

**Transcriptome analysis of production of poly- $\gamma$ -glutamic acid in recombinant  
*Escherichia coli***

윤성호, Jiang Hao, 이상엽

한국과학기술원 생명화학공학과

전화 (042) 869-3930, FAX (042) 869-8800 (이상엽)

**Abstract**

Poly- $\gamma$ -glutamic acid ( $\gamma$ -PGA) is biodegradable and water-soluble polymer which can be applied in fields of food, medicine, cosmetics, waste water treatment and surgical adhesive<sup>1)</sup>. Although some wild type *Bacillus* species produce  $\gamma$ -PGA as extracellular products with reasonably high efficiency, there are some disadvantages: extreme strain instability leading to appearance of  $\gamma$ -PGA non-producing cells, degradation of  $\gamma$ -PGA and production of byproducts. To solve these problems, there was attempts to produce  $\gamma$ -PGA in *E. coli*. Transcriptome analysis employing high-density DNA microarray enabled global understanding of cellular physiology and metabolism, and consequently can be used to identify connections between regulatory circuits and metabolic pathways that were previously unknown<sup>2)</sup>. Even though the microarray-based studies can provide useful information on gene expression profiles under various conditions, little is reported about the application of microarray data to real industrial bioprocess. In this study, we made recombinant *E. coli* producing high molecular  $\gamma$ -PGA, and fed-batch cultures were carried out to overproduce  $\gamma$ -PGA in *E. coli*. Transcriptome analysis using *E. coli* microarray containing 2,850 genes including all functionally known and putative ones, was performed for finding out physiological and metabolic change during fed-batch cultivation of this strain. We also show how the microarray analysis can contribute to enhance the productivity of bioproduct in real bioprocess.

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**References**

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