Proteomic Insights into Fungal-Mediated PFAS Precursor Biotransformations

Kshitija Shah, Yifan Gao, and Shaily Mahendra (Department of Civil and Environmental Engineering, University of California, Los Angeles, CA)
Glenn Nurwono and Junyoung O. Park (Department of Chemical & Biomolecular Engineering, University of California, Los Angeles, CA)
Vijaya Pandey, Adarsh Mayank, and James Wohlschlegel (Department of Biological Chemistry, University of California, Los Angeles, CA)

Background/Objectives. Per- and polyfluoroalkyl substances (PFAS) are extensively found in the environment due to their widespread use in industrial and consumer products. They are also categorized as emerging contaminants and are potential endocrine disruptors and carcinogens due to which a collective effort to identify PFAS degradation mechanisms is underway.

At AFFF-impacted sites, fungi are more frequently found in the vadose zones of soil. Some fungal isolates have been shown to bio-transform PFAS in Mahendra laboratory at UCLA. But the relevant enzymes and biochemical pathways are yet to be elucidated. The objectives of this work were to conduct a proteomics analysis to investigate PFAS biotransformation mechanisms.

Approach/Activities. A well-characterized strain of wood-decaying fungus was cultivated in defined growth medium containing 20 g/L glucose under aerobic conditions. Disappearance of 10 mg/L 6:2 FTS was measured in triplicate experimental flasks over 30 days. Abiotic, killed and PFAS free controls were also monitored simultaneously. The sample's pellet and supernatant were separated via centrifugation and the total protein content in both conditions was quantified using the Lowry assay. The pellets were washed with deionized water prior to freezing. The proteomics analysis was then conducted by the UCLA Proteomics Center through Mass Spectroscopy, and data analysis was performed using MaxQuant and enrichment analysis.

Results/Lessons Learned. Forty-seven oxidoreductases and eight peroxidases were differentially expressed in fungal secretome of fungi cultivated in PFAS exposed conditions as opposed to those grown in conditions without PFAS. Approximately 20 putative P450 proteins appeared to be candidates of interest among the intracellular protein components. Comprehensive data reporting their induction mechanisms and specific roles in PFAS biotransformation are still being characterized via proteomics enrichment analysis and will be presented at the conference. These results will be valuable in deepening our understanding of fungal transformation of PFAS precursors that have been proposed to not result in the production of terminal perfluoroalkyl acids.