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Risk analysis of the spread of cattle viral diarrhea in Kazakhstan

S.A. Kan*[1,2], A.V. Zhigailov[1,2], A.V. Lushova[1,2,3], E.O. Ostapchuk[1,2], Y.V. Perfilieva[1,2], S. Kuatbekova[1], N. Abdolla[1,2], A.V. Kuligin[1], S.A. Mashzhan[1,2,3], S.M. Mamadaliyev[1]

[1] *National Center for Biotechnology, Almaty, Kazakhstan*
[2] *Institute of Molecular Biology and Biochemistry named after M.A. Aitkhozhin, Almaty, Kazakhstan*
[3] *Kazakh National University named after Al-Farabi, Almaty, Kazakhstan*

**Corresponding author: kan.soofiya@gmail.com*

Abstract. Bovine viral diarrhea (BVD) is the most common infectious disease of cattle and is registered in many countries of the world. The disease causes significant economic damage to livestock, primarily due to a decrease in the reproductive capacity of infected animals. Infection of cattle during pregnancy results in transmission of the infection to the fetus, which can lead to embryonic death or the birth of persistently infected (PI) calves. PI-animals excrete BVDV in their feces and secretions throughout their lives, which is why they are the main pathway of transmission of the virus. Moreover, acute BVDV infection leads to transient viremia and immunosuppression, resulting in an increase in secondary infections. In recent years, outbreaks of BVD cattle have been reported in several regions of Russia and China bordering Kazakhstan, indicating a high risk of introducing the infection into the country. Although Kazakhstan is officially considered free from BVD cattle, there is ample evidence that this infection is present in many regions of the country. However, the lack of a clear understanding of the epizootic situation in the country in terms of BVD cattle does not allow the full use of effective control measures, such as total vaccination of livestock in regions at risk of infection. This article provides data on the epizootic situation in Kazakhstan on BVD cattle, as well as an epidemiological analysis of the risks of the spread of BVD cattle in the country.

Key words: bovine viral diarrhea, risk analysis, BVDV, epidemiology, animal husbandry.

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Introduction

Bovine viral diarrhea (BVD) is an acute disease of cattle, characterized by erosive and ulcerative inflammation of the mucous membranes of the digestive tract, rhinitis, swollen lymph nodes, fever, general depression, leukopenia, persistent or intermittent diarrhea, erosive and ulcerative stomatitis with profuse salivation, the appearance of mucopurulent discharge from the nasal cavity, abortion, stillbirth, diarrhea of newborn calves and immunodeficiency. The disease proceeds in the form of an epizootic, the incidence is from 10 to 100% of the animals in the herd, and the mortality rate is 10-90%. The disease causes significant economic damage to livestock. The losses to the farms from the BVD of cattle consist of the death and forced slaughter of young animals, a decrease in milk production, abortions, the birth of non-viable calves, and exposure to other diseases [1].

Bovine viral diarrhea virus (BVDV) belongs to the genus *Pestivirus* from the family *Flaviviridae.* Pestiviruses are enveloped viruses containing a single-stranded (+)-strand RNA as a genome. The genomic (g) RNA of pestiviruses lacks a poly(A) tail at 3' end and contains an internal ribosome entry site (IRES) in 5' untranslated region (5' UTR) [2].

Two main genotypes, BVDV-1 and BVDV-2, have been described based on the 5'-UTR sequence of viral gRNA (they are currently distinguished as viruses of different species). These genetic subtypes, in fact, are separate serogroups, and virus-neutralizing antibodies developed for the first group have only a minor cross-reactivity with the second serogroup of the virus [2]. More than two dozen different BVDV-1 genetic subtypes are isolated and several BVDV-2 subtypes also identified. These include non-cytopathic (NCP) and cytopathic (CP) biotypes that differ in the severity of clinical manifestations and the manner of reproduction in cell cultures *in vitro.* In Eurasia, the BVDV1a, 1b, and 2a genotypes are the most frequently circulated [3].

The genetic subtypes of BVDV-1 and BVDV-2 differ greatly in terms of virulence, intensity, and clinical manifestations in animals [4]. The BVDV-2 subtype combines mostly highly virulent strains that cause acute and hyperacute forms of the disease with thrombocytopenia, hemorrhages and high mortality. This genetic subtype of the virus is more widespread in North America, and only sporadic outbreaks of infection are recorded in Eurasia. BVDV-1 is distributed almost everywhere and represented mainly by mesogenic strains that cause transplacental infection and immunosuppression in the postnatal period and an increase in abortions [5].

Susceptible to the virus are cows and buffaloes, as well as sheep, goats, wild bovids (deer, roe deer), pigs and camels. Animals aged 6 months to 2 years are most susceptible. The disease is observed throughout the year, but the number of outbreaks increases during cold periods. [5]. Although infection is often asymptomatic in heterologous species (non-bovine), abortions have been reported in sheep and goats infected with BVDV [6].

The primary source of the infectious agent is sick and recovered animals that excrete the virus with urine, feces, saliva, nasal secretions, milk, and exudate from inflammatory foci [5]. There is information that bloodsucking flies, such as flies and bloodsucker flies, can serve as mechanical vectors of infection [7,8]. Despite the fact that the effectiveness of the transmission

of bovine BVD by these insects is questioned [9], the virus RNA is detected in biting flies, so they can be an important object for infection monitoring, especially in natural reservoirs.

The disease can develop into a lifelong, persistent state during which the ability to infect other animals is retained. The percentage of persistent forms in herds is an important indicator of the epizotological process (more than 1% is considered high [10]. The main task of diagnosing this infection is to identify animals with persistent infection (PI) and exclude them from the herd. The sooner this can be done, the sooner the infection can be eradicated. PI animals can only be detected by highly sensitive direct virus detection methods (virus isolation, PCR-based methods, and direct antigen ELISA).

Serological methods are almost impossible to differentiate vaccinated and animals that have been ill with field strains of the virus. To some extent, differences between such animals can be revealed by ELISA tests based on testing of monoclonal antibodies to p80 [11]. However, it should be noted that even ELISA test systems that use monoclonal antibodies to NS3 (p80) or E0 (Erns) proteins show very high cross-reactivity against other pestiviruses that can infect cows (HoBi viruses) [12]. Only specific antibodies to the E2 protein of BVDV exhibit a sufficient level of specificity to differentiate BVDV from other pestiviruses [12].

