A systems biology analysis of metastatic melanoma using a three-dimensional difference in gel electrophoresis

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Melanoma is an ideal model to study molecular mechanisms of metastatic progression because melanoma usually develops through a series of architecturally and phenotypically distinct stages that are progressively more aggressive, culminating in highly metastatic cells. In this study, to identify key proteins and pathways involved in tumor progression, comparative proteome analysis on two melanoma cells with low and high metastatic potentials was conducted using a three-dimensional difference in gel electrophoresis (3-D DIGE) technology, consisting of sample cydyes-labeling, microscale solution isoelectric focusing prefractionation, and 2-D DIGE. The majority of protein changes are closely associated with many aspects of the pathophysiology of cancers, such as cell death and growth and tumorigenesis. In addition, cellular pathways related in oncogenes and tumor suppressor genes were found to be prevalent metastatic melanoma progression by the Ingenuity Pathway Analysis. Here, these results will be discussed in detail. [This work was supported by the Basic Science Research Program (2010-0008826) through the National Research Foundation of Korea funded by the Ministry of Education, Science and Technology]