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CHARACTERISTICS OF miRNA INTERACTION WITH mRNA GENES OF *T. AESTIVUM* C2H2, ERF, GRAS TRANSCRIPTION FACTORS FAMILIES

Abstract. The molecular mechanisms for increasing plant productivity remain poorly understood. Genes of C2H2, GRAS, ERF transcription factors (TFs) families play a key role in the physiological processes of plants, including wheat. In recent years, the important role of miRNAs in the regulation of the expression of many genes involved in the formation of productivity has been established. Wheat miRNA (mRNA-inhibiting RNA) target genes are involved in the regulation of the development of flowers, seeds, root, shoots, and responses to abiotic and biotic stresses. The miRNAs binding sites in mRNAs of C2H2, ERF, GRAS TFs families were performed using the MirTarget program, which calculates the free energy of miRNA binding with mRNA, the schemes and positions of nucleotide interactions with binding sites. Wheat genes were used as the object of the study, since wheat is one of the main grain crops in Kazakhstan and in many other countries. The presence of miRNA binding sites with high nucleotide complementarity in mRNA of C2H2, ERF, GRAS TF genes of wheat was shown. All binding sites of these miRNAs were located in the CDS of mRNA target genes. Of the 125 miRNAs of *T. aestivum,* miR319-3p efficiently bound with mRNA of C2H2 family genes with the value of ΔG/ΔGm equal 91 %. miR7757-5p interacted with mRNA of ERF and GRAS family genes with the value of ΔG/ΔGm equal to 92 % and 90 % respectively. miR9778-5p bound with mRNA of C2H2, ERF, GRAS family genes to varying degrees. Each of the miR408-3p, miR9780-3p, and miR9778-5p had four target genes with the value of ΔG/ΔGm equal to 87 % and 89 %. These data indicate the dependency of C2H2, GRAS, ERF TFs families expression on miRNA. The obtained results expand the fundamental ideas about the regulatory mechanisms of miRNA in the process of plant growth and development.

Key words: *T. aestivum*, transcription factor, gene regulation, miRNA, mRNA.

Introduction. The present work is aimed to study the participation of miRNA (mRNA-inhibiting RNA) in the growth and development of wheat plants, and to study the characteristics of the interaction of miRNA with mRNA of target genes of C2H2, GRAS, ERF transcription factor (TF) families. C2H2 proteins are transcription factors containing «zinc fingers». They are responsible for the processes of embryogenesis, regulate the development of flowers, shoots and seeds, control the flowering time and the formation of nodules [1, 2]. C2H2 genes are significantly involved in drought, heat and salt response [3]. AP2/ERF (ethylene response factor) – transcription factors family is involved in the regulation of flower and seed development and responses to environmental stresses [4-7]. GRAS TF family is involved

in the regulation of root and shoot development, in responses to gibberellins, and in the transmission of the phytochrome signal [8-11]. Currently, there is limitted information available on the interaction of miRNA with the expression of these genes. miRNAs play an important role in the regulation of many biological processes of plants [12, 13]. The identification of miRNA targets will improve understanding of miRNA-mediated mechanisms of wheat growth and development. This is important for increasing wheat productivity. Most miRNAs affect various plant development processes by regulating the expression of transcription factors [14]. Therefore, it seems important to study the effect of miRNA on the expression of the C2H2, GRAS, and ERF genes involved in all key processes of plant cells.

Materials and methods. The nucleotide sequences of *T. aestivum* genes of the C2H2, ERF, GRAS families were borrowed from Plant Transcription Factor Database v4.0 (http://planttfdb.cbi.pku.edu.cn/). The nucleotide sequences of miRNAs were taken from miRBase v.22 (http://www.mirbase.org/). The miRNAs binding sites in mRNA of several genes were predicted using the MirTarget program [15]. 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. The ratio ΔG/ΔGm (%) was determined for each site (ΔGm equals the free energy of miRNA binding with its fully complementary nucleotide sequence). The MirTarget program found hydrogen bonds between adenine (A) and uracil (U), guanine (G) and cytosine (C), G and U, A and C. The distances between A and C (1.04 nanometers nm), G and U (1.02 nm) were similar to those between G and C, A and U, and equal to 1.03 nm [16]. The numbers of hydrogen bonds in the G-C, A-U, G-U and A-C interactions were found to be 3, 2, 1 and 1, respectively.

