

## MICROBIAL COMMUNITIES SHIFTS IN DARK FERMENTATIVE H<sub>2</sub> PRODUCTION AT MESOPHILIC, THERMOPHILIC AND HYPERTHERMOPHILIC CONDITIONS

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Hydrogen is foreseen as a viable CO<sub>2</sub>-neutral alternative to fossil fuels for generation of energy. Production of H<sub>2</sub> from wastes/wastewaters is possible as this is one of the main products resulting from anaerobic fermentation of organic compounds. If hydrogenotrophic methanogens are suppressed, H<sub>2</sub>-rich biogas can be recovered from anaerobic reactors. In order to optimize and improve H<sub>2</sub> production, it is essential to get more insight into the composition and structure of the microbial communities involved in the process. In this study microbial community shifts in expanded granular sludge blanket (EGSB) reactors producing H<sub>2</sub> at different temperatures and organic loading rates (OLR) were studied using PCR-DGGE fingerprinting analysis. The aim was to get more insight into the microbiology of dark fermentative hydrogen production at mesophilic, thermophilic and hyperthermophilic temperatures. Three EGSB reactors were inoculated with granular biomass previously treated with heat to suppress methanogens. Reactors were operated at 37, 55 and 70 °C with 5gCOD L<sup>-1</sup> of a mixture containing glucose and L-arabinose (1:1); pH was kept at 5.5. OLR applied varied from 5 to 16. PCR amplification of the 16S rRNA gene and subsequent DGGE analysis of sludge samples collected from the reactors at different operational times showed different profiling, mainly correlated with differences in temperature. Bacterial diversity (measured as the number of bands) in sludge samples from reactors operating at 55 °C and 70°C was remarkably lower than in sludges growing at 37°C. No significant changes on DGGE profiles diversity were observed with the increase of OLR over time.