

13C MFA and transcriptome of High Recombinant Protein Expression Sugar Transporter knockout E. coli

한재호, 정휘민, 임대균, 정규열<sup>1</sup>, 오민규<sup>†</sup>  
고려대학교; <sup>1</sup>포항공대  
(mkoh@korea.ac.kr<sup>†</sup>)

Most bacteria have evolved to maximize growth rate, with rapid consumption of carbon sources from the surroundings. However, fast growing phenotypes feature secretion of organic acid or ethanol and have reduced biomass yield in aerobic conditions. Several glucose uptake pathways' transporters or their subunits were knocked out in E. coli, the growth and glucose uptake rates decreased but acetate overflow was relieved and biomass yield was improved. Alteration of intracellular metabolism caused by the mutations was investigated with transcriptome analysis and 13C metabolic flux analysis (13C MFA). Transcription of genes related to glycolysis, chemotaxis, and flagella synthesis was downregulated, and that of gluconeogenesis, Krebs cycle, alternative transporters, quorum sensing, and stress induced proteins was activated in the sugar transporter mutants. Based on these findings, robust production hosts were constructed using the sugar transporter mutants. When pathway genes for producing value-added compounds ( $\gamma$ -aminobutyrate, lycopene) were introduced, the specific production yields of the compounds were improved significantly in the sugar transporter mutants.