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CONCERNING MODERN SYSTEM BIOLOGY MATERIALS DISCUSSED AT THE SCIENTIFIC CONFERENCE «ASSESSMENT OF QUALITY OF LIFE IN CANCER PATIENTS COVERED IN EXPERIMENTAL AND CLINICAL ONCOLOGY PUBLICATIONS: CHALLENGES AND OPPORTUNITIES»

October 3—4, 2024, Kyiv, Ukraine

The Conference was organized on the initiative of the R.E. Kavetsky Institute of Experimental Pathology, Oncology and Radiobiology of the National Academy of Sciences of Ukraine, the State Institution "SP Grigoriev Institute of Medical Radiology and Oncology of the National Academy of Medical Sciences of Ukraine", and public organizations "National Association of Oncologists of Ukraine" and "Ukrainian Society for Cancer Research". The cancer patient's health and the quality of life (QoL) was put in the focus of this conference. Various edges of cancer research were discussed by researchers together with medical doctors, clinical scientists, specialists in demography, economics, law, and the general public.

Presentations and discussions also concerned new technologies, big data assessment, system biology, bioinformatics, and the current diagnostic and therapeutic approaches. Two famous Swedish scientists spoke at the conference via video link.

Professor Ingemar Ernberg (Karolinska Institutet, Stockholm, Sweden) presented a talk «The Origin of Life, Cancer Biology and Drug Development». It was a very interesting and philosophical lecture discussing the cross-talks between theoretical physics, biology, medicine, and mathematics, including the historical development.

Professor Ernberg spoke about the Swedish chemist, baron Jöns Jacob Berzelius (1779—1848) who was one of the greatest scientists, a medical

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Professor Ingemar Ernberg

Professor Erik Aurell

doctor and a chemist. His experimental research was on the edge of medicine and chemistry, and he tried to explain the phenomenon of living organisms by complex interaction between chemical compounds. Actually, a modern approach is to consider that "Living things are made up of interactions in networks resulting in complex systems".

Physicists tried to explain life, starting from 1944, when Erwin Schrödinger wrote the book "What is life? Physical aspects of the living cell with mind and matter". This question was thought to be answered, when Francis Crick and James Watson discovered the DNA structure in 1953. However, even today, after 71 years, the question "What is life?" remains unsolved, because there is a gap between understanding of single molecules (DNA, RNA, proteins, etc.) and life of cell and cellular organisms. This is the reason why a new field of science appeared — complex systems biology. All living organisms are complex systems, they are parts of more complicated networks. And yet, all living organisms are built of networks upon networks. Moreover, not a single gene but a complex network determines the morphology of cells.

Prof. Ernberg mentioned the suggestion that the Origin of Life is in an ancient network of 404 reactions, converting hydrogen, CO_2, and NH_3 into amino acids, bases, and co-factors. He thinks that cell types could be considered as "attractors" upon the change in cell plasticity, when cellular internal network could be re-shuffled. In other words, the cell choses the most negative potential energy to function and behave.

Cancer arises when cancer cells occupy novel, illegitimate attractors among the certain cell type attractors, i.e., the original attractor is re-established. Prof. Ernberg presented this point of view together with co-authors in their book "Rethinking Cancer. A new paradigm in the postgenomic era", published in 2021.

Due to the complex cellular networks, Prof. Ernberg proposed to develop anticancer drugs against libraries of peptides.

Another very important talk was presented by Prof. Erik Aurell (KTH Royal Institute of Technology, Stockholm, Sweden).

Prof. Aurell discussed the recent advances in using large amounts of genome data. He talked about the revolution in biology that started upon the development of artificial intelligence (AI), and machine learning.

The collection of big data and their analysis is a highly important and promising task. A bright example of the possibility to share and work with big data is illustrated by the finding of epistatic interactions which were stable in GISAID data until August 2020, using 50,000 genomes. GISAID is the abbreviation of the Global Initiative on Sharing Avian Influenza Data, based in Germany. During the COVID19 pandemic, GISAID became one of the main repositories for the data on SARS-CoV-2 genome, containing millions sequences of viral genomes.

The proposed mathematical analysis of big data collection can be used in cancer biology, when many traits are not well explained by variability of single genes.

These talks were taken with great enthusiasm and with a fruitful panel discussion. More such works should be done to shed light on the cancer development and possible ways to cure cancer.