

BACKGROUND

The African Trypanosomes, protozoan parasites, are transmitted throughout sub-Saharan Africa by the tsetse fly (*Glossina* spp.). Human African Trypanosomiasis (HAT) is fatal unless treated and takes two geographically disparate forms: gHAT (chronic; *Trypanosoma brucei gambiense*; Western and Central Africa) and rHAT (acute; *Trypanosoma brucei rhodesiense*; Eastern and Southern Africa). Uganda is currently the only country with active foci of both rHAT and gHAT.

Animal African Trypanosomiasis (AAT) is a severe disease associated with food insecurity and economic hardship. AAT is caused by a range of trypanosome species. In cattle, *Trypanosoma vivax* and *Trypanosoma congolense* cause severe disease, whilst *T.b.brucei* and *T.b.rhodesiense* infections are asymptomatic or cause only mild disease. Importantly, ***T.b.rhodesiense* is a zoonotic parasite, and human cases are associated with spill-over from livestock and wild animal populations.**

AIMS AND OBJECTIVES

This project aimed to determine the prevalence of three trypanosome species in cattle in Northern Uganda: *Trypanosoma brucei* sensu lato, *Trypanosoma vivax* and *Trypanosoma congolense*.

METHODS

Blood samples from 989 cattle across three districts in Northern Uganda were collected in a 2018 cross-sectional survey. Blood drawn from the auricular vein was stored on Whatman FTA Cards from which DNA was then extracted.

Two variations of the Polymerase Chain Reaction were used to screen samples for trypanosome DNA: ITS (for *T.brucei* sl., *T.vivax* and *T.congolense*) and TBR (for *T.brucei* sl.). PCR products were examined using gel electrophoresis. Statistical analysis was conducted using GraphPad PRISM (Fisher's Exact Test) software and VasserStats (95% Confidence Intervals).

RESULTS

The prevalence of trypanosome infections across cattle was 15.17% (13.07% - 17.54%; 150/989). Figure 1 shows the composition of infection types: most were caused by a single species (135/150; 90.00%), and a small number were caused by two (11/150; 7.33%) or three species of trypanosome (4/150; 2.67%).

As shown in Figure 2, ***T.brucei* sl. was the most prevalent species** (6.88%; 5.46% - 8.63%; 68/989), followed by *T.congolense* (5.46%; 4.21% - 7.06%; 54/989) and *T.vivax* (4.75%; 3.59% - 6.26%; 47/989). The difference in prevalence between species was not considered statistically significant when the Fisher's Exact Test was applied ($p > 0.05$).

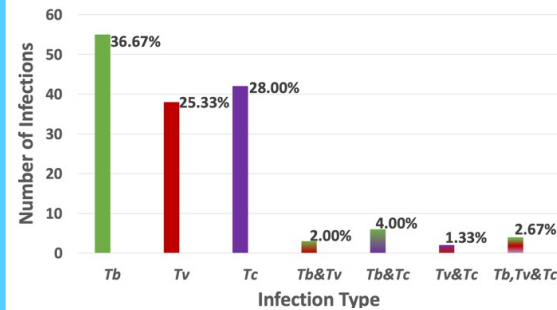


Figure 1: Composition of Infection Types in Cattle (2018).
 Tb = *T.brucei* sl.; Tv = *T.vivax*; Tc = *T.congolense*. % = Percentage of total infections.

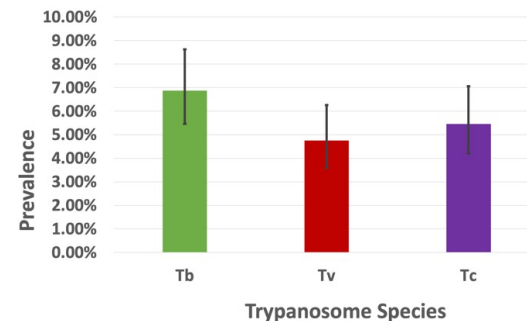


Figure 2: Trypanosome Species Prevalence in Cattle (2018).
 Tb = *T.brucei* sl.; Tv = *T.vivax*; Tc = *T.congolense*. Error bars = 95% confidence intervals.

DISCUSSION

T.brucei sl. was the most prevalent species of trypanosome present, as reported in an adjacent area, using a similar methodology¹. *T.vivax* and *T.congolense*, however, have been more prevalent than *T.brucei* sl. in other studies from Uganda using only the ITS PCR (or a variation)^{2,3}. The TBR PCR has a higher number of target copies than the ITS PCR target^{4,5}; this greater sensitivity might explain differences in reported trypanosome prevalence, depending on methodology used.

The screening and surveillance of cattle populations can serve an important role in disease control and epidemiological understanding. The geographical distributions of gHAT and rHAT in Uganda were estimated to be separated by only 150km in 2005⁶. Given that gHAT and rHAT require different treatments and are diagnosed by microscopy, the morphologically indistinguishable nature of the parasites would be a major obstacle in diagnosis and treatment if distributions were to overlap in Uganda.

Migration of cattle has already been associated with the northward spread of *T.b.rhodesiense* in Uganda^{7,8}. Unpublished analysis of these samples will **investigate the presence of *T.b.rhodesiense* in this cattle population**, confirming if the human-infective parasites are present, and if so, in what proportion.

REFERENCES

- Hamill, L., et al., 2017. Evaluating the impact of targeting livestock for the prevention of human and animal trypanosomiasis, at village level, in districts newly affected with *T. b. rhodesiense* in Uganda. *Infectious diseases of poverty*, **6**(1), pp.1-12.
- Mandela, W.R., et al., 2020. Prevalence and control implications of bovine trypanosomes in endemic areas of northern Uganda. *Tropical Animal Health and Production*, **52**(6), pp.3259-3264.
- Muhanguzi, D., et al., 2014. The burden and spatial distribution of bovine African trypanosomes in small holder crop-livestock production systems in Tororo District, south-eastern Uganda. *Parasites & vectors*, **7**(1), pp.1-10.
- Ahmed, H.A., et al., 2013. A comparative evaluation of PCR-based methods for species-specific determination of African animal trypanosomes in Ugandan cattle. *Parasites & vectors*, **6**(1), pp.1-7.
- Desquesnes, M. and Davila, A.M.R., 2002. Applications of PCR-based tools for detection and identification of animal trypanosomes: a review and perspectives. *Veterinary parasitology*, **109**(3-4), pp.213-231.
- Picozzi, K., et al. 2005. Sleeping sickness in Uganda: a thin line between two fatal diseases. *Bmj*, **331**(7527), pp.1238-1241.
- Fèvre, E.M., et al., 2001. The origins of a new *Trypanosoma brucei rhodesiense* sleeping sickness outbreak in eastern Uganda. *The Lancet*, **358**(9282), pp.625-628.
- Selby, R., et al. 2013. Cattle movements and trypanosomes: restocking efforts and the spread of *Trypanosoma brucei rhodesiense* sleeping sickness in post-conflict Uganda. *Parasites & vectors*, **6**(1), pp.1-12.