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UDC 578:578.4:578.42 **Review article**

The role of Culicoides vectors in the transmission of the bluetongue virus in Kazakhstan and adjacent regions

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Abstract

The bluetongue virus (BTV) is a transmissible pathogen whose circulation in natural and economic systems is determined by the triad "susceptible hosts – competent *Culicoides* woodlice – seasonal and climatic conditions". The non-contact nature of transmission (mainly through Culicoides bites) means that the risk of outbreaks is determined not so much by the "density of animal–animal contacts" as by the intensity of host-vector contacts and the timing of host viremia with vector activity.

Epizootologically cattle are often the key "hidden" link: infection in cattle is usually asymptomatic, but viremia can be relatively long-lasting, which increases the likelihood of infection by woodlice and maintenance of transmission when co-grazing with sheep (clinically the most vulnerable).

Complementary evidence of BTV circulation has been published for Kazakhstan: a 1997-1998 serological examination revealed widespread seropositivity in cattle/sheep/goats (~21-25%), which was interpreted as endemic in the absence of clinical recognition, and a 2021 review of the model risk assessment showed pronounced seasonality of potential transmission (spring-summer, peak in July) and a spatial gradient risk assessment, molecular research 2022-2024. The detection of BTV RNA in animals and in some *Culicoides* species in the southern regions was confirmed, while typing indicates the presence of at least separate genetic lines (BTV-9 "western topotype" was reported). Together, this justifies the transition from "serological confirmation of contact" to risk-based continuous surveillance with simultaneous monitoring of hosts and vectors.

Keywords: bluetongue; virus; blood-sucking woodlouse of the genus *Culicoides*; serotype; vector.

Introduction

Bluetongue is a non-contagious transmissible viral disease of ruminants, mainly sheep, whose clinical manifestations are associated with systemic damage to the microcirculatory vessels and impaired tissue blood supply [1].

The causative agent of the disease is a virus belonging to the genus *Orbivirus* of the family Reoviridae. *Orbiviruses* are non-enveloped virions composed of a three-layered icosahedral capsid and containing a segmented genome. The bluetongue virus genome consists of ten segments of double-stranded RNA (S1-S10), which encode seven structural proteins (VP1-VP7) that form the architecture of the virion, as well as at least four non-structural proteins (NS1-NS4) involved in virus replication and interaction with the host cell [2].

BTV is one of the transboundary animal diseases that pose a significant threat to livestock farming due to its ability to spread rapidly across geographical areas and infect large populations of susceptible hosts

[3, 4]. The main feature of bluetongue epizootiology is the vector transmission route, which is carried out through blood-sucking midges of the genus *Culicoides*, allowing the virus to spread independently of direct contact between animals and to cross state and natural borders [4,5].

The transboundary significance of bluetongue is exacerbated by international trade in animals and animal products, as well as by changes in climatic factors that contribute to the expansion of the range and seasonal activity of vectors [5]. Outbreaks of the disease have been repeatedly recorded in regions previously considered non-endemic, highlighting the virus's ability to re-establish itself and circulate sustainably in new epizootic conditions [3].

Both domestic and wild cloven-hoofed animals are susceptible to BTV, although the degree of susceptibility and epizootiological role of different species vary. Sheep are considered to be the most susceptible, as the infection often takes a clinically pronounced form in them and serves as an epizootological indicator of the pathogen's circulation [6].

The incidence rate among sheep can reach 100%, and the mortality rate can reach 50%, which determines their key role in the epizootic process. Cattle, goats, and camels usually carry the infection in a subclinical or inapparent form and act as reservoirs for the virus, contributing to its preservation and spread in the epizootic system. It has been established that the virus is capable of persisting in the body of animals for a long time in the presence of specific antibodies. Cases of intrauterine infection are of particular epizootological significance, as the birth of dead or non-viable embryos may occur long after the mother's body has been infected [6].

In this regard, bluetongue is included in the list of priority diseases of the World Organisation for Animal Health (WOAH), and its control requires coordinated international measures, including epizootic surveillance, vector monitoring, restrictions on animal movements, and the application of preventive strategies [4, 5]. For countries with long borders and developed pastoral livestock farming, including Kazakhstan, bluetongue is of particular epizootic significance as a potential factor in cross-border risks [5].

Currently, the status of BTV in Kazakhstan shows active circulation with increasing seroprevalence, while in neighboring Central Asian countries, data are limited or outdated. The main risk factor is the presence of *Culicoides* vectors throughout the region [7].

