

Distribution of Crimean–Congo hemorrhagic fever virus in ticks of the Turkestan Region of Kazakhstan based on PCR surveillance data in 2025

Talgat Nurmakhanov, Altyn Rysbekova*, Nurkeldi Turebekov, Nur Tukhanova, B.K. Aimakhanov, Zauresh Zhumadilova, Gulnara Tokmurzieva, S.K. Umarova, Olzhas Yeskhozhayev, G.M. Sairambekova, T.Z. Sagidulin

Aikimbayev National Research Center for Especially Dangerous Infections, QazBioPharm National Holding, Almaty, Kazakhstan

* Corresponding author's Email: rysbekova570@gmail.com

ABSTRACT

Crimean–Congo hemorrhagic fever (CCHF) is a natural focal zoonotic infection of high epidemiological significance for the southern regions of Kazakhstan. This study aimed to detect Crimean–Congo hemorrhagic fever virus (CCHFV) RNA in ixodid ticks collected in the Turkestan region in spring 2025 using real-time reverse transcription polymerase chain reaction (RT-qPCR). A total of 468 ticks were examined and grouped into 96 pools according to species and collection site. CCHFV RNA was detected in four pools: three pools of *Hyalomma asiaticum* collected from small ruminants in the Sozak district and one pool of *H. scupense* from cattle in the Maktaaral district. The minimum infection rate (MIR) was 8.55 per 1,000 examined ticks (equivalent to 0.855%), indicating the activity of natural CCHFV foci in the surveyed locations with a relatively low intensity of virus circulation. Ticks of the genus *Hyalomma* predominated, accounting for 78.0% of all collected specimens, which is consistent with their leading role in the maintenance and transmission of CCHFV in endemic regions. The obtained results highlight the necessity of regular entomological and molecular surveillance within the One Health framework for early risk assessment and evidence-based planning of preventive measures.

Keywords: Crimean–Congo hemorrhagic fever virus, CCHFV, Ixodid ticks, *Hyalomma*, Real-time PCR, Turkestan region, Kazakhstan; Natural foci, Minimum Infection Rate (MIR).

Article type: Research Article.

INTRODUCTION

Crimean–Congo hemorrhagic fever virus (CCHFV; genus *Orthonairovirus*, family Nairoviridae) is the causative agent of one of the most clinically severe and epidemiologically significant viral hemorrhagic fevers affecting humans. The disease is endemic across vast territories of Africa, the Balkan Peninsula, the Middle East, Central Asia, and southern regions of Eastern Europe, predominantly south of the 50th parallel north latitude (CDC 2024; WHO 2025). CCHF is characterized by an acute onset, pronounced intoxication syndrome, hemorrhagic manifestations of varying severity, and a high risk of fatal outcome, particularly in the absence of timely medical care and adequate infection control measures. According to the World Health Organization (WHO), case fatality rates during CCHF outbreaks may reach up to 40%; however, most clinical series and systematic reviews report a wide range of fatality rates—from 5% to 30%—reflecting substantial variability in circulating viral strains, healthcare capacity, surveillance systems, and timeliness of diagnosis (Ergönül *et al.* 2018; Bente *et al.* 2013; WHO R&D Blueprint 2018; CDC 2024; WHO 2025). The high potential lethality of the disease, the absence of a licensed and widely available vaccine, and the risk of nosocomial transmission have led to the inclusion of CCHF among WHO priority pathogens requiring enhanced epidemiological surveillance and intensified research efforts (WHO R&D Blueprint 2018; WHO 2025). The primary route of CCHFV transmission to humans is

