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THE PROPERTIES OF MIRNA INTERACTION WITH 5' AND 3' UTR MRNA GENES HAVING NUCLEOTIDE REPEATS

A.M. Belkozhayev, R.E. Niyazova

Al-Farabi Kazakh National University, Faculty of Biology and Biotechnology, Almaty, Republic of Kazakhstan

Several diseases are caused by above – threshold expansion of certain trinucleotide repeats occurring in a protein-coding or non-coding region [1]. miRNAs are regulators of the expression of genes involved in the development of nucleotide repeat disorders. The expression of many genes is regulated by the binding of their mRNA with miRNA, so it is required to identify which candidate genes of nucleotide repeat disorders and to what extent can interact with miRNA.

In this work we have been studied the characteristics of miRNAs binding sites located in 5' UTR and 3' UTR mRNA genes having nucleotide repeats.

miRNA binding sites were predicted by the MirTarget program, which determines: a) the start of the initiation of miRNA binding to mRNAs; b) the localization of miRNA binding sites in 5' UTRs, CDSs and 3' UTRs of the mRNAs; c) the free energy of interaction miRNA and the mRNA (ΔG , kJ/mole); d) the schemes of nucleotide interactions between miRNAs and mRNAs [2].

The nucleotide sequences of human genes mRNAs have been downloaded from NCBI (<http://www.ncbi.nlm.nih.gov>). Nucleotide sequences of human 2567 miRNAs have been downloaded from the miRBase database (<http://mirbase.org>).

100 candidate genes with nucleotide repeats have 897 miRNAs binding sites in the 5'UTR and 3'UTR mRNA. The $\Delta G/\Delta G_m$ values equal to 87 % or more. From this results only 19 miRNAs have binding sites in 20 mRNAs of genes with a free interaction energy greater than -120 kJ/mol.