The purpose of this review article is to analyze the role of *Culicoides* vectors in the transmission of bluetongue virus in Kazakhstan and neighboring regions based on current data on their species composition, biological and ecological characteristics, as well as factors affecting the circulation of the pathogen, with an assessment of the epizootological situation and current approaches to the control and prevention of infection.

Materials and Methods

This review article was conducted using a systematic analysis of scientific literature and available epizootological data on bluetongue virus circulation and Culicoides vectors in Kazakhstan and adjacent regions.

Scientific publications indexed in international databases, including Web of Science, Scopus, and PubMed, as well as reports from international organizations such as the World Organisation for Animal Health (WOAH), were analyzed. In addition, regional studies and epizootological monitoring reports related to bluetongue virus circulation in Central Asia were included in the analysis.

The selection of literature sources was based on their relevance to the epidemiology of bluetongue virus, vector ecology, host susceptibility, and environmental factors influencing virus transmission. Publications from the last decades with particular emphasis on recent studies were prioritized. The collected information was systematized and analyzed to identify key patterns in the circulation of bluetongue virus, the role of Culicoides vectors, and the environmental and biological factors affecting the epizootic process in Kazakhstan and neighboring regions.

Results and Discussion

Virus hosts and the epizootic role of populations

BTV belongs to the genus Orbivirus of the family Reoviridae and causes a transmissible non-contagious infection in domestic and wild ruminants, in which the pathogen is not transmitted through normal direct contact between susceptible hosts [8, 9]. The BTV genome consists of ten segments of double-stranded RNA, and the virion is characterized by a double-layer capsid structure that plays a key role in the formation of the virus's antigenic properties. In particular, the internal capsid protein VP7 determines serogroup specificity, while the outer protein VP2 is the main determinant of the serotype-specific immune response and is used in serotype identification of the virus [8, 9].

From a biological point of view, BTV is a strictly vector-dependent pathogen transmitted by blood-sucking midges of the genus *Culicoides*. Carriers become infected when they feed on viremic animals, after which the virus undergoes an exogenous replication cycle in the insect's body. According to data from the World Organisation for Animal Health, the replication period required to achieve infectivity lasts an average of 6-8 days, after which infected midges remain capable of transmitting the virus throughout their lives [8]. This feature ensures the effective maintenance of virus circulation in natural and agricultural ecosystems.

The epizootological significance of various species of ruminants is determined not only by their susceptibility to infection, but also by the nature of the clinical course of the disease. These parameters do not always coincide: for example, cattle are often infected subclinically, but are capable of maintaining viremia for a long time and serving as an important reservoir of infection, ensuring the infection of vector populations and the further spread of the virus [8, 9, 10].

For vertebrate hosts, the difference between infectious viremia and persistent viremia is of fundamental importance. Infectious viremia is characterized by the presence of viable virus in the blood capable of infecting *Culicoides* midges during blood feeding, whereas viremia reflects only the detection of the viral genome by PCR and can persist for much longer without necessarily retaining transmissibility [10, 11]. Experimental studies have shown that the duration of viremia infectious to vectors is limited in time and depends on the host species, despite the longer detection of viral RNA in the blood of infected animals [10].

Table 1. Epizootological parameters of bluetongue virus infection in major domestic and wild ruminant species [8-16]

Host / Population	Susceptibility to Infection	Clinical Manifestation (Typical)	Duration of Infectious Viremia (Approx.)
Sheep	High	High; severe forms and mortality possible in susceptible breeds	11-54 days (depending on serotype/conditions and method)
Cattle	High	Often asymptomatic; clinical signs possible with certain serotypes	Usually <60 days; in datasets up to ~63 days; in some experiments up to 49 days with proven infectiousness to Culicoides
Goats	High	Often asymptomatic or mild; clinical disease possible	27-54 days (experimental data for European breeds)
Saiga (wild populations)	Not specified (limited direct evidence of infection)	Not specified	Not specified
Roe deer (Capreolus capreolus)	Susceptibility confirmed by serological and molecular findings in Europe	Often subclinical; clinical signs variable	Not specified
Red deer (Cervus elaphus)	High (experimentally confirmed)	Often without obvious clinical signs; prolonged viremia possible	Not specified (for “infectious” viremia, Xeno diagnostic/vector-competent data required)

Mechanically prolonged viremia in ruminants is associated with the interaction of the virus with erythrocytes, which ensures long-term circulation of the virus in the bloodstream without active replication in blood cells. Unlike vertebrate hosts, the infection is persistent in carriers, and after the end of the exogenous incubation period, ticks remain infectious throughout their lives [10]. This feature forms a stable system for maintaining the virus in natural and agricultural ecosystems.

