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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**AU**A**AUCU-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**CUGAGUU**G**AA**A**CAUG**A**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'-CGGGAGCUGCCCU**CC**GGUCCA**G**-3' 3'-UCCCUCGA-GGGA**AG**UCAGGU**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'-CGGGAGCUGCCCU**CC**GGUCCA**G**-3' 3'-UCCCUCGA-GGGA**AG**UCAGGU**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'-CGGGAGCUGCCCU**CC**GGUCCA**G**-3' 3'-UCCCUCGA-GGGA**AG**UCAGGU**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**AUGG**G**UCGCUGAAGGUUUCAU-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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INFLUENZA D VIRUSES - PATHOGENS FORMING A NEW GENUS IN THE ORTHOMYXOVIRIDAE FAMILY

Abstract. Influenza pathogens belong to the Orthomyxoviridae family and are divided into genera: Influenzavirus A, B, C, D, as well as Quaranjavirus, Thogotovirus, and Isavirus. For the first time, the influenza D virus was isolated from swine nasal swabs in 2011 in the United States, and its widespread distribution among cattle in France, China, Italy, Ireland, Japan, and several African countries, as well as its ability to infect ferrets, guinea pigs, is further shown. Antibodies to influenza D virus are found in the blood serum of horses, sheep, goats, and in people who have been in contact with cattle. The RNA genome of the influenza D virus is represented by seven fragments responsible for the synthesis of nine proteins. The longest three segments encode for polymerases PB2, PB1, and P3; the fourth and fifth segments encode for hemagglutinin-esterase fusion protein – HEF and nucleoprotein – NP, respectively. The sixth fragment is involved in the synthesis of membrane polypeptides DM1 and DM2, which, in accordance, lines the viral membrane from the inside and performs the function of proton channels. The seventh segment encodes the non-structural protein NS1 and the nuclear export protein NEP; NS1 helps to neutralize cellular interferon and NEP mediates the nuclear export of ribonucleoprotein. Three phylogenetic lines of the influenza virus D are described – D/OK, D/660, and D/Japan, which must be taken into account when preparing vaccines. It is concluded that from its epidemiological, pathological and biological characteristics, the potential ability to cause disease in humans and be transmitted from person to person, new, more in-depth studies are required using ecological-virological and molecular genetic methods.

Key words: virus, influenza D, genome, variability, cattle, phylogenesis, clade, HEF fusion protein, serology.

Characteristics of the Orthomyxoviridae family. Influenza occupies one of the first places among infectious diseases in terms of the number of species involved in the infectious process and is characterized by global distribution and high economic and social significance [1].

All currently known influenza pathogens belong to the family *Orthomyxoviridae* and are divided into genera: *Influenzavirus A, B, C, D*, as well as *Quaranjavirus, Thogotovirus* and *Isavirus*; the last two infect rabbit-like mammals and salmon fish [2,3,4]. Representatives of *Quaranjavirus* found among both invertebrates (ticks) and vertebrates (water birds) hosts [5].

Influenza A viruses are widespread in the environment and infect humans, mammals and birds. The global spread of influenza A pathogens is due to unique variability, which is based on point mutations and recombinations of eight segments of the genome. The classification of influenza A viruses is determined by a combination of the known subtypes of surface antigens of hemagglutinin (HA) and neuraminidase

(NA) – H1N1, H3N2, H5N1, H7N7, etc. [6]. In Kazakhstan, as a result of long-term studies of influenza A virus ecology, eight different subtypes of this pathogen were identified [7,8,9,10,11,12,13].

The causative agents of influenza A along with influenza B viruses, cause annual epidemics, accompanied by 3-5 million cases of severe morbidity and about 300,000 deaths, with a mortality rate reaching 16 % and 10 %, respectively [14,15].

Modern epidemic influenza B viruses are phylogenetically and antigenically divided into two lines - Yamagata-like and Victoria-like, which are easily differentiable in the hemagglutination inhibition assay (HI) [16]. The natural host of influenza B virus is human but sporadic infections of pheasants, horses, and dogs have been reported in 1960-1980 [17,18,19]. Further, this virus was isolated from a seal *(Phoca vitulina)* in the Netherlands in 1999, the B/Seal/Netherlands/1/99 [20]. Antibodies to influenza B virus were detected in pig sera in China in 2015, their sensitivity to experimental infection was also shown [21].

Representatives of the genus C predominantly infect the children's contingent and differ significantly in structural characteristics from A and B viruses. They possess an RNA genome consisting of seven fragments, one of which encodes hemagglutinin-esterase (HEF) synthesis, which combines the functions of HA and NA in the virion. Another feature of the influenza C virus (ICV) is the ability to infect pigs, which was first demonstrated in China in 1982 [22], in addition to this, antibodies to it were detected in 2015 in the horse sera of in the USA [23].

The Orthomyxoviridae family is represented by the so-called newly emerging infectious diseases, the number of which is growing in the world, and many of them pose a serious threat to wildlife, domestic animals, and public health [24,25].

In April 2011, B.M. Hause et al. [26] in Oklahoma (USA), during the virological study of nasal swabs from pigs, isolated an influenza virus with an RNA genome consisting of 7 fragments that are 50% structurally similar in amino acid sequence to ICV. Originally designated as C/Oklahoma/1334/2011, it diverged from ICV in phylogenetic analysis to the same extent as influenza A viruses differ from representatives of genus B. No cross-reactivity was observed between the new isolate and ICV in HI. Antibodies to this strain were found in 9.5 % and 1.3 % of pig sera and staff, respectively; in addition, it was transmitted to healthy animals through direct contact and was able to infect pigs, ferrets, and guinea pigs in the experiment. Cell tropism of the new virus was superior to that of ICV, while conservative enzymatic and divergent receptor-binding sites were detected in the HEF fusion protein. In experiments with two human ICVs and two newly isolated swine and cattle viruses, no reassortment and production of viable generation were found. In experiments with specific polyclonal antibodies, cross-recognition was not observed in agar gel immunodiffusion. Based on the data obtained, the isolated virus was assigned to the new genus D [27], which was adopted by the decision of the International Committee on Taxonomy of Viruses (ICTV) in 2018 [28]. Subsequent molecular genetic studies have identified several characteristics of the causative agent of influenza D.

Structural features of the influenza D virus. The RNA genome of the influenza D virus (IDV) is represented by seven fragments responsible for the synthesis of 9 proteins. The longest three segments encode polymerases PB2, PB1, and P3, the fourth – protein HEF, the fifth – NP. The sixth fragment is involved in the synthesis of membrane polypeptides DM1 and DM2, one of which underlines the viral membrane from the inside, the other performs the function of proton channels [29]. The seventh segment encodes the non-structural protein NS1, and the nuclear export protein NEP; NS1 helps neutralize cellular interferon, NEP mediates the nuclear export of ribonucleoprotein [30]. IDV, like ICV, uses cellular 9-*O*-acetylated sialic acid as its receptor but exhibits a broader cellular and host tropism [31]. The reason for this lies in the structural features of the molecule of the HEF monomer, consisting of two subunits HEF1 and HEF2, As revealed by comparative X-ray crystallographic study and following the domain nomenclature previously used for ICV, H. Song et al. [31] divided the structure of IDV HEF into three domains: a receptor-binding domain (R), an esterase domain (consisting of subdomains E1, E' and E2) and a fusion domain (consisting of subdomains F1, F2, and F3). The general structure and structural folds of the individual HEF subdomains of both viruses were similar. E domains are the most conserved; the F1 and F2 subdomains are less identical, while the F3 subdomain contains the fusion peptide, which is essential for the viral membrane fusion.

The E domain of IDV HEF, harboring the receptor-destroying enzyme (RDE) activity, has a hydrolase fold that is highly similar to that of ICV HEF. The active-site architecture of the HEF sialate-9-O-acetylesterase is fully conserved in ICV and IDV HEF and has oxyanion hole. The pocket is

extremely conserved not only in IDV HEF and ICV HEF but also in some nidovirus hemagglutinin-esterase (HE) proteins such as bovine coronavirus, porcine torovirus and bovine torovirus HE [32]. Phylogenetic analysis also shows the relationship between HEF and HE to be much closer than the relationship between HEF and HA or hemagglutinin-neuraminidase (HN) proteins, implying common ancestral origins.

Epidemiology of influenza D. Following the first report on the isolation of IDV in 2013, L. Ferguson et al. [33] in 2014 recovered 15 IDVs from surveillance of bovine herds in Mississippi belonging to two genetic lines. Based on the serological analysis of "archived" sera, it was shown that the pathogen has been circulating in cattle stock in this region since at least 2014. Active transmission of the virus has been detected in places where newborn, weaned, and comingled calves were maintained. The detection rate of IDV in RT-PCR was 2.4 % of 82 healthy calves, which was significantly higher than in Chinese Shandong – 0.7 % of 453 calves [34], which indicates its possible participation in the etiology of respiratory cattle disease, as an infection with many potential pathogens. Continuing his research, L. Ferguson et al. [29] conducted an experimental intranasal infection of three dairy calves with the influenza virus D/bovine/Mississippi/C00046N/2014 followed by replanting of a seronegative contact calf. Seroconversion and the presence of the virus in the respiratory tract were detected in all animals. The infection of ferrets with nasal discharge from calves has not yielded results. These data are consistent with Koch's postulates and confirm the hypothesis that cattle are a natural reservoir of the virus.

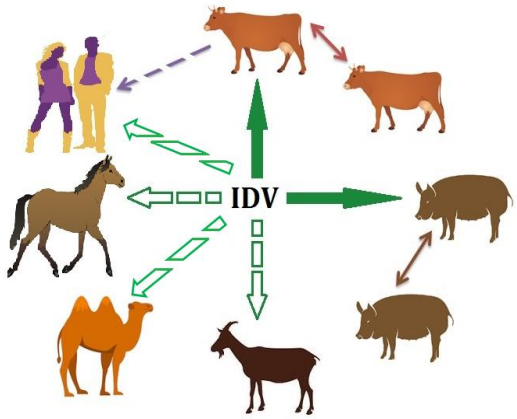
In subsequent years, IDVs were found in cattle in France, China, Italy, and Japan [35,34,36,37]. E. Collin et al. [38] studied 208 biological samples from cattle from 12 US states in real-time PCR and found 10 positives for IDV samples, using passages on cell cultures, they isolated six IDV strains.

O. Flynn et al. [38] examined 320 "archival" samples in the form of nasal swabs taken from cattle in Ireland during 2014–2016. Using RT-PCR on IDV and Sanger sequencing, five partial RNA sequences suitable for phylogenetic analysis were obtained from 18 positive samples.

In Japan, according to a national serological study, the average level of seropositivity in cattle for the influenza virus is 30%, and the values vary depending on the region [37,40]. At the same time, a molecular epidemiological analysis of cattle samples with symptoms of respiratory disease collected from 23 different farms in this country revealed 2.1 % (8/377) influenza D infection [41].

E. Salem et al. [42] conducted a serological search for antibodies to influenza C and D viruses among ruminants and camelids in Africa in 1991–2015, and for this purpose, they collected 2083 blood serum samples from a cattle, pigs, small ruminants, and dromedary camels in Morocco (n=200), Togo (n=540), Côte d'Ivoire (n=203), Benin (n=308) and Kenya (n=1231). The percentage of positive samples from cattle in Morocco was 35 %, Togo – 10.4 %, Côte d'Ivoire – 0 %, Benin – 1.9 %, Kenya – 0 %. Noteworthy is the high percentage (99 %) of positive blood serum from camels in Kenya (287 out of 293), but the serum was not pre-adsorbed by ICV in this test. The results indicated a wide circulation in Africa of IDV, and its significant tropism to all the hosts studied.

H. Nedland et al. [23] examined 364 serum samples from horses of 141 farms in the Midwestern United States and showed that animals are susceptible to two IDV lines represented by D/swine/Oklahoma/1334/2011 (D/OK line) and D/bovine/Oklahoma/660/2013 (line D/660), as 12 % and 11 % of sera, respectively, were seropositive in HI.



The hosts of the influenza D virus. IDV can be transmitted between cattle and also between pigs as indicated by the solid line. Antibody specific for IDV were also detected in sera from small ruminants (sheep and goat), horses, camels and humans, especially in people with cattle exposure, but no virus was isolated (indicated by the broken line), indicating that IDV may be transmitted from cattle to humans (broken line)

M. Quast et al. [43] in a serological analysis of 648 sheep and goat blood serum samples collected in 2014 in the USA and Canada, detected antibodies to IDV in 5.2 % (29/557) of the studied sheep from 13.5 % (17/126) of farms. In turn, 8.8 % (8/91) of goats from 13.3 % (2/15) of the tested farms also contained antibodies against IDV.

IDV was first isolated from pigs and then from cattle. Since cattle seropositivity is much higher than that of pigs, it is believed that it is the main natural reservoir. Currently known IDV hosts are shown in figure. In addition, the ability of D/OK to infect ferrets, guinea pigs, and transmit them to native animals by direct contact is shown [26,44], which allows them to be used as models in the study of IDV.

Phylogenesis of influenza D. viruses. With the accumulation of IDV strains of various origins and places of isolation, the possibility of their comparative antigenic and phylogenetic studies appeared. E.A. Collin et al. [38] performed full genome sequencing and phylogenetic analysis of 7 viral RNA segments of six new strains and four previously registered IDVs and revealed two different circulating lines – D/OK and D/660, which often reassorted with each other. Antigenic analysis using representative viruses D/swine/Oklahoma/1334/2011 and D/bovine/Oklahoma/660/2013 and their antisera in the HI showed an approximately 10-fold loss of cross-reactivity. An important finding was that one of the isolates (D/bovine/Texas/3-13/2011) belonged to the D/bovine/Oklahoma/660/2013 cluster, but was characterized by high titers with a serum to the heterologous variant D/swine/Oklahoma/1334/2011. Molecular modeling of the HEF fusion protein of strain D/bovine/Texas/3-13/2011 made it possible to identify the mutation at position 212 responsible for unusual serological test titers. The obtained data indicate the widespread prevalence of at least two genetically different IDV lines in cattle, and also the vital role of lysine (K212) in antigenic recognition of D/swine/Oklahoma/1334/2011-like viruses. IDVs related to D/bovine/Oklahoma/660/2013 clade carried arginine in this position (R212).

Phylogenetic analysis of the HEF sequence of the USA IDV isolates performed by L. Ferguson et al. [26], aligned them into two genetic clusters: viruses D/bovine/Mississippi/C00046N/2014 and D/bovine/Mississippi/C00030P/2014 were genetically close toD/swine/Oklahoma/1334/2011 (D/OK), while D/bovine/Mississippi/C00013N/2014 and D/bovine/Mississippi/C00014N/2014 were genetically related to D/bovine/Oklahoma/660/2013 (D / 660).

O. Flynn et al. [39] found that five IDV strains isolated in Ireland in 2014–2016 were grouped in the same clade together with the virus from Europe D/swine/OK/1334/2011.

S. Murakami et al. [37] using reverse transcription-PCR successfully amplified the complete genome sequence of the first Japanese IDV strain (D/bovine/Ibaraki/7768/2016), sequenced its seven segments and built their phylogenetic trees. The results indicated that it occupies a separate position from strains from other countries, and only the M gene is included in one cluster with isolates from France (D/bovine/France/2986/2012) and China (D/bovine/Shandong/Y127/2014, D/bovine/Shandong/Y217/2014, D/bovine/Shandong/Y125/2014). Later on, in Japan, from a cow with signs of respiratory disease, the D/bovine/Yamagata/10710/2016 strain highly related D/bovine/Ibaraki/7768/2016 according to the HEF gene was isolated, the homology of the nucleotide and amino acid sequences was 99.8 % and 100 %, respectively [45]. H. Mekata et al. [41] performed analysis of 46 nasal swabs from cattle with signs of respiratory disease from 26 different farms in Japan, using the Next Generation Sequencing, the nucleotide sequence of the complete IDV genome was determined, and it was shown that it forms a separate cluster. According to the authors, the virus could develop uniquely over a long period, and its pathogenic properties differ from the strains found in other countries. In 2018 T. Odagiri et al. [46] studied IDV phylogenesis and established the presence of three genetically distinct lines: D/OK, D/660, and D/Japan. In addition, in the cross-linked HI, it was found that representatives of three lines in the composition of the surface protein HEF present both common for all and line-specific antigens.

The most conserved PB1 viral protein gene is often used to evaluate the evolutionary relationships of influenza viruses. S. Su et al. [2] based on the nucleotide sequences of the PB1 genes of influenza A, B, C, and D viruses, constructed a phylogenetic tree to determine the relationship between them. IDV clusters turned out to be the most closely related to ICV, which suggests their common ancestor. Sequence analysis of the PB2, P3, NP, M, and NS genes also confirmed the origin of IDV from human ICV [26]. To study the origin and evolutionary history of IDV, the authors conducted a Bayesian analysis of the HEF ICV gene sequences, indicating 1896 as the average time (t-MRCA) of the most recent common ancestor, which is consistent with previously obtained data [47]. For the HEF genes of ICV and

IDV, the t-MRCA value was 482 A.D. It is shown that two IDV lines – D/OK and D/660 had the last common ancestor (t-MRCA) about 44.6 years ago. The average frequency of substitution for the HEF IDV gene was calculated using Bayesian analysis and amounted to 1.54×10^{-3}, which exceeds the frequency of ICV [47]. From this point of view, the causative agent of influenza D has great epidemic potential, and in the future, it is necessary to monitor its development constantly.

Conclusion. To date, an intensive study of IDV has shown that it infects pigs, cattle, and small ruminants, but the full spectrum of its susceptible hosts remains to be determined. To better understand the causative agent of influenza D from epidemiological, pathological and biological characteristics, in particular, the ability to cause disease in humans and be transmitted from person to person, new, more in-depth studies using molecular genetic tools are required. A significant stock of broad species range of susceptible farm animals needs a study of IDV prevalence in Kazakhstan.

Taken together, the epidemiological and metagenomic data, as well as experimental infection of animals, showed that the influenza virus D is the causative agent of respiratory disease of cattle, and therefore there is the task of appropriate vaccination. Moreover, the antigenic heterogeneity of HEF IDV explains the need to take into account which strains of which line circulate in a given region to prepare the most effective vaccine against this infection.

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ТҰМАУ D ВИРУСЫ – ORTHOMYXOVIRIDAE ТҰҚЫМДАСЫНДАҒЫ ЖАҢА ТҮР ҚАЛЫПТАСТЫРАТЫН ПАТОГЕНДЕР

Аңдатпа. Тұмау қоздырғыштары Orthomyxoviridae тұқымдасына жатады және A, B, C, D тұмауы болып, сондай-ақ Quaranjavirus, Thogotovirus және Isavirus туыстықтарына бөлінеді. D тұмауы вирусы алғаш рет 2011 ж. АҚШ-та шошқаның кеңсірік шайындысынан бөлініп алынды, кейінірек Франция, Қытай, Италия, Ирландия, Жапония, бірқатар Африка елдерінде ірі қара малдың арасында кең тарағаны, сонымен қатар оның күзендер мен теңіз шошқаларына жұғатыны анықталған. D тұмауы вирусына қарсы антиденелер жылқылардың, қой мен ешкілердің және малмен байланыста болған адамдардың қан сарысуынан кездеседі. D тұмауы вирусының РНҚ геномы 9 ақуыз синтезіне жауап беретін жеті фрагменттен тұрады. Ең ұзын үш сегмент PB2, PB1 және P3 полимеразаларын кодтайды, төртіншісі – HEF гемагглютинин-эстераза тұтасу ақуызы, бесінші – NP нуклеопротеині. Алтыншы фрагмент мембрана полипептидтерінің DM1 және DM2 синтезіне қатысады, олардың бірі вирустық мембрананы ішінен қаптап жатады, екіншісі протон арналарының қызметін орындайды. Жетінші сегмент NS1 құрылымдық емес ақуызды және NEP ядролық экспорт ақуызын кодтайды; NS1 жасушалық интерферонды бейтараптандыруға көмектеседі, NEP рибонуклеопротеиннің ядролық экспортын жүзеге асырады. Тұмау D вирусының үш – D/OK, D/660 және D/Japan филогенетикалық желісі сипатталған, олар вакцина дайындау кезінде ескерілуі керек. Оның эпидемиологиялық, патологиялық және биологиялық сипаттамалары тұрғысынан, адамдарда ауру тудыруы және адамнан адамға берілуі мүмкін болатын қазіргі заманғы экологиялық-вирусологиялық және молекулалық-генетикалық әдістерді қолдана отырып, жаңа, тереңірек зерттеулер қажет деген тұжырым жасалды. Аса консервативті вирустық PB1 ақуыз гені тұмау вирустарының эволюциялық қатынастарын бағалау үшін жиі қолданылады. S. Su et al. [2] A, B, C және D вирустарының PB1 генінің нуклеотидтік тізбегі негізінде олардың арасындағы байланысты анықтау үшін филогенетикалық дарақ құрастырылды. IDV кластерлері ICV-мен ең жақын байланыста болды, бұл олардың ата-бабаларының ортақ екенін білдіреді. PB2, P3, NP, M, NS гендерінің тізбегін талдау нәтижесіде, олардың адам ICV-нен IDV шыққанын растады [26]. IDV-ның пайда болуы мен эволюциялық тарихын зерттеу үшін авторлар HEF ICV гендік тізбегіне байесовский талдауын жүргізді, бұл 1896 ж., ортақ туыстастықтың орташа уақыты (t-MRCA) деп көрсетеді, бұл алдыңғы деректермен сәйкес келеді [47]. HEF гендері, ICV және IDV үшін t-MRCA мәні 482 н.т., болды. Екі линия IDV-D/OK және D/660 шамамен 44.6 жыл бұрын соңғы жалпы ата-бабалары (t-MRCA) болғанын көрсетеді. HEF IDV гені алмасуының орташа жиілігі Байес анализінің көмегімен есептелді және 1,54×10-3 құрады, бұл ICV жиілігінен асып түсті [47]. Осы тұрғыдан алғанда, D тұмауының қоздырғышы үлкен эпидемиялық потенциалға ие және заманауи экологиялық-вирусологиялық және молекулалық-генетикалық әдістерді қолдану арқылы болашақта оның дамуын үнемі бақылау қажет.

Түйін сөздер: вирус, тұмау D, геном, өзгергіштік, мүйізді ірі қара, филогенез, клайд, тұтасу ақуызы HEF, серология.

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ВИРУСЫ ГРИППА D – ПАТОГЕНЫ, ОБРАЗУЮЩИЕ НОВЫЙ РОД В СЕМЕЙСТВЕ ORTHOMYXOVIRIDAE

Аннотация. Возбудители гриппа относятся к семейству Orthomyxoviridae и разделяются на роды: Influenzavirus A, B, C, D, а также Quaranjavirus, Thogotovirus и Isavirus. Впервые вирус гриппа D выделили из назальных смывов свиней в 2011 г. в США, в дальнейшем показана его широкая распространенность среди крупного рогатого скота во Франции, Китае, Италии, Ирландии, Японии, ряде африканских стран, а также способность инфицировать хорьков, морских свинок. Антитела к вирусу гриппа D обнаружены в сыворотках крови лошадей, овец, коз и у людей, контактировавших с крупным рогатым скотом. РНК-геном вируса гриппа D представлен семью фрагментами, ответственными за синтез 9 белков. Самые длинные три сегмента кодируют полимеразы PB2, PB1 и P3, четвертый – белок слияния гемагглютинин-эстеразу HEF, пятый – нуклеопротеин NP. Шестой фрагмент участвует в синтезе мембранных полипептидов DM1 и DM2, один из которых выстилает вирусную мембрану изнутри, другой осуществляет функцию протонных каналов. Седьмой сегмент кодирует неструктурный белок NS1 и белок ядерного экспорта NEP; NS1 способствует нейтрализации клеточного интерферона, NEP опосредует ядерный экспорт рибонуклеопротеина. Описаны три филогенетические линии вируса гриппа D – D/OK, D/660 и D/Japan, что необходимо учитывать при приготовлении вакцин. Делается вывод о том, что с точки зрения его эпидемиологических, патологических и биологических характеристик, потенциальной способности вызывать заболевание у людей и передаваться от человека человеку требуются новые, более углубленные исследования. Наиболее консервативный ген вирусного белка PB1 часто используется для оценки эволюционных взаимоотношений вирусов гриппа. S.. Su et al. [2] на основе нуклеотидных последовательностей генов PB1 вирусов гриппа A, B, C и D построили филогенетическое древо для определения взаимосвязи между ними. Кластеры IDV оказались наиболее тесно связаны с ICV, что предполагает их общего предка. Анализ последовательности генов PB2, P3, NP, M и NS также подтвердил происхождение IDV из ICV человека [26]. Чтобы изучить происхождение и эволюционную историю IDV, авторы провели байесовский анализ последовательностей генов HEF ICV, указав 1896 год как среднее время (t-MRCA) самого последнего общего предка, что согласуется с ранее полученными данными [47]. Для генов HEF ICV и IDV значение t-MRCA было 482 н.э. Показано, что две линии IDV – D/OK и D/660 имели последнего общего предка (t-MRCA) около 44,6 лет назад. Средняя частота замещения гена HEF IDV была рассчитана с использованием байесовского анализа и составила 1,54 × 10-3, что превышает частоту ICV [47]. С этой точки зрения возбудитель гриппа D обладает огромным эпидемическим потенциалом, и в будущем необходимо постоянно следить за его развитием. использованием современных эколого-вирусологических и молекулярно-генетических методов.

Ключевые слова: вирус, грипп D, геном, изменчивость, крупный рогатый скот, филогенез, кластер, белок слияния HEF, серология.

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CONSTRUCTION, EXPRESSION AND PURIFICATION OF *BRUCELLA SPP*. RECOMBINANT PROTEINS L7/L12 AND SODC IN *E. COLI*

Abstract. Brucellosis is still an important public health problem as long as natural reservoirs of infection exist. Currently, live attenuated vaccines based on strains S19, RB51 and Rev1 are used for the prevention of brucellosis in animals, the main disadvantage of which is virulence for humans. However, animal immunization programs should be implemented to reduce the incidence of humans. The development of safe and effective new generation vaccines using "omix" technology is a promising direction of vaccinology. A number of immunogenic Brucella proteins that elicit both a humoral and cellular immune response has been identified. The aim of these research was to optimize the expression and purification conditions of the *Brucella spp*. recombinant proteins L7/L12 and SodC. As a result, expressing plasmids pET/Br-L7/L12 and pET/Br-SodC were obtained. The parameters of target genes expression in *E. coli* were established and the method for purification of recombinant proteins was optimized. Purification of the L7/L12 protein was performed under hybrid conditions on HisPur agarose using a binding buffer containing 6 M guanidine hydrochloride, a wash buffer with 20 mM imidazole and an elution buffer with 300 mM imidazole. Protein SodC was purified under denaturing conditions with the addition of 1 % Triton X-100 and 1 % sodium deoxycholate to the lysis buffer. Inclusions were solubilized with a buffer containing 8 M urea and 5 mM imidazole. The target protein was eluted from HisPur agarose with buffer containing 8 M urea and 100 mM imidazole. The use of modified purification protocols made it possible to obtain purified recombinant proteins with a yield of 13 mg/L for the L7/L12 protein and 10 mg/L for the protein SodC, respectively. The specificity of the proteins was confirmed by a Western blot. Immunization of mice with recombinant proteins led to the production of specific antibodies, the titer of which in ELISA was 1:20480 and 1:20480, respectively.

Key words: *Brucella spp.*, ribosomal protein L7/L12, superoxide dismutase, expression, protein purification.

Introduction. Brucellosis is one of the widespread zoonotic diseases causing great economic damage to agriculture. According to the Joint FAO Expert Committee, brucellosis of livestock is prevalent in almost the whole world and since animals with brucellosis are a source of infection for humans, this disease is a high degree of danger [1-4]. The annual identification of farm animals and people reacting to brucellosis in certain regions of Kazakhstan indicates an extremely unstable situation for this infection and the real possibility of forming foci of brucellosis with varying degrees of activity of manifestations of epizootic and epidemic processes in farms [5,6]. In this regard, this infection is a serious problem for veterinary and medical science.

Today, recombinant proteins having antigenic and immunogenic properties are widely used in the development of prophylactic and diagnostic preparations, as well as candidates for vaccine against various zoonotic diseases. A lot of work has been devoted to the study of immunogenic proteins of *Brucella spp* and a number of proteins have been discovered, such as: L7/L12, SodC, BP26, BCSP31, Omp16, Omp19, Omp31, which have immunogenic properties that can be used for diagnostic purposes. These proteins are conserved and their identity is 100 % between *Brucella* species [7-12].

In the study of Brucella antigens capable of inducing cellular immunity, a 12 kDa protein was detected that causes lymphocyte proliferation and is a L7/L12 ribosomal protein. It was shown that purified recombinant L7/L12 protein produced in *E. coli* stimulates CD4 T cell immunity in mice infected with *B. abortus*. It was also shown that immunization of mice with the recombinant ribosomal protein L7/L12 protects them from control infection with *B. abortus*. According to published data, L7/L12 is an immunodominant *B. abortus* protein that elicits a cellular immune response (Th1 and CD8 + T cells) [13-15].

The periplasmic protein SodC (Cu-Zn superoxide dismutase) is one of the main enzymes of the antioxidant system of microorganisms, which is considered as one of the universal mechanisms of the pathogenesis of infectious diseases, and indicators reflecting shifts in the levels of antioxidant enzymes are key factors in predicting the outcome of the disease. The researchers determined the protective effect of the antioxidant enzyme SodC *B.abortus*, expressed in significant induction of T-cell proliferation and production of gamma-interferon in infected mice. Thus, vaccination of mice with *E. coli* cells expressing the SodC *B.abortus* enzyme formed a defense against brucella infection. The use for this purpose of plasmid DNA, including the SodC gene *B.abortus*, also induced a humoral and cellular immune response against the causative agent of brucellosis [8,16].

The purpose of these studies was the construction of expression vectors, the expression and optimization of the purification conditions of the recombinant *Brucella spp* L7/L12 and SodC proteins, as well as the production of specific sera to them. Recombinant proteins and their specific sera will be used in the development of a vector anti-brucellosis vaccine based on sheep pox virus.

