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The Link Between Microbial Community Composition and Organic Matter Transformations in a Laboratory System.

The carbon cycle in aquifer systems is poorly understood. In particular, the role of prokaryotic and eukaryotic microbes in the cycling of organic matter (OM) has not been well documented. The goal of this work was to utilize stable isotopes in combination with geochemical and microbial methods to study microbially-mediated OM transformations in aquifers and aquifer sediments. A laboratory flow-through column experiment was conducted with sediment collected from a pristine, shallow, coastal plain aquifer. The groundwater medium was amended with low levels of isotopically labeled nutrients,  $^{13}\text{C}$ -acetate and  $^{15}\text{N}$ -ammonium. At pre-determined time points, DNA, RNA, and relevant biomarkers were isolated from the sediment and groundwater. The labeled nucleic acids were separated from non-labeled nucleic acids by ultra-centrifugation and then sequenced to determine the composition of the actively-respiring microbial consortia. In parallel, the organic matter was analyzed by GC-MS and ESI-FT-ICR-MS. The incorporation of  $^{13}\text{C}$  and  $^{15}\text{N}$  was examined for both the aqueous phase and sediment bound microbial communities along with the dissolved and adsorbed OM. Analyzing both dissolved and adsorbed fractions enabled us to determine the relative importance of each on microbial activity and OM transformations. The incorporation of  $^{13}\text{C}$  and  $^{15}\text{N}$  allowed us to estimate residence times of different organic matter fractions and to answer fundamental questions about organic matter lability and microbial community dynamics in the subsurface environment.