

Comparison of periplasmic proteomes in *Escherichia coli* K-12 and B strains한미정*

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Here, periplasmic proteome reference maps of the *E. coli* K-12 and B strains were compared. Of the 145 proteins identified, 61 proteins were conserved in the two strains, whereas 11 and 12 strain-specific proteins were identified for the *E. coli* K-12 and B strains, respectively. In addition, 27 proteins exhibited differences in intensities greater than 2-fold between the K-12 and B strains. Distinctive differences between the two strains included several proteins that were caused by genetic variations, hydrolytic enzymes, particularly phosphatases, glycosylases, and proteases, and many uncharacterized proteins. Compared to previous studies, the localization of many proteins, including 30 proteins for the K-12 strain and 53 proteins for the B strain, was newly identified as periplasmic. This study identifies the largest number of proteins in the *E. coli* periplasm as well as the dynamics of these proteins. Additionally, these findings will be useful for studying protein secretion and may provide new strategies for the enhanced secretory production of recombinant proteins. [This work was supported by the Basic Science Research Program (2010-0008826) through the NRF of Korea funded by the MEST]