

EGU22-6868

<https://doi.org/10.5194/egusphere-egu22-6868>

EGU General Assembly 2022

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Variation in soil microbial communities following vegetation restoration in a Rare Earth Elements Mine area

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Rare earth elements (REEs) exploitation has led to severe soil degradation in Southern China. Revegetation is a promising way to minimize the negative environmental impact of abandoned REEs mine tailings. However, little is known about how soil microbial communities respond to the vegetation restoration in degraded REEs mine lands, although much research has emphasized their important roles in ecological restoration. Here, we evaluated soil nutrients, microbial community structure and enzyme activities in both surface and deep soils where vegetation restoration was implemented using arbor-shrub-grass pattern for 9 years. Our results showed that vegetation restoration have significantly altered the diversity, structure and co-occurrence patterns of microbial community, especially in surface soil. The bacterial phyla Proteobacteria, Actinobacteria, and Acidobacteria were more abundant at the restored site than at the unrestored site. Potential plant growth promoting bacteria (PGPB) were identified by comparing 16S sequences against a self-constructed PGPB database via BLAST, and it was found that the abundance of nutrient (e.g. P, N and Fe) accumulating-bacteria was greater, but the abundance of ACC deaminase-producing bacteria was lower at the restored site than at the unrestored site. This provides evidence for the potential role of plant beneficial bacteria in improving the performance of vegetation restoration in degraded mine lands.