Transcriptome Analysis of *Escherichia coli* during Overproduction of Recombinant Protein by Fed-batch Fermentation

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Abstract

Escherichia coli has been the workhorse for the production of various useful recombinant proteins. In *E. coli*, recombinant proteins can be produced as soluble form or insoluble form by the expression conditions such as host, expression system, concentration of inducer, culture temperature and so on. Large-scale production of recombinant proteins is generally achieved by fed-batch cultivation. Recently, various techniques to compare the whole cellular transcriptome in response to various environmental changes have been developed, which are able to understand global cellular physiology and metabolism. Transcriptome analysis allows comparison of global changes in gene expression that occur in response to varying environmental conditions. In this study, we report analysis of transcriptomes of *E. coli* during overexpression of recombinant human leptin protein as an insoluble form by using Panorama™ DNA array. Fed-batch fermentation of *E. coli* was carried out by pH-stat strategy until the maximum human leptin contents as an inclusion body was as high as 18% of the total protein contents and transcriptomes were analysed to understand metabolic and physiological changes by the inclusion body formation.

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