PROTEOMIC STUDIES OF GLIOMA CELL LINE T98G AND BRAIN TISSUES: PAVING THE WAY FOR CONSTRUCTION OF GLIOMA GEL DATABASE.

^{1,2,3} <u>Gimenez, M.</u>; ³ Solano, K.R.; ³ Orellana, M.D.; ⁴ Oba-Shinjo, S.M.; ⁴ Marie, S.K.N; ^{1,2,3} Rosa, J.C.

Depto. Biologia Celular e Molecular e Bioagentes Patogênicos, Faculdade de Medicina de Ribeirão Preto, Universidade de São Paulo; ² Centro de Química de Proteínas; ³ Fundação Hemocentro de Ribeirão Preto, ⁴ Depto. de Neurologia, Faculdade de Medicina de São Paulo, Universidade de São Paulo.

The most common form of glioma is the glioblastoma multiforme (GBM) grade IV, an aggressive and malignant tumor which can either develop in a rapid de novo manner (primary) or by secondary progression from less malignant glioma (astrocytoma grade II or III). We developed a proteomic study based on 2D gel electrophoresis (2DGE) and mass spectrometry (MS) to compare and identify differential protein expression between T98G cell lines derived from GBM and surgical fragment of "normal" brain tissue (n=3) excised from epileptic patients. T98G was used to compare protein profiling as cultured cells versus brain tissue and to develop a proteomic platform to analyze proteins in very limited amount mimicking raw samples from brain tumors. We will attempt to construct a consistent and reproducible glioma gel database which will correlate protein pattern of glioma (grade II, III and IV) by 2DGE, protein identification by MS and clinical histopathological records from individual patient. This strategy may contribute to elucidate biological process involved in glioma tumoral progression. FAPESP