The epizootiological role of different ruminant species varies significantly depending on their clinical susceptibility and ability to maintain viremia. In mixed herds (sheep, goats, and cattle), a unique epizootiological "bridge" is formed, ensuring the circulation of the virus. Sheep, as a rule, show pronounced clinical symptoms and serve as an indicator of virus circulation, while cattle and, probably, goats often carry the infection subclinically but are capable of maintaining longer viremia, which is infectious for carriers [8, 12]. As a result, subclinically infected animals play a key role in maintaining the epizootic process and creating a prolonged period of risk of virus transmission.

The practical significance of this feature is that the absence of clinical signs of disease in cattle cannot be considered an indicator of the epizootic well-being of the farm. On the contrary, asymptomatic infected animals can serve as a reservoir for the virus and ensure its hidden circulation, including the possibility of unnoticed introduction and persistence of infection in the carrier population [9, 10].

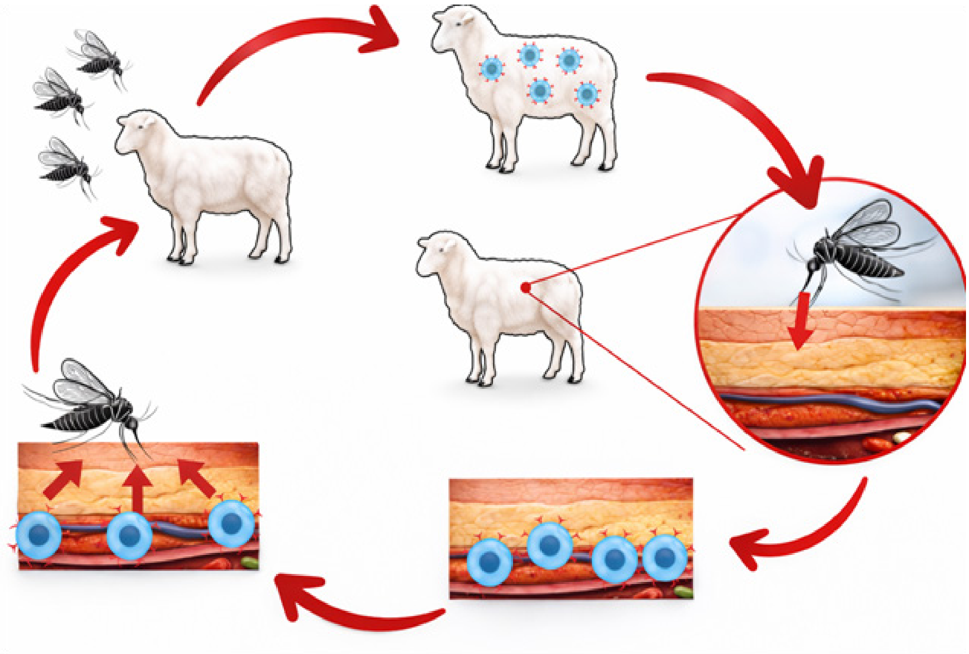


Figure 1. Diagram of transmissible transmission of BTV involving *Culicoides* midges and susceptible hosts (sheep)

The role of migratory wild animals in the spread of BTV is limited by a number of biological and environmental conditions. For effective transmission of the virus, a viremic host and active competent vectors must be present simultaneously along the migration route. Serological studies of saiga antelope (Saiga tatarica) in Kazakhstan have not detected antibodies to BTV, indicating no evidence of sustained virus circulation in populations of this species and making its role as a reservoir host unlikely under current conditions [17, 18]. However, the occasional involvement of wild ungulates in the circulation of the virus cannot be completely ruled out, especially in the presence of local epizootic foci.

Experimental and field studies conducted in Europe demonstrate the ambiguous role of wild ruminants in maintaining bluetongue virus circulation. In particular, red deer (Cervus elaphus) have been shown in experimental conditions to be capable of prolonged viremia, persisting for up to 98-112 days after infection, which could theoretically contribute to interaction with vector populations [15]. However, the results of long-term monitoring of natural populations in France did not confirm the role of red deer as a reservoir host for the virus, indicating the limited epizootological significance of this species in natural conditions [16].

Overall, the available data indicate that wild ruminants cannot be considered a proven reservoir of the bluetongue virus, but they can serve as epizootic indicators of virus circulation. Studies conducted in various regions of Europe have shown that monitoring the serological status of wild ruminants can be used for early detection of virus circulation and assessment of the spatio-temporal dynamics of infection [19, 20]. In this regard, wild ruminants in Kazakhstan should be considered primarily as potential "sentinel" species and subjects of epizootological monitoring, rather than as a confirmed reservoir of the virus.

