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Molecular ecological network complexity drives stand resilience of soil bacteria to mining disturbances among typical damaged ecosystems in China

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Understanding the interactions among different soil microbial species and how they responded to disturbances are essential to ecological restoration and resilience in the damaged mining areas. This information, however, remains unclear and poorly understood. In this study, we investigated the bacterial distribution in disturbed mining areas across three provinces of China, and constructed molecular ecological networks to reveal the interactions among soil bacterial communities. Furthermore, we examined the relationship between the microbial network topology and environmental factors to show if there is a correlation between the resilience of bacterial community and external pressure. Bacterial community composition differed dramatically among the different disturbed mining areas, and bacterial diversity decreased as microbial networks became more complex. Additionally, based on the network topology, we distinguished key microbial populations among the different mining areas, such as Proteobacteria, Acidobacteria, Actinobacteria, and Chloroflexi. Moreover, the network structure was significantly correlated with soil properties (e.g., pH value, electrical conductivity value, and available phosphorus value), which suggested that microbial network interactions might change the soil resilience, then affect soil ecosystem functions. Overall, our findings provided insight into the ways in which microorganisms responded to mining activities and change the resilience by regulating their interactions in different ecosystems.