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CRIMEAN-CONGO HEMORRHAGIC FEVER: REVIEW OF THE EPIDEMIOLOGICAL SITUATION, DISTRIBUTION AREA, VIRUS CHARACTERISTICS, DIAGNOSIS, AND DISEASE PREVENTION

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Abstract. This review article addresses the etiology, epidemiology, distribution of Crimean-Congo hemorrhagic fever (CCHF), and its diagnosis and prevention. Crimean-Congo hemorrhagic fever (CCHF) is one of the deadly hemorrhagic fevers endemic in Africa, Asia, and Europe. It is a tick-borne zoonotic viral disease caused by the CCHF virus of the genus *Nairovirus*, family *Bunyaviridae*. In Kazakhstan, natural foci of CCHF are located in the Zhambyl, Turkestan, and Kyzylorda regions, as well as the city of Shymkent. In Kazakhstan, 108 confirmed cases of CCHF were registered in humans during the period from 2021 to 2023. The virus genome consists of small (S), medium (M), and large (L) segments, encoding nucleocapsid proteins (N), envelope glycoproteins (G1 and G2), and polymerase complex proteins, respectively. Most human cases were associated with agricultural activities such as animal husbandry, haymaking, and livestock slaughter. Humans are most commonly infected by tick bites. Clinical signs usually indicate the rapid progression of the disease, which is accompanied by bleeding, muscle pain, and fever. Now, there is no specific treatment, and the most important measures are preventive safety practices. For the diagnosis of CCHF, methods such as ELISA, RT-PCR, and real-time RT-PCR are used.

Keywords: CCHF; arboviruses; infection; review; diagnosis; prevention.

Introduction

Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne viral disease widely distributed around the world, belonging to the order *Bunyavirales*, family *Nairoviridae*, genus *Orthonairovirus*. The disease affects only humans, with its natural cycle involving wild mammals, livestock, birds, and ticks [1]. More than 30 species of ixodid ticks serve as reservoirs and vectors for the CCHF virus. Ticks of the genus *Hyalomma* are recognized as the primary vectors, with *H. marginatum* being the most effective carrier. The main hosts for these ticks are domestic livestock. However, humans can become infected through contact with the blood, biological fluids, and tissues of infected livestock or through the bite of an infected tick. The infection can also be transmitted from person to person through direct contact with the blood and biological fluids of infected individuals, particularly in healthcare settings [2,3].

Viral hemorrhagic fevers today present a significant challenge to both national and international health systems. The registration of new endemic areas for these dangerous infectious diseases, active migration processes with a high risk of pathogen introduction into non-endemic

areas, as well as the potential use of the virus as a biological weapon, underscore the importance of addressing this issue.

According to the Ministry of Health of the Republic of Kazakhstan, CCHF and its natural foci hold special significance for the country. To successfully combat this infectious disease, further research in several areas is necessary.

Kazakhstan's diverse natural and climatic conditions are home to a wide range of ixodid tick species, including *Hyalomma asiaticum*, *H. anatolicum*, *H. scupense*, *H. marginatum*, *Dermacentor niveus*, *D. marginatus*, *Haemaphysalis punctata*, *H. sulcata*, and *Boophilus calcaratus* [4].

The aim of this article is to present information on current knowledge and achievements in the field of CCHF epidemiology and distribution based on literature data.

The first studies of CCHF as a viral zoonotic disease affecting humans began in 1944-1945. During this time, cases of infection were recorded in the northwestern part of Crimea among residents and soldiers assisting in the harvest for collective farms [5]. The number of cases reached over 200, with a significant number being fatal. A scientific expedition led by M.P. Chumakov and a group of military doctors proved the pathological nature of the disease [6].

In June 1967, Soviet virologist Mikhail Chumakov registered an isolate from a fatal case in Samarkand, identifying the virus from arthropods [7].

From 1967-1969, it became known that the Congo virus, which shares antigenic properties with the CCHF virus, existed. Unlike Crimean hemorrhagic fever, the disease associated with the Congo virus was rarely observed in humans (fewer than 20 cases), but the virus was frequently detected in animals [8]. As a result, in 1973, the International Committee on Taxonomy of Viruses officially named the virus Crimean-Congo hemorrhagic fever [9].

