Enhancement of Lycopene Biosynthesis in *Escherichia coli* using Metabolic Control and Pathway Analysis

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Abstract

In post-genomic era the fascinating approaches of metabolic engineering are constraints-based flux analysis on genome-scale model and metabolic control analysis on kinetics model. Constraints-based flux analysis is to calculate metabolic fluxes using linear programming with several constraints such as thermodynamic capacities, mass and charge conservation, and external measurements. On the other hand, metabolic control analysis is to find rate-controlling steps on metabolic networks. Metabolic control coefficients and elasticity represent the normalized partial derivative of the objective flux with respect to perturbed enzyme activities and concentrations, respectively. Metabolic control analysis on kinetic model, however, allows selecting potential rate-controlling reactions for enhancement of the interesting flux[1]. It was applied to lycopene production in *Escherichia coli*. Kinetics model containing lumped lycopene pathways with glycolysis and pentose phosphate pathway of *E. coli* was constructed. Metabolic control coefficients were calculated using Jarnac[2] (http://www.sbml.org). Consequently the dxs gene encoding for 1-deoxy-D-xylulose 5-phosphate synthase recorded the highest flux control coefficient. Then, metabolic control and pathway analysis was applied after the overexpression of the *dxs* gene. It has suggested that 6-phosphofroctokinase and phosphotransferase system be increased and pyruvate kinase decreased. It promises metabolic control analysis is useful for lycopene production in *E. coli*. Financially supported by the Korean Systems Biology Research program of the Korean Ministry of Science and Technology, and LG chemicals Chair Professorship. Hardware for computational analysis supported by the IBM-SUR program.

References

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