Integrated Approach to Study Mouse Embryonic Stem Cell Proteome

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Study of the proteome of the embryonic stem cells (ES) cells is important to understand active pathways, regulatory networks and their dynamics. We have been studying protein expression in mouse embryonic stem cell line R1-9 and ABI and have integrated the data with transcriptomics studies as well as with proteomics studies with the same and other cell lines from other laboratories. Such integrated approach would help in consolidation of the protein expression data and the biochemical pathways operational in the stem cells and their differentiation lineages. Proteins expressed in mouse ES cells R1-9, AB1 were studied using LC-ESI MS/MS and LC-MALDI MS/MS approaches after pre fractionation (SDS PAGE) of total cellular proteins or the proteins from the ES cells nuclei. Proteins were identified and identifications verified against the transcriptomics data - DNA microarrays, SAGE, and ESTs. We have thus identified more than 2000 proteins with high confidence. Pathway analysis of these short listed proteins was carried out using KEGG, IPA, GenMAPP and their gene ontology classification revealed among them transcription regulators, signal transducers, cell cycle and differentiation molecules along with other general classes of proteins. Using this list of proteins and those identified by other groups with the same stem cell lines, putative regulatory pathways operational in these cells are being constructed to further explore their role in stem cells. In addition, functional annotation of proteins corresponding to many still unidentified / uncharacterized mouse genes is also being attempted and will be discussed.

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