Metabolomics and Systems Biotechnology

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Recent advances in high-throughput experimental techniques supported by bioinformatics have resulted in rapid accumulation of a wide range of omics data at various levels, thus providing a foundation for in-depth understanding of biological processes. Even though our ability to analyze these omics data in a truly integrated manner is currently limited, new targets for strain improvement can be identified from these global data. Along with these high-throughput experimental techniques, *in silico* modeling and simulation are providing powerful solutions for deciphering the functions and characteristics of biological systems. Consequently, systems-level engineering of microorganisms can be best achieved by integrating high-throughput experiments and *in silico* experiments. High-throughput quantitative analysis of metabolites has become possible as increasingly sophisticated NMR, gas chromatography mass-mass spectrometry (GC-MS), gas chromatography time-of-flight mass spectrometry (GC-TOF), and liquid chromatography-mass spectrometry (LC-MS) equipments have been developed. Comparative analysis of metabolite profiles under genetic and environmental perturbations renders it possible to analyze physiological states of the cells. Given that metabolome data can be analyzed together with the fluxome data, metabolome profiling will become an increasingly popular tool in systems biotechnological research. In this lecture, I will focus on metabolome profiling and its use in systems biotechnology. [This work has been supported by the KSBRG from the MOST, IBM SUR program, LG Chem Chair Professorship and BK21 program.]