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

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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.]