Veterinary Integrative Sciences 2023; 21(3): 865 - 877 DOI; 10.12982/VIS.2023.062

Vet Integr Sci
Veterinary Integrative Sciences

ISSN; 2629-9968 (online)

Website; www.vet.cmu.ac.th/cmvj

Review article

Crimean-Congo hemorrhagic fever favouring factors virus transmission: Special focus on Iraq and neighbouring countries

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Abstract

Arthropod-borne infections, also known as vector-borne diseases, are a significant threat to both humans and animals. These diseases are transmitted to humans and animals through the bites of infected arthropods such as mosquitoes, ticks, fleas, and flies. In the last half century, there have been a number of unexpected viral outbreaks in Middle Eastern countries. Recently, Iraq has witnessed an outbreak of the Crimean-Congo Hemorrhagic Fever virus (CCHFV) with high morbidity and mortality rates in humans. However, very little is known about the prevalence and distribution of CCHFV in Iraq, and therefore, it is impossible to quantify the risk of infection.

(CCHFV) is primarily transmitted to humans through the bite of infected ticks. However, transmission can also occur through contact with the blood or tissues of infected animals during slaughter or through contact with contaminated objects or surfaces. In addition, healthcare workers and family members caring for infected individuals are at risk of infection through exposure to contaminated body fluids and aerosols. There are still many unknowns about the role that vertebrates play in the upkeep and spread of CCHFV. Critical information for our comprehension of CCHFV ecology may be gleaned through experimental studies conducted on wild animals and cattle. Therefore, the purpose of this review article is to draw attention to current studies and publications that shed light on the intricate dynamic between CCHFV, vector, and host also demonstrates how bio-surveillance at each stage aids in our knowledge of disease transmission, risk, and future research prospects.

Keywords: Cattle, Crimean-Congo Hemorrhagic Fever virus (CCHFV), Iraq, Outbreak, Tick, Vector, Zoonotic

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Article history;	*received manuscript: 20 May 2023,* *revised manuscript: 17 June 2023,* *accepted manuscript: 19 June 2023,* *published online: 3 July 2023*
Academic editor;	*Korakot Nganvongpanit*

INTRODUCTION

Crimean-Congo Hemorrhagic Fever (CCHF) is a zoonotic disease caused by a tick-borne virus (CCHFV). CCHFV is a negative sense RNA virus that belongs to the genus Orthonairovirus of the Nairoviridae family within the Bunyavirales order. CCHFV causes severe hemorrhagic sickness with high fatality rates (up to 40%) (Gonzalez et al., 1992; Hawman and Feldmann, 2018). The name of the disease and virus is taken from the locations where the disease was originally documented [Crimea, 1945, and Belgian Congo (currently the Democratic Republic of Congo), 1956]. Virus isolates from the two areas were indistinguishable in terms of antigenicity (Casals, 1969; Elevli et al., 2010). Hard-body ticks, particularly those of the Hyalomma genus, are the primary vectors and reservoir of CCHFV, while there is some possibility that other tick genera, such as Rhipicephalus and Dermacentor, may also act as carriers (Bente et al., 2013). Ticks get infected with CCHFV when they feed on viremic animals or when they co-feed with infected ticks, and vertebrate hosts, including cattle and wild animals like hares, likely function as amplifying hosts (Spengler et al., 2016b; Gargili et al., 2017). Cases of CCHF are reported throughout Africa, Southern and Eastern Europe, the Middle East, India, and some other Asian countries (where the Hyalomma vector can be found); an estimated 10,000 to 15,000 human infections by CCHFV occur annually, although the majority of these infections are subclinical and unrecognized (World Health Organization, 2017).

To effectively control the transmission of CCHFV in Iraq and neighbouring countries, it is essential to have a comprehensive knowledge of virus ecology. This requires not only continued research into the mechanisms of transmission and persistence but also efforts to monitor and track the spread of the virus and its vectors in different ecological contexts. Only with a better understanding of these factors can we hope to develop effective strategies for preventing and controlling CCHFV outbreaks.

CCHF is endemic in Turkey, Saudi Arabia, and Iran, which are situated to the north, west and east of Iraq, respectively (El-Azazy and Scrimgeour, 1997; Sisman, 2013; GÜRBÜZ et al., 2021). Since the first case of CCHF was recorded in Iraq in 1979, there have been intermittent outbreaks followed by years with no new cases. Cases were not recorded at all in four years (2008, 2014, 2016, and 2017) while the highest annual total was 10 from 2007 to 2020. According to statistics from the Ministry of Health, Iraq, the number of confirmed cases in Iraq has recently increased, from 19 in 2021 to 219 in the first half of 2022 (Alhilfi et al., 2023).

This review seeks to summarize the existing knowledge on the transmission of CCHFV in Iraq and nearby countries, as well as identify the areas where our understanding is lacking. Furthermore, there are plans to enhance our understanding of the vectors and prevalence of the virus.

SPREAD OF CCHFV TO IRAQ AND NEIGHBOURING COUNTRIES

World Health Organization has classified CCHFV as a high priority pathogen due to the virus's geographically widespread vector, high mortality rate, and lack of medical countermeasures for treatment/prevention of sickness. From 1978 to 2021, nine of the 22 Arabic countries including Iraq, Kuwait, the United Arab Emirates (UAE), Saudi Arabia, Oman, Sudan, Egypt, Tunisia, and Mauritania—reported death rates for the CCHF that varied from 24 to 61% (mean: 29%) throughout the various outbreaks. Those employed in abattoirs/slaughterhouses, livestock fields, and healthcare were the most exposed. The most prevalent mode of transmission was the exposure to the blood or secretions that carrying the virus (Perveen and Khan, 2022). Expanding tick distribution due to climate change, human influences, and movement on afflicted birds, imported animals, or both is also raising concerns about the spread of CCHFV into previously unaffected regions (Gale et al., 2012). CCHF is widespread in the Middle East, including in Iraq. The epidemiology of CCHF in close geographic neighbours like Iran (Chinikar et al., 2010; Telmadarraiy et al., 2010) and Turkey (Karti et al., 2004; Ertugrul et al., 2009) is well documented in the scientific literature. Nevertheless, there is a lack of information on CCHF in Iraq, and the literature that does exist goes back to the 1980s (Al-Tikriti et al., 1981; Tantawi et al., 1981), when the virus was originally discovered.

