



Fund “Nauka” Project № 17019 Resume – Competitive-based Session 2017:

“Study of single nucleotide polymorphisms in genes for non-coding RNAs in patients with colorectal cancer in order to identify new diagnostic, prognostic and predictive biomarkers for the Bulgarian population”

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Colorectal cancer is the second most common cancer in women and the third most common cancer in men and is one of the leading causes of cancer-related deaths. New approaches in the stratification of colorectal cancer, based on the establishing of the status of individual patients in terms of molecular mechanisms could determine and regulate carcinogenesis, and indicate diagnostic, prognostic and predictive biomarkers and define new therapeutic strategies.

This project is aimed to study single nucleotide polymorphisms (SNPs) as new genetic biomarkers in Bulgarian patients with colorectal cancer. The used methods are SNPs genotyping by validated TaqMan PCR test and qPCR expression analysis.

Studies of the presence of SNPs in the genes for non-coding RNAs and their role as diagnostic, prognostic and predictive factors are new, few in the literature, especially for Caucasians. This study is the first for the Bulgarian population. Therefore, the present study will also contribute to increasing scientific knowledge in the field.

As a result of the completed project tasks, the following scientific results were obtained:

- ❖ The genotypic distribution and allelic frequencies of five selected SNPs in miRNAs genes among a sample of the Bulgarian population were established – rs7372209 (in the miRNA-26a-1 gene), rs2910164 (in the miRNA-146a gene), rs2682818 (in the miRNA-618 gene), rs3593 (in the gene cluster for miRNA-143 and miRNA-145), and rs322931 (in the gene for miRNA-181b);
- ❖ Polymorphisms – rs2682818 and rs353293 were studied for the first time for association with colorectal cancer in Caucasian patients;
- ❖ Recessive G allele of rs353293 was associated with a low risk of CRC among the Caucasians or at least among the Bulgarian population;
- ❖ The heterozygous genotypes of rs2910164-miRNA-146a and rs2682818-miR-618 were associated with a low risk of CRC;

- ❖ The TT rs7372209 and AA rs353293 genotypes were associated with better overall survival in CRC patient;
- ❖ The TT rs7372209 genotype was assessed as a risk factor for right colon tumor development.

Publications with results of the project from 2019-2022 have been cited, so far - February 2022, four times in foreign studies.