Results and discussion. As a result of studying the interaction of several families of miRNAs with mRNA of *T. aestivum* genes, it was found that only 38 genes were targets for these miRNAs. The miRNA binding sites were located in the protein coding region (CDS) of mRNA target genes (table). We selected miRNA targets genes, with which mRNA bound with ΔG/ΔGm value of 86 % or more. The mRNA of Traes_5AL_903412779.2, Traes_5BL_C3F3A871A.1, Traes_5DL_3FBCC4C48.1, Traes_5BL_7F0FD1538.2 genes had binding sites with miRNAs with the value of ΔG/ΔGm higher than 90 % and in the remaining mRNAs, ΔG/ΔGm value was 86-90 %. Such criterion indicates a high probability of miRNAs binding to mRNA genes of C2H2, ERF, GRAS TF families. It was found that miR10520-5p, miR1127b-3p, miR398-3p, miR1119-3p, miR5200-3p, miR9674a-5p, miR9677b-5p, miR399-3p, miR530-3p, miR9672a-3p had only one target gene. The miR9657b,c-3p and miR408-3p had similar binding sites in the mRNA of the Traes_2BL_58A855C7B.2, Traes_2DL_540050272.2 genes, and miR408-3p had two more interaction sites in the mRNA of the Traes_2AL_7ABA7B7C8.1 and Traes_5BL_D53A846BE.1 genes of C2H2 family and one binding site in the mRNA of Traes_2BL_88A78A71E.1 gene of GRAS family. Each of miR1128-5p and miR319-3p had three target genes of C2H2 family with value of ΔG/ΔGm from 87 % to 91 %. This indicates a strong interaction of mRNA with miRNA. Traes_5BL_7F0FD1538.2 gene of ERF family was the target for miR5200-3p and miR7757-5p. The miR7757-5p bound to mRNA of Traes_5BL_7F0FD1538.2 gene completely complementary and ΔG/ΔGm value was 92 %, which indicates a strong interaction of these RNAs. The possibility of binding of several miRNAs to one mRNA or one miRNA at sites of different mRNAs indicates an increased control of the expression of the corresponding genes by miRNAs. The miRNA analysis of target genes showed that miR9778-5p, miR9780-3p, and miR7757-5p had binding sites in the studied families, which indicates a high probability of their significance for the regulation of mRNA translation of the corresponding genes. The targets for miR9778-5p were mRNA of four genes in the CDS regions of three studied families: Traes_1DS_75AF80583.1 (C2H2), Traes_4AS_19FA06316.1 (GRAS) and Traes_1AL_08BAD7CD3.1 (ERF), Traes_1BL_09D8BE2C9.1 (ERF) with the value of ΔG/ΔGm equal 87 % and 89 % respectively. miR9780-3p had three binding sites in the mRNA genes of ERF family (Traes_2AL_0F08552FB.1, Traes_2BL_984787AC0.1, Traes_5BL_199A847E4.1) and one binding site in the mRNA TRAES3BF064300010CFD_t1 gene of C2H2 family, while miR7757-5p had three binding sites in mRNA of GRAS genes (Traes_5BL_1E751EF1F.1, Traes_5BL_A7C4DAE11.2, Traes_5DL_B89CD8432.1) and one binding site in mRNA of Traes_5BL_7F0FD1538.2 gene of ERF family. The miR156-5p, miR171b-3p and miR531-5p had two binding sites in the mRNA genes of GRAS and ERF transcription factors families. The miR156-5p and miR171b-3p bound to mRNA of

Traes_6AL_4084532FC1.1, Traes_6DL_26DDCA106.1 and Traes_4AS_19FA06316.1 Traes_4DL_5B3B57371.1 genes, respectively, of GRAS TF family with the value of ΔG/Δm equal 87%. miR531-5p interacted with mRNA of Traes_4AS_D20DF472E.1 and Traes_4DL_6EBD74330.2 genes with value of ΔG/ΔGm equal 88%.

