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RICE miRNAs ARE POTENTIAL REGULATORS OF HUMAN GENES EXPRESSION

Abstract. Plant miRNAs are able to enter the human cells through the gastrointestinal tract with food and to affect the processes occurring in the body like endogenous miRNAs. These exogenous miRNAs can regulate the expression of human genes, affecting various physiological processes. The interactions of miRNAs with mRNAs were calculated using the MirTarget program. Rice miRNAs were chosen, because rice, in comparison with other plants, contains the largest amount of miRNAs and is the most common nutrition of the population. It was found that 32 human genes were targets for 17 osa-miRNAs (miR408-3p, miR408-5p, miR1320-3p, miR1847.1-5p, miR1860-3p, miR2093-3p, miR2102-5p, miR2866-5p, miR2867-5p, miR2868-5p, miR2919, miR2931-5p, miR5075-3p, miR5339-5p, miR5514-5p, miR5534a-5p, miR5833-5p). Detected binding sites were located at 5'-untranslated region (5'UTR), protein-coding region (CDS) and 3'-untranslated region(3'UTR) mRNA target genes. These 32 genes were influenced by human miRNAs. Of particular interest are *RBMS2, KATNAL1* genes with binding sites for several human miRNAs. The mRNA of the *RBMS2* gene had binding sites for seven members of the miR-1273 family. The *KATNAL1* gene was target for 38 miRNAs of the large miR-548 family. Rice miRNA target genes are involved in the development of oncological, cardiovascular and neurodegenerative diseases.

Keywords: miRNA, mRNA, binding site, gene regulation, plant, human.

Introduction. MiRNAs are short RNA sequences, approximately 22 nucleotides in length that binds to targeted messenger RNAs to inhibit protein synthesis [1].On the basis of many studies, it has been shown that plant miRNAs are able to penetrate the blood and host tissues during meals. miRNAs are transferred from cell to cell with blood, being packed in exosomes [2].They are not destroyed by digestive enzymes in the gastrointestinal tract, from where they enter the blood vessels and, as a result, accumulate in the blood and internal organs [3]. Exogenous miRNA that has penetrated the host organism from food can regulate the course of physiological processes in organism by regulating the target genes of the host [4-7]. In the present work, using bioinformatics approaches, the quantitative characteristics of the interaction of rice miRNAs with mRNAs of human genes were predicted.

Materials and methods. The nucleotide sequences of the mRNAs of human genes were downloaded from NCBI (https://www.ncbi.nlm.nih.gov/). The nucleotide sequences of human and rice miRNAs were taken from miRBase v.22 (http://www.mirbase.org/). The miRNA binding sites in mRNA of several genes were predicted using the MirTarget program [8]. This program defines the following features of miRNA binding to mRNA: a) the start of the initiation of miRNA binding to mRNAs from the first nucleotide of the mRNA's 5'UTR; 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.

Results and discussion. Study of 738 osa-miRNAs binding to mRNAs of 17494 human genes revealed that only 32 genes were targets for 17osa-miRNAswith the selection criteria ΔG/ΔGm equal 95% and over. The interaction patterns of the nucleotide sequences of rice miRNAs with the mRNAs of human genes are presented in figure. It can be seen from the schemes that all miRNA nucleotides form hydrogen

bonds. The advantage of the MirTarget program is the incorporation of hydrogen bonds in non-canonical pairs of nucleotides U-G, A-C into the free energy of miRNA interaction with mRNA [9].

The largest number of target genes was osa-miR2102-5p. miR2102-5p bound to mRNA of 11 genes (*AFAP1*, *C19orf6*, *CHSY1*, *DIRC2*, *KATNAL1*, *NR1D2*, *PDAP1*, *PPP2R5C*, *RHOBTB2*, *UHRF1BP1*, *WT1*) with energy from -115 kJ/mole to -121 kJ/mole and ΔG/ΔGm value from 95% to 100%.miR2919

