

Population Dynamics Pre and Post Oil Metagenomic Analysis of Water and Soil from Beaches Affected by the BP Oil Spill

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The Estimates of 60,000 gallons of oil a day for 100+ days spilled into the Gulf of Mexico leaving thousands of square miles covered in crude oil. While visible damages are seen in wildlife populations and marine estuaries, the most damaging and significant affect is on the most basic level of the ecosystems: the bacterial and plankton populations.

We present results from the ultra high throughput sequencing of water and soil samples collected in Louisiana and Mississippi, before and during the appearance of oil, in order to estimate the changes in the microbial population. DNA from sixteen samples taken at approximately two week intervals from Grand Isle, LA and Gulfport, MS were sequenced using an Illumina GAIIx Genome Analyzer. Analysis of the genomic composition of the near-shore water and beach soil samples was performed using *de-novo* assembly and reference based search and base mapping approaches. The metagenomic composition of samples, suggest a significant loss in oxygen producing photosynthetic organisms, absence of aromatic oxidizers, and increases in anaerobic bacteria. Such changes are in agreement with reported decreases in the water oxygen levels. Significant fluctuations were observed in bacteria including a large spike in the human pathogen *Vibrio cholera* in the water samples from both locations. *Vibrio cholera* was among the most abundant bacteria in the June 14th sample in both water and soil samples from Grand Isle and to a lesser extent in Gulfport soil and water samples. In all cases, the *V. cholera* spiked in June and was very low in July. This suggests that the bacteria had a bloom seen in all four samples analyzed on June 14th. Other detectable genomes included *Vibrio parahaemolyticus* and *Vibrio vulnificus* all showing different patterns of abundance; *V. cholera* phage show an inverse relation to the appearance of the *V. cholera*.