



Anaerobes beyond anaerobic digestion

Diana Sousa, M. Alcina Pereira, Madalena Alves

*IBB-Institute for Biotechnology and Bioengineering, Centre of Biological Engineering,
Universidade do Minho, Campus de Gualtar, 4710-057 Braga, Portugal.*

Anaerobic microorganisms are widespread in nature. Sediments, gastrointestinal tracks, volcanic vents, geothermal sources are examples of habitats where anaerobic metabolism prevail, in some cases at extreme temperature, pH and pressure conditions. In such microbial ecosystems waste of some is food for others in a true integrated structure. Anaerobic microorganisms are able to use a wide variety of organic and inorganic compounds. Recalcitrant compounds, such as hydrocarbons, aromatics, fatty-acids, can be converted by anaerobic microbial mixed communities to a range of intermediary products or, ultimately, to methane and carbon dioxide. Inorganic compounds, for example sulphur and sulphur oxides, nitrogen oxides, iron, can act as electron acceptors during anaerobic conversion of organic molecules. A complex food-chain takes place in anaerobic microbial ecosystems with a great potential for the recovery of products with biotechnological interest. We focus on the study of microbial ecology and physiology of anaerobic mixed communities aiming at potential biotechnological applications. In parallel, pure culture studies are important to assess novel physiological traits and metabolic routes of anaerobic microorganisms. Bio-hydrogen production, syngas fermentation and long chain fatty-acids degradation are examples of microbial processes currently studied at our laboratory. Microbial communities involved in the production of bio-hydrogen were characterized by DGGE and cloning and sequencing approach¹. Fermentation of syngas to methane and study of metabolic alternative routes for the production of other products, such as butanol, is being assessed by using pure cultures and defined mixed cultures. Microorganisms involved in the degradation of long chain fatty-acids have been extensively studied and a novel syntrophic bacterium, *Syntrophomonas zehnderi*, was isolated². Complete genome sequencing of this bacterium is currently ongoing.

¹ Alves, J.I., Abreu, A.A., Alves, M.A. & Sousa, D.Z. Microbial communities shifts in dark fermentative H₂ production at mesophilic, thermophilic and hyper-thermophilic conditions. 12th International Symposium on Microbial Ecology - ISME 12. Cairns, Australia, 17-22 August, 2008.

² Sousa D.Z., Smidt H., Alves M.M. & Stams A.J.M. (2007) *Syntrophomonas zehnderi* sp. nov., an anaerobe that degrades long chain fatty acids in co-culture with *Methanobacterium formicicum*. Int J Syst Evol Microbiol 57: 609-615.