Gene, miRNA, start of site, characteristics of binding	Gene, miRNA, start of site, characteristics of binding
PSEN2, miR1847.1-5p, 1785, 3'UTR, -108, 96, 21 5'-GUGCCACA**G**GCUGCAA**G**CUGCA-3' 3'-CACGGUGU**U**-GACGUU**U**GACGU-5'	*C19orf6*, miR2102-5p, 193, CDS, -115, 95, 20 5'-G**C**GGCGGCGGCGGC**CC**GGCCC-3' 3'-C**A**CCGCCGCCGCCG**AA**C-GGG-5'
KLHDC10, miR1860-3p, 3134, 3'UTR, -108, 96, 22 5'-AGAGAAAACCGUAGC**C**UCCAGA**C**-3' 3'-UCUCUUUUGG-AUCG**A**AGGUCU**A**-5'	*ZNF442*, miR2866-5p, 1020, CDS, -98, 96, 20 5'-GAUGCUG**G**ACACAAAC**C**AGA-3' 3'-CUACGAC**U**UGUGUUUG**A**UCU-5'
OSTM1, miR2093-3p, 848, CDS, -93, 96, 20 5'-AUGCAUU**G**AUGUGGAAGAUG**C**-3' 3'-UACGUAA**U**UA-ACCUUCUAC**A**-5'	*ATP13A3*, miR2867-5p, 3035, CDS, -115, 95, 22 5'-U**U**GGGAUGUGUGGUGAUGGC**G**CA-3' 3'-A**G**CCCUACACACC-CUACCG**U**GU-5'
WT1, miR2102-5p, 450, CDS, -121, 100, 20 5'-GUGGCGGCGGCGGCUGUGCCC-3' 3'-CACCGCCGCCGCCGA-ACGGG-5'	*HK2*, miR2868-5p, 6645, 3'UTR, -93, 96, 20 5'-UU**C**CU**G**CUACACAAAAGCCAA-3' 3'-AA**A**GA**U**GAUGUGUUUU-GGUU-5'
KATNAL1, miR2102-5p, 80, 5'UTR, -117, 96, 20 5'-G**C**GGCGGCGGCGGC**C**UGCGCC-3' 3'-C**A**CCGCCGCCGCCG**AA**CG-GG-5'	*KIAA1161*, miR2919, 3436, 3'UTR, -106, 98, 19 5'-UCUU**C**CCCCCGCCCCCCCUU-3' 3'-AGAA**A**GGGGG-GGGGGGGAA-5'
NR1D2, miR2102-5p, 254, 5'UTR, -117, 96, 20 5'-G**C**GGCGGCGGCGGCG**C**UGCCC-3' 3'-C**A**CCGCCGCCGCCG-**A**ACGGG-5'	*BDNF*, miR2919, 2681, 3'UTR, -106, 98, 19 5'-UCUUUCCCCCCCUCCCCCU**C**-3' 3'-AGAAAGGGGGGG-GGGGGA**A**-5'
CHSY1, miR2102-5p, 348, 5'UTR, -117, 96, 20 5'-G**C**GGCGGCGGCGGCG**C**UGCCC-3' 3'-C**A**CCGCCGCCGCCG-**A**ACGGG-5'	*ADAMTS5*, miR2102-5p, 1494, CDS, -113, 93, 20 5'-GUGGCGGCGGCGGCG**CC**GC**U**C-3' 3'-CACCGCCGCCGCCG-**AA**CG**G**G-5'
DIRC2, miR2102-5p, 233, CDS, -117, 96, 20 5'-G**C**GGCGGCGGCGGCG**C**UGCCC-3' 3'-C**A**CCGCCGCCGCCG-**A**ACGGG-5'	*UFSP1*, miR2931-5p, 960, 3'UTR, -91, 96, 20 5'-UUUUGACAUCAA**U**AAUAAAAG-3' 3'-AAAACUGUAGUU**G**UUAUU-UC-5'
RHOBTB2, miR2102-5p, 158, 5'UTR, -115, 95, 20 5'-GU**A**GCGGCGGCGGC**C**UCGCCC-3' 3'-CA**C**CGCCGCCGCCG**AA**-CGGG-5'	*RPS6KA5*, miR5075-3p, 261, CDS, -121, 98, 21 5'-GCGGACGGCGGCGACGGAG**GA**-3' 3'-CGCCUGCCGCCGCUGCCUC**UU**-5'
UHRF1BP1, miR2102-5p, 112, 5'UTR, -115, 95, 20 5'-G**C**GGCGGCGGCGGCUGUG**U**CC-3' 3'-C**A**CCGCCGCCGCCGA-AC**G**GG-5'	*NR2F2*, miR5075-3p,350,5'UTR,-117, 95, 21 5'-GCGG**G**CGGCGGCG**G**CCGGAGA**G**-3' 3'-CGCC**U**GCCGCCGC**U**G-CCUCU**U**-5'
PDAP1, miR2102-5p, 29, 5'UTR, -115, 95, 20 5'-G**C**GGCGGCGGCGGCUGGCCC-3' 3'-C**A**CCGCCGCCGCCGAACGGG-5'	*SLC35D1*, miR5339-5p, 795, CDS, -102, 96, 21 5'-UCUGAGAAG**G**UUCUC**CA**UCCUG-3' 3'-AGACUCUUC**U**AAGAG**A**UAG-AC-5'
PPP2R5C, miR2102-5p, 72, 5'UTR, -115, 95, 20 5'-G**C**GGCGGCGGCGGC**CC**GCUCC-3' 3'-C**A**CCGCCGCCGCCG**AA**CG-GG-5'	*NANOS1*, miR5534a-5p, 1967, 3'UTR, -106, 96, 21 5'-CCAUUC**C**AGCUGUUG**C**CUGUCA-3' 3'-GGUAAG**A**UCGACAAC**A**G-CAGU-5'
AFAP1, miR2102-5p, 144, 5'UTR, -115, 95 5'-G**C**GGCGGCGGCGGC**CC**GCCC-3' 3'-C**A**CCGCCGCCGCCG**AA**-CGGG-5'	*COX20*, miR5833-5p, 396, CDS, -117, 96, 21 5'-GCCCG**G**UGAGCCCGAGGAGAG**G**-3' 3'-CGGGC**U**ACUCGGGCUCCUC-C**U**-5'