Materials and methods. *Bacterial strains.* The studies used the vaccine strain *B.abortus* S19 obtained from the laboratory of the collection of microorganisms of the Research Institute of Biological Safety Problems RK ME&S – Science Committee, Kazakhstan. *B.abortus* S19 genomic DNA was isolated using the PrepMan Ultra kit (Applied Biosystems, USA). For manipulation with plasmid DNA, *E. coli* strain TOP10 (Invitrogen, USA) was used. For bacterial expression, E. coli T7 express strain (New England Biolabs, USA) was used.

Construction of expression cassettes and obtaining producer strains. The *Brucella* genes *L7/L12* and *sodC* were amplified with the genomic DNA *B.abortus* S19 using pairs of primers FP-*L7/L12*-5'-CGCAT*ATG*GCTGATCTCGCAAAGATCGT-3', RP-*L7/L12*-5'-CGCTCGAGCTTGA GTTCAACCTTGGCGCCA-3' and FP-*SodC-5*'-CGCC*ATGG*TTAAGTCCTTATTTATTGC-3', RP-*SodC-5*'-CGCTCGAGTTCGATCAC GCCGCAGGCAAAA-3', respectively.

Amplification was performed in 50 µl containing 5 µl of 10 × PCR buffer (Qiagen), 1 µl of 10 mM dNTPs (New England Biolabs, USA), 0.1 µl of DNA, 1 µl of each primer (20 pMol/µl), 0.5 µl of Taq DNA polymerase (2.5 units, Qiagen). Amplification conditions: 94 ºC 5 min; then 30 cycles of 94 ºC, 1 min, 50 ºC, 1 min, 72 ºC, 2 min, and 1 cycle of 72 ºC, 7 min.

The obtained products were digested with respective enzymes *NdeI – XhoI* (L7/L12), *NcoI – XhoI* (SodC) and cloned into the plasmid vector pET28b(+) (Novogen, USA).

As a result, recombinant plasmids pET/Br-L7/L12 and pET/Br-SodC were obtained containing the sequence coding the SodC protein fragment (1-173 aa) and the C-terminal peptide LEHHHHHH; and the sequence encoding the L7/L12 protein fragment (21-144 aa), the N-terminal peptide MSSHHHHHHSS and the C-terminal peptide LEHHHHHH. Plasmids were sequenced to verify the integrity of the inserts.

Plasmids were transformed into *E.coli* cells, strain T7 express (New England Biolabs, USA). As the result *E. coli* clones, producers of the recombinant proteins SodC and L7/L12, were obtained.

Gene expression. To expression the genes of the target proteins L7/L12 and SodC, bacterial cells were grown in LB-kan (Luria-Bertani broth, containing 50 µg/mL of kanamycin) at 37 °C on a shaker (250 rpm) to optical density OD600 = 0.6-1.0. Gene expression was induced by addition IPTG to final concentration 1 mM to the bacterial suspension with subsequent incubation for 4 h at 37 °C. The cells were harvested by centrifugation at 5000 × g for 15 min and stored at - 70 °C until further use. Aliquots

selected before and after induction were examined by PAGE electrophoresis. The solubility of the recombinant protein was determined using a BugBuster master mix reagent (Novagen, USA) according to the manufacturer's instructions.

Protein L7/L12 purification. Cell pellet was resuspended in NB buffer (50 мМ NaH_2PO_4, 300 мМ NaCl, 6 М guanidine hydrochloride, 10 мМ imidazole, pH 7,4) at the rate of 5 ml of buffer per 1 g of crude cell pellet. Suspension was incubated in ice for 30 min and sonicated. Cell lysate was clarified by centrifugation at 3000 g for 15 min. The supernatant (soluble protein fraction) was filtered through a 0.22 μm membrane and uploaded to HisPur ™ Cobalt Superflow (Thermo Scientific, USA) agarose pre-equilibrated with NB buffer. The agarose resin was washed using NW buffer (50 mM NaH_2PO_4, 300 mM NaCl, 20 mM imidazole, pH 7.4), the protein was eluted with NE buffer (50 mM NaH_2PO_4, 300 mM NaCl, 300 mM imidazole, pH 7.4). The pure protein fraction was dialyzed against 10 times the volume of the buffer (20 mM PBS, 300 mM NaCl, pH 7.4) overnight at 4°C.

Protein SodC purification. Protein purification was performed as [17] with modifications. Cells were resuspended in buffer 1 (100 mM Tris HCl pH 8.0, 150 mM NaCl, 1 % Triton X-100, 1 % Sodium deoxycholate) at the rate of 15 ml per 1 g of crude cell pellet. Lysozyme was added to the resulting suspension to a final concentration of 1 mg/ml. Cell lysis was performed by freezing twice at - 70 °C and thawing at 37 °C of the suspension. The cell lysate was incubated at 4 °C overnight, then centrifuged at 4 °C for 15,000 × g for 15 min. The pellet was washed successively with buffer 2 (100 mM Tris HCl, pH 8.0, 150 mM NaCl, 1 % Triton X-100), buffer 3 (100 mMTris HCl, pH 8.0, 1 M NaCl), buffer 4 (50 mM Tris HCl, pH 7.5). The pellet was resuspended in buffer 5 (20 mM PBS, pH 7.4, 300 mM NaCl, 8 M urea, 5 mM imidazole, pH 7.4) and incubated at 4°C overnight to completely solubilize. The dissolved inclusion fraction was filtered through a 0.22 μm membrane. Protein purification was carried out using HisPur ™ Cobalt Superflow agarose. After sorption of protein, resin was washed with DW buffer (50 mM NaH_2PO_4, 300 mM NaCl, 8 M urea, 5 mM imidazole, pH 7.4). Protein was eluted with DE buffer (50 mM NaH_2PO_4, 300 mM NaCl, 8 M urea, 100 mM imidazole, pH 7.4). Refolding of the protein was performed by dialysis sequentially against buffer 7 (20 mM PBS, 300 mM NaCl, 4 M urea, pH 7.4), buffer 8 (20 mM PBS, 300 mM NaCl, 2 M urea, pH 7.4), buffer 9 (20 mM PBS, 300 mM NaCl, 1 mM DTT (dithiothreitol), pH 7.4) and buffer 10 (20 mM PBS, 300 mM NaCl, pH 7.4). Protein concentration was determined by the method of Lowry et al. [18], using BSA as a standard.

Polyacrylamide gel electrophoresis and Western blot. Electrophoretic analysis of polypeptides was performed in 12 % SDS-PAGE under denaturing reducing conditions according to Laemmli [19]. For visualization of proteins, Coomassie G-250 staining was used. For Western blot analysis, proteins were transferred onto a nitrocellulose membrane and detected as described in [20] using anti-His (Cterm)/AP antibodies (Invitrogen, USA) and sera from sick cattle.

Obtaining specific serum to recombinant proteins. Animal experiments were carried out in accordance with applicable national and international legislation. The protocol was approved by the Bioethics Commission of the RIBSP RK ME&S of the Republic of Kazakhstan (No. 6 dated September 25, 2017).

To obtain specific sera, outbred white mice (females, 6-8 weeks old, weight 18-20 g) were immunized with a target protein. Proteins were prepared as follows: purified protein was mixed with Montanide Gel 01 (SEPPIC, USA) in a ratio of 9:1 (v/v). The final protein concentration was 150 μg/ml. Before administration of the drug, animals were bled to obtain normal serum. Immunization was carried out subcutaneously four times in a dose of 30 μg of protein. 14 days after the last injection, the animals were bled. The serum was tested in ELISA (enzyme-linked immunosorbent assay).

ELISA. 96-wells plates were coated with the 2 mg/ml of affinity purified recombinant proteins in 0.05 M carbonate-bicarbonate buffer, pH 9.6 (100 μL/well), and incubated overnight at 4 °C. Plates were washed four times with TBST buffer (150 мМ NaCl, 20 мМ tris-HCl, pH 7.5, 0,1 % tween-20) and blocked with TBST containing 5 % fat free dry milk for 1 h at 37 °C. Double dilutions of test sera in the blocking buffer, were added to wells (100 μL/well). Plates were incubated for 1 h at 37 °C and washed three times with TBST. Anti-mouse immunoglobulin IgG conjugated to alkaline phosphatase (1:5000) was added (100 μL/well) and the plates were incubated for 1 h at 37 °C. After washing, the substrate for alkaline phosphatase (pNPP, Sigma, USA) was added into each well (100 μL). The plates were incubated

for 30 min. Optical density was read at 405/630 nm on ELISA plates reader ImmunoChem-2100. Cut-off values were determined using the mean optical density values from negative control sera plus three standard deviations.

Results and discussion. *Construction of recombinant plasmids.* A comparative analysis of the amino acid sequences of the L7/L12 and SodC proteins showed their high identity (95-100 %) for *Brucella spp.* Using the SignalP [21] and TMHMM2.0 [22] software, the signal peptide was established for the SodC protein, while transmembrane domains were absent in both proteins (figure 1).

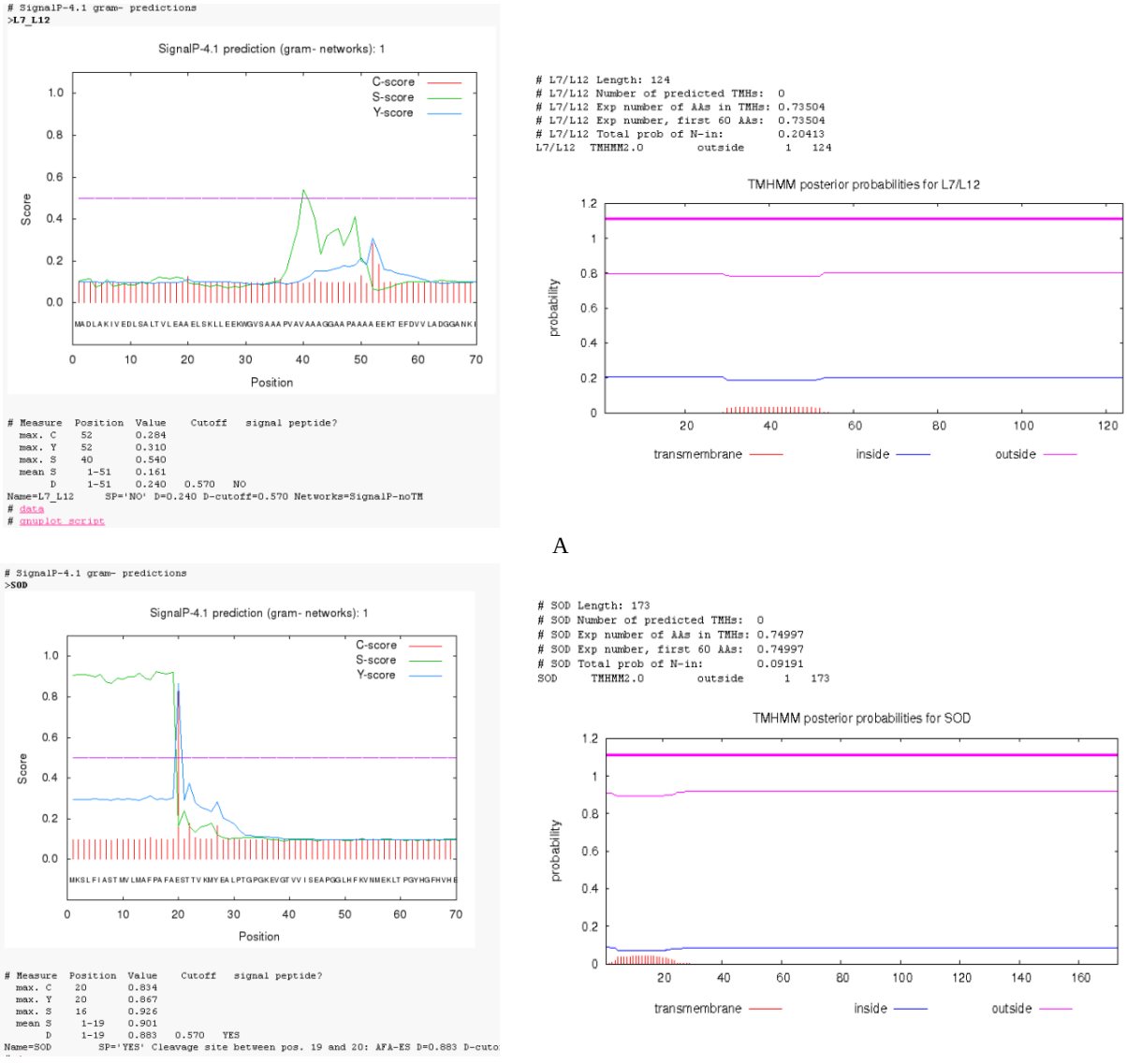


Figure 1 – The results of the analysis of the amino acid sequences of the target proteins for the presence of signal peptides and transmembrane domains: A – L7/L12, B – SodC

Amplified DNA fragments encoding the L7/L12 and SodC genes were cloned into the pET28b(+) vector. As a result, plasmids expressing recombinant proteins flanked at the N- and/or C-terminus by 6HIS oligopeptides were obtained (figure 2). The predicted molecular weights of SodC and L7/L12 proteins were 19.87 and 15.77 kDa, respectively. The obtained plasmids were transformed into *E. coli* T7 cells.

Analysis	Entire Protein
Length	152 aa
Molecular Weight	15774.20
1 microgram =	63.395 pMoles
Molar Extinction coefficient	5690
1 A[280] corr. to	2.77 mg/ml
A[280] of 1 mg/ml	0.36 AU
Isoelectric Point	6.10
Charge at pH 7	-5.07

```
  1  MGSSHHHHHH SSGLVPRGSH MADLAKIVED LSALTVLEAA ELSKLLEEKW
 51  GVSAAAPVAV AAAGGAAPAA AAEEKTEFDV VLADGGANKI NVIKEVRALT
101  GLGLKEAKDL VEGAPKAVKE GASKDEAEKI KAQLEAAGAK VELKLEHHHH
151  HH
```

A

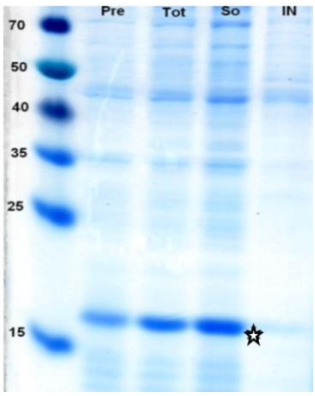
Analysis	Entire Protein
Length	188 aa
Molecular Weight	19875.26
1 microgram =	50.314 pMoles
Molar Extinction coefficient	5360
1 A[280] corr. to	3.71 mg/ml
A[280] of 1 mg/ml	0.27 AU
Isoelectric Point	6.37
Charge at pH 7	-3.75

```
  1  MKSLFIASTM VLMAFPAFAE STTVKMYEAL PTGPGKEVGT VVISEAPGGL
 51  HFKVNMEKLT PGYHGFHVHE NPSCAPGEKD GKIVPALAAG GHYDPGNTHH
101  HLGPEGDGHM GDLPRLSANA DGKVSETVVA PHLKKLAEIK QRSLMVHVGG
151  DNYSDKPEPL GGGGARFACG VIEDKLAAAL EHHHHHH*
```

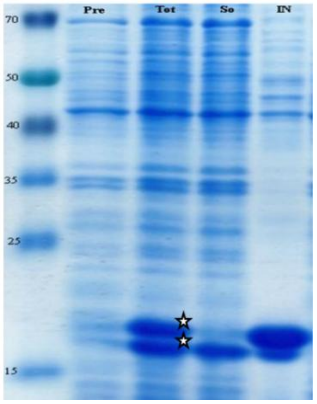
B

Figure 2 – Prediction and analysis of amino acid sequences of recombinant proteins L7/L12 (A) and SodC (B)

The expression of genes encoding recombinant proteins. Induction of target genes expression resulted in the production of L7/L12 (figure 3A) and SodC (Figure 3B) proteins. The molecular weight of the recombinant proteins corresponded to the calculated values (figures 2, 3). As a result of gene SodC expression, two protein products were formed (figure 3B, Tot), which is associated with the presence of a signal peptide in the sequence of the recombinant protein. Modified protein (without signal peptide) was in the soluble protein fraction (figure 3B, So), while unmodified protein formed inclusions bodies (figure 3B, IN).



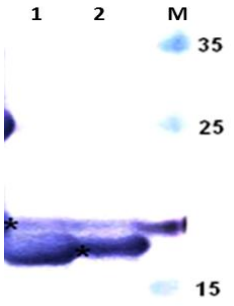
A



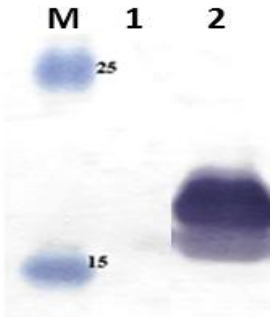
B

Figure 3 – Electrophoretic analysis of proteins of the cell lysate of E. coli strain T7, transformed with plasmids pL7/L12 (A) and pSodC (B): Pre – cell lysate before induction, Tot – after induction IPTG, So – soluble proteins, IN – inclusions. Recombinant proteins are marked with asterisks

The expression of the target Brucella L7/L12 and SodC proteins was confirmed by the Western blot using anti-His-antibodies (figure 4). Recombinant proteins also interacted with sera from brucellosis sick cattle, which confirms their specificity (figure 5).



A



B

Figure 4 – Immunoblotting of proteins of the cell lysate of *E. coli* strain T7, transformed with recombinant pET plasmids, using serum to polyhistidine. A:1 – cell lysate prior to induction of L7/L12; 2 – after induction of IPTG; B:1 – cell lysate prior to SodC induction; 2 – after induction of IPTG

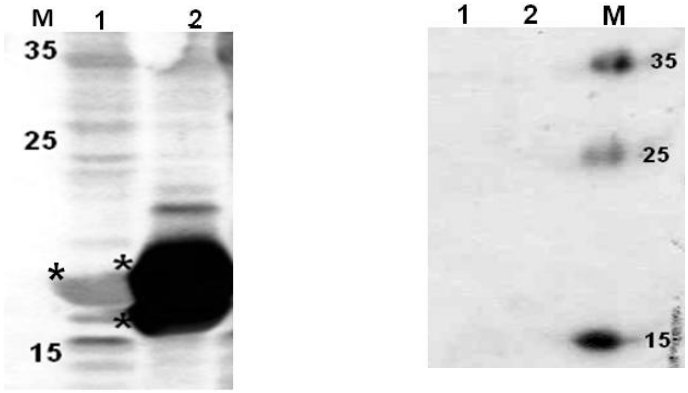


Figure 5 – Immunoblotting of proteins of the cell lysate of E. coli strain T7, transformed with recombinant pET plasmids, using serum from cattle with brucellosis: A – serum from cattle with brucellosis, B – normal cattle serum. 1 – cell lysate L7/L12; 2 – cell lysate SodC. Recombinant proteins are marked with asterisks

B. abortus Cu-Zn супероксиддисмутаза (SodC) была идентифицирована Beck et al. (1990) [23]. Using western blot, Betsy et al. (1990) proved that superoxide dismutase is found in most *Brucella* strains and species except *B. neotomae* and *B. suis* biovar 2 [24]. Both SodC and L7/L12 are immunodominant proteins and induce antibody production. Rajagunalan et al. (2014) in their studies, found antibodies to the recombinant protein L7/L12 of *B. melitensis* 16M in the sera from patients with acute brucellosis [25]. Proteins SodC and L7 / L12 were used in the development of DNA and vector vaccines. Recombinant vaccines elicited an immune response in animals [13, 14, 26].

Protein purification L7/L12. At the first stage, the purification of L7/L12 protein was carried out under native conditions (figure 6).

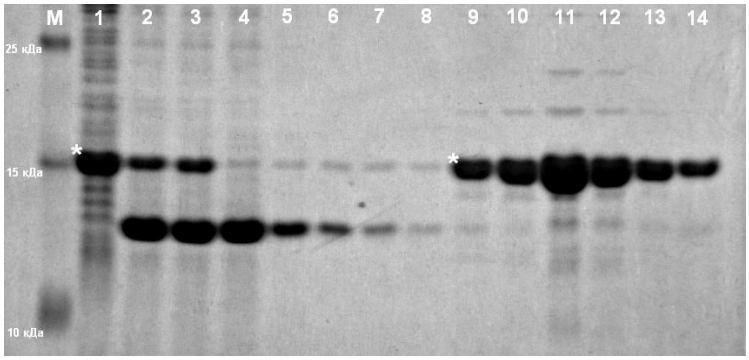


Figure 6 – Electrophoretic analysis of the recombinant protein L7/L12 during the cleaning process: M – molecular weight marker; 1 – total cell lysate; 2 – cell lysate after treatment with lysozyme; 3 – cell lysate after filtration through 0.22 μm; 4 – flow-through; 5-8 – wash fraction; 9-14 – fractions of purified protein. Recombinant proteins are marked with asterisks

As seen in the figure 6, lane 4, the cell lysate was not completely adsorbed onto resin. Washing the agarose with a buffer containing both 20 mM imidazole (figure 6, lane 7, 8) and 10 mM imidazole (figure 6, lane 5, 6) resulted in the loss of the target protein. The target protein eluted with a buffer containing both 300 mM imidazole (figure 6, lane 11-14) and 100 mM imidazole (figure 6, lane 9, 10) contained cell protein impurities. Purification of the protein under standard native conditions according to the recommendations of the resin manufacturer did not give satisfactory results. The protein purification protocol was optimized.

Hybrid conditions were selected for purification (see the Materials and Methods section), which made it possible to obtain a protein preparation with a high degree of purification without significant losses at intermediate stages (figure 7). The yield of recombinant protein L7/L12 was 13 mg per 1 liter of culture.

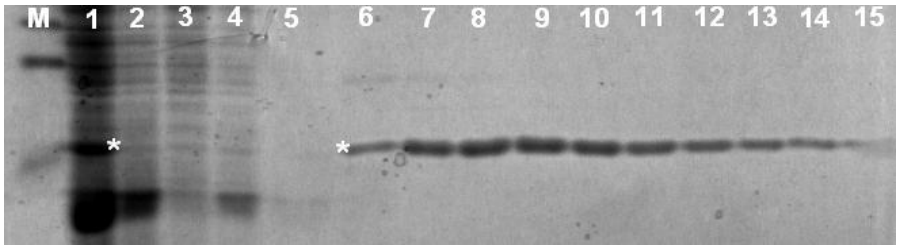


Figure 7 – Electrophoretic analysis of the recombinant protein L7/L12 during the purification process using optimal (hybrid) conditions. M – molecular weight marker; 1 – cell lysate after treatment with lysozyme; 2 – flow-through; 3-5 – washing fractions; 6-15 – fractions of purified protein. Recombinant proteins are marked with asterisks

SodC Protein Purification. Protein purification was performed under denaturing conditions (figure 8). When purifying the recombinant SodC protein, there were also problems with its adsorption to agarose. Only a small amount of protein was bound to the resin (figure 8, lane 2). Washing the resin led to the loss of the target protein (figure 8, lane 3-6), and the protein eluate contained a significant amount of impurities of cellular proteins (figure 8, lanes 7-10). An optimized purification protocol (see the Materials and Methods section) made it possible to obtain a SodC protein preparation with a high degree of purity (figure 9).

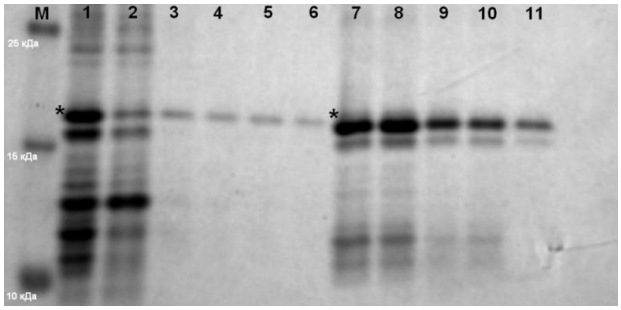


Figure 8 –
Electrophoretic analysis of recombinant SodC protein during purification under denaturing conditions.
M – molecular weight marker;
1 – cell lysate after treatment with lysozyme;
2 – flow-through; 3-6 – wash fraction;
7-12 – fractions of purified protein.
Recombinant proteins are marked with asterisks

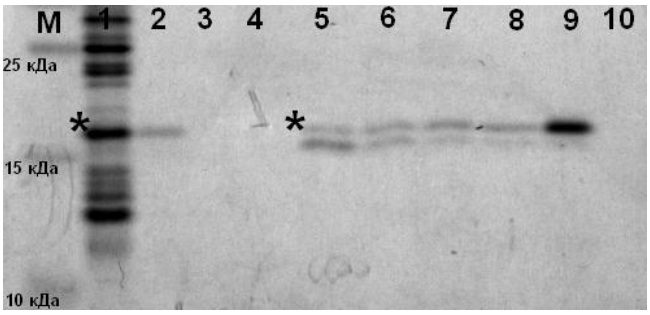


Figure 9 –
Electrophoretic analysis of recombinant SodC protein during purification under optimal denaturing conditions: M – molecular weight marker;
1 – cell lysate after treatment with lysozyme;
2 – flow-through; 3-4 – washing fractions;
5-10 – fractions of purified protein.
Recombinant proteins are marked with asterisks

As seen in the figure 9, a slight loss of the target protein was observed upon binding to agarose (lane 2). Loss of the target protein during resin washing was not detected (lanes 3-4). There were no impurities of cell protein in the eluate (lanes 5–9), which confirms the high purity of the obtained recombinant protein preparation. The yield of purified SodC protein was 10 mg per 1 liter of culture.

In addition, mouse specific sera for recombinant SodC and L7 / L12 proteins were obtained. For this, mice were immunized with triply recombinant proteins mixed with Montanide 01 gel (seppic, USA). Recombinant proteins induced the production of specific antibodies in animals. The antibody titer in ELISA for both SodC and L7 / L12 proteins was 1: 20480.

Purified recombinant proteins and their specific sera are suitable for use in the development of specific diagnostic and prophylactic agents against *Brucella* spp.

Conclusion. As a result of studies, purified preparations of recombinant proteins SodC and L7/L12 were obtained. Optimal protocols have been developed for the expression and purification of recombinant proteins in E.coli. The specificity of the obtained purified recombinant proteins was established using the western blot with sera from animals with brucellosis. Highly active specific sera for recombinant proteins were obtained, an antibody titer was 1:20480 for both the SodC and the L7/L12 proteins. Proteins and

serums for them will be further used in the development of specific diagnostic and prophylactic agents against *Brucella* spp.

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E. COLI-ДЕ *BRUCELLA SPP.* L7/L12 ЖӘНЕ SODC РЕКОМБИНАНТТЫ БЕЛОКТАРДЫ КОНСТРУИРЛЕУ, ЭКСПРЕССИЯЛАУ ЖӘНЕ ТАЗАЛАУ

Аннотация. Бруцеллез инфекцияның табиғи резервуарлары бар болғандықтан, денсаулық сақтаудың маңызды проблемасы болып қала береді. Қазақстанның жеке аудандарында жыл сайын адамдардың және ауыл шаруашылығындағы малдардан бруцеллездің анықталуы індет бойынша тұрақсыз, құбылмалы жағдайды және шаруашылықтардағы эпизоотиялық және эпидемиялық процестердің әртүрлі деңгейдегі белсенді көріністерімен бруцеллез ошақтарының қалыптастыруының нақты мүмкіндігінің бар екенін білдіреді. Осыған байланысты, бұл індет ветеринария және медицина ғылымы үшін үлкен мәселе болып отыр. Қазіргі таңда бруцеллезді мал шаруашылығында алдын алу үшін S19 және RB51 штамдары негізінде алынған тірі аттенуирленген вакциналар қолданылады. Олардың басты кемшілігі – адамдарға тигізетін жұқпалы әсері. Сонда да адамдардың бұл індетпен ауруын төмендету үшін ауыл шарушылығындағы малдарды иммундау бағдарламалары жүзеге асырылуы қажет. Омиксті технологияларды қолдана отырып, қауіпсіз және тиімді болатын жаңа дәуір вакциналарын жасақтау – вакцинологияның перспективті бағыты. Бүгінгі күні алдын алу және балау, препараттарды әзірлеу кезінде, сонымен қатар әртүрлі зоонозды ауруларға қарсы вакцина жасау барысында қолданылатын, антигендік және иммуногендік қасиеттері бар рекомбинантты белоктар кеңінен қолданылады. Гуморалды және жасуша деңгейінде иммунды жауап қайтаратын бруцелланың бірқатар иммуногенді белоктары айқындалған болатын. Бұл мақаланы жазудың мақсаты *Brucella spp.* L7/L12 және SodC рекомбинантты белоктарды экспрессиялау және тазалау барысындағы жағдайларды оңтайландырумен байланысты. Жасалған жұмыстардың нәтижесінде экспрессиялайтын плазмидалық ДНҚ *pET/Br-L7/L12* және *pET/Br-SodC* алынды. Тұтас гендердің *E.coli* -де экспрессиялау параметрлері анықталды және рекомбинантты белоктарды тазалау әдісі оңтайландырылды. Нәтижесінде L7/L12 белокты тазалау үшін келесідей гибридті жағдай таңдалды: жасушаларды лизистеу барысында құрамында 6М гуанидин гидрохлориді бар буферді қолдану, жуып-шаю барысында құрамында 20 мМ имидазол бар буферді қолдану, HisPur агарозадан тұтас белокты элюирлеу барысында, құрамында 300 мМ имидазол бар буферді қолдану. SodC белокты денатурациялы жағдайда лизис буферіне 1 % тритон Х-100 және 1 % натрий дезоксихолаты қосылып тазаланды. Алынған тұнбалар құрамында 8 М мочевина және 5 мМ имидазол бар буферді қолдана отырып, ерітіліп алынды. HisPur агарозадан тұтас белокты құрамында 8 М мочевина және 100 мМ имидозол бар буферді қолдана отырып, элюирлеп алынды. Тазалау барысының өзгертілген жағдайларын қолдана отырып, тазартылған рекомбинантты белоктар келесідей мөлшерде алынды: L7/L12 шығымдылығы 13 мг/л, SodC шығымдылығы 10 мг/л. Белоктардың телімділігі вестр блотты қолдана отырып расталды. Рекомбинантты белоктармен тышқандарды егу нәтижесінде ИФА-де титрлері 1:20480 және 1:20480 сәйкес телімді антиденелердің пайда болуы анықталды. Рекомбинантты белоктар мен оларға алынған сарысулар бруцеллезге қарсы қой шешегі вирусы негізде векторлық вакцинаны жасауда қолданылатын болады.

Түйін сөздер: *Brucella spp.,* рибосомалық белок L7/L12, супероксиддисмутаза, экспрессия, тазалау.

