

Methanogenesis Coupled Bioremediation of Hydrocarbon Contaminated Soil and Groundwater

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Extended Abstract

At the moment, the global economy is based on petrochemical products; hence hydrocarbons are among the main pollutants all over the world. Hydrocarbon contaminations pose a serious threat to the environment and human health. Therefore, removal of such pollutants is among the top environmental challenges. A number of biotechnologies have been developed for aerobic oxidation of various hydrocarbons, however, remediation under anoxic conditions such as in the deep soil layers is still a big challenge requiring economic solutions. The innate microflora might have the metabolic capacity to utilize hydrocarbons as a carbon and energy source. However, under anaerobic conditions, alternative, expensive electron acceptors are required, or in their absence, a portion of the mineralized hydrocarbons can be converted into methane, thus can be collected as an energy carrier and can decrease the costs of remediation.

In this study, we investigated an area which has been used as an army airport in the past. The remediation of the area has already been attempted but – likely due to the groundwater flows – the pollution appeared again. The area was remonitored: samples (12) were taken up to the groundwater level (7.5 - 8m) and were chemically and microbiologically characterized. Metagenomic analyses revealed that the most abundant genera were *Smithella* (16%) alongside with *Rhodoferrax* (9%). The members of these two genera were recognized as alkane [1] and aromatics [2] degraders respectively. *Methanosaeta* (3%) and *Methanoregula* (6%) were also found among the most abundant genera. Applying a binning method, the genomes belonging to the genera above were recovered with the exception of *Methanosaeta*. In the reconstructed genome of *Smithella sp.*, we identified an alkylsuccinate synthase gene that participates in the activation of aliphatic hydrocarbons under anaerobic conditions [3]. Genes participating in the degradation of aromatic compounds were also found in the *Rhodoferrax* genome. Batch fermentation experiments showed that the enrichment culture derived from this soil sample was able to convert hydrocarbons into methane, therefore it can be used for microbial enhanced energy recovery.

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References

- [1] B. Tan, C. Nesbø, and J. Foght, "Re-analysis of omics data indicates *Smithella* may degrade alkanes by addition to fumarate under methanogenic conditions," *The ISME Journal*, vol. 8, no. 12, pp. 2353–2356, 2014.
- [2] C. Risso, J. Sun, K. Zhuang, R. Mahadevan, R. DeBoy, W. Ismail, S. Shrivastava, H. Huot, S. Kothari, S. Daugherty, O. Bui, C.H. Schilling, D.R. Lovley, and B.A. Methé, "Genome-scale comparison and constraint-based metabolic reconstruction of the facultative anaerobic Fe(III)-reducer *Rhodoferrax ferrireducens*," *BMC Genomics*, vol. 10, pp. 447, 2009.

- [3] A. V. Callaghan, I. A. Davidova, K. Savage-Ashlock, V. A. Parisi, L. M. Gieg, J. M. Suflita, J. J. Kukor, and B. Wawrik, "Diversity of benzyl- and alkylsuccinate synthase genes in hydrocarbon-impacted environments and enrichment cultures," *Environmental Science & Technology*, vol. 44, no. 19, pp. 7287–7294, 2010.