



Category: Metagenomics

Genome scale metabolic network reconstruction of *Spirochaeta cellobiosiphila*

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Abstract

Substantial rise in the global energy demand is one of the biggest challenges in this century. Environmental pollution due to rapid depletion of the fossil fuel resources and its alarming impact on the climate change and Global Warming have motivated researchers to look for non-petroleum-based sustainable, eco-friendly, renewable, low-cost energy alternatives, such as biofuel. Lignocellulosic biomass is one of the most promising bio-resources with huge potential to contribute to this worldwide energy demand. However, the complex organization of the Cellulose, Hemicellulose and Lignin in the Lignocellulosic biomass requires extensive pre-treatment and enzymatic hydrolysis followed by fermentation, raising overall production cost of biofuel. This encourages researchers to design cost-effective approaches for the production of second generation biofuels. The products from enzymatic hydrolysis of cellulose are mostly glucose monomer or cellobiose unit that are subjected to fermentation. *Spirochaeta* genus is a well-known group of obligate or facultative anaerobes, living primarily on carbohydrate metabolism. *Spirochaeta cellobiosiphila* sp. is a facultative anaerobe under this genus, which uses a variety of monosaccharides and disaccharides as energy sources. However, most rapid growth occurs on cellobiose and fermentation yields significant amount of ethanol, acetate, CO₂, H₂ and small amounts of formate. It is predicted to be promising microbial machinery for industrial fermentation processes for biofuel production. The metabolic pathways that govern cellobiose metabolism in *Spirochaeta cellobiosiphila* are yet to be explored. The function annotation of the genome sequence of *Spirochaeta cellobiosiphila* is in progress. In this work we aim to map all the metabolic activities for reconstruction of genome-scale metabolic model of *Spirochaeta cellobiosiphila*.

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