

***Hyalomma* Ticks and Human and Animal Health**

Subjects: Entomology

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Ticks are obligatory hematophagous ectoparasites that act as vectors for many important human and livestock pathogens worldwide. Like spiders and scorpions, they belong to the class Arachnida. Within the order Ixodida, most species of ticks belong to one of the two main large families, Argasidae or Ixodidae. The latter are known as “hard” ticks since they have a sclerotized dorsal plaque or scutum. In contrast, those belonging to the family *Argasidae* lack this physical feature and are therefore known as “soft ticks”. Tick-borne infectious diseases spread following the bite of infected ticks, which can carry and be infected by bacteria, viruses, or parasites. Some of the most important bacteria-infecting ticks include species of the genera *Rickettsia*, *Borrelia*, *Francisella*, *Anaplasma*, and *Ehrlichia*, as well as viruses such as the Crimea–Congo hemorrhagic fever (CCHF) virus, the West Nile virus, and the tick-borne encephalitis virus, among others.

Keywords: tick microbiome ; endosymbiont ; tick symbiosis ; climate change ; pathogen

1. The Increase in Ticks and Tick-Borne Diseases in the Era of Climate Change

In recent years, there has been an increase in the population of these ectoparasites, possibly as a result of the modification of the environmental biomass caused by humans, but also due to climate change and global warming, the altered migration patterns of birds, as well as human migrations due to wars and geopolitical conflicts, among others ^{[1][2][3][4][5]}.

There are rising reports that advocate for the northward spread of thermophilic ixodid species, such as *Hyalomma*. In this particular case, there have been many studies that evidence the dwindling success of these Afro-Mediterranean tick species in continental climates in Europe, and with contact with animals and humans.

For example, early in 2012, an adult case of *H. marginatum rufipes* was reported on cattle under a continental climate in Hungary ^[6]. Since then, many other studies have also identified other *Hyalomma* species in animals and humans in Hungary ^[7], the Netherlands ^[8], and Germany ^[9]; in cattle of Corsica in France ^[10]; in an English horse ^[11]; and in a migrant in Malta ^[2]. Furthermore, the first human exposure to a locally acquired adult *H. marginatum* was recently described in England in 2021 ^[12]. Most of these reports have detected the successful molting of these *Hyalomma* species in newly colonized regions of Europe.

Both climate change and other human activities (deforestation, urbanization, and international travel) ^[13] play a decisive role in the increase in infectious pathogens and their transmission vectors. In a recent study, the impact of climate trends in the distribution of *H. marginatum* was explored. The authors generated annual models of environmental suitability for the tick in the period 1970–2018, using harmonic regression-derived data of the daily maximum and minimum temperature, soil moisture, and water vapor deficit. It was concluded that climate change could create new areas in Europe with suitable climates for *H. marginatum*, while keeping its “historical” distribution in the Mediterranean ^[3]. Moreover, other works have discussed the importance of migratory birds in the international dispersion of *Hyalomma* ticks. They may play an important role in the changing climatic and environmental conditions in Europe because birds that cover long distances over a short time and stay temporarily in different habitats in the context of climate change can introduce tick and pathogen species in areas where they have never been ^[4].

This appearance of vectors and zoonotic infectious diseases in areas where no disease had been previously reported so far ^{[14][15]} reaffirms the prompt needed for further strategies for dispersion control, especially considering both the impact of tick-borne diseases and also their potential social and economic impact ^[16].

2. The Impact of Ticks of the Genus *Hyalomma* on Human and Animal Health

The genus *Hyalomma* is included in the family *Ixodidae* and is considered one of the main transmission vectors of the CCHF virus in humans and theileriosis in cattle. This genus comprises more than 20 species, mainly distributed across three continents: Europe, Asia, and Africa ^[17] (**Table 1**). Up to half of them are capable of transmitting disease-causing pathogens, and due to their adaptability, they are usually found in tropical or subtropical areas, mainly where arid climates predominate ^[18]. Despite being transmitters of potentially fatal diseases, ticks from this genus are not particularly anthropophilic, and the risk of transmitting diseases to humans is lower than in other genera, such as *Ixodes* or *Dermacentor* ^[17].

