107f Quantitative Proteomic Analysis of E. Coli Using Isobaric Tags

Kunal Aggarwal, Leila H. Choe, Zsofia Franck, and Kelvin H. Lee

We will examine the use of an isobaric tagging shotgun approach to simultaneously study protein expression of *E. coli* at four different biological states. In this study, 780 unique proteins, representing all the major functional groups, were identified at p<0.05. These include some low abundance proteins and transcription factors. The choice of a more stringent protein identification criteria (p<0.01) did not significantly change the functional groups that were represented in the data set. In general, the genes corresponding to the detected proteins were observed to have relatively higher mRNA expression than all the protein coding genes that were expressed. Proteins were quantified using independent measurements from multiple peptides. Exclusion of outliers using multiple statistical tests significantly improved the observed coefficients of variation for quantified proteins. Protein quantitation using isobaric tags and 2-DE was compared and both these methods were observed to yield reasonably similar protein expression ratios. However, the isobaric tagging method demonstrated lower coefficients of variation in quantitation of proteins that were poorly stained on 2-DE gels. Not all the proteins detected using 2-DE were identified using the isobaric tagging shotgun approach.