

Bacteria ate some toxins, but worst remain, according to Gulf oil spill researcher

July 31 2014, by Kathleen Haughney

A Florida State University researcher found that bacteria in the Gulf of Mexico consumed many of the toxic components of the oil released during the Deepwater Horizon spill in the months after the spill, but not the most toxic contaminants.

In two new studies conducted in a deep sea plume, Assistant Professor Olivia Mason found a species of [bacteria](#) called Colwellia likely consumed gaseous hydrocarbons and perhaps benzene, toluene, ethylbenzene and xylene compounds that were released as part of the oil spill.

But, her research also showed that bacteria did not consume the most toxic parts of the oil spill in the water column plume or in the oil that settled on the seafloor.

The most toxic contaminants are called [polycyclic aromatic hydrocarbons](#) or PAHs. PAHs are a group of semi-volatile organic compounds that are present in crude oil and can cause long-term health problems such as cancer.

"Those PAHs could persist for a long time, particularly if they are buried in the ocean floor where lack of oxygen would slow PAH degradation by microorganisms," Mason said. "They're going to persist in the environment and have deleterious effects on whatever is living in the sediment."

When the Deepwater Horizon spill occurred, more than 4 million barrels of oil spilled into the Gulf of Mexico. Some of that oil has never been accounted for, and thus has unknown environmental and health consequences for the region.

Mason and colleagues investigated the [oil deposits](#) on 64 sediment samples in different areas around the oil wellhead.

To understand the functional capacity of the microorganisms to degrade oil, microbial DNA was sequenced in 14 of those samples. Of those 14, seven of the samples were so contaminated with PAHs that they exceeded the U.S. Environmental Protection Agency's water quality benchmarks for aquatic life.

Mason's first paper, which specifically examined how the bacteria ate—or didn't eat—toxins in the sediments, appeared in the *International Society for Microbial Ecology Journal*. The second, which focused on how and why the bacteria *Colwellia* flourished in the water column in the deep-sea plume, was published in *Frontiers in Microbiology*.

More information: "Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill." Olivia U Mason, et al. The *ISME Journal* (2014) 8, 1464–1475; [DOI: 10.1038/ismej.2013.254](#); published online 23 January 2014

The report, "Single-cell genomics reveals features of a *Colwellia* species that was dominant during the Deepwater Horizon oil spill," is available online: [journal.frontiersin.org/Journal/2014.00332/abstract](http://journal.frontiersin.org/Journal/2014/00332/abstract)

Provided by Florida State University

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