Note: The upper and lower nucleotide sequences of mRNA and miRNA, respectively. The bold type indicates the nucleotide of non-canonical pairs U-G, A-C.

Schemes of the interaction of osa-miRNA with CDS mRNA human genes

had two binding sites in the 5'UTR mRNA of the *ADAMTS5*, *GPBP1L1* genes and two sites in the 3'UTR mRNA of the *BDNF*, *KIAA1161*genes with a ΔG/ΔGm value of 96% and 98%, respectively. For miR5075-3p, binding sites were found in mRNA of the *NR2F2*, *PARP2*, *RPS6KA5* genes. The rest 13 miRNAs (miR408-3p, miR408-5p, miR1320-3p, miR1847.1-5p, miR1860-3p, miR2093-3p, miR2866-5p, miR2867-5p, miR2868-5p, miR2931-5p, miR5339-5p, miR5514-5p, miR5534a-5p, miR5833-5p)could bind to mRNAs of one target gene, with a ΔG/ΔGm value of 95% to 96%. The detected miRNA binding sites were located at 5'UTR, CDS, and 3'UTR.

osa-miRNA target genes are involved in the development of various diseases, including breast cancer (*RBMS2*, *RHOBTB2*, *RPS6KA5*, *WT1*[10-13]), colorectal cancer (*ADAMTS5*, *CHSY1*[14,15]), carcinoma in various organs (*C19orf6*, *PPM1F*, *AFAP1*, *PPP2R5C*, *DIRC2*, *UHRF1BP1* [16-21]), leukemia (*HK2*, *PDAP1*[22, 23]), cardiovascular disease (*NR2F2*, *UFSP1*, *ATP13A3* [24-26]), neurodegenerative diseases (*BDNF*, *PSEN2*, *ZNF442* [27-29]).

