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Prevalence and risk factors of bovine trypanosomosis in Kilwa district, Lindi region of southern Tanzania

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ABSTRACT

African animal trypanosomosis (AAT) and human African trypanosomosis (HAT) are complex chronic, debilitating, emaciating and often fatal diseases of animals and humans, respectively. This cross-sectional study was conducted to determine the prevalence and risk factors associated with bovine trypanosomosis in tsetse-infested Kilwa district, Lindi region, southern Tanzania. Blood samples were collected from 420 cattle randomly selected from 86 herds from ten villages. A maximum of ten herds per village and at most six animals from each herd were selected for sampling. At the same time, a questionnaire was administered. Individual animal samples were analysed using microscopy and pooled sample at herd level were analysed by loop mediated isothermal amplification (LAMP). A herd was considered positive if at least one animal in the herd was positive for AAT. A prevalence of 9.3% (95% CI: 2.9–14.9) was recorded for AAT by microscopy, mainly caused by *Trypanosoma congolense* (5.8%, 95% CI = 0.9–10.7), *Trypanosoma brucei* species (5.8%, 95%, CI = 0.9–10.7) and *Trypanosoma vivax* (3.5%, 95% CI = 0–7.4). Loop mediated isothermal amplification (LAMP) recorded a heard prevalence of 41.9% (95% CI: 30.0–51.4%), mainly caused by *T. congolense* (30.2%, 95% CI: 20.5–39.9), *T. brucei* species (25.6%, 95% CI: 16.4–34.8) and *T. vivax* (20.9%, 95% CI: 12.3–29.7). Most of the cattle herds had mixed infections of these parasites. According to LAMP, Miteja and Matandu villages had the highest AAT herd prevalence of 57% (95% CI: 20.3–93.7) while Mavuji had the lowest prevalence of 14% (95% CI: 0–39.7). Data from the present study suggest that district of origin, grazing in game reserve, water source and form of watering point are risk factors associated with AAT in Kilwa district, southern Tanzania. Continuous surveillance and monitoring of AAT using more sensitive are recommended.

1. Introduction

African animal trypanosomosis (AAT) or *nagana* and human African trypanosomosis (HAT) or sleeping sickness are complex chronic, debilitating, emaciating and often fatal diseases of animals and humans, respectively. The outcome of the infection differs substantially among humans, livestock species and within a livestock species and breeds (Connor and Van den Bossche, 2004). The disease is endemic in sub-Saharan Africa between latitudes 14°N and 29°S. HAT, transmitted through the bite of an infected tsetse fly, is caused by trypanosomes belonging to the subgenus *Trypanozoon* namely *Trypanosoma brucei rhodesiense* and *Trypanosoma brucei gambiense*. While *T. b. rhodesiense* causes the disease in eastern and southern parts of Africa, *T. b. gambiense* causes HAT in west and central Africa (Brun et al., 2010). HAT is invariably fatal when untreated. Because of the difficult and cost of surveillance and treatment, HAT has been considered to have profound impact on the socio-economic development of Africa (Mersha et al., 2013). According to Kibona et al. (2002), the disease was first recorded in Tanzania in 1922 in Maswa district, south of Lake Victoria. It then spread throughout mainland Tanzania such that it is currently endemic in 9 regions namely Arusha, Manyara, Mara, Lindi, Ruvuma, Kagera, Tabora, Mbeya and Rukwa.

In livestock, AAT is caused by *T. congolense*, *T. vivax*, *T. brucei brucei*, *T. evansi*, *T. simiae*, *T. suis* and *T. equiperdum*. AAT is one of the most intractable diseases affecting most species of livestock in Africa (Zewdu et al., 2013). Infection results in high mortality rate in acute cases and in a severe loss of production in chronic cases. The main economic losses attributed to AAT are related to cattle mortality and morbidity, diagnosis and treatment costs, the reduction in meat and milk production and the reduction of livestock production areas (Kristjanson et al., 1999). Because of the complexity of the disease-vector inter-relationship, little

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progress has been made in controlling the disease since its discovery by Bruce late in the nineteenth century (Murray and Gray, 1984).

Within the Lindi region, Kilwa people are traditionally non-livestock keepers. In 1996, Kilwa district had 1436 cattle, 4879 goats and 5000 sheep (DED Kilwa, 2009). Since 2007, following the evacuation of livestock from Usangu and Ihefu areas in Mbarali district, Mbeya region, which were declared conservation areas and the key water sources for hydroelectric power generation, pastoralist and agro-pastoralist have been migrating to Kilwa from the southern highland and western circuits of the country, bringing with them large herds of cattle (Ngairo, 2011). Following these movements, Kilwa district received 12,554 cattle, 18,110 goats and 2173 sheep from Ihefu, Mbeya region, and other parts of Tanzania. This has brought the number of livestock kept in Kilwa to increase up to 14,756 cattle, 28,742 goats and 5143 sheep (DED Kilwa, 2009). Many pastoralists opted to settle in the districts which had a low human population density to ensures ample grazing land for their animals (Malele et al., 2011). However, animal populations in Kilwa district increased rapidly as a result of this eviction from the wetland sources, settlement of these animals came without much preparation to avert the problem caused by tsetse and AAT in the pasture areas. Despite the availability of plenty of grazing areas for animals, the pastoralists were confronted with a serious challenge of tsetse and AAT, which has become a major stumbling block to livestock sector development in Kilwa district. Before this study was conducted, there was little documented literature on AAT prevalence in Kilwa district (Coonor and Halliwell, 1987). Therefore, this study aimed at evaluated the performance of the trypanosome species-specific LAMP, using parasite DNA obtained from Kilwa cattle in southern Tanzania, against the reference method of microscopy.

