Russian Academy of Sciences, Siberian Branch
Institute of Cytology and Genetics

The Ninth International Conference on Bioinformatics of Genome Regulation and Structure\Systems Biology

ABSTRACTS

BGRS\SB-2014
NOVOSIBIRSK, RUSSIA
JUNE 23–28, 2014

THE FEATURES OF BINDING SITES OF miR-619-5P, miR-5095, miR-5096 AND miR-5585-3P IN THE mRNAs OF HUMAN GENES

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Key words: miRNA, mRNA, miR-619, binding site, human

Motivation and Aim: The actions of miRNAs on the cell cycle, apoptosis, differentiation, growth and development in animals have been shown. Connections between miRNA expression and the development of various diseases has been established. miRNA concentrations change in cancer and cardiovascular diseases. Metabolic disturbances necessarily change miRNA concentrations in cells. It is possible to normalize some processes using miRNAs. The aforementioned roles do not encompass the full list of the biological processes in which miRNAs participate, which proves the importance of their biological functions. The connections between the majority of miRNAs and their target genes will remain unknown.

Methods and Algorithms: MirTarget program defines the localization of miRNA binding sites in the 5'UTRs, CDSs and 3'UTRs of the mRNAs; it calculates the free energy of hybridization (ΔG, kJ/mole) and the ratio $\Delta G/\Delta G_m$ (%), where ΔG_m equal to the free energy of miRNA binding with completely complementary nucleotide sequence. The binding sites of miRNAs with mRNAs were selected with $\Delta G/\Delta G_m$ ratio of 90% or more.

Results: The binding of 2,563 human miRNAs with the mRNAs of 12,175 human genes was calculated. It was established that miR-619-5p, miR-5095, miR-5096 and miR-5585-3p bind with high affinity to the mRNAs of the 1215, 832, 725 and 655 genes, respectively.

miR-619-5p has 1811 binding sites on 1215 target mRNAs. Of these, 1772 miR-619-5p binding sites are located in 3'UTRs, 26 sites are located in 5'UTRs and 13 sites are located in CDSs. The mRNAs of 197 genes have completely complementary binding sites for miR-619-5p ($\Delta G/\Delta G_m = 100\%$). The mRNAs of 27 genes have four binding sites. Seven genes have five binding sites, and the mRNAs of the *CATAD1, ICA1L, GK5, POLH* and *PRR11* genes have six miR-619-5p binding sites. The mRNAs of the *OPA3* and *CYP20A1* genes have eight and ten binding sites, respectively. All of these sites are located in 3'UTRs. miR-5096 has 997 binding sites on 832 target mRNAs. Of these, 984 miR-5096 binding sites are located in 3'UTRs, nine sites are located in 5'UTRs and four sites are located in CDSs. The mRNAs of 42 genes have completely complementary binding sites for miR-5096 ($\Delta G/\Delta G_m = 100\%$). The mRNAs of the *IP09* gene have four binding sites. The *PRR11* gene have five binding sites. The mRNAs of the *OPA3* and *CYP20A1* genes have six and eleven miR-5096 binding sites, respectively. All of these sites are located in 3'UTRs. We found that 655 target gene mRNAs have 734 binding sites. Fourteen of these binding sites are located in 5'UTRs, eight sites are located in CDSs and 712 sites are located in 3'UTRs. The mRNAs of two genes have completely complementary binding sites for miR-5095. The mRNAs of the *OPA3,* and *SPN* genes each have four binding sites.

The mRNAs of 725 target gene have 844 binding sites for miR-5585-3p. Nine of these binding sites are located in 5'UTRs, two sites are located in CDSs and 833 sites are located in 3'UTRs. The mRNAs of the *CYP20A1* and *GPR155* genes each have four binding sites.

Conclusion: Studied miRNAs have binding sites in the 3'UTRs, CDSs and 5'UTRs. The mRNAs of many genes have multiple miR-619-5p, miR-5095, miR-5096 and miR-5585-3p binding sites. Groups of mRNAs with the ordering of the miR-619-5p, miR-5095, miR-5096 and miR-5585-3p binding sites were established.