## The impact of oil contamination on the geochemistry and microbiology of salt marsh sediment and seawater microcosms

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an effort to better understand the impact of the In Deepwater Horizon oil spill and future oil spills on the U.S. Gulf Coast, experiments were conducted to study the effect of oil contamination on the geochemistry and microbiology of salt marsh sediment and seawater microcosms. Salt marsh sediment and seawater samples were collected on the Gulf Coast of Alabama, near the town of Bayou la Batre. Microcosms consisting of 200 g sediment and 250 g seawater were constructed soon after sample collection, spiked with MC-252 oil, and incubated for 21 days. Duplicate sterile controls, with and without oil, and duplicate non-sterile controls without oil were also set up. Duplicate microcosms were sacrificed periodically, the solid phase and aqueous phase separated by centrifugation and filtration, and samples prepared for analysis. The aqueous phase inorganic chemistry was analyzed by ICP-OES and ion chromatography. The composition and concentrations of alkanes and PAHs in the sediments and the concentrations of dissolved inorganic nitrogen, phosphorous, and dissolved organic carbon were also characterized. Bacterial community responses to oil contamination were examined using the high-throughput 16S rRNA bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP) technology.

Analytical data reveal several interesting temporal trends. Changes in aqueous Fe and Mn concentrations resulted from microbially mediated redox reactions which transferred these metals from the sediment to solution. Over the course of the 21 day incubation, 54.6% of the total alkanes in the sediment was lost within the first six hours, and 71.5% was lost after 14 days. Total PAHs decreased by 90.1% within the first six hours, but did not show subsequent decreases. Analysis of the bacterial communities present in the experimental substrates showed that the 14 day oil-contaminated substrate exhibited positive detection of alkene hydroxylase (alkB), catechol 2,3-dioxygenase (C23DO) and biophenyl dioxygenase (bph) genes, but these genes were not detected in the non-oiled control substrate. The indigenous microbial communities quickly shifted their structure to accommodate organisms which can survive in the oil-contaminated environment.