through the bite of infected ixodid ticks, predominantly of the genus *Hyalomma*, as well as through contact with blood and tissues of viremic livestock (large and small ruminants, camels) and infected humans. Nosocomial outbreaks associated with breaches in biosafety measures during patient care and invasive medical procedures pose a particular epidemiological threat (Maltezou *et al.* 2010; Ergönül *et al.* 2018; Bente *et al.* 2013; CDC 2024; WHO 2025). In this context, CCHF is regarded not only as a natural focal infection, but also as a significant challenge to healthcare systems, especially in endemic regions. In the Republic of Kazakhstan, natural foci of CCHF have historically been concentrated in the southern regions—namely, the Turkestan, Zhambyl, and Kyzylorda regions, as well as the city of Shymkent—where human cases are reported annually and comprehensive anti-epidemic and preventive measures are implemented. According to the epidemiological forecast of the National Center for Public Health (HLS/KZ), 25 confirmed cases of CCHF were registered in the country in 2025 [National Center for Public Health (HLS/KZ) 2025]. The Turkestan region represents one of the most stable endemic areas, with official case registration dating back to the mid-20th century, indicating the long-term persistence of natural foci and continuous circulation of the virus (Dobritsa 1965; Levchenko 1978). Ticks of the genus *Hyalomma* (*H. asiaticum*, *H. anatolicum*, *H. scupense*, and *H. marginatum*) are considered the principal vectors and, simultaneously, reservoirs of CCHFV in Eurasia. Their biological characteristics—high mobility, pronounced aggressiveness toward hosts, and the capacity for transstadial and transovarial virus transmission—facilitate sustained circulation of the pathogen in natural ecosystems (Hoogstraal & Kaiser 1966; Bente *et al.* 2013; Sultankulova *et al.* 2022; Berdikulov *et al.* 2025). Massive infestation of livestock by these ticks creates a persistent risk of human infection, particularly among livestock workers, veterinary personnel, and rural populations (Maltezou *et al.* 2010; Sultankulova *et al.* 2022). Previous studies conducted in Kazakhstan and neighboring countries have investigated CCHFV infection in ticks, including molecular genetic characterization of the virus, revealing the circulation of multiple genetic lineages belonging to the Euro-Asian and Asian clades (Hoogstraal 1979; Yashina *et al.* 2003; Deyde *et al.* 2006; Papa *et al.* 2017; Sultankulova *et al.* 2022; Berdikulov *et al.* 2025). At the same time, the high genetic variability of CCHFV—driven by its segmented genome organization and evolutionary pressure within natural foci—necessitates regular updating of data on virus distribution and circulation activity across specific administrative territories and seasons (Yashina *et al.* 2003; Deyde *et al.* 2006; Papa *et al.* 2017; Carroll *et al.* 2020). One of the most widely used indicators for assessing the intensity of pathogen circulation in vector populations is the minimum infection rate (MIR), which provides a quantitative estimate of the proportion of infected ticks when pooled samples are analyzed and is commonly applied in epidemiological studies of arboviral and naireoviral infections (Gu & Novak 2004; Biggerstaff 2009). Despite known methodological limitations, MIR remains a practical tool for comparative analyses between regions and seasons in surveillance studies. In this context, obtaining up-to-date data on CCHFV circulation in *Hyalomma* tick populations in the Turkestan region is of considerable importance for epidemiological risk assessment, improvement of surveillance systems, and scientific substantiation of preventive measures. The aim of this study was to investigate the circulation of Crimean–Congo hemorrhagic fever virus in the Turkestan region during the spring period of 2025 through molecular genetic analysis of pooled tick samples using real-time RT-PCR and calculation of the minimum infection rate (MIR).

MATERIALS AND METHODS

Study design

A cross-sectional field-based epizootological and epidemiological study was conducted to assess the circulation of Crimean–Congo hemorrhagic fever virus (CCHFV) in ixodid tick populations. Sampling was performed during the period of high seasonal tick activity (*Hyalomma* spp.) in April 2025, which corresponds to the peak risk of virus transmission to humans in endemic regions of Central Asia (Messina *et al.* 2015; Estrada-Peña & de la Fuente 2017). The study comprised field collection of ticks, laboratory species identification, pooling of specimens, molecular detection of viral RNA, and calculation of infection indicators.

