Metabolic flux analysis for Poly(3-hydroxybutyrate) production by recombinant *Escherichia coli*

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The variation of intracellular metabolic flux distributions of normal and poly(3-hydroxybutyrate) [(P3HB)] producing *Escherichia coli* was simulated by metabolic flux analysis to evaluate the effect of P(3HB) production on intracellular metabolic fluxes of *E. coli* [2, 3, 4]. The metabolic network consists of 310 reactions and 295 metabolites were used. The TCA cycle flux competes with P(3HB) biosynthesis pathway for acetyl-CoA decreased significantly during P(3HB) production. Increase of Entner-Doudoroff (ED) pathway flux supply acetyl-CoA to P(3HB) biosynthesis pathway was also found out [1]. To estimate the role of ED pathway on the P(3HB) production, the mutant strain HM114, which is defective in the activity of 2-keto-3-deoxy-6-phosphogluconate aldolase (Eda) was used as host strain. The P(3HB) content of HM114 (pJC4) decreased to one half of that obtained with parent strain KS272 (pJC4), and HM114 recovered P(3HB) productivity when *eda* gene was co-overexpressed.

Acknowledgement

This work was supported by the National Research Laboratory Program (2000-N-NL-01-C-237) of the Korean Ministry of Science and Technology (MOST).

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