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Presentation Abstract

- Session: P-007-Making a living on Hydrocarbons: Diversity, metabolic potential, and regulation of microbial hydrocarbon oxidation Tuesday, Feb 17, 2015, 5:30 PM - 8:00 PM Presentation: 163 - Unraveling Who Is Who In Methanogenic Oil Degradation Woodway Hall, Poster Board: P-007-02 Location: Pres. Time: Tuesday, Feb 17, 2015, 5:30 PM - 8:30 PM A. J. Cavaleiro¹, A. F. Salvador¹, J. I. Alves¹, A. A. M. Langenhoff^{2,1}, A. J. M. Stams^{3,1}, M. Author(s): M. Alves¹, D. Z. Sousa^{3,1}; ¹Centre of Biological Engineering, University of Minho, Braga, PORTUGAL, ²Subdepartment of Environmental Technology, Wageningen University, Wageningen, NETHERLANDS, ³Laboratory of Microbiology, Wageningen University, Wageningen, NETHERLANDS. Abstract: Methanogenesis from hydrocarbons is a potentially important component of attenuation in
- water and sediments impacted by oil spills. The largest fraction of crude oil consists of aliphatic hydrocarbons (AHC). Current knowledge on key microorganisms degrading alkenes is scarce and is a central question addressed in our research. A methanogenic hexadecene (Hxd)-degrading consortium was obtained from laboratory microcosms inoculated with anaerobic granular sludge, and characterized by 16S rRNA gene amplification, cloning and sequencing. We have learned by community analysis that the present bacteria belong mainly to Syntrophaceae and Synergistaceae families. A Syntrophus-like microorganism (96% similarity at genera level) is possibly involved in Hxd degradation. Known methanogens utilizing acetate and H2/CO2 were identified, namely Methanosaeta-, Methanobacterium- and Methanolinearelated microorganisms, and were likely the syntrophic partners in Hxd degradation. With these results we find hints for similar pathways involved in alkenes and alkanes biodegradation. For alkanes, complete degradation to methane can occur through syntrophic interactions between bacteria and methanogens. This is the first time that an alkene-degrading methanogenic mixed community is characterized. Novel microorganisms involved in AHC degradation could be identified. This information is useful for understanding "who is doing what", and at what rate. It can be used for innovative biotechnological solutions for deep contaminated sites clean-up.