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Proteomic Analysis of Human Embryonic Stem Cells

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The application of embryonic stem(ES) cells in biomedical field provide us new therapeutic paradigm to cure unsolving human diseases. Above all, to establish and develope ES cell therapeutics, the mass production of undifferentiated ES cells and the characterization of ES cells is strongly need. However in spite of the possibility of ES cell therapeutics, its basic characteristics still remains unclear probably due to shortage of our knowledge about proteins functioning in the ES cells. There have been few studies about proteome of mouse ES cells, however, the proteome of human ES cells has never been reported. In this study, we performed proteomic analysis of undifferentiated human ES cells based on 2D gel electrophoresis with Coomassie and silver staining and mass-spectrometry. We detected 675 individual spots, some of which we identified by mass spectrometry and database searching. We present here a first set of 85 proteins identified which are the normally expressed of human embryonic stem cells. They include house keeping genes, all type of t-complex gene, cytoskeleton-related proteins, a protein previously shown to be involved in cell proliferation, enzymes, oxidative-stress related proteins, and a few of transcription-regulating factors. We may suggest that these proteins may have certain roles in the maintenance of the undifferentiated state of human ES cells. Spinal cord injury is a major medical problem worldwide, and realistic goals of functional repair have only recently been acknowledged. Recent advances in neural injury and repair, and the progress towards development of neuroprotective and regenerative interventions are basis for increased optimism. A number of potential approaches

aim to optimize functional recovery after spinal cord injury. They include minimizing the progression of secondary injury, manipulating the neuroinhibitory environment of the spinal cord, replacing lost tissue with transplanted cells or peripheral nerve grafts, remyelinating denuded axons, and maximizing the intrinsic regenerative potential of endogenous progenitor cells. Embryonic stem (ES) cells can give rise to all neural progenitors and they represent an important scientific tool for approaching neural repair. However functional recovery in movement after stem cell transplantation into spinal cord have been reported from several case in laboratory animals, it still remains unclear to understand the molecular mechanism of recover after transplantation of stem cells. Selective marker expression in transplanted ES cell derived neural cells is providing new insights into transplantation and repair not possible previously. These features of ES cells will produce a predictable and explosive growth in scientific tools that will translate into discoveries and rapid progress in neural repair. Two dimensional-based Proteome analysis was employed to identify the proteins associated with functional recovery after spinal cord injury. Male Sprague-Dawley rats were anesthetized with sodium pentobarbital and subjected to spinal cord injury (SCI) model. Rats were laminectomized and SCI was induced using NYU spinal impactor at T9 spinal segment. Human embryonic stem (ES) cells were transplanted into a rat spinal cord 1 week after SCI. A behavioral test using BBB locomotor rating scaling was performed every one week for 1 months. Hindlimb performance was modestly improved in human ES cell-transplanted rats compared to vehicle-treated rats. Five proteins displayed different expression levels in the spinal cords of stem cell transplanted rats. Among these proteins, GFAP is dramatically changed in the spinal cords of stem cell transplanted rats, even though the total expression level of GFAP is not quietly changed. GFAP immunoreactivity is quietly distinct in the spinal cords of stem cell transplanted rats with immunohistochemical localization. It may be suggested that GFAP act an important role during functional recovery of movement after stem cell-transplant into injured rat spinal cords. To our knowledge, this is the first report about the 2DE based proteome of human embryonic stem cells and insight into differentiation-related proteins.