Environmental and climatic characteristics and sampling areas

The Turkestan region is located in the southern part of the Republic of Kazakhstan (41–46° N, 65–74° E) and is characterized by pronounced environmental and climatic heterogeneity, including forest–meadow–steppe zones of foothill areas, as well as semi-desert and desert lowland territories. This combination of landscapes, climatic conditions, and land-use patterns promotes the formation of stable natural foci of vector-borne infections, including CCHF, and supports a high diversity of tick hosts (Gaidamovich *et al.* 1981; WHO R&D Blueprint

2018). Sampling was carried out in rural settlements and pasturelands traditionally associated with reported human cases and infection among animals.

Tick collection

Ixodid ticks were collected using two principal methods: (i) in open habitats by the flagging method using a white cotton cloth measuring 60 × 100 cm, which represents a standard approach for tick surveillance in natural biotopes; (ii) from livestock (large and small ruminants) by manual removal of ticks using sterile medical forceps. Each tick was placed into an individually numbered tube labeled with information on the district and sampling site, date of collection, and source (habitat type or animal host). All field activities were conducted in compliance with biosafety requirements: personnel wore protective clothing and gloves and used repellents, while collected material was transported in sealed containers [World Health Organization 2020; Centers for Disease Control and Prevention (CDC) 2020].

Species identification

Tick species identification was performed under laboratory conditions using a stereomicroscope based on morphological characteristics, including scutum shape, structure of the gnathosoma, legs, and anal shield. Identification was conducted using widely accepted taxonomic keys for ixodid ticks, including representatives of the genus *Hyalomma*, as well as members of the family Argasidae (Hoogstraal & Kaiser 1966; Levchenko 1978; Gu & Novak 2004; Maltezou *et al.* 2010). When necessary, species identification was independently verified by a second specialist.

Pooling strategy and homogenate preparation

For molecular analysis, ticks were combined into pools according to species and sampling location in order to optimize reagent consumption and increase analytical throughput. Pool sizes averaged 4–6 specimens, with a range of 1–10 ticks depending on sample availability, in accordance with recommendations for surveillance studies of vector-borne viruses (Mackay *et al.* 2002; Biggerstaff 2009). Tick homogenization was performed in 2.0 mL DNase/RNase-free tubes containing Dulbecco's Modified Eagle Medium (DMEM) and zirconia–silica beads (5 mm in diameter). Mechanical disruption of tick tissues was carried out using a TissueLyser II homogenizer (QIAGEN, Germany) following the manufacturer's recommendations for processing arthropod samples (Papa *et al.* 2017). After homogenization, the suspension was clarified by centrifugation at 800 × g for 5 minutes, and the supernatant was used for subsequent RNA extraction.

RNA extraction

Viral RNA was extracted from the clarified homogenate using a column-based method with the QIAamp Viral RNA Mini Kit (QIAGEN, Germany) or an equivalent certified kit routinely used in the laboratory, strictly following the manufacturer's instructions (Yashina *et al.* 2003). Each extraction run included a negative extraction control (buffer without sample) and, when provided by the kit, an internal extraction control to assess extraction efficiency and exclude cross-contamination (World Health Organization 2014).

Real-time RT-PCR

Detection of CCHFV RNA was performed by reverse transcription followed by real-time polymerase chain reaction (RT-qPCR) using the commercial reagent kit *AmpliSens® CCHFV-FL* (Central Research Institute of Epidemiology, Rospotrebnadzor, Russian Federation), which is validated for CCHF diagnostics. Amplification was carried out on a Rotor-Gene 3000 real-time PCR instrument (QIAGEN, Germany) in accordance with the manufacturer's instructions (Deyde *et al.* 2006; Carroll *et al.* 2020). Each RT-qPCR run included a positive control, a negative amplification control, and an internal control for inhibition (if provided by the kit), in compliance with the requirements for laboratory diagnosis of especially dangerous viral infections (Estrada-Peña & de la Fuente 2016).