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КОНСТРУИРОВАНИЕ, ЭКСПРЕССИЯ И ОЧИСТКА РЕКОМБИНАНТНЫХ БЕЛКОВ L7/L12 И SODC *BRUCELLA SPP.* В *E. COLI*

Аннотация. Бруцеллез продолжает оставаться важной проблемой здравоохранения, пока существуют естественные резервуары инфекции. Ежегодное выявление реагирующих на бруцеллез сельскохозяйственных животных и людей в отдельных районах Казахстана свидетельствует о крайне неустойчивой ситуации по этой инфекции и о реальной возможности формирования очагов бруцеллеза с разной степенью активности проявления эпизоотических и эпидемических процессов в хозяйствах. В связи с этим данная инфекция представляет серьезнейшую проблему для ветеринарной и медицинской науки. В настоящее время для профилактики бруцеллеза у животных используют живые аттенуированные вакцины на основе штаммов S19 и RB51, главным недостатком которых является вирулентность для человека. Тем не менее, программы иммунизации животных должны проводиться, чтобы снизить заболеваемость людей. Разработка безопасных и эффективных вакцин нового поколения с использованием омиксных технологий является перспективным направлением вакцинологии. Сегодня при разработке профилактических и диагностических препаратов, а также в качестве кандидатов на вакцину против различных зоонозных заболеваний широко используются рекомбинантные белки, обладающие антигенными и иммуногенными свойствами. Установлен ряд иммуногенных белков бруцелл, индуцирующих как гуморальный, так и клеточный иммунный ответ. Целью данных исследований являлась оптимизация условий экспрессии и очистки рекомбинантных белков L7/L12 и SodC *Brucella spp.* В результате проведенных исследований получены экспрессирующие плазмидные ДНК *pET/Br-L7/L12* и *pET/Br-SodC*. Установлены параметры экспрессии целевых генов в *E.coli* и оптимизирован метод очистки рекомбинантных белков. В результате проведенных работ для очистки белка L7/L12 подобраны гибридные условия с использованием буфера содержащего 6М гуанидина гидрохлорида на этапе лизиса клеток, 20 мМ имидазола на этапе отмывки и 300 мМ имидазола на этапе элюирования целевого белка с агарозы HisPur. Белок SodC очищали в денатурирующих условия с добавлением в лизирующий буфер 1 % тритон Х-100 и 1 % дезоксихолата натрия. Включения солюбилизировали буфером, содержащим 8 М мочевины и 5 мМ имидозола. Элюировали целевой белок с агарозы HisPur буфером содержащим 8 М мочевины и 100 мМ имидозола. Использование модифицированных протоколов очистки позволило получить очищенные рекомбинантные белки с выходом 13 мг/л для белка L7/L12 и 10 мг/л для белка SodC, соответственно. Специфичность белков была подтверждена в вестерн блоте. Иммунизация мышей рекомбинантными белками приводила к выработке специфических антител, титр которых в ИФА составил 1:20480 и 1:20480 соответственно. Рекомбинантные белки и специфические сыворотки к ним будут использованы при разработке векторной противобруцеллезной вакцины на основе вируса оспы овец.

Ключевые слова: *Brucella spp.,* рибосомальный белок L7/L12, супероксиддисмутаза, экспрессия, очистка.

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OXIDATIVE STRESS AND MITOCHONDRIAL DYSFUNCTION

Abstract. The process of cell damage resulting from the action of free radicals – reactive oxygen species (ROS) – is called oxidative stress. Most ROS are constantly formed in the cell – about 5 % of the oxygen consumed by tissues is converted into free radicals, but their level is normally so small that the cell inactivates them with the help of an antioxidant system. Different organs and tissues are exposed to different degrees of ROS and demonstrate different stability during the implementation of oxidative stress. The mechanisms of ROS formation by mitochondria under oxidative stress are still unclear.

At the same time, it was found that mitochondrial dysfunction and the accumulation of mitochondrial mutations in tissues make a significant contribution to the aging process, as well as to the pathogenesis of a number of diseases characterized by neurodegeneration. Mutations lead to increased generation of free radicals, reduced ATP levels, and energy failure of cells.

Coenzyme Q10 is a component of the mitochondrial respiratory chain. Violation of the biosynthesis of coenzyme Q10 can lead to a number of mitochondrial diseases. When coenzyme Q10 is deficient, sulfide metabolism plays a critical role. Sulfide metabolism in mammalian cells includes trans-sulfuration (biosynthetic) and hydrogen sulfide oxidation (H_2S) (catabolic). Violation of H_2S oxidation may contribute to oxidative stress in coenzyme Q deficiency or may play a synergistic role with oxidative stress in the pathogenesis of tissue specificity in coenzyme Q deficiency.

Key words: oxidative stress, reactive oxygen species, mitochondria, mitochondrial diseases, coenzyme Q10, glutathione.

Mechanisms of oxidative stress.

The processes of free radicals and the body's responses are roughly balanced. It is easy enough to shift this relative balance in favor of radicals. As a result, the cell's biochemistry is disrupted and oxidative stress occurs. Most elements are able to tolerate a moderate degree of imbalance. This is due to the presence of reparative structures in cells [1]. They identify and remove damaged molecules. New elements take the place of the latter. In addition, cells have the ability to increase protection by responding to oxidative stress [2].

Oxidative stress is an imbalance between oxidants (active forms of oxygen) and antioxidant protection in the body towards oxidants. In cells, oxidants actively interact with biomolecules (phospholipids, proteins, and nucleic acids). As a result, these biomolecules are irreversibly damaged, which leads to cellular dysfunction and, as a result, various pathologies in the body and cell death [3].

However, oxidative stress cannot be unequivocally considered as absolutely harmful to the body. In some cases, oxidative stress is used by the body as a defense mechanism. The immune system uses it to fight antigens [4].

Oxidative stress is the process of cell damage as a result of the action of free radicals-reactive oxygen species (ROS). Most ROS are constantly formed in the cell – about 5 % of the oxygen consumed by tissues is converted into free radicals, but their level is normally so small that the cell either inactivates

them with the help of an antioxidant system (reduced glutathione, vitamins C and E, coenzyme Q, neutralizing short – lived ROS free radicals, while turning into long-lived or stable radicals in which the unpaired electron is delocalized-oxidized glutathione, ascorbate-radical, tocopheroxyl radical, coenzyme q radicals), or replaces damaged molecules. Thus, ROS formed as byproducts of normal cellular metabolism in the respiratory chain of mitochondria, as well as other cytoplasmic reactions, do not cause cell damage [5, 6].

Oxidative stress and its consequences for the body.

The level of ROS that exceeds the protective capabilities of the cell causes serious cellular disorders (for example, ATP depletion). As a result, one of the least ROS, superoxide, becomes more aggressive (hydroxyl radical, etc.), which can cause oxidation and destruction of many cellular components – proteins and lipids of membranes, DNA [7]. The cells can return to their original state with small abnormalities. However, more severe oxidative stress causes cell death. When necrosis occurs, the cell membrane is destroyed and the cell contents are released into the intercellular space, which can result in damage to the surrounding cells and tissues and cause a cascade of pathological processes.

Exposure to ionizing radiation, high temperatures, and certain chemicals (nitrates, etc.) triggers oxidative stress as a pathological process, increasing the formation of ROS. It is known that different organs and tissues are exposed to different degrees of ROS and demonstrate different stability during the implementation of oxidative stress (figure 1) [8].

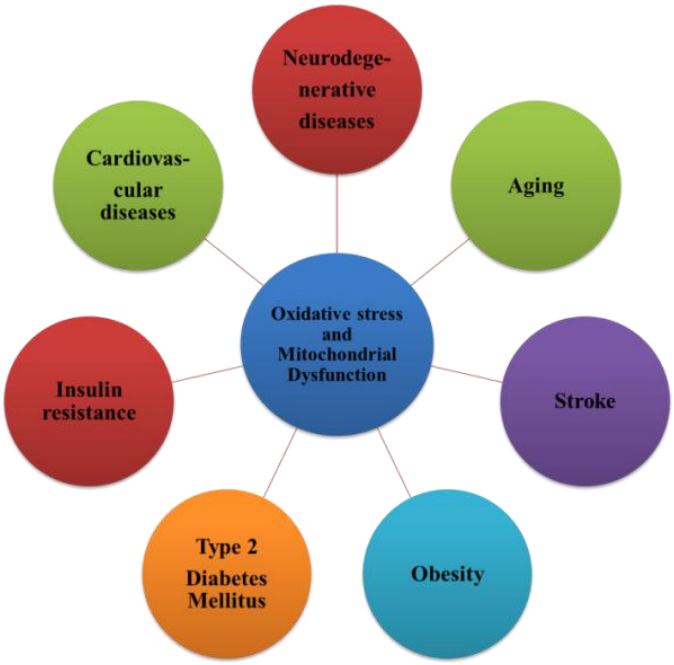

Figure 1 – Oxidative stress and mitochondrial dysfunction

Since the formation of oxygen derivatives and the level of the antioxidant defense system are approximately balanced, it is easy to shift the balance in favor of oxygen derivatives and disrupt the cell's biochemistry. Most cells can tolerate a moderate degree of oxidative stress due to the fact that they have a reparative system that detects and removes molecules damaged by oxidation, which are then replaced (figure 2).

In addition, cells can increase their antioxidant defense in response to oxidative stress. For example, rats placed in an atmosphere of pure oxygen (and the air contains 21 % oxygen) die after a few days. But exposure to animals with gradually increasing oxygen concentrations over a few days can increase the activity of the antioxidant defense in the lungs, and ultimately they can tolerate 100 % oxygen content. However, severe oxidative stress can damage or destroy cells [9-11].

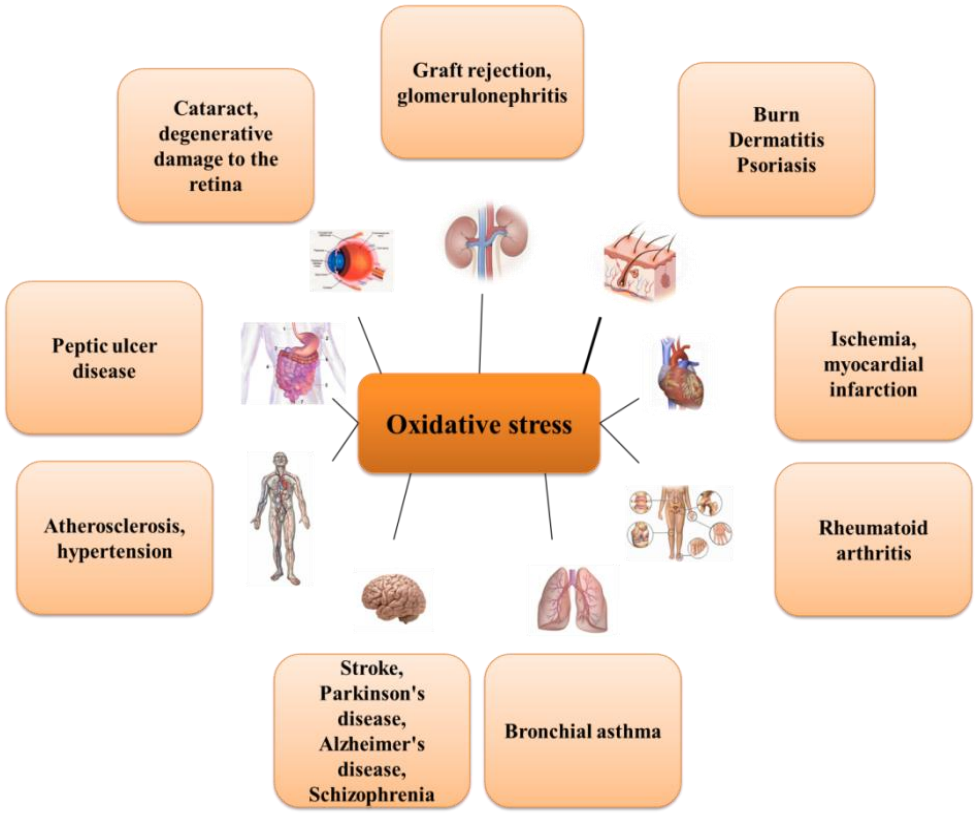

Figure 2 – Diseases associated with oxidative stress

In a healthy human body, there is a normal balance between the formation of oxygen derivatives and antioxidant protection. It follows that there are at least two reasons for the development of oxidative stress: a decrease in the number of antioxidants or an increase in the formation of oxygen derivatives in such a way that antioxidants can no longer cope with protection [12].

Physiological role of reactive oxygen species.

The action of ROS in the body is actually directed at 3 types of cell targets: proteins, nucleic acids, and lipids. Normally, they are actively involved in their metabolism, and in pathological conditions – in their oxidative destruction.

Various stimuli, such as ionizing radiation, inflammation, increased oxygen stress, ozone, and aging processes contribute to the formation of increased concentrations of ROS. Ozone, ozonides and industrial pollutants contained in the air activate the processes of radical formation in the lung tissues [13].

Oxidative modification of proteins, nucleic acids, and lipids with the participation of ROS is constantly observed in tissues and plays an important role in the breakdown of these compounds. This is one of the stages of updating the chemical composition of tissues. ROS cause oxidative modification of nucleotides and nucleic acids, especially DNA. This leads to the formation of ROOH hydroperoxides (for example, 5-CH_2OOH-uracil is formed from thymine), and then the hydroxy derivatives ROH or $R(OH)_2$, the main of which are 8-OH-2'-deoxyguanosine and timinglicol (their determination in tissues and urine is used as indices of oxidative DNA modification).). Of ROS, only NO• causes DNA damage (oxidation of bases, their modifications, chain breaks, chromosome damage), while it is now believed that ROS cause more mutations than another class of mutagens – alkylating substances. Mutations can lead to pathology and death of cells or their malignant degeneration (cancer, leukemia, etc.), and mutations in the DNA of germ cells – to inherited diseases. High concentrations of ROS and lipid hydroperoxides inhibit DNA synthesis and cell division and can activate apoptosis [14,15].

Lipid peroxidation is carried out in the presence of metals of variable valency and is accompanied by the formation of a group of radical products – R•, RO•, ROO•, cytotoxic aldehydes of the 4-hydroxy-2, 3-trans-nonenal type, or less toxic, as Malon dialdehyde.

Reactive oxygen species have not only cytotoxic properties, but can also act as secondary messengers, participating in maintaining the physical and chemical properties of biological membranes, regulating the state of intracellular redox systems, protein kinase activity, and regulating cellular reactions such as proliferation, differentiation, and apoptosis.

Generation of moderate amounts of ROS is an absolutely necessary element of the physiological state of cells of all types. Active oxygen forms take part in the cellular immune system, providing the function of all phagocytes in the fight against infection. Regulation of prostaglandin, thromboxane, and leukotriene synthesis. Oxidative destruction of xenobiotics (exogenous substances foreign to the body), destruction of own damaged or abnormal cells. Regulation of cell growth, proliferation and differentiation. Participation in cell membrane renewal and modification [16-18].

The role of mitochondria in the development of oxidative stress.

Mitochondria are cellular organelles that perform important functions: supplying cells with energy in the form of ATP, generating and regulating calcium ions in the cytoplasm, and initiating apoptosis. Violations of the function of these organelles play a leading role in the origin and clinical manifestations of mitochondrial diseases caused by mutations of mitochondrial or nuclear DNA genes that encode energy metabolism.

At the same time, it was found that mitochondrial dysfunction and the accumulation of mitochondrial mutations in tissues make a significant contribution to the aging process, as well as to the pathogenesis of a number of diseases characterized by neurodegeneration [19]. Mutations lead to increased generation of free radicals, reduced ATP levels, and energy failure of cells.

The mechanisms of ROS formation by mitochondria under oxidative stress are still unclear. Numerous data obtained in experiments with isolated mitochondria and submitochondrial particles indicate that the main superoxide-forming components of the respiratory chain are NADH: ubiquinone-oxidoreductase (complex I) and ubiquinone-cytochrome C reductase (complex III). However, it is not clear which component of complex I serves as a single-electron donor for oxygen recovery. Moreover, under physiological conditions, cells maintain a high level of NADH, which can prevent the formation of superoxide by complex I. Probably for this reason, experiments on cell cultures give conflicting results about the role of complex I in the generation of ROS. Inhibition of complex I activity in cell culture can lead to both an increase and a decrease in ROS levels, depending on the cell type and the stimulus that causes oxidative stress. This ambiguity indicates the complexity of the mechanisms of ROS generation by mitochondria in physiological conditions [20].

The role of coenzyme Q10 as a biomarker of oxidative stress.

Coenzyme Q10 is a component of the mitochondrial respiratory chain. In recent years, the antioxidant properties of its reduced form have been actively studied. In its reduced form, coenzyme Q10 is found in all cell membranes, blood plasma, and lipoproteins. Coenzyme Q10 successfully protects membrane phospholipids and low-density lipoproteins from peroxidation, as well as mitochondrial membrane proteins and mitochondrial DNA from damage by free radicals. These properties of coenzyme Q10 are not related to the action of exogenous antioxidants, although coenzyme Q10 is able to enhance the effects of vitamin E by restoring it from the oxidized form. The content of Q10 in tissues increases with oxidative stress and decreases with age, primarily in the myocardium.

Coenzyme Q10 (Q10) is a fat – soluble vitamin-like substance. Q10 is found in the human body literally everywhere, which is why its second official name – "ubiquinone" (from lat. ubique-everywhere, everywhere). Inside cells, Q10 is mostly found in mitochondria (40-50 %). There is twice as much of this substance in the heart muscle as in any other organ or tissue.

Two main functions of Q10 in living organisms are known today. Q10 is involved in the production of energy in any of the cells. Coenzyme Q10 in mitochondria is involved in the synthesis of ATP as an electron Transporter that interacts with the processes of electronic transport and oxidative phosphorylation. It is a necessary link for the transfer of electrons from complexes I and II to complex III of the respiratory chain. With a lack of Q10 (difficulty in transmitting electrons through the respiratory chain), complexes I and III become the main generators of superoxide radicals (figure 3) [21].

Violation of the biosynthesis of coenzyme Q10 can lead to a number of mitochondrial diseases. Mitochondrial diseases are a complex heterogeneous group of hereditary diseases and pathological conditions caused by violations of the structure and function of mitochondria and tissue respiration. One of the most well-known diseases is Leigh Syndrome.

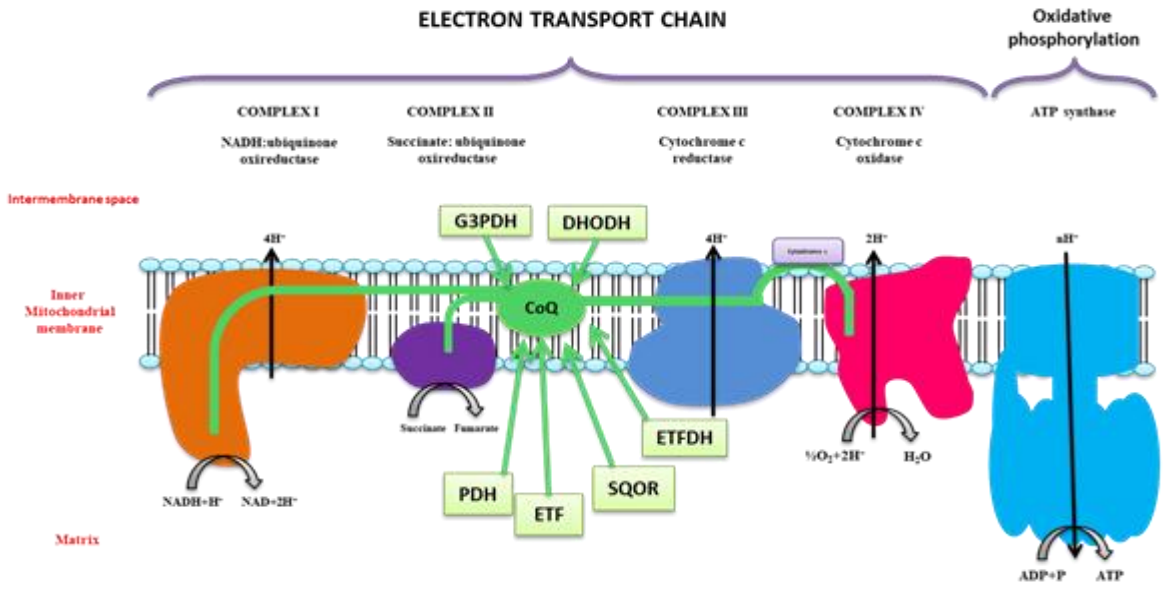

Figure 3 – Electron transport chain

Leigh syndrome (SL) or subacute necrotizing encephalomyelopathy is a rare progressive disease of the Central nervous system that manifests in early childhood and is characterized by symptoms of gray matter damage to the brain the prevalence of SL at birth is approximately 1: 36,000 cases. Leigh syndrome is a genetically heterogeneous disease: it is caused by mutations in genes encoding energy exchange proteins, including proteins of complexes I, II, III, IV, V of the mitochondrial respiratory chain, which are involved in oxidative phosphorylation and ATP generation, as well as components of the pyruvate dehydrogenase complex.

This syndrome can be inherited by an autosomal recessive type. It is known from literature data that the onset of the disease occurs in early childhood and is characterized by progressive neurological disorders, lactate acidosis and characteristic neuroradiological changes. To date, there is no etiotropic treatment for Li syndrome.

Pathogenetic and symptomatic treatment is performed. Therapy is carried out with energotropic drugs, which include: cofactors of energy exchange (b vitamins, PP, L-carnitine), antioxidants (vitamins C, E), substances that transfer electrons (coenzyme Q, succinic acid) [22].

Antioxidant role of coenzyme Q10.

Another important function of Q10 is antioxidant. Q10 is the only fat-soluble antioxidant that can be synthesized in humans and animals. The direct (direct) antioxidant effect of Q10 is to capture free radicals. Due to its ability to dissolve in fats, Q10 is most represented in lipid structures-membranes, liposomes, and low-density lipoproteins (LDL). The plasma concentration of Q10 is proportional to the LDL concentration. Plasma LDL oxidation is one of the starting points in atherogenesis (development of atherosclerosis) and other diseases associated with increased formation of free radicals. Q10 is able to prevent the development of chain reactions of free radical oxidation, including peroxidation of cell membrane phospholipids and plasma lipoproteins.

Another unique property of coenzyme Q10 is the constant regeneration of its oxidized form with the help of the body's enzyme systems and non-enzymatic antioxidants (ascorbate, alpha-tocopherol), which returns its antioxidant activity.

The indirect antioxidant effect of Q10 is to prevent the formation of phenoxyl radicals of α-tocopherol, that is, to prevent the possible Pro-oxidant action of α-tocopherol [23].

Vitamin E or α-tocopherol is another fat-soluble antioxidant (human blood plasma), along with Q10 is present in large quantities in the inner membrane of mitochondria. With a lack of coenzyme Q10, α-tocopherol in the reduced form begins to act as a prooxidant, triggering lipid peroxidation reactions, including the oxidation of atherogenic LDL.

Thus, Q10 as an antioxidant inhibits the development of atherosclerosis in two ways (through two mechanisms), catching free radicals and preventing the Pro-oxidant effect of vitamin E. one of the causes of Q10 deficiency in the body may be changes in the genes involved in the synthesis of Q10. For example, changes in the COQ2 and PDSS2 genes were detected in children with encephalomyopathies, cerebral ataxia, and pure myopathy. Rapid depletion of Q10 reserves is observed during intense physical or psychoemotional loads, severe diseases and operations, taking cardiotoxic cytostatics (doxorubicin, adriamycin), as well as taking such widely used drugs in the clinic as statins. Very low levels of Q10 were observed in hyperthyroidism. Given the involvement of oxidative stress in the pathogenesis of Parkinson's disease (PD) and other neurodegenerative diseases, the use of Q10 in therapy to slow the progression of the disease is of great interest. A factor that contributes to the development of PD is also a decrease in the Q10 content with age.

BP is associated with progressive loss of dopamine neurons in the black substance of the brain. In most cases, the disease manifests itself after the age of 60. Typical symptoms of PD – tremor at rest, gait instability, muscle rigidity, and bradykinesia occur when about 80% of dopamine neurons are lost. One of the main hypotheses for the development of PD is oxidative stress caused by violations of dopamine metabolism or neurotoxins that enter the body from the environment, such as rotenone, MANEB or paraquat (organic pesticides). It was found that the activity of complex I of the respiratory chain of mitochondria was reduced by 30-40 % in the black substance of the brain in PD, which is not observed in other areas of the brain [24].

Role of sulfide metabolism in coenzyme Q10 deficiency.

Sulfide metabolism in mammalian cells includes TRANS-sulfuration (biosynthetic) and hydrogen sulfide oxidation (H_2S) (catabolic). H_2S catabolism involves several pathways: oxidation in mitochondria, methylation in the cytosol, and binding to hemoglobin. Oxidation proceeds sequentially through the formation of intermediate products (thiosulfate and sulfite), and at the end there is a main product – sulfate. The result of methylation is dimethyl sulfide, and binding to heme iron gives sulfhemoglobin.

Cystathionine-γ-lyase catalyzes the conversion of cystine to thiocysteine, pyruvate, and ammonia; thiocysteine is then non-enzymatically converted to cysteine and H_2S. Cystathionine-β-synthase condenses homocysteine with cysteine, and cystathionine and H_2S are formed. Cysteinaminotransferase converts cysteine and α-Ketoglutarate to 3-mercaptopyruvate, which is further metabolized by the enzyme 3-mercaptopyruvate sulfotransferase to form H_2S and pyruvate. Oxidation of H_2S to thiosulfate is a non-enzymatic process associated with the respiratory electronic chain in mitochondria. Thiosulfate is converted to sulfite through a series of reactions, and then to sulfate.

The second way of H_2S metabolism is methylation with the formation of dimethyl sulfide. Finally, H_2S binds to hemoglobin, forming sulfhemoglobin. H_2S can modify protein molecules: restore disulfide bonds (S = S), attach to thiol groups (–SH), as a result of which they turn into-SSH [25].

The evolution of living nature on Earth since the appearance of oxygen in the atmosphere was accompanied by the formation of a biochemical system of antioxidant protection in cells. One of its most important components is reduced glutathione (GSH), which is a Tripeptide L-γ-glutamyl-L-cysteinyl-glycine. The small size of the molecule and the presence of a sulfhydryl group in the cysteine side chain make glutathione a universal participant in the vast majority of reactions, aimed at preventing the damaging effects of reactive oxygen species (ROS) and free radical processes. GSH plays a key role in maintaining redox status in the cell, determined by the ratio of concentrations of oxidative and reducing equivalents It exists in two redox forms, reduced and oxidized. Most of the biological functions of glutathione are performed by converting the reduced GSH to the oxidized form (GSSG) using the enzyme glutathione peroxidase and then returning to the reduced form (GSH). Glutathione can affect the process of cell death by modulating the level of mitochondrial ROS. Loss of GSH by mitochondria leads to an increase in the level of ROS and active nitrogen, dysfunction of these organelles, and leakage of ATP, which can lead to the transfer of the cell death process from apoptosis to necrosis. One of the most important functions of GSH is to store and preserve cysteine, since this amino acid is extremely unstable in extracellular conditions and is very quickly oxidized to cystine in processes that produce potentially toxic ROS. There is a gamma-glutamic acid cycle that allows GSH to be used as a continuous source of cysteine [26,27].

In mammals, CoQ is a fat-soluble component of the mitochondrial respiratory chain present in all cell membranes and involved in many metabolic functions. One of these functions is the transfer of electrons in the first H_2S oxidation reaction catalyzed by SQOR. Several *in vitro* and *in vivo* evidence shows that

Coq deficiency causes disruption of the regulation of H_2S oxidation and accumulation of H_2S, which can affect multiple physiological processes, possibly through modification of s-sulfhydration of the protein. Violation of H_2S oxidation may contribute to oxidative stress in CoQ deficiency or may play a synergistic role with oxidative stress in the pathogenesis of tissue specificity in CoQ deficiency. The role of H_2S metabolic disorders in CoQ deficiency deserves further study, as it may have therapeutic implications [28].

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ТОТЫҒУ СТРЕСІ ЖӘНЕ МИТОХОНДРИЯЛЫҚ ДИСФУНКЦИЯЛАР

Аннотация. Бос радикалдардың, яғни оттегінің активті формаларының (ОАФ) әсерінен жасушалардың зақымдану процесі тотығу стресі деп аталады.

Жасушада көптеген ОАФ үнемі қалыптасып отырады, тіндер тұтынатын оттегінің шамамен 5 % бос радикалдарға айналады, бірақ олардың деңгейі қалыпты жағдайға қарағанда аз болады, сондықтан жасуша оларды антиоксиданттық жүйенің көмегімен белсенді етпейді. Жасушаның қорғаныш қабілеттерін арттыратын ОАФ деңгейі, жасушалық ауытқуларды тудырады (мысалы, АҮФ-ң азаюы). Нәтижесінде оттегінің белсенді түрлерінің бірі – супероксид агрессивті формаларға (гидроксил радикалдары және т.б.) айналады, бұл көптеген жасушалық компоненттердің – ақуыздар мен мембрана липидтерінің, ДНҚ-ның тотығуына және бұзылуына әкелуі мүмкін.

Әр түрлі мүшелер мен тіндерге ОАФ әртүрлі дәрежеде әсер етеді және тотығу стресс процесінде әртүрлі тұрақтылықты көрсетеді. Тотығу процесінің жағдайында митохондрия арқылы ОАФ түзілу механизмі әлі де түсініксіз.

Оттегі туындысының түзілуі және антиоксиданттық қорғаныс жүйесінің деңгейі шамамен теңдестірілгенде, оттегі туындыларының тепе-теңдігін жылжыту және жасушаның биохимиясын бұзылуы оңай болады. Жасушалардың көпшілігі репаративті жүйеге ие болғандықтан тотығу стрестің орташа дәрежесіне шыдай алады, тотыққан молекулаларын анықтап алып тастайды, содан кейін оларды ауыстырады.Сонымен қатар, жасушалар тотығу стресіне жауап ретінде антиоксидантты қорғаныш жүйесін күшейте алады.

Митохондриялардың дисфункциясы және тіндердегі митохондриялық мутациялардың жинақталуы қартаю процесіне, сонымен қатар нейродегенерациямен сипатталатын бірқатар аурулардың патогенезіне айтарлықтай үлес қосатындығы анықталды. Мутациялар бос радикалдардың көбеюіне, АҮФ деңгейінің төмендеуіне және жасушалардың энергия тапшылығына әкеледі.

