

Hydrocarbon biodegradation and bacterial succession in surface and seafloor pressure incubations

S.A. LINCOLN^{1*}, A.G. VALLADARES JUÁREZ²,
M. SCHEDLER², H.S. KADIMESETTY², R. MÜLLER²,
J.L. MACALADY¹ AND K.H. FREEMAN¹

¹Dept. of Geosciences, Penn State University, University Park, PA 16801 (*correspondence: slincoln@psu.edu)

²Institute of Technical Biocatalysis, Technical University Hamburg-Harburg, Hamburg, Germany

The 2010 Deepwater Horizon (DWH) blowout released ~4.1 billion barrels of oil into the Gulf of Mexico [1]. A significant fraction of the “residual” 22% of oil not depleted by natural processes or remediation strategies [2] reached marine sediments [3-4].

Understanding the long-term fate and impact of this oil on benthic communities is critical for informing remediation policies, but gaps in our knowledge of hydrocarbon biodegradation hinder this effort. In particular, how high hydrostatic pressures (~150 bars at the DWH site) impact biodegradation is unclear, and is increasingly salient as deep water drilling expands. Although early experiments showed that biodegradation proceeded more slowly at elevated pressures [5], most studies have been conducted at surface pressure, and their results may not be applicable to the deep ocean.

Here, we revisit this problem using Macondo oil and mixed microbial communities in Gulf of Mexico surface sediments collected near the DWH site. Sediment slurries amended with oil were incubated in pressure cells at 1 and 150 bars with continuous online measurement of O₂ and CO₂. We compare hydrocarbon concentrations and bacterial community composition (determined by rDNA amplicon sequencing) in samples collected at different stages of O₂ drawdown, putatively correlating to different growth phases of the community. These experiments enable us to evaluate potential differences in microbial community succession and the efficiency of hydrocarbon degradation at surface and DWH pressures.

[1] Zukunft, P.F. (2010). Operational science advisory team report. [2] Ramseur, J.L. (2010). Cong Res Serv: 1-20, R41531. [3] Montagna, P.A. *et al*, (2013). *PLOS One*. **8**, e70540. [4] Romero, I.C. *et al*, (2014). *Deep-sea Research II*, in review. [5] Schwarz *et al*, (1974). *Appl. Microbiol.* **28**, 982-986.