OIE-recommended direct detection methods for BVDV antigen include virus isolation, direct antigen ELISA, and RT-PCR [13]. For virus detection by RT-PCR, the most conserved loci of the viral genome are selected, namely, 5'-UTR and the NS3 (p80) open reading frame. In this case, it is recommended to use an additional, more specific locus, for a clear differentiation of BVDV from other pestiviruses [13].

There is no information on the status of BVD cattle in the territory of Kazakhstan in open government sources. However, it follows from unofficial sources and scientific articles by foreign authors that the causative agent of this disease is already circulating in some regions of the country [14]. The absence of a clear unified system of state control leads to the fact that farmers privately vaccinate their animals, and often the herd is only partially vaccinated (for example, only heifers, or only breeding animals). However, the effectiveness of privately administered vaccination remains unknown. In addition to inactivated vaccines, attenuated vaccines against bovine viral diarrhea containing more than one virus genotype are also available on the market. The use of such vaccines in virus-free areas, as well as non-100% vaccination with attenuated vaccines of herds in which animals with clinical signs of BVDV are detected, contribute to the stable emergence of a sufficiently large number of PI- animals [15].

Among other things, the uncontrolled use of attenuated vaccines opens gateways for infection into the wild (wild ruminants such as deer and roe deer are susceptible to BVDV), forming natural reservoirs of infection that will contribute to the rapid spread of infection in the territory of Kazakhstan [16].

This article provides information about the epizootic situation in Kazakhstan on viral diarrhea in cattle, the results of an epidemiological assessment of the risks of the spread of infection in the country. Also, samples from cattle were evaluated for a monitoring program to study the circulation of this infection in the country.

Methodology

Epidemiological methods

All calculations of epidemiological parameters were carried out using the EpiInfo v. 7.2.2.2 (CDC).

The total sample size for conducting a monitoring study in relation to BVD cattle was determined by formula (1) [17].

$$Size\ samples\ (n) = N^* [Z^2 * p * (1-p)/e^2] / [N - 1 + (Z^2 * p * (1-p)/e^2] \quad (1)$$

Where:

N is the population size;

Z is the critical value of the normal distribution at the required confidence level;

p is the expected level of prevalence, %;

e is the permissible error.

Collection of samples from animals

The collection of samples was carried out within the framework of the state monitoring program funded by the Ministry of Agriculture of the Republic of Kazakhstan. The conclusion of the ethical commission of the RSE on REM "National Center for Biotechnology" was received (protocol No. 4 dated December 3, 2021).

The collection of blood and serum was carried out by qualified veterinarians. At the place where it was supposed to make a puncture, sheared wool and skin, disinfected with a 5% solution iodine. Blood was taken from the jugular animal veins into Venosafe collection tubes whole blood (containing K2 EDTA) and serum tubes (containing coagulation activator) fitted with a safety needle (Venoject Quick fit needle). To obtain serum, Venosafe tubes with the blood collected in them after the formation of a clot was centrifuged at 1200 xg for 10 min at 4°C.

Nucleotide sequence analysis

Computer analysis of nucleic acid sequences was performed using the VNTI- Viewer 11.5.1, MEGA-X, and RNA- structure 3.5 programs.

Risk Analysis

For risk analysis and forecasting, we used an additional add-in in Microsoft Excel - Decision Tools Suite 6.0 Professional from Palisade.

Discussion

Analysis of the epizootic process for BVD cattle in the world

OIE data for ehe epizootic situation in the world over the past 3 years (2019-2022) is shown in Figure 1.

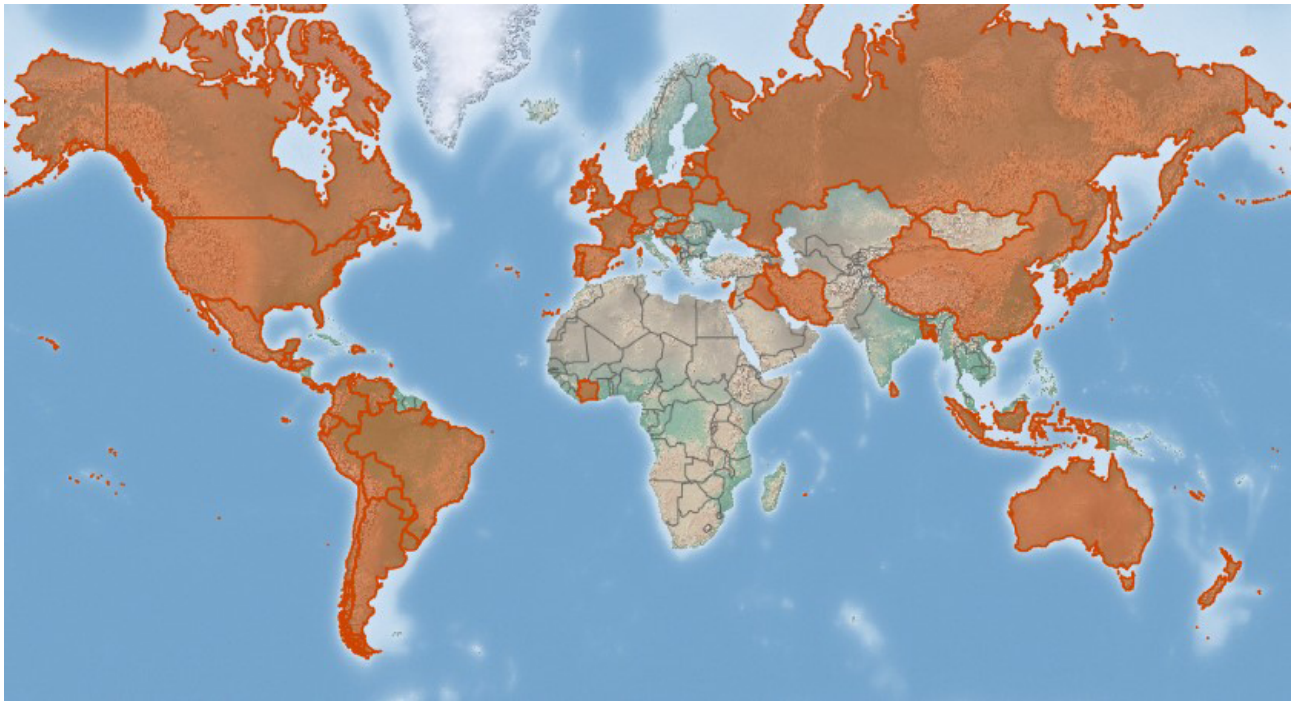

Figure 1. Regions and states in which outbreaks of BVD cattle were recorded at the official level according to OIE data for 2011-2022 [18]

In general, the disease is very widespread and is considered endemic in Asia, Europe, Australia, South and North America.

