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Diversity-triggered deterministic bacterial assembly constrains community functions

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A growing body of evidence suggests that microbial α -diversity (local species richness) may have positive effects on ecosystem function. However, less attention has been paid to β -diversity (the variation among local microbial assemblages). Here we studied the impact of microbial α -diversity on stochastic/deterministic microbial community assembly processes, which are related to β -diversity, and the consequences for community function. Bacterial communities differing in α -diversity were generated and their structures and potential community functional traits were inferred from DNA sequencing. Phylogenetic null modeling analysis suggests that stochastic assembly processes are dominant in high-diversity communities. However, in low-diversity communities, deterministic assembly processes are dominant, associating with the reduction of specialized functions that are correlated with specific bacterial taxa. Overall, we suggest that the low-diversity-induced deterministic community assembly processes may constrain community functions, highlighting the potential roles of specialized functions in community assembly and in generating and sustaining the function of soil ecosystems.

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