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UDC 595.421 **Research article**

First report of *Hyalomma marginatum* (Arachnida, Ixodidae) in *Saiga tatarica* from Ural antelope population: Western Kazakhstan

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Abstract

Background and Aim. Ixodid ticks (Acari, Ixodidae) are among the most important groups of arachnids globally, significantly impacting human and veterinary practice. Five genera of ticks of the Ixodidae family have been registered in Kazakhstan. Ticks of the genus *Hyalomma* are particularly important from epizootiological and epidemiological perspectives. Bites from infected ticks can transmit pathogens of bacterial and viral diseases.

Materials and Methods. The research was conducted in the Bokeyorda State Nature Reserve, located in the Bokeyorda, Zhanibek, Kaztalov, and Zhanakala districts of the West Kazakhstan region of Kazakhstan, under a permit from the Ministry of Ecology and Natural Resources of the Republic of Kazakhstan. Trapping for parasite carriage studies was conducted using the Coral method without harming animal health. To avoid stress, each captured animal was examined as quickly as possible. One or two ticks were removed safely, after which the animals were immediately released. The collected samples were placed in sterile laboratory Eppendorf tubes and stored at 2-4 °C. Tick species identification was performed under a trinocular stereoscopic microscope using identification tables.

Results. During the study, *Hyalomma marginatum* ticks, a major vector of the Crimean-Congo hemorrhagic fever virus (CCHF), were discovered for the first time in representatives of the Ural saiga population (*Saiga tatarica*) in Western Kazakhstan. This species have not previously been recorded on saiga in Kazakhstan. Morphological identification allowed us to clarify the characteristic diagnostic features of the discovered specimens, distinguishing them from other species of the genus *Hyalomma*.

Conclusion. The detection of H. marginatum in saigas is of epizootiological significance, as this tick species actively parasitizes farm animals, creating conditions for the circulation and possible transmission of zoonotic pathogens between wild and domestic animals. Saiga migrations between Kazakhstan and Russia contribute to the expansion of the range of *H. marginatum* and likely increase the risk of tick-borne infections in the steppe ecosystems of the Urals.

Keywords: ectoparasites; *Hyalomma marginatum;* transmissible diseases; *Saiga tatarica.*

Introduction

Ticks are vectors of numerous infectious diseases, including some highly pathogenic ones. Bites from infected ticks can transmit bacterial pathogens (tick-borne borreliosis, Lyme disease), relapsing fever, tularemia, and babesiosis), rickettsial infections (spotted fever, Q fever, ehrlichiosis, and anaplasmosis), and viral diseases (tick-borne encephalitis, colitis, Crimean-Congo hemorrhagic fever, etc.).

Ixodid ticks (Acari, Ixodidae) are one of the most important groups of arachnids globally, significantly impacting human and veterinary practice. They are highly resilient to adverse environmental conditions, capable of overwintering, and surviving habitat flooding for up to two weeks. In a state of starvation, a female can survive for up to three years and may lay up to 5,000 eggs, transmitting pathogens to subsequent generations transovarially, which is why biotopes infested with parasites are dangerous foci of infection for many years [1, 2]. In Kazakhstan, 5 genera of ticks in the family Ixodidae are recorded. Ticks of the genus *Hyalomma* are of particular epizootiological and epidemiological significance. Some species of ticks of this genus are the main carriers of pathogens of diseases such as human granulocytic anaplasmosis (HGA), sheep anaplasmosis (*Anaplasma ovis*), theileriosis of horses, small and large cattle (*Theileria annulata, T equi, T. orientalis, T. ovis*), babesiosis of cattle and horses (*Babesia occultans, B. caballi*), ehrlichia [3, 4]. Studies conducted in the Balkhash district of the Almaty region and in the adjacent territory of northwestern China have shown the presence of *B. caballi* in *H. asiaticum* [5, 6]. Tacheng tick virus 2 (TcTV-2) was detected in *H. scupense* from the East Kazakhstan and Almaty regions, in *H. asiaticum* from the Almaty region, and *H. anatolicum* from the Zhambyl region [7]. In the southern region of the republic, DNA of four pathogens (LSDV (lumpy skin disease virus), *Coxiella burnetii, Theileria annulata,* and *Babesia caballi*) were detected in *Hyalomma asiaticum, H. scupense,* and *H. anatolicum* by PCR. Infection with LSDV was detected in *Hyalomma asiaticum* ticks collected from cattle in the West Kazakhstan region. *Coxiella burnetti* (the causative agent of Q fever) was detected in Hyalomma anatolicum ticks in the Zhambyl region. *Theileria annulata* and *Babesia caballi* were detected in *Hyalomma* scupense ticks from cattle in the Turkestan region [8].

