

Differential Display Proteomics and Transcriptome Analyses of a Hydrogen Metabolism Mutant of the Archaeon *Methanococcus maripaludis*.

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Methanococcus maripaludis is a mesophilic archaeon that reduces CO₂ to methane with H₂ or formate as a source of energy. It contains two membrane-bound energy-conserving hydrogenases (Eha and Ehb). Ehb is believed to reduce low potential ferredoxins for CO₂ assimilation and other anabolic reactions. An insertion in the *ehb* operon yielded the mutant, strain S40. Growth of S40 was severely impaired in minimal medium. Both acetate and yeast extract were necessary to restore growth to nearly wild-type levels, suggesting that Ehb was involved in multiple biosynthetic steps. Methanogenesis with pyruvate as the electron donor was also reduced by 30 % in S40, suggesting a defect in coupling to pyruvate oxidoreductase (POR). Out of 1722 ORFs in the genome, expression of 939 ORFs was observed in the proteome. Both array and proteomic analyses found increases in the mutant in expression of CO dehydrogenase/acetyl-CoA synthase, pyruvate oxidoreductase and AMP-forming acetyl-CoA synthetase. Some of these changes were confirmed by enzymatic assay and real-time PCR. Changes in expression of genes involved in energy metabolism were also observed. These observations support a role for Ehb in anabolic CO₂ assimilation in methanococci.