It was important to find out whether these osa-miRNA target genes are targets for hsa-miRNA. The effect of 2565 hsa-miRNA on osa-miRNA target genes was studied. The mRNAs of almost all of these target genes could bind hsa-miRNA. The quantitative characteristics of the binding of hsa-miRNAs to the mRNAs of the target genes listed in figure are shown in table 1. Specifically, the *ADAMTS5*, *C19orf6*, *DIRC2*, *GPBP1L1*, *KIAA1161*, *KLHDC10*, *NR1D2*, *NR2F2*, *OSTM1*, *PM20D2*, *PPM1F*, *PSEN2*, *RHOBDB1*, and *RHOBTB1* geneseachhad one binding site to hsa-miRNA. Consequently, osa-miRNAs and hsa-miRNAs can bind simultaneously to enhance their suppression of translation.

Table 1 – Characteristics of hsa-miRNA binding sites in mRNA of human genes

Gene	hsa-miRNA	Start of site, nt	Region of miRNA	ΔG, kJ/mole	ΔG/ΔGm, %	Length, nt
1	2	3	4	5	6	7
ADAMTS5	miR-511-5p	2728	CDS	-102	92	21
ATP13A3	miR-182-5p	6258	3'UTR	-110	90	24
ATP13A3	miR-183-5p	6260	3'UTR	-104	92	22
C19orf6	miR-6808-5p	2441	3'UTR	-113	90	22
CHSY1	miR-1273e	3542	3'UTR	-108	93	22
CHSY1	miR-1273g-3p	3499	3'UTR	-108	93	21
COX20	miR-3191-3p	47	5'UTR	-121	93	23
COX20	miR-5096	2121	3'UTR	-106	94	21
COX20	miR-5585-3p	2189	3'UTR	-106	91	22
COX20	miR-619-5p	2047	3'UTR	-117	96	22
DIRC2	miR-1199-5p	178	CDS	-113	93	20
GPBP1L1	miR-574-5p	3012	3'UTR	-117	96	23
HK2	miR-1273g-3p	617	5'UTR	-106	91	21
HK2	miR-1285-3p	770	5'UTR	-106	91	22
KIAA1161	miR-1273g-3p	3476	3'UTR	-108	93	21
KLHDC10	miR-4298	23	5'UTR	-113	90	22
NANOS1	miR-3960	584	CDS	-121	97	20
NANOS1	miR-5096	3285	3'UTR	-106	94	21
NANOS1	miR-551a	4459	3'UTR	-108	94	21
NANOS1	miR-619-5p	3218	3'UTR	-121	100	22
NR1D2	miR-466	3337	3'UTR	-110	95	23
NR2F2	miR-483-5p	2322	CDS	-108	91	22
OSTM1	miR-6880-3p	36	5'UTR	-110	91	21
PDAP1	miR-5096	1998	3'UTR	-106	94	21
PDAP1	miR-619-5p	1925	3'UTR	-121	100	22

Continuation of table 1

1	2	3	4	5	6	7
PM20D2	miR-1273g-3p	2662	3'UTR	-115	98	21
PPM1F	miR-6779-3p	1442	CDS	-104	91	21
PPP2R5C	miR-152-5p	435	CDS	-110	91	23
PPP2R5C	miR-6746-3p	41	5'UTR	-117	92	22
PSEN2	miR-4520a,b-5p	1988	3'UTR	-96	90	20
RHOBTB2	miR-6124	3431	3'UTR	-102	92	20
SLC35D1	miR-5695	2821	3'UTR	-102	91	22
UFSP1	miR-548az-3p	782	CDS	-93	90	21
UHRF1BP1	miR-5096	6450	3'UTR	-104	92	21
UHRF1BP1	miR-619-5p	6378	3'UTR	-119	98	22
WT1	miR-3960	573	CDS	-113	90	20
WT1	miR-466	2704-2714(6)	3'UTR	-106	91	23
WT1	miR-466	2755-2765(6)	3'UTR	-106	91	23

The *COX20*, *NANOS1*, *PDAP1*,and *UHRF1BP1* genes are targets for miR-5096, miR-5585-3p, and miR-619-5p. These miRNAs also belong to a group of unique miRNAs [30, 31]. For example, miR-619-5p targets 201 genes with fully complementary binding sites and more than three hundred that have 98% homology with its nucleotide-binding sites.

miR-5096 and miR-619-5p bound to the mRNAs of the four genes *COX20*, *NANOS1*, *PDAP1* and *UHRF1BP1*. hsa-miR-466 has polysites in two regions in the 3′UTR of *WT1* gene, forming two clusters as in the work [13].