Characteristics of miRNA binding sites in the coding region mRNA of C2H2, ERF, GRAS transcription factors genes of *T. aestivum*

Gene	miRNA	Start of site, nt	ΔG, kJ/mole	ΔG/ΔGm, %	Length, nt
C2H2 transcription factor family					
TRAES3BF064300010CFD_t1	miR9780-3p	1366	-110	87	21
Traes_1DS_75AF80583.1	miR9778-5p	480	-98	87	21
Traes_2BL_58A855C7B.2	miR9657b,c-3p	132	-102	87	21
Traes_2DL_540050272.2	miR9657b,c-3p	132	-102	87	21
Traes_4AS_D20DF472E.1	miR531-5p	270	-108	88	21
Traes_4DL_6EBD74330.2	miR531-5p	360	-108	88	21
Traes_2AL_7ABA7B7C8.1	miR408-3p	1631	-104	87	21
Traes_2BL_58A855C7B.2	miR408-3p	1625	-104	87	21
Traes_2DL_540050272.2	miR408-3p	1625	-104	87	21
Traes_5BL_D53A846BE.1	miR408-3p	297	-104	87	21
Traes_5BL_C3F3A871A.1	miR398-3p	2846	-104	87	21
Traes_5AL_903412779.2	miR319-3p	2343	-104	91	21
Traes_5BL_C3F3A871A.1	miR319-3p	3231	-104	91	21
Traes_5DL_3FBCC4C48.1	miR319-3p	2409	-104	91	21
Traes_4BL_3B919C814.1	miR1128-5p	335	-98	87	21
Traes_4BS_6BEE72C38.1	miR1128-5p	335	-98	87	21
Traes_4DL_AA51A43E7.1	miR1128-5p	332	-98	87	21
Traes_5BL_46BDE583B.1	miR1127b-3p	356	-96	87	21
Traes_1BL_4026DC5011.2	miR10520-5p	373	-91	88	20
ERF transcription factor family					
Traes_2AL_0F08552FB.1	miR9780-3p	360	-110	87	21
Traes_2BL_984787AC0.1	miR9780-3p	357	-110	87	21
Traes_5BL_199A847E4.1	miR9780-3p	128	-110	87	21
Traes_1AL_08BAD7CD3.1	miR9778-5p	435	-100	89	21
Traes_1BL_09D8BE2C9.1	miR9778-5p	435	-100	89	21
Traes_2BL_FC0F8A3DC.1	miR9677b-5p	304	-110	90	21
TRAES3BF051200070CFD_t1	miR9674a-5p	89	-96	87	21
Traes_5BL_7F0FD1538.2	miR7757-5p	2096	-102	92	22
Traes_5BL_7F0FD1538.2	miR5200-3p	3396	-96	88	21
Traes_4DS_9C01B536B.1	miR1119-3p	786	-115	86	24
GRAS transcription factor family					
Traes_4AS_19FA06316.1	miR9778-5p	1382	-98	87	21
Traes_1AL_FB0C83DD9.1	miR9672a-3p	402	-96	87	21
Traes_4AL_04B7D5758.1	miR9657b-5p	888	-98	87	21
Traes_4DS_258687ACC.1	miR9657b-5p	888	-98	87	21
Traes_5BL_1E751EF1F.1	miR7757-5p	1799	-100	90	22
Traes_5BL_A7C4DAE11.2	miR7757-5p	1811	-98	88	22
Traes_5DL_B89CD8432.1	miR7757-5p	1823	-98	88	22
Traes_4BL_86941BB78.1	miR530-3p	6	-98	88	21
Traes_2BL_88A78A71E.1	miR408-3p	1171	-104	87	21
Traes_4AL_C217A20A1.2	miR399-3p	1469	-91	90	19
Traes_4AS_19FA06316.1	miR171b-3p	432	-98	87	21
Traes_4DL_5B3B57371.1	miR171b-3p	420	-98	87	21
Traes_6AL_4084532FC1.1	miR156-5p	774	-96	87	21
Traes_6DL_26DDCA106.1	miR156-5p	774	-96	87	21

