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Posterior cranial fossa pediatric brain tumors: a comparative proteomic study

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Introduction: The oncogenesis mechanisms of brain tumours are still partly unknown. Genetic alterations that drive cell transformation and malignant progression result in tumour-specific changes in protein expression. The identification of individual proteins or protein clusters expressed in neoplastic tissue could uncover critical mediators of tumour progression and identify surrogate markers for diagnosis, prognosis, and therapeutic response. Proteome profiles reflect the biological phenotype of individual tumours more accurately than transcriptome analyses, bacause changes in gene expression do not always correlate with protein expression. Moreover proteomic analyses can detect post-translational modifications and different isoforms which may specifically affect disease progression. Preliminary results of the comparative proteomic study of pylocitic astrocytoma and medulloblastoma posterior cranial fossa pediatric brain tumors tissues is here presented.

Methods: Tumor tissues soluble fraction was analyzed by LC-MS following both top-down and bottom-up approaches, respectively analyzing entire and enzymatic (trypsin) digested proteins. Protein and peptides characterization was achieved by high resolution LC-ESI-LTQ-Orbitrap-MS manually and with auxiliary bioinformatic software for tandem MS data elaboration.

Conclusions: The combination of the top-down and bottom-up approaches for the proteomic characterization of pylocitic astrocytoma and medulloblastoma tumor tissues allowed the identification of different proteins and peptides with high confidence. The data evidenced interesting differences in the presence of interesting peptides and truncated proteins strongly characterizing the most malignant medulloblastoma. These data could be of great help for the individuation of diagnosis and prognosis biomarkers, potential therapeutic targets and for the elucidation of pediatric posterior cranial fossa tumors tumorigenesis processes.