

Proteomic study of Streptomyces for Secondary Metabolites

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Bacterial genome project spurred on the level of understanding a microorganism from several genes involved in specific cellular processes to metabolic network and its system as a whole. With the genome information, recent fast development in analytical tools and their automation in separation science and protein chemistry made a great stride in proteomics. The major contribution was exerted by mass spectrometry on high throughput protein sequence analysis. Combined with 2D-gel image analysis, specific tagging molecule design and nano-scale chromatography, large-scale comparative proteome analysis enabled us to do reevaluation of old findings as well as to identify new key biomarkers and control elements in the secondary metabolite production of industrial microorganisms, such as Streptomyces. We were interested in more detailed understanding of global regulatory and pathway specific regulatory genes which govern the synthesis of antibiotics in Streptomyces. As the global regulatory genes and pathway specific regulatory genes, quorum sensing(QS) pathway and pathway specific transcriptional regulatory genes, their protein-protein interactions and sigma factors were analyzed and investigated, respectively. In this talk, we will compare the QS pathway in the three different Streptomyces species, and show our approaches and preliminary results in proteomic study of using mass spectrometry, DNA-bound beads and 2D-gel.