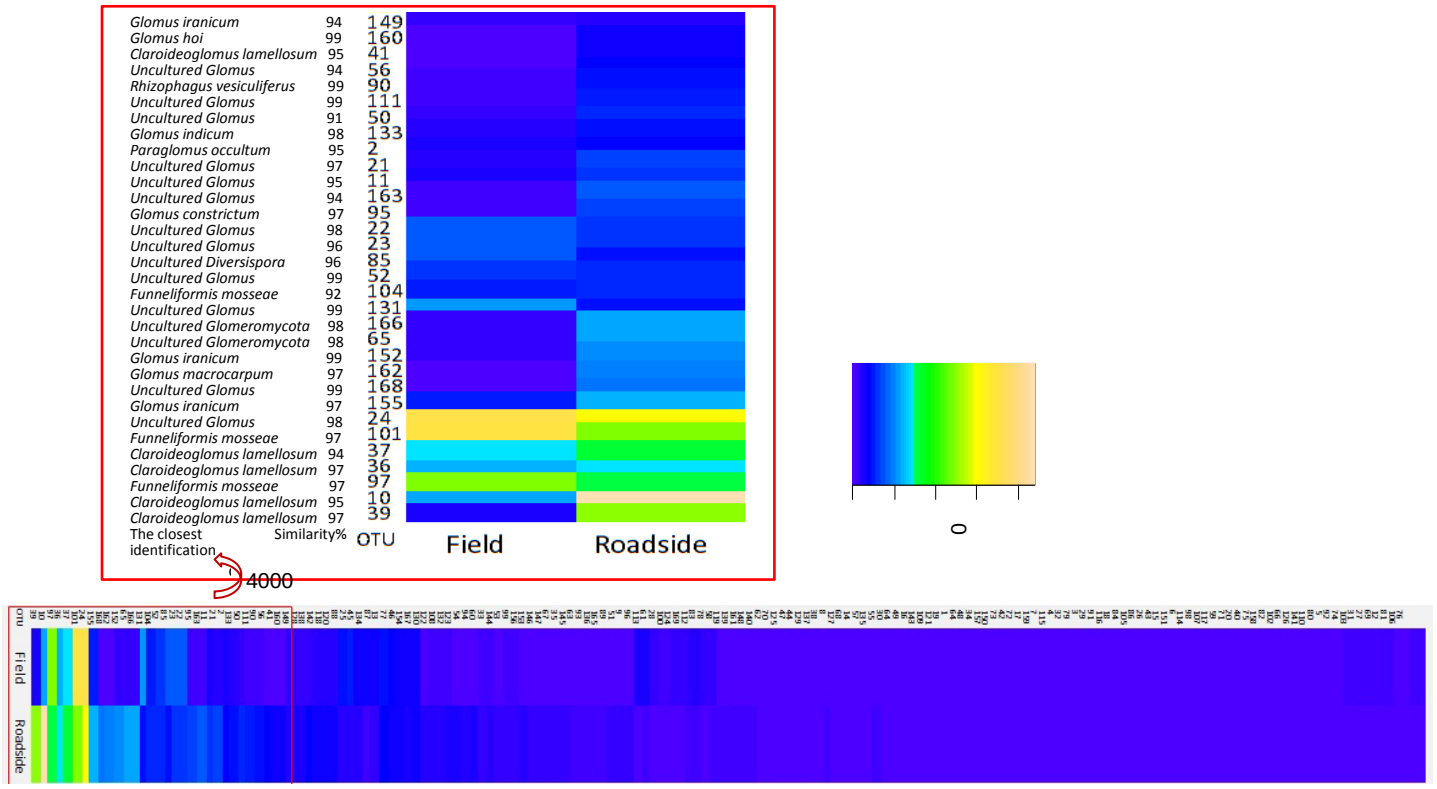

Figure 2. Diversity of AM fungal community disclosed by OTUs (3% dissimilarity) and their richness was colored as a heatmap. Colours from purple to orange show increasing read abundance. The section of the heatmap with dominant AM fungal OTUs was enlarged and rotated 90° in red box to show the identification and similarity level obtained from BLAST in GenBank.

Conclusion

Agriculture importantly modified and impoverished AM fungal communities compared to corresponding more stable roadside ecosystems.

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