
Bacterial "social" network in French soils: a Metagenomics insight.

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Abstract

High-throughput sequencing technologies evidenced that soil houses a huge microbial biodiversity. Based on these observations, it is now possible to better describe the spatial distribution of soil microbial communities, to study the ecological processes lying behind (environmental selection, dispersal limitations), and to mine the data to define the ecological attributes of soil microbial taxa. These huge datasets also offer the opportunity to study how soil microbial populations are interrelated.

The objective of this study was to design the first bacterial "social" network in French soils, to characterize how bacterial taxa are potentially related to one-another. To do so, the bacterial community composition was characterized for the 2,200 soils of the French Soil Quality Monitoring Network using 454-pyrosequencing based on 16S rRNA genes directly amplified from soil DNA. Bacterial taxa were then identified based on SILVA database. The bacterial "social" network was designed by means of a network analysis. First results at the phylum level demonstrate that the soil bacterial "social" network is highly complex (density 0.585), with different relationships between bacterial phyla (positive/negative, strong/weak). This complexity is determined both by biotic relationships between bacterial phyla and by environmental conditions. Indeed, soil bacterial "social" networks from different ecosystem types did not have the same complexity (density gradient: forests (0.440), grasslands (0.375), croplands (0.346), vineyards (0.021)).

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Understanding these relationships represents a cornerstone of soil microbial ecology to go further in understanding ecological processes shaping soil microbial communities; and to identify land-use practices preserving soil bacterial "social" network complexity.

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