Analysis of the epizootic process for BVD cattle in Kazakhstan

Previously, outbreaks of BVD cattle occurred on the territory of the country: they were recorded in the North Kazakhstan, Karaganda, Kyzylorda, Almaty regions.

For the period from 2019 to 2020, there was no official information on outbreaks of BVD cattle in the territory of the Republic of Kazakhstan. However, according to KazInform, in 2019 in the Atyrau region there was an outbreak of infection among cattle with the death of several animals; diagnosis made by local veterinary services – BVD cattle. Temporary restrictive measures were established in the territories bordering the farm.

In October 2021, in the village of Mortuk, Ualikhanov district, North Kazakhstan oblast, an outbreak of BVD cattle occurred with the death of livestock, and a limited quarantine for BVD cattle was declared [19]. In December 2021, in the village of Akzhal, Shet district, Karaganda region, an outbreak of cattle infection occurred with the death of livestock; confirmed laboratory diagnosis - BVD cattle [20].

In February 2022, more than 700 animals fell ill in the Kyzylkoginsky district of the Atyrau region; laboratory analyzes revealed BVD cattle; quarantine for BVD cattle was declared [21]. In August 2022, in the village of Kok uy, Khobdinsky district, Aktobe region, cows died, the diagnosis established by veterinary services was BVD cattle [22]. In June 2022, an outbreak of an unknown cattle infection with the death of livestock was recorded in the Mibulak rural district of the Ulytau region; the reason is established [23].

Analysis of the risks of introduction and spread of BVD cattle in the territory of Kazakhstan

To a large extent, the growth in the number of cattle in recent years is provided by the massive importation of breeding stock from abroad. Thanks to state subsidies for the purchase of imported breeding stock and its laboratory testing, it becomes more profitable for farmers to purchase breeding stock abroad than in domestic breeding centers. It is the importation of breeding stock that is the main risk of introducing BVD cattle into the country. Visual inspection and serological methods of analysis do not reveal animals with persistent infection (PI animals can rarely be distinguished from non-infected animals by external signs). Although in rare cases animals with persistent infection may have specific antibodies to the virus (newborn calves may have maternal antibodies, antibodies may appear for a short time after vaccination, or if the animal is infected with a virus of a different genotype), as a rule, antibodies to BVDV in such animals are completely absent.

It is not possible to test all imported livestock using expensive real-time PCR-based direct analytical tests that require highly qualified laboratory personnel. Both vaccinated and non-vaccinated against BVDV cattle are imported to Kazakhstan.

The leader among exporters of breeding cattle to our country is Russia (more than 50%), followed by Germany and Austria. All these countries are endemic in terms of BVD of cattle (infection outbreaks have been recorded here for the last 5 years) [18]. Also in the list of exporters are Belarus (endemic for BVD cattle [18]), Estonia (endemic for BVD cattle [18]), Ukraine, the Netherlands (endemic for BVD cattle [18]), Slovakia (endemic for BVD cattle [18]), Lithuania (endemic for BVD [18]), Northern Ireland (endemic for BVD [18]), Hungary (endemic for BVD [18]), Australia. When assessing the risk of bringing the infection into the country on the epizootic situation in terms of BVD cattle, it is in these countries that special attention should be paid.

Livestock and density of cattle in Kazakhstan

The most important parameters that should be taken into account when assessing the risks of outbreaks and the spread of BVD cattle are considered to be the density of cattle, the presence or absence of a state infection control system, whether conditions are suitable for the reproduction of mechanical infection vectors, and the volume of livestock imported into a given region [24].

The highest density of cattle in our country is in the southern regions of Turkestan, Zhambyl and Almaty regions, the northern regions of Aktobe, Kostanay and North Kazakhstan (NK), West Kazakhstan (WK) regions, as well as in some areas of Akmola, Pavlodar and East Kazakhstan areas (Figure 2). It is in these areas of the country that the maximum risk of the spread of BVD cattle remains.

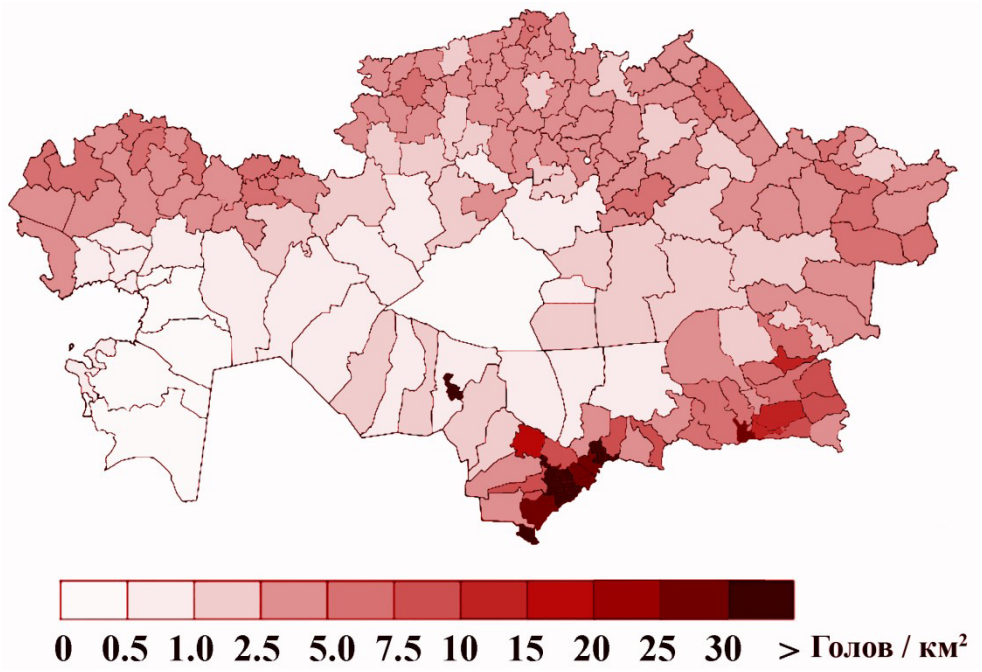

Figure 2. Density of livestock susceptible to BVDV in Kazakhstan [25]

The leaders in the number of cattle are Turkestan, Abai, WK and Almaty regions (Figure 3).

