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ABSTRACT TITLE: Toward a predictive understanding of microbial carbon turnover in a northern peatland.

ABSTRACT: Global peatlands sequester one-third of all soil carbon and currently act as major sinks of atmospheric CO₂. The goal of this project is to investigate changes in the lability of soil organic matter and the composition of decomposer microbial communities in response to the climatic forcing of environmental processes that determine carbon storage and sequestration in peatlands. A combination of cutting-edge analytical chemistry approaches and next generation sequencing of microbial genes has been applied to bog and fen habitats in the Marcell Experimental Forest (MEF), northern Minnesota. Chemical and spectroscopic analyses of soil organic matter (SOM) in the solid phase peat from different sites throughout the MEF identified three distinct zones within the peat core each with unique properties: (1) a poorly decomposed surface portion; (2) a more decomposed middle section and (3) a more homogeneous and constant lower section. Solid phase FT IR, ¹³C NMR and ³¹P NMR spectroscopy data indicated shifts in abundance of different classes of compounds within each zone. Ultrahigh resolution (UHR) mass spectrometry and PARAFAC modeled 3-D excitation-emission matrix [EEM] fluorescence spectroscopy were used to identify the reactive and refractory dissolved organic matter (DOM) pools with depth in peat porewaters at each site. Radiocarbon signatures of microbial respiration products (dissolved inorganic carbon, DIC; CH₄) more closely resemble that of DOM rather than solid peat, indicating that carbon from recent photosynthate is fueling the majority of the decomposition. Microbial community structure, genes encoding plant polymer-degrading enzymes, properties of DOM, and numerous other variables show strong vertical stratification patterns. Surface peat, characterized by high DOC concentrations and relatively low aromaticity, harbored diverse and abundant bacteria and fungi. Bacterial communities were dominated by the Acidobacteria, Verrucomicrobia, and Proteobacteria phyla. The majority of phenol oxidase genes are assigned to Acidobacteria and Proteobacteria. In more decomposed and anoxic layers at 30-50 cm depth, anaerobic metabolic pathways and fractions of methanogens and syntrophic fermenters became elevated. The abundance of fungi as determined by qPCR of rRNA genes attenuates more rapidly with depth than do other domains, leading to bacterial and then archaeal dominance with depth below the surface. All domains show elevated abundance in the subsurface below 50 cm depth in the fen compared to the bog. The relative abundance of archaea increased with depth. Below 75 cm, methanogens were progressively replaced by uncultivated Crenarchaeota lineages that accounted for up to 60% of the microbial community. The deeper peat shows a less dynamic microbial community, depressed exoenzymatic activity, and accumulation of more aromatic DOM compounds. Marked differences are observed in the active microbial community composition as determined from rRNA amplicon sequences in comparison to DNA-derived rRNA genes. Isotope mass balance indicates that processes other than methanogenesis (fermentation, anaerobic respiration) predominate in the deep peat leading to dominance of CO₂ production at depth. A multivariate linear model identified quantity and quality of DOM and surface vegetation as most significant variables governing microbial community turnover spatially and seasonally, and pointed to the dominant microbial groups and metabolic pathways associated with carbon and nutrient cycling in the peatland.