MICROBIAL CONSORTIA INVOLVED IN ANAEROBIC DEGRADATION OF UNSATURATED AND SATURATED-LCFA SHOW A DIFFERENT COMPOSITION

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Background and aims:
The biochemical pathways and microbial consortia involved in anaerobic degradation of saturated- and unsaturated-LCFA have not been fully resolved yet. Here, the microbial composition of anaerobic sludge samples that degraded unsaturated- and saturated-LCFA was studied. The aim was to determine and compare the microbial populations involved in unsaturated and saturated-LCFA degradation, and elucidate differences in both processes.

Methods:
Diverse sludge samples were incubated with unsaturated- and saturated-LCFA, at different conditions, i.e. continuous LCFA-feeding, batch-LCFA feeding, and successive dilutions with LCFA in the presence and absence of sulphate. Oleate and palmitate were used as model substrates for unsaturated- and saturated-LCFA, respectively. The microbial community composition of anaerobic consortia after incubation with LCFA under different conditions, were analysed by DGGE fingerprinting and subsequent cloning and sequence analysis.

Results:
Microorganisms closely related to syntrophic fatty-acid oxidising bacteria were detected in all samples after incubation with LCFA. Dominant DGGE-bands corresponded to bacteria clustering within Syntrophomonadaceae, Syntrophaceae, and Syntrophobacteraceae families. A specific dominant DGGE-band corresponding to a bacterium affiliated with the Syntrophomonas genus, closely related to the uncultured bacterium clone R6b2 (94%), was found to be only present in sludges that had been incubated with the unsaturated-LCFA oleate. Moreover, a palmitate-adapted consortium was not able to degrade oleate, until the bacterium corresponding to this dominant DGGE-band appeared in the DGGE-profile.

Conclusions:
The identification of a bacterium exclusively present in oleate-fed sludges suggests its involvement in degradation of unsaturated-LCFA and emphasises the differences between unsaturated- and saturated-LCFA degradation.