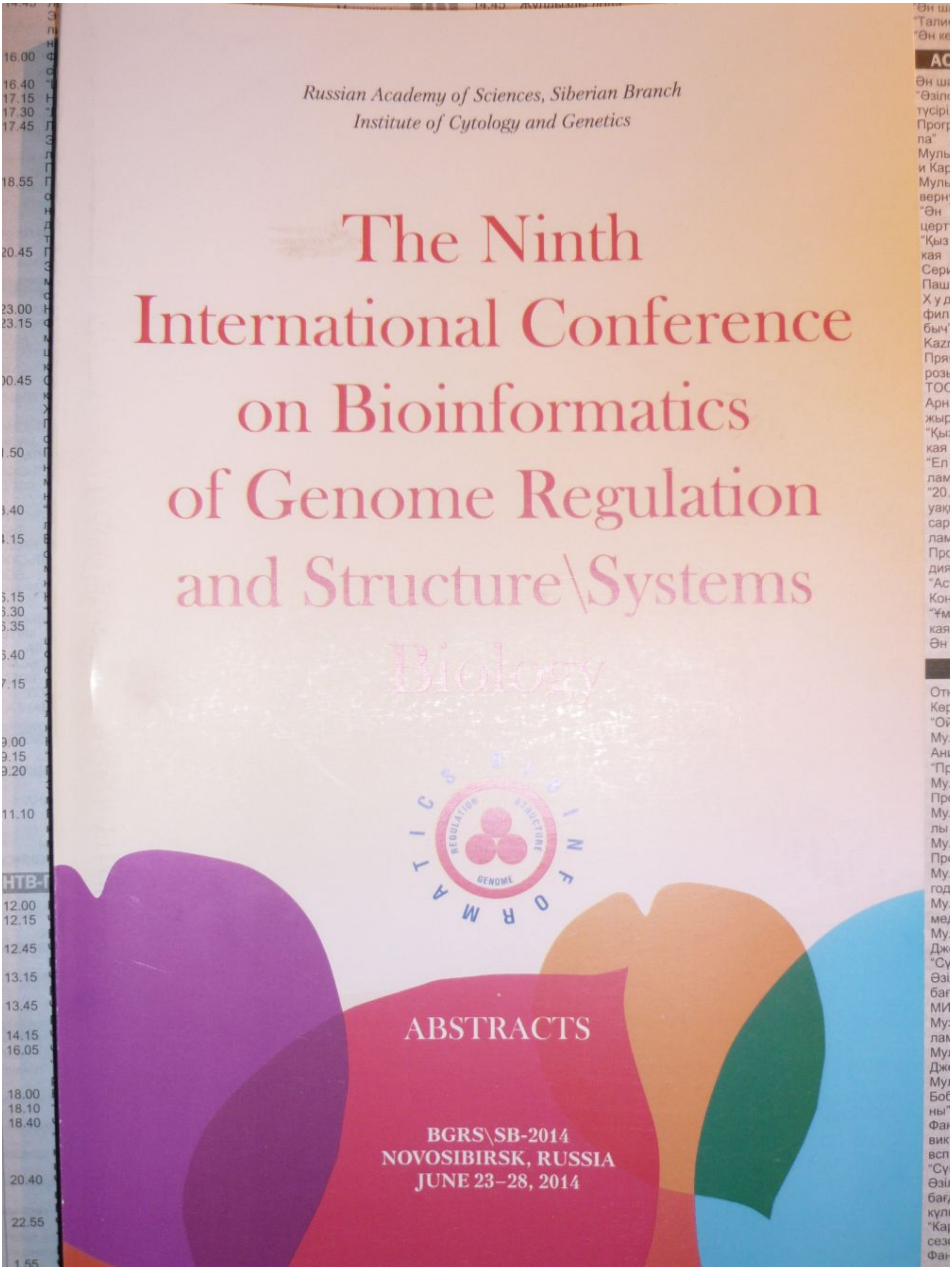

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ABSTRACTS

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FEATURES OF INTERACTIONS BETWEEN miR-1273 FAMILY AND mRNA OF TARGET GENES

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Motivation and Aim: miRNAs participate in the post-transcription regulation of gene expression. miRNAs participate in many pathological processes. Changes in the miRNA concentration have been shown to occur during the development of breast, lung, esophageal, stomach, intestine, prostate and other cancers. In this work, we studied the binding of 2,563 miRNAs with 12,175 mRNAs. The majority of these genes participate in the development of cancer and other diseases.

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 by $\Delta G/\Delta G_m$ ratio of 90% or more.

Results: The miR-1273 family consists of miR-1273a, miR-1273c, miR-1273d, miR-1273e, miR-1273f, miR-1273g-3p, miR-1273g-5p, miR-1273h-3p and miR-1273h-5p. It was found that the miRNAs of miR-1273 family have binding sites on mRNAs of 33 to 1,074 target genes, with a free energy hybridization of 90% or more of its maximum value.

We found that miR-1273g-3p has 1,330 binding sites on 1,074 mRNAs. Of those, 69 miR-1273g-3p binding sites are located in 5'UTRs, 38 sites are located in CDSs and 1,223 sites are located in 3'UTRs. The mRNAs of seven genes have completely complementary binding sites for miR-1273g-3p ($\Delta G/\Delta G_m = 100\%$).

The mRNAs of 766 genes contain 886 miR-1273f binding sites. Of those, 45 sites are located in 5'UTRs, 40 sites are located in CDSs and 801 sites are located in 3'UTRs. The mRNAs of ten genes have completely complementary binding sites for miR-1273f ($\Delta G/\Delta G_m = 100\%$). The mRNAs of 582 general target genes have pair sites for both miR-1273g-3p and miR-1273f. Of those, 24 mRNAs are located in 5'UTRs, 18 are located in CDSs and 540 are located in 3'UTRs. miR-1273g-3p and miR-1273f binding sites in all of the tested mRNA are located at distance of 12 nucleotides.

We found 449 miR-1273e binding sites on the mRNAs of 413 target genes. Of those, 19 binding sites are located in 5'UTRs, nine sites are located in CDSs and 421 sites are located in 3'UTRs. The nucleotide sequences of paired miR-1273g-3p and miR-1273e binding sites located in the 5'UTR and their adjacent parts have high homology level. The mRNA segments in CDSs containing paired miR-1273g-3p and miR-1273e binding sites also have a high degree of homology. The paired miR-1273g-3p and miR-1273e binding sites are found in the 3'UTR of 300 genes, and they have a high degree of homology. The 3'UTR of target genes have paired miR-1273g-3p and miR-1273a binding sites that are also located in the 5'UTR, with three overlapped nucleotides.

Conclusion: The arranged binding sites of the miR-1273 family are located in the 5'UTR, CDS or 3'UTR of many mRNAs. Five repeating regions containing some of the miR-1273 family's binding sites were found in the 3'UTR of several target genes. The oligonucleotides of miR-1273 family binding sites that are located in CDSs coded for homologous oligopeptides in the proteins of target genes. The nucleotide sequences of mRNAs (99nt) with arranged binding sites for the miR-1273 family were established. Many target genes for miR-1273 family participate in tumorigenesis.