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Bacterial community structure of biohydrogen production process in extreme thermophilic conditions (70ºC)

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Abstract

The search for new energies is a priority and hydrogen is one of the most promising alternatives to fossil fuels, since water is the only product of oxidation. The attention on dark fermentation has increased recently due to the fact that H_2 can be generated continuously at high rate from renewable organic materials [1]. Fermentation under extreme-thermophilic conditions (70ºC) promote better pathogenic destruction, better thermodynamics conditions and less contamination with methanogenic organisms, comparing with mesophilic and thermophilic systems [2]. In this study, two different granular systems were investigated in order to get insight into the structure of the bacterial communities involved in H_2 production under extreme-thermophilic conditions. Heat treated methanogenic granules (HTG) and engineered heat treated methanogenic granules (EHTG) were individually inoculated in two EGSB reactors, fed with arabinose and glucose (1:1 (w/w)) at a final concentration of 5gCOD l^{-1}. EHTG were obtained by contact of granules with an enriched H_2-producing culture in batch mode for 3 days. The EHTG system showed more stable and efficient H_2 production achieving a maximum production rate of 2.7lH_2 $l^{-1}d^{-1}$ and a conversion of 175mlH_2g^{-1}substrate. In the HTG system no steady state was achieved and only a transient H_2 production was observed with two maximum peaks of 0.8 and 1.5lH_2 $l^{-1}d^{-1}$. Granular samples collected during the experiment as well as the enriched H_2-producing culture were analyzed by molecular ecology techniques, such as PCR-DGGE, cloning and sequencing. The dominant bacterial ribotypes found in the EHTG system DGGE profiles were closely related to *Clostridium* sp., *Sporolactobacillus* sp., *Bacillus* sp., *Klebsiella* sp. and *Thermoanaerobacterium* sp.. *Thermoanaerobacter*-like organism corresponded to dominant DGGE bands in the enriched culture but could not be found in the continuous EHTG system. Nevertheless, the contact of HTG with this culture contributed to the development of a stable and efficient hydrogen production during the EHTG system operation. The presence of active hydrogen producers in the EHTG system during the reactor start-up, seems to have created favourable conditions for the development of an efficient H_2-producing bacteria community. This seems to be the case of organisms affiliated to *Clostridium* sp. and *Klebsiella* sp. that corresponded to dominant bands in the EHTG system DGGE profiles, but were not detected in the HTG system.

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