In 1979, Congo/Crimean haemorrhagic fever was first identified in Iraq. The initial case was reported on September 3rd of that year, and an additional nine patients have been examined since. Of those patients, eight had contact with sheep or cattle, while two contracted the disease while working in a hospital and coming into direct contact with patients. The virus responsible for the illness was isolated from the blood and post-mortem liver samples of the patients, and was found to be serologically similar to other members of the Congo/Crimean haemorrhagic fever virus group. The patients were from various areas surrounding Baghdad and Ramadi (110 Km west of Baghdad), and had no known connection to each other (Al-Tikriti et al., 1981).

In 1980, a study was conducted in three different faunal areas of Iraq to determine the prevalence of the CCHFV through seroprevalence testing. The study found that the serological positivity rates for the virus were different across animal species. Specifically, sheep had a rate of 57.6%, goats 49.64%, cattle 29.28%, horses 58.73%, and camels 23.23% (Tantawi et al., 1981). From 1998 to 2009, the annual number of confirmed cases fluctuated between zero and six. Later, the National Surveillance System received case reports from 1990 to 2010 that showed the trend and pattern of CCHF in Iraq. There were 11 confirmed cases and 28 suspected cases reported. The case fatality rate for confirmed cases was 36%, while it was 4% for suspected cases (Majeed et al., 2012). In general, between 1979 and 2014, there were 55 confirmed cases of CCHFV in Iraq, with 24 fatalities and a mortality rate of 44% (Al-Tikriti et al., 1981; Tantawi et al., 1981; Majeed et al., 2012; Ibrahim et al., 2014). This changes in 2022 when between January 1st, 2022 and June 26th, 2022, a total of 219 cases of CCHF were confirmed. The initial case was reported in March 2022, and subsequent cases persisted until June 2022 (Table 1). Cases have been recorded in all Iraqi Governorates except Salah Al-Din and Al-Sulaymaniyah, but most of the cases occurred in the southeast portion of the country, with 39.7% of the total cases recorded in Thi Qar (Figure 1).

The rise in the prevalence of CCHF in Iraq in 2022 may be attributed to an increase in hard tick infestations of livestock and farms. The lack of pest control activities in 2020 and 2021 during the coronavirus disease 2019 (COVID-19) pandemic may have contributed to this rise. Moreover, butchers, farmers, and the general public are unaware of CCHF and it's route of transmission. Since humans are more likely to get the virus if they have a history of tick bites or animal handling, this is a significant contributing reason to the rising infection incidence. The majority of cases of CCHF occur in rural settings where wild and domestic animals act as tick hosts, resulting in viraemia that promotes the maintenance and transmission of the virus in the environment (Alhilfi et al., 2023).

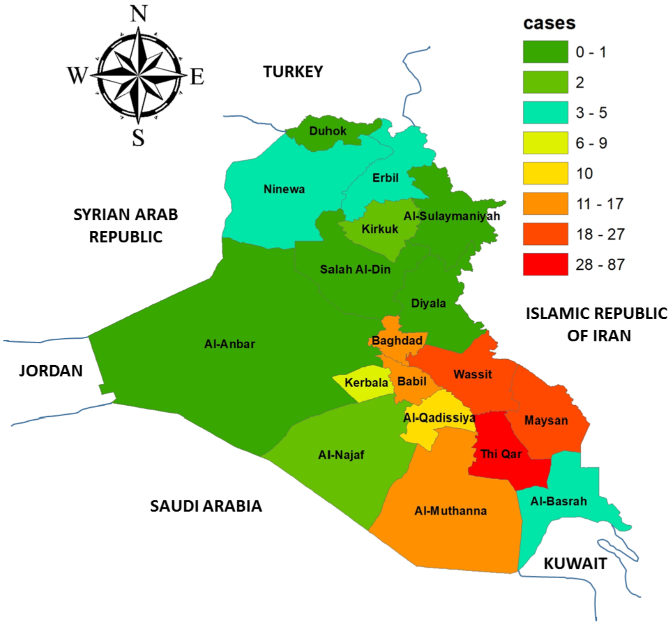

Figure 1 Cases (n=219) of CCHF verified by Central Public Health Laboratory (CPHL) in Baghdad, Iraq from January 1st, 2022, to June 26th, 2022. Figure adapted from (Alhilfi et al., 2023).