2. Material and methods

2.1. Ethical considerations

Approval and clearance for the study was obtained from the Regional and District veterinary authorities (reference No 10/20/I/Vol.III/181). Informed consent was sought from cattle owners to participate in the study and collect blood from their animals.

2.2. Study site and design

A cross-sectional survey of AAT involving a total of 420 cattle from 86 cattle herds was conducted in 10 villages within the tsetse-infested Kilwa district, Lindi region of southern Tanzania (Fig. 1). Kilwa district lies on Latitude 8°20′ S to 9°56′ S and Longitude 38°36′ E to 39°50′ E. To the north, it borders Rufiji district, Coast Region, Lindi and Ruangwa districts in the South, Liwale district in the West and to the East, the Indian Ocean (MacLennan, 1980). Kilwa district is administratively divided into 6 divisions, 20 wards, and 96 villages, 14 of which are occupied by agro-pastoralists and their livestock (DED Kilwa, 2009). The total area of Kilwa district is 13,347.50 square Kilometers (1,334,750 ha) of which 12,125.9 km^2 is surface land and 1221.52 km^2 is the ocean.

2.3. Blood sample collection and questionnaire administration

Blood samples were collected from cattle whose owners consented to participate in the study. All the animals presented for sampling were subjected to clinical examination. About 2 ml of blood was drawn from the jugular vein of each animal into EDTA vacutainer tubes and Giemsa-stained thin blood smears from each animal examined as described (Haji et al., 2014). In addition, about 200 μl of each blood sample was placed on a labeled FTA® Elute card (Whatman FTA® Elute Cards, Whatman, UK) for DNA extraction according to the manufacturer's suggested protocol. At the same time of blood collection, a structured questionnaire was administered to the head of each household whose animals were sampled. The information that was collected included demographic data, livestock species, numbers and their management.

2.4. DNA extraction and LAMP analysis

DNA was extracted from each of the 420 cattle blood samples as previously described (Namangala et al., 2013). In order to circumvent the limited LAMP reagents, 1.0 μl of the obtained DNA from each of the 10 samples, based on chronological sample labelling, was then pooled to make one tube, giving a total of 42 pooled samples stored at minus 20 °C until use. The resultant pooled DNA was then used for the LAMP assay as previously described (Namangala et al., 2013), using

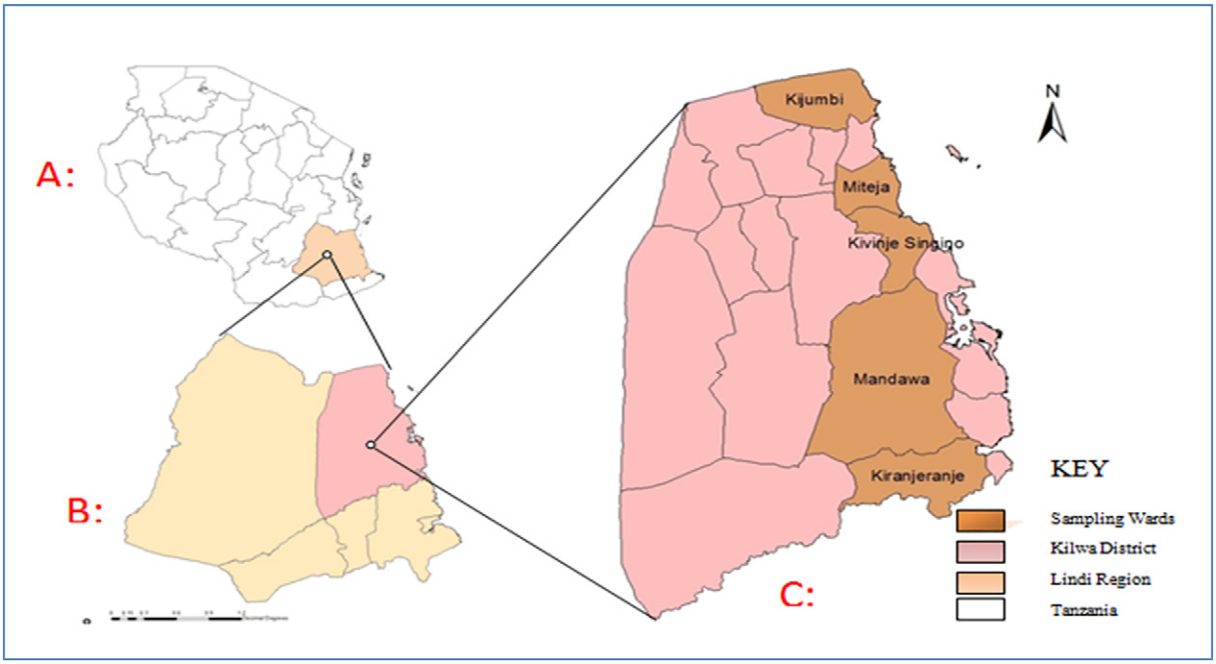

Fig. 1. Map of the study area showing (A) Tanzania (B) Lindi region and (C) Kilwa district showing sampling wards.