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PROTEOMICS OF SYNTROPHOMONAS ZEHNDERI AND METHANOBACTERIUM FORMICICUM GROWING ON LONG-CHAIN FATTY ACIDS

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Background: Conversion of long-chain fatty acids (LCFA) in anaerobic digesters relies on syntrophic relationship between acetogenic bacteria and methanogenic archaea. Conversion of unsaturated- and saturated-LCFA has been previously shown by a coculture of Syntrophomonas zehnderi and Methanobacterium formicium. Degradation of unsaturated-LCFA is rare among Syntrophomonas species; the best studied fatty acid oxidizer, S. wolfei, can only grow on saturated-LCFA.

Objectives: Major differences are expected in the pathways and enzymes involved in the degradation of unsaturated-LCFA. In this work we used proteogenomic approach to study these differences.

Methods: A draft genome of S. zehnderi was obtained by Illumina HiSeq sequencing. Genomes of S. zehnderi and S. wolfei (available at NCBI) were compared. S. zehnderi and M. formicicum co-cultures grown on oleate (unsaturated LCFA, C18:1) and on stearate (saturated LCFA, C18:0) were further studied using a proteomics approach.

Conclusions: Genomic comparison of S. zehnderi and S. wolfei revealed approximately 900 different proteins and 1200 common proteins. In the genome of S. zehnderi, two replicates of the unsaturated acyl-CoA dehydrogenase genes were identified, one of which differs considerably from the acyl-CoA gene found in S. wolfei. Proteomic analysis of S. zehnderi and M. formicium co-cultures revealed high expression levels of proteins related to the β-oxidation of LCFA (up to 30% of total proteins identified). Different protein expression levels were observed during the degradation of oleate (44% unique proteins) and stearate (23% unique proteins). In addition, proteins involved in electron transfer were highly expressed, including electron transfer flavoproteins, ATP synthases and a number of hydrogenases and formate dehydrogenases.