

Genomic and metabolic analyses of microbial cellulose producer

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Bacterial cellulose nanofiber (CNF) is a polymer with a wide range of potential industrial applications. Several Komagataeibacter species, including Komagataeibacter xylinus as a model organism, produce CNF. However, industrial application of CNF has been hampered due to inefficient CNF production. Here, we present complete genome sequence and a genome-scale metabolic model (GEM) of *K. xylinus* DSM 2325 for metabolic engineering applications. To understand the metabolic characteristics of *K. xylinus*, its GEM KxyMBEL1810 was reconstructed using genome annotation. Random flux sampling analysis was used to predict gene overexpression targets, *pgi* and *gnd* genes, for the enhanced CNF production. This prediction was experimentally validated by individually introducing heterologous *pgi* and *gnd* genes. Batch fermentation of engineered *K. xylinus* overexpressing the *E. coli* *pgi* gene produced 3.15 g/L of CNF in a complex medium containing glucose, which was 115.5% higher than that (1.46 g/L) obtained with the control strain. These results should be useful resources for metabolic engineering of *K. xylinus* for the CNF production [Funding information: Samsung Advanced Institute of Technology].