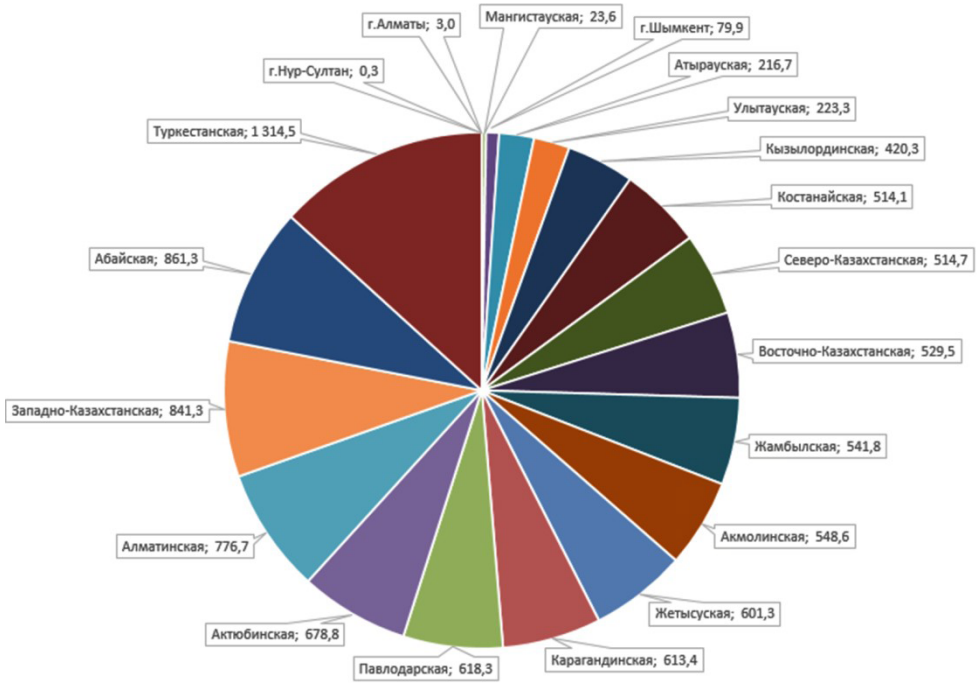

Figure 3. The total number of cattle in the regions of the Republic of Kazakhstan in thousand heads (as of July 1, 2022) [25]

Thanks to state programs to support and develop agriculture, over the past ten years, a systematic increase in the number of cattle has been observed in Kazakhstan. The first steps to expand animal husbandry were made back in 2011, when the Sybaga program was launched in the country. After Kazakhstan joined the WTO in 2015, export subsidies and other types of state support related to import substitution were banned. Despite this, the Republic of Kazakhstan is the leader among the CIS countries in terms of the increase in the number of cattle (with the exception of Kyrgyzstan, other members of the union experience stagnation or even negative dynamics in this indicator). So, if in 2011 the number of cattle in our country was estimated at 5702 thousand heads, as of July 1, 2022 it was already 9921.3 thousand heads [25]. This circumstance significantly increases the risks associated with the rate of spread of BVD cattle in the territory of Kazakhstan. Data on the change in the number of cattle in the country for 1990-2022 are shown in Figure 4.

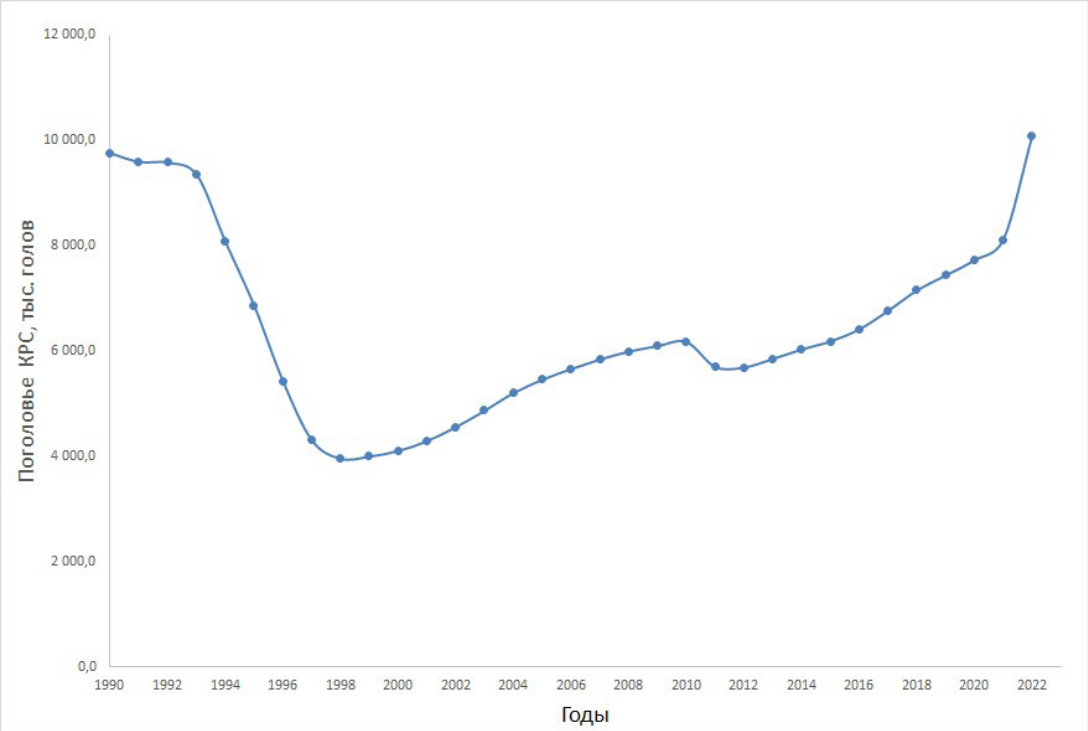

Figure 4. Change in the total number of cattle in Kazakhstan [25]

