The rate limiting step in biogenic coal bed methane production has been attributed to the predominantly recalcitrant composition of coal, making it difficult for bacteria to anaerobically break down into methanogenic substrates. The significance of different carbon (C) cycling pathways involved in the turnover of recalcitrant, terrestrial C under various redox conditions is still a topic of debate, and in fact, unknown C cycling metabolic pathways are still being discovered in sub-oxic and anoxic environments. Redox transitions exist along gradients of increasingly recalcitrant C in many environments, and subsurface environments represent a large reservoir of C. The Powder River Basin in southeastern Montana is a model environment for studying in situ redox gradients for terrestrial subsurface C and were selected to investigate i) the temporal and spatial variation in the microbial assemblage from four different coal seams with varying depth profiles, ii) the physicochemical controls that impact the turnover of recalcitrant coal to methane, and iii) the functional potential for hydrocarbon degradation under different sulfate concentrations. Similar to the methane-sulfate critical zone in marine habitats, the presented work highlights the crucial role sulfate has on microbial assemblages, methane production, and C consumption in shallow coal seams.

Given the accepted differences between groundwater and surface-associated communities of subsurface porous media, diffusive microbial samplers packed with native coal material were used to enhance the establishment of microbial communities that better re-capitulated in situ communities. The microbial community inhabiting low sulfate coal seams consisted of sequences indicative of syntrophic bacteria such as *Syntrophomonas* and *Hydrogenophaga* which have previously demonstrated degradation of polycyclic aromatic hydrocarbons (PAH) and coupled growth with hydrogenotrophic methanogens. The assemblages inhabiting high sulfate coal seams were comprised of methylotrophic methanogens and sulfate reducing bacteria. Methylotrophic methanogens are observed in methane producing coal seams that have intermediate levels of sulfate, suggesting an important transition role in early stage methanogenesis. Low sulfate microcosms experienced an increase in humic-like material and consumed more C compared to high sulfate conditions that demonstrated changes in more labile C, including amino acid-like molecules. Moreover, we used a highly curated anaerobic and aerobic hydrocarbon degradation (AnHyDeg and AromaDeg) and redox (nitrogen, sulfur, methane cycle) gene database and pipeline to analyze metagenomic samples that were obtained from three different coal beds that had increasing sulfate levels. While the functional potential for methanogenesis *(mcrA)* was detected in all metagenomes, the diversity and relative quantity of these genes was greater in the coal beds that contained methane. Of interest was a significantly greater percentage of aerobic hydrocarbon degradation genes (dioxygenases) from one of the methane-containing coal bed samples. These metabolic markers were identified in co-assembled metagenomes. These results provide an enhanced understanding of recalcitrant carbon turnover in the terrestrial subsurface under different redox conditions and the presumptive metabolic capacities involved in subsurface C turnover in relationship to biogenic CH4.