PS.06.001 STRATEGIES FOR SELECTNG HYDROGEN PRODUCING MICROORGANISMS AFFECT MICRO AND MACRO STRUTURE OF GRANULAR SLUDGE

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Mixed-culture dark fermentation is an environmentally friendly bio-hydrogen production process. In this work we study the potential for directing microbial anaerobic mixed communities towards improved hydrogen production. Strategies applied for promoting the selection of hydrogen-producing bacteria in anaerobic granular sludge consisted of heat treatment and chemical treatment with 2-bromo-ethane sulfonate (BES) and with BES+Chloroform. Three expanded granular sludge bed reactors, R_{Heat}, R_{BES} and R_{BES+Chlo}, where inoculated with the treated sludges and fed with synthetic sugar-based wastewater. Hydrogen production was monitored. Morphological integrity and microbial diversity of the granules were studied by using image analysis technique and molecular techniques (DGGE, cloning and sequencing), respectively. Hydrogen production in R_{Heat} was below 300 mLH₂L⁻¹d⁻¹. In R_{BES+Chlo} hydrogen production rate never exceeded 300 mLH₂L⁻¹d⁻¹. In this sludge, a physical deterioration of the granules was observed with a decrease of their density and microbial diversity. In R_{BES}, a transient period of unstable H₂ production was observed but an additional pulse of BES triggered hydrogen production rate to an average value of 700 ± 200 mLH₂L⁻¹d⁻¹, which was kept for 30 days. This strategy did not affect significantly granular sludge structure. The dominant bacterial ribotypes displayed in the DGGE profiles along the R_{BES} operation were found to be closely related to Clostridium species, e.g. Clostridium ljungdahlii (99% identity), Clostridium drakei (94% identity), and to uncultured microorganisms belonging to Clostridiaceae and Ruminococcaceae. The strategies used for selecting hydrogen producing microorganisms affected both, micro and macro structure of granular sludge. Image analysis allowed the identification and quantification of changes on the morphological properties of granular sludge that could be related to bacterial community dynamics and diversity.

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