

## METHANE PRODUCTION FROM FAT: ASSESSING THE BIOAUGMENTATION POTENTIAL OF *SYNTROPHOMONAS ZEHNDERI*

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**Introduction:** Long-chain fatty acids (LCFA) are common pollutants in fat-rich wastewater, but their conversion to methane is difficult. Bioaugmentation of anaerobic sludge with LCFA-degrading bacteria can be strategically used to enhance methane production from LCFA. *Syntrophomonas zehnderi* is an anaerobic bacterium able to degrade saturated and unsaturated fatty acids with 4 to 18 carbons<sup>1</sup>, which makes it potentially suitable as bioaugmenting strain to enhance degradation of the wide range of LCFA present in wastewaters.

**Aim:** The aim of this work was to evaluate the potential of bioaugmenting anaerobic sludge with *S. zehnderi*, for improving methane production from LCFA.

**Methods:** A co-culture of *S. zehnderi* and *Methanobacterium formicicum* was pre-grown in a bicarbonate-buffered medium supplemented with oleate. Cultivation was done with and without carrier (sepiolite). Anaerobic granular sludge was subsequently added to bottles containing pre-grown cultures of *S. zehnderi*. Control vials with autoclaved-inactivated co-culture and without co-culture (only sludge) were also prepared. All the incubations were done with 1 mM oleate. Blank assays (without oleate) were also done. Methane, LCFA and VFA were monitored by GC and HPLC.

**Results:** In the bioaugmented assays methane recovery from oleate was completed in up to 20 days. No lag phases were observed preceding methane production in the bottles containing *S. zehnderi* supplemented sludge, while the onset of methane production in the non-bioaugmented sludge did not occur before 15 to 20 days of incubation. Sepiolite stimulated degradation of oleate, both in bioaugmented and non-bioaugmented assays.

**Conclusion:** Bioaugmentation of anaerobic sludge with *S. zehnderi* improved methane recovery from oleate, by enhancing its production rate and yield.

**Reference:** <sup>1</sup> Sousa DZ, Smidt H, Alves MM & Stams AJM. *Int J Syst Evol Microbiol* (2007), 57, 609-615.

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