

PATHOGEN SURVEILLANCE IN WILD VERTEBRATES AS A BASIS FOR RISK MODELLING OF EMERGING VECTOR-BORNE DISEASES

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Most vector-borne pathogens that cause disease in humans are zoonotic, and most of these circulate in enzootic cycles in which wild hosts are key. The likelihood of human interaction with infected vectors is, in part, the result of the complex web of interactions between wild vertebrate hosts of pathogens and vectors that determine the density of infected vectors and the risk of transmission following a vector bite. Many of these vector-borne pathogens can replicate in a large number of vertebrates and may also have numerous competent vector species that transmit them. Thus, for these multi-host and multi-vector pathogens, the local vertebrate and arthropod vector community structure is key in determining when and where the risk of pathogen transmission may be greatest. Identifying key vertebrate and arthropod species in the ecology of these pathogens can help overcome the lack of knowledge of the web of interactions that modulate the transmission of these pathogens. Wildlife health surveillance programmes can be a useful tool for the construction of spatio-temporal risk models of vector-borne disease emergence. This presentation will focus on the progress made in Spain in estimating the spatiotemporal risks of West Nile fever virus and Crimean-Congo haemorrhagic disease virus transmission.