

## Peatland topography influences microbial function at SPRUCE

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Microbial activities are central for modeling soil carbon (C) and nitrogen (N) cycling because microorganisms release extracellular enzymes to decompose soil organic matter (SOM) and produce bioavailable C and N. However, scaling microbial traits, such as biomass or enzyme potentials, is challenging, particularly in boreal wetlands, which are vulnerable to shifting climate, and spatially complex due to micro-topographic features. Characterizing spatial variability in microbial traits can improve our ability to detect and accurately scale microbial mechanisms that influence C and N cycling. To quantify the spatial variation and functional characteristics related to microbial decomposition of peat organic matter, we measured microbial traits along a micro-topographic gradient at the Spruce and Peatland Responses Under Climatic and Environmental Change Experimental (SPRUCE) site in the Marcell National Forest, Minnesota, USA. Fresh peat cores were collected from hummocks and hollows from 0 to 20 cm below hollow surface at the beginning (June) and the end (September) of the 2013 growing season. Fungal community composition, microbial biomass and potential extracellular enzyme activities were assayed at 10 cm increments. We found that depth and topography were central drivers of differences in microbial biomass and activity, while seasonality influenced fungal community membership. While the majority of microbial biomass resides in the surface of hummocks, at equivalent peat depths, microbial biomass was higher in hollows compared to hummocks, with greatest concentrations in September. Higher microbial biomass coincided with greater polypeptide-degrading enzymes in hollows in both June and September, while carbon cycling enzymes were greater in hollows only in September. Differences in enzyme activity were not supported by changes in fungal community composition (relative OTU abundance) across topography, depth, or season, suggesting that shifts in bacterial community composition or physiological responses may be driving differences in microbial function. Together these results demonstrate how consideration of micro-habitats within the peatland provides greater resolution for understanding the biological responses driving ecosystem scale biogeochemistry.