

In-depth analysis of proteomic differences between *Escherichia coli* K-12 and B strains using multiplexed isobaric tandem mass tag (TMT) labeling

한미정[†], 이훈재, 이진모, 김일순
동양대학교
(mjhan75@dyu.ac.kr[†])

In this study, an in-depth analysis of the physiological behavior of the *Escherichia coli* K-12 and B strains at the proteomic level was performed using six-plex isobaric tandem mass tag (TMT)-based quantitative mass spectrometry. Additionally, the best lysis buffer for increasing the efficiency of protein extraction was selected from three tested buffers prior to quantitative proteomics analysis. This study was the first to identify the largest number of proteins in both *E. coli* strains and to show the dynamics of these proteins. In this poster, distinctive differences in the proteomes between the two strains will be presented. Compared to previous studies, these proteomic results provided a more holistic view of the overall state of the *E. coli* cell in a single proteomic study and revealed significant insights into why the two strains show considerably distinct phenotypes. [This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (No. 2010-0008826 and 2015R1D1A1A01057315)]