

## SYNTROPHIC LCFA-DEGRADERS - “BACTERIA THAT CAN CLEAN SOAP”

D.Z. Sousa<sup>1,2</sup>, H. Smidt<sup>2</sup>, A.J.M. Stams<sup>2</sup>, M.M. Alves<sup>1</sup>

<sup>1</sup>*IBB-Institute for Biotechnology and Bioengineering, Centre for Biological Engineering, University of Minho, Braga, Portugal,* <sup>2</sup>*Laboratory of Microbiology, Wageningen University, Wageningen, Netherlands*

Wastewaters contain substantial amounts of long-chain fatty acids (LCFA) which, when in the form of sodium salts, are what we normally call soaps. These compounds, resulting from fats' hydrolysis, can be converted to high amounts of methane. Developing new technological solutions for LCFA methanation, but also understanding the physiology and microbiology of LCFA degradation is fundamental for the bioenergy valorization of fatty wastewaters. In this work we present an overview of our results on anaerobic LCFA microbial degradation. Molecular techniques were used to investigate the structure of microbial communities present in different LCFA-degrading communities, such as continuous oleate- and palmitate-fed bioreactors and several enrichment cultures degrading these two LCFA as well. Choice of oleate and palmitate as model substrates was due to their predominance in wastewaters and to the fact that they represent mono-unsaturated and saturated LCFA, respectively. DGGE fingerprinting and sequencing evidenced the importance of syntrophic bacteria, affiliated with the *Syntrophomonas* genus, in the degradation of these compounds. Enrichment on oleate or palmitate resulted in distinct bacterial communities, which might be related to LCFA chain-saturation differences. A new obligately syntrophic bacterium, *Syntrophomonas zehnderi*, was isolated from an oleate-degrading culture. The fact that *S. zehnderi* can degrade a wide range of fatty-acids with different chain length (C4-C18) and is also able to use unsaturated LCFA (e.g. oleate) makes it a destined and dedicated key for the anaerobic treatment of wastewaters, in which an assembly of different fatty-acids is normally present. Genome sequencing of *S. zehnderi* is currently undergoing.