

Genome-scale reconstruction and *in silico* analysis of *Escherichia coli* W for the elucidation of physiological features

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We newly reconstructed the genome-scale metabolic model of *Escherichia coli* W based on *E. coli* K-12 MG1655 model. *E. coli* W has several physiological features, such as fast-growing, low acetic acid production. After the genome-scale metabolic model of *E. coli* W was published, we 1) reflected the result of genome comparative analysis that was demonstrated with whole genome sequence and annotation data of *E. coli* W and K-12 MG1655, 2) utilized the genome-scale model to describe the growth phenotype and specific physiological features of *E. coli* W using fermentation data, and 3) also applied the model as a tool for generating the metabolic engineering strategy to improve the production of biochemicals such as L-valine. In conclusion, the revised genome-scale metabolic model successfully represented the physiological features of *E. coli* W. [This work was supported by the Technology Development Program to Solve Climate Changes from the Ministry of Education, Science and Technology (MEST) through the National Research Foundation of Korea (NRF-2012-C1AAA001-2012M1A2A2026556)]