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RESEARCH ARTICLE

Identification of Ticks Infesting Cattle in Konya Region and Investigation of the Presence of Crimean-Congo Hemorrhagic Fever (CCHF) in Ticks

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Konya Bölgesindeki Sığırları Enfeste Eden Kenelerin Tiplendirilmesi ve Kenelerde Kırım Kongo Kanamalı Ateşi (KKKA) Varlığının Araştırılması

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Öz

Amaç: Bu çalışma Konya ilinin güneyinde yer alan ve halk elinde bulunan sığırları enfeste eden kene türlerinin tanımlanması ve bu kenelerde Kırım Kongo Kanamalı Ateşi (KKKA) varlığının araştırılması amacıyla planlanmıştır.

Gereç ve Yöntem: Kene örnekleri halk elinde bulunan ve makroskobik olarak kene enfestasyonu bulunan, 30 işletmeden seçilen 60 büyükbaş hayvandan elde edilmiştir. RT-PCR yöntemi ile KKKA varlığı moleküler olarak araştırılmıştır. Çalışma sahası olarak belirlenen 5 lokasyondaki (Karabayır, Karacahisar, Arslantaş, Kozağaç ve Kayapınar mahalleleri) 30 işletmeden 60 sığırı enfeste eden keneler toplanmıştır. Toplanan kenelerin tür tayinleri yapılmıştır.

Bulgular: 117 kenenin tür tayini yapılmış ve 111 tanesinin (%94,87) *Hyalomma marginatum*, 3 tanesinin (%2,56) *Hyalomma excavatum* ve yine 3 tanesinin (%2,56) *Dermacentor marginatus* olduğu belirlenmiştir. Kenelerden oluşturulan 35 havuzda (kene türü, kene cinsiyeti, toplama alanı dikkate alınarak) yapılan RT-PCR analizinde ise KKKA virusu varlığı tespit edilememiştir.

Öneri: Bu çalışmada tespit edilen kenelerin büyük çoğunluğunun *Hyalomma marginatum* olarak belirlenmesi dikkat çekici bulunmuştur. KKKA hastalığının Türkiye'deki vektörünün *H. marginatum* olması, artan endişeleri destekler niteliktedir. Bölgede daha önce KKKA virusu varlığını sınırlı da olsa gösteren moleküler ve serolojik kanıtlar hastalıkla ilgili daha geniş kapsamlı çalışmalar yapılması gerektiğini göstermektedir.

Anahtar kelimeler: *Hyalomma marginatum*, kene, KKKA

Abstract

Aim: This study was designed to identify the tick species infesting cattle in the southern region of Konya and to investigate the presence of Crimean-Congo Hemorrhagic Fever (CCHF) in these ticks.

Materials and Methods: Tick samples were obtained from 60 cattle selected from 30 farms, where tick infestations were macroscopically observed in the livestock. The presence of CCHF was investigated molecularly by RT-PCR method. Ticks infesting 60 cattle from 30 farms located in the five designated study areas (Karabayır, Karacahisar, Arslantaş, Kozağaç, and Kayapınar neighborhoods) were collected. The collected ticks were identified to species.

Results: A total of 117 ticks were identified, with 111 (94.87%) identified as *Hyalomma marginatum*, 3 (2.56%) identified as *Hyalomma excavatum*, and 3 (2.56%) identified as *Dermacentor marginatus.* In the RT-PCR analysis conducted on 35 pools of ticks (considering tick species, sex, and collection area), no presence of the CCHF virus was detected.

Conclusion: The identification of the majority of the ticks in this study as *Hyalomma marginatum* is noteworthy. The identification of *Hyalomma marginatum* as the vector of the CCHF disease in Türkiye is indicative of increasing concerns. Molecular and serological evidence showing the presence of the CCHF virus in the region, albeit limited, indicates that more comprehensive studies related to the disease are necessary.

Keywords: CCHF, *Hyalomma marginatum*, tick

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Introduction

Crimean-Congo Hemorrhagic Fever (CCHF) is one of the most common tick-borne diseases geographically seen in more than 30 countries in Asia, Africa, Europe and the Middle East. The annual incidence is estimated to be over 10,000 worldwide. It is a significant viral zoonotic disease, responsible for approximately 500 deaths annually (WHO 2022, Frank et al 2024).

