Identification of the Characteristics between the Biomass Formation and Succinic Acid Production Based on the Flux Balance Analysis in *Escherichia coli*

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In this work, the specific strategy is applied for identifying the correlation between the biomass formation and succinic acid production by limiting the levels of succinic acid production. This approach for succinic acid production is based on the correlation by the deletions of candidate genes of the C3-C4 reactions present in the central metabolic networks. This metabolic networks of the model incorporate 814 metabolites and 979 metabolic reactions. Specific growth rate is quantified by a biomass equation derived from the drain of biosynthetic precursors into *E. coli* biomass with their appropriate ratios (Neidhardt et al., 1996). The metabolic network is constructed under steady state assumption on the basis of flux measurements, the unknown fluxes within the metabolic reaction network are evaluated by flux balance analysis (FBA), subject to the constraints satisfying mass conservation and reaction thermodynamics (Edwards et al., 2002; Lee and Papoutsakis, 1999). The effect of gene deletion is achieved by fixation of the reaction flux at zero. In all genes tested in C3-C4 reactions, nine cases are identified necessary for overproduction of succinate. The resultant gene deletion list are selected and disrupted to redirect for succinate production experimentally.

References

1. Edwards JS, Covert M, Palsson B. 2002.Metabolic modelling of microbes: the flux-balance approach. Environ. Microbiol. 4: 133-140.
2. Ma H, Zeng A. 2003. Reconstruction of metabolic networks fromgenome data and analysis of their global structure for various organisms. Bioinformatics 19: 270-277
3. Neidhardt FC, Curtiss R, Ingraham JL, Lin ECC, Low KB, Magasanik B, Reznikoff WS, Riley M, Schaechter M, Umbarger HE. 1996. Escherichia coli and Salmonella. Washington DC: ASM Press.
4. Lee SY, Papoutsakis ET. 1999. Metabolic engineering. New York: Marcel Dekker.