Geographical Distribution of CCHF

The current distribution area of the CCHF pathogen coincides with the distribution of ticks, such as ixodid ticks of the genus *Hyalomma*, which covers Africa, Europe, and Asia [10]. European-Asian epidemic foci of this infection have been identified in Kazakhstan, Bulgaria, Greece, Hungary, Yugoslavia, France, Portugal, Turkey, as well as southern Europe and Russia, Ukraine, Moldova, Azerbaijan, Armenia, Pakistan, Afghanistan, China, Iran, India, the UAE, most countries in sub-Saharan Africa (Congo), Iraq [11,12].

Since the mid-1990s, there has been a clear increase in the number of natural disease foci in Afghanistan, Pakistan, South Africa, Kosovo, and Mauritania [13].

At the beginning of the new millennium, there was also a significant increase in CCHF cases in southern Russia. For the first time, CCHF was registered in Kalmykia and Ingushetia. During the same years (1999-2006), it appeared in Albania and Bulgaria [12,14].

According to ProMED-mail, in 2022, outbreaks of CCHF were reported in the UK - 1 case (imported from Central Asia), Côte d'Ivoire - 1 case, Uganda - 2 cases, Spain - 2 cases (1 fatal), Senegal - 2 cases, South Africa - 3 cases (1 fatal), Pakistan - 4 cases (1 fatal), Mauritania - 6 cases (2 fatal), Kazakhstan - 33 cases (4 fatal), Georgia - 45 cases (3 fatal), Turkey - 27 cases (1 fatal), Iran - 78 cases (9 fatal), Afghanistan - 250 cases (14 fatal), Iraq - 299 cases (55 deaths) [15]. Since January 2023, countries in these regions have been reporting unusually high numbers of cases.

From 1944 to 2022, a total of 13,042 cases of the disease were registered in 37 CCHF-endemic countries worldwide since official records began. Of these, 7,378 cases occurred in Asia, 5,297 in Europe, and 367 in Africa. As can be seen, a high incidence of CCHF is recorded in Asia, particularly in Afghanistan, Iraq, Iran, Pakistan, and Turkey [16].

Due to global climate change (increased average temperatures, changes in hydrological regimes, and intense anthropogenic landscape transformation), the territory of natural foci is gradually expanding in various parts of the world.

In Kazakhstan, natural foci of CCHF are found in the Kyzylorda, Turkestan, and Zhambyl regions, as well as the city of Shymkent. The main vectors of the virus in these areas are the ticks *H. asiaticum*, *H. anatolicum*, *H. scupense*, *H. marginatum*, and *D. niveus* (Figure 1). Each year, approximately 16 clinical cases are registered in Kazakhstan [17], with an average mortality rate of 14.8% [18].

