ABSTRACT

A study was conducted to characterize infectious trypanosomes in domestic animals within Lamu County, Kenya, using parasitological and molecular techniques. Fifteen trypanosome stabilates and 92 whole blood samples collected from parasitologically negative animals were randomly retrieved from the cryobank freezer at the Biotechnology Research Institute, (KALRO-BioRI), Kenya, and characterized. Human serum resistance associated (SRA) gene present in *T. b. rhodesiense* was used to differentiate *T. brucei* positive stabilates. Results showed that 10/15(67%) trypanosome stabilates and 13/92(14%) whole blood samples from cattle, donkeys and goats were positive using PCR. Positive *T. congolense* 5/23(22%) yielded a product size of 700bp using ITS1 primers. The Brucei group 7/23(30%) and *T. vivax* 11/23(48%) amplicons were 480bp and 250bp, respectively. Identified trypanosome stabilates were *T. b. brucei* (7) T. vivax (2) and *T. congolense* Savannah (1). Whole blood PCR profiles revealed 13 isolates namely *T. vivax* (9) and *T. congolense* Savannah *(4)*. *Trypanosoma b. brucei*, *T. vivax* and *T. congolense* Savannah were the etiological agents for AAT in donkeys. In contrast, *T. vivax* and *T. congolense* Savannah caused the disease in cattle, and *T. b. brucei* in goat within Lamu County. The study underscores the significance of molecular and parasitological methods during epidemiological monitoring and surveillance of disease.

Keywords: Trypanosomes, livestock, PCR, Lamu County, Kenya