

FUNCTIONAL CHARACTERIZATION AND COMPARATIVE METAGENOMICS OF INDIGENOUS BACTERIA ISOLATED FROM THE SAN JACINTO RIVER FOR BIODEGRADATION OF RECALCITRANT CHLORINATED AND NON-CHLORINATED AROMATIC WASTE

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Abstract: Partial submergence of two paper mill waste pits along the banks of the San Jacinto River (SJR) east of Houston, Texas has led to the accumulation and spread of polychlorinated dibenzo-p-dioxins and dibenzofurans (PCDDs/PCDFs) across this river system. The World Health Organization (WHO) classifies several PCDD and PCDF congeners as class 1 human carcinogens. Monitoring data shows that while PCDD/PCDF toxicity decreases sharply as you move downstream towards Galveston Bay (>5 ng/kg TEQ), sediment sampled from Bear Lake to the northwest as well as areas associated with the Houston Ship Channel to the southwest and southeast range from 20 ng/kg TEQ to as high as 85 ng/kg TEQ along Buffalo Bayou. At immediate risk are communities lying within three census tracts cited by the Texas Department of State Health Services for unknown elevated incidences of unusual cancers. We hypothesize that bacteria collected from SJR sediment are likely capable of degrading PCDDs/PCDFs and could be utilized in the bioremediation of these compounds as well as in pollution monitoring through the distribution of bacterial degradation activity and biomarkers. To test our hypotheses, soil from public parks and sediment from along the banks of the SJR was collected within the three census tracts located near the waste pits. Initial screenings of SJR sediment samples have yielded several bacterial strains including *Pseudomonas putida*, *Pseudomonas nitroreducens*, *Stenotrophomonas maltophilia*, *Enterobacter aerogenes*, *Raoultella ornithinolytica* and multiple species of *Klebsiella*. Isolated bacterial strains will be tested against PCDD/PCDF/biphenyl substrates and analyzed through GCMS to identify the best degraders. Environmental samples will be subjected to 16S rDNA and shotgun metagenomic analysis to compare their underlying bacterial populations and abundance of PCDD/PCDF degradation genes. Taken together, our preliminary results suggest that metabolically versatile pseudomonads and opportunistic human pathogens will be among the dominant contributors to PCDD/PCDF degradation in the SJR and could be utilized in bioremediation as well as pollution monitoring.

Keywords: Biphenyl, dioxin, environmental sampling, furan, metagenomics, whole genome sequencing