Geophysical Research Abstracts
Vol. 12, EGU2010-14488, 2010
EGU General Assembly 2010

Microbial Physiology of the Conversion of Residual Oil to Methane: A Protein Prospective

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Abstract

Traditional petroleum recovery techniques are unable to extract the majority of oil in most petroliferous deposits. The recovery of even a fraction of residual hydrocarbon in conventional reserves could represent a substantive energy supply. To this end, the microbial conversion of residual oil to methane has gained increasing relevance in recent years [1,2]. Worldwide demand for methane is expected to increase through 2030 [3], as it is a cleaner-burning alternative to traditional fuels [4]. To investigate the microbial physiology of hydrocarbon-decomposition and ultimate methanogenesis, we initiated a two-pronged approach. First, a model alkane-degrading sulfate-reducing bacterium, Desulfoglaeba alkanexedens, was used to interrogate the predominant metabolic pathway(s) differentially expressed during growth on either n-decane or butyrate. A total of 81 proteins were differentially expressed during bacterial growth on butyrate, while 100 proteins were unique to the alkane-grown condition. Proteins related to alkylsuccinate synthase, or the homologous 1-methyl alkylsuccinate synthase, were identified only in the presence of the hydrocarbon. Secondly, we used a newly developed stable isotope probing technique [5] targeted towards proteins to monitor the flux of carbon through a residual oil-degrading bacterial consortium enriched from a gas-condensate contaminated aquifer [1]. Combined carbon and hydrogen stable isotope fractionation identified acetoclastic methanogenesis as the dominant process in this system. Such findings agree with the previous clone library characterization of the consortium. Furthermore, hydrocarbon activation was determined to be the rate-limiting process during the net conversion of residual oil to methane.

References

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