PS.06.092 PREDOMINANCE OF *SYNTROPHOMONAS ZEHNDERI* IN OLEATE-FED BIOREACTORS AND ITS POTENTIAL AS BIOAUGMENTING STRAIN

Sousa, D*; Cavaleiro, A; Alves, M
IBB-Institute for Biotechnology and Bioengineering, Centre for Biological Engineering, University of Minho, Braga, Portugal

Denaturing gradient gel electrophoresis (DGGE) of PCR-amplified 16S rRNA genes was used to follow the changes in bacterial communities during anaerobic continuous and fed-batch reactors operation with oleate, an unsaturated long-chain fatty acid (LCFA).

Throughout continuous operation, bacterial profiles of the sludge showed an average similarity with the inoculum of 9±5%. Bacterial profiles were also altered during fed-batch operation; similarity between sludges before and after fed-batch cycles was 50%. A predominant DGGE-band was identified in all the DGGE profiles of sludges contacting with oleate. 16S rRNA gene sequences retrieved from the different sludges, and corresponding to this position in the DGGE profiles, where found to be closely related to *Syntrophomonas zehnderi* (99% identity). *S. zehnderi* is known to degrade saturated and unsaturated LCFA [1], and could potentially be used to bioaugment anaerobic sludge for improving methane recovery from LCFA. This hypothesis was tested in batch assays performed with and without the solid microcarrier sepiolite. Oleate was added to the medium at a final concentration of 1 mM. Methane production and volatile fatty-acids were monitored throughout the experiment and LCFA were quantified at the end of the assays. The results obtained show that methane production from oleate was enhanced through *S. zehnderi* addition to the anaerobic sludge. After 15 days of incubation, methane yield in bioaugmented assays with sepiolite was as high as 71±3%, whereas in non-bioaugmented bottles only 27±1% of the theoretical methane could be accounted. Methane yield in bioaugmented bottles without sepiolite was also lower, i.e. 36±12%. The use of a microcarrier might facilitate interspecies metabolite exchange, favoring faster methane production. This approach can be potentially useful for a faster reactor start-up or recovery of an LCFA-inhibited anaerobic bioreactor.

[1] Sousa DZ, Smidt H, Alves MM & Stams AJM (2007) Int J Syst Evo

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06 Engineered Environments