

Study of Genomic Parameters in the Case of Lung Cancer

Nano Mikaia

e-mail: nano.mikaia957@ens.tsu.edu.ge

Department of Biology

Faculty of Exact and Natural Sciences

Ivane Javakhishvili Tbilisi State University

Cancer is one of the leading causes of morbidity and mortality in the world. According to World Health Organization data, the current level of death caused by cancer, which is about 8.2 million in the world, will increase by more than 13 million before 2030 (Cancer Statistics Center 2016).

The purpose of our work was: to determine the variation of the genomic parameters in individuals with lung cancer; to study the activity of ribosomal cistrones; to determine the level of mutations of the chromosomes (aberrations, aneuploidy, polyploidy, early chromatid segregation (ECS), fragile sites); to measure the frequency of acrocentric chromosomes and ribosomal cistrones, also determining the overall level of methylation.

The study material was the cells of stimulated peripheral blood lymphocytes from lung cancer patients and healthy donors.

The results show that in cells of lung cancer patients statistically significant was increased the structural (aberrations, fragile sites) and quantitative (ECS, aneuploidy, polyploidy) disorders of chromosomes compared to the control group. In the 58% of male patients the aneuploidy was induced by the lost of Y chromosomes. In patients with lung cancer, the frequency of centromeric fringe sites have increased in comparison to the control group, while the frequency of medial fragile sites decreased.

In patients with lung cancer, the frequency of acrocentric chromosomes is relatively higher than in control group that is indicating the increase of transcriptional activity of ribosomal genes.

The intensity of 15 chromosome entering in associations in all patients with lung cancer was increased compared to the control group. The frequency of Ag⁺ chromatids in patients with lung cancer is significantly increased and the frequency of 2-point Ag⁺ chromatids is reduced compared to the control data.

The overall level of DNA-methylation is reduced, which is consistent with literature data regarding DNA-methylation changes in lung cancer.

Reference:

- Cancer Statistic Centre 2016
- Key Statistics for Lung Cancer. American cancer society. National Center for Health Statistics (NCHS), Centers for Disease Control and Prevention, 2016.