Of particular interest are gene mRNAs with binding sites for several specific miRNAs (table 2). The mRNA of the *RBMS2* gene has binding sites for miR-1273a, miR-1273c, miR-1273e, miR-1273e, miR-1273f, miR-1273g-3p, and miR-1273h-5p. Some members of the miR-1273 family are unique in that they target several hundred genes [32]. Therefore, osa-miR408-3p can compete with the miR-1273 miRNAs to regulate *RBMS2* gene expression.

Table 2 – Characteristics of hsa-miRNA binding sites in mRNA of *RBMS2, KATNAL1*genes

Gene	hsa-miRNA	Startof site, nt	RegionofmiRNA	ΔG, kJ/mole	ΔG/ΔGm, %	Length, nt
1	2	3	4	5	6	7
RBMS2	miR-1273a	4818	3'UTR	-121	92	25
RBMS2	miR-1273a	5854	3'UTR	-119	90	25
RBMS2	miR-1273c	5856	3'UTR	-110	91	22
RBMS2	miR-1273e	5919	3'UTR	-108	93	22
RBMS2	miR-1273e	4883	3'UTR	-106	91	22
RBMS2	miR-1273f	4873	3'UTR	-100	96	19
RBMS2	miR-1273f	5909	3'UTR	-98	94	19
RBMS2	miR-1273g-3p	5470	3'UTR	-113	96	21
RBMS2	miR-1273g-3p	5876	3'UTR	-113	96	21
RBMS2	miR-1273g-3p	5136	3'UTR	-110	95	21
RBMS2	miR-1273g-3p	4840	3'UTR	-108	93	21
RBMS2	miR-1273g-5p	5500	3'UTR	-108	91	22
RBMS2	miR-1273h-5p	5504	3'UTR	-115	98	21
RBMS2	miR-1285-3p	5453	3'UTR	-108	93	22
RBMS2	miR-1972	5081	3'UTR	-110	90	22
RBMS2	miR-6124	64	5'UTR	-104	94	20

Continuation of table 2

1	2	3	4	5	6	7
RBMS2	miR-6803-3p	7181	3'UTR	-110	90	22
KATNAL1	miR-1273a	3903	3'UTR	-119	90	25
KATNAL1	miR-1273g-3p	3925	3'UTR	-113	96	21
KATNAL1	miR-1972	4492	3'UTR	-113	91	22
KATNAL1	miR-548a-5p	3534	3'UTR	-98	90	22
KATNAL1	miR-548aa	3495	3'UTR	-123	100	25
KATNAL1	miR-548ab	3534	3'UTR	-98	92	22
KATNAL1	miR-548ag	3535	3'UTR	-96	90	21
KATNAL1	miR-548aj-5p	3536	3'UTR	-110	98	23
KATNAL1	miR-548ak	3535	3'UTR	-96	92	21
KATNAL1	miR-548am-5p	3534	3'UTR	-110	100	22
KATNAL1	miR-548ap-3p	3501	3'UTR	-89	100	19
KATNAL1	miR-548ap-5p	3537	3'UTR	-89	95	19
KATNAL1	miR-548aq-5p	3534	3'UTR	-102	92	22
KATNAL1	miR-548ar-5p	3535	3'UTR	-100	98	21
KATNAL1	miR-548as-5p	3534	3'UTR	-106	94	22
KATNAL1	miR-548au-5p	3535	3'UTR	-104	100	21
KATNAL1	miR-548ax	3533	3'UTR	-108	96	22
KATNAL1	miR-548ay-5p	3535	3'UTR	-100	98	21
KATNAL1	miR-548az-3p	3499	3'UTR	-93	90	21
KATNAL1	miR-548az-5p	3535	3'UTR	-104	94	22
KATNAL1	miR-548b-5p	3534	3'UTR	-102	92	22
KATNAL1	miR-548c-5p	3534	3'UTR	-110	100	22
KATNAL1	miR-548d-5p	3534	3'UTR	-106	98	22
KATNAL1	miR-548e-5p	3535	3'UTR	-106	93	22
KATNAL1	miR-548f-5p	3537	3'UTR	-98	92	22
KATNAL1	miR-548g-3p	3497	3'UTR	-93	90	22
KATNAL1	miR-548g-5p	3536	3'UTR	-110	98	23
KATNAL1	miR-548h-3p	3498	3'UTR	-104	91	23
KATNAL1	miR-548h-5p	3534	3'UTR	-104	94	22
KATNAL1	miR-548i	3534	3'UTR	-106	96	22
KATNAL1	miR-548m	3536	3'UTR	-93	90	21
KATNAL1	miR-548n	3535	3'UTR	-98	92	22
KATNAL1	miR-548o-5p	3534	3'UTR	-110	100	22
KATNAL1	miR-548q	3542	3'UTR	-113	95	22
KATNAL1	miR-548t-3p	3495	3'UTR	-123	100	25
KATNAL1	miR-548t-5p	3536	3'UTR	-96	90	21
KATNAL1	miR-548v	3495	3'UTR	-102	91	22
KATNAL1	miR-548w	3533	3'UTR	-108	93	23
KATNAL1	miR-548x-5p	3536	3'UTR	-110	98	23
KATNAL1	miR-548y	3534	3'UTR	-98	90	22
KATNAL1	miR-548z	3498	3'UTR	-104	91	23
KATNAL1	miR-574-5p	4197-4236(20)	3'UTR	-113	93	23
KATNAL1	miR-574-5p	4394-4410(9)	3'UTR	-113	93	23

