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ABSTRACT BOOK

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In silico prognosis of miRNAs interaction with human mRNA genes having di- and trinucleotide repeats

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Abstract

Many socially significant diseases, including neurodegenerative, oncological and diabetes diseases are caused by unstable di- and trinucleotide repeat expansions located in disease-associated genes, but their biological function is not understood. Several studies point that miRNAs are involved in a variety of physiological and pathological processes in humans, and the alteration of miRNA expression is considered to be a hallmark of many diseases, including nucleotide repeat diseases. However, the function of these repeat-associated miRNAs is unclear. Therefore, *in silico* search the features of miRNA binding with genes associated with the development of nucleotide repeat disorders are significant. The miRNA binding sites were predicted by the MirTarget program. The MirTarget program defines the following features of binding: the start of the initiation of miRNA binding to mRNAs; the localization of miRNA binding sites in 5'UTRs, CDSs and 3'UTRs; the free energy of binding; and the schemes of nucleotide interactions between miRNAs and mRNAs. The nucleotide sequences of human miRNAs were downloaded from miRBase (http://mirbase.org), also, the nucleotide sequences of the human mRNA genes were obtained from GenBank (http://www.ncbi.nlm.nih.gov). Characteristics of binding sites of miRNAs with mRNAs of human genes were determined. Our findings suggest that the miR-574-5p, miR-466, ID00436.3p-miR, ID00470.5p-miR, ID00061.3p-miR and ID00296.3p-miR have binding sites in the 5′UTR, 3′UTR and CDS mRNAs of 53 genes involved in the development of neurodegenerative, oncological diseases and diabetes with GU, AC and CCG nucleotide repeats. The binding sites for ID00436.3p-miR and ID00470.5p-miR were identified in 3′UTR and 5′UTR mRNAs of 44 genes with GU and AC nucleotides with a free energy value equal to -104 kJ/mole – -113 kJ/mole. The free energy for ID00296.3p-miR binding in CCG nucleotide repeated regions in 5′UTR and CDS is significantly larger than for miR-574-5p, miR-466, ID00436.3p-miR, ID00470.5p-miR, ID00061.3p-miR and equal to -142 kJ/mole. Based on these results, the associations of miRNAs and candidate target genes are recommended for developing methods for diagnosing socially significant diseases, including neurodegenerative, oncological diseases and diabetes.