



Soil aggregates as habitats for different microbial functional communities: Impact of different aggregate sizes and land-use

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Soil is a complex environment containing a huge diversity of microhabitats. This diversity of microhabitats can be taken into consideration when studying soil microbial communities by investigating soil aggregates as specific soil compartments. However, there is still an intense debate about the potential role of soil aggregates in structuring microbial communities. Thus, the aim of this study was to investigate the geochemical conditions and abundance of microbial communities among soil aggregates.

Four different field sites with contrasting land-use (e.g. grassland, cropland, forest) were sampled from Critical Zone Observatory Fuchsenbigl/Marchfeld near Vienna (Austria). Aggregates of six different size classes were obtained by dry-sieving (0-0.25, 0.25-0.5, 0.5-1.0, 1-2, 2-5, 5-10 mm), and characterized geochemically. Quantitative-PCR (Q-PCR) was used to investigate the abundance of bacteria, archaea and fungi, and indicator genes for functional guilds like N-fixation, denitrification, metal reduction, sulphate reduction, and methanogenesis.

The Q-PCR results showed that different land-use had significantly different abundances for all the genes, with the cropland site showing the lowest abundance for most of the genes. In contrast, fewer differences were found in gene abundance between the different sizes of soil aggregates, with no specific trends across all the genes, but significant differences related to individual genes and land-use.