Mycoremediation: Evaluating Fungal Metagenomics and Biofilm Association in PAH-contaminated Estuarine Sediments

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Overview: Polycyclic aromatic hydrocarbons (PAHs) are ubiquitous environmental contaminants, that enter the environment via natural and industrial processes. In sediment, microbes complexed within biofilms may be good targets for bioremediation of PAHs because of their resilience and cooperation. Fungi within biofilms may play an important role in initiating the degradation of high molecular weight PAHs, a current limitation for bacterial degradation. While most bioremediation strategies target basidiomycetes, our findings suggest that ascomycetes may be a more appropriate target community in soils with higher levels of PAH contamination.

Background/Objectives: PAHs are ubiquitous environmental contaminants, some of which are included in EPA's Priority Pollutant List for their carcinogenicity. In sediment, PAH degradation occurs via microbial catabolic processes. Engineered bioremediation strategies are designed to harness microbial capabilities, which are often more effective and economical approaches for removing complex contaminants, than physical removal processes. Biofilms are cooperative communities that are resilient to environmental stressors and facilitate the sharing of nutrients and exchange of genetic material. Fungi complexed within biofilms may employ extracellular enzymes to scavenge nutrients for the community. Focusing bioremediation strategies on fungi may be particularly useful for the degradation of high molecular weight PAHs, which are challenging compounds for bacteria.

Approach/Activities: Biofilms were collected from the sediment-water interface at four sites in the Elizabeth River, Virginia featuring low, medium, and high levels of PAH contamination. Biofilms were extracted from 3D-printed devices and isolated using culture media with various nutrient concentrations. Treatments were designed to target both bacterial and fungal communities assembled within biofilms. Microbial community composition between sites was analyzed using next-generation sequencing for 18S/ITS/16S gene regions. Two bacterial and one fungal strains were strategically selected to form a model biofilm for evaluation and manipulation. Biofilms were assessed for PAH-degradation capabilities through various screening methods, including treatment with PAHs detected in Elizabeth River sediments. These studies aim to evaluate whether co-cultured microbes complexed within a biofilm structure are more adept at degrading PAHs than planktonic forms.

Results/Lessons Learned: Fungal taxonomy correlated with changes in PAH profiles and concentrations at individual sites. For example, chytrids dominated soils with minimal PAH pollution, but lost their advantage to ascomycetes and basidiomycetes as pollutant levels increased, suggesting that the latter two fungal communities are more suitable biostimulation targets at sites with higher PAH concentrations. Further, this demonstrates that changes in microbial community structure can be used as an indicator of changing pollution conditions. Further analyses indicated that basidiomycetes, which are commonly studied for bioremediation, were less abundant and less diverse than ascomycetes in more heavily polluted soils.