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Manipulating soil microbial communities to unravel biotic interactions

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Abstract:

The importance of microbial communities and the complex functional roles they perform is becoming increasingly evident. Yet, we know little about the ecological processes driving the assembly of these communities in the environment. In this context, our objectives were to unravel how biotic interactions within complex microbial communities determine microbial community assembly and functioning. For building a predictive understanding of community assembly, we used a manipulation approach to remove or enrich targeted groups in a soil microbial community. Soil suspensions were either subjected to antibiotic, antimicrobial peptide, heat or osmotic shock as well as directed enrichment treatments before being inoculated in a total of 325 sterile soil microcosms (n=25). Interactions between microbial taxa were evidenced 45 days after recolonization of the sterilized soils by sequencing the bacterial 16S rRNA gene and the fungal ITS region using Illumina Miseq sequencing. Causal effects of microbial community manipulations for soil functioning were assessed by measuring a range of activities related to C and N cycling. A model-based biclustering approach allowed the identification of strong associations between specific microbial groups and applied treatments. We also identified keystone species conserved between the different treatments using comparative analysis of OTU-based co-occurrence networks. Large differences in community composition were related to changes in C and N cycling. By explicitly testing biotic interactions using a manipulation approach, this study provides insights into the role of interactions between bacterial taxa in the assembly of soil microbial communities.