

Factors associated with Rift Valley fever in south-west Saudi Arabia

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Summary

The authors undertook a study of environmental and animal risk factors associated with Rift Valley fever (RVF) in south-west Saudi Arabia. An enzyme-linked immunosorbent assay was used to detect the presence of immunoglobulin M (IgM) and immunoglobulin G (IgG) antibodies against the RVF virus in serum samples from sentinel animals. In addition, a further 32 known IgM-positive serum samples were tested using the reverse transcription polymerase chain reaction (RT-PCR) to detect the RVF virus genome.

The results were analysed using the univariate odds ratio (OR). To control for confounding, Mantel-Haenszel adjusted odds ratio (M-H OR) was used. Positive associations were found between RVF and the following factors: a dense mosquito population (OR = 4.2), high rainfall (M-H OR = 2) and the presence of lakes and/or ponds (M-H OR = 2.2). The RVF virus genome was detected in four (12.5%) serum samples, indicating an early stage of RVF. The study found that the probability of detecting the virus genome was greater in animals with a high percentage of IgM antibodies against the virus (OR = 3) and in animals who had aborted (OR = 4.3). In addition, more sheep than goats tested positive for the presence of the genome (OR = 4).

The authors conclude that the environmental and animal risk factors identified in this study can be considered good predictors for RVF and that the animal factors, in particular, should be considered when developing an efficient and cost-effective control strategy.

Keywords Association – Confounding factor – Middle East – Reverse transcription polymerase chain reaction – Rift Valley fever – Rift Valley fever virus genome – Risk factor – Saudi Arabia – Sentinel animal.