The first clinical records of the disease came from Crimean lands during the Second World War and the disease was called Crimean Hemorrhagic Fever during this period. In 1956, it was isolated in the Democratic Republic of Congo and the disease was called Congo Hemorrhagic Fever in this region. In 1969, it was determined that both viruses causing the disease were the same, leading to the disease being named Crimean-Congo Hemorrhagic Fever as it is known today (Hoogstraal 1979). CCHF has been endemic in Türkiye since it was first identified in a human case in Tokat province in 2002. Since the first detection in Türkiye in 2002, a total of 16,499 confirmed human cases have been reported (Karti et al 2004, Welch et al 2024). In Türkiye, it was reported that the cases reached the highest number with 1,318 cases in 2009 (HSGM 2023). In addition, it was reported that human cases were generally seen between April and September on a yearly basis with the number of cases reaching a peak in July (Welch et al 2024).

The causative agent of the disease is the *Crimean-Congo Hemorrhagic Fever virus*, which belongs to the family Nairoviridae and the genus orthonairovirus, and has been reclassified by the International Committee on Taxonomy of Viruses (ICTV) as Orthonairovirus haemorrhagiae (Kuhn et al 2024). Orthonairovirus genomes consist of three linear RNA molecules with negative polarity. Each of the three segments encodes different proteins: the S (small) segment encodes the nucleocapsid (N) protein, the M (medium) segment encodes glycoproteins (Gn and Gc), and the L (large) segment encodes RNA-dependent RNA polymerase (Bente et al 2013).

The disease is primarily transmitted through bites from infected ticks. Ticks acquire the virus by feeding on infected vertebrates and can transmit it to other hosts during feeding. However, the disease can also be transmitted directly to individuals in contact with the tissues and organs of infected animals, and to healthcare workers nosocomially (Whitehouse 2004).

The transmission route for CCHF varies during the incubation period. The incubation period varies between 3 to 7 days; however, this duration is shorter after tick exposure and longer in cases of contact with infected blood or tissues compared to tick bites (Bente et al 2013).

The disease associated with CCHF presents clinical symptoms exclusively in humans among vertebrate hosts. The causative agent previously demonstrated in various domestic and wild vertebrates causes asymptomatic viremia lasting between 7 to 15 days (Bente et al 2013). The disease presents in humans with clinical manifestations ranging from subclinical cases to fatal outcomes, and the case fatality rates in humans can rise to as high as 30% (Bente et al 2013, Welch et al 2024). In Türkiye, the case fatality rate (CFR) has been reported to be 4.8% (Welch et al 2024).

To date, over 950 tick species have been identified worldwide. In Türkiye, 55 species belonging to the families *Argasidae* and *Ixodidae* have been identified. The *Ixodidae* family comprises genera such as *Rhipicephalus, Dermacentor, Hyalomma, Haemaphysalis*, and *Ixodes*, represented by 47 species, while the Argasidae family is represented by 8 species (Touray ve et al 2023).

The primary vectors responsible for the transmission of CCHF are ticks belonging to the *Hyalomma* genus within the *Ixodidae* family. In particular, the ticks classified as *Hyalomma marginatum* serve as the primary vector and reservoir for the disease in Türkiye (Hoogstraal 1979, Estrada-Peña et al 2007). Additionally, ticks such as *Hyalomma excavatum, Hyalomma lusitanicum, Hyalomma rufipes*, and *Hyalomma turuncatum* within the genus *Hyalomma* have been reported to carry the disease in various regions of the world and play significant roles as vectors (Gonzalez et al 1991, Estrada-Peña et al 2012, Akuffo et al 2016, Nasirian 2022). In addition to the species belonging to the genus *Hyalomma, the Haemaphysalis, Dermacentor, Rhipicephalus, Ixodes, and Ambylomma* genera have also yielded 33 species of ticks in which the CCHF virus has been isolated (Hoogstraal 1979, Tsapko et al 2022). The presence of transovarial and transstadial transmission in ticks carrying the CCHF virus facilitates the intergenerational transfer of the disease, thereby ensuring their survival. Additionally, due to co-feeding, uninfected ticks can also become infected (Bente et al 2013).

