



First serological evidence of hantavirus among febrile patients in Mozambique



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ABSTRACT

Objective: The occurrence of hantavirus in Sub-Saharan Africa is poorly studied and its clinical implications are unknown. This study aimed to determine the occurrence of hantavirus infection among febrile patients attending an outpatient clinic at a primary health care center located in a suburban area of the city of Maputo in Mozambique.

Methods: Paired acute and convalescent samples from a total of 200 febrile patients aged >5 years who were recruited between February 2012 and October 2014 were screened for IgM and IgG antibodies against hantavirus using an ELISA. Acute samples were also screened for malaria and to determine hematological and clinical chemistry parameters.

Results: Of the 200 patients enrolled, four had IgM antibodies in their acute sample and IgG antibodies in their convalescent sample, yielding a prevalence rate of 2%.

Contact with rodents was higher among IgM-positive participants than IgM-negative participants (50.0% (2/4) vs. 15.3% (30/196)). IgM-positive patients presented significantly higher levels of creatinine and alanine aminotransferase and lower platelet counts than IgM-negative patients.

Conclusions: The findings of this study demonstrate human exposure to hantavirus in Mozambique for the first time; however, further studies should be conducted to investigate its clinical implications.

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Introduction

Hantaviruses are emerging yet neglected viruses of the *Bunyaviridae* family harbored by small mammals. They are known to cause life-threatening diseases in humans in Eurasia and the Americas (Avsic-Zupanc et al., 2015; Jonsson et al., 2010; Klempa et al., 2006). Hantaviruses represent a genetically complex group of viruses, and 22 strains are so far known to be associated with disease in humans (Bi et al., 2008; Jonsson et al., 2010; Manigold and Vial, 2014).

The public health importance of this virus has increased tremendously in recent decades. A rapidly growing number of

countries are reporting cases of hantavirus in humans or infection in their reservoirs, and new species of hantavirus have recently been discovered in several parts of the world (Bi et al., 2008; Manigold and Vial, 2014). Transmission occurs mostly by direct contact with the feces, saliva, or urine of infected mammals, or by inhalation of the virus in their excreta (Enria and Levis, 2004; Jonsson et al., 2010).

For many years, rodents were considered the primary reservoirs of hantaviruses. However, recent reports of novel hantavirus in bats and shrews in Africa have expanded the host range for this virus. Thus, the epidemiology and ecology of hantavirus in Africa might be even more complex (Kang et al., 2014; Klempa et al., 2007; Weiss et al., 2012; Witkowski et al., 2014).

Although hantavirus causes chronic and unapparent infections in its animal reservoirs, the virus causes severe disease in humans, which can present as two different clinical syndromes: hemorrhagic fever with renal syndrome (HFRS), which occurs in Europe

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and Asia (Eurasia), and hantavirus pulmonary syndrome (HPS), which occurs in the Americas (Jonsson et al., 2010; Nichol et al., 1993).

It is estimated that more than 150 000 cases of HFRS have occurred worldwide (Jonsson et al., 2010). The fatality rate is high and can vary between 12% in HFRS and 60% in HPS (Jonsson et al., 2010; Kruger et al., 2015).

Most studies on hantavirus infections in humans have been conducted in Europe (Bergstedt Oscarsson et al., 2016; Geurts-vanKessel et al., 2016; Mailles et al., 2005a; Mailles et al., 2005b; Rose et al., 2003), Asia (Chen et al., 1986), and the Americas (Bellomo et al., 2015; Dusi Rde et al., 2016; Padula et al., 2000a). In contrast, hantavirus is greatly neglected in Sub-Saharan Africa, where vulnerability to severe outbreaks might be the highest worldwide due to poor health systems; furthermore, the clinical implications of the virus in humans remain unknown, as only a few cases of HFRS have been reported so far in Sub-Saharan Africa (Coulaud et al., 1987; Klempa et al., 2010). In addition, genetic material for hantavirus was not identified in Sub-Saharan Africa until 2006, when a novel hantavirus, Sangassou virus (SANGV) – the first indigenous African hantavirus – was isolated for the first

time in rodents in the forest of Guinea, West Africa (Klempa et al., 2006).

