Examination of metabolic control mechanism in glycolysis: using MCA (metabolic control analysis) methods

Jong hwa Jin¹, Bum soo Lee¹, Bo ra Kim¹, Ui sub Jung¹, Sukmin Hong¹, Sang Yup Lee², Yong-Ho In³, Jinwon Lee¹

¹Department of Chemical Engineering, Kwangwoon University, Seoul 139-701, Korea

²Department of Chemical & Biomolecular Engineering, Korea Advanced Institute of Science and Technology, Daejeon, Korea

³Eighth floor, Sung Woo Bldg., 1424-2, Seocho 1-dong, Seocho-gu, Seoul 137-864 Bioinformatix Inc., Korea

Abstract

Glycolysis is central pathway and it has very important function that connected with other metabolic pathways (TCA cycle, pentose phosphate pathway, fatty acid synthesis, amino acid synthesis, oxidation, respiratory chain). The study of glycolysis pathway is very actively being investigated more than others in the metabolic pathways. So, its reaction mechanisms, metabolites, and reaction steps have been examined in many other researches. But most of these researches have been studied not overall study but individual steps independently.

Therefore we need clearly examination and elucidation of glycolysis metabolic mechanism. In this study, first we have investigated for construction of glycolysis metabolic network and second we tried to collect all the variables as much as possible which might affect the glycolysis metabolic pathway. Also we could know a time course glycolysis' metabolites with simulation

References

- 1. Gregory N., Stephanopoulos, Aristos A. Aristidou, Jens Nielsen (1998), "Metabolic engineering", Academic Press.
- 2. Agius, L., Sherrat, H. S. A., (Eds.), "Channeling in intermediary Metabolism", 53-70, Portland Press.
- Varma, A., Pallson, B. O. (1994), "Metabolic flux balancing: basic concepts, scientific and pratical use", Biotechnology 12, 994-998.
- 4. Edwards, J. S., Ramakrishna, R., Schilling, C. H., Palsson, B., O., Lee, S. Y. (1999), "Metabolic Engineering", *Marcel Deker*, 13-57.
- 5. Morgan, J., A., Rhodes, D. (2002), "Mathematical modeling of plant metabolic pathways", Journal of Metabolic Engineering 4, 80-89.

- Neal Mitra (2001), "Whole cell simulations: an exponential increase in biological data and in computational power allow for and integrative approach and cellular biology", MBB 752a.
- 7. Tomita, M. (2001), "Whole-cell simulation: a grand challenge of the 21st century", *Trends Biotechnol.* **19**(6), 205-210.
- 8. http://www.genome.ad.jp/kegg/kegg2.html
- 9. http://biocyc.org/
- 10. http://www.brenda.uni-koeln.de/
- 11. Tomita, M., et al., "E-CELL: software environment for whole-cell simulation", Bioinformatics 15(1), 72-84.
- 12. http://mbel.kaist.ac.kr/mfn/requirements.html
- 13. Mendes P. (1997), "Biochemistry by numbers: simulation of biochemical pathways with gepasi 3", *Trends Biochemical Sci.* **22**(9), 361-363.
- 14. Mendes P. (1993), "Gepasi: a software package for modelling the dynamics, steady states and control of biochemical and other systems", *Computer Applicated Bioscience* **9**(5), 563-571.
- Hoefnagel, M. H. N., Starrenburin, M., J. C., Martens, D. E., Hugenholtz, J., Kleerebezem, M., Van Swam, I. I., Bongers, R., Westerhoff, H. V., Snoep, J. L. (2002), "Metabolic engineering of lactic acid bacteria, the combined approach: kinetic modelling, metabolic control and experimental analysis", *J. Microbiology* 148, 1003-1013.
- 16. Fell, D. (1997), "Understanding the control of metabolism," Portland press.
- 17. Stephanopoulos, G., Sinskey, A. J. (1993), "Metabolic engineering methodologies and future prospects", *TibTech.* 11, 392-396.