Geographical visualization

Geographic coordinates (GPS) of sampling sites, as well as associated metadata (tick species, sampling source, number of specimens per pool, and RT-qPCR results), were recorded in an electronic database (Microsoft Excel). Spatial analysis and visualization were performed using ArcGIS software to generate maps showing the distribution of sampling locations and identified positive pools. During map preparation, requirements for proper

citation of cartographic basemaps and accurate data attribution were strictly followed (Yashina *et al.* 2003; Carroll *et al.* 2020).

Statistical analysis and MIR calculation

The minimum infection rate (MIR) was calculated as the ratio of the number of positive pools to the total number of examined ticks, multiplied by 1,000 (number of infected ticks per 1,000 examined specimens), which represents a standard indicator for the analysis of pooled samples (Biggerstaff 2009). In addition, MIR may be expressed as a percentage, provided that the units of measurement are explicitly stated. It should be noted that the MIR method is based on the assumption that no more than one infected individual is present in each positive pool, which limits its applicability when infection prevalence is high. In such cases, the use of maximum likelihood estimation (MLE) methods is recommended for more accurate prevalence assessment, as these approaches are also widely applied in the epidemiology of vector-borne infections (Yashina *et al.* 2003; Gu & Novak 2004).

RESULTS

General characteristics of the sample

During field-based epizootological investigations conducted in the spring of 2025 in the Turkestan region, a total of 468 ixodid ticks were collected and analyzed. Sampling covered nine administrative districts of the region (Kazygurt, Zhetysay, Maktaaral, Ordabasy, Sairam, Sozak, Tulkibas, Shardara, and Baidibek), as well as the suburban area of the city of Shymkent, thereby providing spatial coverage of both traditionally endemic areas and adjacent territories (Table 1). Tick collection was carried out across diverse ecological and epidemiological settings, including natural habitats (shrub vegetation and soil surface), livestock (large and small ruminants), and farm buildings. This approach allowed assessment of virus circulation across different components of natural–anthropogenic foci. The combination of sampling sources reflects real-world conditions of contact between vectors, hosts, and humans, thereby increasing the representativeness of the obtained sample. Geographic coordinates of tick collection sites were entered into an Excel database for subsequent mapping. Sampling locations were visualized on a regional map (Fig. 1).

Tick species composition

Morphological identification revealed seven tick species belonging to three genera: *Hyalomma asiaticum*, *H. scupense*, *H. turanicum*, *H. anatolicum*, *Haemaphysalis punctata*, *Haemaphysalis sulcata*, and *Argas persicus*. Ticks of the genus *Hyalomma* predominated in the sample, accounting for 365 of 468 specimens (78.0%), which is consistent with existing evidence of the leading role of this genus in maintaining natural foci of Crimean–Congo hemorrhagic fever in arid and semi-arid regions of Central Asia.

Representatives of the genus *Haemaphysalis* comprised 98 specimens (20.9%), whereas argasid ticks (*Argas persicus*) were detected at a minimal frequency, with only five specimens (1.1%). The predominance of *Hyalomma* spp. confirms the epidemiological significance of this group of ticks in the southern regions of Kazakhstan and supports the rationale for targeted surveillance of these species when assessing the risk of CCHFV circulation. Based on the data obtained during field investigations, a distribution map of the identified tick species was generated (Fig. 2).

Table 1. Data on tick collection from natural habitats and livestock in the Turkestan region, Kazakhstan.

Sampling district	Tick species identified	Sampling source	Number of ticks collected
Kazygurt district	<i>Hyalomma scupense</i>	Cattle	29
Maktaaral district	<i>Hyalomma scupense</i>	Cattle	34
Ordabasy district	<i>Hyalomma scupense</i>	Cattle	25
	<i>Hyalomma anatolicum</i>	Cattle	5
	<i>Hyalomma turanicum</i>	Cattle	20
	<i>Argas persicus</i>	Poultry (chickens)	5
	<i>Hyalomma turanicum</i>	Natural habitat	60
Sairam district	<i>Hyalomma scupense</i>	Cattle	28
	<i>Hyalomma anatolicum</i>	Cattle	7
	<i>Haemaphysalis punctata</i>	Natural habitat	60
Sozak district	<i>Hyalomma asiaticum</i>	Small ruminants	87
	<i>Hyalomma asiaticum</i>	Cattle	14
	<i>Hyalomma asiaticum</i>	Natural habitat	56
Shymkent city, Turan	<i>Haemaphysalis sulcata</i>	Natural habitat	8
Shymkent city, Al-Farabi	<i>Haemaphysalis sulcata</i>	Natural habitat	3
Total			468