Figure shows examples of the interaction of some miRNAs with mRNAs of their target genes, which illustrate hydrogen bonds between interacting nucleotides. With full complementarity and high interaction of free energy, the probability of miRNAs interaction with mRNA molecules increases. The data presented demonstrate the important role of non-canonical A-C and G-U pairs in increasing the free energy of interaction between miRNAs and mRNAs of the C2H2, ERF, GRAS genes that control various processes of wheat development. For example, when miR319-3p interacted with the mRNA of the Traes_5DL_3FBCC4C48.1, Traes_5BL_C3F3A871A.1, Traes_5AL_903412779.2 genes, two non-canonical G-U pairs and one A-C pair were formed. When miR7757-5p and miR399-3p interacted with mRNA of Traes_5BL_7F0FD1538.2 and Traes_4AL_C217A20A1.2 genes, respectively, two A-C pairs. These schemes demonstrate the advantage of the MirTarget program over other commonly used programs when determining the free energy of interaction between miRNA and their target genes in animals and plants, which is calculated taking into account the formation of non-canonical pairs of nucleotides A and C, G and U [17–20].

Gene, miRNA, start of site, characteristics of binding	Gene, miRNA, start of site, characteristics of binding
●Traes_4BL_581E788ED.1; miR1122c-3p; 48; -93; 86; 21 5'-CCUCCGCCCCAU**GG**U**G**CCGGA-3' 3'-GGAGGCAGGGUA**UU**A**U**AAUCU-5'	▲Traes_2BL_FC0F8A3DC.1; miR9677b-5p; 304; -110; 90; 21 5'-GCCCACCUGCUGCCCCGCCCGG-3' 3'-CCGGUGGACAA-GGGGCGGGAC-5'
● Traes_2BS_ACA52BC08.1; miR1137a-3p; 778; -87; 87; 20 5'-GA**C**GACUCA**G**CUCUGUUC**C**A-3' 3'-CU**A**CUGAGU**U**GA**A**ACAUGA**U**-5'	▲ Traes_1AL_08BAD7CD3.1; miR9778-5p; 435; -100; 89; 21 5'-CGACGUGUUCGAGAUGC**C**GC**G**-3' 3'-GCUGCUCAAGCUCUACU**A**CGU-5'
●Traes_5DL_3FBCC4C48.1; miR319-3p; 2409; -104; 91; 21 5'-CGGGAGCUGCCCUCC**G**GUCCA**G**-3' 3'-UCCCUCGA-GGGA**A**GUCAGGU**U**-5'	▲ Traes_1BL_09D8BE2C9.1; miR9778-5p; 435; -100; 89; 21 5'-CGACGUGUUCGAGAUGC**C**GC**G**-3' 3'-GCUGCUCAAGCUCUACU**A**CGU-5'
●Traes_5BL_C3F3A871A.1; miR319-3p; 3231; -104; 91; 21 5'-CGGGAGCUGCCCUCC**G**GUCCA**G**-3' 3'-UCCCUCGA-GGGA**A**GUCAGGU**U**-5'	■ Traes_5BL_1E751EF1F.1; miR7757-5p; 1799; -100; 90; 22 5'-AAUGG**G**UUGCUGAAGGUUUUAU-3' 3'-CUACC**U**AUCGACUUCCAAAAUA-5'
● Traes_5AL_903412779.2; miR319-3p; 2343; -104; 91; 21 5'-CGGGAGCUGCCCUCC**G**GUCCA**G**-3' 3'-UCCCUCGA-GGGA**A**GUCAGGU**U**-5'	■ Traes_4AL_C217A20A1.2; miR399-3p; 1469; -91; 90; 19 5'-GGGUAACUCUCCU**CC**AGGCA-3' 3'-CCCGUUAAGAGGA**AA**-CCGU-5'
▲Traes_5BL_7F0FD1538.2; miR7757-5p; 2096; -102; 92; 22 5'-**A**AUGGAUAGCUGAA**A**GUUUUAU-3' 3'-**C**UACCUAUCGACUU**C**CAAAAUA-5'	■ Traes_5DL_B89CD8432.1; miR7757-5p; 1823; -98; 88; 22 5'-**A**AUGGG**U**CGCUGAAGGUUUCAU-3' 3'-**C**UACC**U**AUCGACUUCCAAAAUA-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. ● - C2H2 TF family, ▲ - ERF TF family, ■ - GRAS TF family.

