Application of metabolic flux analysis on the prediction of optimum metabolic pathways of various metabolites

Soon Ho Hong, Soo Yun Moon, Sang Yup Lee
Dept. of Chemical&Biomolecular Engineering,
Korea Advanced Institute of Science and Technology
TEL: +82-042-869-3930, FAX: +82-42-869-8800

The intracellular metabolic fluxes can be calculated by metabolic flux analysis, which uses a stoichiometric model for the intracellular reactions along with mass balances around the intracellular metabolites (1, 2, 3). In this study, metabolic flux analyses were carried out to estimate flux distributions for the maximum *in silico* yields of various metabolites in *Escherichia coli*. The maximum *in silico* yields of acetic acid and lactic acid were identical to their theoretical yields. On the other hand, the *in silico* yields of succinic acid and ethanol were only 83% and 6.5% of their theoretical yields, respectively. The lower *in silico* yield of succinic acid was found to be due to the insufficient reducing power, which could be increased to its theoretical yield by supplying more reducing power. The maximum theoretical yield of ethanol could be achieved when a reaction catalyzed by pyruvate decarboxylase was added in the metabolic network. Furthermore, the optimal metabolic pathways for the production of various metabolites could be proposed based on the results of metabolic flux analyses. In the case of succinic acid production, it was found that pyruvate carboxylation pathway should be used rather than phosphoenolpyruvate carboxylation pathway for its optimal production in *E. coli*.

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