The virus exhibits significant genetic diversity due to its complex biology. The CCHF virus S segment has been classified into seven distinct genotypes based on phylogenetic analyses. This classification is often correlated with the geographical region from which the isolates are obtained. The genotypes are designated as Africa 1 (Genotype 1), Africa 2 (Genotype 2), Africa 3 (Genotype 3), Asia 1 (Genotype 4a), Asia 2 (Genotype 4b), Europe 1 (Genotype 5), and Europe 2 (Genotype 6) (Anagnostou and Papa 2009).

The genetic diversity of the virus is related to recombination (the base exchange between the nucleic acids of different viruses) and reassortment (the exchange of segments among RNA viruses with segmented genomes), which occur

due to its segmented RNA genome (Deyde et al 2006, Burt et al 2009). These mutational changes cause concerns about the appearance of new variants that will cause effects such as increasing the pathogenicity of the virus, changing the host range or expanding the geographical areas where it is effective (Kalaycioglu 2019).

Phylogenetic studies conducted on the CCHF virus in Türkiye have reported that a significant portion of the obtained isolates cluster within the European 1 lineage, similar to isolates from the Balkans and Eastern European countries (Ozdarendeli et al 2010, Orkun et al 2017). Additionally, the *Aigai virus* (AP-92), which was classified under the Europe 2 lineage until recently and has been renamed under a new classification, has also been observed in Türkiye (Midilli et al 2009, Papa et al 2022).

The observation of viruses from different genotypes outside the regions where they were isolated indicates the potential for spread through factors such as migratory birds and transboundary animal transport (Mild et al 2010). Indeed, a study conducted in sheep in Iran, which shares a border with Türkiye, revealed through phylogenetic analyses based on the S segment of the virus that the virus detected in sheep is closely related to the virus previously identified in humans in Türkiye and belonging to the European 2 lineage (Mehravaran et al 2013). Some members of the *Hyalomma* genus feed on small animals such as rodents, wild rabbits, and ground-feeding birds during their larval and nymph stages, while in their adult stages, they are multi-host ticks that feed on sheep, cattle, and other large mammals (Bente et al 2013). Türkiye due to its geographical location, has many migration routes preferred by migratory birds. In the fall, birds migrating from north to south enter Türkiye through the Thrace region, the Bosphorus, and Artvin, spreading into Anatolia and exiting the country through Hatay. In spring, they pass through Türkiye via the opposite routes (Oztemel 2021). There is no evidence that birds have become viremic. However, the role of birds in CCHF is primarily considered to be the mechanical transportation of infected ticks over long distances, thereby introducing the disease to areas where it has not previously been observed (Bente et al 2013). In this regard, continuous monitoring of circulating viruses and tracking of available vectors and vector candidates with molecular analyses are very important in terms of understanding the epidemiology of the disease and increasing public health concerns (Kalaycioglu 2019).

Positive findings were found in serologic and virologic screening of various vertebrates and ticks in the region on different dates. The study conducted in this context aimed to determine the tick types infesting farm animals on the outskirts of Mount Taurus in the south of Konya province in the Central Anatolia Region, identify the presence of the virus by investigating the presence of CCHF in ticks, determine the types that potentially have the vector capability, and perform phylogenetic analyses of the isolates to be obtained (Ozdemir et al 2016, Dincer et al 2022, Şevik 2023).

Material and Methods

Determination of the study area

This study was conducted between August 2024 and September 2024 in the southern region of Konya, located in the Central Anatolia Region of Türkiye, specifically in the Bozkır district at the following coordinates: (37 10′ 59″ N, 32 15′ 0″ E) in the neighborhoods of Karabayır (37 6'52.98" N, 32 15'23.27" E), Arslantaş (37 7'11.14" N, 32 13'35.26" E), Kayapınar (37 8'14.51" N, 32 12'50.32" E), Kozağaç (37 9'34.01" N, 32 14'28.28" E), and Karacahisar (37 8'6.28" N, 32 8'34.60" E).

The animals from which samples will be collected in the study consist of cattle owned by the community. Despite this livestock potential in the region, information about infecting ticks and the diseases they transmit is very limited. In this study, sampling was performed between August and September. Five different locations were selected, taking into

Table 1. Oligonucleotide sequences of PCR primers used in the study.