Analysis of the risk of infection spread across the territory of Kazakhstan

The analysis of the risk of spread of infection was carried out based on the available data on the history of outbreaks of BVD cattle in the territory of the Republic of Kazakhstan, the density and total number of cattle by region, the method of transmission of the pathogen (including conditions for the spread and reproduction of blood-sucking flies), the availability of preventive methods to minimize the risks associated with the spread of infection (coverage by vaccination against BVD cattle, carried out both at the state level and privately), the actual state of the epizootic process for BVD cattle in a given region of the country, including the average level

of antibody seroprevalence in herds, as well as the risks of introducing infection from endemic diseases of regions or states. Based on all the processed data, a risk map of the occurrence of large outbreaks of BVD cattle in the territory of Kazakhstan was built. The map is shown in Figure 5.

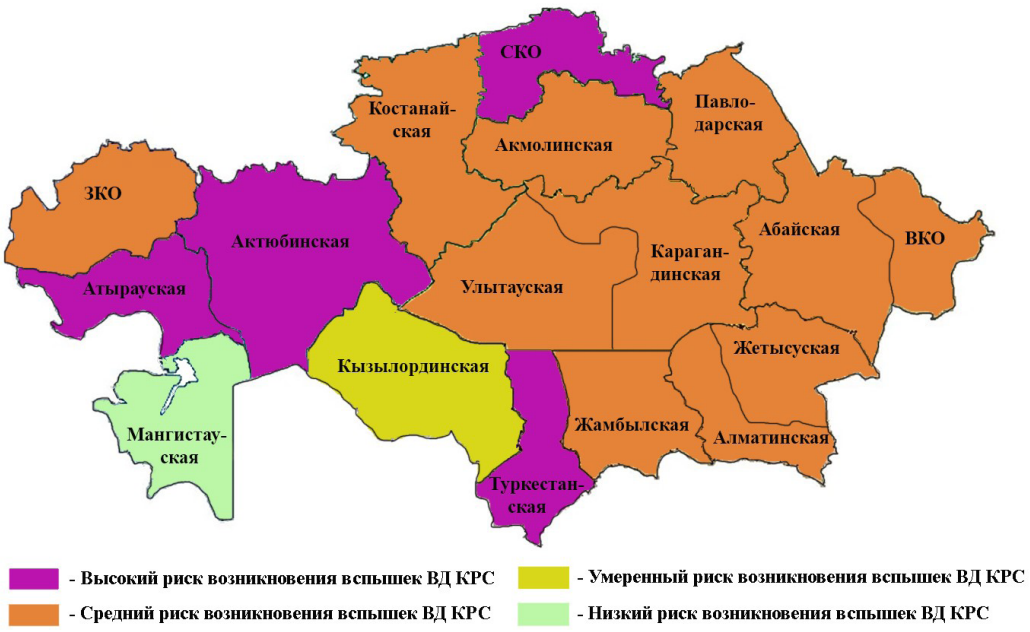

Figure 5. Map of risks in relation to the occurrence of large outbreaks of BVD cattle in the territory of Kazakhstan (at the time of 09.01.2022)

Determination of sample size and collection of field samples of BVD cattle

As of 07/01/2022, according to the official data of the bureau of statistics in the Republic of Kazakhstan [25], the country contains 9921.3 thousand heads of cattle. Since no large-scale monitoring of the BVD of cattle has been carried out in the country before, the level of antibody seroprevalence should be taken equal to 50% (according to [17]). For epidemiological studies, the confidence interval in most cases is assumed to be 95%; therefore, this value is recommended for calculations [17]. The permissible error in calculations is usually assumed to be 5% [17]. Thus, for groups of five to forty animals, the minimum required number of animals, according to calculations, was 400 per year (no more than forty animals from each location). As a rule, the number of animals exceeding the critical sample size by at least 10% is involved in monitoring, since some proportion of the samples may not be suitable for analysis (for example, serum may be hemolyzed, and blood clotted). Thus, the minimum threshold for the number of animals involved in the monitoring study for BVD cattle was determined to be 450 animals. Table 1 presents data on the number of samples we collected for further monitoring of the prevalence of BVD in the country.

Table 1

Data on the number of collected biological samples

Region	Area	Samples collected		
		total animals	sera	blood samples
Turkestan	Kazygurtsky	60	60	60
	Baidibek	50	50	50
	Ordabasinsky	140	140	120
	Total:	250	250	230
North Kazakhstan region	Taiynshinsky	111	111	98
	Timiryazevsky	100	100	100
	Mamlyutsky	56	56	56
	Akkayinsky	20	20	0
	Aiyrtau	20	20	0
	Akzharsky	10	10	0
	Total:	317	317	254
Akmola	Arshalinskiy	100	100	100
	Zerendinskiy	100	100	100
	Astrakhan	20	20	0
	Burobaisky	20	20	0
	Kokchetavskiy	24	24	0
	Total:	264	264	200
Pavlodar	Shcherbaktinsky	100	100	100
	Pavlodar	100	100	100
	Uspensky	50	50	0
	Total:	250	250	200
Karaganda	Osakarovsky	25	25	0
Kostanay	Fedorovsky	15	15	0
Total:		1121	1121	884

In addition, in addition to the planned oblasts, a small number of serum samples were collected in Karaganda and Kostanai oblasts. Based on the analysis carried out and the biological material collected, it is planned to monitor the prevalence of BVD in the country in the future. The samples will be analyzed by serological methods for the detection of antibodies to the BVDV pathogen, and the detection of BVDV RNA in the collected biological materials will also be carried out.

Primer development for the genetic characterization of BVDV.