TICK VECTORS AND RESERVOIRS OF CCHFV IN IRAQ

Although the participation of *Hyalomma* and *Rhipicephalus* ticks in CCHFV replication and transmission is verified and well documented, the contribution of the other tick genera is less apparent (Biglari et al., 2016; Shahhosseini et al., 2017). Assessing tick's epidemiology likely lead to complicate the situation of the fact that finding the viral nucleic acid or viral isolation in ticks does not necessarily mean that it can survive and virus replication, particularly when the tick is collecting from an infected animal during tick feeding on vertebrate host. Additionally, being a competent vector for a virus (i.e., having the capacity to contract the virus during tick feeding, maintain it, and then spread it to vertebrate host through infestation) does not always lead to effective spread in wild conditions because of numerous conditions, including endemic area with ticks, engorgement rate and trophic as well as seasonality and susceptibility of vertebrate hosts (Turell, 2007). Thus, horizontal transmission mechanisms (which describe the potential role of the invertebrate host as reservoirs); the biological role of hard ticks has a critical role in CCHF epidemiology. This is particularly true when ticks are required to sustain CCHFV infection during seasons like as winter in temperate locations like Iraq, which restrict active viral transmission and when the risk of infection from viremic animal hosts is minimal. During winter, these animals may be less active or migrate to warmer regions, reducing the chances of humans coming into contact with infected animals (Gargili et al., 2017). Further confounding that CCHFV can survive throughout the tick's lifespan without any negative impact on the tick itself (Gargili et al., 2017). Furthermore, tick vectors may serve as a biological harbour for the CCHFVs, enabling the virus to survive during winter season. After 10 months at 4 ℃, *H. marginatum* stay capable to transfer the virus to a vertebrate host (Turell, 2007). *H. marginatum* is the primary vector of CCHFV in Europe, while *H. asiaticum* is the primary vector of CCHFV in Asia (Maltezou and Papa, 2010). Ticks belonging to the genus *Hyalomma* are the principal vectors of CCHFV in people as well as wild animals and domestic animals. CCHFV has been found in over 35 different species of ticks around the globe (Spengler et al., 2016a; Vakalova et al., 2019). An article discussed the prevalence of tick infestations in domestic animals in several regions of Iraq during three different seasons (spring, winter and autumn). The study focused on the Liwas of Diwaniya (Al-Qadissiya) and Nasiriya (Thi Qar) in the spring, Kerbala in the winter, and Hilla (Babil) in the autumn and winter. The researchers collected and identified various tick species from animals such as cattle, sheep, and goats. They found that *Rhipicephalus turanicus* was the most prevalent tick species in all regions, followed by *H. anatolicum excavatum*. Other species identified included *H. marginatum turanicum*, *H. detritum*, and *R. annulatus* (Robson et al., 1969). The distribution of tick species in Iraq is explored briefly using available data. A study, which was carried out in Al-Sulaymaniyah, Iraq, which is located 265 km north of Baghdad, found that the four species with the highest overall prevalence of tick infestation in sheep were *H. anatolicum anatolicum*, *H. marginatum*, *R. turanicus*, and *R. sanguineus*. The study also found that sheep and goats (Omer et al., 2007). During an investigation conducted in the Kurdistan region of Iraq, three different genera of ticks were collected and identified on cattle. *Boophilus* spp. was found to have the highest prevalence, followed by *Hyalomma* spp. and *Rhipicephalus* spp. (Mustafa and Faraj, 2013). *Boophilus* spp. may be more common because they can survive in dry, harsh environments with few hiding spots (Kettle, 1995). A research was undertaken in the Aldoura region of southern Baghdad for a full calendar year, from January 2010 to December of the same year. Ticks were found on 79 out of 284 animals (7.8%), with a frequency of 19.7% in sheep and 8.1% in cattle. May and July had the highest tick populations. *Hyalomma* (70%), *Rhipicephalus* (25%), and *Boophilus* (5%) ticks were found in the collection. There were a total of thirteen species found; *H. anatolicum anatolicum* had the highest tick index, followed by numerous species in the *Hyalomma* and *Rhipicephalus* genera (Hasson, 2012). On the other hand, there is evidence that ~28 additional species related to 7 genera, including *Hyalomma, Rhipicephalus, Boophilus, Ambylomma, Haemaphysalis,* and *Ixodes*, are capable of transmitting the virus. Yet, there have been no reports of the finding of such species in any study conducted in Iraq (Akuffo et al., 2016).

A research was conducted in Iran found that *R. sanguineus* and *H. marginatum* were the two most frequent of 642 ixodid species found in sheep and goats (Razmi et al., 2002). Another study, revealed that of the 49 ticks collected, CCHFV was found in only three of them. The ticks belonged to five different species: *R. sanguineus*, *H. anatolicum*, *H. asiaticum*, *H. dromedarii*, and *H. marginatum*, with a prevalence of 46.9%, 32.7%, 4.1%, 2.1%, and 2.1%, respectively (Shahhosseini et al., 2017). In the year 2000, CCHFV was isolated from ticks: *Hyalomma, Rhipicephalus*, and *Amblyomma* that were found on small ruminants that had been brought from Sudan to the Saudi Arabia Kingdom (Hassanein and El-Azazy, 2000). CCHFV was discovered in ticks taken from cattle, goats, wild boar, hare, and the ground in Turkey, but not in samples obtained from people, donkeys, dogs, or other small animals (Orkun et al., 2017). A research has shown that CCHF virus is a migratory pathogen, although the full scope of its movement remains unclear. The first study to assess the global migratory pattern of CCHF virus found that Turkey may be the source of migration to Europe from both the east and the west and the UAE is the source of migration to the Middle East (Mild et al., 2010). The average prevalence of CCHFV antibodies in various hosts and vectors has been documented. Camels, for example, had a 29% prevalence of CCHFV antibodies, whereas cattle had a 22% prevalence, buffaloes had a 0.4% prevalence, sheep had a 14% prevalence, goats had a 15% prevalence, and small mammals had a 14% prevalence. As a result of the data analysis, camels have the highest seroprevalence of CCHFV in the Arab globe. In ticks, the seroprevalence rate was 10%, but in Europe, CCHFV antibodies were found in 11.76% of ticks (Albayrak et al., 2012; Perveen and Khan, 2022). CCHFV was found in *H. schulzei*, *H. onatoli*, and *H. dromedarii* ticks in Saudi Arabia when they were tested for hemorrhagic fever viruses (Mohamed et al., 2017). Also, different studies have found *Hyalomma* ticks in Kuwait, which suggests that they could be involved in the spread of CCHFV (Converse and Moussa, 1982; Perveen et al., 2021).