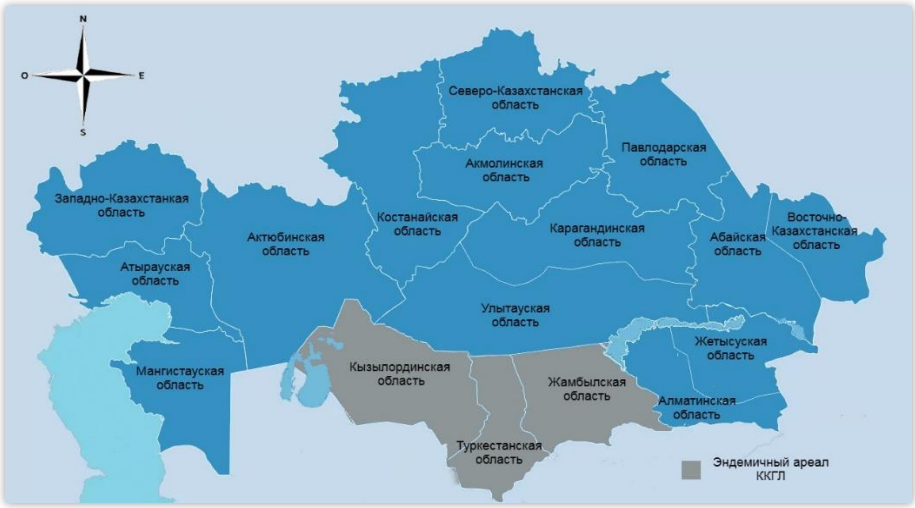

Figure 1 - Geographical Distribution of CCHF in Kazakhstan

The first cases of CCHF in Kazakhstan were registered in 1948 in the Maktaaral and Keles (Saryagash) districts of the Turkestan region, where the disease was known as “Central Asian fever.” Six cases were recorded [19]. From 1948 to 2022, a total of 357 cases of CCHF were reported. An analysis of morbidity showed that the highest rate of infections was in the Sozak district, accounting for 38% of cases. In recent years, cases have been most frequently reported in the Kazygurt, Ordabasy, Sauran, Otyrar, Tolebi, Keles, Maktaaral, Zhetisay districts, and in the city of Shymkent [20].

During a study conducted in 2011, 3,495 people were reported to have been bitten by ticks over the course of the year, with 108 individuals hospitalized with suspected CCHF, 47 of whom had a fever [21].

H. anatolicum and *H. scupense* are the most widespread tick species in the Turkestan region, and representatives of these species are found in almost all districts. *H. scupense* is the second most common, but with a low infection rate of 0.136. The highest infection rate was found in *H. anatolicum*, with an infection index of 0.542% [20].

In the Kyzylorda region, 215 cases of CCHF were registered among people from 1964 to 2022. An analysis of morbidity by district showed that the highest number of cases occurred in the Shieli district, accounting for 49% of all CCHF cases. Recently, cases have been reported in the Syrdarya, Zhalagash, Zhanakorgan, and Karmakshy districts. The main tick vectors in the region are *H. asiaticum* (32%), *H. scupense* (11%), and *Dermacentor niveus* (32%) [22]. It is worth noting that *Ixodes ricinus* ticks, which are not typical for this area, were identified in the Kyzylorda region.

Ixodes ricinus is a new species for the Kyzylorda region and for Kazakhstan. It is most likely introduced by migratory birds and mammals and requires more detailed study. Due to their small population, the role of this species in the epidemiology of natural epidemics is insufficiently understood [23].

In 1974, signs of CCHF circulation were detected during the monitoring of animals in the Zhambyl region [24]. The first case of the disease in humans was not reported for the next eight years. From 1982 to 2022, a total of 300 cases of CCHF were registered, 73% of which were in the Sarysu district, and the remaining 27% in the Moyynkum district. Recently, cases have been reported in the Talas, Zhambyl, Shu, and Baizak districts of the region. According to monitoring data, the vectors of ticks in the Zhambyl region are *H. asiaticum* and *H. scupense*, along with a significant number of *Dermacentor* species [22].

The most recent data on registered cases of CCHF in the republic from 2021 to 2023 was obtained from the National Center for Public Health under the Ministry of Health of the Republic of Kazakhstan, as well as from online resources [25-28]. This data is shown in the diagram (Figure 2).

