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Enhanced production of recombinant proteins by systems biotechnological approaches

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The recent development of high-throughput experimental techniques has resulted in rapid accumulation of a wide range of biological data and information at different levels: genome, transcriptome, proteome, metabolome, and fluxome data. This technology-driven discovery science is now allowing the identification of unprecedentedly large numbers of individual components and molecules of a biological system, thus providing a foundation for a profound understanding of biological processes. It is currently true that the identification of these components and molecules alone is not sufficient to characterize their functions and interactions in a global scale. However, even not truly global scale information and knowledge newly found from such omics studies can be successfully employed for strain development. Also, it is increasingly accepted that *in silico* analysis of the cellular network is promising to discover a knowledge map for deciphering the functions and characteristics of the biological systems. *In silico* genome-scale metabolic models can be used to understand the status of the complex cellular system and investigate inherent cellular properties. As such, hypothesis-driven *in silico* experiments can be invaluable to improve our ability to predict the cellular behavior of microorganisms under various genetic and environmental conditions. In this lecture, I will show some successful examples of "local engineering of cellular components based on global omics data" toward enhanced production of recombinant proteins. Also, systems biotechnological research cycle that allows efficient strain development by combining *in silico* and wet experiments will be discussed.

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