

Hydrocarbon Bioconversion to Methane by Crude Oil Reservoir-Associated Microbial Communities

LISA M. GIEG^{1*}, CAROLINA BERDUGO-CLAVIJO¹,
COURTNEY TOTH¹, JANE FOWLER¹
AND LISA OBERDING¹

¹University of Calgary, Department of Biological Sciences,
2500 University Drive NW, Calgary, AB T2N 1N4
(*correspondence: lmgieg@ucalgary.ca)

The microbial metabolism of hydrocarbons under methanogenic conditions is known to occur, but the microbial communities and pathways by which this process occurs in conventional crude oil reservoirs are poorly understood. Hydrocarbon methanogenesis has led to the generation of heavy oil over geological time but it remains unclear whether this process occurs in real time within reservoirs, a process that may find application in microbial enhanced energy recovery. We thus sought to determine whether reservoir-associated microbial communities have the potential to metabolize hydrocarbons. We enriched a microbial community from production waters of a conventional oil field using light crude oil as the sole substrate. Incubations were conducted as liquid cultures in serum bottles (planktonic system), as well as in sandstone-packed residual oil columns as model systems to simulate a marginal reservoir (sessile system). Hydrocarbon composition, methane production, anaerobic hydrocarbon metabolites and associated genes, and microbial community composition were assessed in the incubations. Substantial methane production was measured in both systems relative to controls, and hydrocarbon analysis revealed that over 50% of the *n*-alkanes and up to 50% of select PAHs were depleted. Alkylsuccinates indicative of C₅ and C₆ alkane degradation were detected at higher abundance in the oil-amended liquid cultures relative to controls. In accordance, the *assA* gene was detected. Microbial community analysis based on the 16S rRNA gene revealed a dramatic difference in the dominant bacteria when the culture was incubated planktonically or in a sessile system. While methanogens were prevalent in both systems, the liquid cultures were dominated by *Smithella* sp. often associated with methanogenic oil degradation, while the sessile cultures were dominated by bacteria known for their biofilm forming abilities (e.g., *Pseudomonas* and *Halomonas*). The results show that reservoir-associated microbes can potentially metabolize hydrocarbons to methane in real time, and also suggest that different organisms may carry out this process in different compartments (e.g., liquid or attached environments) within a subsurface crude oil reservoir.