Biodegradation of Fluorotelomer-Based PFAS by Soil Cultures Enriched with Various Carbon Sources

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Background/Objectives. Fluorotelomer-based per- and polyfluoroalkyl substances (PFAS) such as 6:2 FTOH and 6:2 FTS are precursors to perfluoroalkyl acids (PFAAs) that are toxic and persistent in the environment. These precursors have also shown to be toxic to mammalian species and they are frequently detected in soils and/or groundwater of aqueous film forming foam (AFFF)-impacted sites. Previous studies have shown that different carbon source amendments promoted biodegradation of these precursors by 6:2 FTOH-degrading strains. However, studies on examining the effects of carbon sources on biodegradation of precursors by mixed cultures are limited. In this study, the biodegradation potential of fluorotelomer-based PFAS by soil microbial cultures that were enriched with a wide range of carbon sources - alcohols, alkanes, aromatics, and surfactants - were investigated.

Approach/Activities. Lab-scale sequencing batch reactors were operated at 1-day or 2-day solid retention time (SRT), depending on the amended carbon sources. A 1-day SRT was used for reactors receiving EtOH, 1-PrOH, 1-BuOH, phenol, cocamidopropyl betaine (CPB) while a 2-day SRT was used for reactors receiving hexane and octane. When the reactors reached quasi steady-state conditions (i.e., at least five times of its respective SRT), the cell suspensions were collected and then spiked with n:2 FTOH (n=4,6,8) to initiate FTOH biodegradation. Fluoride release and metabolite production were monitored. The ability of these cultures to use 6:2 FTS for cell growth was also examined under sulfur-free conditions. Target/non-target PFAS metabolite analysis and microbial community analysis were conducted and used to link between microbial community structures/functions to PFAS biodegradation, and to predict presumptive functional genes that might be responsible for PFAS degradation metabolite profiles.

Results/Lessons Learned. A trend was observed in which long chain-length alcohol-grown enrichments released higher fluoride as the chain length of n:2 FTOHs increased. 1-BuOH grown enrichment exhibited the highest released fluoride from n:2 FTOH. Alkane-, aromatic compound-, surfactant-grown enrichments were able to release fluoride from FTOH biodegradation but showed no significant differences. Compared to all the enrichment cultures, the EtOH enrichments released the least amounts of fluoride from the FTOH biodegradation. In terms of the degradation products of 6:2 FTOH, 1-BuOH, octane, and CPB enrichments showed highly diverse metabolite formation. Overall, the generally 1-BuOH-enriched cultures showed high FTOH degradation and might be explained by the highest microbial diversity observed in the microbial community and a highly dominant *Rhodococcus erythropolis*. This species is known to possess a large set of oxygenase enzymes that could participate in vast type of biodegradations. On-going research efforts are placed on evaluating 6:2 FTS degradation under sulfur-limited conditions by the corresponding enrichments through target and non-target PFAS analysis.