

## Characterizing PFAS-Degrading Microbial Communities in Environmental Samples Collected from a PFAS-Contaminated Site

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**Background/Objectives.** Per- and polyfluoroalkyl substances (PFAS) are synthetic chemicals of emerging concern that have recently attracted regulatory attention. A deeper understanding of the molecular mechanisms, governed by naturally abundant microorganisms, underlying the cleavage of the highly stable carbon-fluorine (C-F) bond is of growing importance for the development of efficient strategies for degrading fluorinated organic compounds. The current literature on PFAS removal via microbial degradation has had contradictory results and the biodegradation process of PFAS compounds has not been understood yet. The main goal of this work is to enrich microorganisms exhibiting the highest potential for per- and polyfluorinated alkyl substances (PFAS) transformation and degradation by performing an exploratory lab-based enrichment study using environmental samples from a PFAS-contaminated site. The outcomes of the proposed research will generate enrichment cultures containing microorganisms and enzymes involved in (co-) metabolic transformation of fluoroorganics, including PFAS.

**Approach/Activities.** Applying knowledge about the range of fluorinated compounds utilized by already known microbial strains, the most promising primary growth substrates have been selected to test co-metabolic degradation of selected PFAS (i.e., PFOS, PFOA etc.). The selection of primary substrates has been based on the extent of co-metabolic transformation of target PFAS, and the ease of monitoring their degradation. Analysis of free fluoride generated during the biodegradation process will be used to establish understanding on PFAS defluorination. The samples will be analyzed to determine parent PFAS compound and the PFAS transformation products generated in this co-metabolic process via ultra-performance liquid chromatography (UPLC)-high-resolution mass spectrometry (MS/MS) on a UPLC-Q Exactive Orbitrap mass spectrometer using proven methodologies.

**Results/Lessons Learned.** PFAS-degrading microbial consortia with a broad spectrum of microbial diversity responsible for potential degradation and/or defluorination of PFOA and AFFF compounds spiked to the microcosms will be subject to chemical and biological analyses. If microbial degradation occurs in the enrichments, the microorganism(s) will be identified and PFAS biodegradation pathways will be elaborated. These identified and isolated indigenous microbial species that are capable of degrading PFAS can be used for in situ PFAS degradation through bioaugmentation and biostimulation for PFAS-contaminated sites.