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Can diversified cropping systems shape maize rhizosphere microbiomes towards more robust, interconnected communities?

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We have little insight into whether differences in agricultural management and the forms of fertilization affect the recruitment and metabolic activities of the root-associated microbiome over the course of plant development. We investigated these questions in two contrasting cropping systems; a conventional (two-year rotation, inorganic fertilization) and a diversified (four-year rotation, manure amendments) system. Despite large differences in management, diversified cropping systems can be as productive as conventional systems, reduce N losses to ground-water, and promote retention of C and N. These documented ecosystem services allow us to explore how agricultural management affects the coupling between microbial communities and plant roots, and how this interaction may factor into increased nitrogen use efficiency. In this study, we examined prokaryotic and fungal communities of the maize root-associated microbiome at various maize developmental stages with varying predicted N demand in the field and laboratory. We show that root-associated prokaryotic and fungal community composition shifts significantly over the course of plant development in a cropping-system specific manner. Moreover, total resident (DNA-based) and metabolically active (rRNA-based) community profiling indicates prokaryotic species richness and the number of differentially abundant taxa is greater in diversified systems, but in a manner influenced by proximity to the root. Co-occurrence analysis suggest diversified cropping system prokaryotic communities exhibit more robust and efficient networks as they generally have more nodes with greater connectivity (links). It is unclear whether the similarity between rhizosphere and bulk soil prokaryotic communities and greater interconnectedness contributes to the crop yield benefit and reduced N losses in the diversified system.