

INTRODUCTION TO PROTEOMICS AND AN EXAMPLE OF ITS APPLICATION

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In this seminar, use of proteomic analysis to study microorganism will be discussed. In particular, our recently published work [Kim, Y. et al., *Fungal Genet. Biol.* (2007), doi:10.1016/j.fgb.2006.12.001] using proteomic analysis to study the model filamentous fungus *Aspergillus nidulans*' adaptation to mild osmotic stress will be highlighted. Comparative proteomic analysis via two dimensional gel electrophoresis (2DE) and matrix-assisted laser desorption ionization/time-of-flight (MALDI-TOF) mass spectrometry was used to assess molecular level events associated with this phenomenon. Thirty of 90 differentially expressed proteins were identified. Sequence homology and conserved domains were used to assign probable function to twenty-one proteins currently annotated as "hypothetical." In osmoadapted cells, there was an increased expression of glyceraldehyde-3-phosphate dehydrogenase and aldehyde dehydrogenase, as well as a decreased expression of enolase, suggesting an increased glycerol biosynthesis and decreased use of the TCA cycle. There also was an increased expression of heat shock proteins and Shp1-like protein degradation protein, implicating increased protein turnover. Five novel osmoadaptation proteins of unknown functions were also identified. This work therefore demonstrates that proteomic analysis is a valuable tool to study filamentous fungi and allows us to elucidate systematic protein level changes in the fungi even under minor perturbations in their environment.