The role of vectors as a key link in the epizootic process

The spread of the bluetongue virus is determined by the presence and activity of biological vectors, whose numbers and epizootic significance depend on a complex of micro- and macroclimatic factors, including temperature, humidity, wind speed, light intensity, and habitat characteristics [21, 22]. These parameters influence the growth rate, survival, feeding intensity, and spatial distribution of vector populations, determining the temporal and geographical boundaries of virus circulation.

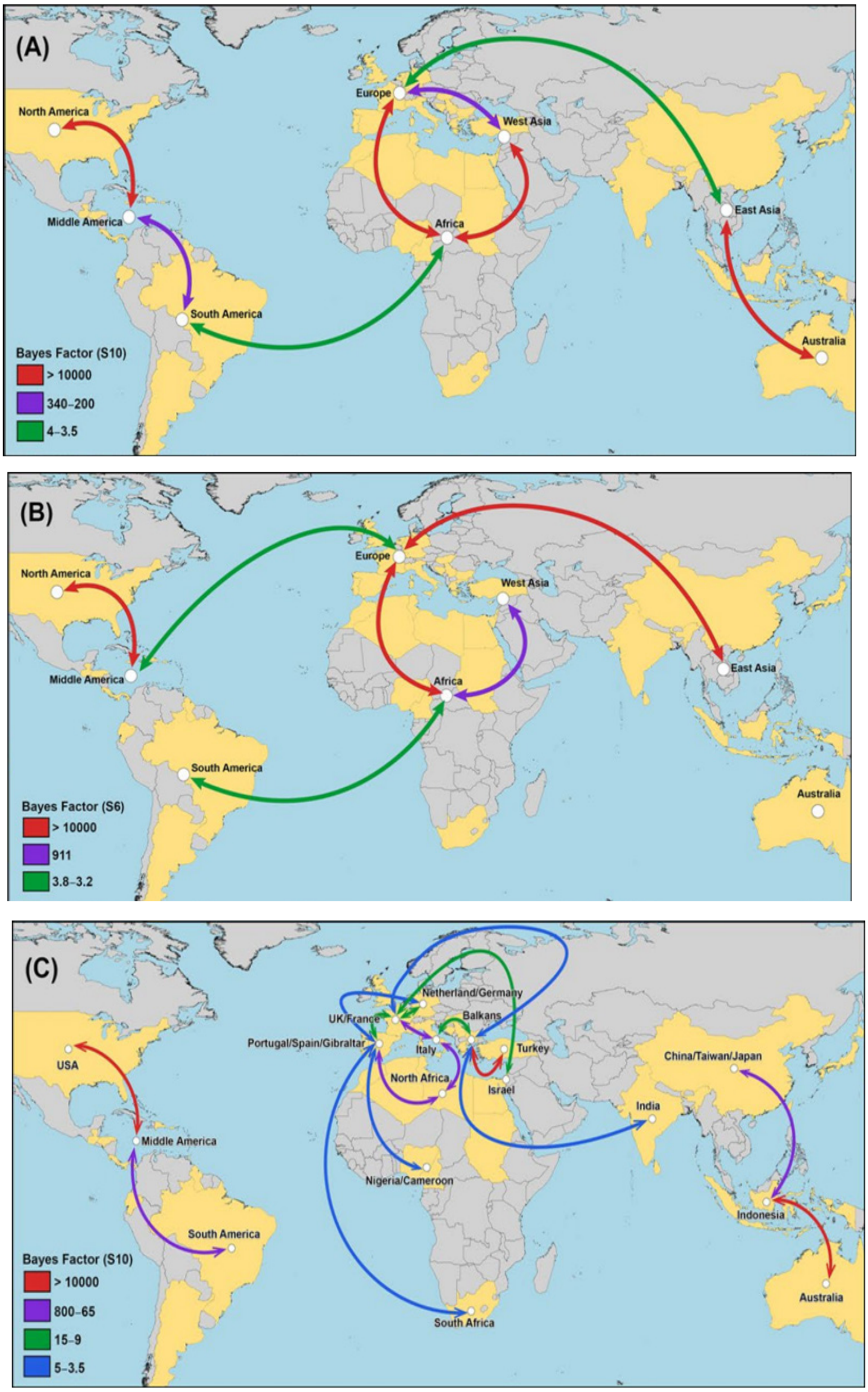
The bluetongue virus is transmitted mainly by blood-sucking midges of the genus *Culicoides,* which are the main biological vectors of the infection [6]. Currently, about 1,500 species of the genus *Culicoides* have been described, but the epizootological significance has been confirmed for at least 50 species, which is about 3% of their total diversity and reflects the expansion of understanding of the vector potential of this group [23]. These insects act not only as mechanical vectors but also as biological intermediate hosts, since the virus is capable of replicating in their bodies for a long time, ensuring subsequent transmission to susceptible vertebrate hosts [6].

