

**МАТЕРИАЛЫ
КОНГРЕССА**

**CONGRESS
PROCEEDINGS**



ТОМ 1 / PART 1

IX МЕЖДУНАРОДНЫЙ КОНГРЕСС

IX INTERNATIONAL CONGRESS

**БИОТЕХНОЛОГИЯ:
СОСТОЯНИЕ
И ПЕРСПЕКТИВЫ
РАЗВИТИЯ**

**BIOTECHNOLOGY:
STATE OF THE ART
AND PERSPECTIVES**

**20-22 ФЕВРАЛЯ 2017
МОСКВА, ГОСТИНЫЙ ДВОР,
ИЛЬИНКА, 4**

**20-22 FEBRUARY, 2017
ILYNKA 4, GOSTINY DVOR,
MOSCOW**

Ген	miRNA	Начало сайта, нт.	ΔG , кДж/моль	$\Delta G/\Delta G_m$, %	Длина, нт.
NFE2L2	miR-2-3313-3p	442-448	-138÷-144	87-91	25
NFE2L2	miR-3-8100-5p	443-446	-129÷-132	88-90	24
NFE2L2	miR-9-28523-5p	441-453	-115	92	20
NFE2L2	miR-2-4453-3p	444-447	-121÷-123	92-94	21

Примечание. * - сайты в 3'UTR, ** - сайты в CDS

Результаты этого исследования продемонстрировали, что miRNA могут осуществлять регуляцию экспрессии генов в 3'UTR, 5'UTR и CDS. Эти данные показали важность поиска сайтов в 5'UTR, так как там выявлена повышенная плотность сайтов.

Литература:

1. Londin E. et al. Analysis of 13 cell types reveals evidence for the expression of numerous novel primate- and tissue-specific microRNAs//PNAS. 2015. E1106-E1115.

UDC 577.21

INTERACTION OF miRNAs WITH mRNAs OF SOME GENES IN THE DEVELOPMENT OF STOMACH CANCER

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Identified miRNA binding sites with mRNA of genes that are key participants in stomach cancer. Established binding sites with high energy of hybridization which are arranged in the 5'UTR, CDS and 3'UTR in mRNA of these genes. Found four miRNA binding sites with full complementarity. The research results are useful for the development of methods for early diagnosis of cancer.

Key words: miRNA, mRNA, stomach cancer.

miRNA plays the important role in the regulation of oncogenes. Worldwide developed molecular non-invasive methods of early diagnosis of stomach cancer based on the analysis of blood changes in the concentration of metabolites, proteins, DNA, miRNA etc. Prediction of miRNA binding sites and searching them in mRNA oncogene essential for the development of methods for early diagnosis of cancer.

For this work it was created a database for the genes involved in the development of stomach cancer and a database of miRNAs. As the targets for miRNA was studied genes, which proteins are involved in carcinogenesis of the stomach. Search of target genes for miRNA was performed using MirTarget program, created in our laboratory. The program defines the beginning of the binding sites of miRNA with mRNA; the location of binding sites in 5'UTR, CDS, 3'UTR; the free energy of hybridization ($\Delta G/\Delta G_m$, where ΔG_m is the free energy of interaction of the miRNA with complementary nucleotide sequence), and interactions of nucleotides of miRNA with mRNA. For analysis it was selected 106 genes from Genbank (<http://www.ncbi.nlm.nih.gov/>), most frequently involved in the development of stomach cancer.

The binding sites of miRNA was considered in the ratio $\Delta G/\Delta G_m$ is equal to more than 85%. It is established that 20% of the studied genes do not have binding sites with 3701 miRNAs [1]. 106 mRNAs of genes associated with 255 miRNAs in 431 binding sites with $\Delta G/\Delta G_m$ ratio more than 87%. Among them, 103 binding sites located in CDS, 157 binding sites – in 5'UTR and 171 binding sites – in 3'UTR. Identified mRNA of *KDM1A*, *HDAC4* and *NFE2L2* genes, having fully complementary binding sites with miRNA. mRNA of *NFE2L2* gene has multiple binding sites in 5'UTR. miR-2-4453-3p, miR-19-21199-3p and miR-15-32047-5p, miR-1-155-3p, miR-2-3313-3p and miR-19-33623-3p have homological binding sites in mRNA of *NFE2L2* gene. mRNA of *HDAC4* gene has in 5'UTR thirty two binding sites with miRNA. In mRNA of *HDAC4* gene miR-19-21199-3p, miR-1-2121-3p, miR-2-3313-3p binding sites located in 5'UTR; miR-16-40163-5p in 3'UTR; miR-6-17789-3p in CDS of mRNA. Consequently, all regions of mRNA could interact with miRNA. In mRNA of *HDAC4*