Table 1. Pathogens of human and animal importance transmitted by ticks of the *Hyalomma* species.

<i>Hyalomma</i> Species	Human Pathogens	Animal Pathogens	Continent	Reference
<i>H. aegyptium</i>	– - <i>Anaplasma phagocitophilum</i>		Africa Europe	^{[19][20]}
	– - <i>Ehrlichia canis</i>	– <i>Theileria annulata</i>		
	– - <i>Coxiella burnetti</i>	– <i>Hepatozoon kisrae</i>		
	– - <i>Rickettsia aeschlimannii</i>	– <i>Hemolivia mauritanica</i>		
	– - <i>Rickettsia africae</i>	– <i>Theileria lestoquardi</i>		
	– - <i>Borrelia turcica</i>	– <i>Candidatus</i>		
	– - <i>Borrelia burgdoferi</i>	– <i>Midichloria mitochondrii</i>		
<i>H. albigatum</i>	– - <i>Leishmania infantum</i>		Africa	^{[21][22]}
	– - <i>R.conorii</i>			
<i>H. anatolicum</i>	– - Crimean–Congo hemorrhagic fever (CCHF) virus		Africa Asia Europe	^{[23][24]}
	– - Virus Kadam			
	– - Virus Kundal	– <i>Theileria annulata</i>		
	– - Virus Karyana	– <i>Theileria equi</i>		
	– - <i>Rickettsia</i> spp.	– <i>Theileria lestoquardi</i>		
	– <i>Ehrlichia</i> spp.	– <i>Theileria ovis</i>		
	– <i>Anaplasma</i> spp.			
<i>H. arabica</i>	– <i>Babesia</i> spp.		Asia	^[25]
<i>H. brevipunctata</i>	– <i>Anaplasma marginale</i>		Asia	^[23]
	– <i>Babesia bigemina</i>			

<i>Hyalomma Species</i>	Human Pathogens	Animal Pathogens	Continent	Reference
<i>H. detritum</i>	– <i>Bhanja virus</i>			
	– <i>Rickettsia aeschlimannii</i>		Africa Europe	[26]
	– <i>Theileria annulata</i>			
	– CCHF virus			
	– Dhori virus			
	– Kadam virus			
	– Sindilbis virus			
<i>H. dromedarii</i>	– Chick Ross virus	– <i>Theileria annulata</i>		
	– Thogoto virus	– <i>Theileria camelensis</i>	África Asia Europa	[27]
	– Bhanja virus	– <i>Coxiella burnetti</i>		
	– <i>Coxiella burnetti</i>			
	– <i>Rickettsia aeschlimannii</i>			
	– <i>Rickettsia rickettsii</i>			
	– <i>Babesia</i> spp.			
<i>H. erythraeum</i> o <i>H. somaliticum</i>			Africa Asia Europe	[28]
<i>H. excavatum</i>		– <i>Theileria lestoquardi</i>		
	– <i>Rickettsia aeschlimannii</i>	– <i>Anaplasma marginale</i>		
		– <i>Anaplasma centrale</i>	Africa Europe	[17]
		– <i>Theileria annulata</i>		
<i>H. franchinii</i>			Europe	[21]
<i>H. husainii</i>			Asia	[23]
<i>H. impeltatum</i>	– CCHF virus			
	– Dhori virus	– <i>Babesia ocutans</i>		
	– <i>Rickettsia aeschlimannii</i>	– <i>Theileria lestoquardi</i>	Africa Asia Europe	[28][29]
	– <i>Rickettsia africae</i>			
<i>H. impressum</i>		– <i>Babesia ocutans</i>	Africa	[23]
<i>H. kumari</i>				[30]

