## Network Based Molecular Profiling of Intracranial Ependymoma over Spinal Ependymoma

Authors : Hyeon Su Kim, Sungjin Park, Hae Ryung Chang, Hae Rim Jung, Young Zoo Ahn, Yon Hui Kim, Seungyoon Nam Abstract : Ependymoma, one of the most common parenchymal spinal cord tumor, represents 3-6% of all CNS tumor. Especially intracranial ependymomas, which are more frequent in childhood, have a more poor prognosis and more malignant than spinal ependymomas. Although there are growing needs to understand pathogenesis, detailed molecular understanding of pathogenesis remains to be explored. A cancer cell is composed of complex signaling pathway networks, and identifying interaction between genes and/or proteins are crucial for understanding these pathways. Therefore, we explored each ependymoma in terms of differential expressed genes and signaling networks. We used Microsoft Excel<sup>™</sup> to manipulate microarray data gathered from NCBI's GEO Database. To analyze and visualize signaling network, we used web-based PATHOME algorithm and Cytoscape. We show HOX family and NEFL are down-regulated but SCL family is up-regulated in cerebrum and posterior fossa cancers over a spinal cancer, and JAK/STAT signaling pathway and Chemokine signaling pathway are significantly different in the both intracranial ependymoma comparing to spinal ependymoma. We are considering there may be an age-dependent mechanism under different histological pathogenesis. We annotated mutation data of each gene subsequently in order to find potential target genes.

Keywords : systems biology, ependymoma, deg, network analysis

Conference Title : ICMSB 2016 : International Conference on Metabolomics and Systems Biology

Conference Location : Paris, France

Conference Dates : July 25-26, 2016