Коэнзим Q10 митохондрияның тыныс алу тізбегінің құрамдас бөлігі болып табылады. Соңғы жылдары оның тотықсызданған формасындағы антиоксиданттық қабілеттері белсенді түрде зерттелуде. Коэнзим Q10-ң тотықсызданған түрі барлық жасуша мембраналарында, қан плазмасында және липопротеидтерде болады. Коэнзим Q10 мембраналық фосфолипидтер мен төмен тығыздықтағы липопротеидтерді асқын тотығудан сақтайды, сондай-ақ митохондриялық мембрана ақуыздары мен митохондриялық ДНҚ-ны бос радикалдардың әсерінен қорғайды.

Коэнзим Q10 биосинтезінің бұзылуы бірқатар митохондриялық ауруларға әкелуі мүмкін. Коэнзим Q10 жетіспеушілігінде сульфидтердің алмасуы шешуші рөл атқарады. Сүтқоректілердің жасушаларында суль-фидтердің алмасуы транс-күкірттенуді (биосинтетикалық) және күкіртсутектің (H_2S) тотығуын (катаболика-лық) қамтиды. H_2S тотығуының бұзылуы коэнзим Q тапшылығы жағдайында тотығу стресінің жоғары-лауына ықпал етуі мүмкін немесе коэнзим Q жетіспеушілігінде тіндердің спецификалық патогенезінде синергетикалық рөл атқаруы мүмкін.

Сүтқоректілерде CoQ митохондрияның тыныс алу тізбегінің майда еритін компоненті болып табылады, барлық жасуша мембраналарында болады және көптеген метаболикалық қызметтерге қатысады. Осы функциялардың бірі - H_2S алғашқы тотығу реакциясындағы бірінші электронды сульфид-хинон оксидордуктазасымен катализденеді In vitro және in vivo жағдайында CoQ жетіспеушілігі H_2S тотығуы мен H_2S жинақталуының жоғарылауын туындатады, S-сульфидратация арқылы көптеген физиологиялық процестерге әсер етуі мүмкін. H_2S ақуыз молекулаларын өзгерте алады: дисульфидті байланыстарды қалпына келтіреді (S = S), тиолдар тобына қосылады (–SH), нәтижесінде олар –SSH болады.

Глутатион (GSH) тотығу және тотықсыздану эквиваленттерінің концентрацияларының қатынасы арқылы анықталатын жасушадағы тотығу күйін сақтауда маңызды рөл атқарады. Ол тотығу және тотықсыздану түрінде болады. GSH биологиялық функцияларының көпшілігі глутатион пероксидазасы

ферментін қолданып, тотықсызданған глутатионды тотығатын формаға (GSSG) айналдыру арқылы жүзеге асырылады, содан кейін тотықсызданған күйіне (GSH) келеді. Глутатион митохондриялық ОАФ деңгейінің модуляциясы арқылы жасушалардың өліміне әсер етуі мүмкін. Митохондриямен GSH жоғалуы ROS мен белсенді азот деңгейінің жоғарылауына, осы органеллалардың дисфункциясына және АҮФ азаюына әкеледі, бұл жасуша өлімін апоптоздан некрозға өткізуге әкелуі мүмкін. GSH-ның маңызды функцияларының бірі цистеинді сақтау болып табылады, өйткені бұл амин қышқылы жасушадан тыс жағдайларда өте тұрақсыз және өнімдері улы ОАФ болатын процестерде цистинді тез тотықтырады. CoQ жетіспеушілігінде H_2S метаболизмінің рөлі қосымша зерттеуді қажет етеді, өйткені оның терапиялық әсері болуы мүмкін.

Түйін сөздер: тотығу стресі, оттегінің активті формалары, митохондрия, митохондрия аурулары, коэнзим Q10, глутатион.

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ОКИСЛИТЕЛЬНЫЙ СТРЕСС И МИТОХОНДРИАЛЬНЫЕ ДИСФУНКЦИИ

Аннотация. Процесс повреждения клетки в результате действия свободных радикалов – активных форм кислорода (АФК) – называется окислительным стрессом. Большинство АФК постоянно образуются в клетке – около 5 % потребляемого тканями кислорода превращается в свободные радикалы, но их уровень в норме настолько небольшой, что клетка инактивирует их с помощью антиоксидантной системы.

Уровень АФК, превышающий защитные возможности клетки, вызывает серьезные клеточные нарушения (например, истощение АТФ). В результате один из активных форм кислорода - супероксид превращается в более агрессивные формы (гидроксильный радикал и т.п.), что может вызвать окисление и разрушение многих клеточных компонентов – белков и липидов мембран, ДНК.

Различные органы и ткани в разной степени подвержены действию АФК и демонстрируют различную устойчивость в процессе реализации окислительного стресса. Механизмы образования АФК митохондриями в условиях окислительного стресса до сих пор остаются неясными.

Поскольку образование производных кислорода и уровень антиоксидантной защитной системы приблизительно сбалансированы, то легко сдвинуть баланс в пользу производных кислорода и нарушить биохимию клетки. Большинство клеток может переносить умеренную степень окислительного стресса благодаря тому, что они обладают репаративной системой, выявляющей и удаляющей поврежденные окислением молекулы, которые затем заменяются. Кроме того, клетки могут повысить свою антиоксидантную защиту в ответ на окислительный стресс.

В то же время установлено, что дисфункция митохондрий и накопление в тканях митохондриальных мутаций вносят существенный вклад в процессы старения, а также в патогенез ряда заболеваний, характеризующихся нейродегенерацией. Мутации ведут к усиленной генерации свободных радикалов, снижению уровня АТФ и энергетической недостаточности клеток.

Коэнзим Q10 является компонентом дыхательной цепи митохондрий. В последние годы активно изучаются антиоксидантные способности его восстановленной формы. В восстановленном виде коэнзим Q10 встречается во всех клеточных мембранах, плазме крови и липопротеинах. Коэнзим Q10 успешно предохраняет фосфолипиды мембран и липопротеины низкой плотности от перекисного окисления, а также белки мембран митохондрий и митохондриальную ДНК от повреждения свободными радикалами.

Нарушение биосинтеза коэнзима Q10 может привести к ряду митохондриальных заболеваний. При дефиците коэнзима Q10 сульфидный метаболизм играет важнейшую роль. Сульфидный метаболизм в клетках млекопитающих включает транс-сульфурацию (биосинтетический) и окисление сероводорода (H_2S) (катаболический). Нарушение окисления H_2S может способствовать окислительному стрессу при дефиците коэнзима Q или может играть синергетическую роль в патогенезе тканеспецифичности при дефиците коэнзима Q.

У млекопитающих CoQ является жирорастворимым компонентом дыхательной цепи митохондрий, присутствует во всех клеточных мембранах и участвует во многих метаболических функциях. Одна из этих функций заключается в переносе электронов в первой реакции окисления H_2S, катализируемой *сульфид-хинон оксидоредуктазы*. В условиях *in vitro* и *in vivo* установлено, что дефицит CoQ вызывает нарушение регуляции окисления H_2S и накопление H_2S, которое может влиять на множественные физиологические процессы, возможно, через модификацию S-сульфгидратации белка. H_2S может модифицировать белковые молекулы: восстанавливать дисульфидные связи (S=S), присоединяться к тиоловым группам (–SH), в результате чего они превращаются в –SSH.

GSH (глутатион) играет ключевую роль в поддержании редокс-статуса в клетке, определяемого соотношением концентраций окислительных и восстановительных эквивалентов. Он существует в двух редокс-формах, восстановленной и окисленной. Большая часть биологических функций глутатиона осуществляется путем превращения восстановленного GSH в окисленную форму (GSSG) с помощью фермента глутатионпероксидазы и последующего возвращения в восстановленную форму (GSH). Глутатион может влиять на процесс гибели клетки через модуляцию уровня митохондриальных АФК. Потеря GSH митохондриями ведет к росту уровня АФК и активного азота, дисфункции этих органелл и утечке АТФ, что может приводить к переводу процесса гибели клетки из апоптоза в некроз. Одной из наиболее важных функций GSH является запасание и сохранение цистеина, поскольку эта аминокислота крайне нестабильна во внеклеточных условиях и очень быстро окисляется до цистина в процессах, продуктами которых являются потенциально токсичные АФК. Роль нарушений метаболизма H_2S при дефиците CoQ заслуживает дальнейшего изучения, поскольку он может иметь терапевтические последствия.

Ключевые слова: окислительный стресс, активные формы кислорода, митохондрия, митохондриальные заболеваний, коэнзим Q10, глутатион.

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MATERIALS FOR THE HEMIPTERANS FAUNA (HETEROPTERA) OF KOLSAI KOLDERY STATE NATIONAL NATURE PARK

Abstract. As a result of the research performed at SNNP “Kolsai Koldery”, we noted 26 species of hemipterans, belonging to 3 families. According to nutrition connections the identified hemipterans are 6 species are phytophages: polyphages (4 %), wide oligophages (22 %), 1 species - zoophytophage (4 %), the remaining 16 species are mycetophages (70 %). By confinement to the habitats, the hemipterans of SNNP “Kolsai Koldery”are divided into several groups: dendrobionts (15 species), hortobionts (6 species), herpetobionts (2 species). On the territory of SNNP “Kolsai Koldery”according to ecological features, all identified species are mesophiles. For the true bugs of SNNP “Kolsai Koldery” all known types of voltinism are characteristic: monovoltinism (6 species), bivoltinism (1 species), acyclic species (16 species).

Key words: Hemiptera, Heteroptera, “Kolsai Koldery” National Nature Park.

Introduction. The unique landscape diversity of SNNP “Kolsai Koldery” many natural and historical monuments determines the intensified development of tourism, both domestic and international. Also, this zone is interesting from the point of view of species diversity of insects, as it is a plain and mountains and is influenced by mesofauna of various biotopes.

Hemipterans (Heteroptera) are a group of insects that inhabit a wide variety of biotopes and play an important role in biological processes in biogeocenoses. Among the above-ground hemipterans, some live openly on plants, others under bark, and others in plant bedding or soil. Many species are serious plant pests. These are, for example, pine submissive bugs , harmful turtle, cruciferous bugs and many others.

The purpose of the study is to identify the biodiversity of hemipterans insects that inhabit the territory of the study, to study the ecological, biological characteristics and spread of hemipterans species in the territory of the SNNP “Kolsai Koldery”.

In the natural park “Kolsai koldery” despite the important economic importance of hemipterans, their species composition, biology, ecology, vertical belt distribution and economic importance are not sufficiently studied, which determines the relevance of the present study.

The basis for this work was the authors collected material and field observations. Collections of material were carried out from June to August 2018-2019 in various biotopes of SNNP “Kolsai Koldery”.

Field work was carried out in the gorge: Kurmeti, Saty, Karabulak, Kok-Zhazyk, Sary-Naua, Kayyndy, Taldy, Zhaman-bulak, Lake Kolsai, the species composition of hemipterans insects was studied.

Methods of researches. In the course of research, conventional techniques [1-4] with original modifications were used to collect field faunistic entomological materials.

Results of researches. The following are the species found in the territories studied and an analysis of this material is given.

Class: Insecta

Order: Hemiptera

Family: Aradidae

Aneurus avenius avenius (Dufour, 1833). Almaty region, Rayymbek district, SNNP "Kolsai Koldery", 12.06.2018, 5 ♀, 4 ♂; 20.07.2019, 3♀, 4♂; gorge Sata, flood plain of the Saty River, 25.06.1919, 3 ♀, 2 ♂; the surroundings of Kaiynda Lake. 18.07.2018, 3♀, 4♂; 22.07.2019, 3 ♀, 2 ♂. Dendrobiont (under the lagging behind bark of stubs and trees and in crevices of wood of deciduous trees, in bark cracks on branches and thin trunks); mezofit; there is no narrow food specialization; Feeds on possibly phloem juice, there is an indication of the juice nutrition of Coriolus fungi [5]; acyclic; winters imago and larvae of all stages.

Aradus angularis J. Sahlberg, 1886. Almaty region, Rayymbek district, SNNP "Kolsai Koldery", 06/12/2018, 2♂; Kurmeti cordon, 06/19/2019, 2♀, 1♂; Sary-Nahua cordon. 08/07/2019.2♀, 3♂. Dendrobiont (inhabits under the bark of coniferous trees, in cracks of the bark on branches and thin trunks); mesophile, mycetophagus (on tinder fungus); acyclic; winters imago [5, 6].

Aradus aterrimus Fieber, 1864. Almaty region, Rayymbek district, SNNP "Kolsai Koldery", gorge Karabulak, Kok-Zhazyk cordon. 06/14/2018, 2♀, 3♂; Kurmeti cordon, 06/19/2019, 2♀, 2♂; 1st lake Kolsay. 07/21/2019, 1♀, 2♂. Dendrobiont (on Pinus pine); mesophile (in the mountains rises to a height of 2300-2500 m above sea level); mycetophage; eats mushroom juice; acyclic; winters imago and larvae of all stages [5].

Aradus betulae (Linnaeus, 1758). Almaty region, Rayymbek district, SNNP "Kolsai Koldery", lake Kayyndy. 06.15.2018, 2♀, 3♂; 06/23/2018, 3♀, 3♂; 07/23/2018, 4♀, 3♂; 06/17/2019, 2♀, 2♂. Dendrobiont (inhabits on sick and dead birch trees and other deciduous trees affected by trutovitics from the polyporacea group [7]; mycetofage; mesophil; acyclic; winters imago and larvae of all stages.

Aradus bimaculatus Reuter, 1872. Almaty region, Raiymbek district, SNNP "Kolsai Koldery", gorge Saty, 06/25/2018, 1♀, 2♂; gorge Karabulak. 07/17/2018, 3♀, 2♂; 07/21/2019, 1♀, 2♂. Dendrobiont (on the dying bark of white and silver poplars, as well as on aspen, oak, alder, etc. affected by mushrooms); mesophyll, mycetophagus, feeds on mushroom juice; acyclic; winters imago and larvae of all stages. Rare. It was found under the bark of Picea excelsa [8].

Aradus cinnamomeus Panzer, 1794. Almaty region, Raiymbek district, "Kolsai kolderi"SNPP, Kok-Zhazyk cordon. 06/14/2018, 3♀, 4♂; Kurmeti cordon, 06/19/2019, 1♀, 2♂; 1st lake Kolsai. 07/21/2019, 2♀, 2♂. Dndrobiont (inhabits on young pines); mesophil; mycetofag, eats mushroom juice; acyclic; winters imago and larvae of all stages [9].

Aradus corticolis Linnaeus, 1758. Raiymbek district, SNNP "Kolsai Koldery", 1st lake Kolsai. 05/16/2018. 3♀, 2♂; gorge Taldy. 07/17/2019. , 2♀, 2♂; gorge: Karabulak, Sary Nahua. 08.24.2019.1♀, 2♂. Dendrobiont [under the bark of trees and in the folds of the tinder fungus Fomesmarginalis (on pines and other trees) and Daedaleaquercina (on oak and conifers); mesophyll; eats the juice of fungus- trutoviki (mycetophagus); acyclic; winters imago and larvae of all stages [10].

Aradus crenaticollisR.F.Sahlberg, 1848. Almaty Region, Raiymbek District, SNNP "Kolsai Koldery", gorge Karabulak, Sary-Nahua. 12.06.2018, 2♀, 1♂; 07/20/2019, 1♀, 2♂; gorge Saty, the Saty river floodplain, 06/25/1919, 2♀, 2♂; gorge Taldy. 07/18/2018, 3♀, 2♂; 07/22/2019, 3♀, 2♂. Dendrobiont (lives on conifers, pines on fungus- trutoviki); mesophil, mycetophague, eats mushroom juice; non-cyclic; winters imago and larvae of all stages [11].

Aradus distinctusFieber, 1860. Almaty region, Raiymbek district, SNNP "Kolsai Koldery", gorge Karabulak, Sary-Nahua. 12.06.2018, 2♀, 2♂; 07/20/2019, 3♀, 2♂; gorge Saty, the Saty river floodplain, 06/25/1919, 2♀, 1♂; gorge Taldy. 07/18/2018, 1♀, 2♂; 07/22/2019, 3♀, 2♂. Herpetobiont (in detritus on dry and moist soils; in oak forests near rivers, on sand dunes near Populusnigra); mesophyll; mycetophagus, feeds on fungi growing among plant debris); acyclic; winters imago and larvae of all stages [5]. West Eurasian species.

Aradus flavicornis Dalman, 1823. Almaty region, Raiymbek district, SNNP "Kolsai Koldery", gorge Karabulak, 06/14/2018, 2♀, 1♂; Kurmeti cordon, 06/19/2019, 1♀, 2♂; gorge Taldy. 07/18/2018, 3♀, 2♂; 07/22/2019, 2♀, 2♂. Dendrobiont (inhabits on deciduous); mesophil, mycetophague, eats mushroom juice; acyclic; winters imago and larvae of all stages [12].

Aradus pictus Baerensprung, 1859. Almaty region, Raiymbek district, SNNP "Kolsai Koldery", Kok-Zhazyk cordon. 06/14/2018, 3♀, 2♂; Kurmeti cordon, 06/19/2019, 2♀, 2♂; 1st lake Kolsay. 07/21/2019, 2♀, 3♂. Dendrobiont (on the fungus- trutoviki on conifers); mesophyll, mycetophagus, eats on mushroom juice; acyclic; winters imago and larvae of all stages [13].

Aradus hieroglyphicus J. Sahlberg, 1878. Almaty region, Raiymbek district, SNNP "Kolsai Koldery", gorge Karabulak, 06/14/2018, 2♀, 2♂; Kurmeti cordon, 06/19/2019, 1♀, 2♂; gorge Taldy. 07/18/2018, 3♀, 2♂; 07/22/2019, 3♀, 2♂; gorge Zhaman-bulak. 06/15/2018. 1♀, 2♂. Dendrobiont (on tinder-stands on aspen and willow, as well as under the bark of pyramidal and other poplars and white acacia; mesophile, mycetophage (eats on mushroom juice); acyclic; winters imago and larvae of all stages [7].

Aradus lugubris Fallen, 1807. Almaty region, Raiymbek district, SNNP "Kolsai Koldery", Kok-Zhazyk cordon. 06/14/2018, 3♀, 2♂; Kurmeti cordon, 06/19/2019, 2♀, 3♂; 1st lake Kolsay. 07/21/2019, 4♀, 3♂. Dendrobiont (lives on coniferous trees in the mountains); mesophil, mycetophagus, feeds on juice of mushrooms [4]; acyclic; winters imago and larvae of all stages

Aradus obtectus Vasarhelyi, 1988. Almaty region, Raiymbek district, SNNP "Kolsai Koldery", 1st lake Kolsay. 05/16/2018. 2♀, 2♂; gorge Taldy. 07/17/2019. 3♀, 2♂; gorge Karabulak, Sary Nahua. 08/24/2019. 1♀, 2♂; Lake Kayyndy. 06/15/2018, 2♀, 2♂; 06/23/2018, 3♀, 2♂. Dendrobiont (on Pinus, Betula, Acer); usually on the fungus- trutoviki on conifers; growing on stumps of birch; mesophile, mycetophagus, feeds on the juice of fungi-tinder fungi; acyclic [5]; winterslarvae.

Aradus ribautiE.Wagner, 1956. Almaty Region, Rayymbek District, SNNP "Kolsai Koldery", gorge Karabulak, 06/14/2018, 2♀, 2♂; 06/21/2019, 3♀, 2♂; gorge Taldy. 07/18/2018, 1♀, 2♂; 07/22/2019, 3♀, 2♂; gorge Zhaman-bulak. 06/15/2018. 3♀, 2♂. Dendrobiont (on Populus tremula and other Populus); mesophile, mycetophagus, feeds on the juice of fungus- trutoviki; acyclic; winters imago and larvae of all stages [7].

Aradus setiger Kiritshenko, 1913. Almaty region, Raiymbek district, SNNP "Kolsai Koldery", gorge Karabulak, 06/14/2018, 2♀, 2♂; 06/21/2019, 1♀, 2♂; gorge Taldy. 07/18/2018, 3♀, 2♂. Dendrobiont (on the fungus- trutoviki, on aspen and willow, as well as under the bark of poplars and white acacia [11]; mesophilus, mycetophage, feeds on mushroom juice; acyclic; winters imago and larvae of all stages.

The Berytida Family – Berytidae.

Berytinus clavipes (Fabricius, 1775). Almaty region, Rayymbek district, SNNP "Kolsai Koldery", gorge Karabulak, 06/14/2018, 2♀, 3♂; Kurmeti cordon, 06/19/2019, 2♀, 1♂; gorge Taldy. 07/18/2018, 3♀, 2♂; 07/22/2019, 2♀, 2♂; gorge Zhaman-bulak. 06/15/2018. 3♀, 2♂. Hortobiont; mesophil (inhabits in forest steppe, rarefied forests, forest edges and forest glades, parks, mesophite meadows, in the middle belt of mountains); wide oligophythofag (feeds on grassy legumes: Ononis, etc. [5]; monovoltine; winters imago.Kazakhstan it is ubiquitous.

Berytinus crassipes (Herrich-Schaeffer, 1835). Almaty region, Rayymbek district, SNNP "Kolsai Koldery", gorge Karabulak, 06/14/2018, 2♀, 1♂; Kurmeti cordon, 06/19/2019, 2♀, 2♂; gorge Taldy. 07/18/2018, 3♀, 2♂; 07/22/2019, 2♀, 3♂; gorge Zhaman-bulak. 06/15/2018. 2♀, 2♂. Hortobiont; mesophil (lives in rarefied forests, forest edges and forest glades, parks); polyphitofag (easts legumes, sedge, cereals, seeds ([5]; monovoltine; winters imago.

Berytinus distinguendus (Ferrari, 1874). Almaty region, Rayymbek district, SNNP "Kolsai Koldery", gorge. Karabulak, 06/14/2018, 2♀, 1♂; Kurmeti cordon, 06/19/2019, 2♀, 2♂; gorge Taldy. 07/18/2018, 3♀, 2♂; 07/22/2019, 2♀, 3♂; gorge Zhaman-bulak. 06/15/2018. 2♀, 2♂. Hortobiont; mesophyll (in places of growth of stunted alfalfa: Medicago rigidula, M. minima [5]; narrow oligophytophage; monovoltine; winters imago.

Berytinus hirticornis Brulle, 1835. Almaty Region, Raiymbek District, SNNP "Kolsai Koldery", Kok-Zhazyk cordon. 06/14/2018, 1♀, 2♂; Kurmeti cordon, 06/19/2019, 2♀, 2♂; gorge Karabulak, 06/14/2018, 2♀, 3♂; Kurmeti cordon, 06/19/2019, 3♀, 2♂; gorge Taldy. 07/18/2018, 1♀, 2♂; 07/22/2019, 2♀, 1♂; gorge Zhaman-bulak. 06/15/2018. 2♀, 3♂. Hortobiont; mesophyll; wide oligophytophage (on legumes); monovoltine; winters imago [5].

Berytinus minor minor (Herrich-Schaeffer, 1835). Almaty region, Raiymbek district, SNNP "Kolsai Koldery", Kok-Zhazyk cordon. 06/14/2018, 3♀, 2♂; Kurmeti cordon, 06/19/2019, 2♀, 2♂; gorge Karabulak, 06/14/2018, 2♀, 1♂; Kurmeti cordon, 06/19/2019, 3♀, 2♂; gorge Taldy. 07/18/2018, 3♀, 2♂; 07/22/2019, 2♀, 1♂; gorge Zhaman-bulak. 06/15/2018. 3♀, 3♂. Hortobiont (On and under different-level vegetation); mesophile (sparse forests, forest edges and forest glades, parks, hillsides and river terraces, meadows: numerous in the middle mountain belt); wide oligophytophage (on legumes: Trifolium, Medicago, Ononis); monovoltine; winters imago [5,14].

Berytinus montivagus (Meyer-Dur, 1841). Almaty region, Raiymbek district, SNNP "Kolsai Koldery", Kok-Zhazyk cordon. 06/14/2018, 2♀, 2♂; Kurmeti cordon, 06/19/2019, 3♀, 2♂; gorge Karabulak, 06/14/2018, 3♀, 3♂; Kurmeti cordon, 06/19/2019, 3♀, 4♂; gorge Taldy. 07/18/2018, 1♀, 2♂; 07/22/2019, 2♀, 3♂; gorge Zhaman-bulak. 06/15/2018. 2♀, 3♂. Hortobiont; mesophile (dry slopes of hills, river terraces and other places covered with Medicago lupula and other types of low alfalfa); wide oligophytophage (Medicago and Trifolium); monovoltine [5]; winters imago.

Redbug Family – Pyrrhocoridae.

Pyrrhocoris apterus (Linnaeus, 1758). Almaty region, Raiymbek district, SNNP "Kolsai Koldery", Kok-Zhazyk cordon. 06/14/2018, 3♀, 4♂; Kurmeti cordon, 06/19/2019, 5♀, 6♂; gorge Karabulak, 06/14/2018, 4♀, 3♂; Kurmeti cordon, 06/19/2019, 4♀, 4♂; gorge Taldy. 07/18/2018, 6♀, 5♂; 07/22/2019, 3♀, 5♂; gorge Zhaman-bulak. 06/15/2018. 4♀, 3♂; 07/12/1920, 4♀, 6♂. Herpetobiont; mesophil (lives in forests and clearings, forest strips, parks, protective plantations and other mesophilic biotops; among detritus; often feeds on plants, small insects and ticks, dead insects, fallen seeds and juice of green parts of plants (Malvaneglecta, Alcea rosea, Lavatera thuringiaca, Caragana arborescens); up to 2 generations per year; winters imago, in groups among plant residues [5,15,16].

Table 1 – Taxonomic composition of hemipterans in the SNPP "Kolsai Koldery"

Family	Species name	number of species	%
Aradidae	*Aneurusaveniusaven*ius (Dufour, 1833)	16	70
	Aradus angularis J.Sahlberg, 1886		
	Aradus aterrimus Fieber, 1864		
	Aradusbetulae(Linnaeus, 1758)		
	Aradus bimaculatus Reuter, 1872		
	Aradus cinnamomeus Panzer, 1794		
	Aradus corticolis Linnaeus, 1758		
	*Araduscrenaticollis*R.F.Sahlberg, 1848		
	*Aradusdistinctus*Fieber, 1860		
	*Aradusflavicornis*Dalman, 1823		
	Aradus pictus Baerensprung, 1859		
	Aradus hieroglyphicus J.Sahlberg, 1878		
	Aradus lugubris Fallen, 1807		
	*Aradusobtectus*Vasarhelyi, 1988		
	*Aradusribauti*E.Wagner, 1956		
	*Aradussetiger*Kiritshenko, 1913		
Berytidae	*Berytinus clavipes* (Fabricius, 1775)	6	27
	Berytinuscrassipes(Herrich-Schaeffer, 1835)		
	Berytinus distinguendus (Ferrari, 1874)		
	Berytinushirticornis Brulle, 1835		
	Berytinus minor minor (Herrich-Schaeffer, 1835)		
	Berytinus montivagus (Meyer-Dur, 1841)		
Pyrrhocoridae	*Pyrrhocoris apterus* (Linnaeus, 1758)	1	3
In total:		23	100

As can be seen from the data presented in table 1, representatives of the Aradidae family – 16 species, and Berytidae – 6 species predominate in species diversity from the identified bugs.

The seasonal development of the hemipterans is heterodynamic. Voltinism of the population reflects the number of annual generations realized by the population in a certain part of the species range. For the hemipterans of SNNP "Kolsai Koldery" all known species of Voltinism are characteristic:

– monovoltinism (one generation per year) – 6 species;
– bivoltinism (two generations per year) – 1 species;
– acyclic species have a stretched life cycle, i.e. throughout a year there are different phases and stages of development – 16 species.

The nutrition of hemipterans is extremely varied. There are mycetophages, phytophages and zoophythages on the SNNP "Kolsai Koldery" area (table 2).

Table 2 – Food specialization of hemiptera of "SNNP "Kolsai Koldery"

Species groups		Number of species	%
Zoophytophages		1	4
mycetophages		16	70
phytophages	polyphages	1	4
	wide oligophages	5	22
In total:		23	100

According to nutrition connections the identified hemipterans – 6 species are phytophages: polyphages (4 %), wide oligophages (22 %), 1 species – zoophytophage (4 %), the remaining 16 species are mycetophages (70 %).

According to habitat, the hemipterans in the SNNP "Kolsai Koldery"are divided into several groups: dendrobionts (15 species), hortobionts (6 species), herpetobionts (2 species).

On the territory of the SNNP "Kolsai Koldery", according to ecological features, all identified species are mesophiles.

Conclusion. As a result of the research conducted at SNNP "Kolsai Koldery", we noted 26 species of hemipterans, belonging to 3 families. According to nutrition connections the identified hemipterans are 6 species are phytophages: polyphages (4 %), wide oligophages (22 %), 1 species - zoophytophage (4 %), the remaining 16 species are mycetophages (70 %). By confinement to the habitats, the hemipterans of SNNP "Kolsai Koldery" are divided into several groups: dendrobionts (15 species), hortobionts (6 species), herpetobionts (2 species). On the territory of the SNNP "Kolsai Koldery", all identified species are mesophiles according to environmental features. For the hemipterans of SNNP "Kolsai Koldery", all known species of Voltinism are characteristic: monovoltinism (6 species), bivoltinism (1 species), acyclic species (16 species).

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«КӨЛСАЙ КӨЛДЕРІ» МЕМЛЕКЕТТІК ҰЛТТЫҚ ТАБИҒИ ПАРКІ ЖАРТЫЛАЙ ҚАТТЫҚАНАТТЫЛАР (HETEROPTERA) ФАУНАСЫНА МАТЕРИАЛДАР

Аннотация. «Көлсай көлдері» МҰТП-нің қайталанбас ландшафттық алуан түрлілігі, көптеген табиғи және тарихи ескерткіштер ішкі және халықаралық туризмнің дамуын айқындайды. Бұл аймақ жәндіктердің алуан түрлілігі тұрғысынан да қызықты, өйткені бұған жазық таулар және әртүрлі биотоптардың мезофаунасы әсер етеді.

