





# **10th Tick and Tick-Borne** Pathogen Conference

## 29 August-2 September 2022 Murighiol, Danube Delta, Romania

Abstracts



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Platinum





Gold



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Silver



#### Bronze



FULLER









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### Symposium "Rethinking our approach to understanding tick-borne hemorrhagic fever viruses: why we need a transdisciplinary approach" (SY5.1-SY5.4)





# SY5.1 Crimean-Congo hemorrhagic fever enzootic cycle and factors favouring virus transmission: special focus on France, an apparently free-disease area

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Crimean-Congo hemorrhagic fever (CCHF) is a viral zoonotic disease resulting in hemorrhagic syndrome in humans. Its causative agent is naturally transmitted by ticks to non-human vertebrate hosts within an enzootic sylvatic cycle. Ticks are considered as biological vectors but also reservoirs for CCHF virus (CCHFv), as they are able to maintain the virus for several months or years and to transmit CCHFv from ticks to ticks. Although animals are not symptomatic, some of them can sufficiently replicate the virus to become a source of infection for both ticks, as well as humans through contact with contaminated body fluids. The recent emergence of CCHF in Spain indicates that the geographic range of the virus is expanding. In other European countries like France, the presence of its main tick vector and the detection of CCHFv antibodies in animals, without necessarily human cases, suggest that CCHFv has been continuing to spread silently. Based on a systematic review of the literature, we investigated the different CCHF epidemiological cycles already known in endemic countries and determined the one as hypothesized in the French local context. This work made it possible to point out tick species that seem to be the best candidate vectors of CCHFv in France, but also to highlight the importance of the abundance and composition of local host communities on the infection prevalence of vectors. We also identified parameters that may influence the virus transmission among tick vectors and non-human vertebrate hosts. Considering all these components, we understand why tick vectors may remain weakly infected in France and predict a low probability of disease emergence in humans in the current situation. The likelihood of factors that can modify this equilibrium is discussed.