

Population dynamics of LCFA-degrading syntrophic communities exposed to extended contact with sulfate

D.Z. Sousa¹^{a,b,§}, J.I. Alves^{a,b}, H. Smidt^b, M.M. Alves^a, A.J.M. Stams^b

^a IBB-Institute for Biotechnology and Bioengineering, Centre of Biological Engineering, University of Minho, Braga, Portugal, ^b Laboratory of Microbiology, Wageningen University, Wageningen, The Netherlands,
[§] dianasousa@deb.uminho.pt

Competition between sulfate-reducing bacteria (SRB) and methane-producing archaea in high rate wastewater treatment processes has been extensively described [e.g. 1,2,3]. A range of substrates, such as starch, glucose, hydrogen and volatile fatty-acids were used as energy sources. Long chain fatty acids (LCFA) however, are not usually used, though they are common substrates in wastewaters with high sulfate levels, such as the one produced in slaughterhouses, food-processing industries and edible oil production. Therefore, it is important to get insights into the effects of biological sulfate reduction on anaerobic treatment of LCFA-containing wastewater, including dynamics of competition between SRB and syntrophic bacteria and/or methanogenic archaea [4].

Bacteria involved in the anaerobic degradation of LCFA in the presence of sulfate, were studied by a combination of cultivation-dependent and molecular techniques. Bacterial diversity in four mesophilic sulfate-reducing enrichment cultures, growing on oleate (C18:1, unsaturated LCFA) or palmitate (C16:0, saturated LCFA), was studied by 16S rRNA gene fingerprinting (DGGE). These enrichment cultures were started using methanogenic inocula in order to assess the competition between methanogenic communities and SRB. Phylogenetic affiliation of 16S rRNA gene sequences corresponding to predominant DGGE-bands demonstrated that members of the *Syntrophomonadaceae*, together with sulfate-reducers mainly belonging to the *Desulfovibrionales* and *Syntrophobacteraceae* groups, were present in the sulfate-reducing enrichment cultures. Subculturing of LCFA-degrading methanogenic cultures in the presence of sulfate resulted in the inhibition of methanogenesis and, after several transfers, archaea could no longer be detected by real-time PCR. This indicated that sulfate-reducers out-competed methanogens in the competition for hydrogen and acetate. Conversely, SRB known as fatty acid oxidizers were not detected in the enrichment cultures after subculturing with sulfate, suggesting that acetogenic syntrophic bacteria were the major LCFA-degrading organisms present in the mixed cultures.

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