Combining in silicogenome scale metabolic analysis with comparative genomics for strain improvement

Sang Yup Lee

Korea Advanced Institute of Science and Technology Dept. Chemical & Biomolecular Eng., 373-1 Guseong-dong, Yuseong-gu, Daejeon, Chungnam, 305-701, Korea T: 82-42-869-3930, F: 82-42-869-3910, leesy@kaist.ac.kr

As the number of completely sequenced genomes increases, the use of genome-scale *in silico* metabolic models for strain improvement has been receiving great attention. Using these genome-scale models, the effects of genetic and/or environmental perturbations on cellular metabolism can be analyzed and predicted by means of various modeling and simulation approaches. Here I report the results obtained in my group towards strain improvement by combined use of *in silico* metabolic flux analysis and comparative genomics. The method of multiple optimization in designing improved microorganisms will also be reported. Using a primary metabolite not abundant in *E. coli* as examples, the impact of this new strategy on strain design will be described. For instance, double knock-out strains showing improved performance could be designed based on these *in silico* dual optimization studies, which otherwise would have been extremely difficult to perform. Finally, approaches being taken in my group towards integrating various high-throughput omics data with the results of genome-scale *in silico* modeling and simulation will be described. [This work was supported by the Korean Systems Biology Research Program from the MOST. Further supports by the BK21 program, LG Chem Chair Professorship, and IBM-SUR program are appreciated.]