CCHF TRENDS IN IRAQ AND NEIGHBOURING COUNTRIES

Iraq is a CCHF-endemic country. The first mention of CCHF in Iraq was in 1979 (Al-Tikriti et al., 1981). According to a seroprevalence study done in 1980 in three different faunal areas of Iraq, the serological positivity rates for the CCHFV virus were, respectively, 57.6%, 49.64%, 29.28%, 58.73%, and 23.23% in sheep, goats, cattle, horses, and camels (Tantawi et al., 1981). Between 1998 and 2009, the number of CCHF cases that were verified each year ranged from 0 to 6. However, there were 28 suspected cases and 11 confirmed cases recorded in 2010 (Majeed et al., 2012). In eight Iraqi provinces in 2010, 11 out of 44 suspected human samples tested positive for the CCHF virus, and ELISA was utilised to find CCHF virus-specific IgM in human blood samples. It was discovered that one patient caught the illness after butchering a sheep at home (Abul-Eis, 2012). There have been sporadic occurrences and outbreaks of CCHF in Iraq, including many nosocomial reports with a case fatality ratio of 36%, such as two confirmed fatal cases in 1979 (one doctor and one nurse), two confirmed cases in 1992 (physicians), and one confirmed case in 1996 (physician) (Ibrahim et al., 2014). In 1979, an index case and five subsequent nosocomial cases of CCHF were initially reported in Dubai, the UAE. People at the time speculated that infected cattle had been brought in from places like Iraq, Kenya, and Pakistan (Longson et al., 1996). In addition, a new lineage of CCHFV with potential genome reassortment of the M segment was found in dromedary camels (*Camelus dromedarius*) and camel ticks (*H. dromedarii*) in UAE (Camp et al., 2020; Camp et al., 2021; Khalafalla et al., 2021). In Saudi Arabia, after an outbreak of viral hemorrhagic fever in 1990 that infected seven slaughterhouse employees in Mecca, western Saudi Arabia, CCHF was finally identified and named. 40 confirmed or probable cases (12 fatalities) of CCHF were found in Mecca by serosurveys of slaughterhouse employees in 1989 and 1990. Ticks on imported sheep that entered the country via the port of Jeddah have been blamed for bringing CCHFV to Saudi Arabia (El-Azazy and Scrimgeour, 1997; Memish, 2002). In another study conducted in Saudi Arabia, CCHFV was found in 0.8% of people, 4.1% of sheep, 3.2% of goats, and 0.6% of cattle (Hassanein et al., 1997). In Kuwait, 4% of the human sera collected between 1979 and 1982, the subject of a serological analysis at two hospitals, were positive for anti-CCHFV antibodies (Al-Nakib et al., 1984). Since that time, Kuwait's CCHFV circulation has not been the subject of any more published statistics. In 1995, an epidemiological study focus on tick distribution in the Sultanate of Oman, CCHF was identified in four individuals based on their clinical symptoms. Later, serological testing for CCHFV exposure was performed on samples from both imported and domestic animals, with 22% of samples expressing CCHFV IgG positive. Sixteen tick pools were identified as *H. anatolicum*, out of a total of nine teen, that tested positive for CCHFV antigen in a screening of 235 tick pools (Williams et al., 2000). Generally, CCHF is more common in males than in women, and this disparity is likely due to tick or infected tissue/blood contact on the occupational for example farmers, field workers, butchers, and healthcare professionals, are particularly at risk (Tishkova et al., 2012).

Table 1 Chronological reporting of CCHFV human cases in Iraq from 2021-2022

Country	Year	Case number	Death number	Notes
Iraq	2021	19	ND*	(Alhilfi et al., 2023)
	2022	219	ND*	(Alhilfi et al., 2023)
	2022	212	27	According to WHO data between 1st January-22nd May 2022. There were 115 suspected cases and 97 verified ones. In all, 27 people passed away, with 13 having laboratory-confirmed causes of death (World Health Organization, 2022).

**ND: not detected*

VITAL ROLE OF TICK VECTORS AND VERTEBRATE HOST POPULATIONS

The number of hosts used by a tick throughout its three parasitic phases of development (larva, nymph, and adult) is what determines the length of the tick's life cycle. The adult female tick will then drop off the host to oviposit when she has finished feeding (Figure 2) (Hoogstraal, 1979; Tahmasebi et al., 2010). Yet, it is unclear whether or not many of these species are capable of acting as vectors or reservoirs for CCHFV. Some ticks, known as "one-host ticks," (e.g., *Rhipicephalus microplus*, *R. decoloratus* and *R. annulatus*) spend their whole lives attached to a single host, usually a larger mammal such as a cow. Ticks that feed on and live on two separate hosts throughout their lives like the *H. marginatum, H. anatolicum*, and *H. detritum*) are called "two-host ticks". During their larval and nymphal life phases, these ticks feed and live on a small animal, before dropping off and attaching to a different host (larger mammals) as adults for a final blood meal. However, ticks that need three hosts to complete their life cycle (like *Dermacentor marginatus*, *Ixodes ricinus* and *Haemaphysalis punctata*) feed on small mammals during the first two phases of their lives and then switch to large vertebrates for the third (final blood meal). It's hard to think about CCHFV without taking ticks and vertebrate hosts into account. Some species of vectors may have a restricted host range in a given area (such as *H. dromedarii* for dromedary camels and *H. aegyptium* for Testudo species tortoises), this is often only the case at the local level (Široký et al., 2007; McCoy et al., 2013; Estrada-Peña and de la Fuente, 2014).