Жартылай қаттықанаттылар (Heteroptera) – биогеоценоздарда биологиялық процестерде маңызды рөл атқаратын және әртүрлі биотоптарды мекендейтін жәндіктер тобы. Жер үсті жартылай қаттықанаттылардың

арасында, біреуі өсімдіктерде, басқалары өсімдік қабықтарының астында, үшіншісі – өсімдік төсенішінде немесе топырақта ашық өмір сүреді. Көптеген түрлер – өсімдіктердің маңызды зиянкестері. Бұл, мысалы, қарағай түбегі, зиянды тасбақалар, крест гүл шоғыры және тағы басқалар.

Зерттеудің мақсаты – зерттеу аумағын мекендейтін жартылай қаттықанатты жәндіктердің биологиялық алуан түрлілігін анықтау, "Көлсай көлдері" МҰТП аумағында жартылай қаттықанаттылар түрлерінің экологиялық, биологиялық ерекшеліктерін және таралуын зерттеу.

"Көлсай көлдері" табиғи паркінде жартылай қаттықанаттылардың маңызды шаруашылық маңызына қарамастан, олардың түрлік құрамы, биологиясы, экологиясы, белдеулер бойынша бөлу және шаруашылық маңызы жеткілікті түрде зерттелмеген, зерттеудің өзектілігі осымен анықталады.

Бұл жұмыс авторлардың жеке жиындары мен далалық бақылаулары негізінде жазылды. "Көлсай көлдері" МҰТП әртүрлі биотоптарында материалды жинау 2018-2019 жылдары жүргізілді. Дала жұмыстары – Құрметі шатқалы, Саты шатқалы, Қарабұлақ, Көк-жазық, Сары-Науа шатқалы, Қайынды шатқалы, Талды, Жаман-бұлақ, Құрмет, Көлсай көлдері аумағында жартылай қаттықанатты жәндіктердің түрлік құрамы зерттелді.

«Көлсай көлдері» МҰТП территориясында жүргізілген зерттеулер нәтижесінде жартылай қаттықанаттылардың 3 тұқымдасына жататын 26 түр анықталды. Табылған жартылай қаттықанаттылар қоректік байланысы жағынан фитофагтар – 6 түр: полифагтар (4 %), кең олигофагтар (22 %), 1 түр – зоофитофаг (4 %), 16 түр – мицетофагтар (70 %). «Көлсай көлдері» МҰТП жартылай қаттықанаттылар тіршілік ету ортасына байланысты бірнеше топқа бөлінеді: дендробионттар (15 түр), хортобионттар (6 түр), герпетобионттар (2 түр). Зерттелген аймақ жартылай қаттықанаттылары экологиялық ерекшеліктері жағынан – мезофильдер. Оларға вольтинизмнің белгілі бар типі тән: моновольтинизм (6 түр), бивольтинизм (1 түр), ациклды түрлер (16 түр).

Түйін сөздер: жартылай қаттықанаттылар, Heteroptera, «Көлсай көлдері» мемлекеттік ұлттық табиғи паркі.

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МАТЕРИАЛЫ К ФАУНЕ ПОЛУЖЕСТКОКРЫЛЫХ (HETEROPTERA) ГОСУДАРСТВЕННОГО НАЦИОНАЛЬНОГО ПРИРОДНОГО ПАРКА «КӨЛСАЙ КӨЛДЕРІ»

Аннотация. Уникальное ландшафтное разнообразие ГНПП «Көлсай көлдері», множество памятников природы и истории обусловливает усиленное развитие туризма как внутреннего, так и международного. Также эта зона интересна с точки зрения видового разнообразия насекомых, так как является равниной и горами и испытывает на себе влияние мезофаун различных биотопов.

Полужесткокрылые – группа насекомых, заселяющих самые разнообразные биотопы и играющих важную роль в биологических процессах в биогеоценозах. Среди наземных полужесткокрылых одни живут открыто на растениях, другие под корой, третьи – в растительной подстилке или в почве. Многие виды – серьезные вредители растений. Это, например, сосновый подкорный клоп, вредная черепашка, крестоцветные клопы и др.

Цель исследования – выявление биоразнообразия полужесткокрылых насекомых, населяющих территорию исследования, изучить экологические, биологические особенности и распространение видов полужесткокрылыхнасекомых на территории ГНПП «Көлсай көлдері».

В ГНПП «Көлсай көлдері», несмотря на важное хозяйственное значение полужесткокрылых, их видовой состав, биология, экология, распределение по вертикальным поясам и хозяйственное значение изучены недостаточно, что и определяет актуальность настоящего исследования.

Сборы материала проводились с июня по август 2018-2019 гг. в различных биотопах ГНПП «Көлсай көлдері». Полевые работы проводились в ущ. Курмети, Саты, Карабулак, Кок-Жазык, Сары-Науа, Кайынды, Талды, Жаманбулак, Курмети, оз. Колсай, изучался видовой состав полужесткокрылых насекомых.

В результате проведенных исследований в ГНПП «Көлсай көлдері» нами было отмечено 26 видов полужесткокрылых, относящихся к 3 семействам. По пищевым связям из них – 6 видов являются фитофагами: полифаги (4 %), широкие олигофаги (22 %), 1 вид – зоофитофаг (4 %), остальные 16 видов – мицетофаги (70 %). По приуроченности к местам обитания полужесткокрылые ГНПП «Көлсай көлдері» подразделяются на несколько групп: дендробионты (15 видов), хортобионты (6 видов), герпетобионты (2 вида). На территории парка по экологическим особенностям все выявленные виды – мезофилы. Для

полужесткокрылых ГНПП «Көлсай көлдері» характерны все известные типы вольтинизма: моновольтинизм (6 видов), бивольтинизм (1 вид), ацикличные виды (16 видов).

Ключевые слова: полужесткокрылые, Heteroptera, национальный природный парк «Көлсай көлдері».

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PLANT BIODIVERSITY OF MONITORING POINTS V.AMANGELDY ALMATY REGION

Abstract. The article provides a systematic analysis of the species composition of plants of the flora of v. Amangeldy, Almaty region.

The comprehensive study of regional floras is becoming increasingly important in connection with the implementation of the solution to the problem of studying and preserving biological diversity. Complete information about the composition of the flora of a territory is of great theoretical importance, it allows establishing the structure and Genesis of its components, to identify individual characteristics, to restore the history of formation and trends. This ultimately is the basis of rational use of plant resources and protection of rare and endangered plants, as well as to solve many important economic problems - identifying new sources and resources of medicinal, food, fodder, ornamental and other plants.

One of the main characteristics of any flora is its systematic structure, namely the ratio of families, genera and species, on the one hand, and the quantitative indicators of these taxa that determine its wealth, on the other. These indicators are components of a systematic analysis of flora in general and coenoflora in particular, the data obtained using such analysis are important material for comparative floristry. From this point of view, the systematic structure of the flora acquires the significance of one of the essential indicators that characterize the flora in the regional plan.

The study of the species composition of the flora is of great importance both for understanding the history of flora and landscapes of the region as a whole, and for finding ways to conserve and use biodiversity under conditions of increasing anthropogenic pressure.

Research was carried out by route-reconnaissance method in combination with a detailed study of experimental sites. In the study area – V. Amangeldy was first identified: 112 species from 88 genera and 29 families, with the dominance of the families *Asteraceae* (24 species or 21.4 %, 17 genera), *Rosaceae* (15 species or 13.39%, 11 genera), *Brassicaceae* (11 species, or 9.82 %, 9 genera) from Dicotyledons, and *Poaceae* (11 genera, 12 species, or 10.71 %) from Monocotyledonous plants. The dominant families account for 62 species, which is 55.36 % of the total number of plant species growing in this territory. Leading genera *Artemisia*, *Potentilla* and *Rumex*. On the territory of the study, 33 forage plant species were identified: *Bromus inermis* (Leyss.) Holub., *Rumex confertus* Willd., *Trifolium pratense* L., *Poa bulbosa* L., etc. In connection with the degradation of the vegetation cover number of weed plants was 75 species, among which are: *Rumex crispus* L., *Capsella bursa-pastoris* (L.) Medik., *Cannabis ruderalis* Janisch., *Lathyrus tuberosus* L. and other. Endemic and rare species were not found.

The results of the research will serve as a basis for the rational use of the flora of Amangeldy village in Almaty region, as well as for the conservation of biodiversity. Obtained as a result of a systematic analysis of the flora of Amangeldy, it will help to identify the centers of endemism and relict, as well as to solve the issues of the place and role of this flora in a number of other adjacent floras.

Key words: village Amangeldy, systematic analysis, species composition, species, genus, families.

Introduction. Vegetation cover is an organized system whose components, ranging from the organismic to the population-species or even phytocenotic, are more or less evolutionarily adapted to the set of abiotic and biotic environmental conditions, functional and structural units. The above seems to us to be true with regard to the vegetation cover as a whole in its relations with the relief-landscape structure

of the natural historical region within which it is formed. In this regard, each natural flora and phytocenoses formed by its species is not just a random set of plant species in a certain area, but a multitude of them, which has its own internal patterns of addition, geographical and genetic relationships [1]. The most important aspect of geobotanical research is the study of the species diversity of the vegetation cover [2].

One of the most important problems of our time is the conservation of biological diversity, both of natural populations and by placing species in artificially created reserves. Kazakhstan, as a modern state, has ratified the Convention on Biological Diversity (1994) over the years of independence. However, to carry out the tasks set in the Convention, it is necessary to take an inventory of floristic diversity in order to determine its main components, which can be further balanced and used [3].

Biodiversity is by no means the only, or even the primary, driver of ecosystem functions [4,5,13]. Both biodiversity and ecosystem functions have been known to be driven by common drivers of contemporary environments, such as climate and biotic and abiotic attributes [6-9, 13]. Biodiversity could be also shaped by long-term drivers, such as geological processes, which impart lasting legacies on contemporary environments [10-14].

A standard analysis of the flora is the basis of any floristic study, since it allows you to determine the specifics of the studied flora, its difference from the border flora and flora of remote territories. A systematic analysis aims to identify the taxonomic structure of the studied flora, which is necessary to determine its specificity and place in the phytogeographic hierarchy of large land regions. Each flora has its own quantitative characteristic and, in addition to the total number of species, a certain set of genera and families, which can significantly differ from other floras [15].

The analysis of flora occupies a leading position in comparative floristry and forms the basis of its study. The analysis reveals the taxonomic, coenecological, and chorological parameters of the flora, on the basis of which conclusions are drawn about its wealth, origin, and the role of individual taxa of the rank of a family, genus, and species, including endemic and relict species, of ecological, coenotic, and biomorphological nature components of the flora, the basis is being created for conducting fractional botanical and geographical zoning of the territory and making recommendations for the protection and rational use of certain species [16].

The study of flora is the basis for solving many theoretical and practical issues of taxonomy, Botanical geography, resource studies, as well as to clarify the history of flora and predict its further changes. The inventory of flora is important for the implementation of environmental measures. Intensive human impact on nature leads not only to the loss of many native species, but also to the degradation of vegetation in large areas [17].

The study of the species composition of flora is important both for the knowledge of the history of flora and landscapes of the region as a whole, and for the search for ways to preserve and use biodiversity in the conditions of increasing anthropogenic pressure. In recent years, a number of scientific works have been devoted to the study of biodiversity of terrestrial plants in the Almaty region and numerous field studies have been carried out [18-22].

In recent years, all studies on flora and vegetation have been aimed at preserving biodiversity at different levels of its structural organization (species, population, coenotic, ecosystem, landscape).

Materials and methods. The objects of research are flora and vegetation of Amangeldy village (N 43°17.951′E 077°12.509′), Almaty region. The research was conducted by route-reconnaissance method in combination with a detailed study of experimental sites. To solve the tasks in each region, three typical experimental plots of 10 m^2 were selected. At each site, three sites with an area of 1 m^2 were selected by random sampling. The main research methods were geobotanical and floristic [23]. Floral lists were compiled during walking tours.

When determining plant species, a geobotanical description of the communities of Amangeldy was originally made. According to the geobotanical method: the laying of sites was carried out in tenfold repetition. The species were identified according to the collections of Flora of Kazakhstan, Volume 1-9 [24]. The refinement of the Latin names took place according to the summary of S.K. Cherepanov [25].

Results and Discussion. The systematic list of flora of v. Amangeldy village that we have compiled includes 112 plant species belonging to 88 genera and 29 families. Table 1 provides information on the number of species and genera in the families of the studied flora of the Amangeldy territory.

Table 1 – Species wealth of the families of Amangeldy

№	Families	Number of genera	Number of species
1	*Asteraceae* Dumort.	17	24
2	*Rosaceae* Juss.	11	15
3	*Poaceae* Barnhart	11	12
4	*Brassicaceae* Burnett	9	11
5	*Fabaceae* Lindl.	5	6
6	*Chenopodiaceae* Vent.	4	6
7	*Lamiaceae* Lindl.	3	3
8	*Caryophyllaceae* Juss.	2	2
9	*Polygonaceae* Juss.	2	4
10	*Malvaceae* Juss.	2	2
11	*Balsaminaceae* A. Rich.	2	2
12	*Boraginaceae* Juss.	2	2
13	*Cyperaceae* Juss.	2	2
14	*Ranunculaceae* Juss.	1	1
15	*Hypecoaceae* (Dumort) Willk.	1	1
16	*Fumariaceae* DC.	1	1
17	*Amaranthaceae* Juss.	1	2
18	*Salicaceae* Mirb.	1	1
19	*Cucurbitaceae* Juss.	1	1
20	*Ulmaceae* Mirb.	1	1
21	*Cannabaceae* Endl.	1	1
22	*Urticaceae* Juss.	1	1
23	*Euphorbiaceae* Juss.	1	2
24	*Apiaceae* Lindl.	1	1
25	*Rubiaceae* Juss.	1	1
26	*Solanaceae* Juss.	1	2
27	*Convolvulaceae* Juss.	1	2
28	*Scrophulariaceae* Juss.	1	2
29	*Plantaginaceae* Juss.	1	2

In the study area of Amangeldy, 112 species were identified from 88 genera and 29 families, with the dominance of the families *Asteraceae* (24 species or 21.4 %, 17 genera), *Rosaceae* (15 species or 13.39%, 11 genera), *Brassicaceae* (11 species or 9.82 %, 9 genera) from dicotyledons, and *Poaceae* (11 genera, 12 species, or 10.71 %) from monocotyledonous plants. The dominant families account for 62 species, which is 55.36 % of the total number of plant species growing in this territory (figure 1). Leading genera *Artemisia, Potentilla* and *Rumex*. No endemic species have been identified. The ratio of the main taxonomic groups shows that all species belong to the Department Angiospermae (angiospermae) – 112 species.

Table 2 – Distribution of plants of Amangeldy in systematic groups

Systematic group	Number of families	Number of genera	Number of species	% of the total number of species
Angiosperms:				
1) dicotyledonous	27	75	98	87,5 %
2) monocotyledonous	2	13	14	12,5 %

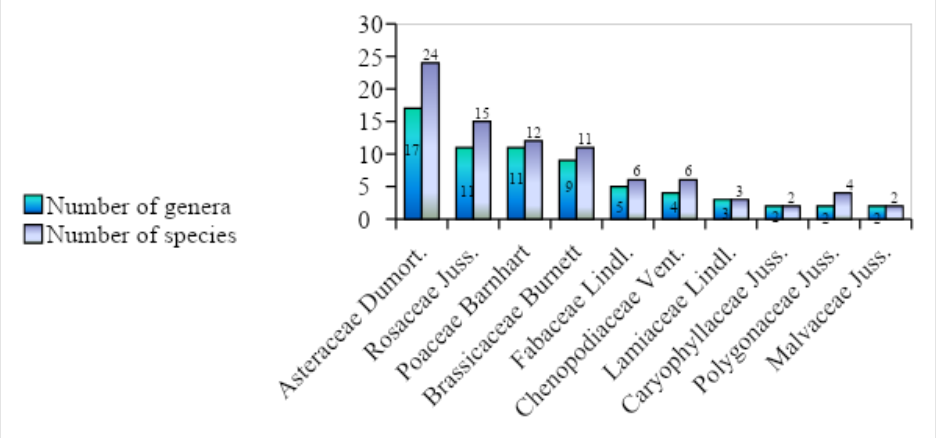

Figure 1 – 10 leading Amangeldy point families

The flora of v. Amangeldy has 28 families, out of 4 (13.79 % of the total) with the largest number of species, which are the head part of the spectrum of flora families. In the remaining 25 families, the number of species is represented by a smaller number.

The top 10 families comprise 85 species (75.89 % of the total), more than half of all species in the region. The first three families include 51 species (45.5 % of the total).

The richest in the number of species is the family, significantly "breaking away" in the number of species from all others: *Asteraceae* Dumort-24 species (21.4 %).

At the point of Amangeldy, plants were harvested in a dandelion-motley community. The projective coverage of the community is 70-80 %. A change of grass stand was also observed. Fodder species (cereals, wormwood) in some places were replaced by weeds, plants of low value in terms of forage qualities (gingerbread - *Xanthium strumaruim*) and poisonous (brunets – *Sophora alopecuroides*).

a – *Artemisia annua* L

b – *Trifolium pratense* L

c – *Bromus inermis* (Leyss.) Holub

d – *Rumex confertus* Willd

Figure 2 – Variety of plants at the monitoring point of Amangeldy village

The following dominant and fodder species were collected for analysis in the dandelion-herb community: *Artemisia annua* L. (figure 2 a) – annual wormwood from the family *Asteraceae* Dumort, *Trifolium pratense* L. (figure 2 b) - meadow clover from the family *Fabaceae* Lindl. In the second community taken – *Bromus inermis* (Leyss.) Holub. (figure 2 c) – boneless bonfire from the family *Poaceae* Barnhart, *Rumex confertus* Willd. (figure 2 d) - horse sorrel from the family *Polygonaecae* Juss.

On the territory of Amangeldy, 33 forage plant species grow. The following plants are representatives of fodder species: *Bromus inermis* (Leyss.) Holub., *Rumex confertus* Willd., *Trifolium pratense* L., *Poa bulbosa* L., *Artemisia scoparia* Waldst. & Kit., *Stipa capillata* L., *Lathyrus tuberosus* L., *Chenopodium album* L., *Carex physodes* Bieb., *Achillea millefolium* L., etc.

The degradation of the natural vegetation cover was also observed, and now fodder plants were replaced by weedy species of little value. On the territory of Amangeldy, 75 weed species of plants were identified. These include the following plant species: *Rumex crispus* L., *Capsella bursa-pastoris* (L.) Medik., *Cannabis ruderalis* Janisch., *Lathyrus tuberosus* L., *Artemisia vulgaris* L., *Xanthium strumarium* L., *Stipa capillata* L., *Inula britannica* L., *Hypecoum parviflorum* Kar. &Kir.and etc.

Conclusion. Based on the research and analysis of the results, the data obtained, the following conclusions are made:

– based on the analysis of literature data, as well as our own research on the study and collection of plants at the monitoring point v. Amangeldy compiled a list of plants, including 112 species belonging to 88 genera and 29 families.

– the first ten leading families contain 85 species and make up 75.2 % of the total species composition of the flora of the study area. The leading families in this taxonomic composition are *Asteraceae* (24 species, or 21.2 % of the total number of species, 17 genera), *Rosaceae* (15 species or 13.2%, 11 genera), *Poaceae* (12 species, which is 10.6 % of the total, 11 species).

– leading of the genus *Artemisia, Potentilla* and *Rumex*.

No endemic species have been identified.

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АЛМАТЫ ОБЛЫСЫНДАҒЫ МОНИТОРИНГТІ НҮКТЕ, АМАНГЕЛДІ АУЫЛЫНЫҢ ӨСІМДІКТЕРІНІҢ АЛУАНТҮРЛІЛІГІ

Аннотация. Мақалада Алматы облысы, Амангелді ауылы флорасының өсімдіктерінің түрлік құрамына жүйелі талдау жүргізілді.

Аймақтық флораны жан-жақты зерттеу биологиялық әртүрлілікті зерттеу және сақтау проблемасын шешуді жүзеге асыруға байланысты аса маңызды болып келеді. Белгілі бір аумақ флорасының құрамы туралы толық мәліметтер маңызды теориялық мәнге ие, себебі оның компоненттерінің құрылымы мен генезисін орнатуға, жеке ерекшеліктерін анықтауға, қалыптасу тарихын және өзгеру үрдісін қалпына келтіруге мүмкіндік береді. Бұл өсімдік ресурстарын ұтымды пайдаланудың және өсімдіктердің сирек кездесетін және жойылып бара жатқан түрлерін қорғауды ұйымдастырудың негізі болып саналады, сондай-ақ көптеген маңызды шаруашылық проблемаларды шешу үшін дәрілік, тағамдық, жемдік, сәндік және басқа да өсімдіктердің жаңа көздері мен ресурстарын анықтау үшін маңызды.

Кез келген флораның негізгі сипаттамаларының бірі – оның жүйелі құрылымы, атап айтқанда, бір жағынан, тұқымдастардың, тектер мен түрлердің арақатынасы және екінші жағынан, осы таксондардың байлығын анықтайтын сандық көрсеткіштері. Бұл көрсеткіштер, тұтас алғанда, флораны жүйелі талдаудың құрамдас бөлігі болып табылады және мұндай талдаудың көмегімен алынған деректер салыстырмалы

флористика үшін маңызды материал болып есептеледі. Осы тұрғыдан алғанда, флораның жүйелі құрылымы аймақтық жоспарда флораны сипаттайтын маңызды көрсеткіштердің біріне ие болады.

Флораның түрлік құрамын зерттеу жалпы аймақтың флорасы мен ландшафттарының тарихын тану үшін де, өсіп келе жатқан антропогендік қысым жағдайында биоалуантүрлілікті сақтау және пайдалану жолдарын іздеу үшін де маңызды мәнге ие.

Зерттеулер эксперименттік учаскелерді егжей-тегжейлі зерттеумен ұштастыра отырып, маршруттық-рекогносцировкалық әдіспен жүргізілді. Зерттелетін Амангелді аумағында алғаш рет: *Asteraceae* (24 түр немесе 21,4 %, 17 түр), *Rosaceae* (15 түр немесе 13,39 %, 11 түр), *Brassicaceae* (11 түр немесе 9,82 %, 9 түр) қос жарнақты өсімдіктерден және *Poaceae* (11 түр, 12 түр немесе 10,71 %) дара жарнақты өсімдіктерден 112 түр анықталды. Басым тұқымдастардың үлесіне 62 түр келеді, бұл осы аумақта өсетін өсімдіктердің жалпы санының 55,36 %-ын құрайды. Жетекші туыстар: *Artemisia, Potentilla* және *Rumex*. Зерттеу аумағында өсімдіктердің 33 жемдік түрі анықталды: *Bromus inermis* (Leyss.) Holub., *Rumex confertus* Willd. Өсімдік жамылғысының тозуына байланысты арамшөптің саны 75 түрді құрады, олардың ішінде: *Rumex crispus* l., *Capsella bursa-pastoris* (L.) Medik., *Cannabis ruderalis* Janisch., *Lathyrus tuberosus* L. және т.б. бар. Эндем және сирек кездесетін түрлер табылған жоқ.

Жүргізілген зерттеулердің нәтижелері Алматы облысы, Амангелді ауылының флорасын тиімді пайдалануға, сондай-ақ биоәртүрлілікті сақтауға негіз болады. Амангелді кентінің флорасына жүйелі талдау жүргізу нәтижесінде алынған эндемизм және реликтілік орталықтарын анықтауға, сондай-ақ осы флораның басқа жақын флоралар қатарындағы орны мен рөлі мәселелерін шешуге мүмкіндік береді.

Түйін сөздер: Амангелді ауылы, систематикалық анализ, түрлік құрылым, түр, туыс, тұқымдас.

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БИОРАЗНООБРАЗИЕ РАСТЕНИЙ МОНИТОРИНГОВОЙ ТОЧКИ С. АМАНГЕЛДЫ АЛМАТИНСКОЙ ОБЛАСТИ

Аннотация. В статье приведен систематический анализ видового состава растений флоры с. Амангельды Алматинской области.

Всестороннее изучение региональных флор приобретает всё большее значение в связи с реализацией решения проблемы изучения и сохранения биологического разнообразия. Полные сведения о составе флоры той или иной территории имеют важное теоретическое значение, позволяют установить структуру и генезис ее компонентов, выявить индивидуальные особенности, восстановить историю формирования и тенденции изменения. Это, в конечном итоге, является основой рационального использования растительных ресурсов и организации охраны редких и исчезающих видов растений, а также для решения многих хозяйственно важных проблем – выявления новых источников и ресурсов лекарственных, пищевых, кормовых, декоративных и других растений.

Одной из основных характеристик любой флоры является её систематическая структура, а именно соотношение семейств, родов и видов, с одной стороны, и количественные показатели этих таксонов, определяющие её богатство – с другой. Эти показатели являются составляющими систематического анализа флор в целом и ценофлор в частности, полученные при помощи такого анализа данные являются важным материалом для сравнительной флористики. С этой точки зрения систематическая структура флоры приобретает значение одного из существенных показателей, характеризующих флору в региональном плане.

Изучение видового состава флоры имеет большое значение как для познания истории флоры и ландшафтов региона в целом, так и для поиска путей сохранения и использования биоразнообразия в условиях нарастающего антропогенного давления.

Исследования проводили маршрутно-рекогносцировочными методом в сочетании с детальным исследованием экспериментальных участков. По результатам исследований флоры в Алматинской области, села Амангельды, с использованием маршрутного метода и метода закладывания пробных площадок в

100 м2, определено количество видов. На исследуемой территории Амангельды впервые выявлено: 112 видов из 88 родов и 29 семейств, с доминированием семейств *Asteraceae* (24 вида или 21,4 %, 17 родов), *Rosaceae* (15 видов или 13,39 %, 11 родов), *Brassicaceae* (11 видов или 9,82%, 9 родов) из Двудольных, и *Poacea* (11 родов, 12 видов или 10,71 %) из Однодольных растений. На долю доминирующих семейств приходится 62 вида, что составляет 55,36 % от общего количества видов растений, произрастающих на данной территории. Ведущие рода *Artemisia, Potentilla* и *Rumex.* На территории исследования выявлено 33 кормовых видов растений*: Bromus inermis* (Leyss.) Holub.*, Rumex confertus* Willd.*, Trifolium pratense* L., *Poa bulbosa* L. и др. В связи с деградацией растительного покрова количество сорных растения составило 75 видов, среди которых: *Rumex crispus* L., *Capsella bursa-pastoris* (L.) Medik., *Cannabis ruderalis* Janisch., *Lathyrus tuberosus* L. и др. Эндемичных и редких видов не обнаружено.

Результаты проведенных исследований послужат основой для рационального использования флоры с. Амангельды Алматинской области, а также сохранения биоразнообразия. Полученные в результате проведения систематического анализа флоры с. Амангельды, позволят выявить центры эндемизма и реликтовости, а также решать вопросы места и роли данной флоры в ряду других прилежащих флор.

Ключевые слова: с. Амангельды, систематический анализ, видовой состав, вид, род, семейства.

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SARCOCYSTIS IN SOME RODENTS AND BIRDS

Abstract. Sarkosporidiosis is a chronic animal disease that often results in death. In animals with severe damage to the body by sarkosporidiosis, weakness, tissue depletion and hydremia are observed. Sarcocyst development occurs in muscle cells and tissues.

It is known that in vivo predators become infected by eating meat from animals affected by sarcocysts. Sarcocysts secrete toxic substances, sarcocystin and sarcosporiocin, which lead to the death of animals within 5-20 hours.

In chronic conditions in animals, salt deposits form around numerous sarcocysts and pronounced skeletal muscle hydremia is also observed. Sarcocystosis can be detected only after the death of animals. The corpses of animals must be examined microscopically, severely damaged corpses should be buried to a depth of 2 meters. When conducting microscopic studies of slices taken from samples of affected animal meat, a diagnosis is established.

The proposed work is devoted to study the fauna and cycles of the development of micromorphology of representatives of the genus Sarcocystis of some rodents and birds. To achieve this research, an experiment was conducted with small vertebrates. The goal of our work is to identify the distribution of sarcosporidia of some species of rodents and birds, to study the morphology of the detected sarcosporidia, and their life cycle. The results of the study can be used for the epizootological characterization of sarcocystosis of rodents and birds. The study of the life cycle and specific structure is necessary for the diagnosis of species of the genus Sarcocystis. Yellow ground squirrel, house mouse and chukar can serve as a laboratory example in the study of mammalian and bird sarcocystosis. Ultrastructure materials and the life cycle of sarcosporidia can be used in studying the courses "Parasitology" and "Invertebrate Zoology". There are 5 articles that were published on materials of this work.

Key words: sarcocyst, sarcosporidiosis, fauna, development cycle, micromorphology, definitive host, schizogony, gametogony, sporogony, merozoite.

Introduction. Sarcosporidia – parasitic species belonging to genus Sporozoa, class Sarcocystis and is widespread in wildlife. It is found in various mammals species, including humans, birds, and reptiles in the different parts of the globe. Contamination of farm animals by sarcosporidia has reached 60 %.

Infection by Sarcocystis is more common in the relatively immotile animals (in marmots – 41 %, in alectoris – 2-5.7 %). Sarcosporidia in wild animals are studied to a lesser extent than in farm animals. Bearing in mind the detriments to farm animal, it can be used to predict that they control the wild animals` population number.

Life cycle of Sporocystis depends on its intermediate and terminal hosts and is related to its trophic connections.

Materials and Research Methods. Research was conducted in 2018-2019 in the research complex-laboratory of the Institute of Geography and Natural Sciences and in the laboratory of invertebrate zoology in the Faculty of Biology.

Target of the research is the Southeastern part of Kazakhstan, in other words, Almaty region. Species found in the studied areas and brief information about each species are shown below.

While samples were studied by the compressive method, Darling`s method was used to extract Sporocysts from the intermediate hosts. Skeleton, diaphragm, and cardiac muscles were used in the samples. By compressive method, muscles with the volume of 3x3x10 mm were pressed by two glasses; then, cysts were counted.

Cystozoids were studied in the drops of sterile physiologic solution; then, preparations were stained according to Romanowsky-Giemsa staining and placed in methanol smears.

For the experimental study of the life cycle of Sarcosporidia, we used the following animals as the final host: a cat (Fells catus). During the study of sexual reproduction of Sarcosporidia, it was found by the samples taken from the final hosts that they were infected by preying on intermediate hosts. During the electro-microscopic examination of the cystic phase of Sarcosporidia, yellow ground squirrel, house mice, and bird muscles, which were slaughtered on the 27th, 40th and 120th days after being infected by sporocysts, were used as a special study material [2].

