Proteomic Analysis of Mesenchymal Stem Cells Isolated from Low Grade and High Grade Glioma

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Introduction

Malignant brain tumors comprise a small percentage of tumors in adult population with an incidence of 4–5 in 100,000 per year; however, their malignant nature has made them the fourth leading cause of cancer death. Gliomas are the most common primary brain tumors. Management of these tumors is implicated with several challenges; identification of molecular biomarkers for glial tumors can improve management of them in several aspects including diagnosis, classification, and treatment. Proteins as the functional molecules in the cells are the main effectors of normal cellular and disease processes. Proteomics is the large-scale analysis of protein expression and post-translational modifications. Through comparative proteomic profiling of brain tumor tissue versus normal tissue, molecular alterations leading to tumorigenesis can be detected. Also proteomics can be used for detection of potential diagnostic, prognostic and treatment-assessing biomarkers. Isolation of mesenchymal stem cells (MSC) from gliomas have been reported recently. These cells contribute to the aggressive behavior of glial tumors by altering the environment favorable for the proliferation of glioma stem cells. Proteomic analysis of these cells can elucidate their molecular properties and mechanism of action.

Methods

Nine patients with newly diagnosed intracranial glioma of different grades were included. Isolation and culture of mesenchymal stem cells was done in DMEM/F12 culture medium containing 10% fetal bovine serum and 1% penicillin/streptomycin. Differential proteomic analysis of cells cultured from low grade vs. high grade tumors was performed by 2-DE and MALDI -TOF-MS.

Results

In the cells isolated from low grade glioma, three isoforms of vimentin, two isoforms of transgelin and cathepsin-B, mitochondrial Mn-SOD, endoplasmin and ezrin were detected to be upregulated; whereas in the cells isolated from high grade tumors, five isoforms of vimentin, transgelin, Mn-SOD, pyruvate kinase (PKM), GTP-binding nuclear protein Ran and 40S ribosomal protein SA were detected to be overexpressed.

Conclusions

For the first time we analyzed the proteomic profile of mesenchymal stem cells isolated from glioma tumors. Endoplasmin was introduced as a novel protein found to be associated with glioma brain tumors.

Learning Objectives

Through proteomic analyses the molecular mechanisms of tumorigenesis and malignant behaviors of tumoral cells can be elucidated.

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