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(KEGG) pathway database, at the moment there are 140 known apoptosis-associated genes in human genome. In addition, it is known that many microRNA molecules, a major class of small RNA molecules that post-transcriptionally inhibit gene expression, can regulate those apoptosis-associated genes. Therefore, there is a need for better elucidation of the interplay between microRNA molecules and apoptosis-associated genes.

In this talk I will present our research on microRNA and gene expression profiling of high-grade serous ovarian cancer. We used microarray technology which allows us to determine the expression patterns of more than 2,500 human microRNAs or over 26,000 protein-coding genes in a single experiment. Furthermore, from this sea of data, using various bioinformatic tools and databases, we were able to construct the microRNA:target gene interaction networks related to (dys)regulation of apoptosis in high-grade serous ovarian cancer. These results could help us to understand better the etiology of this type of ovarian cancer and to discover new diagnostic and prognostic biomarkers, as well as new targets for therapies.

Keywords: apoptosis genes; microRNAs; expression; microarrays; ovarian cancer.

THE ROLE OF DISHEVELLED GENE AND PROTEIN IN ASTROCYTIC BRAINE TUMORS

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Astrocytic brain tumors are the most common primary central nervous system neoplasms and are classified according to their lineage of origin, histology, behavior and prognosis into four WHO grades. Wnt signaling pathway is one of the basic mechanisms of cell signaling as evidenced by its participation in a numerous processes in the cell. The most interesting role of this signaling pathway for us is its involvement in brain tumorigenesis. We aim to investigate the incompletely understood role of Dishevelled (DVL) gene family, which is considered to be the central hub of wnt signaling.

Genetic changes of *DVL1*, *DVL2* and *DVL3* genes were analysed by PCR/loss of heterozygosity (LOH)/microsatellite instability (MSI) methods using Spreadex elec-

trophoresis. Protein expressions and localizations of DVL1, DVL2 and DVL3 proteins were analyzed by immunohistochemistry.

In this study, results showed that DVL expression is significantly higher in astrocytomas than in normal brain tissue. Furthermore, expression increases with the pathological grade of tumors.

DVLs may play a important role in formation and invasion of astrocytic brain tumors. Future studies using an expanded cohort may help to improve the understanding of the role of individual DVL in astrocytoma as well as its potential as a molecular diagnostic marker or a therapeutic target.

Keywords: DVL1; DVL2; DVL3; Wnt signaling pathway; astrocytic brain tumors.

EXPRESSION OF SURVIVIN IN INVASIVE AND NONINVASIVE UROTHELIAL CARCINOMA OF THE URINARY BLADDER

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Objective: The inhibitor of apoptosis protein survivin regulates apoptosis and cell cycle. There are conflicting data in the literature regarding relationship between the degree and localisation of survivin expression and behavior of urinary bladder carcinoma. Here, we correlated immunohistochemical localization of survivin with the histologic diagnosis of noninvasive and invasive urothelial carcinoma of the bladder (UCB).

Methods: A total of 82 histopathologically confirmed UCB were recruited. Of these 32 were non-invasive, 27 had invasion of lamina propria and 23 had confirmed invasion of muscularis propria of the urinary bladder. Immunohistochemistry was used to detect survivin expression in tumor tissues. The intensity of the reactions was assessed semiquantitatively, using three expression categories; 0-5% (low expression), >5%-50% (moderate expression), and >50% (high expression).