
Physical interactions between *Desulfovibrio vulgaris* Hildenborough and *Clostridium acetobutylicum* are required to induce metabolic changes in the consortia

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Abstract

Numerous microorganisms can produce hydrogen by "dark fermentation". Isolated from various environments, they present a broad range of different metabolisms. Until now, literature reports have mainly dealt with the use of pure microbial cultures producing biohydrogen from simple sugars, such as glucose and sucrose. More recently, studies on biohydrogen production by mixed cultures from complex organic sources have been developed. Even though biohydrogen productivities and conversion yields can be interesting for industrial purposes, several scientific and technical constraints remain to be addressed. In particular, the presence of alternative metabolic ways of hydrogen consumption generally results in chronic instability of the biological processes. To increase the stability and the efficiency of dark fermentative processes, it is now necessary to acquire a better understanding of the metabolic interaction networks existing between producing and consuming microorganisms. We have developed an innovative and multidisciplinary approach to ecological engineering, which consists of the construction and study of synthetic microbial consortia to establish the metabolic networks existing between microorganisms for further optimization of biohydrogen production. First we have studied the networks of metabolic interactions between two bacterial models known as involved in a natural bacterial consortium: a bacterium from *Clostridium* genus; *Clostridium acetobutylicum* and one from *Desulfovibrio* genus, *Desulfovibrio vulgaris* Hildenborough. The first one being producing of hydrogen by fermentation of complex sugars and the second in the production or consumption of hydrogen according to its environment. After the definition of a minimal medium, we investigated the effect of a bacterium on the other one within the framework of the production of hydrogen using metabolic studies. Using different approaches ie microbiology, FISH, RT-PCR and metabolic quantification, we demonstrate (i) the coexistence of the two bacteria in the consortium; (ii) an higher hydrogen production by the consortium compared to isolated bacteria in line with a modification in the metabolic pathway in the clostridium strain; (iii) a physical interaction between the strains via nanotubes.

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Keywords: metabolism, consortia, hydrogen production, bioenergy