Sequence	Annealing (°C)	Amplicon lengths (bp)
S-F2: TGGACACCTTCACAAACTC	57	536
S-R3: GACAAATTCCCTGCACCA		
S-F3: GAATGTGCATGGGTTAGCTC	57	260
S-R2: GACATCACAATTTCACCAGG		

Table 2. Reaction mixtures and thermal cycles.

1.Mix	Amount(µl) total 50 µl	2.Mix	Amount (µl) total 20 µl
5 x Rt PCR buffer	10	2x ExPrime TaqTM Premix	10
Forward+Revers Primer10pmol	2+2	Forward+Revers Primer10pmol	1+1
dNTP Mix (10mM)	2	-	-
OneStep RT-PCR Enzyme Mix	2	-	-
RNase-free water	27	DNase-free water	6
RNA	5	*DNA	2

1. One-Step rt-PCR Cycles			2. PCR Cycles		
Temperature (◦ C) and Steps	Reaction Time	Cycles	Temperature (◦ C) and Steps	Reaction Time	Cycles
50 (cDNA)	30 min	1	-	-	-
95 (İnitial)	15 min	1	94(İnitial)	5 min	1
94(Denaturation)	30 sec		94(Denaturation)	30 sec	
57 (Annealing)	50 sec	30	57(Annealing)	50 sec	28
72 (Extension)	50 sec		72(Extension)	50 sec	
72(Final Extension)	10 min	1	72(Final Extension)	5 min	1

*1st PCR products were used as templates.

account factors such as climatic conditions and the feeding practices of the animals. The locations of the investigated regions are shown in Figure 1.

Sample collection

Tick samples were collected from grazing domestic cattle (*Bos taurus*) between August 2024 and September 2024. Tick samples were collected from the perineum, scrotum, udder, inner ear, and lower neck regions of cattle infested by ticks in the neighborhoods of Karacahisar, Arslantaş, Karabayır, Kayapınar, and Kozağaç. The collected ticks were transferred to the Department of Parasitology at Selçuk University Faculty of Veterinary Medicine on the same day, adhering to biosafety precautions for species identification. Tick samples were morphologically identified as suggested by Estrada-Peña et al. (2018), and pools were created for molecular analyses. Pools were created considering tick species, gender, and collection area. Additionally, the ticks obtained based on different species, gender, and collection area were not mixed within the pools. The samples were stored at -80°C until the analysis process.

Homogenization

A total of 117 ticks that underwent species identification were categorized into 35 pools based on species, sex, and collection area. Each tick pool was mechanically homogenized using RNAse-free pestles and transferred to tubes containing 600 µL of sterile phosphate-buffered saline (PBS) to create a suspension. Subsequently, the suspension was homogenized using a homogenizer (IKA T–25 Ultra-Turrax, Germany) at 6000 rpm for 10 minutes. The resulting homogenate was centrifuged at 14,000 rpm for 5 minutes, and the supernatant was collected and stored at -80°C until use in the extraction process.

Viral RNA extraction and PCR

To obtain viral RNA from the pool homogenates, RNA extraction was performed in accordance with the manufacturers instructions (QIAamp Viral RNA Mini Kit; Qiagen, Germany). In the study, a two-step nested RT-PCR test method was employed to investigate the presence of viral RNA from the extraction products obtained. For this purpose, a single-step RT-PCR procedure was performed using RNA extraction samples for the first reaction. For this purpose, single step RT-PCR was performed from RNA extraction samples for the first reaction. In this way, both the cDNA synthesis process and the first reaction of the RT-PCR test were completed with the use of primer sets designed specifically for the viral S segment (One Step RT-PCR kiti; Qiagen). The PCR products obtained at the end of the first reaction were used as templates, and the second reaction of

Table 3. Numerical data of the species, location and gender of the ticks collected in the study area.

