

FEATURES OF miR-1322 BINDING SITES IN THE CODING AREA OF mRNA ORTHOLOGIC GENES

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miR-1322 can regulate the expression of genes that are involved in the development of cancer, cardiovascular and neurodegenerative diseases [1]. It is important to identify the features of miR-1322 binding sites in the protein coding region of the mRNA of the orthologous genes *AFF3*, *AR* and *ATXN2*. miR-1322 binding sites in the mRNA were predicted using the MirTarget program [2].

AFF3 gene encodes a transcription factors that may function in lymphoid development and oncogenesis [3]. The protein coding region of the mRNA (CDS) of *AFF3* gene has several miR-1322 binding sites. The beginning of these binding sites is sequentially located through three nucleotides and this CDS region encodes the oligopeptide SSSSSSSGSSSSSS. The oligopeptide is conserved in *AFF3* protein of the following species: *Homo sapiens*, *Rhinopithecus roxellana*, *Chlorocebus sabaeus*, *Pan troglodytes*, *Nomascus leucogenys*, *Macaca fascicularis*, *Pan paniscus*, *Callithrix jacchus*, and *Saimiri boliviensis*. Before the N-end of the polyserine in the *AFF3* protein of all objects, there is a hexapeptide SVPSSKG, and after the C-end there is a hexapeptide DSESSSG. The miR-1322 binding sites are located in the conservative mRNA region and remain in the studied species for more than ten million years of their divergence. Probably the interaction of miR-1322 with the mRNA of *AFF3* gene is a functionally important necessity.

Androgen receptor (*AR*) gene encode several polyglutamine domain of its protein. Increase in the length of the polyglutamine tract from the normal 9-34 glutamine to the pathogenic 38-62 glutamine causes Kennedy's disease and Breast Cancers [4]. We have established that CDS sites encoding polyglutamine are the binding sites of miR-1322 in the mRNA of *AR* gene of thirteen animal species. We should note, that depending on the reading frame, miR-1322 binding sites can encode polyglutamine, polyserine or polyalanine. In the CDS of mRNA of *H.sapiens's AR* gene there are sequentially located through three nucleotide binding sites of miR-1322, that encoding 23 glutamine. In *AR* protein of *Pan troglodytes*, *Oryctolagus cuniculus*, *Ailuropoda melanoleuca*, *Pan paniscus*, *C.sabaeus*, *Canis familiaris* and *Felis catus*, there are 22, 18, 17, 16, 14, 10, 9 glutamine residues, respectively. In *AR* protein of *M.fascicularis*, *M.mulatta*, *Loxodonta africana*, *Sus scrofa* there are eight glutamine and in *AR* protein of *Balaenoptera acutorostratas* there are six glutamine. In *AR*

protein of all studied animal species, the conservative pentapeptide APPGA is located from the N-end of the polyglutamine, and the nonapeptide ETSPRQQQQ from the C-end.

Another region of the mRNA of AR gene of *H.sapiens*, *P.troglodytes*, *P.paniscus*, *M.mulatta*, *C.jacchus* encodes pentaglutamine: QQQQQ. In the AR protein of these primates, from the N-end of the polyglutamine there is a conservative oligopeptide SEASTMQLL, and from the C-end is the oligopeptide EAVSEGSSSG. AR protein of *A.melanoleuca*, *Balaenoptera acutorostrata*, and *Rattus norvegicus* contains polyglutamine from 6, 9 and 10 glutamine residues, respectively. AR protein of *F.catus*, *Rattus norvegicus*, *C. familiaris* contains 20, 22 and 24 glutamine, respectively.

H.sapiens's *ATXN2* gene encoded cytoplasmic protein involved in endocytosis and modulates mTOR signals. The N-end region of the protein contains a polyglutamine tract of 14-31 residues that can be expanded in the pathogenic state to 32-200 residues [5].

In the mRNA of *ATXN2* gene of *P.troglodytes*, the multiple binding sites of miR-1322 encode a polyglutamine of 26 glutamine residues. In the *ATXN2* protein of *H.sapiens*, there are 23 residues of glutamine, *Nomascus leucogenys* has 19 glutamine, *C.sabaeus* - 17 glutamine, *M.mulatta* and *M.fascicularis* have 16 glutamine, *F.catus* and *S.scrofa* have for 9 glutamine. In *ATXN2* protein of these mammalian species from the N-end of polyglutamine, there is a conservative oligopeptide MSLKP. From the C-end in *H.sapiens*, *P.troglodytes*, *C.sabaeus* located oligopeptide PPPAAANVRK, in *M.mulatta*, *M.fascicularis*, *F.catus* located oligopeptide PPAAANVRK.

The number of miR-1322 binding sites in the mRNA of the orthologous genes of the animal species studied can vary over a wide range. The miR-1322 binding sites can encode oligopeptides within different reading frames, which confirms the importance of the nucleotide composition for binding miRNA, rather than the oligopeptide coded by them. The miR-1322 binding sites are usually located in the conservative region of mRNA's CDS and persist in the studied species for more than ten million years of their divergence. Probably the interaction of miR-1322 with mRNA target genes is a functionally important necessity for the studied organisms. Choosing an animal model for studying the role of miRNA in various diseases should take into account the peculiarities of interaction with mRNA corresponding miRNA target genes.

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