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Factors Governing Microbially-Mediated Geochemical Processes and Microbial Community Composition Across Watershed Ecosystem Compartments

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Microorganisms mediate virtually all geochemical cycles in the terrestrial near-surface. While the predominant transformations that community members can perform are expected to vary considerably with site-specific conditions, we do not know which factors are most important or how functions are distributed across landscapes. We are investigating the drivers for release and uptake of nutrients and other compound transformations across a watershed by subdividing the system into major compartments, three of which are being intensively studied. First, we identified four major vegetation types and are evaluating their distinct soil ecosystems in the upper reaches, mid watershed and lower reaches of the East River, Colorado. Results show significant variation in both microbial community composition and metabolic potential as a function of vegetation types and soil depths. Location in terms of watershed longitudinal position also exerts a significant impact on metabolic potential of microbial communities. We find that vegetation type and location are important determinants of nitrification and C1 metabolism while soil depth influences processes such as organohalide reduction, impacting fluxes of compounds across hillslopes, into riparian zone soils, and exports to the river. Second, we considered position on the hillslope as a control on microbial community structure and functions within the watershed. By analysis of soil and sub-soil communities, we show substantial variation with depth as well as some lateral variations, particularly associated with proximity to the East River. We found that the intersection of the hillslope and riparian zone at the floodplain is compositionally and functionally distinct from communities on the hillslope. Microbial communities in the floodplain soils are similar to those found throughout the soils of the riparian zone. Third, we intensively sampled three meander floodplains along the East River corridor to test for variation within the regions circled by the river and to compare them to each other. Gradients in community composition and metabolic potential occur within the soils flanking each meander. However, there are striking features shared by the meanders. Notably, certain strains of bacteria are consistently abundant across floodplains and play similar roles in biogeochemical cycling at each site. For instance, the capacity for sulfur metabolism seems persistent among organisms that are abundant across sites. Overall, the results have begun to elucidate which parameters are more and less important for shaping community composition and microbial capacities within the watershed. Additionally, this inventory of watershed microbial metabolic potential is being used to inform reaction networks in models across scales.