

Microtopographic controls on microbial community structure

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<https://www.anl.gov/bio/project/subsurface-biogeochemical-research> **Project Abstract:**

Wetlands are key features of watersheds that play an outsized role in affecting water quality because of their position within the landscape. The sharp and dynamic redox gradients typical of wetlands support a variety of microbial metabolisms and drive elemental transformations. Indeed, within wetland ecosystems even small changes in elevation can affect the local hydroperiod and alter the fate and transport of nutrients and contaminants. In this study, we examined the distribution of microbial taxa across microtopographic variation within the Tims Branch watershed on the Savannah River Site. Across the watershed, hydroperiod was an apparent driver of differences in microbial community composition. Microbial community composition aligned along this primary axis of variation, with lower elevation spots in the creek bed having the most dissimilar communities from higher elevation communities across all samples. Pit and mound microsites (formed when trees uproot) had distinct microbial communities, and these communities also varied by tree species. Further, local cm-scale heterogeneity in elevation at locations near the waterline resulted in differentiation of microbial community composition, with hummocks and hollows having consistently separable communities regardless of vegetation cover or position along Tims Branch. Considered together, these results suggest that fine scale variation in flooding regime and soil moisture can impact the structure of microbial communities and the functioning of watersheds.

We also examined the influence of contamination and disturbance (i.e. wild boar wallows) on microbial communities in this watershed. The effects of contamination and disturbance had a lesser effect. Microbial communities were mostly differentiated in response to disturbance, with communities that were different but overlapping in response to site contamination. While there were over 1,500 taxa that were unique to contaminated sites (of more than 20,000 taxa present in the communities from the contaminated sites), each of these taxa had low relative abundance. There was no effect of site contamination or disturbance on microbial diversity.