Schemes of miRNAs interaction
with CDS mRNAs of C2H2, ERF, GRAS transcription factors genes in *T. aestivum*

Conclusion. It can be concluded from the study that most miRNAs regulate plant development by controlling the expression of transcription factors, which play an important role in the growth and development process. The binding sites of miRNAs with mRNA genes involved in the growth and development of wheat were characterized by high complementarity. Establishing the properties of miRNA binding sites with mRNA genes of C2H2, ERF, GRAS transcription factors significantly expands the understanding of the role of miRNA in the regulation of plant gene expression. The data obtained will contribute to the creation of new varieties of wheat in order to increase their productivity and resistance to stress factors.

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C2H2, ERF, GRAS *T. AESTIVUM* ТРАНСКРИПЦИОНДЫ ФАКТОРЛЫ ТҰҚЫМДАС ГЕНДЕРІНДЕГІ мРНҚ-МЕН миРНҚ-НЫҢ ӨЗАРА ӘРЕКЕТТЕСУЛЕРІНІҢ СИПАТТАМАЛАРЫ

Аннотация. Өсімдіктердің өнімділігін арттырудың молекулалық механизмдері әлі де жақсы зерттелмеген. Транскрипция факторларының (ТФ) гендік тұқымдастары C2H2, GRAS, ERF өсімдіктердің, оның ішінде бидайдың физиологиялық процестерінде маңызды рөл атқарады. Соңғы жылдары өнімділікті қалыптастыруға қатысатын көптеген гендердің экспрессиясын реттеудегі miRNA (mRNA-inhibiting RNA)-ның маңызды рөлі анықталды. Бидай miRNA -ның нысана гендері гүлдердің, тұқымдардың, тамырлардың және өркендердің дамуын реттеуге, сондай-ақ өсімдіктің биотикалық және абиотикалық стресстерін реттеуге қатысады. MirTarget бағдарламасының көмегімен miRNA-ның C2H2, ERF, GRAS TF тұқымдарының mRNA-мен байланысатын сайттар анықталды. Бағдарлама miRNA-мен mRNA байланыстыратын учаскелердің басталуын, орналасқан жерін, miRNA -ның бос энергиясы мен mRNA-дың өзара әрекеттесуінің (ΔG, кДж/моль) және miRNA-мен mRNA-дың нуклеотидтерінің өзара әрекеттесу схемаларын анықтайды. Бидай генінің нуклеотидтік тізбегі зерттеу объектісі ретінде қолданылды, өйткені бидай Қазақстанда және көптеген елдерде негізгі дәнді дақылдардың бірі болып табылады. Бидайдың ТФ генінің mRNA-да жоғары нуклеотидті комплементарлы miRNA-мен байланыстыратын учаскелердің болуы көрсетілді. Осы miRNA-лардың барлық байланыстыратын сайттары нысана гендердің mRNA-ның белокты кодтайтын бөлігінде орналасқан. *T. aestivum* C2H2 тұқымдасының 125 miRNA-ның 211 геннің mRNA-мен әрекеттесуін зерттеу нәтижесінде miRNA үшін тек 16 нысан анықталды. miR10520-5p, miR1127b-3p, miR1128-5p, miR319-3p, miR398-3p, miR408-3p, miR531-5p, miR9657b, c-3p, miR9778-5p, miR9780-3p осы нысана гендердің mRNA-мен байланысады. 