

Hydrobiogeochemical controls on a low-carbon emitting energy extraction mechanism: exploring methanogenic crude oil biodegradation

Jenna Shelton (1,2), Jennifer McIntosh (3,2), Denise Akob (4), John Spear (1), Peter Warwick (2), and John McCray (1)

(1) Department of Civil and Environmental Engineering, Colorado School of Mines, Golden, CO 80401 USA (jlshelton@usgs.gov), (2) Eastern Energy Resources Science Center, U.S. Geological Survey, Reston, VA 20192 USA, (3) Department of Hydrology and Atmospheric Sciences, University of Arizona, Tucson, AZ 85721 USA, (4) National Research Program, U.S. Geological Survey, Reston, VA 20192 USA

Exploiting naturally-occurring microbial communities in the deep subsurface could help mitigate the effects of CO_2 emissions to the atmosphere. These microbial communities, a combination of methanogens and syntrophic bacteria, can perform methanogenic crude oil biodegradation, namely the conversion of crude oil to natural gas, and have also been detected in biodegraded, methanogenic reservoirs. These microbes could target residual crude oil, a high-carbon, hard-to-obtain fossil fuel source, and convert it to natural gas, effectively "producing" a lower CO_2 per BTU fuel source. Yet, little is known about what geochemical parameters are driving microbial population dynamics in biodegraded, methanogenic oil reservoirs, and how the presence of specific microbial communities may impact methanogenic crude oil biodegradation. To investigate methanogenic crude oil biodegradation, 22 wells along a subsurface hydrogeochemical gradient in the southeastern USA were sampled for DNA analysis of the microbial community, and geochemical analysis of produced water and crude oil.

A statistical comparison of microbial community structure to formation fluid geochemical parameters, amount of crude oil biodegradation, and relative extent of methanogenesis revealed that relative degree of biodegradation (high, medium, or low), chloride concentration (550 mM to 2100 mM), well depth (393 m to 1588 m), and spatial location within the reservoir (i.e. oil field location) are the major drivers of microbial diversity. There was no statistical evidence for correlation between extent of methanogenesis and the subsurface community composition. Despite the dominance of methanogens in these sampled wells, methanogenic activity was not predicted solely based on the microbial community composition. Crude oil biodegradation, however, correlates with both communities associated with degree of crude oil biodegradation may not actually be statistically significant (dependent on formation water chemistry). Together, this suggests that a single microbial population is not indicative of a reservoir's ability to degrade crude oil to methane, and that formation water geochemistry may be a more important indicator for selecting a reservoir for the enhancement of natural gas generation than microbial community structure.