MICROBIAL COMMUNITIES INVOLVED IN ANAEROBIC DEGRADATION OF UNSATURATED- AND SATURATED-LCFA UNDER SULFIDOGENIC CONDITIONS

J.I. Alves[1,2], D.Z. Sousa[1,2], H. Smidt[2], A.J.M. Stams[2], M.M. Alves[1]

[1]Centre of Biological Engineering, University of Minho, Braga, Portugal
[2]Laboratory of Microbiology, Wageningen University, Wageningen, The Netherlands

Background and aims:

Several long chain fatty acids (LCFA)-rich wastewaters contain sulfate which can interfere with LCFA-methanization. Here, sulfidogenic LCFA-degrading consortia and methanogenic LCFA-degrading consortia incubated with sulfate were studied using cultivation-dependent and molecular methods. The aim was to get insight into the structure and function of LCFA-degrading microbial communities and methanogens/sulfate-reducers competition.

Methods:

Two sulfidogenic oleate- and palmitate-enrichments were obtained by successive dilutions in mineral media. Additionally, bottles seeded with stable methanogenic oleate- and palmitate-enrichment cultures were incubated with sulfate. Bacterial-specific 16S rRNA gene sequencing and PCR-DGGE profiling were used to follow microbial consortia upon enrichment under sulfidogenic conditions. Same approach was used to study changes in methanogenic consortia after incubation with sulfate. Archaea were quantified by real-time PCR.

Results:

Sulfidogenic oleate- and palmitate-enrichments showed differences in bacterial-specific DGGE-profiles. Nevertheless, 16S rRNA gene sequencing demonstrated that members of *Syntrophomonadaceae* and *Syntrophobacteraceae*, together with sulfate-reducers belonging to *Desulfovibrionales*, were prominent members of both enrichments. The DGGE-profile of the methanogenic oleate-enrichment shifted during incubation with sulfate, with clear appearance of a dominant band corresponding to a *Desulforhabdus amnigenus* related bacterium, possibly involved in acetate utilization. Conversely, the DGGE-profile of methanogenic palmitate-enrichment did not change significantly during incubation with sulfate. Addition of sulfate to methanogenic enrichments resulted in inhibition of methanogenesis. No archaea were detected by real-time PCR after prolonged incubation with sulfate.

Conclusions:

Dominant organisms in LCFA-enrichments clustered within *Syntrophomonadacea*, *Syntrophobacteraceae*, and *Desulfovibrionales* groups. Sulfate reduction became more important than methanogenesis when stable methanogenic enrichments were incubated with sulfate.