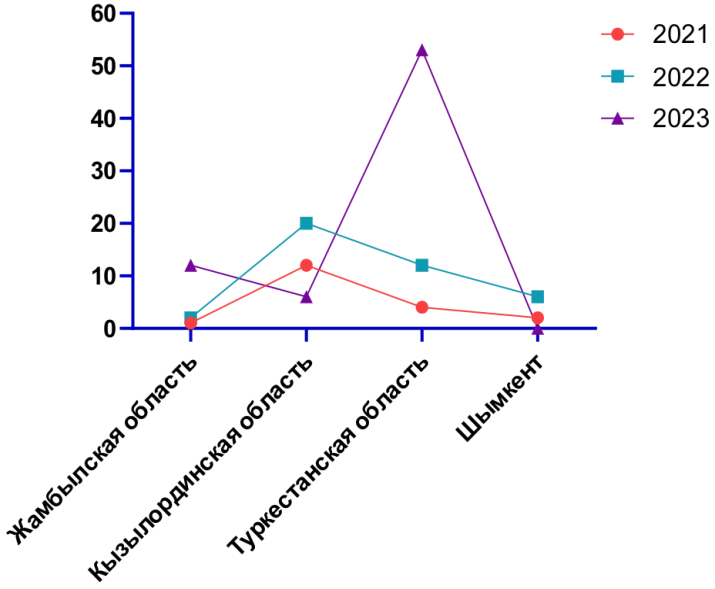

Figure 2 - Cases of CCHF Registered in Kazakhstan from 2021 to 2023

As seen in the diagram (Figure 2), 19 cases of CCHF were registered among the population of the republic in 2021. Among them, 1 case occurred in the Zhambyl region (1 fatal), 12 in the Kyzylorda region, 4 in the Turkestan region (1 fatal), and 2 in the city of Shymkent.

The incidence of CCHF across the republic doubled in 2023 compared to 2022. In 2022, 36 cases of CCHF were registered, including 20 cases in the Kyzylorda region (5 fatal), 12 cases in the Turkestan region (1 fatal), 2 cases in the Zhambyl region (1 fatal), and 6 cases in the city of Shymkent (6 fatal). One fatality each was recorded in the Zhambyl and Turkestan regions.

In 2023, the highest number of outbreaks occurred in the Turkestan region, where the number of cases reached 53, with 1 fatality. Over the past year, 12 cases were registered in the Zhambyl region, with 1 fatality, and 6 cases in the Kyzylorda region, with 3 fatalities.

Based on the above data, it can be noted that the incidence of CCHF is increasing annually across our republic. Therefore, it is necessary to improve the following preventive measures: provide training to healthcare workers on the diagnosis, treatment, and prevention of CCHF.

CCHF Virus Genome. CCHF virions have a spherical or oval shape, measuring 80-120 nm. They possess a single-layer lipoprotein envelope, 5-7 nm thick, covered with spikes 5-10 nm high, composed of two glycoproteins, Gn and Gc. The viral glycoproteins Gn and Gc are responsible for binding to receptors and enabling the virus to enter the host cell (Figure 3). These glycoproteins are mainly localized in the cytoplasm. The most susceptible cell cultures include porcine embryonic kidney, Syrian hamster kidney, and monkey kidney cells [29]. The RNA genome consists of three segments: small (S), medium (M), and large (L). Upon entry, these proteins produce positive-sense viral RNA using negative-sense genomic viral RNA as a template to initiate the production and replication of viral proteins (Figure 3) [30]. The virus genome is shown in Figure 3 [31].