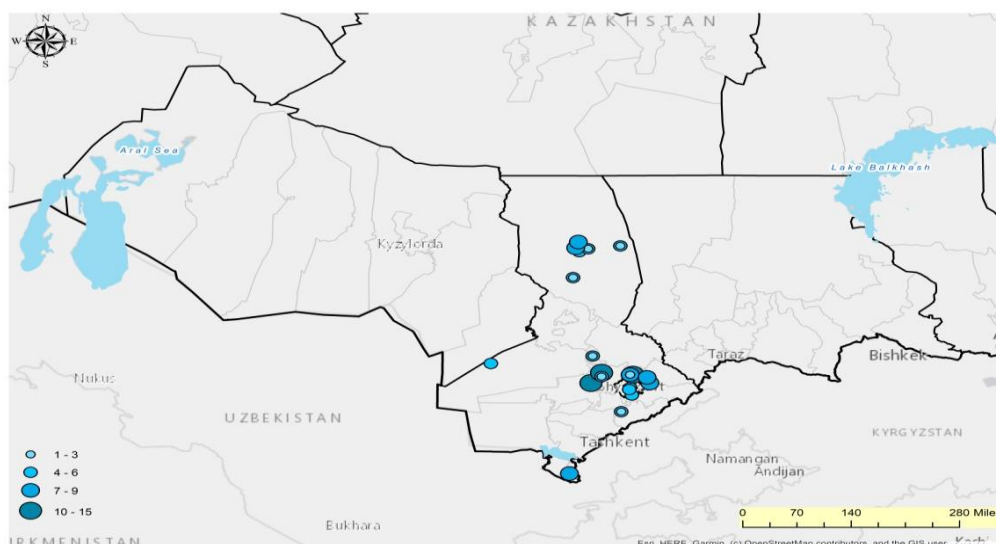


Fig. 1. Map showing tick sampling sites in the Turkestan region in spring 2025. Blue circles indicate tick collection locations and the number of field-collected specimens at each site.

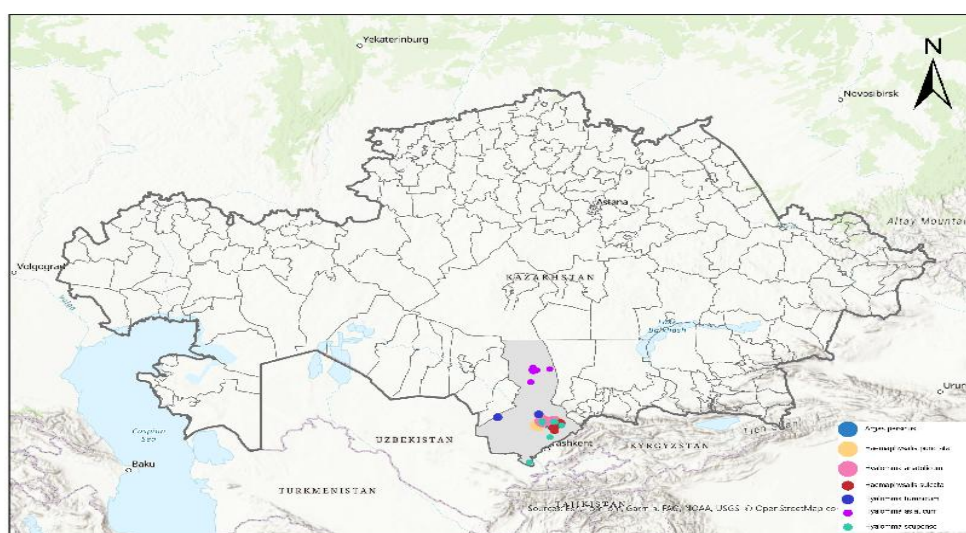


Fig. 2. Map showing the species diversity of ixodid ticks collected for the study in the Turkestan region in 2025.

