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Biogeochemical Conditions and Microbial Populations Linked to Biodegradation of Per- and Polyfluoroalkyl Substances in Soil and Sediment

MICHELLE M. LORAH[1], DENISE M. AKOB[1], CASSANDRA HARRIS[1], KE HE[2], LEE BLANEY[2], LARA SCHULTES[3], ELSIE SUNDERLAND[3] AND CHAD VECITIS[3]

[1]US Geological Survey
[2]University of Maryland, Baltimore County
[3]Harvard University

Presenting Author: mmlorah@usgs.gov

Per- and polyfluoroalkyl substances (PFAS) are widespread emerging contaminants with many source areas resulting from the use of aqueous film-forming foams (AFFFs) for hydrocarbon firefighting. Perfluorinated compounds, including perfluorooctanesulfonic acid (PFOS) and perfluorohexane sulfonic acid (PFHxS), are substantial components of legacy AFFFs and are also produced in the environment from degradation of polyfluorinated precursor compounds. Understanding of the biogeochemical conditions and microbial populations linked to PFAS degradation is lacking, especially for perfluorinated compounds that are believed to be resistant to biodegradation. We evaluated biodegradation and associated microbial communities in batch experiments using (1) aerobically incubated near-shore sediment that was amended with the precursor N-(3-dimethylaminopropan-1-yl)perfluoro-1-hexane-sulfonamide (PFHxSAm) and (2) anaerobically incubated soil that was amended with the perfluorinated compound PFOS.

Aerobic degradation of PFHxSAm occurred within 20 days and was associated with an increase in nitrate; and, after 13 days of incubation, accumulation of an intermediate polyfluoroalkyl compound occurred. PFHxSAm amendment resulted in pronounced differences in microbial community structure, with significant increases in several ammonia-oxidizing populations (*Proteobacteria*, *Nitrospirota*, and *Archaea*) indicating these taxa play a role in aerobic biodegradation of PFHxSAm. In anaerobic PFOS-amended experiments, a substantial decrease in total mass of PFOS was observed with the indigenous soil microbes, with and without addition of a known dehalogenating culture (WBC-2), compared to controls over the 45-day experiment. However, addition of the dehalogenating culture resulted in greater removal of PFOS (45 percent) than observed with only the indigenous soil microbes (29 percent). Mass balance of total fluorinated organics by total oxidizable precursor analyses indicated that most of the PFOS removed in the soil amended with the dehalogenating culture was completely defluorinated. The predominant change in the microbial populations linked to PFOS removal over time, however, was in the sulfate-reducers *Desulfosporosinus*, rather than in the known dehalorespirers in the culture. The results of our experiments indicate that relatively ubiquitous microbes carrying out metabolic functions of ammonia oxidation and sulfate reduction could be linked to PFAS degradation under environmentally relevant conditions. Additional research is needed to explore these microbial associations and the potential for enhanced degradation of PFOS with known dehalorespirers.