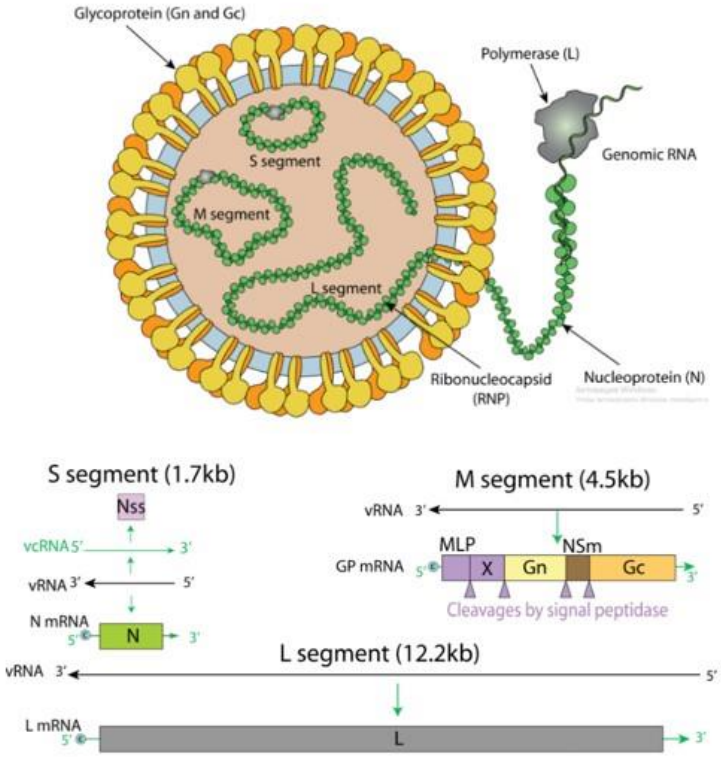

Figure 3 – Molecular Structure of the CCHF Virus

S-Segment. The small genome segment (S~1700 bp) encodes the viral nucleocapsid (N) along with a small non-structural protein (NSs) in the opposite reading frame (Fig. 3). In addition to interacting with viral RNA to form ribonucleoprotein complexes, NP has endonuclease activity, interacts with host heat shock proteins during viral intracellular replication, and in infectious particles, facilitates translation of viral mRNA, demonstrating NP protein's multifactorial role in the life cycle of CCHFV [32].

M-Segment. The M segment (~4500 bp) of the CCHFV genome encodes a viral glycoprotein precursor (GP). Compared to the M segment of other Bunyavirales, the M segment of CCHFV is more complex as the viral glycoprotein GP undergoes proteolytic processing, forming separate viral glycoproteins Gn and Gc28, the GP160/85 protein, which is further processed into a highly

glycosylated mucin-like domain (MLD), the GP38 protein, and a medium non-structural protein (NSm), which assists in glycoprotein processing and virion assembly (Fig. 3) [33].

L-Segment. Consisting of more than ~12,000 bp, the large (L) segments of CCHFV and its related orthonairoviruses are unusually large for the Bunyavirales order (Fig. 3). The encoded L protein contains an RNA-dependent RNA polymerase with cap-snatching functions [34-36].

The virus is unstable in the environment, dying instantly when boiled, after 20 hours at 37°C, and after 2 hours at 45°C. In a lyophilized state, it can persist for over two years. The RNA polymerase has a mass of 200 kDa [37].

Transmission Routes. The primary transmission route of CCHFV is via tick bites, either by sucking blood or biting an infected tick. Contact transmission is also possible when a tick is crushed, or through damaged skin when in contact with infected animals or humans, and aerosol transmission when the virus is present in the air. Additionally, there is a risk of nosocomial transmission, i.e., when medical instruments and equipment are insufficiently processed or sterilized, and needles are reused.

Humans have a high natural susceptibility to CCHFV. Transmission to humans through tick bites can occur in open fields, hay-fields, animal enclosures, during nature trips, on farms, and especially in rookeries of rooks. Moreover, other birds such as crows and magpies can also carry ticks [38].

The highest risk group includes rural residents who have large and small livestock, livestock workers, and shepherds who come into contact with ticks when tending to livestock. The first contact between ticks and livestock grazing on pastures occurs in the spring, after the livestock leaves its winter quarters. In the spring, when the average daily temperature exceeds 10°C, ticks become active, emerging from the soil and seeking food (warm-blooded animals). While caring for animals, people may unintentionally come into contact with ticks. Some rural residents remove ticks from animals with unprotected hands or crush them, which is most dangerous for transmitting CCHFV. Slaughtering or butchering livestock infected with ticks, and handling skins without protection can also lead to CCHFV transmission. Human infection cases are most frequently reported in the spring-summer period (May-June). During this time, the people most affected are those engaged in agricultural work, nature outings, and those in forested or green areas [39].

