

Proteomic analysis of *Escherichia coli* cultured in oleic acid and its application

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Abstract

Many proteomic studies have been reported for response to extreme stresses including pH, temperature, antibiotics, organic solvents, cell density, nutrients starvation and anaerobiosis¹. Such a comprehensive analysis of every protein induced or repressed by stimuli may be provide the necessary information to understand a response in the cell².

Proteome profiles were compared to identify global translational differences in cultures of *Escherichia coli* W3110 strain grown in the presence of glucose and oleic acid. From over 2,000 spots on the 2D-gels, we identified about 100 proteins by comparing them with the *E. coli* database SWISS-2DPAGE or by Q-TOF MS/MS analysis. To examine the influence of the presence of oleic acid in the protein level, we compared the proteome of *E. coli* W3110 strain cultured in oleic acid with that of glucose. The levels of about 33% (29 proteins) of total identified proteins were altered in the presence of oleic acids. Also, we identified a new interesting protein for protein production, the results of which will be reported in detail.

In conclusion, we identified global translational changes in the presence of oleic acid, applied them to foreign protein production and confirmed that its yield was notably higher than conventionally available protein production system. Furthermore, it could be a new strategy of metabolic engineering based on proteomic analysis for utilizing diverse carbon sources such as oleic acid for protein production. This work was supported by the Korean Systems Biology Research Grant (M10309020000-03B5002-00000) from the Korean Ministry of Science and Technology. Further supports by LG Chem Chair Professorship and IBM SUR program are greatly appreciated.

Reference

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