

Linking Microbial Community Structure to Spatial and Vertical Variation of Soil Biogeochemical Properties

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To better understand biogeochemical processes affecting the fate of contaminants in subsurface environments, high-resolution site characterization (HRSC) research was performed in a test-bed site (100 m x 60 m) formerly used as a farm land for several decades. Total 72 soil samples were collected from three depths (10-40, 80-110, and 160-190 cm). The results of 16S rRNA gene sequencing showed that 68 different phylum-level lineages were present in soils. Microbial diversity in soils significantly decreased with depth. Chloroflexi increased with depth, while Proteobacteria and Acidobacteria decreased with depth. The shared genera at three depths only accounted for 8% of the bacterial community suggesting that each soil layer contained distinct microbial communities. The results also well correlated with toxic metal concentrations and other physical and chemical properties in soils. Water content, As, Ni, and Pb, significantly increased with depth, but soil pH, bacterial population, nitrate, Cd, Cu, Zn and bioavailable iron (0.5N HCl extractable iron) decreased with depth. Hierarchical cluster analysis indicated that for the top soil layer, the first cluster contained Cr, Ni, Cu, Pb, As, and Zn, while the second cluster included Cd, nitrate, water content, bacterial numbers, and soil pH. For the mid soil layer, the first cluster contained Pb, Cu, and Zn. For the bottom soil layer, the first cluster contained Ni, Zn, Cr, Cu, and water. The results suggest that the distinct microbial communities and their associated metabolic activity in three soil layers at the site are tightly linked to the physical and geochemical variables, and subsequently influences on the distribution of metals and nitrate.