

P-137 - PRESSURIZED SYNGAS BIOCONVERSION: PHYSIOLOGICAL AND MICROBIAL CHARACTERIZATION

Joana Isabel Alves¹; Marlene Lopes¹; Ana Luísa Arantes¹; Isabel Belo¹; Diana Zita Sousa^{1,2}; M. Madalena Alves¹

1 - Centre of Biological Engineering, University of Minho, 4710-057 Braga, Portugal.; 2 - Laboratory of Microbiology, Wageningen University, Stippeneng 4, 6708 WE Wageningen, The Netherlands.

Background

Syngas is mainly composed by CO, H₂ and CO₂ and represents one of the most inexpensive substrates for microbial fermentation. Bioconversion of syngas is a promising technology to recycle lignocellulosic biomass or carbon-based wastes, producing a variety of biofuels and biochemicals. However, a potential bottleneck in industrial implementation of syngas bioconversion technology is the gas-to-liquid mass transfer limitation, reducing the amount of gases available to be used as substrate by microorganisms. In this work, a pressurized bioreactor was used to improve syngas components solubility, assessing the influence of initial syngas pressure on methane and biochemicals production, on CO and H₂ consumption rate and on microbial communities' structure.

Method

Batch syngas bioconversion was performed in a pressurized bioreactor. Phosphate-buffered mineral salt medium was inoculated with anaerobic granular sludge. Bioreactor headspace was pressurized with syngas (60% CO, 30% H₂ and 10% CO₂) until the desired pressure (1.2×10⁵ Pa, 3.0×10⁵ Pa or 5.2×10⁵ Pa). Throughout the bioconversion, CH₄, CO and H₂ in headspace were quantified by GC and liquid products by HPLC. Microbial communities' structure was assessed by 16S rRNA-based techniques (PCR-DGGE); RNA samples were sequenced (Illumina Miseq platform).

Results & Conclusions

The rise of syngas pressure led to a decrease on CO and H₂ consumption rates and CH₄ production rate. When methanogenesis was partially inhibited, propionate and butyrate were the main metabolites produced, showing a metabolic change with increasing syngas pressure. From the Illumina sequencing analysis, it was observed that the relative abundance of bacterial communities tend to decrease (72% to 46%), and archaeal communities increased (25% to 54%) by raising the pressure of syngas from 1.2×10⁵ Pa to 5.2×10⁵ Pa. In the inoculum and biomass incubated at 1.2×10⁵ Pa syngas, 40% of total population were from *Deltraproteobacteria* class and their abundance was reduced 4-fold at 5.2×10⁵ Pa. As a direct effect of high pressures of syngas, organisms belonging to *Firmicutes*, *Synergistetes* and *Thermotogae* phyla increased over 10-fold. The predominant phylotypes at highest pressures were related to *Methanobacterium* genus (archaea) and to *Eubacteriaceae*, *Synergistaceae* and *Syntrophobacteraceae* families (bacteria). These results showed a microbial population enrichment suggesting a high specialization for the substrate.

References & Acknowledgments

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