The seasonal dynamics of *Culicoides* midge populations is a key factor determining the formation of the so-called "epizootological window" for bluetongue virus transmission. A model risk analysis for Kazakhstan showed pronounced seasonality of conditions favorable for virus transmission. According to forecasts, conditions for BTV transmission are absent during the winter period (approximately from October to March), while in April a low level of risk appears in the south of the country, which gradually expands geographically and reaches its maximum in July. Subsequently, there is a decrease in risk in September and its almost complete disappearance by October, reflecting the seasonal activity of vector populations and the climatic determinants of their numbers [13].

For most species, optimal conditions for flight and activity are observed at temperatures between +7 and +17 °C, while lower temperatures significantly limit their activity, especially at night [21, 22]. In addition, high light intensity can partially or completely suppress the activity of midges, while increased wind reduces the intensity of attacks on hosts, limiting the effectiveness of virus transmission. The characteristics of the habitat, including the type of ecosystem, vegetation index, soil cover properties, and degree of salinity, also have a significant impact, creating favorable or unfavorable conditions for maintaining stable vector populations [21, 22]. Thus, the epizootological role of vertebrate hosts is directly related to the phenology of herds and seasonal characteristics of animal husbandry, since spring and summer animal movements, the formation of herds, and the use of pastures coincide with the period of maximum risk of virus transmission.

The geographical spread of the bluetongue virus is closely linked to the habitat of various species of midges of the genus *Culicoides*, which are widespread in tropical and temperate climatic zones. The expansion of the range of vectors contributes to the emergence of new epizootic foci and changes in the spatial structure of virus circulation [24, 25].

Phylogeographic analysis of the bluetongue virus confirmed the existence of numerous intercontinental routes of spread, with Africa considered to be the key center of virus dispersion. It has been established that the most significant routes include the spread of the virus from Africa to Europe, Asia, and Australia, which is associated with a combination of factors, including the movement of infected animals, the spread of *Culicoides* vectors, and anthropogenic activity [26].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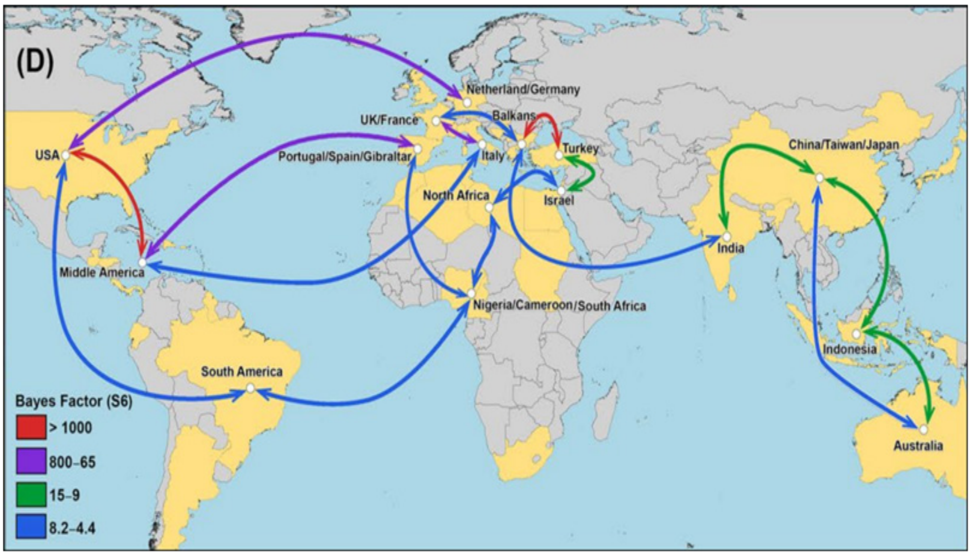


Figure 2. Phylogeographic reconstruction of the global distribution of the bluetongue virus based on genetic data analysis [26]

Thus, *Culicoides* midges are a key link in the epizootic process, ensuring biological transmission of the virus between susceptible hosts. Their population dynamics, ecological adaptation, and dependence on climatic factors determine the spatio-temporal patterns of bluetongue virus circulation and shape the epizootological risk of infection emergence and spread.