In addition to BVDV-1 and BVDV-2, pestiviruses include the classical swine fever virus (CSFV) and border disease virus (BDV) sheep, as well as more seven species : pronghorn antelope pestivirus (Pestivirus E), Bungowannah virus (Pestivirus F), giraffe pestivirus (Pestivirus G),

Hobi-like pestivirus (Pestivirus H), Aydin-like pestivirus (Pestivirus I), rat pestivirus (Pestivirus J) and atypical porcinepestivirus (Pestivirus K) [5, 26]. Although the main hosts of BVDV -1 and BVDV -2 are cattle, C S FV is pigs, and BDV is small cattle, pestiviruses have a fairly wide level of tropism, so bovine VDV can also infect pigs, sheep, goats, and also wild ruminants and even calluses [16], and vice versa, representatives of the other two main types of pestiviruses can theoretically be found in the blood of cattle [27]. Since all currently known species of pestiviruses are detected in Asia [28], it is important to develop universal primers for the detection of BVDV, eliminating false positive responses against CSFV, BDV and other pestiviruses.

BVDV RNA in the blood of animals, standard primers were selected for the conservative region of the pestivirus genome, for the 5'-untranslated sequence of genomic RNA (“BVDV_UTR_ DL1F” and “ BVDV_UTR_DL4R”) [29]. Although this locus is often used for pestivirus typing, it is not an ideal target for phylogenetic analysis [30]. Primers were synthesized and purified by reverse phase high performance liquid chromatography (HPLC) and tested by RT-PCR on an RNA control sample isolated from a commercially available Bovi-Shield Gold vaccine containing inactivated BVDV -1 virus. The results of the analysis are shown in Figure 2.

Designations: “BVDV - Vac”, total RNA preparation isolated from Bovi-Shield Gold vaccine; "K-" - negative control; M - DNA reference.

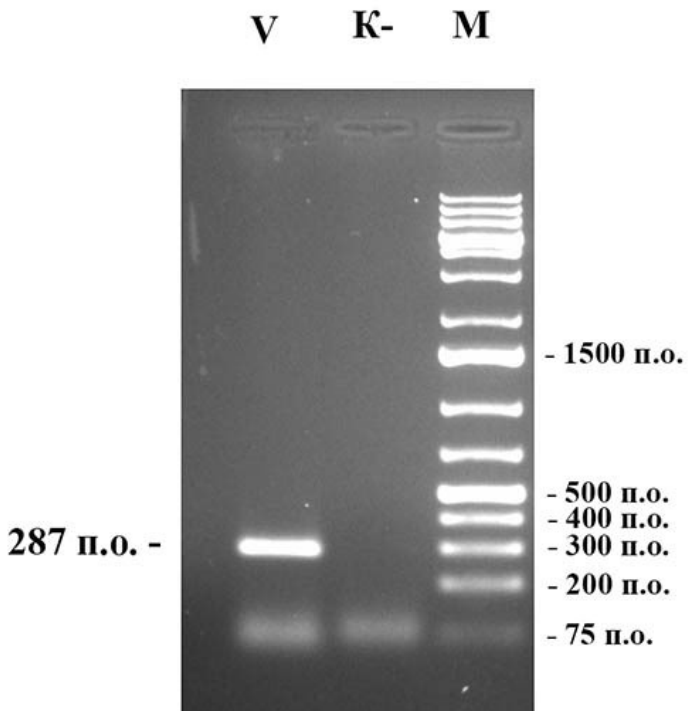

Figure 6. Electrophoretic analysis in 1.5% agarose gel of RT-PCR products with primers "BVDV_UTR_ DL1F" and " BVDV _ UTR _ DL 4 R " for testing the BVDV detection method

For genetic characterization of the virus isolates, primers “BVDV 1_Npro - F” and “BVDV 1_ Npro - R” were chosen, targeting the moderately variable locus of the Npro viral protease [31].

Primers for 5'-UTP gRNA loci BVDV and Npro were tested for their ability to detect new lines and genotypes of BVDV circulating in Russia and China bordering Kazakhstan. In Western China bordering Kazakhstan, the following virus genotypes are common: 1a, 1b, 1c, 1d, 1m, 1o, 1p, 1q, and 1u [32]. In the regions of Russia bordering Kazakhstan (Tyumen, Omsk and Novosibirsk regions), seven subtypes were identified BVDV -1 - 1a (5%), 1b (35%), 1c (5%), 1d (10%), 1f (20%), 1i (5%), 1p (5%) and two subtypes BVDV -2 — 2b (10%) and 2c (5%) [33, 34].

Currently, the use of more than two gene loci is recommended for phylogenetic analysis [5], and although the use of the 5'UTR and Nrpo loci is widespread, the most promising for genotyping is the region encoding the viral glycoprotein E 2. This immunodominant surface protein is the most variable in pestiviruses and mediates the formation of a serotype, and it is to it that a large proportion of neutralizing antibodies to the virus is formed [35].

In this regard, the nucleotide sequences of the E2 locus of BVDV genotypes potentially circulating in Kazakhstan were analyzed and primers were developed for the genetic characterization of BVDV isolates at this locus. The alignment of the target sequences of the forward and reverse primers is shown in Figure 3.

