

Prevalence of Trypanosomosis of small ruminants in Guangua district of Awi Zone, northwestern Ethiopia

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Small ruminant Trypanosomosis

Sheep and goats play an important role in improving the economy of small holder farmers in Ethiopia. Tsetse-transmitted animal trypanosomosis is one of the most significant and costly diseases in the country, hindering the efforts being made for food self-sufficiency. In Ethiopia, about 200,000 km² of the land is infested with tsetse flies [1] and the main pathogenic trypanosomes in animals are *Trypanosoma congolense*, *T. vivax*, and *T. brucei*. Although there have been several reports on livestock trypanosomosis, there is little data on the prevalence of trypanosomosis in sheep and goats in northwestern Ethiopia.

To provide this data, we collected blood into ethylenediaminetetraacetic acid (EDTA) from 600 adult sheep and 1,810 goats in five peasant associations (PAs) in the Guangua district of northwestern Ethiopia.

The packed cell volume (PCV) was measured and the buffy coat and uppermost layer of red blood cells were examined with phase contrast at x 400 for the presence of motile trypanosomes [2]. Thick and thin blood smears were stained with Giemsa at 1:10 dilution for 30 minutes and examined under oil immersion for trypanosomes [3].

Standard tsetse fly traps (66 NGU and 20 Monoconical) [4] were deployed in the study PAs during the late rainy season and early dry season. All the traps were baited uniformly with octenol (1-oct-3-ene) and acetone and left for 72 hours before collection.

Overall, trypanosomes were found in 5.6% (102/1810) of the samples, with more sheep being infected (8.7%) than goats (4.1%) ($P > 0.01$). The

highest prevalence in a PA was recorded in sheep (11.7%) but prevalences in each species did not vary significantly between PAs.

The trypanosomes identified in the blood smears were *T. vivax*, *T. congolense*, and *T. brucei*. All these organisms were found in sheep in each PA, but only *T. vivax* and *T. congolense* were found in goats in each PA. *Trypanosoma brucei* had the lowest overall prevalence, infecting only one goat (0.1%) and eight sheep (1.3%) in the five PAs. *Trypanosoma vivax* was the most common species found in sheep (2.7%; 1.8-4.2%) and goats (1.6%; 1.3-1.7%). *Trypanosoma congolense* was more common in goats (1.5%; 1.2-2.2%) than sheep (2.3; 1.3-3.3%). Mixed infections with *T. vivax* and *T. congolense* were common in both sheep and goats.

Animals with trypanosomes had significantly ($P < 0.001$) lower PCVs than uninfected animals (sheep 19.1% vs. 26%; goats 20.3% vs. 25.4%).

Significantly more trypanosomes were trapped in the late rainy season (9.5%; 94/986) than in the early dry season (1.0%; 8/824) ($P < 0.001$). The trypanosome vectors identified in the traps were *Glossina morsitans submorsitans*, *Glossina tachinoides* and other biting flies of the *Tabanidae* (*Tabanus* and *Chrysops*) and *Stomoxysinae* (*Stomoxys calcitrans*) families.

Our findings on trypanosomes in northwestern Ethiopia are similar to those previously reported from the southwest of the country [5]. We found more sheep were infected than goats, which is consistent with findings in other studies [6,7,8,9]. The species we identified, *T. congolense*, *T. vivax*, and *T. brucei*, are the most notable causes of trypanosomosis of

livestock in Sub-Saharan Africa. Further studies are indicated to determine whether the infected small ruminants we found are acting as reservoirs of infections for cattle in the area. Because cattle have lower trypanotolerance, infections in these animals result in greater economic losses.

We found that the prevalence of trypanosomosis was significantly higher in the wet season as compared to the dry season. This is likely because the tsetse fly vectors we found are more prevalent in the wet season [10,11], leading to increased transmission of disease.

Although the microscopic technique used in our study has limited sensitivity, it provided important additional information on the prevalence of trypanosomosis in small ruminants in Ethiopia and showed the importance of the disease in the Guangua district. Further data can be provided with more sensitive techniques such as ELISA and PCR.

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