<i>Hyalomma Species</i>	Human Pathogens	Animal Pathogens	Continent	Reference
<i>H. lussitanicum</i>	– <i>Rickettsia</i> spp.			
	– <i>Anaplasma phagocytophilum</i>			
	– <i>Borrelia</i>		Europe	[31][32]
	– <i>Coxiella burnetii</i>			
	– <i>Francisella tularensis</i>			
<i>H. marginatum</i>	– CCHF virus			
	– Dhori virus			
	– West Nile virus			
	– Bhanja virus	– <i>Babesia</i> spp.	Africa Asia Europe	[12][33][34]
	– <i>Ricketssia aeschlimannii</i>	– <i>Theileria annulata</i>		
<i>H. nitidum</i>	– <i>Ricketssia sibirica</i>			
	– <i>Ricketssia africae</i>			
	– Thogoto virus			
	– CCHF virus		Africa	[22]
<i>H. punctata</i>			Africa Asia	[35]
<i>H. rhipicephaloides</i>			Africa Asia	[35]
<i>H. rufipes</i>	– Thogoto virus			
	– CCHF virus			
	– <i>Ricketssia aeschlimannii</i>	– <i>Babesia ocutans</i>	Africa Asia Europe	[2][36]
	– <i>R.conorii</i>			
		– <i>Anaplasma ovis</i>		
<i>H. schulzei</i>	– Dhori virus	– <i>Anaplasma marginale</i> – <i>Ehrlichia ewingii</i>	Asia	[37]
<i>H. scupense</i>	– <i>Coxiella burnetii</i>	– <i>Theileria annulata</i>	Africa Asia Europe	[38][39]

<i>Hyalomma Species</i>	Human Pathogens	Animal Pathogens	Continent	Reference
<i>H. truncatum</i>	– CCHF virus			
	– Bhanja virus			
	– Rift Valley fever virus	– Venezuelan equine encephalitis	Africa Asia Europe	[22][40]
	– <i>Coxiella burnetti</i>			
	– <i>Rickettsia aeschlimannii</i>	– Rift Valley fever virus		
	– <i>R. sibirica</i>			
<i>H. turanicum</i>	– <i>R. conorii</i>			
		– <i>B. ocutans</i>		
		– <i>B. caballi</i>		
	– CCHF virus	– Venezuelan equine encephalitis	Africa Asia Europe	[36]
	– <i>R. sibirica</i>	– Rift Valley fever virus		

Firstly, *Hyalomma aegyptum* constitutes one of the best known species within the genus. This species of tick is abundantly distributed throughout the eastern parts of European territory and the northern parts of the African continent. Characteristically, it has been seen to use camels and tortoises of the genus *Testudo* as hosts [19]. In a study conducted in Qatar, the most frequently identified pathogen in these latter hosts was *Hemolivia mauritanica*. This justifies the need to increase control over species such as *Testudo* tortoises in order to reduce the spread of infectious diseases caused by *H. mauritanica*, *Candidatus Midichloria mitochondrii*, or *Ehrlichia* spp. [20]. This same study shows that *H. dromedarii* uses the same intermediate hosts as *H. aegyptum* and is also one of the main vectors of the transmission of Q fever and theileriosis among camels in North Africa [27].

Secondly, *H. albiparmatum*, *H. nitidum*, and *H. truncatum* are morphologically very similar species that are differentiated by the identification and comparison of somatic primary or secondary sexual characteristics that they develop throughout adult life [21]. Both *H. albiparmatum* and *H. nitidum* extend through the central areas of the African continent (Senegal, Kenya, and the Democratic Republic of Congo), while *H. truncatum* has been found to be widely distributed [22].

