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The Ech Hydrogenase is Important for Growth of Desulfovibrio vulgaris with Hydrogen

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INTRODUCTION

One objective of the Virtual Institute for Microbial Stress and Survival (VIMSS) and the Environmental Stress Pathway Project (ESPP) is to determine the genetic and physiological bases for cooperative and competitive interactions among environmental microbial populations of relevance to the DOE. The ESPP Applied Environmental Core (AEC) and Functional Genomics Core (FFG) have identified a number of genes that may participate in cooperative interactions between sulfate reducers and methanogens under low sulfate conditions.

The Deltaproteobacterium D. vulgaris is able to grow in the absence of an electron acceptor via syntrophy with hydrogenotrophic organisms. Despite decades of research, energy conservation in D. vulgaris is not well understood. The presence of multiple hydrogenases, including many located in the periplasm in all studied Desulfovibrio strains - and the observation that hydrogen is produced and then consumed during growth with lactate and sulfate (Tuji and Yagi, 1980) - lead to the formulation of the hydrogen cycling hypothesis as a mechanism for energy conservation (Odum and Peck, 1981). The completed genome sequence of D. vulgaris Hildenborough has since revealed genes for at least six different hydrogenases: four periplasmic and two cytoplasmic. Although several have been partially characterized biochemically and genetically, their roles in D. vulgaris under different growth conditions remain mostly undefined.

One of the membrane-bound hydrogenases, Ech, is very similar to a proton pumping hydrogenase from Psychrobacter furiosus DSM 1638 (Supra et al., 2004) and Thermotoga maritima DSM 2093 (Soboh et al., 2004). It was suggested that a role for the Ech of DvH is hydrogen production using ferredoxin as a redox partner (Pohorelic et al., 2003). In this work we examined the growth and metabolite production of an echA (DVU0434) D. vulgaris Hildenborough mutant under three different growth conditions: i) in medium amended with lactate and sulfate and ii) in medium amended with acetate, hydrogen and sulfate, and iii) in coculture with the hydrogenotrophic methanogen Methanothermobacter maripaludis.

RESULTS

**Growth of D. vulgaris JW380 monoculture**

- With lactate and sulfate
- Hydrogen in head space during growth with lactate and sulfate
- With H2, CO2 and sulfate

- Figure 3

**Growth of D. vulgaris JW380 in syntrophic association with M. maripaludis without sulfate**

- Figure 4

**REFERENCES**


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On lactate, the mutant demonstrated a growth rate and yield comparable to the wild type strain, but evolved more hydrogen as measured by its accumulation in the headspace during growth in batch culture (Figure 2A and B). A coculture consisting of the mutant strain and a hydrogenotrophic methanogen (M. maripaludis) demonstrated only slightly reduced growth rate and increased hydrogen accumulation in stationary phase when lactate was consumed relative to the wild type (Figure 4). This suggested a minor role of Ech in energy conservation during syntrophic growth. The hypothetical mechanism of hydrogen oxidation under these two growth conditions are shown on Figure 5.

In a medium containing acetate and an atmosphere of H2/CO2, growth of the mutant was severely impaired relative to the wild type (Figure 2C). Thus, the available data suggest that the primary role of the Ech hydrogenase is oxidation of hydrogen during sulfate respiration, possibly also contributing to the production of reduced ferredoxin required for conversion of Acetyl CoA to pyruvate by pyruvate oxidoreductase, as was previously demonstrated for the homologous hydrogenases in M. barkeri and M. maripaludis (Meuer et al., 2002; Pora et al., 2006). The hypothetical mechanism of hydrogen oxidation under this growth condition are shown on Figure 6.

Additional information on function of another hydrogenases in D. vulgaris you can find on Poster 059.