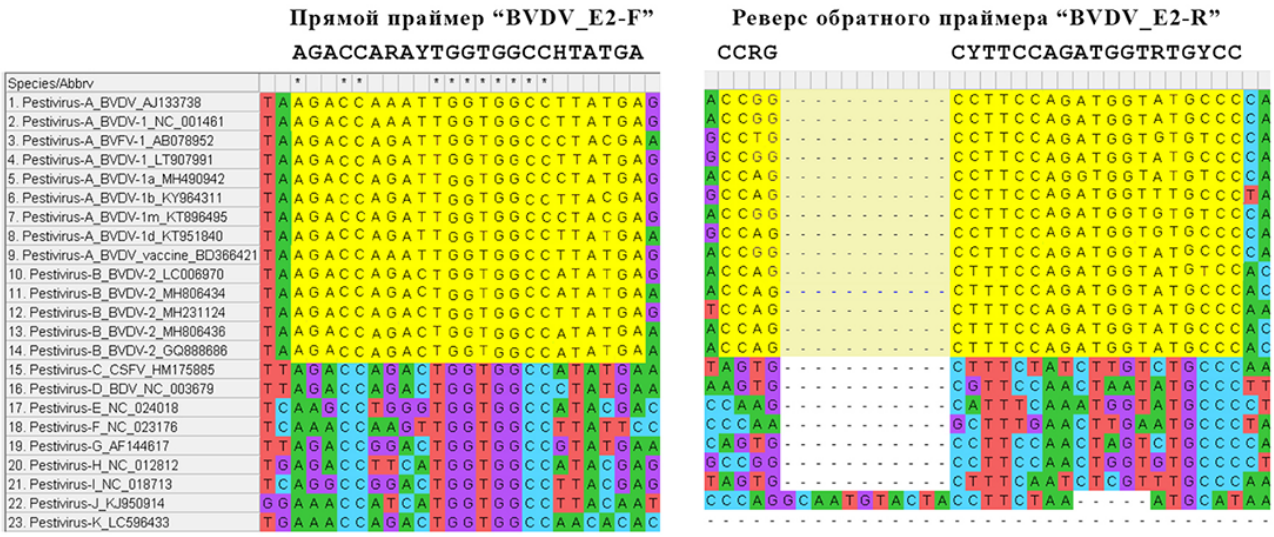

Figure 7. Alignment of the nucleotide sequences of the genome of various pestiviruses at the E 2 locus in the MEGA - X program

As can be seen from the presented data, the developed primers are specific for all BVDV -1 and BVDV- 2 variants used in the analysis, and are not suitable for other pestiviruses.

In the course of the research, we developed an epizootic visualization map with indicators of risk zones for the spread of BVD cattle in the Republic of Kazakhstan, taking into account the analysis of such indicators as the report on outbreaks of BVD cattle with a diagnosis from open official sources for 2013-2022, the population density of cattle, reports of outbreaks of BVD cattle in neighboring regions and states.

According to official data, epizootic foci of BVD cattle were first registered in 2013, after which single outbreaks of BVD were recorded almost every year and they occurred in Karaganda,

North Kazakhstan, Almaty, Atyrau and Aktobe regions in different years. These results allow us to conclude that BVD cattle is quite widespread in a number of regions of the country.

Accordingly, based on the results of this study, it can be concluded that the most unfavorable regions in relation to BVD cattle, with the highest risk of spreading the virus, are Atyrau, Aktobe, Turkestan and North Kazakhstan regions. West Kazakhstan, Kyzylorda, Pavlodar, Akmola, Kostanay, Ulytau, Zhetysu, Abay, Almaty, Zhambyl, Turkestan and East Kazakhstan regions are characterized by medium and moderate risk of virus spread. And only Mangistau region is safe in relation to BVD cattle, with a low risk of infection.

However, since the number of cattle has significantly increased in the country in recent years, and the share of imported livestock remains at a high level, this creates additional threats for the emergence of new outbreaks of BVD cattle in various regions of the country. In this regard, it is obvious that there is an urgent need to develop additional measures to prevent further spread of the pathogen to non-endemic regions of the Republic of Kazakhstan and measures to eradicate the infection in herds in which the circulation of the BVDV has been proven. Based on the data obtained in the context of the study, it is recommended to conduct a general state vaccination of livestock against BVDV in areas that are unfavorable for this infection, as well as in the border regions of Kazakhstan to eliminate the threat of further spread to regions that are not endemic for the infection.

Furthermore, as BVD cattle is a relatively new animal disease in our country, which farmers and livestock owners have not encountered before; in order to increase the effectiveness of the program to control this dangerous livestock infection, work should immediately begin to bring information about BVD cattle to the target audience. For completeness the study of the epizootic process of BVD cattle in the country, it is necessary to monitor the prevalence of the prevalence agent of this disease in all regions of the Republic of Kazakhstan and carry out work on the genetic characterization of BVDV isolates circulating in the country.

Conclusion

Thus, based on the results of the risk analysis, it can be concluded that the most disadvantaged regions in relation to BVD cattle, with the highest risk of spreading the virus, are Atyrau, Aktobe, Turkestan and North Kazakhstan regions. West Kazakhstan, Kyzylorda, Pavlodar, Akmola, Kostanay, Ulytau, Zhetysu, Abay, Almaty, Zhambyl, Turkestan and East Kazakhstan regions are characterized by medium and moderate risk of virus spread. And only Mangistau region is safe in relation to BVD cattle, with a low risk of infection. Also, primers were developed for characterizing the BVD cattle, the sample size was determined, and biological material was collected from animals for monitoring by BVD of cattle.

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Conflict of interest

There is no conflict of interest between the authors.

Authors' contribution

Kan S.A.: contribution to the concept; execution of the claimed scientific research; creation of a scientific article.

Zhigailov A.V.: scientific design.

Lushova A.V.: contribution to the concept.

Ostapchuk E.O.: contribution to the concept.

Perfilieva Y.V.: scientific design.

Kuatbekova S.: interpretation of the claimed scientific research.

Abdolla N.: contribution to the concept.

Kuligin A.V.: interpretation of the claimed scientific research.

Mashzhan S.A.: interpretation of the claimed scientific research.

Mamadaliyev S.M.: interpretation of the claimed scientific research.

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С.А. Кан*[1,2], А.В. Жигайлов[1,2], А.В. Лушова[1,2,3], Е.О. Остапчук[1,2], Ю.В. Перфильева[1,2], С. Куатбекова[1], Н. Абдолла[1,2], А.В. Кулигин[1], С.А. Машжан[1,3], С.М. Мамадалиев[1]

[1]Ұлттық биотехнология орталығы, Алматы, Қазақстан

[2]М.А. Айтхожин атындағы молекулалық биология және биохимия институты, Алматы, Қазақстан

[3]Әл-Фараби атындағы Қазақ ұлттық университеті, Алматы, Қазақстан

Қазақстанда ірі қара малдың вирустық диареясының таралу қаупін талдау

Аңдатпа. Ірі қара малдың вирустық диареясы ірі қара малдың ең таралған жұқпалы ауруы болып табылады және әлемнің көптеген елдерінде тіркелген. Бұл ауру ең алдымен ауру малдың көбею қабілетінің төмендеуіне байланысты мал шаруашылығына айтарлықтай экономикалық зиян келтіреді. Буаздық кезінде малды жұқтыру инфекцияның ұрыққа берілуіне әкеледі, бұл