The presence of antibodies to BTV in farm animals in Kazakhstan indicates the natural circulation of the pathogen in susceptible host populations in the absence of vaccination. Serological studies conducted in Central Kazakhstan in 1996-1998 revealed antibodies to BTV in 23.2% of the animals examined, confirming the circulation of the virus in the country during that period and indicating its persistent presence in the region [17].

The detection of antibodies in various farms in Central Kazakhstan indicates the focal nature of the infection and confirms the possibility of the formation of natural and economic epizootic foci. Additional serological data obtained from farm animals also confirm the circulation of the virus in the absence of vaccination, indicating natural mechanisms for maintaining the infection, probably associated with the presence of competent vectors of the genus *Culicoides* [27].

Recent studies confirm the continued circulation of the bluetongue virus in Kazakhstan. Specifically, between 2018 and 2020, antibodies to BTV were detected in 3.8% of the agricultural animals examined, and viral RNA was detected in 0.7%, mainly in sheep, which indicates the continuing epizootic process and the activity of natural focal transmission mechanisms [28].

Genetic analysis of the identified isolates showed that they belong to the western topotype of serotype BTV-9, which indicates the stable presence of this genetic variant of the virus in the region and confirms its circulation in local populations of susceptible hosts [28].

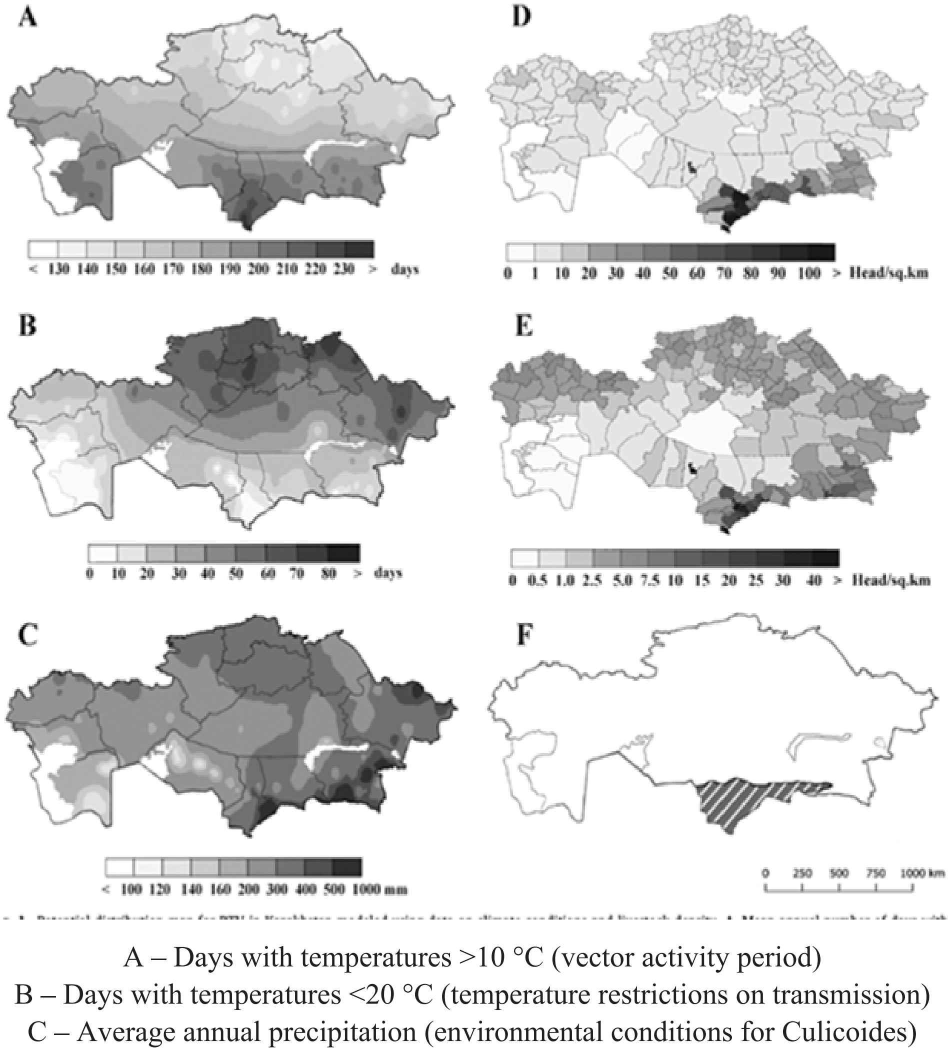
The persistence of bluetongue virus circulation in Kazakhstan is directly linked to the presence and seasonal activity of *Culicoides* vectors. Epizootic risk modeling has shown that virus transmission in Kazakhstan is highly seasonal and occurs mainly from April to September, with the highest risk in July, which corresponds to the period of maximum activity of midge populations [13]. During the winter period, from October to March, the basic reproduction number (R_0) remains below the threshold level required for sustained transmission of the infection, making the occurrence of epizootic outbreaks unlikely [13].

