Assessing the environmental and public health impacts of the Deepwater Horizon oil spill is difficult owing to the extreme depth of the blowout and the large volumes of oil released. One strategy for remediation of the plume is to use the intrinsic bioremediation potential of deep-sea microorganisms to degrade the oil. This strategy depends on a number of environmental factors, including a favorable response of indigenous microorganisms to an increased concentration of hydrocarbons and/or dispersant. To study the effects of the spill, researchers collected deep-water samples from across the Gulf of Mexico and analyzed their physical, chemical, and microbiological properties using a variety of techniques, including synchrotron radiation Fourier-transform infrared (SR-FTIR) spectroscopy at ALS Beamline 1.4.3. The studies suggest that the plume did indeed stimulate indigenous deep-sea bacteria that are closely related to known petroleum degraders.

Seventeen deep-water samples were taken between May 25 and June 2, 2010, from across the Gulf of Mexico and analyzed their physical, chemical, and microbiological properties using a variety of techniques, including synchrotron radiation Fourier-transform infrared (SR-FTIR) spectroscopy at ALS Beamline 1.4.3. The studies suggest that the plume did indeed stimulate indigenous deep-sea bacteria that are closely related to known petroleum degraders.

Genetic analysis of in-plume samples revealed that, while cell densities were higher, taxonomic diversity was lower. The enriched bacteria were restricted to a few members of the γ-Proteobacteria subphylum, including psychrophilic and psychrotolerant (cold-water thriving or tolerant) species. Further cloning and sequencing revealed that the samples were dominated by the order Oceanospirillales, with the observed sequences falling into one of two distinct Oceanospirillales groups. One of these groups is largely composed of known psychrophilic hydrocarbon degraders and microorganisms from hydrocarbon-dominated environments, including Oleispira antarctica, Thalassotilus oleivorans [psychrophiles] and Oleiphilus messi...
Scanning electron micrographs of dominant bacteria collected in the plume (1099 to 1219 m deep). The dominant cell type exhibits a distinctive morphology typical of the Oceanospirillales order of Proteobacteria. Insets: Acridine orange stains of samples at two distances from the source.

Infrared images showing the spatial distribution of various oil and microbial products.