Results and discussion. Life cycle and fauna of the sarcocysts in yellow ground squirrel (Spermophilus fulvus).

Table 1 – Research results of sarcocysts in yellow ground squirrel

Year	Studied	Infected %	Studied	Infected %	Studied	Infected %	Identified		In one season
							S.cv	S.cb	S.cv, S.cb
2018	379	28(7.4)	181	13 (7.2)	198	15(7.6)	26	–	2
2019	192	17(8.8)	105	12(11.4)	84	5(5.9)	13	3	1
Total	571	45	286	25	282	20	39	3	3
Note: S.cv – Sarcocystis citellivulpes. S.cb – Sarcocystis citellibuteonis.									

Yellow ground squirrels were caught in their natural habitats. In the muscles of yellow ground squirrel , slaughtered on the 27th day, tiny 14.4x7 μm cysts with intermediate cells, metrocytes, and a few merozoits were found. On the 40th day, a large, 8-14x16-32 μm, with the same types of cells, cysts were found. After infection on the 138th day, 28-420x140-840 μm, large, thin-walled, mature sarcocysts were found. These sarcocysts were further investigated under the electron microscope [3].

As shown in the results of the research, Sarcocystis citellivulpes (5.6 %) is most common species in yellow ground squirrels, it is mainly transmitted by Canidae(dogs), but Sarcocystis citellibuteonis is seen rarely.

Life cycle and fauna of the sarcocysts in house mice (Mus musculus).

Investigation of house mice, which were caught in different parts of Almaty, revealed the variety of their infection. It was due to the density of house mice population and cats being the definitive host [4].

Table 2 – Research results of the sarcocysts in house mice (Mus musculus)

Studied	Infected %	Studied	Infected %	Studied	Infected %
52	5(9, 3)	28	2(8,7)	30	3(10)

In ‘native’ preparations, parasites appeared to be like wide thread, with the value of 150-630x10500-11000 μm. Little amount of cysts were found in the muscle samples. The size of the wall is 2.8-3.5 μm. Merozoits with the value of 2.8-4, 9x14.0-14.5 μm resembling banana and half of Sun emerge from cysts [5,6].

Table 3 – Comparative information of sarcocysts in house mice

Type	Definitive host	Cyst size (μm)	Size of cyst walls (μm)	Value		Authors, year
				Merozoits (μm)	Sporocysts (μm)	
S. murus	Cat	500-600	–	4-6x14-16	7.5-9,Ox 8,7 -11.7 (8.5x10.3)	Ruiz, Frenkel, 1976
S.murus	Cat	20-130x 4230-8500	0.,5-1,5	3.9-6.5x I0.7–16.9	7.2-8.7x8.7-11,6	Levitt, 1984
S.musmustellis	Weasel	150-630x 1000-10500	2.,8-3.5	2.8-4.9x 14.0-14.5	**9** -9.8x I2.2-12.6 (9.6x12.6)	Pak, Orazalinova, Fedoseenko, 1993
S.disperse	Owl	80-90x20-30		8-9x4	11-14x8-12	Cerna,1977
S.crotali	Rattlesnake	500-4000			7.9x10.8	Enzeroth, Chobotar, Scholtyseck, 1985
S.murivi pera	Palestinian viper	150-400x 5000-8000	3,5 *	7x1,3	9.6x12.2 (8.8-10.5)x(11.7-12.9)	Matuschka, Heydorn, Mehihorn, et.al., 1987

Sarcocysts in chukars (Alectoris chucar).

Adult chukars, which were accidentally infected with sarcosporidia, in hunting business in Ile Alatau, Almaty region in 2018-2019 were studied.

To identify the sarcocysts in chukars, 'native' preparations of thigh, chest, and cardiac muscles were used with the light microscope in low magnitude. To identify the life cycle of sarcosporidia in the muscles of chukars, predators were fed by them; then, via analysis, presence of sarcosporidia was determined.

Research results of sarcocysts in chukars are depicted in table 4. As it is shown in the table, infection by sarcocysts was high for chukars. Males were more prone to infection; thigh muscles were especially damaged, but they were absent in cardiac muscles [8,9].

Table 4 – Research results of sarcocysts in chukars

Year	Studied	Infected %	Studied	Infected %	Studied	Infected %	Identified		In one season
							S.av	S.ab	S.av, S.ab
2018	45	4 (9,5)	20	2(10)	10	2 (20)	16	–	–
2019	22	2(9,8)	9	2(10,5)	12	1(10,2)	4	1	3
Total	67	6	29	4	22	3	20	1	3
Note: S.av – Sarcocystis alectorivulpes. S.ab – Sarcocystis alectoributeonis.									

Table 5 – Comparative information of sarcocysts in chukars

Type	Definitive host	Cyst size (μm)	Size of cyst walls (μm)	Value	
				Merozoits (μm)	Sporocysts (μm)
Sarcocystis alectorivulpes	Fox, Corsac fox	20-560x 530-9750	2.0-2.8	2.1-4.2 x 9.8-14.0	8.4-9.8x II,9-13.3
Sarcocystis alectoributeonis	Buzzard	52-130x 260-2600	0.5-1.0	1.4-2.1x 7.0-8.4	8.4-10.5x I1.2-14.7

Conclusions. As a result of the research, two types of sarcocysts Sarcocystis citellivulpes, Sarcocystis citellibuteonis were identified. Sarcocystis citellivulpes (5.6%) was more common, its main carrier was Canidae (dogs), while Sarcocystis citellibuteonis was seen rarely (0.5%).

5 types of sarcocysts were found in house mice. They are Sarcocystis *murus,* Sarcocystis *musmustellis,* Sarcocystis *disperse,* Sarcocystis *crotali,* Sarcocystis *murivipera. Definitive hosts are: cat, weasel, owl, rattlesnake, and Palestinian viper.*

Research results of sarcocysts in chukars are depicted in Table 4. As it is shown in the table, infection by sarcocysts was high for chukars. Males were more prone to infection; thigh muscles were especially damaged, but they were absent in cardiac muscles. Two types of sarcocysts (Sarcocystis alectorivulpes**,** Sarcocystis alectoributeonis) were found in chukars.

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КЕЙБІР КЕМІРГІШТЕР МЕН ҚҰСТАРДАҒЫ SARCOCYSTIS

Аннотация. Саркоспоридиоз – жануарлардың жиі өліммен аяқталатын созылмалы ауруы. Организм саркосцисталармен қатты зақымдалған уақытта, жануарларда әлсіздік, азу, ұлпалардың гидремиясы байқалады. Саркоцисталардың дамуы бұлшықет жасушалары мен ұлпаларында өтеді.

Табиғи жағдайда жыртқыш жануарлар саркоцисталармен зақымдалған ауру жануарлардың етін жеген кезде жұқтыратыны белгілі. Саркоцисталар саркоцистин және саркоспориоцин деп аталатын улы заттар бөледі, олар жануарларды 5-20 сағат ішінде өлімге дұшар етеді.

Саркоцисталармен сүтқоректілер, атап айтсақ еліктер, бұғылар, қабандар, қояндар, егеукұйрықтар, тышқандар, үй жануарлары және құстар (жабайы үйректер) зақымданады. Жабайы жануарлардың саркоцистоздарының этиологиясында осы паразиттердің бірнеше түрлері белгілі, олар елікте (жұтқыншақ бұлшықетінде, тіл тамырларында); қабанда (барлық көлденең салалы бұлшықеттерінде, көбінесе диафрагма бұлшықетінде, тілдің ұшында, құрсақ қабырғаларында, жүрек бұлшықетінде); қояндарда (қаңқаның барлық бұлшықеттерінде); үйректерде (қаңқаның бұлшықеттерінде) кездеседі. Цисталар бұлшықетаралық дәнекер ұлпасында орналасқан.

Саркоцисталармен залалданған ірі қара малдың және шошқаның шикі етін жегеннен кейін, дефинитивті иесі нәжістерімен бірге спороцисталарды бөле бастайды. Адамдар жануарлардың шикі саркоцистоздық еттерін пайдаланған кезде, сондай-ақ шикі етпен жанасқан жағдайда немесе жеке гигиенаны сақтамаған кезде, саркоспоридиоз ауруын жұқтыруы мүмкін.

Саркоцистоз кезінде инкубациялық кезең өте ұзақ уақыт жүреді, жануарлар қатты зақымдалған жағдайда, ең бірінші байқалатын белгісі – азу. Жақ асты және көкірек аймақтарында ісінулер айқын байқалады, жануарлардың қозғалысы нашарлайды, көп жата береді, кейбір жағдайда өлімге әкеледі, егерде ауру жануарлар саркоспоридиоз ауруымен әлсіз зақымдалған жағдайда, аурудың клиникалық белгілерін жыл бойы тасымалдауы мүмкін.

Саркоспоридиоз ауруымен өлген жануарларда, ең алдымен, азу көзге түседі. Олардың ішкі паренхиматозды мүшелерінде күрт айқын көрінетін өзгерістер байқалмайды, бірақ мүшелерінің көлемдерінің кішірейгенін анық байқауға болады. Диафрагмада, құрсақ бөлімінде, тілдің тамырларында, жүрек бұлшықеттерінде сопақша келген ақ немесе сұр қосылыстарды, яғни саркоцисталарды көруге болады.

Созылмалы болған жағдайда көптеген саркоцисталармен қатар олардың айналасында әк тұздардың шөгіндісі пайда болады және сондай-ақ қаңқа бұлшық еттерінде айқын гидремия орын алады. Саркоцистозды тек жануарлар өлгеннен кейін ғана анықтай аламыз. Олардың өлекселерін міндетті түрде микроскопиялық түрде зерттеу қажет, қатты зақымдалған өлекселерді 2 метрлік тереңдікте көму керек.

Зақымдалған мал етінің сынамаларынан алынған кесінділерге микроскопиялық зерттеулер жүргізу арқылы диагноз қойылады. Саркоцисталардың бұлшықет талшықтарында және бұлшықетаралық дәнекер ұлпаларында оқшауланатынын анықтап көрдік. Саркоцистозбен күрес жүргізу шаралары әлі де болса оң нәтижелерін бермей келеді.

Ұсынылып отырған жұмыс кейбір кеміргіштер мен құстардағы Sarcocystis туысы өкілдерінің фаунасын, даму циклдарын және микроморфологиясын зерттеуге арналған. Осы зерттеуге қол жеткізу үшін, ұсақ омыртқалы жануарлармен эксперимент жүргізілді. Біздің жұмысымыздың мақсаты – кеміргіштер мен құстардың кейбір түрлерінде саркоспоридиялардың таралуын анықтау, табылған саркоспоридиялардың морфологиясын, олардың тіршілік циклын зерттеу.

Зерттеу нәтижелері кеміргіштер мен құстардың саркоцистоздарының эпизоотологиялық сипаттамасы үшін пайдаланылуы мүмкін. Даму циклы мен нақты құрылымды зерттеу Sarcocystis туысының түрлерін диагностикалау үшін қажет. Зорман, үй тышқандары, кекіліктер сүтқоректілер мен құстардың саркоцистоз-

дарын зерттеу кезінде зертханалық үлгі ретінде алынады. "Паразитология" және "Омыртқасыздар зоологиясы" курсын оқып үйрену барысында ультрақұрылымы мен даму циклы бойынша материалдарды пайдалануға болады. Осы жұмыс негізінде 5 мақала жарық көрді.

Түйін сөздер: саркоциста, саркоспоридиоз, фауна, даму циклы, микроморфология, мерозоит, дефинитивті иесі, шизогония, гаметогония, спорогония.

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SARCOCYSTIS У НЕКОТОРЫХ ГРЫЗУНОВ И ПТИЦ

Аннотация. Саркоспоридиоз является хроническим заболеванием животных, которое часто заканчивается летальным исходом. У животных при сильном поражении организма саркоспоридиозом наблюдается слабость, истощение и гидремия тканей. Развитие саркоцистов происходит в мышечных клетках и тканях.

Известно, что в естественных условиях хищные животные заражаются при употреблении мяса животных пораженных саркоцистами. Саркоцисты выделяют ядовитые вещества, саркоцистин и саркоспориоцин, которые приводят к летальному исходу животных в течение 5-20 часов.

Саркоцистами поражаются косули, олени, кабаны, кролики, крысы, мыши, домашние животные и дикие утки. В этиологии саркоцистозов диких животных известны несколько видов этих паразитов, которые встречаются у косуль (в мышцах глотки, в корнях языка), у кабана (во всей поперечнополосатой мускулатуре, преимущественно в мышцах диафрагмы, кончиках языка, брюшной стенке, и в сердечной мышце), у кроликов (во всех скелетных мышцах), у уток (в скелетных мышцах). Цисты расположены в межмышечной соединительной ткани.

После приема сырого мяса крупного рогатого скота и свиней, зараженных саркоцистами, дефинитивный хозяин с фекалиями начинает выделять спороцисты. Человек может заразиться саркоспоридиозом при употроблении сырого мяса, зараженного саркоцистозом животных, и при не- соблюдении личной гигиены.

При саркоцистозе инкубационный период продолжается очень длительное время, и при сильном поражении животные подвергаются истощению. Животные плохо передвигаются, больше находятся в состоянии лежа, в подчелюстной и грудной области отмечаются отеки. В некоторых случаях заболевание приводит к гибели животного. При слабом поражении больные животные могут переносить клинические признаки заболевания в течение года.

При болезни саркоспоридиозом в первую очередь наблюдается истощение организма животных. Во всех внутренних паренхиматозных органах резко выраженных изменений не наблюдается, но можно заметить уменьшение размеров органов животных. Можно увидеть саркоцисты – овальные белые или серые соединения – в диафрагме, в брюшной части, в корнях языка и в мышцах сердца.

При хронических состояниях у животных вокруг многочисленных саркоцист образуются отложения солей и также наблюдается выраженная гидремия скелетных мышц. Саркоцистоз можно обнаружить только после смерти животных. Трупы животных необходимо микроскопически исследовать, сильно поврежденные трупы следует погребать на глубину 2 метров.

При проведении микроскопических исследований срезов, приготовленных из проб пораженного мяса животных, устанавливается диагноз. Можно увидить, что саркоцисты изолировано находятся в мышечных волокнах и межмышечных соединительных тканях. Меры по борьбе с саркоцистозом все еще не дают положительных результатов.

Предлагаемая работа предназначена для изучения фауны, циклов развития и микроморфологии представителей рода Sarcocystis некоторых грызунов и птиц. Для достижения этого исследования был проведен эксперимент с мелкими позвоночными животными. Целью нашей работы является выявление распространения саркоспоридий в некоторых видах грызунов и птиц, изучение морфологии обнаруженных саркоспоридий, их жизненного цикла.

Результаты исследования могут быть использованы для эпизоотологической характеристики саркоцистозов грызунов и птиц. Изучение цикла развития и конкретной структуры необходимо для диагностики видов рода Sarcocystis. Желтый суслик, домашние мыши, кеклик могут служить лабораторным примером при исследовании саркоцистозов млекопитающих и птиц. При изучении курса «Паразитология» и «Зоология беспозвоночных» можно использовать материалы по ультраструктуре и циклу развития. На основе этой работы опубликовано 5 статей.

Ключевые слова: саркоциста, саркоспоридиоз, фауна, цикл развития, микроморфология, мерозоит, дефинитивный хозяин, шизогония, гаметогония, спорогония.

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BIOLOGICAL AND ECOLOGICAL FEATURES OF THE SAXAUL-EATING SHEEPSHANKS (COLEOPHORIDAE)

Abstract. Within pests (insects), Lepidoptera, by species composition and harmfulness, are in the front row. As you know, one of the biogenic factors in nature, they have a serious impact on the yield of natural pasture grasses and saxaul. They feed on leaves, stems, roots, flowers and seeds of plants, and prevent the reproduction of saxaul. In this regard, it is now necessary to study the biological characteristics of shells that feed on saxaul, determine the phenology, harmfulness, and organize measures to protect against pests. For many reasons (seed production, agricultural engineering, etc.), it is connected with the fact that in the desert zone of South-Eastern and southern Kazakhstan, issues of increasing the area of the saxaul and protecting it from pests are being solved. One of the main reasons is an incomplete study of the species composition of insects-insects that feed on saxaul. Therefore, the study of bioecological features of pest species and their harmfulness and measures to protect the saxaul from pests is one of the urgent problems. The article deals with the study of biological features of shells that feed on saxaul, determining the phenology, harmfulness and organization of measures to protect against pests.

Key words: saxaul, insects, scapulars, insect pests, Lepidoptera.

Introduction. For many reasons (seed production, agricultural engineering, etc.), it is connected with the fact that in the desert zone of South-Eastern and southern Kazakhstan, issues of increasing the area of the saxaul and protecting it from pests are being solved. One of the main reasons is an incomplete study of the species composition of insects-insects that feed on saxaul. Therefore, the study of bioecological features of pest species and their harmfulness and measures to protect the saxaul from pests is one of the urgent problems.

The article deals with the study of biological features of shells that feed on saxaul, determining the phenology, harmfulness and organization of measures to protect against pests.

Brief description of the parent. The sesame crustacean family (Coleophoridae) is a small butterfly belonging to the relatives of Gelechioidea (1700 species of the family 1425 families in this Taxon are included in the international register) [1,2].

Morphological feature. The margins of the front wing of butterflies are 7-40 mm., the wings have thin, toning, white stripes along the crests and long hair. In the course of life is closely Gldata decides boxes. Fruit carriers are wrapped in silk and made from various plant residues. Some species develop within a class or within a breed, inside a gall (node). Aesthetes spend feeds and plants [3].

Range. It is most commonly found in temperate regions of the Northern hemisphere, desert and desert areas in the Palearctic. In southern Africa, South America, and the continents of Australia [4,5,6,7,8,9,10].

More than 1,000 sesame species are known in the countries of the former USSR, including pests of agricultural crops, forest and fruit trees, and pasture plants [5,6]. The following species of kunduars are found in saxaul: Characia haloxyli (Flkv).), Coleophora captiosa (Flkv.), Ionescumia saxauli (Flkv.), Casignotella gallivora (Flkv.), Coleophora galligena, Coleophora calligoni [7].

Research materials and methods. As a result of a taxonomic survey conducted by scientists around the world recently, it was proved that the kunduna springs are divided into 11 families. Currently, the taxonomic degrees are as follows: family name – arthropods (Arthropoda); only branch – tracheae (Trachiata); class – hexagons (Hexapoda); herd – bunt (Insecta); tap – wings (Pterygota); infratap – janacanates (Neoptera); group – scaly (Lepidoptera); group – nasal (Lepidoptera); group – nasal (Lepidoptera). glossata); related is gelechiidae fracker, 1915; related-Coleophoridae Hübner, 1825 families: Augasma, Coleophora, Corythangela (Batrachedridae), Enscepastra (Batrachedridae), Goniodoma, Iriothyrsa (Agonoxeninae), Ischnophanes, Ischnopsis (Agonoxeninae), Metriotes, Nasamonica; Porotica (agonoxeninae) [9,10].

The largest species of the sesame family genus is in the Coleophora family. Most of the seeds that live in saxaul belong to this breed.

I. seed-a General characteristic of the Coleophora family (Hübner, 1825).

The number of species belonging to the sesame family is 95 % of all known species of the Coleophoridae family, and there are 1,350 known species worldwide that belong to this breed. As a result of subsequent taxonomic studies, on morphological features, many species of the family were again included in this breed. Many continents of the world are inhabited mainly by near-Arctic and Palearctic zoogeographic zones [11,12].

The results of research and analysis. In the desert regions of our South-Eastern Kazakhstan in 2014-2016. as a result of research, it was found that there are 2 types of sesame seeds in the saxaul, living mainly with generative and vegetative members of the saxaul. Information was obtained about the features of their biological development, nutritional relationship and harmfulness. For the phenological development and control of mass species, the stages of their optimal development were determined. Below, we focus separately on species that feed on various members of the saxaul.

1.Saxaulnik-Coleophora haloxyli (Flkv.)

Synonyms: Characia haloxyli (Flkv.)

Morphological feature. The area of the front wing of butterflies is 10-12 mm. the Ink is thin, covered, the outer side is covered with husks. The forewing is white or light grey matting, and has red-brown scales on which the top group is found. The hindwing is dark white, the hair of the fore and hind wings is light. The ink is thin, the outer side is framed with light brown silk. The 2nd chain is covered with short husks (figure 1).

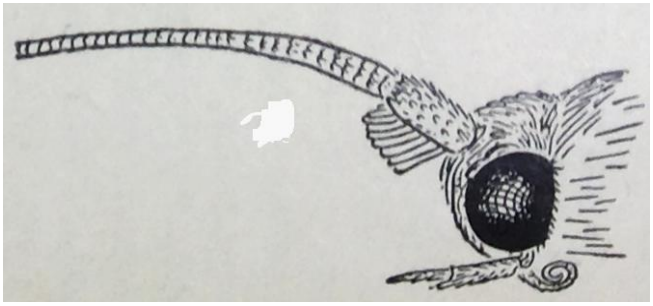

Figure 1 – Saxaul sesame-Coleophora haloxyli (Flkv.) [12]

Distribution. Turkmenistan, Uzbekistan [13], in the desert regions of South-Eastern Kazakhstan.

Biology. Star seeds are made from saxaul. It lives in the White saxaulnik. The length of the shell is 8-9 mm., the color is brown-yellow.

Cereal asterisks are found in September-October [14]. The flight of butterflies will begin in early June. At this time, they also feed on saxaul shoots. In the summer, it falls into the estivation. Inside kundak winter starlets. 1 generation per year.

2. Captiosa (Coleophora captiosa (Flkv.), 1972) morphological and biological features.

Types: Coleophora captiosa captiosa, Coleophora captiosa maior Baldizzone, 1994.

Synonyms. Tritemachia capitosa (Flkv.)

Distribution. Turan-Gobial species: Mongolia, Turkmenistan, Uzbekistan [13, p.817], settlement of saline lands in the desert regions of South-Eastern Kazakhstan.

Morphological feature. The area of the front wing of butterflies is 10-12 mm. the Ink is thin, covered, the outer side is covered with husks. The forewing is white or light grey matting, and has red-brown scales on which the top group is found. The rear wing is Matt white. The hair of the front and rear wings is light. The ink is narrow, the outer side is framed by light brown scales. The 2nd chain is covered with short husks [12, p.50].

The length of the fruit is 5-6. 5 mm., the saxaul leaf is a tubular shape made on shoots, with a well-developed valve, the color is dark brown.

Biology. Butterflies fly in June. Parsley feeds on black saxaul shoots in spring and seeds in autumn. 1 generation per year.

3. The seed of the Haloxylon – Coleophora saxauli (Flkv.) morphological and biological features.

Synonyms. Ionescumia saxauli (Flkv.)

Distribution. Turan-Gobalyk: Mongolia, Turkmenistan, Uzbekistan [13, p.820]. In the desert regions of South-Eastern Kazakhstan, there are lands overgrown with white saxaul.

Morphological feature. The margins of the front wing of butterflies are 11-12 mm. the Ink is thin, covered, and the outer side is covered with husks. The forewing is white or light grey matting, and has red-brown scales on which the top group is found. The rear wing is Matt white. The brushes of the front and rear wings are light. The ink is thin, the outer side is framed with light brown silk. The 2nd chain is covered with short husks (figure 2) [12, p.47]. The length of the sprockets is 6.5-7.5 mm., the saxaul leaf is a tubular shape made on shoots, the rear valve of the kung is well developed, the color is dark brown.

Figure 2 – Coleophora saxauli (Flkv.1972) features of the structure of whiskers and scoops [12, p.89]

Biology. Star worms in kunduk overwinter on the surface of plant residues or soil. Butterflies fly in August. Saxaul shoots feed on stars in the spring, and saxaul seeds in the autumn. 2 generations per year.

1. Calligraphy of Casignotella-Casignotella gallivora (Flkv.)

Distribution. Turan-Gobalyk: Mongolia, Turkmenistan, Uzbekistan. It lives in the desert zones of South-Eastern Kazakhstan.

Morphological feature. The margins of the front wing of butterflies are 8-10 mm the Rollers are white, 2 of which are covered with bugs, without a brush, 1.5 times smaller than the ink of the 3rd chain of the guardrail, twice as large as themselves. Peas at the guardrail-simple, with a white, brown ring. The top of the wings are framed by small, scattered scales, which are often found in some places. The wing shells of females are frequent and dense. The hindwings are dark grey and the hair is light [15].

Threads are knitted with dense silk threads, with a bumpy top, with a back valve three hinged, 6-7 mm long.

Biology. Star worms in kunduk overwinter on the surface of plant residues or soil. In the spring, at the beginning of April, it is fried there. Butterflies of the 1st generation fly in the second half of April, when the eggs are placed in the young shoots of the saxaul (tube leaves). The asterisks of the egg are leaf buds (Psylidae: Caillarida azurea C.), which affect the shoots of the saxaul (Psylidae: Caillarida azurea C.) penetrate inside the galls, feed the core of the shoots. 1 Galle is home to 1 star. The roasting of this generation takes place inside the gall. Butterflies of this generation fly in July, the Gauls have a round hole.

The second-generation asterisks appear from the second half of August to the first days of September. They are located in a tubular droplet, only the head and chest are visible, and when threatened, they get stuck inside the kung. After the first cold, when the saxaul seeds fall out, they go to winter. In the

autumn months, saxaul seeds are eaten from the inside, causing significant damage to the seed yield. In one village, their number reaches 50.

In addition to saxaul, with seeds of eggplant and Circassian, and stars of the 1st generation-inquisitors in the galls of leaf buds in numerous shrub and shrub plants, eat inside the shoot [14, p. 869], and living in two relatives of the breed alabota-the only species [15].

Saxaul shoots feed on stars in the spring, and saxaul seeds in the autumn. 2 generations per year (table) (figure 3).

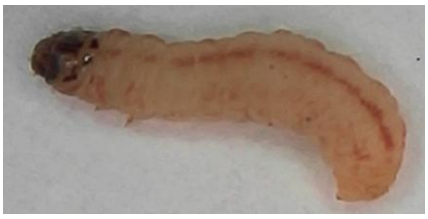

Figure 3 – Casignotella gallivora (Flkv.) ildiri

As a result of the conducted research, 15 star stands were found out of each saxaul breed of this type, collected 1 kg, and the damage reached 5.

1. galligena Kungei-Coleophora galligena (Flkv.)

Distribution. Turan-Gobilyk: Mongolia, Turkmenistan, Uzbekistan, [13, p. 820], Jordan and Pakistan [16]. In the desert regions of South-Eastern Kazakhstan, the saxaul lives.

Morphological feature. The margins of the forewings of butterflies are 12-14 mm the Pockets are white, toning, 2 times longer, 2 of which are covered with burnt husks, without hair, the 3rd chain of the guardrail is shorter than 2. The lower sides of the basal (substep) chain of the guardrail are covered with scales, shaped tassels. The color of peas is White, several chains are covered with husks, in the middle part of the ring is light brown-yellow. The head, back and wings are light yellow [17, p.825]. The length of adult stars of the pest is 4-5 mm, the body is light yellowish, the head is black.

Biology. Asterisks are found in spring in April and may, in autumn from the end of August and in September. The thin branches of the saxaul are white, including the gall. The galls (nodes) are 15 mm long. Two generations per year. The spring generation of saxaul feeds on vegetative, and the autumn generation on seeds.

This species is very similar to the species mentioned above in the striking, nutritional, and biological features of the saxaul. Young and adult starlets hibernate inside a thin elephant, inside plant remains. From seed leaves that are in the breed [18,19].

Casignotella gallivora (Flkv.) phenological calendar. (Almaty region, Balkhash district)

Stage of development	Months																	
	III			IV			V			VI -VIII		VIII	IX			X		
	I	II	III	I	II	III	I	II	III			III	I	II	III	I	II	III
Caterpillars	(—	—																
Doll				**0**	**0**													
Imago					+	+	+											
Egg						●	●											
Caterpillars							—	—	—	—	—							
Doll											**00**							
Imago											+	+						
Egg												●	●					
Caterpillars												—	—	—	—	— V	(— V	(—) V
Symbols: - egg, + - senior butterfly, - star, (-) - Star in the winter range, 0-doll, VVV-the timing of the control measures.																		

Conclusion. As a result, as a result of the conducted research in the desert regions of South-Eastern Kazakhstan, there are 2 types of sesame seeds that live in saxaul forests, which mainly feed on generative and vegetative members of the saxaul. Information was obtained about the features of their biological development, nutritional relationship and harmfulness. For the phenological development and control of mass species, the stages of their optimal development were determined.

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СЕКСЕУІЛМЕН ҚОРЕКТЕНЕТІН ҚҰНДАҚТЫЛАР (*COLEOPHORIDAE*) ТУЫСТАСЫНЫҢ ЗИЯНКЕС ТҮРЛЕРІНІҢ БИОЛОГИЯЛЫҚ ЖӘНЕ ЭКОЛОГИЯЛЫҚ ЕРЕКШЕЛІКТЕРІ

Аннотация. Зиянкес – бунақденелілердің (бөжектер) ішінде қабыршаққанаттыларға жатады, түр құрамы және зияндылығы жағынан алғанда, алдыңғы қатарда тұр. Табиғаттағы биогендік факторлардың бірі ретінде, олардың табиғи жайылым шөптері мен сексеуілдің өнімділігіне әжептеуір ықпалын тигізетіні белгілі. Олар өсімдіктердің жапырағымен, сабағымен, тамырымен, гүлімен және тұқымымен қоректеніп, сексеуілдің өсіп-өнуіне кедергі жасайды. Осыған байланысты қазіргі уақытта сексеуілмен қоректенетін қабыршаққанаттылардың биологиялық ерекшеліктерін зерттеу, фенологиясын, зияндылығын анықтау және зиянкес түрлерден қорғау шараларын ұйымдастыру қажеттілігі туындап отыр.Оңтүстік-Шығыс және Оңтүстік Қазақстанның шөл аймағында қолдан егілген сексеуілдің көлемін ұлғайту және оны зиянкестерден қорғау шаралары көптеген себептерге (тұқым шаруашылығы, агротехникасы т.б.) байланысты. Негізгі себептердің бірі: сексеуілмен қоректенетін зиянкес-қабыршаққанаттылардың түр құрамының толық зерттелмеуі. Сондықтан зиянкес түрлерінің биоэкологиялық ерекшеліктері мен олардың зияндылығын және сексеуілді зиянкес қабыршаққанаттылардан қорғау шараларын зерттеу – өзекті мәселелердің бірі. Мақалада сексеуілмен қоректенетін қабыршаққанаттылардың биологиялық ерекшеліктерін зерттеу, фенологиясын, зияндылығын анықтау және зиянкес түрлерден қорғау шараларын ұйымдастыру мәселелері қарастырылған.

