Crimean-Congo haemorrhagic fever Fact Sheet

1. Disease overview

Crimean-Congo haemorrhagic fever virus (CCHFV) causes Crimean-Congo haemorrhagic fever, a tick-borne viral disease. The virus is maintained in an enzootic cycle involving ticks and various wild and domestic animals. In animals, infection is generally subclinical, although seroconversion is frequent in areas where the virus circulates. Humans are the only species known to develop clinical disease (Ergönül, 2006; Spickler, 2019; Whitehouse, 2004; WOAH, 2025b).

Crimean-Congo haemorrhagic fever is a WOAH-notifiable disease, but it is not listed in the European AHL.

2. Agent

CCHFV is a single-stranded, negative-sense RNA virus of the genus Orthonairovirus. The virus has a tripartite genome, comprising small (S), medium (M), and large (L) RNA segments. These segments encode essential structural and non-structural proteins including the nucleoprotein (NP), glycoproteins (Gn and Gc), and an RNA-dependent RNA polymerase (RdRp). The virus is enveloped and pleomorphic, typically ranging from 80 to 120 nm in diameter. The virus exhibits significant genetic variability, primarily driven by frequent segment reassortment and the error-prone nature of its RdRp during replication. Phylogenetic analyses have identified multiple distinct genotypes, with varying geographic distributions (Bente et al., 2013; Whitehouse, 2004).

3. Geographical Distribution

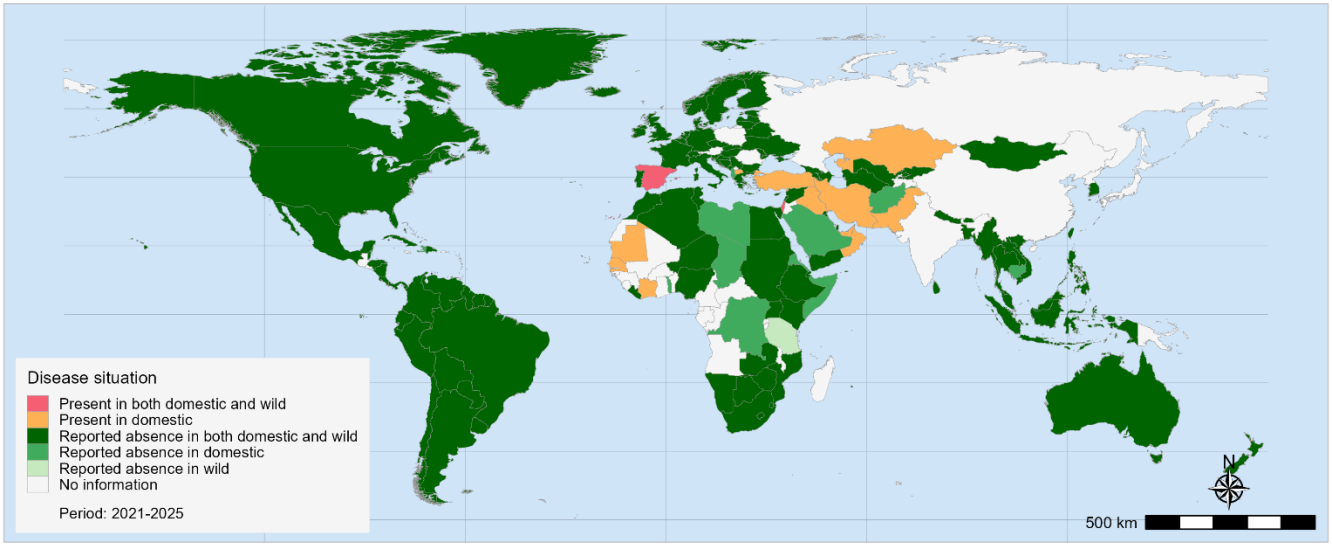

Figure 1. Geographical distribution of CCHFV detected events (2021-2025), as reported to WOAH.

Crimean Congo haemorrhagic fever is endemic in Africa, the Balkans, the Middle East, and Asia, particularly in countries south of the 50th parallel north, which marks the ecological limit of its main tick vector. CCHFV has been reported in the EU over the past 5 years (Figure 1). Up to date maps based on WAHIS are available in the online version of the Disease Profile (accessible via the button in the top right corner).

4. Animal hosts

4.1. Susceptible hosts

Based on epidemiological knowledge of host–pathogen–vector interactions and outbreak reports CCHFV has a wide range of vertebrate hosts with the most important being small wild terrestrial mammals and domestic ruminants, whereas equids are considered as dead-end hosts. However, other susceptible species have been identified by the EFSA's systematic literature review (SLR), with the summary provided in Table 1.

Table 1. Susceptible host species of Crimean-Congo haemorrhagic fever virus.

