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

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 feed 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 virremic 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 (Rikihisa 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. africæ, R. aethiopiana and R. conori. 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 africæ 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. africæ in Rhipicephalus decoloratus ticks did not conclusively prove a vector role for this tick species (Portillo et al. 2007). In South Africa, R. aethiopiana is also thought to be transmitted by Rhipicephalus appendiculatus (Pretorius & Birtles 2002). Rickettsia conori is mainly transmitted by Rhipicephalus sanguineus (Parola, Paddock & Raoult 2005), but has also been isolated from Haemaphysalis (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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Authors’ contributions

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

References