Ticks of the genus *Hyalomma* play an essential role in the transmission of the CCHF pathogen, serving as the primary vectors in natural foci in Kazakhstan. Phylogenetic analysis based on partial S and L segments of the viral genome revealed that Kazakhstani isolates grouped into the Asia-1 and Asia-2 genotypes and shared high sequence similarity with regional strains from Uzbekistan, Turkmenistan, and China, confirming cross-border circulation of the virus. These results provide additional molecular evidence for localized Crimean hemorrhagic fever virus activity in ticks associated with livestock in southern Kazakhstan, thereby expanding knowledge of the virus's geographic distribution and genetic diversity [9]. In the context of climate change and human economic activity over the last decade, significant changes in the ranges of certain tick species in Kazakhstan have been documented [10, 11, 12].

Materials and Methods

The research was conducted at the Bokeyorda State Nature Reserve, located in the Bokeyorda, Zhanibek, Kaztalov, and Zhanakala districts of the West Kazakhstan region of Kazakhstan, in accordance with permission from the Ministry of Ecology and Natural Resources of the Republic of Kazakhstan No. 27-02-19/5707-KLKHZHM dated July 30, 2025. Parasite carriage studies were conducted using the Coral method (Figure 1A), which does not harm the animals [13]. Using this method, saigas were forced into a large mesh enclosure, and the gates were closed once the enclosure was full. Samples were collected from the animals using standard acarological methods [14]. To avoid stress, each captured animal was examined as quickly as possible. Any 1-2 ticks found were removed using specialized tweezers, while observing all safety precautions. The animals were then immediately released. No tick counts were performed on the animals.

Collected samples were placed in sterile laboratory Eppendorf tubes and stored at 2-4 °C. A logistics company with the required temperature control was used to deliver the samples to the laboratory. Tick species identification was performed at the Almaty branch of the National Center for Biotechnology using a trinocular stereoscopic microscope and identification tables [15-17].

Results and Discussion

Since 2006, a Memorandum of Understanding on the Conservation and Sustainable Use of the *Saiga tatarica* has been in effect between Kazakhstan, Russia, Uzbekistan, and Turkmenistan. The document was signed under the Convention on Migratory Species of Wild Fauna [24]. The Ural (Volga-Ural) saiga population inhabits the border of Russia (Volgograd, Astrakhan, and Orenburg regions) and West Kazakhstan, primarily in the steppe regions between the Volga and Ural Rivers. This population migrates between the two countries, especially in the summer, when saigas migrate north to Russia in search of cooler climates and more abundant pastures. In winter, they return to Kazakhstan. The migratory saiga herd shares an epizootiological unit with domestic livestock, increasing the likelihood of re-infection with contagious diseases.

In Kazakhstan, the Ural saiga population inhabits the West Kazakhstan region and Atyrau regions, which border the Russian Federation [25]. The shared use of pastures and the sharing of a single epizootiological unit of *Saiga tatarica* with domestic animals contribute to the intensification of pathogen circulation and, consequently, an increased risk of reinfection. The spread of pathogens causing pasteurellosis, helminthiasis, echinococcosis, and coenurosis has been documented among saigas [26-28]. High levels of theileriosis are known among the Ural, Betpak-dala, and Ustyurt saiga populations, with ticks being the primary vectors of the pathogens [29].

In July 2025, during metagenomic sampling, 2 ticks were found in the sub-tail region of one of the studied saigas (Figure 1B).

A - Fixation of a saiga using the Coral method;
B - Ticks found in the sub-tail region of a saiga (by Sattarova R.)

Figure 1. Capture and study of saiga in the West Kazakhstan region

Upon species identification, it was determined that both specimens were males and belonged to the same species, *Hyalomma marginatum* (Figure 2).

A B

A – Top view; B- Bottom view

Figure 2. *Hyalomma marginatum*, taken from a saiga examined in the Bokeyorda State Nature Reserve (by Sayakova Z.)

Unlike other *Hyalomma* species found in Kazakhstan, the mites we discovered lack a distinct parma. In contrast to *Hyalomma asiaticum*, the cervical grooves are superficial, not reaching the midpoint of the conscutum. Unlike *H. scupense*, the posteromedian groove is narrow and superficial, not reaching the parma. The marginal grooves are long, almost reaching the eyes. The caudal area is clearly defined; large puncturation is relatively sparse, located mainly on the caudal area, lateral fields, and the anterior part of the central field. Small or medium puncturation is evenly scattered throughout the conscutum. The overall coloration is dark, ranging from black to brown. The leg segments exhibit rings of whitish enamel pigment at the articulations. The dorsal process of the peritreme is long, not sharply separated from the main part. The perforated part of the dorsal process of the peritreme is wide, straightened, with a bend at the apex (Figure 3).