Results of molecular genetic analysis

For laboratory analysis, a total of 96 RNA pools were generated, grouped according to tick species and sampling location. Based on real-time RT-PCR results, Crimean–Congo hemorrhagic fever virus (CCHFV) RNA was detected in four pools, corresponding to 4.17% of all tested pools. Geographically, positive samples were identified in two administrative districts of the Turkestan region. In the Sozak district, three positive pools were detected; all belonged to the species *Hyalomma asiaticum* and were collected from sheep within a single livestock farm. In the Maktaaral district, one positive pool was identified, consisting of *Hyalomma scupense* ticks collected from cattle (Table 2). The absence of positive results among ticks of the genera *Haemaphysalis* and *Argas* in this study may indicate their lower epidemiological relevance in CCHFV circulation during the spring period or may reflect the limited sample size for these taxa. Locations of CCHFV-positive findings within the Turkestan region were mapped and are presented in Fig. 3.

Minimum infection rate (MIR)

With a total of 468 examined ticks and four CCHFV-positive pools, the minimum infection rate (MIR) was calculated as 8.55 per 1,000 ticks, which is equivalent to 0.855% when expressed as a percentage. The obtained MIR value indicates a low-to-moderate intensity of CCHFV circulation in the studied tick populations during the spring period of 2025. It should be emphasized that MIR represents a minimum estimate of infection prevalence

and is based on the assumption that each positive pool contains only a single infected individual. Given the clustering of positive pools within a single livestock farm in the Sozak district, the presence of localized areas with a higher true infection prevalence among ticks cannot be excluded. This underscores the need for further detailed surveillance using maximum likelihood estimation approaches and for expanding the sample size.

Table 2. Results of PCR testing of ticks collected in the Turkestan region in 2025.

District	Number of ticks	Number of pools	CCHFV-positive pools
Al-Farabi district	30	6	–
Kazygurt district	29	7	–
Sozak district	157	39	3
Sairam district	95	11	–
Ordabasy district	115	26	–
Shymkent city	8	1	1
Maktaaral district	34	6	–
Total	468	96	4