Tick	Location	Male	Female	Total	%
Hyalomma marginatum	Arslantaş Karabayır Karacahisar Kayapınar Kozağaç	60	51	111	94,87
Hyalomma excavatum	Arslantaş Karabayır	1	2	3	2,56
Dermacentor marginatus	Arslantaş Kozağaç	2	1	3	2,56
Total		63 (53,85%)	54 (46,15%)	117	100

the study was carried out using the (S-F3 and S-R2) primer sets at the annealing temperature specified in the literature (Tonbak et al 2006). The PCR Mastermix protocol used in the study (ExPrimeTaq Premix; GenetBio, South Korea) and the other reaction protocols were prepared according to the method reported by Akyildiz et al. (2021). To enable electrophoresis on the PCR products obtained after the completion of the second stage PCR cycle, 10 µL of each PCR product was aliquoted and transferred to a 2% agarose gel prepared at that concentration. Electrophoresis was performed on PCR products under a current of 100 volts 80 mA for 50 minutes. At the end of the procedure, the products were evaluated on a gel imaging device. (The (+) control samples used in the study were commercially obtained by cloning the complete genome S segment. As a result of the first reaction of the positive control PCR products, a band of 536 bp was detected, and a band of 260 bp was identified in the second reaction. These images are presented in Figure 2. Additionally, the primer oligonucleotide sequences used in the PCR studies are shown in Table 1, and the reaction cycles and temperatures are shown in Table 2)

Results

Morphological findings of ticks

Tick samples were obtained from 60 bovine animals with tick infestation from 30 enterprises selected from five locations. Of the 117 ticks, 94.87% (111) were *H. marginatum*, 2.56% (3) were *H. excavatum*, and 2.56% (3) were *D. marginatus.* Images of the morphological findings of the ticks are shown Figure 3.

Gender distribution of the ticks was determined as follows: for *H. marginatum*, 45.95% female and 54.05% male; for *H. excavatum*, 66.6% female and 33.3% male; and for *D. marginatus*, 66.6% male and 33.3% female. The ratios of ticks by gender, region and species are shown in Table 3.

Findings regarding the CCHF virus

RT-PCR scanning performed in 35 pools consisting of 117 ticks was negative for all pools. Positive controls showed positive amplification during the test process. No amplification was observed in negative controls.

Discussion

Crimean-Congo Hemorrhagic Fever remains important as a major public health threat causing zoonotic infections in humans. The presence of vectors transmitting the disease in a large portion of our country, along with the subclinical course of the disease in domestic and wild vertebrate hosts, and the potential role of birds in the spread of the disease, suggests that there is a potential for the expansion of affected areas (Bente et al 2013, Leblebicioglu et al 2014, İnci et al 2016).

In this study, the species of ticks obtained from cattle were determined as *H. marginatum, D. marginatus* and *H. excavatum.* The identified species are consistent with the results of previous studies conducted in the region (Derinbay Ekici 2008). The identification of species revealed that *Hyalomma marginatum* is predominant in this region, which is noteworthy.

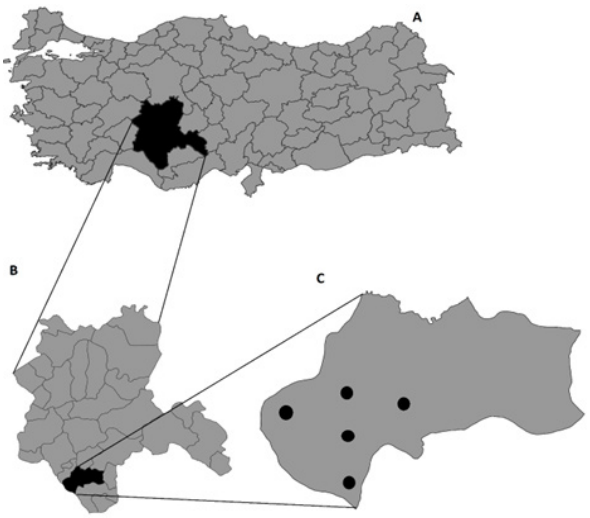

Figure 1. Location of investigated regions in Türkiye A: Türkiye, B: Konya C: Bozkır

