ABSTRACTS

of the 4th Scientific Symposium on *Apoptosis and Neoplasms*

ONLY ONE HEALTH, AND SO MANY OMICS

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The lecture was based on the article (N. Pećina-Šlaus and M. Pećina. Only one health and so many omics. Cancer Cell Int 15:64, 2015, DOI 10.1186/s12935-015-0212-2) in which the modern large-scale analyses have been reviewed. The title is paraphrasing the famous saying of Victor Schlichter from Buenos Aires children hospital in Argentina who said "How unfair! Only one health, and so many diseases". New approaches based on wide profiling methods in studying biological and medical systems are bringing large amounts of data typically stored in big data repositories. Several repositories important for human health today are: The Human Genome Project, The Cancer Genome Atlas (TCGA), The Cancer Genome Project, The Human Proteome Project (HPP), Human Epigenome Project, The Human Metabolome Database, Human Microbiome Project, The Human Connectome Project and The Human Exposome Project. They use specialized algorithms, analyze and present findings to be more comprehendable, thus introducing system sciences. The most common omics employed in the research of complex diseases are genomics -the analysis of complete genetic material of an organism –the complete nucleotide sequence of its DNA. The human genome is comprised of 3.2 billion nucleotides, but contains only 23,500 protein-coding genes. Closely connected to genomics are exomics, the part of the genome formed by exons. Exomes are the protein coding content of the genetic code and the human exome consists of 180,000 exons, roughly 1-2 % of our total genome. Transcriptomics study transcriptome that encompasses

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

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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