Identification of large-scale Escherichia coli periplasmic proteomes

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Typcially, subcellular fractionation has been used for in-depth proteome analysis. This technique has the added benefits of reducing sample complexity, identifying additional unique proteins, localizing newly discovered proteins to specific organelles, and in some cases, allowing functional validation. In contrast to membrane proteins, a complete inventory of E. coli periplasmic proteins has not yet been provided. Here, a more optimized method of periplasmic fractionation was developed. High-resolution periplasmic proteome reference maps of two strains, E. coli K-12 MG1655 and B BL21 (DE3), were constructed using the optimized cold shock method. A total of 137 proteins, 69 proteins from the MG1655 gels and 71 proteins from the E. coli BL21(DE3) gels, were unambiguously identified with LC-MS/MS. The differences of periplasmic proteins between two strains will be discussed. [This work was supported by the Basic Science Research Program (2010-0008826) and Converging Research Center Program (2009-0093652) through the National Research Foundation of Korea funded by the Ministry of Education, Science and Technology]