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Tick-borne pathogens of potential zoonotic importance in the southern African region

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The aim of this communication is to provide preliminary information on the tick-borne pathogens of potential zoonotic importance present in southern Africa, mainly focusing on their geographical distribution and host range, and to identify research gaps. The following tick-borne zoonoses have been reported to occur in southern Africa based mainly on case reports: Crimean–Congo haemorrhagic fever caused by Crimean–Congo haemorrhagic fever virus; ehrlichiosis caused by *Ehrlichia ruminantium*, *Ehrlichia canis* and *Anaplasma phagocytophilum*; babesiosis caused by *Babesia microti*; relapsing fever caused by *Borrelia duttonii* and rickettsioses caused by *Rickettsia africae*, *Rickettsia aeschlimannii* and *Rickettsia conorii*. The epidemiological factors influencing their occurrence are briefly reviewed.

Vector-borne diseases have long been a problem for both animals and humans, causing some of the worst plagues of mankind, such as the Black Death in Europe in the 14th century and yellow fever epidemics in the Americas (Gubler 2009). The 20th century witnessed a steady decline in vector-borne diseases through the implementation of extensive vector control programmes, but the 21st century has witnessed the re-emergence of some of these diseases. This re-emergence has been presumed to be because of new global trends in animal husbandry, urbanisation, modern transportation and globalisation (Gubler 2009). Amongst the re-emerging vector-borne diseases are tick-borne diseases (Estrada-Peña, Ayllon & De la Fuente 2012).

Ticks transmit a wide range of pathogens that include protozoa, bacteria and viruses (Kim *et al.* 2006). In their review on the prevalence, distribution and burden of neglected tropical diseases, Hotez and Kamath (2009) noted that there was lack of information on tick-borne zoonoses in sub-Saharan Africa, thus making it difficult to assess their impact. A study by Horak *et al.* (2002) identified 20 species of ixodid ticks that fed on humans in South Africa, including species known to transmit *Rickettsia conorii* and the virus that causes Crimean–Congo haemorrhagic fever (CCHF). This communication focuses on the information relating to southern Africa.

The following tick-borne zoonoses have been reported in southern Africa: CCHF caused by CCHF virus, tick-borne relapsing fever (TBRF) caused by *Borrelia duttonii*, ehrlichiosis caused by *Ehrlichia ruminantium*, *Ehrlichia canis* and *Anaplasma phagocytophilum*, babesiosis caused by *Babesia microti* and rickettsioses caused by *Rickettsia africae*, *Rickettsia aeschlimannii* and *R. conorii*.

Crimean–Congo haemorrhagic fever is a tick-borne viral disease reported in more than 30 countries in Africa, Asia, south-eastern Europe and the Middle East. It affects mainly people involved in agriculture, the livestock sector and health workers (Ergonul 2012). The virus belongs to the genus *Nairovirus* in the *Bunyaviridae* family. It normally circulates in an enzootic tick-vertebrate-tick cycle, infecting a number of vertebrate hosts, including livestock (Whitehouse 2004). Although a number of tick genera have been reported to be infected by CCHF virus (Hoogstraal 1979), CCHF foci are consistently associated with presence and/or abundance of *Hyalomma* spp. ticks, suggesting a major transmission role for this genus (Burt & Swanepoel 2005; Whitehouse 2004). In the tick vector, the virus is transmitted both trans-stadially and trans-ovarially, confirming that the tick acts as both vector and reservoir of infection (Burt & Swanepoel 2005; Whitehouse 2004). CCHF is the most widespread tick-borne zoonosis (Ergonul 2012). This is thought to be a result of a number of possible factors, including (1) several tick species being able to transmit the virus, (2) several suspected reservoirs of infection and (3) alterations of landscape and vegetation as a result of climatic and social changes (Estrada-Peña *et al.* 2012).

Humans are normally infected through tick bites or after direct contact with blood or tissue from viraemic humans or animals, and clinical disease is characterised by a haemorrhagic fever (Ergonul 2012). In southern Africa, human CCHF has been recorded in the Democratic Republic of Congo (DRC), South Africa and Tanzania, with virological and/or serological evidence of infection in Namibia, Zimbabwe and Madagascar (Burt *et al.* 1996; Mathiot *et al.* 1988; Swanepoel & Burt 2004; Swanepoel *et al.* 1987). However, the tick vector is distributed throughout the southern

African region (Burt & Swanepoel 2005). In Turkey, where CCHF is considered a re-emerging disease, it was observed that the occurrence of the disease was strongly correlated with habitat fragmentation (Estrada-Peña *et al.* 2010).

