Microbial Community Structure in Eroding Crude Oil Asphalt and Emulsion in Shallow Marsh Embayments

William Coronel (wcoron1@lsu.edu), *Vijaikrishnah Elango* (velango@lsu.edu), and John Pardue (jpardue@lsu.edu) (Louisiana State University, Baton Rouge, LA)

Background/Objectives. Marshes impacted by the Macondo spill continue to erode, releasing crude oil in the form of a soft asphalt or emulsion to adjacent shallow embayments. This process moves highly weathered crude oil from an oxygen-limited marsh profile to comparatively high energy shallow open water systems where geochemical and microbiological conditions may promote additional weathering. Specifically, we hypothesize that the erosion process can accelerate biodegradation by moving crude oil asphalts and emulsions from a low energy anoxic environment in the marsh to a higher energy oxic environment in these shallow embayments.

Approach/Activities. Sediment cores were taken in summer 2017 across transects which bisect the boundary between a contaminated marsh and Barataria Bay in the vicinity of Bay Jimmy/Bay Batiste where significant oiling occurred on the marsh surface. Cores (30 cm) from the contaminated marsh, marsh edge and offshore (approximately 10 m from the marsh edge) were analyzed by GC-MS and weathering ratios constructed from 2- and 3-ring PAH compound series (C1-, C2-, C3- and C4-, alkylated naphthalene, phenanthrene, and dibenzothiophenes) and 4-ring PAH series (C1-, C2 and C3-chrysenes). Microbial populations were assessed using the Ilumina platform for MiSeq 16S rRNA protocols. Microbial community structure was evaluated by analysis of molecular variance test, non-parametric homogeneity of molecular variance test and linear discriminant analysis effect size.

Results/Lessons Learned. Total PAHs ranged from 200 to 1,200 µg/g sediment in cores samples from the contaminated marsh. Higher mass of total PAH was observed at a depth of 15 cm from the surface. In core sections from the marsh edge and off shore, measured PAHs were often below or close to our detection limit and total PAH concentrations ranged from 1 to 4 µg/g sediment. Quality analysis of Miseq data by mothur software produced 2.8M sequences for 43 core sections. Microbial diversity (inverse Simpson index) increased from marsh (18-71) to marsh edge (52-109) and was highest in the off shore sediments (23-189). Non-metric multidimensional scaling analysis revealed clustering of microbial communities from each location separately. Clustering microbial communities was statistical different based on homogeneity of molecular variance test between marsh sediments and marsh edge sediments ($p=0.003$) and marsh sediments vs. offshore sediments ($p=0.001$). However, clustering between marsh edge and offshore sediments were not statistically different ($p=0.519$). Data was normalized by subsampling 10,000 sequences and analysis by linear discriminant analysis of effect size of the communities revealed 410 OTUs (Operational Taxonomic Units) at statistically elevated levels in offshore sediments, followed by 366 OTUs in marsh edge sediments and 192 OTUs in marsh sediments. Change in microbial populations will be discussed in light of potential biodegradation of PAHs in offshore environments in the marsh.