At the same time, the greatest potential for the spread of infection is observed in the northern and northeastern regions of the country, which indicates the influence of climatic and environmental factors on the spatial distribution of epizootological risk.

A key element in maintaining the circulation of the virus is the population of midges of the genus *Culicoides*, which are widespread in Kazakhstan. Entomological studies confirm the presence of several species of midges capable of transmitting the bluetongue virus, which creates the necessary conditions for the formation of stable natural foci of infection [30]. The presence of susceptible vertebrate hosts and competent vectors forms a functional epizootic system that ensures the preservation of the virus in the ecosystem and its periodic activation during favorable seasons.

The potential spread of BTV in Kazakhstan is closely linked to climatic conditions and the density of susceptible animals, which determine both the ability to maintain populations of *Culicoides* vectors and the intensity of virus transmission. Spatial risk modeling has shown that the most favorable conditions for virus circulation are found in regions with a sufficient number of warm days, moderate temperatures, and adequate precipitation, as well as a high density of small and large livestock. These factors create environmental conditions that promote the maintenance of stable vector populations and increase the likelihood of virus transmission between susceptible hosts [30].

Phylogeographic analysis of the bluetongue virus confirmed the existence of numerous intercontinental routes of spread, with Africa considered to be the key center of virus dispersion (Figure 2). The most significant routes have been identified as the spread of the virus from Africa to Europe, Asia, and Australia, which is associated with a combination of factors, including the movement of infected animals, the spread of *Culicoides* vectors, and human activity.



A – Days with temperatures >10 °C (vector activity period)
B – Days with temperatures <20 °C (temperature restrictions on transmission)
C – Average annual precipitation (environmental conditions for Culicoides)
D – Small ruminant density
E – Density of cattle
F – Potential spread of BTV based on climate and animal density
Figure 3. Main intercontinental routes of bluetongue virus spread identified by phylogeographic analysis [13]

Modern epizootological studies confirm the active circulation of the bluetongue virus in the southern regions of Kazakhstan. Thus, in the period 2022-2024, antibodies to BTV were detected in 27.4% of the animals examined, and viral RNA in 8.9%, while the virus was successfully isolated in cell culture, confirming the presence of an active epizootic process and the circulation of infectious strains of the virus in the population of susceptible hosts [30]. The isolation of the virus in cell culture is direct confirmation of the presence of a viable pathogen and indicates the continued functioning of the natural focal system of infection transmission.

Analysis of climatic and epizootological parameters has identified key factors determining the risk of BTV spread. These include the number of days with temperatures above +10 °C, corresponding to the period of vector activity, and the number of days with temperatures below +20 °C, reflecting the temperature limitations for effective virus transmission. The average annual precipitation, which determines the habitat conditions for *Culicoides* midges, is also of significant importance, as is the density of susceptible animal populations, including small and large ruminants, which serve as a source of the virus for vectors. These factors together form a spatial model of the potential spread of bluetongue virus and determine regions of increased epizootic risk [30].

The data obtained confirm that the circulation of the bluetongue virus in Kazakhstan is determined by the interaction of climatic factors, the density of susceptible animals, and the presence of competent vectors of the genus *Culicoides*, forming a stable epizootological system capable of sustaining the virus in natural and agricultural ecosystems [29].

The data obtained confirm that the circulation of the bluetongue virus is a complex epizootological process in which biological vectors, primarily midges of the genus *Culicoides*, play a key role. Despite the availability of data on the possible involvement of other arthropods in virus transmission, including mosquitoes of the *Culex* and *Aedes* genera, the sheep louse *Melophagus* ovinus, as well as ixodid ticks (*Dermacentor dagistanicus, Rhipicephalus kochi, Rhipicephalus bursa*), from which the virus has been isolated in natural foci, their epizootiological role remains secondary to that of Culicoides. The ability of ixodid ticks to transmit the virus transovarially and transphasically, as well as their long survival time, potentially contributes to the persistence of the pathogen in natural conditions, but the available data do not confirm their leading role in the formation of the epizootic process [31-33]. The main and most effective vector of the bluetongue virus remains midges of the genus *Culicoides*, which ensure biological transmission of the virus between susceptible vertebrate hosts. These insects are capable of spreading over considerable distances by air currents reaching hundreds of kilometers, which explains the rapid geographical expansion of the infection area and the emergence of new epizootic foci [34]. The spatial distribution of the virus is directly related to the ecology and distribution of vector populations, as confirmed by studies demonstrating a close relationship between the range of *Culicoides* and the circulation of the bluetongue virus [35].

