



Correspondence

The discrepancy of Crimean-Congo hemorrhagic fever-related tick vectors: An urgent need for boosted surveillance

Dear editor;

Crimean-Congo hemorrhagic fever (CCHF) is among the widest tick-borne viral zoonosis diseases worldwide. Crimean-Congo hemorrhagic fever (CCHF) is presented in a wide range of moderate to severe hemorrhagic diseases that could be acute as well as fatal (up to 40%) [1]. CCHF is recognized as the largest tick-transmitted virus that is broadly distributed to the world, except in North America, South America, and Australia. The Crimean-Congo hemorrhagic fever virus is phylogenetically classified into seven sub-lineages, including clade I (Africa 2), clade II (Africa 1), clade III (Europe 2), clade IV (Africa 3), clade V (Europe 1), clade VI (Asia 1) and clade VII (Asia 2) based on the CCHFV S-segment [2].

CCHFV is routinely circulating via natural enzootic tick-vertebrate-tick transmission cycles. However, there was human-to-human transmission through contact with the blood or tissue of infected animals and nosocomial settings [3]. Various susceptible vertebrates (asymptomatic carriage for CCHFV) play an important role in the endemic CCHF cycle of transmission. Hence, the distribution of CCHFV to the new areas occurred following migration, movements, and international travels that involved CCHFV-infected animals, humans, or ticks.

There are two families of ticks: hard-bodied ticks (Ixodidae) and soft-bodied ticks (Argasidae). The genus *Hyalomma* is one of the largest members of the Ixodidae family that is considered a natural niche for CCHFV (both reservoirs and vectors) that have global distribution in Asia, Africa, and European unions. The *Hyalomma* species have great advantages, guaranteeing CCHFV survival without a blood meal for 800 days [4]. Thus, the genus *Hyalomma* tick species appears as a natural niche for long-lasting maintenance of CCHFV in the field. Other *Hyalomma* tick species, e.g., *Amblyomma*, *Boophilus*, *Dermacentor*, *Haemaphysalis*, and *Rhipicephalus* genera, also played crucial roles in the natural circulation of CCHFV transmission chains that be neglected in this issue [5,6]. However, ticks play an important role in the natural maintenance of CCHFV as both reservoirs and vectors. The clinical relevance of ticks is neglected regarding CCHFV in epidemiology.

We postulate that Surveillance of CCHFV in ticks could bring useful information regarding monitoring the introduction or circulation, measuring the risk of exposure in humans, recognizing the natural host, and forecasting further CCHFV outbreaks.

According to the literature reviews, seven major tick genera have been confirmed CCHFV-positive in different regions, including *Hyalomma*, *Rhipicephalus*, *Haemaphysalis*, *Dermacentor*, *Ixodes*, *Amblyomma*, as well as *Ornithodoros* that belong to the *Argasidae* family [7]. The tick species with limited distribution merely play a critical role in enzootic transmission cycle disease. The geographical diversity of tick species in various areas originates from a diverse background in these territories e.g. climate change, temperature, the sampling time course, and

vegetation. In addition, there is diverse tick species distribution based on vertebrate species. For example, the *Ixodidae* family is frequently isolated in female domestic animals due to the high concentration of progesterone and prolactin hormones [8]. Furthermore, we should consider that these tick species can also transfer other infectious agents such as *Borrelia*, *Anaplasma*, *Coxiella*, *Francisella*, *Rickettsia*, *Thieleria*, *Ehrlichia*, and *Babesia* [9].

Nasirian et al., 2022 recently revealed the presence of CCHFV among 31 tick species, that 15 tick species, e.g., *Hyalomma*, *Dermacentor*, and *Rhipicephalus* species, have proven CCHFV vectors as well as 16 suspicion tick vectors [10]. According to the literature, the tick species such as *Hyalomma anatolicum* Koch, *Hy. dromedarii* Koch, *Hy. marginatum* Koch, *Hy. rufipes* Koch, *Rhipicephalus bursa* Canestrini & Fanzago, and *R. sanguineus* (Latreille) are popular species responsible for the upsurge of Crimean-Congo hemorrhagic fever virus worldwide. However, *Hy. Marginatum* species has been considered the biggest vector competence species for global CCHFV outbreaks in the Middle East, Northern Africa, and Southern Europe territories [11–13]. Vertebrates also contribute a fundamental role in viral ecology by acting as connective bridges that CCHFV surpasses from one tick to another species and boosting the transmission cycle through co-feeding (non-systemic) transmission chains [14].

Moreover, Long-distance movement of livestock and wildlife species could introduce CCHFV-infected tick species to other regions, for example, large transport of *Hyalomma glabrum* Delpy, *Hy. Isaaci* Sharif, *Hy. marginatum* sensu stricto, *Hy. rufipes*, and *Hy. Turanicum* Pomerantzev from Africa to Europe unions during 2008–2012 [15]. Tick species play a critical role in the ecology of the virus by maintaining the CCHFV and active contributions to the introduction of CCHFV to the host vertebrates.

Conversely, CCHFV should overcome tick barriers to establish successful infection within the tick species. Identifying predominant competence tick vectors in each exclusive geographic area is a crucial strategy for rapidly controlling local CCHFV outbreaks. Palomar et al., 2016 suggested the elimination of *Hy. marginatum* ticks in the North of Spain do not reduce the risk of human CCHFV infection [16]. Thus, determining circulating tick species in each geographic area has beneficial outcomes in reducing the CCHFV infection rate. We accounted that the environmental and climate change and wild bird movements have played a role in CCHF spreading and the introduction of tick species to other world regions [17]. Hence, surveillance of tick species infested with the Crimean-Congo hemorrhagic fever virus is an essential step in controlling the virus's spread to non-endemic areas.

Finally, regarding the clinical relevance of tick species in virus maintenance and dissemination of CCHFV infection in humans. Tick-borne CCHFV registration and nationwide surveillance are

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recommended to prevent further CCHFV outbreaks in non-endemic regions. Furthermore, there is no comprehensive information regarding vector competence (ability to infect with CCHFV and play a role in the virus transmission) as well as vector capacity (infectious dose) that requires to be elucidated by further investigations to detect the CCHFV expansion to new geographic regions.

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