Clinical Features. The incubation period lasts from 1 to 14 days, with most cases between 2 and 9 days. Following infection, there are various clinical manifestations, and not all patients develop the classic CCHF syndrome. The prodromal phase is absent, with the disease onset being acute. In the first phase, there is a rapid rise in temperature, reaching 39-40°C or higher, along with headaches, chills (sometimes severe), facial and mucosal redness. Symptoms of systemic poisoning (severe weakness, myalgia, arthralgia, nausea, and vomiting) appear. The hemorrhagic second stage occurs after 2-4 days, and the patient’s condition rapidly deteriorates. Hemorrhages manifest as rashes, spots, and hematomas on the skin and mucous membranes. Gum and injection site bleeding intensifies. Epistaxis, gastric, and uterine bleeding may occur. Abdominal pain, liver discomfort, diarrhea, vomiting, and jaundice are possible. The illness lasts 10-12 days, but patients may remain severely weakened for 1-2 months. Complications may include septicemia, pulmonary edema, focal pneumonia, acute renal failure, otitis media, and thrombophlebitis. Fatality rates range between 2-50% [40-42]. Other symptoms may include sweating, nausea, dry mouth, headaches, dizziness, loss of appetite, polyneuritis, and memory loss. Some patients temporarily lose all their hair.

Recovery is typically complete but slow, taking up to a year. Mild fever without hemorrhages has also been reported in some cases [43].

As mentioned earlier, red blood cell and hemoglobin counts in peripheral blood increase. Signs of hypochloremic anemia appear during the hemorrhagic phase of infection.

The most common clinical manifestations of CCHF in Kazakhstan are fever, general weakness, appetite loss, somatic pain, nosebleeds, hemorrhagic rash, headache, hepatomegaly, and facial and neck hyperemia. Laboratory tests on patients with CCHF often reveal thrombocytopenia, anemia, leukocytosis, elevated ALT, ESR, hyperbilirubinemia, and proteinuria. Bleeding, primarily epistaxis and gum bleeding, occurs on days 2-6 of the illness.

A notable feature of the CCHF clinical presentation in the region is the delayed onset of hemorrhagic syndrome, especially internal organ bleeding, occurring on days 8-11 of the disease onset [44].

Diagnosis. Laboratory diagnosis of CCHF is based on detecting the virus, its structural components, and virus-specific antibodies. There are three main groups of methods: virological, immunological, and molecular-genetic [45].

The primary virological method involves isolating the CCHF virus from clinical material. Researchers use methods such as intracerebral infection of newborn white mice and rats with biological material or virus adaptation to several animal-derived cell cultures. These methods are undoubtedly the most reliable but also the most expensive and labor-intensive, making them less competitive with faster analytical methods required for monitoring naturally infected nests [45-47].

Immunological methods in CCHF laboratory diagnostics are used to detect antibodies and antigens in biological samples such as human and animal serum, tissues, and organs, and to characterize the obtained CCHF virus strain. Most often, methods like electron microscopy and enzyme-linked immunosorbent assay (ELISA) are used for this purpose. It should be noted that comparative analysis of modern and classical serological methods has shown that ELISA significantly outperforms classical serological methods in terms of sensitivity [48].

Recently, molecular-genetic methods based on reverse transcription and polymerase chain reaction (RT-PCR) have been used for diagnosing CCHF and genetic characterization of isolates and obtained viruses. This method allows the detection of viral RNA in the early stages of the disease when serological methods do not yield positive results, as the immune response has not yet fully developed [49]. Additionally, this method allows the preliminary genotyping of the virus by directly determining the nucleotide sequence of PCR fragments from the genome if the selected region permits it. However, traditional RT-PCR methods are time-consuming, slow, and prone to amplicon contamination. Real-time RT-PCR (RT-PCR RV) addresses these issues, providing rapid, simultaneous amplification, detection, and quantification of target nucleic acids using specific probes labeled with fluorophores or nonspecific DNA-binding dyes [50].

In Kazakhstan, the main focus of development is ultra-fast test kits and tests that accelerate diagnosis and, consequently, ensure timely treatment, reduce the frequency of secondary infections, and prevent complications. Therefore, it is highly relevant to improve and develop new methods for diagnosing CCHF, including ELISA diagnostics, methods based on RT-PCR, and restriction analysis methods.