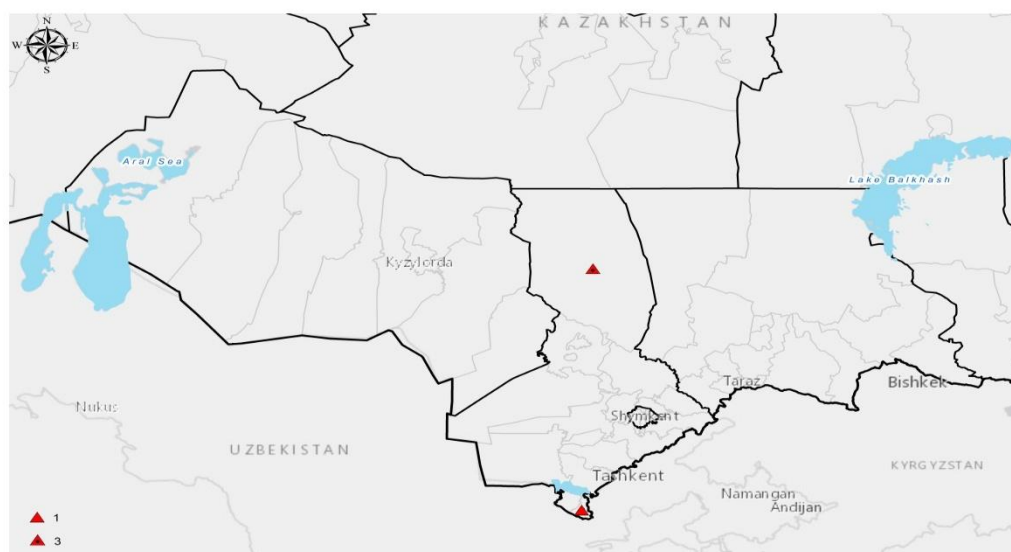


Fig. 3. Map showing locations where CCHFV-infected ticks were detected. Red triangle 1 indicates the site where three CCHFV-positive tick pools were identified in the Sozak district; red triangle 2 indicates the site where one CCHFV-positive pool was detected in the Maktaaral district.

Spatial characteristics of detected positive samples

The concentration of positive pools in two districts of the Turkestan region, together with their association with specific farms and host animal species, indicates a focal pattern of CCHFV circulation. Such spatial heterogeneity is typical of natural focal vector-borne infections and highlights the necessity of locally targeted preventive measures, including acaricidal treatment of livestock and enhanced epidemiological surveillance in high-risk areas.

DISCUSSION

The results obtained in the present study provide strong evidence for the ongoing circulation of Crimean–Congo hemorrhagic fever virus (CCHFV) in ixodid tick populations in the Turkestan region, which is consistent with current understanding of the persistence and stability of natural CCHF foci in the southern regions of the Republic of Kazakhstan [Dobritsa 1965; Hoogstraal 1979; Messina *et al.* 2015; Sultankulova *et al.* 2022; National Center for Public Health (HLS/KZ) 2025; Berdikulov *et al.* 2025). The detection of CCHFV-positive pools in only two of the surveyed administrative districts, alongside the absence of virus detection in the remaining areas, indicates pronounced spatial heterogeneity in CCHFV circulation—a characteristic feature of natural focal vector-borne infections. The localization of three CCHFV-positive pools of *Hyalomma asiaticum* within a single livestock farm in the Sozak district suggests the formation of a localized microfocus in which favorable conditions for vector populations, availability of hosts, and repeated virus transmission cycles coincide. Similar microfoci have been described in endemic regions of Turkey, Iran, and Central Asia and are regarded as key elements of

epidemiological risk for rural populations and livestock workers (Gaidamovich *et al.* 1981; Estrada-Peña & de la Fuente 2017; World Health Organization 2020). The concentration of infected ticks within a single farm substantially increases the likelihood of human exposure to the virus, particularly during periods of intensive agricultural activity. The detection of CCHFV RNA in *H. scupense* collected from cattle in the Maktaaral district further confirms the epizootological role of livestock as transient viremic hosts that contribute to virus amplification in natural foci without developing overt clinical disease [Bente *et al.* 2013; Ergönül *et al.* 2018; Centers for Disease Control and Prevention (CDC) 2020; World Health Organization 2025]. Such animals act as an ecological “bridge” between natural and anthropogenic ecosystems, increasing the risk of human infection both through tick bites and through contact with blood and tissues during animal handling, husbandry, or slaughter. The predominance of ticks of the genus *Hyalomma* in the overall sample (78.0%) fully corresponds with published data identifying this genus as the principal vector of CCHFV in steppe, semi-desert, and desert zones of Eurasia (Maltezou *et al.* 2010; Bente *et al.* 2013; Sultankulova *et al.* 2022; Gu & Novak 2024; Berdikulov *et al.* 2025). Biological characteristics of *Hyalomma* spp., including high aggressiveness, mobility, and the capacity for transstadial and transovarial virus transmission, underpin their leading role in sustaining CCHFV circulation. From a practical perspective, these findings indicate that preventive and anti-epidemic measures in endemic regions should be primarily focused on periods of peak *Hyalomma* activity and on settings involving intensive human–livestock contact.

