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Syngas fermentation: Acetate and ethanol production by pure and mixed-cultures enriched with carbon monoxide

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Fermentation of CO or syngas (CO with H_2 and/or CO_2) can lead to the production of commodity chemicals, including acetate and ethanol. Research has focused on enhancing syngas-conversion by pure cultures to ethanol. However, since syngas composition depends on the feedstock gasified, different substrates, such as $CO:CO_2$, $CO:H_2$ and $CO:CO_2:H_2$, have been used in various studies. Despite increased ethanol/acetate ratios achieved with these different syngas mixtures, the effect of CO_2 and H_2 in the metabolism of carboxidotrophs is not understood. This research focused on understanding how CO, CO_2 and/or H_2 affect the microbial community structure and function. Two carboxidotrophs (SVCO-15 and SVCO-16) were isolated after long-term enrichment of sludge with CO at increasing partial pressure (PCO). Fermentation of CO, $CO:H_0$, $CO:CO_2$, and $CO:CO_2:H_2$ by the CO-enrichment culture and the isolates was tested. Increasing PCO enriched for Clostridiales. CO_2 and H_2 influenced the microbial community structure in the CO-enrichment culture at different stages of CO-fermentation (lag, exponential or stationary phase), but did not affect its overall function or CO-consumption rates. Based on Phylogeny, SVCO-15 is 99% similar to *Acetobacterium wieringae*, and SVCO-16 is a new species within *Pleomorphomonas*. Contrary to the mixed-culture, syngas mixtures affected function of the isolates. SVCO-15 produced mainly ethanol from CO and $CO:H_2$, while acetate was the main product in the presence of CO_2. CO-conversion by SVCO-16 produced $H_2:CO_2$ and was inhibited by external CO_2/H_2. Pure cultures are important for fundamental studies. However, mixed-cultures are promising in large-scale syngas applications because of their flexibility and functional redundancy.

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Candida albicans, comparative *SAP4-6* gene expression from HIV positive patients with oral candidiasis and commensal in healthy individuals

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Gene expression of *SAP4-6* based on the ability of detection of mRNA was observed in *Candida albicans* isolates from HIV-positive patients with oral candidiasis and commensal healthy people. Members of the species of *C. albicans* strains selectively isolated from both sources (habitat) using *CHROMagar* medium. Isolates were then induced to express *SAP4-6* by using gene inducers media *SAP4-6*. Analysis of gene expression was performed by two mechanisms, namely morphogenesis by the formation of hyphae and molecular basis by using RT-PCR. The frequency of *C. albicans* in the sample population was measured by calculating the percentage of samples that carry *C. albicans*. The frequency of *C. albicans* from HIV reached 40%, whereas in healthy people was only 15%. Molecular analysis of gene expression showed that isolates CH_3 derived from HIV-positive patients with oral candidiasis could express *SAP4-6* gene while commensal isolates from healthy people could not. Based on the results of this study it could be concluded that in terms of molecular detection only isolates derived from HIV-positive patients (CH3) could express its *SAP4-6* gene.

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