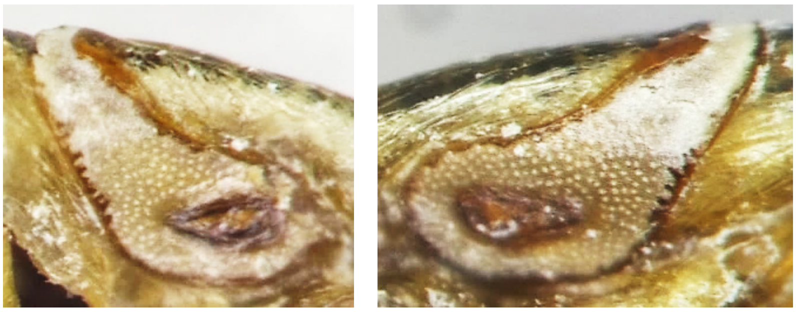

Figure 3. Peritremes of a male *Hyalomma marginatum* taken from a saiga in the Bokeyorda State Nature Reserve (by Sayakova Z.)

Currently, 15 *Hyalomma* species are known to transmit the CCHF virus [18, 19], of which nine species are known in Kazakhstan [17].

The Republic of Kazakhstan borders Russia, China, Kyrgyzstan, Uzbekistan, and Turkmenistan, and therefore, the potential for expansion of the nasal area for transboundary infectious diseases spread by blood-borne ticks cannot be ruled out. Transboundary diseases are those of exceptional relevance to the economies, trade, and/or food security of many countries, capable of widespread interstate spread on an epidemic scale, and the control of which, up to and including eradication, requires the cooperation of several countries [19]. The *Hyalomma marginatum* tick is a vector of such diseases. In southern Russia, this parasite remains the primary vector of the CCHF virus in endemic regions. The high abundance of the species, combined with the constant detection of the pathogen, underscores its central role in the ecology of tick-borne diseases in the country. Sporadic findings outside its primary range indicate the potential for further population expansion. In southern Russia, *Hyalomma marginatum* accounts for nearly 50% of ticks collected from domestic animals, and studies have confirmed the presence of pathogens in this species [19]. Previously, ticks of the genus *Hyalomma* were reported from saiga in Kazakhstan; *Hyalomma scupense* was identified in the Volga-Ural population of the antelope [20].

Hyalomma marginatum primarily inhabits steppes, deserts, and semi-deserts characterized by low to moderate humidity and long, hot, and dry summers [21].

The primary hosts of adult ticks are cattle, small ruminants, camels, horses, and lagomorphs. The pre-imaginal stage feeds primarily on birds. This is the first time we have discovered this species on the saiga. In Kazakhstan, this species is found primarily in the northwest of the country, along the Russian border (West Kazakhstan and Atyrau regions) [22]. Recently, an eastward expansion of this species has been observed. Previously, *H. marginatum* was regularly recorded in the Bokey-Orda and Zhanibek districts of the West Kazakhstan region. Since May 2012, ticks have been reported in the Uralsk region since 2017, in the Baiterek, Taskala, and Burli districts, and since 2019, in the Syrym and Karatobe districts [23]. In the Aktobe region, *H. marginatum* was first discovered by us in April 2023. During an inspection of cattle in the Uil district, 50 ticks (29 females and 21 males) were collected.

In the territory bordering Kazakhstan, *Hyalomma marginatum* is known in the Astrakhan, Saratov, and Volgograd regions [30-33] and coincides with the migration area of the Ural saiga population [25].

Conclusion

The present study documents, for the first time, the occurrence of *Hyalomma marginatum* ticks on the Ural population of *Saiga tatarica*. This observation suggests that shared pastures may facilitate parasite exchange between domestic animals and wildlife. Given the extensive migratory movements of saigas, these animals are likely to contribute to the dispersal and possible range expansion of *H. marginatum* within Kazakhstan.

Authors' contributions

SR, SZ, SK and BF: conceptualized and designed the study, conducted a comprehensive literature search, analyzed the collected data, and prepared the manuscript; AK, KZh RS: conducted final editing and proofreading of the manuscript. All authors read, reviewed, and approved the final version of the manuscript.

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