Соңғы уақытта әлем ғалымдарының жүргізген таксономиялық тексеру нәтижесінде, құндақтылар туыстасының 11 тұқымдасқа бөлінетіндігі дәлелденді. Қазіргі кездегі таксономиялық дәрежелері төмендегідей: тегі – буынаяқтылар (*Arthropoda);* тек тармағы – кеңірдек тыныстылар *(Trachiata)*; таптасы – алтыаяқтылар (*Hexapoda)*; табы – бунақденелілер (*Insecta*); тап тармағы – қанаттылар *(Pterygota)*; инфратап – жаңақанаттылар *(Neoptera);* тобы – қабыршаққанатылар *(Lepidoptera);* топ тармағы – тұмсықтылар *(Glossata);* туыстастары – *Gelechioidea Fracker, 1915*; туыстасы – *Coleophoridae Hübner, 1825* тұқымдастары: *Augasma, Coleophora, Corythangela (Batrachedridae), Enscepastra (Batrachedridae), Goniodoma, Iriothyrsa (Agonoxeninae), Ischnophanes, Ischnopsis (Agonoxeninae), Metriotes, Nasamonica; Porotica (Agonoxeninae*).

Құндақтылар туыстасының ішіндегі ең көп түр *Coleophora* тұқымдасына жатады. Сексеуілде тіршілік ететін құндақтылардың басым көпшілігі осы тұқымдасқа жатады.

Құндақтылар тұқымдасына жататын түрлердің саны *Coleophoridae* туыстасының барлық белгілі түрлердің 95 %-ын құрайды, әлем бойынша осы тұқымдасқа жататын 1350 түр белгілі. Кейінгі кездегі жүргізілген таксономиялық зерттеулердің нәтижесінде, морфологиялық ерекшеліктері бойынша көптеген тұқымдастардағы түрлер осы тұқымдасқа қайтадан енгізілді. Жер шарының көптеген континенттерін, негізінен неарктикалық және палеарктикалық зоогеографиалық аймақтарын мекендейді.

Оңтүстік-Шығыс Қазақстанның шөл аймақтарында 2014-2016 жылдары жүргізілген зерттеулеріміздің нәтижесінде сексеуілде тіршілік ететін құндақтылардың 2 түрі кездесті, олар негізінен сексеуілдің генеративті және вегетативті мүшелерімен қоректенеді. Олардың биологиялық даму ерекшеліктері, қоректік байланысы және зияндылығы туралы мәліметтер алынды. Фенологиялық дамуы және жаппай кездесетін түрлерімен күресу үшін олардың оңтайлы даму сатылары анықталды. Мақалада сексеуілдің әртүрлі мүшелерімен қоректенетін түрлердің сипаммамасы келтірілген.

Құндақтылардың таралу аймағы Солтүстік жарты шардың қоңыржай аймақтарында, Палеарктикадағы шөл және шөлейт жерлерде көбірек кездеседі. Африканың оңтүстігінде, Оңтүстік Америкада және Австралия құрлықтарында аз кездеседі.

Бұрынғы КСРО елдерінде құндақтылардың 1000-нан аса түрлері белгілі, олардың ішінде ауылшаруашылық дақылдарының, орман және жеміс ағаштарының және жайылым өсімдіктерінің зиянкес түрлері бар. Сексеуілде тіршілік ететін құндақтылардың төмендегідей түрлері кездеседі: *Characia haloxyli* (Flkv.),

Coleophora captiosa (Flkv.), *Ionescumia saxauli* (Flkv.), *Casignotella gallivora* (Flkv.), *Coleophora galligena, Coleophora calligoni.*

Оңтүстік-Шығыс Қазақстанның шөл аймақтарында жүргізген зерттеулеріміздің нәтижесінде сексеуілде тіршілік ететін құндақтылардың 2 түрі кездесті, олар негізінен сексеуілдің генеративті және вегетативті мүшелерімен қоректенеді. Олардың биологиялық даму ерекшеліктері, қоректік байланысы және зияндылығы туралы мәліметтер алынды. Фенологиялық дамуы және жаппай кездесетін түрлерімен күресу үшін олардың оңтайлы даму сатылары анықталды.

Түйін сөздер: Сексеуіл, бунақденелілер, құндақтылар, зиянкес-бөжектер, қабыршаққанаттылар.

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БИОЛОГИЧЕСКИЕ И ЭКОЛОГИЧЕСКИЕ ОСОБЕННОСТИ ЧЕХЛОНОСКИ (*COLEOPHORIDAE*), ПИТАЮЩИХСЯ САКСАУЛОМ

Аннотация. Внутри вредителей (насекомые) чешуекрылые, по видовому составу и вредности, находятся в переднем ряду. Как известно, одним из биогенных факторов в природе они оказывают серьезное влияние на урожайность природных пастбищных трав и саксаульников. Они питаются листьями, стеблями, корнями, цветами и семенами растений, препятствуют воспроизводству саксаула. В связи с этим в настоящее время назрела необходимость изучения биологических особенностей раковин, питающихся саксаулом, определения фенологии, вредности и организации мероприятий по защите от вредителей. В пустынной зоне юго - восточного и Южного Казахстана меры по увеличению объема искусственного саксаула и защите его от вредителей зависят от многих причин (семеноводство, агротехника и др.). Одной из основных причин является неполное изучение видового состава насекомых-насекомых, питающихся саксаулом. Поэтому изучение биоэкологических особенностей видов вредителей и их вредоности и мер защиты саксаула от вредителей является одной из актуальных проблем. В статье рассмотрены вопросы изучения биологических особенностей раковин, питающихся саксаулом, определения фенологии, вредоности и организации мероприятий по защите от вредителей.

В результате таксономического обследования, проведенного учеными мира в последнее время, было доказано, что чехлоносики делятся на 11 семейство. В настоящее время таксономические степени следующие: род – членистоногие (Arthropoda); подрод – трахеи (Trachiata); класс – шестиногие (Hexapoda); подкласс – насекомое (Insecta); надкласс- қанаттылар (Pterygota); инфракласс – новокрылые (*Neoptera*); отряд – чешуекрылые (Lepidoptera). glossata); подотряд – *Gelechioidea Fracker, 1915*; надсемейство - *Coleophoridae* Hübner, 1825 семейства: *Augasma, Coleophora, Corythangela (Batrachedridae), Enscepastra (Batrachedridae), Goniodoma, Iriothyrsa (Agonoxeninae), Ischnophanes, Ischnopsis (Agonoxeninae), Metriotes, Nasamonica; Porotica (agonoxeninae).*

Самый крупный вид рода семейства чехлоносок находится к семейству *Coleophora*. Большинство чехлоносок, обитающих в саксауле, относятся к этому виду.

Количество видов, относящихся к семейству чехлоносок, составляет 95% всех известных видов семейства *Coleophoridae*, по всему миру известно 1350 видов, относящихся к данному виду. В результате последующих таксономических исследований, по морфологическим особенностям, многие виды семейства вновь были включены в этот вид. На многих континентах земного шара обитают в основном неарктические и палеарктические зоогеографические зоны.

В пустынных регионах Юго - Восточного Казахстана в 2014 - 2018 гг. в результате проведенных исследований установлено, что в саксауле встречаются 2 вида чехлоносок, питающихся в основном с генеративными и вегетативными органами саксаула. Получены сведения об особенностях их биологического развития, питательной связи и вредности. Для фенологического развития и борьбы с массовыми видами были определены стадии их оптимального развития. В статье приведена характеристика видов, питающихся различными органами саксаула.

Ареал чехлоносок встречается в умеренных районах Северного полушария, пустынных и пустынных местах в Палеарктике. На юге Африки, в Южной Америке и на континентах Австралии встречается мало.

В странах бывшего СССР известно более 1000 видов чехлоносок, среди которых вредители сельскохозяйственных культур, лесных и плодовых деревьев и пастбищных растений. У саксаула встречаются следующие виды чехлоносок, обитающих на саксауле: *Characia haloxyli (Flkv).), Coleophora*

captiosa (Flkv.), Ionescumia saxauli (Flkv.), Casignotella gallivora (Flkv.), Coleophora galligena, Coleophora calligoni.

В результате наших исследований, проведенных в пустынных регионах Юго - Восточного Казахстана, встречаются 2 вида чехлоносок, обитающих на саксауле, которые питаются преимущественно генеративными и вегетативными органами саксаула. Получены сведения об особенностях их биологического развития, питательной связи и вредоности. Для фенологического развития и борьбы с массовыми видами были определены стадии их оптимального развития.

Ключевые слова: саксаул, насекомые, чехлоноски, насекомые-вредители, чешуекрылые.

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EXPERIMENTAL RESEARCH FOR TECHNOLOGICAL PREPARATION OF ARTEMIA (ARTEMIA) ARTIFICIAL CULTIVATION IN SALT LAKES

Abstract. An integral part of the technological preparation of artificial cultivation of brine shrimp in saline water is a set of preliminary experimental work to assess the quality of cysts. It has been shown that during the winter period, activation of Artemia cysts occurs from the initial hatching values of 5-10 % to 72-99 %. The most optimal salinity range for hatching nauplii is a salinity of 20-30 g/l. With an increase in salinity above these indicators, hatching decreases. The size of hatching of Artemia depends on the salinity of a natural reservoir. In reservoirs with salinity of 50-80 g / l, higher hatching rates were obtained than with salinity of 150-160 g/l. Higher hatching rates are observed when using natural lake water for incubation. During incubation of cysts in a standard solution and fixed salinity and temperature conditions, the development rate of various stages of nauplii from the beginning of the opening of cysts (breaking stage) and pre-nauplius to active nauplii is shown. After 1.5–2 h after the mass appearance of pre-nauplii, they completely change into the nauplius stage.

Key words: Artemia, cysts, nauplii, hatching, salinity.

The valuable crustacean *Artemia parthenogenetica Barigozzi 1974* (*Anostraca*, *Artemiidae*) inhabits the salt lakes located on the territory of the Irtysh plain and the Kazakh Uplands [1].

Depending on the water content of the year in lakes with different salinity, 1 to 4 generations are born. Significant variability of climate and water regime is reflected in the species diversity of aquatic organisms, forage availability, productivity, and, as a consequence, in the volumes of cysts extraction. In order to maintain a stable state of Artemia populations in lakes under the conditions of changing environmental factors, there is a need to carry out measures to artificially increase their numbers and create favorable conditions for the reproduction and development of crustaceans.

Currently, there are a number of methods and technologies for artificially increasing the productivity of salt lakes. At the same time, it is proposed to use incubation workshops, special pools and artificial ponds for obtaining juveniles or adult crustaceans [2,3,4,5,6,7]. At the same time, a very promising direction is obtaining of planting material of different ages directly in the lake without using incubation equipment.

To carry out work on experimental reservoirs as part of the technological preparation for the production of juvenile Artemia, a number of laboratory studies was carried out. The material for the experiments was collected in salt ponds of Pavlodar region during expedition trips. This report presents the results of experimental work carried out using artemia cysts collected in lakes with different salinity during the period from March to October.

Analysis of cyst samples from various lakes showed that in the fall thick-celled cysts have a low percentage of hatching nauplii. During the winter period, cysts are activated and in spring the eggs reach a high degree of maturation, hatching reaches 72-99 % (figure 1).

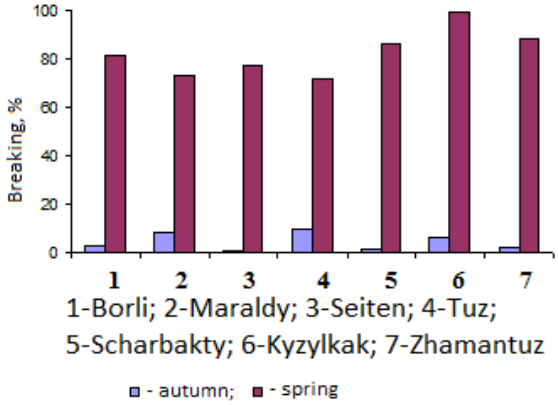

Figure 1 – Breaking of Artemia nauplii in different seasons

Carrying out special works on the activation of cysts from various reservoirs allows you to select Artemia strains with high maturation rates (size, efficiency, production and hatching rate) for use in growing processes.

Due to the fact that the lakes have different salinity values, it is advisable to find out the optimal salinity range for hatching nauplii. Laboratory studies in incubation media with artificial salinity (water + NaCl + NaHCO3) and with cysts collected from lakes with different salinity showed that the highest hatch rates are observed within the salinity of 20-30 g / l (table 1). With an increase in salinity above these indicators, hatching decreases.

Table 1 – Hatching of Artemia nauplii with different salinity of the artificial environment

Salinity of lake water, g / l	Salinity, g / l				
	20	30	50	60	70
50	82±1,3	84±1,2	68±8,7	24±1,5	8±0,9
80	66±4,8	70±1,2	35±3,5	26±0,3	14±4,1
150	32±3,5	29±1,5	3±0	1,8±0,8	0
160	39±2,0	30±2,1	8±0,9	4,5±1,5	0,06±0,01

At the same time, the experiment showed that the hatching rate of Artemia depends on the salinity of the natural reservoir from which the cyst sample was extracted. So, cysts collected in less saline lakes (50-80 g / l) had higher hatching rates than cysts from a reservoir with salinity of 150-160 g / l (figure 2). Thus, obtaining such preliminary data will allow you to plan the collection of material for use in technological processes of cultivation, taking into account the salinity of the mother lake.

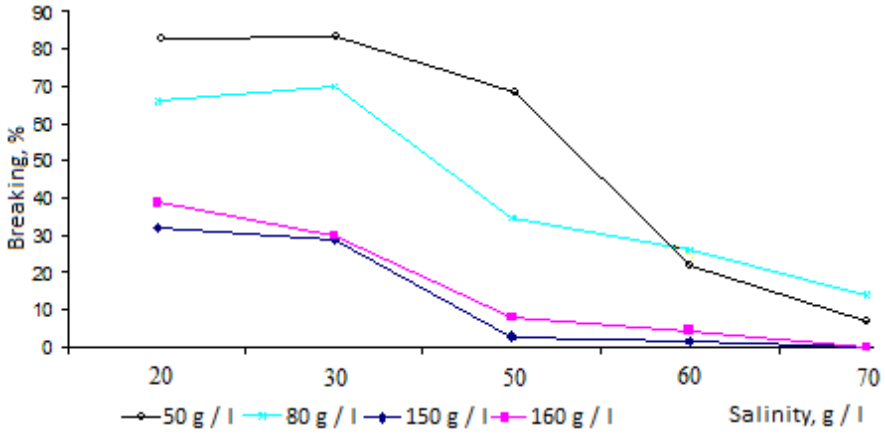

Figure 2 − Breaking of nauplii from lakes with different salinity in different incubation environments

Due to the fact that the artificial medium used in the experiments differs from natural waters in chemical composition, an experiment was conducted to assess the effect of natural water on the hatch rate. The experiments used natural water from Lake Axor (salinity during the season 55-85 g / l, pH 8.5, chloride water, type II). The results of the experiments showed that when using natural water from Lake Axor for incubation (it was diluted to the required concentration), a similar tendency for hatching to decrease with increasing salinity was observed. In the experiments, the number of embryos that left the cyst and hung under an empty shell was separately taken into account (the inner membrane, still attached to the shell – the «parachute» stage). In natural water, hatching at high salinity was higher than in artificial solution (table 2). The number of «parachutes» with increasing salinity of the solution also increases, which indicates a decrease in the rate of hatching in more salty water and the need for a longer time to rupture the egg shell and release the embryo.

Table 2 – Change in the amount of hatching nauplii and «parachutes» in various incubation media, %

Salinity, g / l	Standard solution		Water from Axor lake	
	hatching	«parachutes»	hatching	«parachutes»
20	82±1,3	0,0	75±2,5	2,5±0,2
50	68±8,7	6,2±1,5	59±14,5	5,6±1,6
60	24±1,5	21,3±5,1	35±4,0	17,9±2,8
70	8±0,9	12,7±2,5	34±1,0	6,9±0,1
80	–	–	40±13,0	10,8±0,2

In order to quickly assess the rate of hatching of nauplii during the observation of the incubation process, an experiment was carried out (salinity 20 g / l, 20-22 °C, activation of 3% H_2O_2) with constant fixation of the time of appearance of «parachutes», pre-nauplii and nauplii. According to its results, periods of the appearance of postembryonic stages of development of the crustacean were revealed: 1.5 hours after the beginning of the opening of the cysts (breaking stage), the first «parachutes» appeared, which, after 40 minutes, began to separate and go into the stage of pre-nauplius (figure 3). Over the next hour, pre-nauplii pass into the stage of active nauplii. After 1.5–2 h after the mass appearance of pre-nauplii, their complete transition to the nauplius stage occurs.

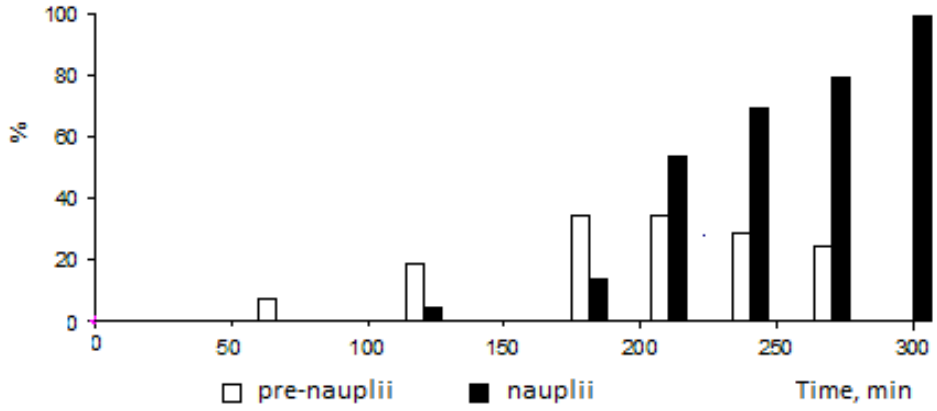

Figure 3 − Dynamics of changes in the initial stages of nauplii development

Thus, the conducted experimental studies indicate that in technological preparation for the cultivation of brine shrimp in salt lakes, it is necessary to conduct laboratory studies of the quality of the cysts used, take into account the influence of salinity of water on the hatching rate of brine shrimp, and select strains of brine shrimp that are most tolerant to the chemical composition of the recipient reservoir water.

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ТҰЗДЫ КӨЛДЕРДЕ АРТЕМИЯНЫ (*ARTEMIA*) ЖАСАНДЫ ЖОЛМЕН ӨСІРУДІ ТЕХНОЛОГИЯЛЫҚ ДАЙЫНДАМА ҮШІН ЭКСПЕРИМЕНТАЛДЫ ЗЕРТТЕУЛЕР

Аннотация. Ертіс жағалауы мен қазақтың ұсақ шоқысы аумақтарында орналасқан тұзды көлдерде Artemia parthenogenetica Barigozzi 1974 бағалы шаяны мекендейді. Шаянның биологиялық және экологиялық сипаттамалары климаттың және су режимінің өзгеруіне айтарлықтай тәуелді.

Артемия популяцияларының жағдайын тұрақты ұстау мақсатында көлдерде шаянды жасанды жолмен молықтыру бойынша іс-шаралар жүргізу қажет.

Тұзды көлдерде артемияны жасанды өсірудің технологиялық дайындығының құрамдас бөлігі шаян цисталарының сапасын бағалау бойынша алдын ала эксперименттік жұмыстар кешені болып табылады. Қыс кезеңі кезінде артемия цисталарының белсенділігі туылудың бастапқы мөлшерлерінен 5-10%-дан бастап 72-99%-ға дейін көрсетілген. Әртүрлі су қоймаларынан цисталарды белсенділендіру бойынша жұмыстарды жүргізу оларды технологиялық өсіру үрдістерінде қолдану үшін артемия штамдарын таңдауға мүмкіндік береді.

Науплиустардың туылуы үшін тұздылықтың аса тиімді шегі 20-30 г/л болып табылатын тұздылық. Осы көрсеткіштерден тұздылықтың артуымен туылымның төмендеуі жүреді.

Артемия туылымының мөлешері табиғи су қоймасының тұздылығына тәуелді. Тұздылығы 150-160 г/л су қоймаларына қарағанда, тұздылығы 50-80 г/л болатын су қоймаларында туылымның аса жоғары көрсеткіштері алынды.

Тәжірибеде қолданылатын жасанды орта химиялық құрамы бойынша табиғи су қоймаларынан ерекшеленеді, осыған байланысты туылымның көрсеткішіне табиғи судың әсер етуін бағалау үшін тәжірибе жүргізілді. Тәжірибеде Ақсор көлінен әкелінген су қолданылды (маусым кезінде тұздылық мөлшері 55-85 г/л, pH 8.5, су хлоридті, II типті). Жүргізілген зерттеулердің нәтижелері Ақсор көлінен әкелінген табиғи суды инкубацияға қолданған кезде, тұздылықтың артуымен туылымның төмендеуінің ұқсас үрдісі байқалды.

Тәжірибелерде цистадан шыққан ұрықтардың саны мен бос қабықшаның астында аспалылардың (әлі қабықшаға жабысқан ішкі мембрана – «парашют» сатысы) мөлшерлері жеке есептелді.

Табиғи суда туылымның мөлшері тұздылықтың жоғары мөлшерлері кезінде жасанды ерітіндіге қарағанда жоғары болды. Ерітіндінің тұздылық мөлшерінің жоғарлауымен «парашюттердің» мөлшері де ұлғаяды, бұл тұздылығы аса жоғары суда туылым қарқындылығының төмендеуін және жұмыртқаның қабығын жару мен ұрықтың босатылуына аса ұзақ уақыт қажет екенін дәлелдейді. Цисталардың стандартты ерітінді мен тұздылық пен температураның тұрақтандырылған шарттарда инкубациясы кезінде цисталардың ашылуынан (breaking stage) бастап, алды-науплиустар (pre-nauplius) мен белсенді науплиустарға дейін науплиустар дамуының әртүрлі кезеңдер қарқындылығы көрсетілген. Алды-науплиустардың жаппай пайда болуынан 1,5-2 сағаттан соң олардың науплиус деңгейіне өтуі жүреді.

Түйін сөздер: артемия, цисталар, науплиустар, туылым, тұздылық.

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ЭКСПЕРИМЕНТАЛЬНЫЕ ИССЛЕДОВАНИЯ ДЛЯ ТЕХНОЛОГИЧЕСКОЙ ПОДГОТОВКИ ИСКУССТВЕННОГО ВЫРАЩИВАНИЯ АРТЕМИИ (*ARTEMIA*) В СОЛЕНЫХ ОЗЕРАХ

Аннотация. В соленых озерах, расположенных на территориях Прииртышской равнины и Казахского мелкосопочника, обитает ценный рачок *Artemia parthenogenetica* Barigozzi 1974.

Биологические и экологические характеристики рачка в значительной степени зависят от изменчивости климата и водного режима. С целью поддержания стабильного состояния популяций артемии в озерах существует необходимость в проведении мероприятий по искусственному воспроизводству рачка.

Составной частью технологической подготовки искусственного выращивание артемии в соленых озерах является комплекс предварительных экспериментальных работ по оценке качества цист рачка. Показано, что в течение зимнего периода происходит активация цист артемии с начальных осенних величин выклева 5-10% до 72-99% весной. Проведение работ по активации цист из различных водоемов позволяет подбирать штаммы артемии для использования их в технологических процессах выращивания. Наиболее

оптимальным диапазоном солености для выклева науплиусов являет соленость 20-30 г/л. С увеличением солености выше этих показателей происходит снижение выклева. Величина выклева артемии зависит от солености природного водоема.

В водоемах с соленостью 50-80 г/л получены более высокие показатели выклева, чем с соленостью 150-160 г/л. Искусственная среда, используемая в экспериментах, отличается от природных вод по химическому составу и поэтому был проведен эксперимент для оценки влияния природной воды на показатель выклева. В опытах использовалась природная вода из озера Аксор (соленость в течение сезона 55-85 г/л, pH 8.5, вода хлоридная, II тип).

Результаты проведенных экспериментов показали, что при использовании для инкубации природной воды из озера Аксор наблюдалась сходная тенденция снижения выклева с увеличением солености. В опытах отдельно учитывали и количество эмбрионов покинувших цисту и висящих под пустой оболочкой (внутренняя мембрана, еще прикрепленная к оболочке − стадия «парашюта»). В природной воде величина выклева при высоких показателях солености, был выше, чем в искусственном растворе. Количество «парашютов» с увеличением солености раствора также увеличивается, что свидетельствует о снижении темпа выклева в более соленой воде и необходимости при этом более продолжительного времени для разрыва оболочки яйца и освобождения эмбриона.

При инкубации цист в стандартном растворе и фиксированных условиях солености и температуры показан темп развития различных стадий науплиусов от начала раскрытия цист (breaking stage) и пред-науплиусов (pre-nauplius) до активных науплиусов.

Спустя 1.5-2 ч после массового появления пред-науплиусов происходит их полный переход в стадию науплиуса.

Ключевые слова: артемия, цисты, науплиусы, выклев, соленость.

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CHANGES OF VERTEBRATE FAUNA IN GREEN AREAS OF ALMATY CITY DUE TO THE URBANIZATION

Abstract. Currently, there are serious changes in the environment in Almaty due to the accentuated urbanization processes. The fauna of wild-living vertebrates of the city is experiencing serious stress pressure in this regard, which forces the animals to adapt to new conditions or leave this territory. The last fundamental research on the species composition of the city's fauna was conducted about 3 decades ago, and therefore there is a necessity for repeated research. The aim of the research is to identify patterns of the vertebrates species composition formation within some Park zones of the southern part of Almaty in the context of the last 30 years. The main methods used in the study are route records of vertebrate fauna and bioindication. An analysis of the data from the research centers, as well as the authors' own bio-indicative studies, revealed an unfavourable state of environmental quality. Based on data from the own records (from February to December), it can be concluded that the species diversity of Almaty fauna has decreased or has undergone a considerable territorial redistribution since the end of the twentieth century.

Key words: fauna, vertebrates, birds, Almaty, urbanization, green zones, pollution.

Introduction. The animal component is most susceptible to dynamic changes under the influence of external factors, and in urban conditions [1], where there is a high degree of mosaic of landscapes, a lower level of ecological sustainability of ecosystems, as well as many other specific environmental conditions, processes occurring inside animal populations differ significantly in intensity from natural, and animals are even more sensitive to environmental factors than they are under natural conditions. Until the middle of the 20th century, the city of Alma-Ata was mainly occupied by one-story buildings, abundantly alternating garden and parking spaces. Now the main part of the territory of Almaty, especially this concerns the central districts, is occupied by multi-story new buildings. The area of the green areas has declined sharply. To date, the area of green plantations is as high as 4.8 m^2 per person at a rate of 13 m^2 (not less than 10m^2) [2,3] and this indicator continues to decrease. Negatively affect the quantity and species diversity of vertebrates not only insufficient array of woody vegetation, but also the violation of the level of park plantations. Recently, the number of shrubby and herbaceous plant species that served as a shelter and food source for many wild animals has sharply decreased within the city.

In the case of Almaty, the mosaic and characteristic features of the habitats included are the most pronounced because of the nature of the urban development that has been historically established, as well as the natural conditions of the area. Also, every urban environment is more or less zoned from the central to the periphery. Different combinations of these conditions lead to the formation of specific zoocenoses in selected areas of the city. In this regard, in an urban landscape, it is most appropriate to use route methods for registering animals, which allows taking into account the difference in biotopes and the spatial distribution of organisms. Bioindication methods are also used in this work. Data from chemical and environmental analyses do not provide objective data on the impact of environmental quality on living organisms, in contrast to biotesting methods that take into account the direct reactions of organisms to environmental factors.

The main purpose of our research was to determine some faunistic changes in wild birds, amphibians, reptiles and mammals in certain green areas of the Almaty city in response to the growing urbanization of the environment. The objectives were:

- To study the development of the urban landscape and its socio-economic and environmental characteristics;
- To clarify the modern species composition of bird fauna, amphibians, reptiles and mammals in the green areas of Almaty;
- Identify possible causes of changes in the population of vertebrate fauna within the green zones of southern Almaty.

Material and Methods. The studies were conducted in 2019, from 24 January to 20 December on the territory of the Main Botanical Garden of Almaty (hereinafter – MBG), the Park of the First President, the Gandhi Park, Park of the 28 Panfilovs Guards. In the MBG area studies were conducted from February to June 2010. There were 116 counts in total (44 of them were conducted in MBG). The length of the routes was 5 km in the MBG, 1.52 km in the park of 28 Panfilovs Guards, 0.88 km in Gandhi Park, 4 km in the Park of the First President. Periodicity of counting was 1-2 times a week for 40-180 minutes. All counts were made in the morning, mostly from 9.00 to 12.00. In the course of the study, the authors used the following methods:

1. Route method of bird population accounting;
2. Observation of behavioral features of birds on model areas;
3. Route method of accounting for amphibians and reptiles;
4. Route method of accounting for mammals;
5. The method of bioindication by measuring fluctuating asymmetry.

The method of route-count is as follows. The recorder moves along the route and marks all members of the counting class that he sees or hears. For each encounter, the species, the number of individuals met and the distance from the record-keeper to the animal at the moment of detection shall be indicated. In addition, the starting and ending times and distance travelled are noted. Weather conditions, characteristics of biota are also recorded [4].

The bio-indication method by measuring the fluctuating asymmetry consists in measuring the asymmetry of the width of the sheet or the length of the hull on the right and left sides [5,6]. Then, using the formula (1) given in the text of the article, the asymmetry coefficient is calculated and the pollution level is determined by comparison with the table values.

Results. The structure of the biotopes of the city is very heterogeneous, with different architectures, nature and density of the greenery, presence of water bodies, etc. The natural landscapes adjacent to the city's boundaries are also very different from each other. From the south side, which has been studied, the pre-mountain areas with tree and shrub vegetation predominate.