H. marginatum and *H. asiaticum* are two examples of *Hyalomma* species that are primarily responsible for CCHFV transmission in Europe and Asia, respectively (Maltezou and Papa, 2010). Besides its native Africa, the vector may also be found in Southern and Eastern Europe, the Middle East, India, and Asia. The *Hyalomma* spp. CCHFV vector is an Ixodid tick, which has three distinct morphological stages: larva, nymph, and adult. Each stage involves a molt during which the tick acquires nutrition via feeding on a host for many days to weeks (Estrada-Peña and de la Fuente, 2014). In western Arabian Peninsula (Mecca) area yielded ticks of the species *H. dromedarii* and *H. impeltatum* (Zakham et al., 2021). Ticks rely heavily on wild animals as hosts, and infected counterparts may then transmit the virus to their uninfected co-feeding ticks. Anti-CCHFV antibodies are often developed during a brief viremic period (2-15 days) during which CCHFV multiplies in small animals. This suggests that small animals are not effective CCHFV reservoirs over the long run. However, they do play a significant role in the ecology of CCHFV, and rising populations of some species (such as hares) have been linked to the spread of the virus. To the best of our knowledge, there have been no experimental investigations conducted on larger mammalian species found in the wild (Spengler et al., 2016a). Ticks that have two or three hosts, such as *H. asiaticum* and *D. marginatus*, find hares (small mammals) to be an ideal source of blood meals. Since the European hare (*Lepus europaeus*) population apparently expanded during the first CCHF epidemic in the Crimea, it was initially thought that this species was crucial in perpetuating CCHFV (Hoogstraal, 1979). Several CCHF outbreaks, notably the first one in Crimea and subsequent ones in the former Soviet Union, Bulgaria, Kosovo, and Turkey, were characterized by an overgrowth of vegetation because of a stop of farming and an increase of the hare population (with the related abundance of ticks) (Hoch et al., 2016). Hedgehogs and ground squirrels are two of the animals that are sometimes consumed as hosts by certain CCHFV-carrying tick species, such as the *D. marginatus* tick. Because these small animals spend a long amount of time rooting about in leaf litter and brush, which is where immature ticks are found, these animals provide excellent hosts for the instar life stages of many different tick species. Experiments have been done in which two distinct species of ground squirrels were infected, and the results of these experiments were quite similar to one another. It has been shown that the Colorado tick fever virus remains active in golden-mantel ground squirrels (*Citellus lateralis*) even when they are hibernating (Emmons, 1966). With long ears, hedgehogs *Hemiechinus auritus* is prevalent in Central Asian locations where CCHFV is endemic, but *Erinaceus europaeus* is found in European countries where CCHFV is typically absent. Experimental research on the susceptibility of hedgehog species to CCHFV showed contradictory findings, indicating that sensitivity to CCHFV and infection dynamics may differ even across closely related species. 2-6 days post infection, with a peak at 4-6 days post infection, viremia was identified in *Hemiechinus auritus* but not in *Erinaceus europaeus* (Nalca and Whitehouse, 2007). Red veld rats (*Aethomys chrysophilus*), white-tailed rats (*Mystromys albicaudatus*), bushveld gerbils (Gerbilliscus leucogaster), and four-striped grass mice (*Rhabdomys pumilio*) were all found to have CCHFV viremia (sampled up to 3-7 days post infection) (Shepherd et al., 1989).

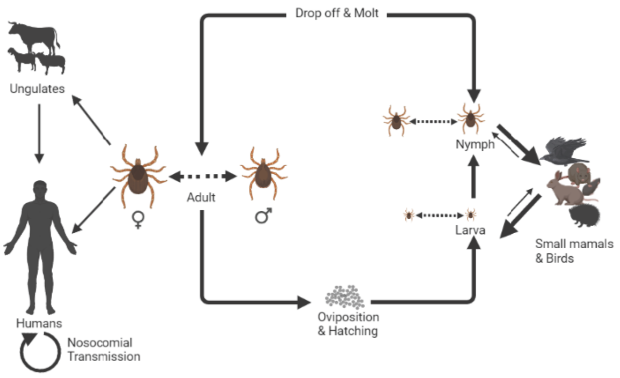

Figure 2 Proposed enzootic cycle of CCHFV transmission in Iraq and neighbouring countries, using the suggested tick vector Hyalomma spp. and its various vertebrate hosts.

CONCLUSION

Unfortunately, there is no available comprehensive genomic or phylogenetic data on the viral strains in Iraq. Control of tick-borne viruses especially zoonotic infections need efficient bio-surveillance to comprehend how the virus remains in the region and find signs of notifiable outbreaks in humans due to the complex enzootic cycle and transmission dynamics of CCHFV and the fact that the virus is silent in nature until it reaches a human host. Additional research is needed on the role that ticks play in the transmission and pathogenesis of the disease, as well as on the role that livestock and other animal species have in maintaining and transmitting CCHFV. This might result in the creation of more effective CCHFV transmission prevention strategies.
A concerted effort must be made to enhance public health campaigns on occupational dangers that are linked to CCHFV infection as well as other infectious diseases, in addition to conducting surveillance. Research institutions and ministries of health should work to share information as rapidly as they can with websites and other scientific outlets in order to increase real-time awareness of CCHFV outbreaks. Finally, to enable quick and accurate detection and diagnosis, approved diagnostic techniques must be available for use in the field and in centralised laboratories. These diagnostic tools must also be utilised periodically in bio-surveillance campaigns in an effort to stop the spread of illness.

CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest regarding the publication and/or funding of this review.

REFERENCES

Abul-Eis, E.S., Mohammad, N.A., Wasein, S.M., 2012. Crimean-congo hemorrhagic fever in Iraq during 2010. Iraqi. J. Vet. Med. 36, 99-103.

Akuffo, R., Brandful, J.A., Zayed, A., Adjei, A., Watany, N., Fahmy, N.T., Hughes, R., Doman, B., Voegborlo, S.V., Aziati, D., Pratt, D., Awuni, J.A., Adams, N., Dueger, E., 2016. Crimean-Congo hemorrhagic fever virus in livestock ticks and animal handler seroprevalence at an abattoir in Ghana. BMC. Infect. Dis. 16, 324.

Al-Nakib, W., Lloyd, G., El-Mekki, A., Platt, G., Beeson, A., Southee, T., 1984. Preliminary report on arbovirus-antibody prevalence among patients in Kuwait: evidence of Congo/Crimean virus infection. Trans. R. Soc. Trop. Med. Hyg. 78, 474–476.

Al-Tikriti, S.K., Al-Ani, F., Jurji, F.J., Tantawi, H., Al-Moslih, M., Al-Janabi, N., Mahmud, M.I., Al-Bana, A., Habib, H., Al-Munthri, H., Al-Janabi, S., K, A.L.-J., Yonan, M., Hassan, F., Simpson, D.I., 1981. Congo/crimean haemorrhagic fever in iraq. Bull. World. Health. Organ. 59(1), 85-90.