The *KATNAL1* gene is the targets of miR-1273a and miR-1273g-3p. An important feature of this gene is the binding of its mRNA to members of the large miR-548 family, which consists of 38 miRNAs. miR-548aa, miR-548am-5, miR-548ap-3p, miR-548au-5p, miR-548c-5p, miR-548o-5p, and miR-548t-3p can fully bind to the 3'UTR mRNA of the *KATNAL1* gene. This gene has one another feature: its 3'UTR mRNA contains 20, and through 136 nucleotides, nine sequentially located miR-574-5p binding sites. It remains a mystery why the *KATNAL1* gene is controlled by such a large number of endogenous miRNAs. In another feature of the mRNA of the *KATNAL1* gene, the distance between the nucleotide-binding sites of miR-548h-3p and miR-548h-5p, miR-548az-3p and miR-548az-5p, and miR-548ap-3p and miR-548ap-5p is 36 nucleotides.osa-miR2102-5p binding sitewere found in mRNAs of the *KATNAL1* gene.

It is of interest to determine which human miRNAs can affect the expression of these genes. The calculation results showed that, of the 32 genes, six are not targeted by any of the 2565 hsa-miRNAs. Several genes, in addition to being targets of osa-miRNAs, have the important feature of being targets of hsa-miRNAs. The mRNA of the RBMS2 gene has binding sites for miR-1273a, miR-1273c, miR-1273e, miR-1273e, miR-1273f, miR-1273g-3p, and miR-1273h-5p. Members of the miR-1273 family are unique because some of them target several hundred genes [32]. The *KATNAL1* gene is the target of miR-1273a and miR-1273g-3p. An important feature of this gene is that its mRNA binds to members of the miR-548 family that bind to 38 miRNAs. miR-548aa, miR-548am-5, miR-548ap-3p, miR-548au-5p, miR-548c-5p, miR-548o-5p, and miR-548t-3p can bind fully to the 3'UTR mRNA of the *KATNAL1* gene. This gene has one more peculiarity: the 3'UTR mRNA contains 20, and through 136 nucleotides, nine are sequentially located miR-574-5p binding sites. It is assumed that miRNA binding to3'UTR mRNA can be significant if the gene contains repeats of site sequences as well asin coding region [33].

Conclusion. The present study provides the evidence that rice miRNAs can be transmitted with food to regulate the expression of human genes. Target genes of the osa-miRNAs are also target genes of the hsa-miRNAs.The established binding sites of osa-miRNAs and their target genes allow targeted insertion of exogenous osa-miRNAs with food to regulate their expression of these human genes.

