

Redox gradient shapes the chemical composition of peatland microbial communities

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The response of soil carbon to climate change and anthropogenic forcing depends on the relationship between the physicochemical variables of the environment and microbial communities. In anoxic soils that store large amounts of organic carbon, it can be hypothesized that the low amount of catabolic energy available leads microbial organisms to minimize the energy costs of biosynthesis, which may shape the composition of microbial communities. To test this hypothesis, thermodynamic modeling was used to assess the link between redox gradients in the ombrotrophic peatland of the Marcell Experimental Forest (Minnesota, USA) and the chemical and taxonomic composition of microbial communities.

The average amino acid composition of community-level proteins, called hereafter model proteins, was calculated from shotgun metagenomic sequencing. The carbon oxidation state of model proteins decreases linearly from -0.14 at 10 cm depth to -0.17 at 150 cm depth. Calculating equilibrium activities of model proteins for a wide range of chemical conditions allows identifying the redox potential of maximum chemical activity. Consistent with redox measurements across peat soils, this model Eh decreases logarithmically from an average value of 300 mV at 10 cm depth, close to the stability domain of goethite relative to Fe^{2+} , to an average value of -200 mV at 150 cm, within the stability domain of CH_4 relative to CO_2 . The correlation identified between the taxonomic abundance and the carbon oxidation state of model proteins enables predicting the evolution of taxonomic abundance as a function of model Eh. The model taxonomic abundance is consistent with the measured gene and taxonomic abundance, which evolves from aerobic bacteria at the surface including Acidobacteria, Proteobacteria, and Verrucomicrobia, to anaerobes at depth dominated by Crenarchaeota.

These results indicate that the thermodynamic forcing imposed by redox gradient across peat soils shapes both the chemical and taxonomic composition of microbial communities. By providing a mechanistic understanding of the relationship between microbial community and environmental conditions, this work sheds new light on the mechanisms that govern soil microbial life and opens up prospects for predicting geochemical and microbial evolution in changing environments.