H. brevipunctata, together with *H. hussaini*, *H. anatolicum*, *H. dromedarii*, and *H. marginatum*, uses the buffalo of northern India as an animal host to transmit diseases such as babesiosis [23]. Babesia has also been identified in other species such as *H. rufipes*, *H. impressum*, *H. truncatum*, *H. marginatum*, and *H. impeltatum*. It is worth mentioning that *H. brevipunctata* is one of the most virulent species, capable of causing otoacariasis and tick paralysis in humans [17]. Surprisingly, despite the fact that *H. marginatum* and *H. impeltatum* act as multi-pathogen reservoirs and have a higher prevalence around the world, it is *H. rufipes* that has the greatest participation and influence in the spread of this disease among Nigerian cattle [36].

H. arabica is the most abundant tick species in the *Hyalomma* genus in Saudi Arabia. It is restricted to the western parts of this country and the Al-Sarawat mountain range in Yemen, and sheep are its main host [25]. It is the closest phylogenetic species to *H. kumari*, which ranges from India to western Iran [30].

H. erythareum has been taxonomically redefined as *H. somaliticum*. Along with *H. impelatum*, both are included in the *H. asiaticum* group [28]. *H. somaliticum* is one of the main vectors of bovine theileriosis in rural areas of Saudi Arabia [29], whilst *H. detritum* is one of the main vectors in parts of North Africa, such as Morocco [26].

H. franchinii is one of eight tick species of the *Ixodes* group that are restricted to the Mediterranean basin [21]. Along with *H. lussitanicum*, it is one of the species undergoing an explosive population increase and has been identified in Spain as a transmitter of the CCHF virus [31]. Up to 80% of the ticks identified in the Iberian Peninsula belong to the species *H.*

lusitanum. Furthermore, *Francisella* were the most common genera in *H. anatolicum*, possibly indicating that some pathogenic species such as *F. tularensis* may be present in the animal population parasitized by this tick species [24].

H. marginatum is one of the most widespread species worldwide. It is the main known vector of the CCHF virus, and, in recent years, its prevalence has increased in areas of northern Europe such as Sweden [33], England [12], and the Czech Republic [34]. Likewise, *H. rufipes* has also recently increased since it was unexpectedly found for the first time in Malta in 2020 [2]. Their increasing incidence evidences the prompt need to epidemiologically control and develop screening strategies for tick-borne infectious diseases in Northern Europe.

H. punctata is predominantly distributed in northern Somalia and Ethiopia, while *H. rhipicephaloides* has been primarily identified round the Dead Sea. Both types of ticks have goats and gazelles as hosts [35]. *H. schulzei* is known to be one of the leading species in the transmission of ehrlichiosis and anaplasmosis among cattle on the border between Iran and Pakistan. It poses a serious problem for the economy of rural parts of the country, given that livestock accounts for their principal income source [37].

H. scupense, along with *H. anatolicum*, stands out as one of the main vectors of theileriosis transmission in Africa [39]. It is mainly distributed in the African Maghreb area [38]. *Theileriosis* is a disease caused by the apicomplexan protist of the genus *Theileria*. They are obligatory intracellular parasites that use cattle as their main host. The two best known species are *T. parva*, which causes East Coast fever, and *T. annulata*, which causes tropical theileriosis. Only *T. annulata*, *T. lestoquardi*, *T. ovis*, and *T. separata* have been identified in ticks of the *Hyalomma* genus. The East Coast fever is characterized by symptoms of generalized lymphadenopathy, fever, anorexia, the appearance of petechiae or ecchymosis on mucous membranes, and neurological signs. Tropical theileriosis also causes the destruction of red blood cells and therefore also causes jaundice, anemia, and hemoglobinuria [41]. In recent years, various strategies have been developed for the control of theileriosis in African cattle. These include vaccination with inactivated *T. annulata* vaccines or with *H. scupense* antigens, which have been associated with a reduction in tropical theileriosis in North Africa [42] and China [43].

Finally, *H. turanicum* and *H. truncatum* are two species mainly implicated in the spread of the Rift Valley fever virus and the CCHF virus, and the horizontal and vertical transmission of these agents have been previously described. They are distributed worldwide and have been reported as one of the main species that cause this disease in sheep and humans [40].

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