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First serological evidence of Crimean-Congo haemorrhagic fever in febrile patients in Mozambique

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ABSTRACT

Objective: Despite its geographical spread, the epidemiology of Crimean-Congo haemorrhagic fever (CCHF) in Sub-Saharan Africa is incompletely understood and its occurrence in Mozambique is unknown. This study was conducted with the aim of investigating the occurrence of CCHF virus (CCHFV) among febrile patients attending an outpatient appointment clinic at three separate primary health care centres in Mozambique.

Methods: Serum samples were collected from a total of 300 febrile patients aged >5 years who were recruited between March 2015 and March 2016 at three health centres in Mozambique. Each patient was screened for IgG antibodies against CCHFV using an ELISA.

Results: Of the 300 patients enrolled, eight had samples that were positive for anti-CCHFV IgG antibodies, yielding a prevalence rate of 2.7%.

Conclusions: This study shows for the first time that humans are exposed to CCHFV in Mozambique. It highlights the need for further work to investigate the broader extent of circulating CCHFV in the country and its clinical implications.

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Introduction

Crimean-Congo haemorrhagic fever (CCHF) is a life-threatening and emerging zoonotic disease caused by the Crimean-Congo hemorrhagic fever virus (CCHFV), which is classified in the *Orthonairovirus* genus of the *Nairoviridae* family within the order *Bunyavirales* (Al-Abri et al., 2017). CCHFV is the most widespread tick-borne virus worldwide (Shayan et al., 2015), occurring in Africa, Eastern and Southern Europe, the Middle East, and Asia (Al-Abri et al., 2017; Flusin et al., 2010). Its emergence into new areas such as India, Morocco, and Spain over the last two decades is concerning (Al-Abri et al., 2017; Messina et al., 2015; Papa et al., 2010).

CCHF is highly contagious and has a fatality rate ranging between 10% and 50% (Flusin et al., 2010). The virus is harboured by wild and domestic mammals, and transmission to humans can occur either through the bite of an infected tick vector, predominantly species of the genus *Hyalomma* (Papa et al., 2015; Shayan et al., 2015), or through direct contact with blood or other bodily fluids from infected individuals or livestock (Lani et al., 2015). CCHFV infection of animals is difficult to identify, making transmission to humans during slaughter a serious risk.

Early infection with CCHFV in humans results in non-specific symptoms, which are often difficult to interpret. Additionally, the virus is not frequently part of a differential diagnosis, especially when evidence of circulating CCHFV is scant, thus its diagnosis is often missed. In circumstances where undiagnosed patients develop haemorrhagic fever or when exploratory surgery is performed, large amounts of highly infectious virus can be released, which may result in nosocomial transmission (Bukbuk et al., 2016)

Although efforts have been made to advance knowledge of CCHFV, most studies are from Eurasia. In Sub-Saharan Africa, CCHFV is often ignored and its epidemiology and clinical profile are still poorly understood (Al-Abri et al., 2017; Messina et al., 2015). In Mozambique, no study has yet been conducted to investigate the

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occurrence of the virus, and the risk it poses to the country is unknown (Messina et al., 2015; Whitehouse, 2004). However, cases of CCHF and significant outbreaks of CCHFV are often reported in humans and animals in South Africa (Shepherd et al., 1987; Swanepoel et al., 1987), a country that shares extensive borders with Mozambique and with which it conducts significant commercial trade. Thus, the hypothesis was that CCHFV represents an important, yet neglected cause of febrile illness in the country,

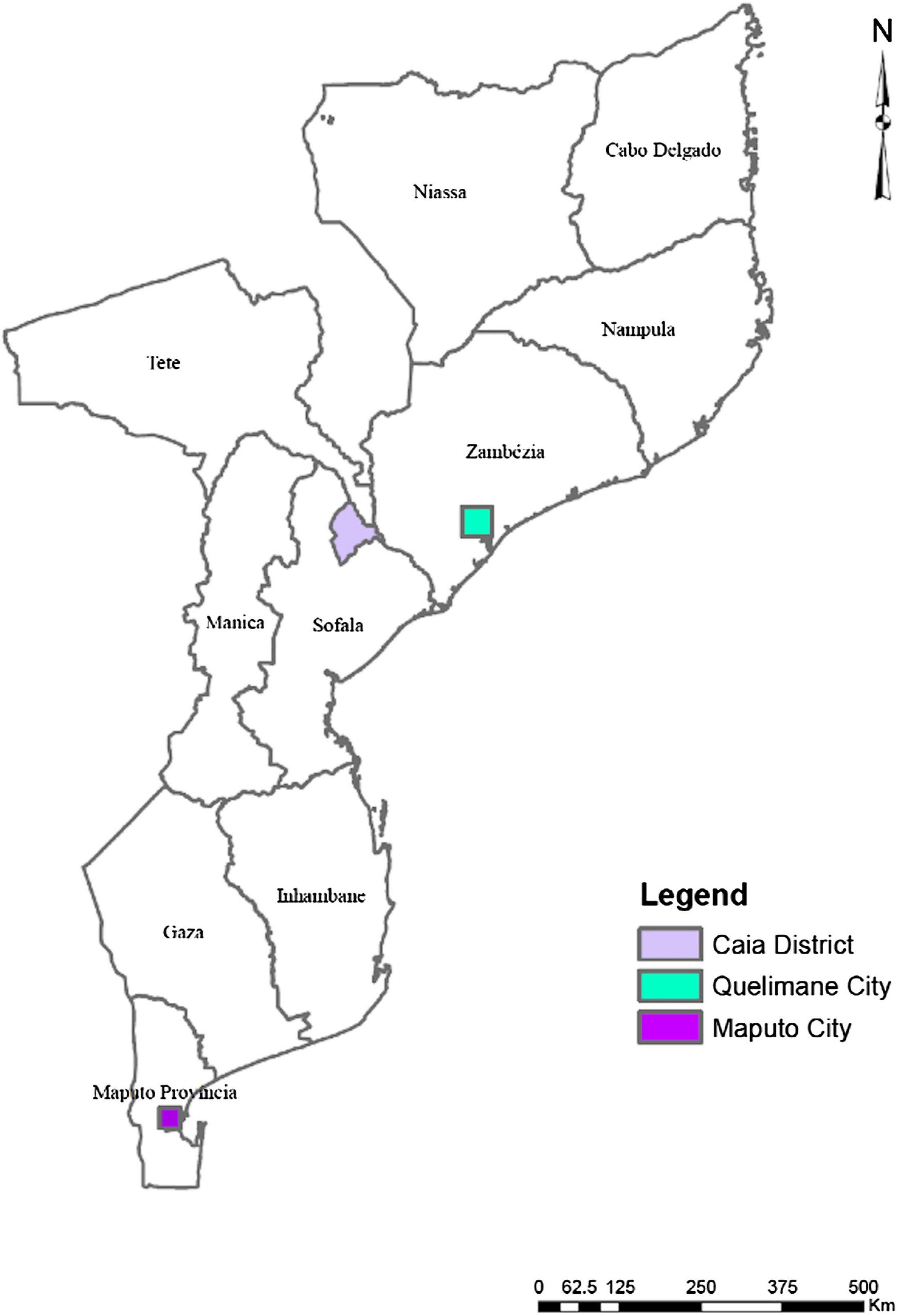

Figure 1. Geographical location of the study sites. Coloured districts depict the localization of the study sites where febrile patients were recruited.

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