Metabolic Control Analysis for the Enhancement of Lycopene Biosynthesis in *Escherichia coli*

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In post-genomic era the fascinating approach of metabolic engineering is metabolic control analysis on kinetics model. Metabolic control analysis on kinetic model allows selecting potential rate-controlling reactions for enhancement of the interesting flux. Kinetics model containing lumped lycopene pathways with glycolysis and pentose phosphate pathway of E. coli was constructed. Metabolic control coefficients were calculated using Jarnac (http://www.sbml.org). Consequently the dxs gene encoding for 1-deoxy-D-xylulose 5-phosphate synthase recorded the highest flux control coefficient. Then, dynamic metabolic control 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. This work was financially supported by the Korean Systems Biology Research program (M10309090000-03B5002-00000) of the Korean Ministry of Science and Technology (MOST), the Brain Korea 21 of the Ministry of Education and LG chemicals Chair Professorship. Hardware for computational analysis supported by the IBM-SUR program.