

The microbial response to the *Deepwater Horizon* deep-sea plume

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In 2010, the *Deepwater Horizon* spill discharged an unprecedented amount of gas and oil into deep-waters of the Gulf of Mexico (Gulf). Hydrocarbons formed a subsurface plume and accumulated at the sea surface. Large amounts of dispersants were applied to the surface oil slick and at the site of the leak. These perturbations substantially altered the Gulf's deep-sea water chemistry and microbial community.

Here, we demonstrate a remarkably rapid response of distinct microbial populations to the deep-sea hydrocarbon infusion. In-depth analysis using a highly sensitive, computational method applied to a spatial and temporal diverse marker gene data set, revealed a previously unrecognized level of diversity of key-players in oil and gas biodegradation. Furthermore, we mimicked oil infusions into Gulf's deep-waters using microcosms amended with either oil, dispersant, dispersed oil or dispersed oil with nutrients. Based on marker gene analysis of microcosm samples, we show that dispersants significantly influenced the microbial community composition, resulting in the selection of specific groups. Moreover, tracer experiments highlighted that dispersant impacts on hydrocarbon biodegradation rates are different than previously expected.