Albayrak, H., Ozan, E., Kurt, M., 2012. Serosurvey and molecular detection of Crimean–Congo hemorrhagic fever virus (CCHFV) in northern Turkey. Trop. Anim. Health. Prod. 44, 1667–1671.

Alhilfi, R.A., Khaleel, H.A., Raheem, B.M., Mahdi, S.G., Tabche, C., Rawaf, S., 2023. Large outbreak of Crimean-Congo haemorrhagic fever in Iraq, 2022. IJID Reg. 6, 76–79.

Bente, D.A., Forrester, N.L., Watts, D.M., McAuley, A.J., Whitehouse, C.A., Bray, M., 2013. Crimean-Congo hemorrhagic fever: history, epidemiology, pathogenesis, clinical syndrome and genetic diversity. Antiviral. Res. 100, 159–189.

Biglari, P., Chinikar, S., Belqeiszadeh, H., Telmadarraiy, Z., Mostafavi, E., Ghaffari, M., Javaherizadeh, S., Nowotny, N., Fooks, A.R., Shahhosseini, N., 2016. Phylogeny of tick-derived Crimean-Congo hemorrhagic fever virus strains in Iran. Ticks. Tick. Borne. Dis. 7, 1216–1221.

Camp, J.V., Kannan, D.O., Osman, B.M., Shah, M.S., Howarth, B., Khafaga, T., Weidinger, P., Karuvantevida, N., Kolodziejek, J., Mazrooei, H., Wolf, N., Loney, T., Nowotny, N., 2020. Crimean-Congo hemorrhagic fever virus endemicity in United Arab Emirates, 2019. Emerg. Infect. Dis. 26, 1019–1021.

Camp, J.V., Weidinger, P., Ramaswamy, S., Kannan, D.O., Osman, B.M., Kolodziejek, J., Karuvantevida, N., Abou Tayoun, A., Loney, T., Nowotny, N., 2021. Association of Dromedary camels and camel ticks with reassortant Crimean-Congo hemorrhagic fever virus, United Arab Emirates. Emerg. Infect. Dis. 27, 2471–2474.

Casals, J., 1969. Antigenic similarity between the virus causing crimean hemorrhagic fever and Congo Virus. Exp. Biol. Med. 131, 233–236.

Chinikar, S., Ghiasi, S.M., Moradi, M., Goya, M.M., Reza Shirzadi, M., Zeinali, M., Mostafavi, E., Pourahmad, M., Haeri, A., 2010. Phylogenetic analysis in a recent controlled outbreak of crimean-congo haemorrhagic fever in the south of iran, december 2008. Euro Surveill. 15(47), 19720.

Converse, J.D., Moussa, M.I., 1982. Quaranfil Virus from Hyalomma Dromedarii (Acari: Ixodoidea) collected in Kuwait, Iraq and Yemen1. J. Med. Entomol. 19, 209–210.

El-Azazy, O.M.E., Scrimgeour, E.M., 1997. Crimean-Congo haemorrhagic fever virus infection in the Western Province of Saudi Arabia. Trans. R. Soc. Trop. Med. Hyg. 91, 275–278.

Elevli, M., Ozkul, A.A., Civilibal, M., Midilli, K., Gargili, A., Duru, N.S., 2010. A newly identified Crimean-Congo hemorrhagic fever virus strain in Turkey. Int. J. Infect. Dis. 14, e213–e216.

Emmons, R.W., 1966. Colorado tick fever: prolonged viremia in hibernating citellus lateralis. Am. J. Trop. Med. Hyg. 15, 428–433.

Ertugrul, B., Uyar, Y., Yavas, K., Turan, C., Oncu, S., Saylak, O., Carhan, A., Ozturk, B., Erol, N., Sakarya, S., 2009. An outbreak of Crimean-Congo hemorrhagic fever in western Anatolia, Turkey. Int. J. Infect. Dis. 13, e431–e436.

Estrada-Peña, A., de la Fuente, J., 2014. The ecology of ticks and epidemiology of tick-borne viral diseases. Antiviral Res. 108, 104–128.

Gale, P., Stephenson, B., Brouwer, A., Martinez, M., de la Torre, A., Bosch, J., Foley-Fisher, M., Bonilauri, P., Lindström, A., Ulrich, R.G., de Vos, C.J., Scremin, M., Liu, Z., Kelly, L., Muñoz, M.J., 2012. Impact of climate change on risk of incursion of Crimean-Congo haemorrhagic fever virus in livestock in Europe through migratory birds. J. Appl. Microbiol. 112, 246–257.

Gargili, A., Estrada-Peña, A., Spengler, J.R., Lukashev, A., Nuttall, P.A., Bente, D.A., 2017. The role of ticks in the maintenance and transmission of Crimean-Congo hemorrhagic fever virus: A review of published field and laboratory studies. Antiviral Res. 144, 93–119.

Gonzalez, J.P., Camicas, J.L., Cornet, J.P., Faye, O., Wilson, M.L., 1992. Sexual and transovarian transmission of Crimean-Congo haemorrhagic fever virus in Hyalomma truncatum ticks. Res. Virol. 143, 23–28.

Gürbüz, E., Ekici, A., Ünlü, A.H., Yılmaz, H., 2021. Evaluation of seroprevalence and clinical and laboratory findings of patients admitted to health institutions in Gümüşhane with suspicion of Crimean-Congo hemorrhagic fever. Turk. J. Med. Sci. 51(4), 1825-1832.

Hassanein, K.M., El-Azazy, O.M.E., 2000. Isolation of Crimean-Congo hemorrhagic fever virus from ticks on imported sudanese sheep in Saudi Arabia. Ann. Saudi. Med. 20, 153–154.