In the history of the formation of the city, researchers distinguish three main periods [7]. Having traced the history of Almaty urban architecture, construction trends and landscape changes, there is a visible movement from a military settlement to a large metropolis. And during the period of its development, the city has undergone a wave-shaped change in the living conditions for wildlife, sometimes for the worse or for the better from the middle of the XVIII century to the present day [8-11]. Accordingly, over three quarters of a century, the population of the city reached 952,000, and since then has increased by 2 times (to 1,854,656 people) [12]. Today, we can talk about the beginning of a new, fourth stage of urban transformation, which is characterized by a significant increase in the anthropogenic load on the landscape. First of all, we should note the significant advance of the city's borders to the South and the inclusion of the territories of mountain stalls in its composition [13]. In this regard, there is a further displacement of wild fauna from natural habitats. The height of residential, industrial and other buildings has increased significantly. Also, due to the increase in the density of the city's population, the appearance of a large number of private vehicles and housing plots, the increase in the capacity of thermal power plants and boiler houses that provide the city with heat and electricity, the level of physical (noise, electromagnetic, vibration and light) and chemical pollution of the environment continues to grow. In the bulletins of "Kazhydromet" on the state of the environment, Almaty always has the status of a city with a very high level of atmospheric pollution [14]. According to the National center of expertise dated November 22, 2019 [15], as a result of planned laboratory monitoring of the atmosphere in Almaty, the MPC was found to exceed many substances (in 431 samples out of 1,576), including NO_2 by 2.2 times,

SO_2 by 1.2 times, and CO by 1.4 times. According to the mayor's office of Almaty, in 2019, the volume of emissions of pollutants into the atmosphere amounted to 123 thousand tons, and API_5 ($ИЗА_5$) ranges between 7-9 units and higher [14-16]. Data from research centers confirm the authors' own research based on the study of fluctuating asymmetry of plant leaves – an indicator used for monitoring environmental quality not only by chemical indicators, but also in connection with its impact on biological systems [17]. Fluctuating asymmetry is random deviations from the ideal symmetry of plants, caused, among other things, by negative deviations from the norm in the quality of the environment.

For this study, 10 leaves were selected from 7 trees of the birch (*Betula spp.*) from different parts of the city. The following parameters were measured for the research: width of half of the leaf; length from the base of the second vein of the second order; the distance between the bases of the first and second veins of the second order (each side); distance between the ends of the first and second veins of the second order; the angle between the main vein and the second vein from the base of the second order.

The leaf asymmetry values were calculated. For this purpose, an integrative indicator showing the average relative difference per topic was found using formula (1):

$$X = \frac{\sum Z}{n} = \frac{Z_1 + Z_2 + \cdots Z_n}{n} \quad (1),$$

where, X – degree of asymmetry of the organism; Z – the average relative difference between the sides per feature of each leaf; n - is the number of leaves.

To determine the quality of atmospheric air, the values were compared with table data for deviations from the norm. To determine the quality of the atmosphere by fluctuating asymmetry, a five-point scale was developed, in which 1 point is a conditional norm, and 5 points is a critical state. Based on the results of the analysis, it can be concluded that the Central and densely populated areas of the city are subject to extremely serious anthropogenic pressure. The calculation results are shown in table 1.

Table 1 – Results of rapid assessment of the state of the environment by bioindication

Sampling location	Indicator of average relative asymmetry per sample	Point	Characteristics of pollution
Timiryazev street, KazNU	0.231	5	Critical condition
s / t Dzerzhinsky	0.022	1	A conditional norm
Kalkaman microdistict	0.035	1	A conditional norm
Koktem 2 microdistict (Park)	0.03	1	A conditional norm
Sairan lake	0.061	3	Dirty
Vesnovka, Bukhar Zhyrau street	0.041	2	Contaminated
Ozhet microdistict	0.12	5	Critical condition

By the end of the last century (1980-1990), about 185 species of birds (including nesting, wintering, migratory and flying species) were regularly recorded in Almaty. Of these, the most common in the spring was a Collared Dove, the Laughing Dove, Pheasant, Great Spotted Woodpecker, Masked Wagtail, Blackbird, Great Tit, Starling, Magpie, Tree and House sparrows, Greenfinch, Chiffchaff and others [8].

In the spring of 2005, the following species were recorded in the territory of the city: Peregrine Falcon, Laughing Dove, Tree Pipit, Masked Wagtail, Isabelline Red-tailed Shrike, Common Mynah, Lesser Whitethroat, Chiffchaff, Stonechat, Blue-headed Redstart, Bluethroat, Blackbird, Great tit, House Sparrow, Chaffinch, Greenfinch [18].

Currently, the study of such green areas of the city as the main Botanical garden of Almaty, the Park of 28 Panfilov guards, the Park of the first President did not reveal a significant number of previously ordinary representatives of the city's avifauna. So, when in the 80 - 90s the spring population of green zone birds numbered 38 species (March-27 species) [8], according to studies of 2019, 18 species were registered in March, 15 in April and 19 in May: mallard (*Anas platyrhynchos*) – March-April; marsh harrier (*Circus aeruginosus*) – March, single occurrence; common buzzard (*Buteo buteo*) – March; pheasant (*Phasianus colchinus*); Wood Sandpiper (*Tringa glareola*) – April, single occurrence; Common Mynah (*Acridotheres tristis*); Woodpigeon (*Columba palumbus*) – April-May; Rock Dove (*Columba livia*); Collared Dove (*Streptopelia decaocto*); Swift (*Apus apus*) – May; Magpie (*Pica pica*); rook

(*Corvus frugilegus*) – March; Carrion Crow (*Corvus corone*); Hooded Crow (*Corvus cornix*) – March; Syke's Warbler (*Hippolais rama*) – May; Chiffchaff (*Phylloscopus collybitus*) – April-May; Blackbird (*Turdus merula*); Coal Tit (*Parus ater*); Great tit (*Parus major*); Grey tit (*Parus bokharensis*); House Sparrow (*Passer domesticus*); chaffinch (*Fringilla coelebs*) – March-April; Brambling (*Fringilla montifringilla*) – March; Red-fronted Serin (*Serinus pusillus*) – March; Greenfinch (*Chloris chloris*) – May; Siskin (*Spinus spinus*) – May; Scarlet Rose Finch (*Carpodacus erythrinus*) – May.

The summer population of birds is represented by 31 species based on the results of surveys conducted in the model plots: Mallard (*Anas platyrhynchos*), Common Buzzard (*Buteo buteo*), Pheasant (*Phasianus colchinus*), Woodpigeon (*Columba palumbus*), Stock Dove (*Columba oenas*), Turtle Dove (*Columba livia*), Collard Dove (*Streptopelia - decaocto*), Long-eared owl (*Asio otus*), Swift (*Apus apus*), hoopoe (*Upupa epops*), House Martin (*Delichon urbica*), white wagtail (*Motacilla alba*), masked wagtail (*Motacilla personata*), Isabelline Red-tailed Shrike (*Lanius isabellius*), Mynah (*Acridotheres tristis*), magpie (*Pica pica*), rook (*Corvus frugilegus*), Carrion Crow (*Corvus corone*), Whitethroat (*Sylvia communis*), Lesser Whitethroat (*Sylvia curruca*), Chiffchaff (*Phylloscopus collybitus*), Spotted Flycatcher (*Muscicapa striata*), Black Redstart (*Phoenicurus ochruros*), blackbird (*Turdus merula*), Coal tit (*Parus ater*), Azure tit (*Parus caeruleus*), Great tits (*Parus major*); house sparrow (*Passer domesticus*), greenfinch (*Chloris chloris*), siskin (*Spinus spinus*), Scarlet Rose Finch (*Carpodacus erythrinus*).

During the autumn surveys 22 species were recorded: Mallard (*Anas platyrhynchos*), Common Buzzard (*Buteo buteo*), Mash Harrier (*Circus aeruginosus*), Hobby (*Falco subbuteo*), Lesser Kestrel (*Falco naumanni*), pheasant *(Phasianus colchinus*), Woodpigeon (*Columba palumbus*), Turtle dove (*Columba livia*), Collard dove (*Streptopelia decaocto*), Mynah (*Acridotheres tristis*), Magpie (*Pica pica*), rook (*Corvus frugilegus*), Carrion crow (*Corvus corone*), Hooded crow (*Corvus cornix*), Lesser Whitethroat (*Sylvia curruca*), Chiffchaff (*Phylloscopus collybitus*), Goldcrest (*Regulus regulus*), Spotted flycatcher (*Muscicapa striata*), Blackbird (*Turdus merula*), Coal tit (*Parus ater*), Great tit (*Parus major*), house sparrow (*Passer domesticus*).

Table 2 – Results of counting the number of birds in the Botanical garden, 2019.

Birds species	Number (unit)				
	February	March	April	May	June
Magpie	36	71	56	62	66
Great tit	68	76	52	57	58
House Sparrow	–	23	20	24	27
Blackbird	21	18	27	27	25
Woodpigeon	–	–	13	10	11
Chiffchaff	~20	~20	~20	~20	~20
Mynah	–	–	–	8	12
Pheasant	–	–	–	5	8

Among other classes of vertebrates, there is much less species diversity in the study areas. A total only 5 species of wild–living mammals and 1 species of reptiles were recorded using route records: Central Asian (steppe) turtle (*Testudo horsfieldi Gray*); Weasel (*Mustela nivalis*), Shrew (*Sorex araneus*), House mouse (*Mus musculus*), grey rat (*Rattus norvegicus*), Squirrel (*Sciurus vulgaris*). Amphibians were not found in the parks. At the same time, in the period of 1980–1990, scientists of the Institute of Zoology registered 10 species of reptiles and 3 species of amphibians on the territory of Almaty: Green toad (*Bufo viridus Laur.*) lake frog (*Rana ridibunda Pall.*), Siberian frog (*Rana amurensis Boul.*), colorful lizard *(Eremias argute Pall.*), fast lizard (*Eremias velox Pall.*), *Asymblepharus alaicus Elpatjewsky,* dice snake (*Natrix tessellate Laur.*), grass snake (*Natrix natrix L.*), *Agkistrodon halys Pall.*, steppe viper (*Vipera ursini Bonap.*), patterned skid (*Elaphe dione Pall.*), *Psammophis lineolatum Brandt.*

According to studies conducted in European cities in the early 1980s, amphibians in the urban environment are more susceptible to death as a result of anthropogenic factors. On roads at that time, about 50 % of all dead vertebrates were amphibians [19]. The result of anthropogenic impact in the case of batrachofauna is also a change in the quantitative ratio of species, location (where the main factor is the

xerification of the environment), the age composition of the population, as well as morphological characteristics of individuals [8].

Discussion. Among the potential reasons for the changes in the species diversity and population decline it is possible to indicate climate change, namely the increase the number of dry and hot days 1–3 every decade over the last seventy years, a decline in precipitation during the summer period, the increase in average annual temperature since 1950, a decrease in ice mass by 15–20 % [20]. Also, a significant impact is caused by the anthropogenic factor, which is manifested in an increase in technogenic pressure on the fauna, a reduction in diversity and area of green spaces, as well as violations of their tiers. An important aspect of the avifauna formation is a sufficient abundance of food and conditions necessary for the reproduction of populations, as well as features of the placement of animals in the spatial and temporal aspect [21]. According to our observations, the number of visitors to certain green areas also significantly affects the occurrence of birds.

Based on the data that was collected as a result of accounting (from February to December), we can conclude that the species diversity of the avifauna of Almaty has decreased in comparison with the end of the XX century. According to research in 1988:

– 37 species of birds were observed in the green (Park) areas of the city in winter: *Accipiter nisus, Falco columbarius, Phasianus colchinus, Streptopelia decaocto, Streptopelia senegalensis, Bubo bubo, Asio otus, Dendrocopos major, Picoides tridactylus, Acridotheres tristis, Pica pica, Corvus monedula, Corvus frugilegus, Corvus corone, Corvus cornix, Troglodytes troglodytes, Prunella atrigularis, Regulus regulus, Leptopoecile sophiae, Turdus atrogularis, Turdus pilaris, Turdus merula, Turdus viscivorus, Parus ater, Parus cyanus, Parus major, Passer domesticus, Passer montanus, Fringilla coelebs, Fringilla montifringilla, Serinus pusillus, Spinus spinus, Carduelis carduelis, Carpodacus rhodochlamys, Uragus sibiricus, Mycerobas carniceps*;

– up to 47 species of birds were observed in spring: *Phasianus colchinus, Streptopelia decaocto, Streptopelia senegalensis, Asio otus, Dendrocopos major, Sturnus vulgaris, Anthus trivialis, Motacilla alba, Motacilla personata, Acridotheres tristis, Pica pica, Corvus monedula, Corvus frugilegus, Corvus corone, Corvus cornix, Prunella fulvescens, Regulus regulus, Phoenicurus phoenicurus, Phylloscopus collybitus, Phylloscopus trochiloides, Phylloscopus inornatus, Phylloscopus griseolus, Phoenicurus erythrogaster, Luscinia svecica, Saxicola torquata, Phoenicurus caeruleocephalus, Phoenicurus erythronotus, Turdus atrogularis, Turdus merula, Turdus viscivorus, Parus ater, Parus cyanus, Parus major, Passer domesticus, Passer montanus, Fringilla coelebs, Fringilla montifringilla, Chloris chloris, Serinus pusillus, Spinus spinus, Carduelis carduelis, Carpodacus rhodochlamys, Uragus sibiricus, Mycerobas carniceps, Emberiza cia;*

– the summer population was represented by 45 species: *Milvus migrans, Accipiter nisus, Falco subbuteo, Falco tinnunculus, Phasianus colchinus, Crex crex, Streptopelia decaocto, Streptopelia turtur, Streptopelia orientalis, Streptopelia senegalensis, Cuculus canorus, Otus scops, Coracias garrulus, Merops piaster, Upupa epops, Hirundo rustica, Hirundo daurica, Delichon urbica, Motacilla cinerea, Motacilla personata, Lanius collurio, Lanius minor, Oriolus oriolus, Acridotheres tristis, Pica pica, Acrocephalus dumetorum, Passer montanus, Sylvia nisoria, Sylvia communis, Sylvia curruca, Phylloscopus collybitus, Phylloscopus trochiloides, Muscicapa striata, Luscinia luscinia, Turdus merula, Remiz pendulinus, Parus cyanus, Parus major, Passer domesticus, Chloris chloris, Carduelis carduelis, Carduelis caniceps, Carpodacus erythrinus, Emberiza bruniceps;*

– and the autumn population – 46 species: *Accipiter nisus, Falco tinnunculus, Phasianus colchinus, Columba palumbus, Streptopelia decaocto, Streptopelia orientalis, Streptopelia senegalensis, Merops apiaster, Dendrocopos major, Hirundo rustica, Motacilla cinerea, Motacilla personata, Sturnus vulgaris, Acridotheres tristis, Pica pica, Corvus monedula, Corvus frugilegus, Corvus corone, Corvus cornix, Prunella atrigularis, Phylloscopus collybitus, Phylloscopus trochiloides, Phylloscopus inornatus, Regulus regulus, Muscicapa striata, Phoenicurus erythronotus, Luscinia svecica, Turdus atrogularis, Turdus viscivorus, Remiz pendulinus, Parus ater, Parus cyanus, Parus major, Passer domesticus, Coracias garrulous, Passer montanus, Fringilla coelebs, Fringilla montifringilla, Serinus pusillus, Chloris chloris, Carduelis carduelis, Carduelis caniceps, Carpodacus erythrinus, Uragus sibiricus, Mycerobas carniceps, Emberiza cia*

According to the results of our surveys we can conclude that the habitat conditions of the above–mentioned representatives of the avifauna have changed, which has led to their disappearance, or a sharp

reduction in the number within urban areas, or a redistribution of habitats within the city. It should be borne in mind, however, that the author's research does not cover all the green areas of the city, based on which it is impossible to draw an unambiguous conclusion about the Park areas of the city as a whole. These studies need to be supplemented with materials from studies of ornithologists (as well as specialists in other classes of vertebrates) and birdwatchers. It is important to note that only 2–5 km South of the upper observation site (the first President's Park) there are already species that were not marked by the author of the work in the model areas (Grey Goldfinch(*Carduelis caniceps)*, Waxwing(*Bombycilla garrulus*), Scops Owl (*Otus scops)*, Roller (*Coracias garullus*), Black Kite (*Milvus migrans*), Rufous Turtle Dove (*Streptopelia orientalis*), Golden Jackal(*Canis aureus*), European Badger (*Meles meles*), Alaian Lidless Skink (*Asymblepharus alaicus*), frogs (*Ranidae*), etc.), which suggests the presence of significant anthropogenic pressure on the species composition of the fauna.

Thus, at this stage of research, we concluded that the active processes of urbanization, reflected in the increase in the number and density of population of the city, the deterioration of environmental quality, as well as changing quantitative and qualitative indicators existing parks have a significant negative impact on the modern condition of fauna in Almaty.

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УРБАНИЗАЦИЯҒА БАЙЛАНЫСТЫ АЛМАТЫ ҚАЛАСЫНЫҢ ЖАСЫЛ АЙМАҚТАРЫНДАҒЫ ОМЫРТҚАЛЫ ЖАНУАРЛАР ФАУНАСЫНЫҢ ӨЗГЕРУІ

Аннотация. Бұл мақалада урбанизация процестерінің Алматы қаласының кейбір жасыл аймақтарында фауна сипаттамаларының өзгеру динамикасына әсері қарастырылады, атап айтқанда, Алматы қаласының Бас ботаникалық бағы, 28 гвардиялық–панфиловшылар паркі, Тұңғыш Президент саябағы. Мақалада қоршаған ортаның ластануы, дәлірек атмосфералық ауаның ластануы және оның құстар мен басқа да жануарлардың қауымдастығына әсері де қозғалады.

Мұндай экожүйелердің қалыптасу және жұмыс істеу процестерін зерттеу қазіргі экологияның ең өзекті мәселелеріне жатады. Зоологиялық элемент сыртқы факторлардың әсерінен динамикалық өзгерістерге ұшырайды, ал қала жағдайында ландшафтардың мозайкалық деңгейінің жоғары болуы, экожүйелердің экологиялық тұрақтылығының төмен деңгейі, сондай–ақ ортаның басқа да ерекше жағдайлары, популяцияның Жануарлар ішінде өтетін процестер табиғи жағдайлардан қарқындылығы жағынан үлкен жағына қарай ерекшеленеді және жануарлар табиғи жағдайларға қарағанда ортаның сыртқы факторларының әсеріне аса сезімталдық танытады.

Жұмыстың мақсаты соңғы 30 жылда Алматы қаласының оңтүстік бөлігінің кейбір саябақ аймақтары шегінде омыртқалы жануарлардың түрлік құрамын қалыптастыру заңдылықтарын анықтау болып табылады. Зерттеу барысында келесі міндеттер шешілді: 1) қалалық ландшафттың даму процестерін және оның әлеуметтік–экономикалық және экологиялық сипаттамаларын зерттеу; 2) Алматы қаласының жасыл аймақтарының аумағында мекендейтін құстар, амфибиялар, рептилиялар және сүтқоректілер фаунасының қазіргі заманғы түр құрамын нақтылау; 3) Алматы қаласының оңтүстік бөлігінің жасыл аймақтары шегінде омыртқалы жануарлар фаунасының өзгеруінің мүмкін себептерін анықтау.

Зерттеу жүргізу барысында авторлар келесі әдістерді пайдаланды:

1. Құстарды есепке алудың маршруттық әдісі.
2. Амфибияларды есепке алудың маршруттық әдісі.
3. Сүтқоректілерді есепке алудың маршруттық әдісі.
4. Флуктуирлеуші асимметрияны өлшеу жолымен биоиндикация әдісі.

Омыртқалы жануарларды есепке алу 2019 жылдың қаңтар айынан желтоқсан айына дейін Алматы қаласының Бас ботаникалық бағында, Тұңғыш Президент саябағында, 28 гвардияшы–панфиловшылар атындағы саябағында, Ганди саябағында жүргізілген. Ауа сапасына биологиялық тестілеу жүргізу үшін материалдарды іріктеу қаланың орталық аудандарына қатысты автомагистральдарға және географиялық

бөлуге жақындық белгісі бойынша сараланған қала аумағындағы 7 нүктеде жүргізілді. Атмосфера сапасын анықтауына ресми зерттеу деректері пайдаланылды.

Жүргізілген есептер түрлік әртүрліліктің төмендеуін (модельдік учаскелер шегінде) анықтауға мүмкіндік берді, ол антропогендік престің үздіксіз күшеюіне байланысты Алматы қаласының омыртқалы жабайы фаунасының тұрақты мекендейтін жерлерінің қайта бөлінуіне байланысты болуы мүмкін, ол ортаның химиялық және физикалық ластануының шамасына, сондай–ақ қала халқының тығыздығы мен санының өсуіне байланысты. Сондай–ақ фауна сипаттамаларының өзгеру себептерінің бірі климаттық көрсеткіштердің өзгеруі болып табылады: соңғы жетпіс жыл ішінде әр онжылдықта құрғақ және ыстық күндер санының 1–3–ге артуы, жазғы кезеңде жауын–шашын мөлшерінің азаюы, орташа жылдық температураның артуы, 1950 жылмен салыстырғанда мұз массасының 15–20 %–ға төмендеуі. Сондай–ақ, жасыл желектердің алуан түрлілігі мен алаңын төмендету, сонымен қатар олардың қабаттылығын бұзу факторы елеулі әсер етеді, өйткені фаунаның қалыптасуының маңызды аспектісі тағамның жеткілікті молдығы және популяцияларды жаңғыртуға қажетті жағдайлар болып табылады. Авторлардың бақылаулары бойынша, сол немесе басқа да көгалдандырылған аймаққа келушілер саны да омыртқалылардың түрлі түрлерінің кездесулеріне айтарлықтай әсер етеді.

Осылайша, биоәртүрліліктің төмендеуінің қаланың урбанизация үдерістерінің қарқындауынан белгілі бір тәуелділігі анықталды. Бұл мәселе осы көрсеткіштерді корреляциялау факторларын одан әрі әзірлеуді және нақтылауды талап етеді.

Түйін сөздер: фауна, омыртқалылар, құстар, Алматы, урбанизация, жасыл аймақтар, ластану.

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ИЗМЕНЕНИЕ ФАУНЫ ПОЗВОНОЧНЫХ В ЗЕЛЕНЫХ ЗОНАХ ГОРОДА АЛМАТЫ В СВЯЗИ С УРБАНИЗАЦИЕЙ

Аннотация. В статье рассматривается влияние процессов урбанизации на динамику изменения характеристик фауны в некоторых зеленых зонах города Алматы таких, как главный ботанический сад г.Алматы, парк 28 гвардейцев–панфиловцев, парк Первого Президента. В статье также затрагивается тема загрязнения окружающей среды, а именно атмосферного воздуха и его влияние на сообщества птиц и других животных.

Исследование процессов формирования и функционирования таких экосистем относится к наиболее актуальным вопросам современной экологии. Зоологический элемент более всего подвержен динамическим переменам под влиянием внешних факторов, а в условиях города, где наблюдается высокая степень мозаичности ландшафтов, меньший уровень экологической устойчивости экосистем, а также многие другие специфические условия среды, процессы, протекающие внутри животных популяций значительно отличаются в большую сторону по интенсивности от естественных, и животные проявляют еще большую чувствительность к воздействию внешних факторов среды, чем в естественных условиях.

Целью работы является выявление закономерностей формирования видового состава позвоночных животных в пределах некоторых парковых зон южной части города Алматы в разрезе последних 30 лет. В ходе исследования решались следующие задачи: 1) изучить процессы развития городского ландшафта и его социально–экономических и экологических характеристик; 2) уточнить современный видовой состав фауны птиц, амфибий, рептилий и млекопитающих, обитающих на территории зеленых зон г.Алматы; 3) установить возможные причины изменений населения фауны позвоночных в пределах зеленых зон южной части г.Алматы.

В процессе проведения исследования авторами использовались следующие методы:

1. Маршрутный метод учета населения птиц;
2. Маршрутный метод учета амфибий и рептилий;
3. Маршрутный метод учета млекопитающих;

4. Метод биоиндикации путем измерения флуктуирующей асимметрии.

Учеты позвоночных животных проводились с января по декабрь 2019 года на территории Главного ботанического сада г. Алматы, парка Первого Президента, парка им. 28 гвардейцев–панфиловцев, парка Ганди. Отбор материала для проведения биологического тестирования качества воздуха производилось в 7 точках на территории города, дифференцированных по признаку приближенности к автомагистралям и географическому распределению относительно центральных районов города. Использованы данные официальных исследований качества атмосферы.

Проведенные учеты позволили выявить снижение видового разнообразия (в пределах модельных участков), которое, вероятно, вызвано перераспределением мест постоянного обитания дикоживущей фауны позвоночных г.Алматы в связи непрерывным усилением антропогенного пресса, который выражается в увеличении ровня химического и физического загрязнения среды, а также ростом плотности и численности населения города. Также одной из причин изменения характеристик фауны может служить изменения климатических показателей: именно увеличение количества сухих и жарких дней на 1–3 каждое десятилетие в течение последних семидесяти лет, сокращение количества осадков в летний период, увеличение среднегодовой температуры, снижение ледниковой массы на 15–20% по сравнению с 1950 г. По результатам анализа загрязнения атмосферного воздуха посредством биоиндикации и изучения данных различных ведомств, можно сделать вывод, что центральные и густонаселенные районы города подвергаются крайне серьезному антропогенному давлению. Также значительное воздействие оказывает фактор снижения разнообразия и площади зеленых насаждений, а также нарушений их ярусности, так как важным аспектом формирования фауны является достаточное обилие пищи и условий, необходимых для воспроизведения популяций. По наблюдениям авторов, количество посетителей тех или иных озелененных зон также значительно влияет на встречаемость различных видов позвоночных.

Таким образом, выявлена определенная зависимость снижения биоразнообразия от интенсификации процессов урбанизации города. Данный вопрос требует дальнейшей разработки и уточнения факторов корреляции данных показателей.

Ключевые слова: фауна, позвоночные, птицы, Алматы, урбанизация, зеленые зоны, загрязнение.

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Жуматов Кайнар Хамзаевич

20 февраля 2020 года на 66-м году жизни скоропостижно скончался известный ученый-вирусолог, доктор биологических наук, профессор, главный научный сотрудник ТОО «Научно-производственный центр микробиологии и вирусологии» Жуматов Кайнар Хамзаевич.

Жуматов К.Х. родился 10 ноября 1954 г. в г. Алмате. В 1977 г. он окончил биологический факультет Казахского государственного университета им. С.М. Кирова и был принят на работу в Институт микробиологии и вирусологии АН Казахской ССР на должность старшего лаборанта. В 1978-80 гг. Жуматов К.Х. прошел стажировку в Институте экспериментальной медицины АМН СССР в г. Ленинграде. В 1980 г. он поступил в аспирантуру при Институте вирусологии им. Д.И. Ивановского АМН СССР, где под руководством академика АМН СССР Косякова П.Н. защитил кандидатскую диссертацию на тему «Антигенная изменчивость гемагглютининов вирусов гриппа В». В 1998 г. Жуматов К.Х. защитил диссертацию на соискание ученой степени доктора биологических наук на тему «Структура популяций и антигенная изменчивость эпидемических вирусов гриппа А и В, циркулирующих в Казахстане» (научный консультант академик НАН РК М.Х. Саятов). Автор диссертации впервые провел анализ особенностей развития эпидемического процесса при гриппе А и В среди населения РК в период с 1990 по 1998 гг. и показал, что наиболее активным был вирус А(Н3N2), явившийся основным возбудителем эпидемий в 1990, 1992, 1996, 1997 гг. Эпидемии 1993 и 1995 гг. были обусловлены преимущественно вирусами серотипа В, а 1994 и 1998 гг. – вирусами А(Н1N1). В сочетанную эпидемию сезона 1992 г. социркулировали вирусы гриппа А(Н3N2) и В.

В составе гемагглютинина эпидемически актуальных штаммов Жуматов К.Х. с помощью моноспецифических антител и иммуносорбционного анализа определил новые антигенные детерминанты: Н3.18; Н3.20, 21, 22; Н3.26; Н3.27 у вирусов А(Н3N2) и Ш.19, Ш20, Ш22 у вирусов серотипа В.

По данным его исследований, антигенный дрейф вирусов гриппа А и В проявляется в виде непрерывного процесса обновления состава антигенных детерминант гемагглютинина, связанного как с появлением оригинальных штаммоспецифических сайтов, так и новыми сочетаниями ранее

идентифицированных маркеров. Показано, что некоторые из вновь возникающих штаммоспецифических детерминант получают наибольшее распространение в последующих эпидемиях и в ходе эволюции становятся группоспецифическими.

В последние годы основными направлениями исследований Жуматова К.Х. являлись экология и эволюционная изменчивость орто- и парамиксовирусов. В ходе эколого-вирусологических исследований Жуматова К.Х. с соавторами впервые на территории РК выделено 189 изолятов вирусов гриппа А от птиц отрядов Поганкообразные, Веслоногие, Голенастые, Фламингообразные, Гусеобразные, Курообразные Журавлеобразные, Ржанкообразные, Воробьинообразные. В составе казахстанских вирусов гриппа птиц идентифицированы варианты с 14 комбинациями поверхностных антигенов – H1N1, H1N2, H3N3, H3N6, H3N8, H4N6, H5N1, H5N3, H10N2, H10N7, H10N8, H11N2, H13N6, H16N3. От представителей отрядов Гусеобразных и Ржанкообразных выделены парамиксовирусы птиц серотипов ПМВ-4, ПМВ-6, ПМВ-8. Многие изученные Жуматовым К.Х. казахстанские изоляты вирусов гриппа депонированы в Национальной коллекции вирусов и защищены предпатентами и авторскими свидетельствами патентного ведомства РК, нуклеотидные последовательности их генов зарегистрированы в международном банке данных GeneBank.

Жуматов К.Х. – автор более 230 научных работ, 17 авторских изобретений и патентов, соавтор первого русско-казахского терминологического словаря по вирусологии, иммунологии, генетике и молекулярной биологии (1993). В 2011 г. удостоен Государственной стипендии для ученых и специалистов, внесших выдающийся вклад в развитие науки по специальности вирусология.

Светлая память о Жуматове Кайнаре Хамзаевиче, большом ученом, блестяще образованном и обаятельном человеке, навсегда сохранится в сердцах его учеников, друзей, коллег, родных и близких.

Академик НАН РК Саятов М.Х.,
доктор ветеринарных наук Кыдырманов А.И.

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