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## **Explicating potential soil development of reclaimed farmlands using the molecular ecological network analysis in mining disturbed area, East China**

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Understanding the interactions among different soil microbial species and how they responded to reclamation is essential to ecological restoration and the land development. In this study, we investigated the bacterial distribution in different reclamation sites and constructed molecular ecological networks to reveal the interactions among soil bacterial communities along the reclamation timeline. The relationship between the microbial network module and environmental factors were also analyzed. Bacterial community diversity and composition changed dramatically along the reclamation timeline. PCA and NMDS analysis showed the microbial distribution patterns varied along the reclamation years. Additionally, based on the network profile, phyla Acidobacteria, Planctomycetes and Proteobacteria were distinguished as the key microbial populations in most reclamation sites. Moreover, different network structures were significantly correlated with different soil properties, such as pH value, soil organic matter, soil dehydrogenase and urease activity, which implied that microbial network interactions might influence the soil ecological functions. The variation of the network complexity along the reclamation years revealed that the microbial development and the persistent agricultural utilization promoted the land development of the reclaimed soil in disturbed mining area. Overall, our findings could provide some information of how microorganisms changed along the increasing reclamation time, and how they responded to reclamation activity by regulating their interactions in different ecosystems.