Hantavirus has been ignored in Sub-Saharan Africa because surveillance systems are weak, laboratory capacity for its diagnosis is not available, clinicians are not aware of HFRS or HPS, and symptoms of hantavirus might overlap with those of other common febrile illnesses (Klempa, 2009; Klempa et al., 2010; Witkowski et al., 2014).

This study aimed to determine the occurrence of hantavirus infection among febrile patients living in the suburban area of the city of Maputo, Mozambique.

Methods

Study setting and population

A cross-sectional study was conducted among febrile patients aged >5 years attending an outpatient clinic at the Polana Caniço Health Center. The health center serves a large population from A and B neighborhoods of Polana Caniço, located in a suburban area of the city of Maputo in Mozambique. Patients were recruited

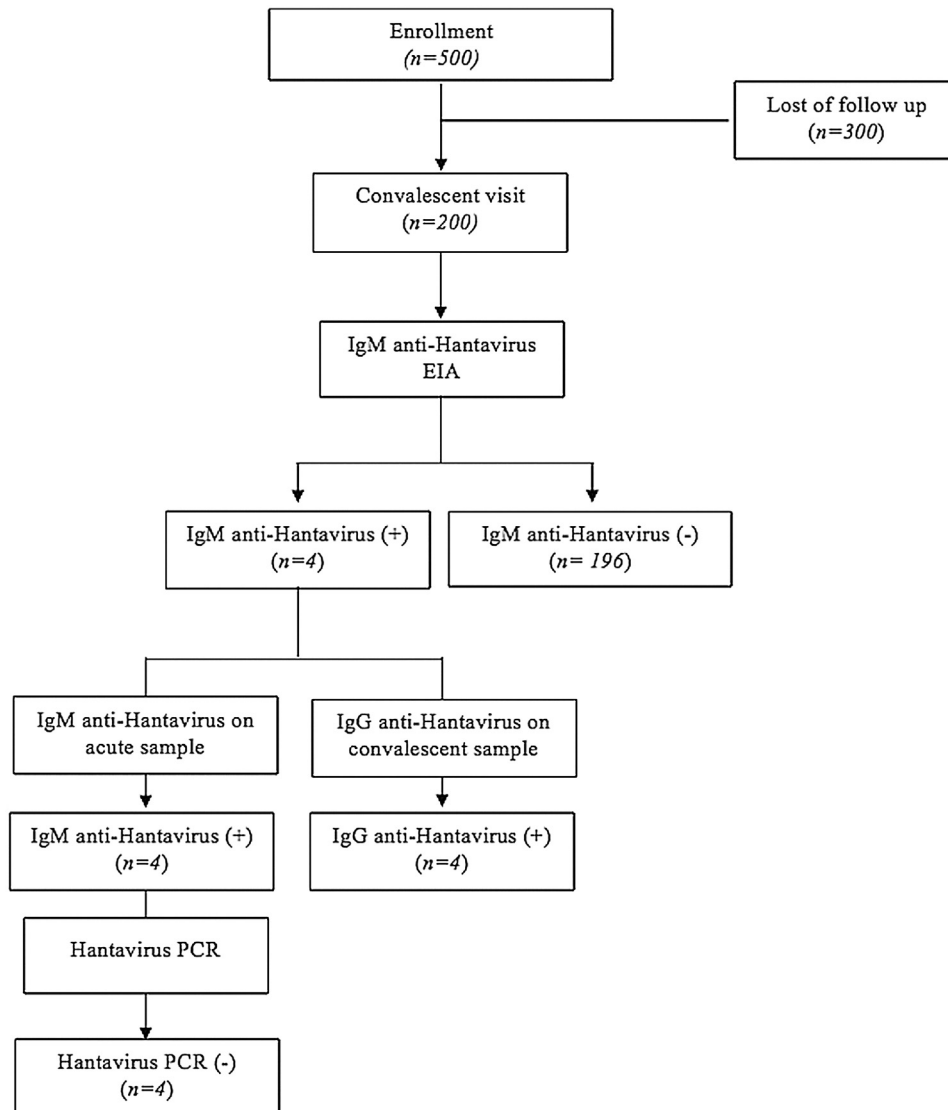


Figure 1. Participant recruitment and sample testing.

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