Hassanein, K.M., El-Azazy, O.M.E., Yousef, H.M., 1997. Detection of Crimean-Congo haemorrhagic fever virus antibodies in humans and imported livestock in Saudi Arabia. Trans. R. Soc. Trop. Med. Hyg. 91, 536–537.

Hasson, R.H., 2012. Tick distribution and infestation among sheep and cattle in Baghdad' s south suburb Raad Hammodi Hasson. Kufa. J. Vet. Med. Sci. 3(1), 77-90.

Hawman, D.W., Feldmann, H., 2018. Recent advances in understanding Crimean–Congo hemorrhagic fever virus. F1000Res. 7, 1715.

Hoch, T., Breton, E., Josse, M., Deniz, A., Guven, E., Vatansever, Z., 2016. Identifying main drivers and testing control strategies for CCHFV spread. Exp. Appl. Acarol. 68, 347–359.

Hoogstraal, H., 1979. Review article: the epidemiology of tick-borne Crimean-Congo hemorrhagic fever in Asia, Europe, and Africa. J. Med. Entomol. 15(4), 307-417.

Ibrahim, A.S., Ibrahim, K.S., Mohammed, M.O., Al-Shaikhani, M.A., Barzanji, A.A., Saeed, S.J., Muhiaden, S., Bhnam, M.N., 2014. Crimean Congo hemorrhagic fever management in Erbil during 2010-2011. Eur. Sci. J. 10(24), 219–229.

Kadir, M.A., Zangana, I.K., Mustafa, B.H.S., 2012. A study on epidemiology of hard tick (Ixodidae) in sheep in Sulaimani governorate - Iraq. Iraqi. J. Vet. Sci. 26, 95–103.

Karti, S.S., Odabasi, Z., Korten, V., Yilmaz, M., Sonmez, M., Caylan, R., Akdogan, E., Eren, N., Koksai, I., Ovali, E., Erickson, B.R., Vincent, M.J., Nichol, S.T., Comer, J.A., Rollin, P.E., Ksiazek, T.G., 2004. Crimean-Congo hemorrhagic fever in Turkey. Emerg. Infect. Dis. 10, 1379–1384.

Kettle D.S., 1995. Medical and veterinary entomology. CAB International, Wallingford, Oxon, UK, pp. 853.

Khalafalla, A.I., Li, Y., Uehara, A., Hussein, N.A., Zhang, J., Tao, Y., Bergeron, E., Ibrahim, I.H., Al Hosani, M.A., Yusof, M.F., Alhammadi, Z.M., Alyammahi, S.M., Gasim, E.F., Ishag, H.Z.A., Hosani, F.A.L., Gerber, S.I., Almuhairi, S.S., Tong, S., 2021. Identification of a novel lineage of Crimean-Congo haemorrhagic fever virus in dromedary camels, United Arab Emirates. J. Gen. Virol. 102(2), 001473.

Longson, M., Shurie, H., Acharya, U.G., Schwarz, T.F., Gilch, S., Zahir, A.R.M., Nitschko, H., Ameen, A., Jager, G., Nsanze, H., 1996. Polymerase chain reaction for diagnosis and identification of distinct variants of Crimean-Congo hemorrhagic fever virus in the United Arab Emirates. Am. J. Trop. Med. Hyg. 55, 190–196.

Majeed, B., Dicker, R., Nawar, A., Badri, S., Noah, A., Muslem, H., 2012. Morbidity and mortality of Crimean-Congo hemorrhagic fever in Iraq: cases reported to the National Surveillance System, 1990–2010. Trans. R. Soc. Trop. Med. Hyg. 106, 480–483.

Maltezou, H.C., Papa, A., 2010. Crimean–Congo hemorrhagic fever: risk for emergence of new endemic foci in Europe? Travel. Med. Infect. Dis. 8, 139–143.

McCoy, K.D., Léger, E., Dietrich, M., 2013. Host specialization in ticks and transmission of tick-borne diseases: a review. Front. Cell. Infect. Microbiol. 3, 57.

Memish, Z.A., 2002. Infection control in Saudi Arabia: meeting the challenge. Am. J. Infect. Control. 30, 57–65.

Mild, M., Simon, M., Albert, J., Mirazimi, A., 2010. Towards an understanding of the migration of Crimean-Congo hemorrhagic fever virus. J. Gen. Virol. 91, 199–207.

Mohamed, R., Mohamed, N., Aleanizy, F.S., Alqahtani, F.Y., Al Khalaf, A., Al-Keridis, L.A., 2017. Investigation of hemorrhagic fever viruses inside wild populations of ticks: One of the pioneer studies in Saudi Arabia. Asian Pacific J. Trop. Dis. 7(5), 299-303.

Mustafa, B.H.S., Faraj, S.H., 2013. Resistance of hard tick (Ixodidae) with some acaricide in cattle (naturally infestation) in sulaimani governorate fields-Kurdistan regional/Iraq. J Agr Sci Tech. 3, 927–934.

Nalca, A., Whitehouse, C.A., 2007. Crimean-Congo hemorrhagic fever virus infection among animals. In: Whitehouse, C.A., Ergonul, O. (Eds.), Crimean-Congo hemorrhagic fever. Springer Netherlands, Dordrecht, pp. 155–165.

Omer, L.T., Kadir, M.A.A., Seitzer, U., Ahmed, J.S., 2007. A survey of ticks (Acari:Ixodidae) on cattle, sheep and goats in the Dohuk Governorate, Iraq. Parasitol. Res. 101, 179–181.

Orkun, Ö., Karaer, Z., Çakmak, A., Nalbantoğlu, S., 2017. Crimean-Congo hemorrhagic fever virus in ticks in Turkey: a broad range tick surveillance study. Infect. Genet. Evol. 52, 59–66.

Perveen, N., Khan, G., 2022. Crimean–Congo hemorrhagic fever in the Arab world: a systematic review. Front. Vet. Sci. 9.