Prevention. Since there is no specific treatment for CCHF, preventive measures are the most important. Preventive measures include avoiding tick bites by using repellents, avoiding tick-infested areas, and systematically inspecting clothing and skin. To prevent tick attachment,

wearing long pants, boots, and long-sleeved shirts is recommended [51-54]. Large and small livestock should be treated with acaricides to control ticks, especially before slaughter and export to other regions. Viruses in meat are usually inactivated by acidification after slaughter. They also die when cooked (at 56°C for 30 minutes). Unpasteurized milk should not be consumed [51,52]. Laboratory workers should strictly adhere to biosafety measures, especially when performing procedures that generate large droplet aerosols, such as coughing or vomiting, and respiratory isolation should be used when negative pressure is present. Strict universal precautions are necessary to prevent nosocomial infections [51-53]. People entering a patient's room should wear gloves and gowns, while those approaching within one meter should wear protective masks or surgical masks and eye protection to prevent contact with blood and other bodily fluids [53].

Currently, no antiviral drug has passed clinical trials for treating patients with viral hemorrhagic fever. Therefore, for a long time, treatment for patients has been limited to symptomatic therapy aimed at relieving the main clinical symptoms. Ribavirin, a drug with direct antiviral activity, has been shown to be effective against CCHFV in vivo and in vitro [55].

There is no globally recognized vaccine against CCHF. However, a vaccine has been used in Bulgaria since 1974. The Bulgarian vaccine originated in the Union of Soviet Socialist Republics (USSR). Data on the immunogenicity of vaccines derived from mouse brain tissue are limited; a 2012 study showed that re-vaccination of healthy volunteers resulted in the production of a high level of antibodies against CCHF [56].

However, the vaccine is approved for use only in Bulgaria and not in other countries.

International approval is unlikely due to the potential for allergic and autoimmune reactions.

Given the limited medical measures for prevention and treatment, supportive therapy remains the standard of care for CCHF.

Conclusion

One of the important tools in combating this infection is epidemiological surveillance. Despite a timely surveillance system in Kazakhstan, more efforts are needed to expand the surveillance system not only within the country but also across all cross-border endemic regions, as identifying the origin of an outbreak generally facilitates the fight against it.

Farmers and private livestock owners should be informed about an outbreak of the disease, especially if it is related to hemorrhagic fever.

Environmental protection workers should raise public awareness of hygiene, sanitation, and tick control, as controlling ticks in the environment is the best way to fight CCHF. Additionally, information about the CCHF virus should be shared on social media, television, radio, billboards, magazines, and newspapers.

Health, environmental protection, and agricultural authorities should cooperate in combating this infection, especially when it involves human-animal interaction.

Given that CCHF is a disease with pandemic potential, it is essential to conduct a risk assessment for the population living in the area where the case occurred. Such data would be useful for determining the level of CCHF exposure in the population and the prevalence of tick-borne infections. Additionally, we propose developing cross-border cooperation between countries to standardize diagnostic procedures and increase awareness among professionals. This includes building diagnostic capacity and networks for sharing case information.

Due to the lack of specific treatments or approved vaccines for CCHF infection, accurate and early detection, reliable epidemiological surveillance, and quantitative virus assessment are needed to improve health outcomes and patient management. To address these challenges, the development of test systems based on the multiplex polymerase chain reaction (PCR) method in real-time (RT-PCR) is necessary.

Furthermore, digital PCR could serve as a valuable complement to the modern quantitative PCR used for the diagnosis of the CCHF virus.

Thus, the implementation of molecular-genetic identification methods for the CCHF virus in laboratory practice and the use of modern bioinformatics analytical approaches in epidemiological studies will improve the effectiveness of CCHF epidemiological surveillance, ensure the quality of epidemiological decryption of disease cases, study virus evolution, and provide a basis for further research.

