



Analysis of microbial diversity and niche in rhizosphere soil of healthy and diseased cotton at the flowering stage in southern Xinjiang

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ABSTRACT. Understanding how microbial community composition and diversity respond to continuous cropping obstacle is not well understood. However, determining the community composition *vs* assessing the diversity of molecular operational taxonomic units is often difficult. In this study, we focused on the microbial diversity and niche differentiation in rhizosphere soils between healthy and diseased cotton using a molecular approach based on a culture-independent method. A total of 124 operational taxonomic units (OTUs) from 1076 DNA fragments were detected, including 46, 57, and 21 OTUs from fungi, bacteria, and actinomycetes, respectively. The identified OTUs were confirmed by sequencing after polymerase chain reaction-restriction

fragment length polymorphism analysis. The number of OTUs from *Fusarium* species in diseased rhizosphere soils was higher than that in healthy rhizosphere, which was consistent with field observations. Overall, the results showed that microbes in healthy rhizosphere soils were more diverse and occupied a wider niche in the healthy rhizosphere soil environment of the cotton field. Beneficial microbes should further be analyzed in studies examining the soil ecology of fields in which continuous cropping of cotton takes place.

Key words: Cotton; Continuous cropping; Culture-independent methods; Microbial communities