Combining geochemical and high-throughput sequencing methods for evaluating the distribution and impact of single and multi-metal pollutions at the soil aggregate scale

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Trace metals, especially in mixtures, can disturb and modify the competitive balance between microorganism species in soils, which in turn induce modifications of biogeochemical cycles (C, N, P...). Soils are spatially heterogeneous environments structured in aggregates of different sizes. Similarly to microorganisms, metals present heterogeneous and specific distribution patterns among these micro-aggregates. The objective of this work was better understand the spatial impact of heavy metals (Cu-Cd-Cr) on soil microbial communities, according to their respective distribution within the different soil microhabitats, and the temporal evolution of microbial communities structure in response to the multi-metal pollution. By applying a high-throughput sequencing approach we studied the restructuring action of a Cu-Cd-Cr contamination on the microbial community of a grassland-soil at the microaggregate-scale. The soil was contaminated with equitoxic concentrations of Cu, Cd and Cr, alone or mixed and regularly physically fractionated (2-64 days). The bulk soil and the size-fractions were analyzed for mass balance, free, soluble and total metals contents and soil properties (pH, Eh, OC and N contents). Microbial biomass, and bacterial density/diversity were measured (16SrDNA rtPCR and Miseq sequencing,). This study provides a new vision of soil bacterial community structure. It opens the way for the detection and identification of rare taxa and potential new bio-indicators of soil health.