

**Identification of flux-coupled genes for the improved prediction of microbial metabolism**

\_\_\_\_\_, \_\_\_\_\_, \_\_\_\_\_,\*  
(leesy@kaist.ac.kr\*)

Various numerical constraints was used to improve simulation accuracy of flux balance analysis (FBA) using genome-scale metabolic network models. In this sense, Flux-Coupled Genes (FCGs) whose expression levels change in a consistent manner with changes in their corresponding reaction fluxes across different conditions were identified. Seven most consistent FCGs (i.e., *zwf*, *gnd*, *rpe*, *sdhB*, *sdhD*, *sucA*, and *pfkB*) were searched from the comparative analysis of transcriptome and  $^{13}\text{C}$ -flux data of *Escherichia coli* at five different dilution rates. Accuracy of FBA with FCGs was then compared with conventional simulation approaches (e.g. FBA without FCGs and MOMA). FBA with FCGs is useful to operate due to the relative easiness of obtaining transcriptional information. [ This work was supported by the Technology Development Program to Solve Climate Changes on Systems Metabolic Engineering for Biorefineries from the Ministry of Science, ICT and Future Planning (MSIP) through the National Research Foundation (NRF) of Korea (NRF-2012M1A2A2026556). ]