all RNA molecules synthesized by the process of transcription, while proteomics can be defined as a large-scale study of proteins, their functions and structures. Since proteins are functional building blocks of cells, the information on proteome of a given cell or tissue in health or disease is a difficult but rewarding task to accomplish. Furthermore, we can also study epigenome (all epigenetic changes), metabolome (complete set of all metabolites in an organism), microbiome (all genomes of microbiota that symbiotically live in or on us), connectome (a map of all the neural connections of human brain) and exposome (the totality of exposures received by an individual during a lifetime). Today there is indeed a whole lot of omics and we wanted to stress the importance of future holistic approach in integrating the knowledge omics has rewarded us.

***Keywords**:* omics; genomics; epigenomics; proteomics; metabolomics; microbiomics; exposomics; connectomics.

THE INTERPLAY BETWEEN MICRO-RNA MOLECULES AND APOPTOSIS-ASSOCIATED GENES IN HIGH-GRADE SEROUS OVARIAN CANCER

Petar Ozretić

Laboratory for Hereditary Cancer, Division of Molecular Medicine, Ruđer Bošković Institute, Zagreb, Croatia

Ovarian cancer is the seventh most frequent tumor type in women and the fifth leading cause of cancer-related deaths among women worldwide. In Croatia there are around 500 new cases annually while about 300 women die every year because of ovarian cancer. Its high death rate, particularly for a serous type which is the most frequent, is a result of the fact that most patients are diagnosed at an advanced stage of the disease. Therefore, there is a need for new knowledge about what causes ovarian cancer as well as new approaches toward better earlier diagnosis and therefore better effect on therapy.

One of the hallmarks of tumor cells is their ability to resist apoptosis, a process of programmed cell death. Deregulation of apoptosis plays a key role in the pathogenesis and progression of cancer, and leads also to chemotherapy resistance, what is a characteristic and one of the reasons of high mortality rate of high-grade serous ovarian cancer. According to the Kyoto Encyclopedia of Genes and Genomes

(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

Anja Kafka

Laboratory of Neuro-Oncology, Croatian Institute for Brain Research, School of Medicine University of Zagreb, Zagreb, Croatia; Department of Biology, School of Medicine University of Zagreb, Zagreb, Croatia

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-