

МАТЕРИАЛЫ
КОНГРЕССА

CONGRESS
PROCEEDINGS



TOM 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

CHKA	mir-1-2121-3p (1)	422	-151	96	24
CHKA	miR-19-33623-3p (1)	422	-140	94	25
HMGAA2	mir-1-2121-3p (1)	544	-146	93	24
HMGAA2	miR-19-33623-3p (1)	544	-142	96	25
LATS2	mir-1-2121-3p (1)	1851	-142	91	24
LATS2	miR-19-33623-3p (1)	1851	-132	89	25
USP7	mir-1-2121-3p (1)	15	-138	88	24
USP7	miR-19-33623-3p (1)	15	-134	90	25
USP7	mir-1-2121-3p (1)	92 ± 99	-140 ± -149	89 ± 95	24
USP7	miR-19-33623-3p (1)	92 ± 99	-132 ± -138	89 ± 93	25

Примечание. В скобках указано число сайтов связывания.

Литература:

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2. Lordin 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.

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INTERACTION MIRNAS WITH MRNAS OF SOME GENES INVOLVED IN LUNG CANCER DEVELOPMENT

Mamirova A.A., Ivashchenko A.T., Niyazova R.E.

Al-Farabi Kazakh National University, Almaty, Kazakhstan
050038, Almaty, al-Farabi avenue 71,
e-mail: Raygul.Niyazova@kaznu.kz

Characteristics of binding sites of miRNA pairs (miR-10-29282-3p and miR-15-36862-3p, miR-11-27078-5p and miR-3-5147-5p, miR-1-2121-3p and miR-19-33623-3p) that have identical binding sites with mRNAs of CDK6, ITGA11, SSX2, CEBPA, CHKA, HMGAA2, LATS2 and USP7 genes involved in lung cancer development were established.

Key words: miRNA, mRNA, gene, lung cancer, diagnostics.

Lung cancer is the leading cause of death in worldwide. MiRNAs, that specifically bind with mRNA of target-genes and inhibit protein translation, are used for the diagnostics of the disease. Search of miRNA and target-genes' mRNA associations aiming for use them in early non-invasive diagnostics of this disease. The MirTarget program defines the following features of binding: the start of the initiation of miRNAs binding to mRNAs; the localization of miRNAs binding sites in the 5'UTRs, CDSs and 3'UTRs of the mRNAs; the free energy of hybridization ΔG (kJ/mole); the ratio $\Delta G/\Delta G_m$ (%) which was determined for each site (ΔG_m equals the free energy of miRNAs binding with its perfect complementary nucleotide sequence); the schemes of nucleotide interactions between the miRNAs and the mRNAs [1]. We identified several pairs of miRNAs from 3701 miRNA [2], which have from one to several identical binding sites with mRNAs of one (single) gene (Table). miR-10-29282-3p and miR-15-36862-3p have six binding sites with mRNAs of genes that indicate strong dependence of gene expression from each miRNA. Starts of binding sites are common for both miRNAs, so only one of them can interact with one mRNA. However, if two miRNAs have similar concentrations, they can bind with equal probability because the values of ΔG are similar.

miR-11-27078-5p and miR-3-5147-5p are more surprising, they bind with mRNA of ITGA11 and SSX2 genes (Table). Both of miRNAs have close characteristics of interaction and 19 identical binding sites with mRNA of ITGA11 gene. These miRNAs have 10 identical binding sites with mRNA of SSX2 gene. miR-1-2121-3p and miR-19-33623-3p have two identical binding sites with mRNA of CEBPA gene. This pair of miRNAs have two binding sites, divided on a few tens of nucleotides in the mRNAs of CHKA and USP7 genes. mRNAs of HMGAA2 and LATS2 genes contain one binding site of both miRNAs. Identified association of miRNAs and genes mRNAs can be used in the diagnosis of lung cancer.