125 miRNA ішінен *T. aestivum* miR319-3p ΔG/ΔGm мәні 91%-ға тең C2H2 ТФ гендерінің mRNA-мен тиімді байланысады. Екі miRNA TRes Traes_2BL_58A855C7B.2, Traes_2DL_540050272.2 және Traes_5BL_C3F3A871A.1 гендерінің mRNA-мен байланысты. ERF тұқымдасының 169 геніндерінің mRNA-мен он miRNA-лар байланысатын сайттар анықталды, олардың мәні 85% -дан асады. Traes_5BL_7F0FD1538.2 генінің mRNA-ның байланыстыратын сайттары үшін miR319-3p және miR398-3p болды. Бір miRNA-мен Traes_1AL_08BAD7CD3.1, Traes_1BL_09D8BE2C9.1, Traes_2AL_0F08552FB.1, Traes_2BL_984787AC0.1, Traes_2BL_FC0F8A3DC.1, Traes_4DS_9C01B536B.1, Traes_5BL_199A847E4.1, TRAES3BF051200070CFD_t1 гендерінің mRNA-лары байланысты. GRAS тұқымдасының 169 генін компьютерлік талдау нәтижесінде тек 13 гендердің miR156-5p, miR156-5p, miR171b-3p, miR399-3p, miR408-3p, miR530-3p, miR7757-5p, miR9657b-5p, miR9672a-3p, miR9778-5p-мен нысана екендігі анықталды. Traes_4AS_19FA06316.1 генінің mRNA-да miR171b-3p және miR9778-5p үшін өзара әрекеттесу сайттары анықталды. Кейбір miRNA-лардың зерттелген бірнеше тұқымдастарында байланысатын сайттар болғанын атап өту керек. miR7757-5p ТФ ERF және GRAS гендерінің mRNA-мен 92% және 90%-да ΔG/ΔGm сәйкесінше байланысты. miR9778-5p әр түрлі деңгейде ТФ гендері C2H2, ERF, GRAS mRNA-мен байланысты болды. miR408-3p, miR9780-3p және miR9778-5p 87 % и 89 %-ға тең ΔG/ΔGm төрт геннің нысаны болып табылды. miRNA және ТФ C2H2, ERF, GRAS гендерінің mRNA-лары өзара әрекеттесу схемалары нуклеотидтердің сутектік байланыстарын анық көрсетеді. miR1122c-3p, miR7757-5p-лардың нуклеотидтік тізбектері Traes_4BL_581E788ED.1 және Traes_5BL_7F0FD1538.2 гендерінің mRNA-ның барлық ұзындықтарымен өзара сәйкесінше әрекеттесті. Бұл мәліметтер ТФ экспрессияларының C2H2, GRAS, ERF тұқымдарының miRNA-ға тәуелділігін көрсетеді. Алынған нәтижелер өсімдіктердің өсуі мен дамуы процесінде miRNA-ны реттеу механизмдері туралы түбегейлі идеяларды кеңейтеді.

Түйін сөздер: *T. aestivum*, транскрипционды фактор, ген регуляциясы, миРНҚ, мРНҚ.

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ХАРАКТЕРИСТИКИ ВЗАИМОДЕЙСТВИЯ миРНК С мРНК ГЕНОВ СЕМЕЙСТВ ТРАНСКРИПЦИОННЫХ ФАКТОРОВ C2H2, ERF, GRAS *T. AESTIVUM*

Аннотация. Молекулярные механизмы повышения продуктивности растений остаются слабо изученными. Семейства генов транскрипционных факторов (ТФ) C2H2, GRAS, ERF играют ключевую роль

