Determinants of Crimean-Congo haemorrhagic fever virus exposure dynamics

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Abstract

Crimean-Congo haemorrhagic fever (CCHF) is an emerging tick-borne human disease in Spain. Understanding the spatiotemporal dynamics and exposure risk determinants of CCHF virus (CCHFV) in animal models is essential to predict the time and areas of highest transmission risk. With this goal, we designed a longitudinal survey in two wild ungulate species, the red deer (*Cervus elaphus*) and the Eurasian wild boar (*Sus scrofa*), in Doñana National Park, a protected Mediterranean biodiversity hotspot with high ungulate and CCHFV vector abundance, and which is also one of the main stopover sites for migratory birds between Africa and western Europe. Both ungulates are hosts to the main CCHFV vector in Spain, *Hyalomma lusitanicum*. We sampled wild ungulates annually from 2005 to 2020 and analysed the frequency of exposure to CCHFV by a double-antigen ELISA. The annual exposure risk was modelled as a function of environmental traits in an approach to understand exposure risk determinants that allow us to predict the most likely places and years for CCHFV transmission. The main findings show that *H. lusitanicum* abundance is a major driver of the fine-scale spatial CCHFV transmission risk, while inter-annual variations in the risk are conditioned by virus/vector hosts, by host community structure and by weather variations. The most relevant conclusion of the study is that the emergence of CCHF in Spain might have been associated with recent wild ungulate population changes promoting higher vector abundance. Decreasing wild ungulate population densities could reduce vector abundance and thus virus prevalence and the risk of CCHFV transmission to humans.

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