OC-NB-06

MICROBIAL CO-CULTIVATION INDUCES A METABOLIC SHIFT, PROMOTING SYNGAS CONVERSION TO CHAIN-ELONGATED ACIDS

Diender, Martijn[1]; Parera Olm, Ivette[1]; Gelderloos, Marten[1]; Koehorst, Jasper[1]; Schaap, Peter[1]; Stams, Alfons[1,2]; Sousa, Diana[1]

1 - Wageningen University & Research; 2 - University of Minho

Keywords: syngas, co-cultures, chain elongation

Introduction:
Syngas, a mixture of H_2, CO and CO_2, can be generated from a wide range of (low-biodegradable wastes) and is a suitable feedstock for biotechnological processes. Several microorganisms are able to use syngas for growth, but main natural products from this fermentation are acetate and ethanol. In order to extend the range of products from syngas fermentation, we constructed a synthetic co-culture of *Clostridium autoethanogenum*, a carboxydotrophic acetogen, with *Clostridium kluyveri*, a bacterium employing the reverse β-oxidation pathway[a]. *C. autoethanogenum* converted syngas to acetate and ethanol, and *C. kluyveri* elongated these products to butyrate and caproate.

Methods:
Experiments in batch bottles and chemostats were conducted to study the differences in physiological behavior between monocultures of *C. autoethanogenum* and co-cultures of *C. autoethanogenu*m and *C. kluyveri*. In addition to physiological characterization a transcriptomics approach was used to unravel the molecular functioning of this co-culture[b].

Results:
Expression of the central carbon- and energy-metabolism of *C. autoethanogenum* in pure or in co-culture with *C. kluyveri* remained unaltered. However, the electron flux from CO to intermediate products (acetate/ethanol) was substantially shifted towards the production of ethanol. In co-culture conditions fed with additional acetate, the metabolism of *C. autoethanogenum* could be pushed to produce only ethanol from CO, resulting in high yields of chain elongated acids by the co-culture.

Conclusions:
The results suggest that thermodynamics and metabolic dependence between the two strains, rather than gene expression, plays a key role in the ratio of products formed during CO fermentation by *C. autoethanogenum*. Overall this suggests that microbial interactions can be exploited to steer the syngas fermentation process towards products of interest, enhancing both the efficiency and the products spectrum of syngas fermentation technology.