The systematic literature review reported in the CCHFV disease profile, identified the following susceptible species (updated until 31/12/2025, for references see online disease profile)
FIELD
Epidemiological studies carried out in the field **Pathogen was detected in the following animal species:** • Bovidae: *Bos taurus, Capra hircus, Ovis aries* • Equidae: No species specified • Hominidae: *Homo sapiens* **Antibodies were detected in the following animal species:** • Bovidae: *Bos taurus, Capra hircus, Ovis aries, Syncerus caffer* • Camelidae: *Camelus dromedarius* • Canidae: *Canis lupus familiaris* • Equidae: *Equus caballus* • Hominidae: *Homo sapiens* • Suidae: *Sus scrofa* **Outbreaks reported to WOAH included the following species:** • Bovidae: *Bos taurus, Capra hircus, Ovis aries*
EXPERIMENTS
Experimental studies demonstrated infection in: • Bovidae: *Ovis aries*

4.2. Clinical Signs

No consistent clinical disease is observed in infected animals. Experimental infections in livestock have demonstrated short-term viremia without observable signs of illness. Therefore, diagnosis relies on serological or molecular detection rather than clinical suspicion.

4.2.1. Incubation Period

The incubation period in animals is not well-defined due to the lack of clinical signs. The systematic literature review identified three experimental studies in sheep, with the reported incubation varying from 3 to 8 days (Gonzalex et al., 1998; Li et al., 2024; Wilson et al., 1991).

4.2.2. Morbidity and case fatality

In livestock and wildlife, morbidity and case fatality are negligible, as infections are generally asymptomatic. However, the presence of high tick infestation rates and animal movement can influence the dynamics of virus circulation (Spickler, 2019).

4.2.3. Zoonotic Potential

CCHFV infection is a zoonotic disease (WHO, 2025).

5. Transmission

CCHFV is transmitted through the bite of infected ticks. For more information on vector distribution, visit the Vector section in the online disease profile.

CCHFV circulates in a tick–vertebrate–tick enzootic transmission cycle. Transovarial and transstadial transmission in ticks allow for sustained circulation across life stages.

Animals become infected through tick bites, and the virus can be acquired by ticks during blood meals. While animals develop a transient viremia (7 – 15 days), they do not transmit the virus directly to other animals or humans. Animal movement and seasonal tick activity contribute to virus spread in endemic areas. Transmission to humans occurs mainly through tick bites or contact with blood or tissues of infected animals (Bente et al., 2013; Ergönül, 2006; Spickler, 2019; Whitehouse, 2004).

6. Diagnostic tests

Recommended tests (WOAH, 2025b) for agent detection: Reverse transcription PCR (RT-PCR), Real-time RT-PCR and virus isolation in cell culture. Virus detection is typically limited to a short viraemic phase. Virus isolation requires BSL-4 containment and is rarely performed outside specialized laboratories.

For immune response detection, the recommended tests are IgM-capture ELISA, IgG-sandwich ELISA, and competitive ELISA. The benefit of competitive ELISA is the capacity to investigate different animal species, because they are host species independent. Virus neutralisation assays, generally considered to be highly specific, are rarely used for CCHFV diagnosis as members of the Orthonairovirus genus generally induce a weaker neutralising antibody response than members of other genera in the family Nairoviridae. Another drawback is the necessity to perform this assay in high biosafety containment because it uses live virus.

Serological tests are commonly used for surveillance in vertebrates. IgG ELISAs are the most widely used and can detect previous exposure. Cross-reactivity with other nairoviruses is possible and should be considered in the interpretation of results.

Table 2 presents data on the sensitivity and specificity of diagnostic tests collected through EFSA's systematic literature review; reported values correspond to the median sensitivity and specificity when multiple study groups investigated the same test and are only included when explicitly stated in the publications.

Table 1. Median sensitivity and specificity of tests to detect AHSV/AHSV antibodies reported in literature included in the systematic literature review.

Target	Test	Species	Sensitivity	N animal groups	Specificity	N animal groups	References
Antibody	ELISA	Human	71.5%	4	93.2%	4	Cosgun et al., 2023
Antibody	ELISA	Sheep	-	-	94.5%	2	Belij-Rammerstorfer et al., 2022
Antibody	I-ELISA	Human	95%	2	99.1%	2	Shrivastava et al., 2022
Antibody	IFAT	Human	100%	1	100%	1	Cosgun et al., 2023
Antibody	LFIA	Human	39.7%	1	92.9%	1	Baniasadi et al., 2019
Antibody	ELISA	Human	71.5%	4	93.2%	4	Cosgun et al., 2023

7. Prevention and control

7.1. Vaccination

There are currently no licensed vaccines for CCHFV in animals.

7.2. Treatment

There is currently no specific treatment available for CCHFV infection in animals. Given the asymptomatic nature of infection, no therapeutic interventions are typically required.

8. References

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