

Comparative proteomic analysis of four biotechnologically important *Escherichia coli* for rational host selection

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Escherichia coli B and K12 derivatives are commonly used in laboratory and bioindustry due to their fast growing and easy cultivation. Here, using two-dimensional gel electrophoresis coupled with MS/MS, we profiled the proteomes of an *E. coli* B derivative and three K12 derivatives grown with a defined medium at exponential phase and stationary phase, respectively. A correlation between the proteome profiling and metabolic pathway analysis revealed significant metabolic differences among the four strains, which provided valuable information for the production of various primary metabolites. Also, analysis of amino acid synthesis and protein processing shed light on rational host selection for recombinant protein production. In conclusion, comparative proteomic analysis provided valuable information for rational host strain selection. [This work was supported by the Korean Systems Biology Research Project (M10309020000-03B5002-00000) of the Ministry of Education, Science and Technology (MEST). Further supports by the World Class University Program from the MEST, LG Chem Chair Professorship, Microsoft, and IBM SUR program are appreciated.]