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КҮРІШТІҢ miRNA-ЛАРЫ АДАМ ГЕНДЕРІНІҢ ЭКСПРЕССИЯСЫНЫҢ ПОТЕНЦИАЛДЫ РЕТТЕГІШТЕРІ

Аннотация. Өсімдік miRNA-лары адамның клеткаларына асқазан-ішек жолымен тағаммен бірге ене алады және эндогенді miRNAретінде организмдегі болып жатқан процестерге әсер етеді. Бұл экзогенді miRNA әртүрлі физиологиялық функцияларға әсер ететін адам гендерінің экспрессиясын реттей алады. miRNA-дың mRNA-мен өзара әрекеттесуі MirTarget бағдарламасын пайдала отырып есептелді.Басқа өсімдіктермен салыстырғанда күріштің құрамында miRNA-ның ең көп мөлшері бар және халық үшін ең көп таралған тамақтану көзі болып табылғандықтан күріш miRNA-лары таңдалды. Адам генінің 32-сі 17 osa-miRNA-ларға (miR408-3p, miR408-5p, miR1320-3p, miR1847.1-5p, miR1860-3p, miR2093-3p, miR2102-5p, miR2866-5p, miR2867-5p) 5p, miR2868-5p, miR2919, miR2931-5p, miR5075-3p, miR5339-5p, miR5514-5p, miR5534a-5p, miR5833-5p) нысана екендігі анықталды. Анықталған байланысу сайттары орындары нысана гендердің mRNA-ның 5'- трансляцияланбайтынаймақта (5'UTR), ақуызды кодтайтын аймақта (CDS) және 3'-аударылмайтын аймағында (3'UTR) орналасқан. Бұл 32 гендерге адам miRNA-лары әсер етті. Адамның бірнеше miRNA-лары мен байланысатын сайттары бар *RBMS2* және *KATNAL1* гендеріне ерекше қызығушылық туды. *RBMS2* генінің mRNA-дары miR-1273 тұқымдасының жеті мүшесі үшін байланысу сайттары болып табылды. *KATNAL1* гені үлкен miR-548 тұқымдасының 38 miRNA-на нысана ретінде болды. Күріш miRNA-ның нысана гендері онкологиялық, жүрек-тамыр және нейродегенеративті аурулардың дамуына қатысады.

Түйін сөздер: miRNA, mRNA, байланысу сайт, геннің реттелуі, өсімдік, адам.

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miRNA РИСА – ПОТЕНЦИАЛЬНЫЕ РЕГУЛЯТОРЫ ЭКСПРЕССИИ ГЕНОВ ЧЕЛОВЕКА

Аннотация. miRNA растений способны с пищей через желудочно-кишечный тракт попадать в клетки человека и как эндогенные miRNA влиять на процессы, происходящие в организме. Эти экзогенные miRNA могут регулировать экспрессию генов человека, влияя на различные физиологические функции. Взаимодействие miRNA с mRNA рассчитывали с помощью программы MirTarget. Были выбраны miRNA риса, потому что рис по сравнению с другими растениями содержит наибольшее количество miRNA и является самым распространенным источником питания населения. Обнаружено, что 32 гена человека были мишенями для 17 osa-miRNAs (miR408-3p, miR408-5p, miR1320-3p, miR1847.1-5p, miR1860-3p, miR2093-3p, miR2102-5p, miR2866-5p, miR2867 -5p, miR2868-5p, miR2919, miR2931-5p, miR5075-3p, miR5339-5p, miR5514-5p, miR5534a-5p, miR5833-5p). Обнаруженные сайты связывания были расположены в 5'-нетранслируемой области (5'UTR), белок-кодирующей области (CDS) и 3'-нетранслируемой области (3'UTR) mRNA генов-мишеней. На эти 32 гена влияли miRNA человека. Особый интерес представляют гены *RBMS2* и *KATNAL1* с сайтами связывания для нескольких miRNA человека. mRNA гена *RBMS2* имела сайты связывания для семи членов семейства miR-1273. Ген *KATNAL1* был мишенью для 38 miRNA большого семейства miR-548. Гены-мишени miRNA риса участвуют в развитии онкологических, сердечно-сосудистых и нейродегенеративных заболеваний.

Ключевые слова: miRNA, mRNA, сайт связывания, регуляция гена, растение, человек.

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