в физиологических процессах растений, в том числе у пшеницы. В последние годы установлена важная роль miRNA (mRNA-inhibiting RNA) в регуляции экспрессии многих генов, участвующих в формировании продуктивности. Гены-мишени miRNA пшеницы участвуют в регуляции развития цветков, семян, корней и побегов, и ответа растения на биотические и абиотические стрессы. Сайты связывания miRNA в mRNA генов семейств C2H2, ERF, GRAS ТФ определяли с помощью программы MirTarget. Программа определяет начало сайтов связывания miRNA с mRNA, расположение сайтов, свободную энергию взаимодействия miRNA и mRNA (ΔG, кДж/моль) и схемы взаимодействия нуклеотидов miRNA с mRNA. В качестве объекта исследования использовали нуклеотидные последовательности генов пшеницы, так как пшеница является одной из основных зерновых культур Казахстана и во многих странах. В работе показано наличие в mRNA генов ТФ пшеницы сайтов связывания miRNA с высокой комплементарностью нуклеотидов. Все сайты связывания этих miRNA расположены в белок-кодирующей части mRNA генов-мишеней. В результате изучения взаимодействия 125 miRNA с mRNA 211 генов семейства C2H2 *T. aestivum* было обнаружено только 16 мишеней для miRNA. miR10520-5p, miR1127b-3p, miR1128-5p, miR319-3p, miR398-3p, miR408-3p, miR531-5p, miR9657b,c-3p, miR9778-5p, miR9780-3p связывались с mRNA этих генов-мишеней. Из 125 miRNA *T. aestivum* miR319-3p эффективно связывалась с mRNA генов ТФ C2H2 с величиной ΔG/ΔGm равной 91%. По две miRNA связывались с mRNA генов Traes_2BL_58A855C7B.2, Traes_2DL_540050272.2 и Traes_5BL_C3F3A871A.1. В mRNA 169 генов семейства ERF, было выявлено десять сайтов связывания miRNA, с величиной ΔG/ΔGm равным более 86%. mRNA гена Traes_5BL_7F0FD1538.2 имела сайты связывания для miR319-3p и miR398-3p. По одной miRNA связывались с mRNA генов Traes_1AL_08BAD7CD3.1, Traes_1BL_09D8BE2C9.1, Traes_2AL_0F08552FB.1, Traes_2BL_984787AC0.1, Traes_2BL_FC0F8A3DC.1, Traes_4DS_9C01B536B.1, Traes_5BL_199A847E4.1, TRAES3BF051200070CFD_t1. В результате компьютерного анализа из 169 генов семейства GRAS было обнаружено, что только 13 генов были мишенями для miR156-5p, miR171b-3p, miR399-3p, miR408-3p, miR530-3p, miR7757-5p, miR9657b-5p, miR9672a-3p, miR9778-5p. Сайты взаимодействия для miR171b-3p и miR9778-5p были обнаружены в mRNA гена Traes_4AS_19FA06316.1. Важно отметить, что некоторые miRNA имели сайты связывания в нескольких изученных семействах. miR7757-5p связывалась с mRNA генов ТФ ERF и GRAS со значением ΔG/ΔGm равным 92% и 90% соответственно. miR9778-5p в разной степени связывались с mRNA генов ТФ C2H2, ERF, GRAS. miR408-3p, miR9780-3p и miR9778-5p имели по четыре гена мишени со значением ΔG/ΔGm равным 87% и 89 %. Схемы взаимодействия miRNA и mRNA генов ТФ C2H2, ERF, GRAS четко показывают образование водородных связей между нуклеотидами. Нуклеотидные последовательности miR1122c-3p, miR7757-5p взаимодействовали по всей длине mRNA генов Traes_4BL_581E788ED.1 и Traes_5BL_7F0FD1538.2, соответственно. Эти данные свидетельствуют о зависимости экспрессии ТФ семейств C2H2, GRAS, ERF от miRNA. Полученные результаты расширяют фундаментальные представления о регуляторных механизмах miRNA в процессе роста и развития растений.

Ключевые слова: *T. aestivum,* транскрипционный фактор, регуляция гена, миРНК, мРНК.

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