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КОНГО-ҚЫРЫМ ГЕМОРРАГИЯЛЫҚ ҚЫЗБАСЫ: ЭПИДЕМИОЛОГИЯЛЫҚ ЖАҒДАЙҒА ШОЛУ, ТАРАЛУ АЙМАҒЫ, ВИРУСТЫҢ СИПАТТАМАСЫ, АУРУДЫҢ ДИАГНОСТИКАСЫ ЖӘНЕ АЛДЫН АЛУ

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Аннотация. Шолу мақалада Конго-Қырым геморрагиялық қызбасының этиологиясы, эпидемиологиясы, таралуы, нақты аурудың диагностикасы және алдын алу мәселелері қарастырылды. Конго-Қырым геморрагиялық қызбасы (КҚГҚ) Африкада, Азияда және Шығыс Еуропада таралған, өлімге әкелетін геморрагиялық қызбалардың бірі болып табылады. Бұл Bunyaviridae тұқымдасының Nairovirus тектес КҚГҚ вирусынан туындаған кене арқылы таралатын зоонозды вирустық ауру. Қазақстанда КҚГҚ табиғи ошақтары

Жамбыл, Түркістан, Қызылорда облыстарының және Шымкент қаласының аумақтарында орналасқан. Қазақстанда 2021-2023 жж. адамдарда ККҒҚ 108 расталған жағдайы тіркелген. Вирустық геном сәйкесінше нуклеокапсид (N) ақуыздарын, конверттік гликопротеиндерді (G1 және G2) және полимеразды кешенді ақуыздарды кодтайтын шағын (S), орташа (M) және үлкен (L) сегменттерден тұрады. Адамдардың ауруларының көпшілігі мал бағу, шөп дайындау және мал сою сияқты ауыл шаруашылығы өндірісімен байланысты болды. Көбінесе адам кене шағуы арқылы жұқтырады. Клиникалық белгілер әдетте аурудың жылдам дамуын көрсетеді. Ол қан кетумен, бұлшықет ауырсынуымен және безгегімен бірге жүреді. Бүгінгі күні арнайы емдеу жоқ, ең маңызды әдіс профилактикалық қауіпсіздік шаралары болып табылады. ККҒҚ диагностикасы үшін ИФА, КТ-ПТР және нақты уақыттағы КТ-ПТР әдістері қолданылады.

Түйін сөздер: ККҒҚ; арбовирустар; инфекция; шолу; диагностика; алдын алу.

КОНГО-КРЫМСКАЯ ГЕМОРРАГИЧЕСКАЯ ЛИХОРАДКА: ОБЗОР ЭПИДЕМИОЛОГИЧЕСКОЙ СИТУАЦИИ, АРЕАЛ РАСПРОСТРАНЕНИЯ, ХАРАКТЕРИСТИКА ВИРУСА, ДИАГНОСТИКА И ПРОФИЛАКТИКА БОЛЕЗНИ

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Аннотация. В обзорной статье были рассмотрены вопросы этиологии, эпидемиологии, распространения Конго-Крымской геморрагической лихорадки, диагностики и профилактики актуальной болезни. Конго-крымская геморрагическая лихорадка (ККГЛ) - одна из смертельных геморрагических лихорадок, эндемичных в Африке, Азии и Европе. Это клещевое зоонозное вирусное заболевание, вызываемое вирусом ККГЛ рода Nairovirus, семейство Bunyaviridae. В Казахстане природные очаги ККГЛ расположены на территориях Жамбылской, Туркестанской, Кызылординской областей и городе Шымкент. В Казахстане за период 2021-2023 гг. зарегистрировано 108 подтвержденных случая ККГЛ у людей. Геном вируса состоит из малых (S), средних (M) и больших (L) сегментов, кодирующих белки нуклеокапсида (N), гликопротеины оболочки (G1 и G2) и белки полимеразного комплекса, соответственно. Большинство случаев заболеваний человека были связаны с сельскохозяйственным производством, такие как уход за животными, заготовкой сен, забоем скота. Чаще всего человек заражается при укусе клещом. Клинические признаки обычно свидетельствуют о быстром прогрессировании заболевания. Оно сопровождается кровотечением, болью в мышцах и лихорадкой. На сегодняшний день не существует определенного лечения, наиболее важными способами являются профилактические меры безопасности. Для диагностики ККГЛ используются методы ИФА, ОТ-ПЦР и ОТ-ПЦР реального времени.

Ключевые слова: ККГЛ; арбовирусы; инфекция; обзор; диагностика; профилактика.