

Pressurized syngas bioconversion: physiological and microbial characterization

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Syngas is composed mainly by CO, H₂ and CO₂ and its fermentation is a promising biological process to produce fuels or commodity chemicals. Experiments under increased initial syngas pressures, up to 5.2×10⁵ Pa, were carried out to evaluate the effects on metabolites production and microbial communities' structure. Two strategies were applied: NB – non-adapted biomass and SB – successively syngas-fed biomass. The rise of syngas pressure from 1.2×10⁵ Pa up to 5.2×10⁵ Pa led to a decrease on CO and H₂ consumption rates and CH₄ production rate. Moreover, when methanogenesis was partially inhibited, propionate and butyrate were the main metabolites produced from syngas. DGGE profiles showed differences on diversity and on similarity indices (SI) with changes in pressure. Regardless the syngas pressure employed, the archaeal communities had higher SI (above 70%) than bacterial community (48% to 62%). 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 *Proteobacteria* phylum and *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 3×10⁵ Pa and 5.2×10⁵ Pa 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.