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Innovative start-up strategies for optimal methane production from lipids in anaerobic bioreactors

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Lipids and long-chain fatty acids (LCFA) are energy-rich compounds that can be used as carbon and energy source by anaerobic microbial communities. Theoretically, large amounts of methane, a valuable energy carrier, may be generated during this process. However, operational problems, mainly associated with LCFA accumulation onto the sludge, have limited the use of anaerobic technology to produce methane from LCFA. In this work, two novel start-up strategies were tested for optimal methane production from LCFA: (i) bioreactor start-up using an intermittent feeding strategy, and (ii) bioreactor bioaugmentation with a LCFA-degrading bacterium. Intermittent feeding start-up resulted in efficient continuous methane production from high LCFA loads (up to 21 kgCOD m⁻³ day⁻¹, 50% COD as oleate (unsaturated LCFA, C18:1)). Alternating continuous bioreactor feeding and batch degradation periods, during bioreactor start-up, was crucial for sludge acclimation and contributed to the development of a metabolically specialized anaerobic microbial community that was able to efficiently convert oleate to methane. After intermittent feeding bioreactor start-up, methane yields higher than 70% were achieved, and neither LCFA nor VFA accumulated in the system. Bioaugmentation experiments were performed using *Syntrophomonas zehnderi*, a bacterium able to degrade saturated and unsaturated LCFA [1]. Anaerobic sludge amended with active and inactive *S. zehnderi* was incubated with 1 mM oleate as sole carbon and energy source. Methane production from oleate in bioaugmented batches was faster and high methane yields (89 ± 5%) were achieved. This work highlights the importance of the start-up strategy for the development of balanced syntrophic communities specialized in methane production from LCFA. Intermittent feeding and bioaugmentation with LCFA-degrading bacteria may be applied as alternative or complementary strategies.

[1] Sousa et al (2007) *Int J Syst Evol Microbiol*, 57: 609 – 615. Part of this study has been funded by FEDER, through the COMPETE program, and by Portuguese funds, through Portuguese Foundation for Science and Technology (FCT), in the frame of the project FCOMP-01-0124-FEDER-014784. Financial support from FCT and the European Social Fund (ESF) through the PhD grant SFRH/BD/24256/2005 attributed to AJ Cavaleiro is also acknowledged.