

Microbial Production of 1,3-Diaminopropane in *Escherichia coli* through *in silico* Metabolic Flux Analysis김지하, 채동연, 김원준, 최 솔, 박시재<sup>1</sup>, 이상엽<sup>†</sup>KAIST; <sup>1</sup>명지대학교(leesy@kaist.ac.kr<sup>†</sup>)

1,3-Diaminopropane (1,3-DAP) is a compound which can be used as an intermediate in the preparation of many applications, including plastics, sequestering agents, and herbicides. Herein, *Escherichia coli* is engineered for the production of 1,3-DAP through genome-scale *in silico* flux analysis to find the most efficient metabolic pathways. By comparing heterologous C<sub>4</sub> and C<sub>5</sub> pathways, the C<sub>4</sub> pathway was found to be more efficient and *Acinetobacter baumannii* *dat* and *ddc* genes were introduced which encode 2-ketoglutarate 4-aminotransferase and L-2,4-diaminobutanolate decarboxylase respectively. The native *ppc* and *aspC* genes were overexpressed and the *pfkA* gene was deleted for increased productivity. Fed-batch fermentation of the final strain resulted in the production of 13 g l<sup>-1</sup> of 1,3-DAP in 69 h with the productivity of 0.19 g l<sup>-1</sup> h<sup>-1</sup> in a glucose minimal medium. [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 and NRF-2012M1A2A2026557).]