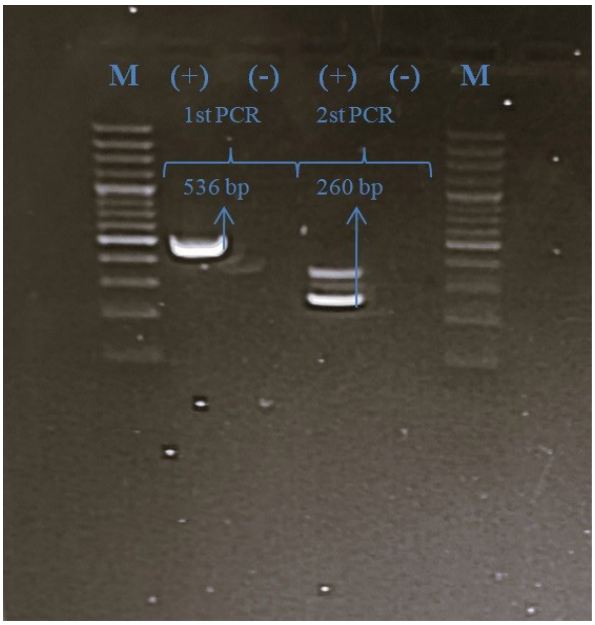

Figure 2. Gel image of the control groups used in the study after PCR. (+): Positive control, (-): Negative control, M: Marker (100bp).

In studies conducted in Türkiye, particularly in the Black Sea region, positivity rates of 3.22% were detected in pools of *H. marginatum* collected from domestic cattle, sheep, and goats in Giresun, Tokat, and Sivas provinces in 2005, while positivity rates of 9.09% were found in pools of *Rhipicephalus bursa* (Tonbak et al 2006). In 2008, out of 1,790 ticks collected from domestic animals in the northern provinces of Samsun, Sinop, Ordu, Giresun, Tokat, Amasya, and Sivas, positivity was determined in 421 pools at a rate of 6.88%. Positive ticks were found in *H. excavatum, H. anatolicum, H. detritum, H. marginatum, R. bursa, R. turanicus* and *I. ricinus* species (Albayrak et al 2010). In another study conducted in Tokat province in 2015, positivity was detected in 12.8% of 78 pools consisting of 335 ticks collected from 114 sheep and goats (Ozupak and Albayrak 2020). In a study conducted between 2008 and 2009, 12.3% positivity was detected in 73 pools consisting of 740 ticks collected from domestic animals in Bursa and Bilecik provinces in the Marmara region, and it was reported that the pools detected positively consisted of *R. turanicus, R. bursa, D. marginatus* and *H. marginatum* ticks (Yesilbag et al 2013). In a study involving the province of Hatay in the Mediterranean Region and neighboring Syria between 2005 and 2007, 30.2% positivity was found in 245 *H. aegyptium* ticks collected from turtles (Široký et al 2014). In a study conducted in 2014 in Kırklareli province in the Marmara region, 51.5% CCHF positivity was detected from 200 *H. marginatum* collected (Akyildiz et al 2021). In a study conducted in 2020 in the Marmara region, specifically in Istanbul, Tekirdağ, Kırklareli, and Edirne, positivity was detected at a rate of 9.49% in 158 pools created from 1,065 ticks collected from turtles and the ground. The positive ticks were found to be *H. aegyptium* (Kar et al 2020). In 2021, 14.28% of the 77 pools formed from 676 ticks collected from the ground in

Figure 3. Morphological findings of ticks A- *Hyalomma marginatum* (male), B- *Dermacentor marginatus* (male), C- *Hyalomma excavatum* (male)

Istanbul province in the Marmara region were found to be positive. It was reported that the ticks reported as positive belonged to *I. ricinus*, *Ixodes* nymphs, *Haemaphysalis* larvae (Ahrabi et al 2023). CCHF positivity was detected in 11.36% of 88 pools consisting of 228 ticks collected from domestic livestock in 2016 in Kütahya province in the Aegean region. The ticks found positive were reported to be *H. marginatum* (İca and Cetin 2016). In a study conducted by Ergünay et al. (2020) covering various regions of Türkiye between 2013 and 2018, pools were prepared from 7,043 tick samples collected from domestic and wild animals as well as the environment, and the CCHF virus was detected in 1.1% of the 602 pools created. It has been reported that the positive pools consisted of 24 ticks, including *H. marginatum, R. bursa, H. scupense, R. sanguineus sensu lato*, and *R. turanicus,* collected from Kırklareli, Diyarbakır, and Mersin.