Human tick-borne ehrlichiosis is caused by any of the following obligate intracellular Gram-negative bacterial species: *Ehrlichia chaffeensis*, *Ehrlichia ewingii*, *E. canis*, *E. ruminantium* and *Anaplasma phagocytophilum* (Ismail, Bloch & McBride 2010). *Anaplasma phagocytophilum* and *E. ewingii* are known to colonise host granulocytes, whilst *E. chaffeensis*, *E. ruminantium* and *E. canis* colonise mononuclear phagocytes (Rikihiya 1991). The first human ehrlichiosis case was reported in 1954 in Japan (Misao & Kobayashi 1954) and there have been reports of possible human infection in Africa, based on serology and/or presence of bacterial DNA in serum (Brouqui *et al.* 1994; Louw, Allsopp & Meyer 2005). Currently there are no reports of either confirmed or suspected cases of human infection by *A. phagocytophilum* in southern Africa. However, Inokuma *et al.* (2005) have reported an *A. phagocytophilum*-related bacterium in a South African dog.

Human babesiosis is caused by either *Babesia microti* or *Babesia divergens* (Hildebrandt *et al.* 2007), with clinical course of disease being reported in asplenic individuals, the elderly and those who are immunocompromised (Benach & Habicht 1981; Hildebrandt *et al.* 2007). The disease is common in temperate regions. The only report of human babesiosis in southern Africa was by Bush *et al.* (1990), in two individuals in South Africa.

Tick-borne relapsing fever is a bacterial infection caused by *Borrelia* spp.; *B. duttonii* is the causative agent in eastern Africa and *Borrelia crocidurae* in western Africa (Cutler 2010; Dupont *et al.* 1997). *Borrelia duttonii* is transmitted by *Ornithodoros moubata* (Cutler 2010). An enzootic cycle in which a vertebrate reservoir species and the tick vectors serve as a ready source of infection for humans has not been demonstrated for *B. duttonii* (Cutler 2010). TBRF is endemic in the DRC and Tanzania, but has not been reported further south. In Tanzania it is listed amongst the top 10 killer diseases in children under 5 years of age (Cutler 2010), associated with perinatal mortality of up to 436/1000 (McConnell 2003). In the DRC, infection was associated with adverse outcomes, including mortalities, especially in pregnant women (Dupont *et al.* 1997).

Rickettsioses are febrile illnesses caused by intracellular bacteria of the genus *Rickettsia*. These bacteria are broadly divided into the spotted fever group and the typhus group; the spotted fever group is of importance in sub-Saharan Africa. Three species of this group that are of medical importance have been reported in southern Africa, namely *R. africae*, *R. aeschlimannii* and *R. conorii*. The distribution of these rickettsiae in ticks and humans in sub-Saharan Africa was reported in the recent review by Cazorla *et al.* (2008).

Rickettsia africae causes African tick bite fever (ATBF) and is mainly transmitted by *Amblyomma* species, with *Amblyomma hebraeum* being the principal vector in southern Africa (Althaus *et al.* 2010; Kelly & Mason 1991). A recent report of

detection of *R. africae* in *Rhipicephalus decoloratus* ticks did not conclusively prove a vector role for this tick species (Portillo *et al.* 2007). In South Africa, *R. aeschlimannii* is also thought to be transmitted by *Rhipicephalus appendiculatus* (Pretorius & Birtles 2002). *Rickettsia conorii* is mainly transmitted by *Rhipicephalus sanguineus* (Parola, Paddock & Raoult 2005), but has also been isolated from *Haemophysalis* (Kelly & Mason 1990). ATBF is the most prevalent and widespread of the rickettsioses in southern Africa. Infection rates in the principal tick vectors have been reported to be as high as 100% (Parola *et al.* 2005). The aggressive nature of the questing *Amblyomma* spp. ticks increases the risk of infection in people who frequent pastures and game areas (Althaus *et al.* 2010). There have been several reports of human infections in people who had visited game reserves (Althaus *et al.* 2010; Consigny *et al.* 2005; McQuiston *et al.* 2004).

Whilst the threat of rickettsioses is real, the precise geographical distribution of infection is unknown, and recent decades have yielded a great deal of new information on rickettsioses as a result of the application of molecular techniques (Parola *et al.* 2005). Whilst there are case reports of tick-borne zoonoses in humans, especially tourists, few surveys have been carried out to determine the level of infection in populations at risk in southern Africa. There is thus a need for structured surveys targeting the populations at risk, and to determine vector and reservoir capacity of various tick species to the tick-borne pathogens.

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Competing interests

The authors declare that they have no financial or personal relationship(s) which may have inappropriately influenced them in writing this article.

Authors' contributions

All authors contributed equally to the literature search and writing of this manuscript.

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