эмбриональды өлімге немесе персистентті жұқтырған (PI) бұзаулардың тууына әкелуі мүмкін. PI-жануарлары өмір бойы вирусты нәжіспен және секрециямен төгеді және вирустың берілуінің негізгі жолы болып табылады. Жедел инфекция өтпелі вирусемияға және иммунитеттің төмендеуіне әкеліп соқтырса, оның салдары екіншілік аурулар санының көбеюіне әкеледі. Соңғы жылдары Ресей мен Қытайдың Қазақстанмен шектесетін бірнеше өңірінде вирустық диареяның өршуі тіркелді, бұл инфекцияның елге ену қаупінің жоғары екендігін көрсетеді. Қазақстан ресми түрде вирустық диареядан таза деп танылғанымен, бұл инфекцияның еліміздің көптеген аймақтарында бар екендігі туралы деректер жеткілікті. Алайда, елдегі ірі қараның вирустық диареясы бойынша эпизоотиялық жағдайды нақты түсінбеу мал басын толық егу және ауру жұқтыру қаупі бар аймақтарда карантиндік шараларды енгізу сияқты тиімді күрес шараларын толық пайдалануға мүмкіндік бермейді. Бұл мақалада Қазақстандағы ірі қара вирустық диарея бойынша эпизоотиялық жағдай туралы деректер, сондай-ақ елдегі ірі қара вирустық диареяның таралу қаупіне эпидемиологиялық талдау жасалған.

Түйін сөздер: ірі қара вирустық диареясы, қауіп талдауы, BVDV, эпидемиология, мал шаруашылығы.

С.А. Кан[1,2]*, А.В. Жигайлов[1,2], А.В. Лушова[1,2,3], Е.О. Остапчук[1,2], Ю.В. Перфильева[1,2], С. Куатбекова[1], Н. Абдолла[1,2], А.В. Кулигин[1], С.А. Машжан[1,3], С.М. Мамадалиев[1]

[1]Национальный центр биотехнологии, Алматы, Казахстан

[2]Институт молекулярной биологии и биохимии им. М.А. Айтхожина, Алматы, Казахстан

[3]Казахский национальный университет им. аль-Фараби, Алматы, Казахстан

Анализ рисков распространения вирусной диареи крупного рогатого скота в Казахстане

Аннотация. Вирусная диарея крупного рогатого скота (ВД КРС) является наиболее распространенным инфекционным заболеванием крупного рогатого скота и регистрируется во многих странах мира. Заболевание наносит значительный экономический ущерб животноводству, в первую очередь из-за снижения репродуктивной способности инфицированных животных. Заражение скота во время беременности приводит к передаче инфекции плоду, что может привести к гибели эмбриона или рождению персистентно инфицированных (PI) телят. PI-животные выделяют вирус со своими экскрементами и выделениями на протяжении всей жизни и являются основным путем передачи вируса. В то время как острая инфекция ВД КРС приводит к транзиторной виремии и иммуносупрессии, последствием чего является увеличение числа вторичных заболеваний. В последние годы вспышки ВД КРС были зарегистрированы в нескольких регионах России и Китая, граничащих с Казахстаном, что указывает на высокий риск заноса инфекции в страну. Хотя Казахстан официально считается свободным от ВД КРС, имеются многочисленные данные указывающие на то, что данная инфекция присутствует во многих регионах страны. Однако, отсутствие четкого понимания эпизоотической ситуации в стране по ВД КРС не позволяет в полной мере использовать эффективные контрольные мероприятия, такие как тотальная вакцинация скота и введение карантинных мероприятий в рисковых по инфекции регионах. В настоящей статье приводятся данные по эпизоотической ситуации в Казахстане по ВД КРС, а также эпидемиологическому анализу рисков распространения ВД КРС в стране.

Ключевые слова: вирусная диарея КРС, анализ рисков, BVDV, эпидемиология, животноводство.

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Information about authors:

Kan S.A. **–** master, junior researcher, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Zhigailov A.V. **–** PhD, head of the Laboratory of Molecular Biology, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Ostapchuk Y.O. **–** PhD, Associate Professor, Head of Laboratory of Immunology and Immunobiotechnology, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Perfilieva Yu.V. **–** PhD, Associate Professor, Lead Researcher, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Lushova A.V. **–** master student, Kazakh National University Al-Farabi, Kazakhstan, Almaty, laboratory assistant, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Kuatbekova S.A. **–** master, researcher, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Abdolla N. **–** PhD, senior researcher, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Kuligin A.V. **–** baccalaureate student, Kazakh National University Al-Farabi, Kazakhstan, Almaty, laboratory assistant, Almaty Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Mashzhan A.S. **–** doctoral student, researcher, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Mamadaliev S.M. **–** doctor of Veterinary Sciences, Professor, Almaty Branch of the National Center for Biotechnology, Zhahanger str., 14, Almaty, Kazakhstan.

Авторлар туралы мәліметтер:

Кан С.А. **–** магистр, кіші ғылыми қызметкер, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Жигайлов А.В. **–** PhD, Молекулярлық биология зертханасының меңгерушісі, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Остапчук Е.О. **–** PhD, қауымдастырылған профессор, Иммунология және иммунобиотехнологиялар зертханасының меңгерушісі, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Перфилиева Ю.В. **–** PhD, қауымдастырылған профессор, жетекші ғылыми қызметкер, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Лушова А.В. **–** магистр, Әл-Фараби атындағы Қазақ ұлттық университеті, лаборант, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Қуатбекова С.А. **–** магистр, ғылыми қызметкер, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Абдолла Н. **–** PhD, аға ғылыми қызметкер, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Кулигин А.В. **–** студент, Әл-Фараби атындағы Қазақ ұлттық университеті, лаборант, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Мәшжан А.С. **–** докторант, ғылыми қызметкер, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.

Мамадалиев С.М. – ветеринария ғылымдарының докторы, профессор, Ұлттық биотехнология орталығы, Джахангер көш., 14, Алматы, Қазақстан.