In another cross-sectional study conducted by Dincer et al. (2017) covering various regions between 2014 and 2016, 187 pools were evaluated from 814 ticks collected from domestic animals and the environment in the provinces of Bayburt, Van, and Mersin, with a positivity rate of 3.2% for the CCHF virus detected. Species found to be positive were reported to be *R. sanguineus* and *R. bursa* ticks. In a study conducted on host-seeking ticks in various regions of Türkiye in 2023, CCHF virus was found to be positive in 690 pools of *H. marginatum* ticks at a rate of 4.5%, in 30 pools of *R. turanicus* ticks at a rate of 8%, and in 4 pools of *R. bursa* ticks at a rate of 25% (Welch et al 2024).

In a study conducted in Ankara, located geographically to the north of the region where this study was carried out, CCHFV positivity was detected at a rate of 3.6% in a total of 736 pools created from 4,283 ticks collected from domestic and wild animals, humans, and the environment. It was reported that the positively identified ticks included *H. marginatum, R. bursa, R. turanicus, H. excavatum,* and *H. parva* (Orkun et al 2017). In a study conducted in Afyon between 2016 and 2017, blood samples collected from 97 cattle containing EDTA were examined using the ELISA method, revealing a seropositivity rate of 2.06% for CCHF antibodies (Şevik 2018). In another study conducted in Afyon in 2022, seropositivity was reported at a rate of 51.54% based on the results of an ELISA test performed on blood samples from 97 equine individuals (Saltik 2022). In a study involving Afyon and Burdur provinces in 2023, serum samples collected from a total of 395 sheep were tested by ELISA method and 16.23% seropositivity was determined in the collected serum samples (Ugdul 2023).

It has been reported that the activity of the vectors responsible for the disease increases during the months when temperatures are high (Hoogstraal 1979). For this reason, sampling was performed between August and September. In this study conducted in a region located in the southern part of Konya, none of the 234 ticks collected were found to contain the CCHF virus. The negative results of the analyses regarding the CCHF virus do not imply the absence of the virus in the region, as the collected samples represent a limited area. In this planned study, the primary aim is the direct detection of the CCHF virus; therefore, no serological investigation was conducted in the sampled animals. However, previous serological screenings conducted in humans and animals in the region, along with molecular screenings in ticks, indicate that the disease is present in the area. In one of the studies conducted in the region, 1,000 healthy human blood samples were examined using the ELISA method in 2016 in Konya province, revealing a seroprevalence of 0.8% for CCHF (Ozdemir et al 2016). Between 2016 and 2017, blood samples collected from 267 sheep and goats in Konya were examined using the ELISA method, revealing a seroprevalence of 21.3% (Şevik 2023). In a study conducted by Dincer et al (2022) between 2020 and 2021, covering the provinces of Çankırı, Konya, Antalya, Kayseri, İzmir, Kütahya, Burdur, Malatya, Bingöl, Şanlıurfa, and Adıyaman, a total of 901 ticks collected from sheep were examined, revealing a positivity rate of 7.2% in *R. bursa* ticks identified in the provinces of Konya and Antalya. The predominance of *H. marginatum* ticks, which are the primary vectors of the disease, in our study demonstrates the existence of risks related to the disease in the region.

In light of all these data, the results of previous studies conducted in the planned region indicate the prevalence of the disease among vertebrates and provide evidence for the serological presence of the disease in the region, albeit at a low level. The presence of the CCHF virus could not be determined as a result of the study since the study covered a limited region, the samples were collected only from adult ticks, the sample size was small, and the study was planned to be only a virological study. In future studies, covering larger areas and incorporating serological screening in addition to virological examinations can shed light on the dynamics of the disease that have not been clarified yet. Thus, effective vaccines and agents that could increase survival rates in treatment and a contribution can be made to the development of a more effective surveillance system in the struggle against the disease.

Conclusion

The identification of *H. marginatum* as the predominant species among the tick species detected in our study supports the growing concerns regarding the disease, as it is recognized as the primary vector of CCHF in Türkiye. The positivity identified in different studies indicates the presence of the virus in the region and suggests that ticks or other domestic and wild animals may serve as potential reservoirs. In light of these results, it is evident that further research is needed regarding the nature of the disease, the risk of its potential spread to different regions, and vector control measures.

Conflict of Interest

Authors declares that there are no conflicts of interest related to the publication of this article.

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Ethical Approval

This study was approved by Selcuk University Faculty of Veterinary Medicine, Experimental Animal Production and Research Center Ethics Committee (Approval no: 2024/107, 2024/09).