Perveen, N., Muzaffar, S. Bin, Al-Deeb, M.A., 2021. Ticks and tick-borne diseases of livestock in the Middle East and North Africa: a review. Insects. 12, 83.

Razmi, G., Naghibi, A., Aslani, M., Fathivand, M., Dastjerdi, K., 2002. An epidemiological study on ovine babesiosis in the Mashhad suburb area, province of Khorasan, Iran. Vet. Parasitol. 108, 109–115.

Robson, J., Robb, J.M., Hawa, N.J., 1969. Ticks (Ixodoidea) of domestic animals in Iraq: Part 5. Infestations in the liwas of diwaniya and nasiriya (spring), karbala (winter), and hilla (autumn and winter). J. Med. Entomol. 6, 120–124.

Shahhosseini, N., Jafarbekloo, A., Telmadarraiy, Z., Chinikar, S., Haeri, A., Nowotny, N., Groschup, M.H., Fooks, A.R., Faghihi, F., 2017. Co-circulation of Crimean-Congo hemorrhagic fever virus strains Asia 1 and 2 between the border of Iran and Pakistan. Heliyon. 3(11), e00439.

Shepherd, A.J., Mathee, O., Cornel, A.J., Swanepoel, R., 1989. Experimental studies on the replication and transmission of Crimean-Congo hemorrhagic fever virus in some African Tick Species. Am. J. Trop. Med. Hyg. 40, 326–331.

Široký, P., Petrželková, K.J., Kamler, M., Mihalca, A.D., Modrý, D., 2007. Hyalomma aegyptium as dominant tick in tortoises of the genus Testudo in Balkan countries, with notes on its host preferences. Exp. Appl. Acarol. 40, 279–290.

Sisman, A., 2013. Epidemiologic features and risk factors of Crimean-Congo hemorrhagic fever in Samsun province, Turkey. J. Epidemiol. 23(2), 95-102.

Spengler, J.R., Bergeron, É., Rollin, P.E., 2016a. Seroepidemiological studies of Crimean-Congo hemorrhagic fever virus in domestic and wild animals. PLoS. Negl. Trop. Dis. 10, e0004210.

Spengler, J.R., Estrada-Peña, A., Garrison, A.R., Schmaljohn, C., Spiropoulou, C.F., Bergeron, É., Bente, D.A., 2016b. A chronological review of experimental infection studies of the role of wild animals and livestock in the maintenance and transmission of Crimean-Congo hemorrhagic fever virus. Antiviral. Res. 135, 31–47.

Tahmasebi, F., Ghiasi, S., Mostafavi, E., Moradi, M., Piazak, N., Mozafari, A., Haeri, A., Fooks, A.R., Chinikar, S., 2010. Molecular epidemiology of Crimean-Congo hemorrhagic fever virus genome isolated from ticks of Hamadan province of Iran. J. Vector Borne Dis. 47, 211–216.

Tantawi, H.H., Shony, M.O., Al-Tikriti, S.K., 1981. Antibodies to Crimean-Congo haemorrhagic fever virus in domestic animals in Iraq: a seroepidemiological survey. Int. J. Zoonoses 8, 115–20.

Telmadarraiy, Z., Ghiasi, S.M., Moradi, M., Vatandoost, H., Eshraghian, M.R., Faghihi, F., Zarei, Z., Haeri, A., Chinikar, S., 2010. A survey of Crimean-Congo haemorrhagic fever in livestock and ticks in Ardabil Province, Iran during 2004–2005. Scand. J. Infect. Dis. 42, 137–141.

Tishkova, F.H., Belobrova, E.A., Valikhodzhaeva, M., Atkinson, B., Hewson, R., Mullojonova, M., 2012. Crimean-congo hemorrhagic fever in Tajikistan. Vector. Borne. Zoonotic. Dis. 12(9), 722-726.

Turell, M.J., 2007. Role of Ticks in the Transmission of Crimean-Congo hemorrhagic fever virus. In: Whitehouse, C.A., Ergonul, O. (Eds.), Crimean-Congo hemorrhagic fever. Springer Netherlands, Dordrecht, pp. 143–154.

Vakalova, E.V., Butenko, A.M., Vishnevskaya, T.V., Dorofeeva, T.E., Gitelman, A.K., Kulikova, L.N., Lvov, D.K., Alkhovsky, S.V., 2019. Results of investigation of ticks in Volga river delta (Astrakhan region, 2017) for Crimean-Congo hemorrhagic fever virus (Nairoviridae, Orthonairovirus, CCHFV) and other tick-borne arboviruses. Probl. Virol. 64, 221–228.

Williams, R.J., Al-Busaidy, S., Mehta, F.R., Maupin, G.O., Wagoner, K.D., Al-Awaidy, S., Suleiman, A.J.M., Khan, A.S., Peters, C.J., Ksiazek, T.G., 2000. Crimean-Congo haemorrhagic fever: a seroepidemiological and tick survey in the Sultanate of Oman. Trop. Med. Int. Heal. 5, 99–106.

World Health Organization, 2022. Crimean-Congo Hemorrhagic Fever in Iraq. Available online: https://www.who.int/emergencies/disease-outbreak-news/item/2022-DON386.

World Health Organization, 2017. Crimean-Congo haemorrhagic fever. Available online: https://www.who.int/news-room/fact-sheets/detail/crimean-congo-haemorrhagic-fever

Zakham, F., Albalawi, A.E., Alanazi, A.D., Truong Nguyen, P., Alouffi, A.S., Alaoui, A., Sironen, T., Smura, T., Vapalahti, O., 2021. Viral RNA metagenomics of hyalomma ticks collected from dromedary camels in Makkah Province, Saudi Arabia. Viruses. 13, 1396.

How to cite this article;

Amer Nubgan and Mohammed Al-Saadi. Crimean-Congo hemorrhagic fever favouring factors virus transmission: Special focus on Iraq and neighbouring countries. Veterinary Integrative Sciences. 2023; 21(3): 865- 877.