The ecological characteristics of individual *Culicoides* species significantly influence their epizootological significance. For example, Culicoides *imicola* mainly inhabits open and well-lit areas, while representatives of the Obsoletus complex prefer shaded areas with dense vegetation, which determines their involvement in virus circulation in various natural and climatic conditions [36]. Field and molecular studies have confirmed the involvement of certain species of midges in virus transmission: in particular, viral RNA was detected in 15.00% of *Culicoides* imicola individuals and in 8.14% of *Culicoides oxystoma* individuals, confirming their role as biological vectors of BTV [37].

Wild ruminants can also participate in the epizootic process, acting as reservoir or indicator hosts. The virus is transmitted between wild and domestic animals via common vectors of the genus *Culicoides,* which contributes to the preservation of the virus in natural foci and its periodic introduction into livestock populations [35, 38].

Current epizootological data confirm the continued spread of bluetongue virus in various regions of Europe, which is associated with the activity of *Culicoides* vectors. In particular, the re-registration of the disease in Austria in 2024-2025 with the detection of serotypes BTV-3, BTV-4, and BTV-8, as well as the confirmation of infection in cattle in Ireland in 2026, indicate the continued circulation of the virus and the cross-border spread of the infection [39].

These data confirm the virus's ability to persist and spread in new regions when favorable climatic conditions and competent vectors are present.

Regional studies in Central Asia also confirm the active circulation of the bluetongue virus. In particular, serological testing of sheep in Kyrgyzstan revealed antibodies to the virus in 36.94% of animals, indicating widespread infection and the presence of conditions conducive to the functioning of a natural focal transmission system involving *Culicoides* vectors [7].

For Uzbekistan, Tajikistan, and Turkmenistan, within the scope of this review, comparable peer-reviewed information on the current circulation of BTV and vector composition in available sources has been identified as unspecified; Therefore, regional risk should be assessed through animal movement and the presence of *Culicoides* and seasonality based on climatic analogues, as well as through targeted surveillance in border areas [13].

Given the similarity of climatic conditions, geographical proximity, and the presence of susceptible animal populations, similar mechanisms of virus circulation may also be characteristic of Kazakhstan.

Given its climate, the presence of susceptible animal populations, and the distribution of *Culicoides* vectors, Kazakhstan is a region with potentially favorable conditions for bluetongue virus circulation. The presence of serological and molecular evidence of virus circulation, as well as environmental conditions conducive to the existence of vectors, indicate the functioning of a natural focal system of infection transmission. Under these conditions, *Culicoides* populations are a key element in the epizootic process, ensuring the maintenance and spread of the virus among susceptible hosts and creating an epizootic risk of disease outbreaks.

Conclusion

The analysis of available scientific data demonstrates that the circulation of bluetongue virus in Kazakhstan is determined by a complex interaction between susceptible hosts, competent Culicoides vectors, and environmental factors. Among these components, biting midges of the genus Culicoides represent the key biological link that ensures virus transmission between vertebrate hosts.

The presence of serological and molecular evidence of bluetongue virus circulation in livestock, together with favorable climatic conditions for vector development, indicates the existence of a natural epizootic system capable of maintaining the pathogen in the region. Seasonal vector activity, animal density, and environmental conditions play a decisive role in shaping the spatial and temporal patterns of virus transmission.

Given the transboundary nature of bluetongue and the presence of competent vectors in Kazakhstan and neighboring regions, continuous epizootological surveillance is required. Integrated monitoring of both susceptible animal populations and Culicoides vectors is essential for early detection of virus circulation and for the implementation of effective preventive and control measures.

Further studies should focus on the detailed investigation of vector species composition, ecological dynamics of Culicoides populations, and molecular characterization of circulating bluetongue virus strains in Central Asia.

Author Contributions

AI and OS: conceptualized and designed the study; NO and MK: performed literature review and data analysis; ZK: wrote the original draft; all authors reviewed and approved the final manuscript.

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