Metabolic Engineering Strategies and Applications Employing Information from Genomics, Transcriptomics, Proteomics and Fluxomics

Sang Yup Lee

Department of Chemical & Biomolecular Engineering, Department of BioSystems, BioProcess Engineering Research Center, and Bioinformatics Research Center, Korea Advanced Institute of Science and Technology, Daejeon, Korea (http://mbel.kaist.ac.kr, leesy@kaist.ac.kr)

Metabolic engineering plays an essential role in modern biotechnology as it allows various bioprocesses to be competitive with existing chemical processes. Metabolic engineering can be defined as the purposeful modification of metabolic pathways to achieve a number of biotechnolgically relevant desired goals. Recent advances in genomics, transcriptomics, proteomics, metabolomics and even fluxomics are allowing us to examine the metabolic pathways and networks at systems level. Here I present the results taken in our group to achieve a number of biotechnological objectives by metabolic engineering based on systems biotechnological approaches. biotechnology, the term coined by Systems biology, can be defined as (by following the definition of biotechnology by the OECD) "The application of science and technology at systems level to living organisms as well as parts, products and models thereof, for the production of knowledge, goods and services". In practice, all the information and data available (and/or generated in house) from traditional and modern biological sciences, including genomics, transcriptomics, proteomics, metabolomics, fluxomics and etc., are all integrated at systems level for the development of bioprocesses as well as parts thereof. In this lecture, systems biotechnological approaches taken to enhance the production of recombinant proteins and primary metabolites will be presented. [This lecture is public presentation of the 5 year research carried out by the recipient of the First Young Scientist's Award from the President of Korea and the KAST.1

References

- 1. Lee, S. Y. and Papoutsakis, E.T. (1999), Metabolic Engineering, Marcel Dekker, USA.
- 2. Lee, D. Y., Yun, H. S., Lee, S.Y., and Park, S.W., MetaFluxNet: the management of metabolic

- reaction information and quantitative metabolic flux analysis, Bioinformatics, in press.
- 3. Han, M. J., Jeong, K. J., Yoo, J. S, and Lee. S. Y. (2003), Engineering *Escherichia coli* for increased production of serine-rich proteins based on proteome profiling, *Appl. Environ. Microbiol.* **69**, 5772-5781.
- 4. Choi, J. H., Lee, S. J., Lee, S. J., and Lee, S. Y. (2003), Enhanced production of insulin-like growth factor I fusion protein in *Escherichia coli* by the coexpression of the down –regulated genes identified by transcriptome profiling, *Appl. Environ. Microbiol.* **69**(8), 4737-4742.
- 5. Han, M. J. and Lee, S. Y., Proteome profiling and its use in metabolic and cellular engineering, *Proteomics*, in press.