Comparative Proteome Profiling of Medulloblastoma and Astrocytomas Cell Lines

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INTRODUCTION: Medulloblastoma is the most common malignant tumor of the central nervous system (CNS) in children. Despite 70–85% of the patients survive for 5 years after diagnostic, most of them will suffer sequelae due to the aggressive treatment. Psychiatric disorders and cognitive dysfunction may be consequences. Thereby, the medulloblastoma research is focused to obtain the early diagnosis and new therapies. Tumor samples are valuable sources for medulloblastoma studies, however, the major limitation is the lack of cerebellar material as non neoplastic tissue. DAOY cell line is widely used in studies of medulloblastoma. The aim of this study was the characterization of proteome of DAOY cell line compared to U87MG and T98G which demonstrated a differential migratory ability.

MATERIAL AND METHODS: DAOY, U87MG and T98G were cultivated in DMEM. Proteomic analysis was based on cation-exchange/reverse phase liquid chromatography coupled to ESI-Q-TOF-MS of tryptic peptides. Proteins were identified by Mascot software using Swiss-Prot database.

RESULTS AND DISCUSSION: Proteomic analysis identified 57 proteins in DAOY, 66 in U87MG and 97 proteins in T98G. Gene Ontology analysis does not discriminate any relevant biological or molecular function within the cell lines. Proteomics analysis showed markedly vimentin abundance in U87MG and T98G compared to DAOY. Vimentin has been described as EMT biomarker and its expression level modulated the cell migratory ability.

CONCLUSION: The differential abundance of vimentin on these cell lines may be implicated in their migratory ability.

Word Keys: medulloblastoma, DAOY, U87MG, T98G, mesenchymal-epithelial transition.

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