



Chronic fertilization of 37 years alters the phylogenetic structure of soil arbuscular mycorrhizal fungi in Chinese Mollisols

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Arbuscular mycorrhizal fungi (AMF) play vital roles in sustaining soil productivity and plant communities. However, adaption and differentiation of AMF in response to commonly used fertilization remain poorly understood. In this study, we showed that the AMF community assembly was primarily driven by soil physiochemical changes associated with chronic inorganic and organic fertilization of 37 years in Mollisols. High-throughput sequencing indicated that inorganic fertilizer negatively affected AMF diversity and richness, implying a reduction of mutualism in plant–AMF symbiosis; however, a reverse trend was observed for the application of inorganic fertilizer combined with manure. With regards to AMF community, order Glomerales was dominant, but the community composition varied significantly among different fertilization treatments. All fertilization treatments decreased family Glomeraceae and genus *Funneliformis*, while *Rhizophagus* abundance increased. Plant-growth-promoting-microorganisms of family *Claroideoglomeraceae* and genus *Claroideoglossus* were stimulated by manure application, and likely resulted in positive effects on pathogen suppression and phosphorus (P) acquisition. Family *Gigasporaceae* and genus *Gigaspora* were negatively correlated with available P in soil. Redundancy analysis further suggested that soil available P, organic matter and pH were the most important factors in shaping AMF community composition. These results provide strong evidence for niche differentiation of phylogenetically distinct AMF populations under different fertilization regimes. Manure likely contributes to restoration and maintenance of plant–AMF symbiosis, and the balanced fertilization would favor the growth of beneficial AMF communities as one optimized management in support of sustainable agriculture in Mollisols.