Interpretation of MIR and epidemiological significance

The minimum infection rate (MIR) calculated in the present study—8.55 per 1,000 ticks (0.855%)—represents a minimum estimate of CCHFV prevalence in the investigated vector populations. As is well recognized, the MIR approach is based on the assumption that no more than one infected individual is present in each positive pool and therefore may underestimate the true proportion of infected ticks, particularly in situations where positive samples are spatially clustered (Mackay *et al.* 2002; Gu & Novak 2004; Biggerstaff 2009). Nevertheless, even relatively low levels of tick infection have substantial epidemiological relevance in settings characterized by high vector abundance, frequent contact with vertebrate hosts, and the high pathogenicity of CCHFV for humans [Bente *et al.* 2013; Ergönül *et al.* 2018; Centers for Disease Control and Prevention (CDC) 2024; World Health Organization 2014, 2025]. Comparable MIR values have previously been reported in endemic regions of Turkey, Bulgaria, and Iran, where they were accompanied by documented human cases of disease, underscoring the practical public health significance of such surveillance data (Estrada-Peña & de la Fuente 2013; Estrada-Peña & de la Fuente 2016; Carroll *et al.* 2020).

Study limitations

The present study has several limitations that should be taken into account when interpreting the results. First, the use of pooled tick samples restricts precise quantitative estimation of infection prevalence and does not allow determination of the actual number of infected individuals within each positive pool. Second, sampling was conducted during the spring period (April), which does not capture the potential summer–autumn peak in tick activity and virus circulation (Gu & Novak 2004; Estrada-Peña & de la Fuente 2016). Third, sequencing of positive samples was not performed within the scope of this study, precluding assessment of the genetic diversity and phylogenetic affiliation of circulating CCHFV strains. Despite these limitations, the obtained data contribute to the updating of information on CCHFV circulation in Turkestan region and may serve as a foundation for further investigations. Such studies should include expanded seasonal surveillance, application of maximum likelihood estimation (MLE) methods for more accurate infection prevalence assessment, and molecular genetic characterization of detected viral strains, as demonstrated in previous studies conducted in Kazakhstan and neighboring territories (Papa *et al.* 2017; Sultankulova *et al.* 2024; Berdikulov *et al.* 2025).

CONCLUSION

The field and laboratory investigations conducted in this study demonstrate that Crimean–Congo hemorrhagic fever virus (CCHFV) continues to actively circulate within natural foci of the Turkestan region. The detection of CCHFV RNA in pooled samples of ixodid ticks collected during the spring of 2025 confirms the epidemiological significance of the region and underscores the necessity of maintaining continuous epizootological and epidemiological surveillance. The identification of positive samples exclusively among ticks of the genus *Hyalomma* associated with livestock highlights the key role of these vectors in sustaining virus circulation within natural–agricultural foci. Small and large ruminants from which infected ticks were collected act as transient

viremic hosts, facilitating viral amplification without the development of clinically apparent disease, thereby increasing the risk of human infection in agricultural settings. The calculated minimum infection rate reflects a low-to-moderate intensity of virus circulation during the study period; however, even such levels have substantial epidemiological significance given the high abundance of vectors, the frequency of human–animal contact, and the high pathogenicity of CCHFV. The quantitative indicators obtained may be applied in epidemiological risk assessment and in planning preventive measures, including acaricidal treatment of livestock, sanitary management of farms, and targeted risk communication for vulnerable population groups. The localization of positive findings to specific districts and farms indicates a focal pattern of virus distribution and supports the need for a locally tailored approach to surveillance and prevention. To enhance understanding of CCHF epidemiology in the region and to strengthen the evidentiary basis of surveillance data, it is advisable to expand monitoring activities by increasing seasonal coverage, applying more accurate statistical methods for infection prevalence estimation, and incorporating molecular genetic analyses, including sequencing of viral genomic fragments. Overall, the results of this study complement existing data on CCHFV circulation in the southern regions of the Republic of Kazakhstan and may serve as a scientific basis for improving regional prevention programs for Crimean–Congo hemorrhagic fever and for strengthening epidemiological surveillance systems for especially dangerous vector-borne infections.

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Conflict of interest

The authors declare that they have no conflict of interest regarding the publication of this paper.

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