



Prevalence of African Animal Trypanosomiasis among Wild Carnivores: A Systematic Review on the Global Distribution of Tsetse Fly Disease

Ghulam Khadija Bashir¹, Iqra Bashir², Umer Ali^{3*}

1. Department of Zoology, Wildlife and Fisheries University of Agriculture Faisalaba.

2. Institute of microbiology, Government college university Faisalabad.

3. Department of Biological Sciences, Tennessee State University, Nashville, TN 37209, USA.

***Correspondence to: Umer Ali**, Department of Biological Sciences, Tennessee State University, Nashville, TN 37209, USA.

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ABSTRACT

This study looks at the prevalence of African animal trypanosomiasis (AAT) in populations of wild carnivores. African wildlife populations particularly those of wild carnivores are seriously threatened by African animal trypanosomiasis (AAT). It also evaluates existing control and preventative methods, identifies contributing factors, and assesses the disease's effects. In order to preserve biodiversity and the integrity of ecosystems, it highlights knowledge gaps, discusses research objectives, and formulates recommendations on how to effectively control and prevent AAT. It is essential for the health of animals and conservation efforts to comprehend the frequency of AAT in these carnivore species. Regional and temporal patterns of AAT incidence, evaluate diagnostic and treatment techniques, examine reservoir host dynamics, and assess the impact of AAT on carnivore populations through a thorough analysis of the body of research and field data gathering are analyzed in this review. This review demonstrates the wide prevalence of AAT in wild predators and its possible effects on ecosystem health and population dynamics. This research advances our knowledge of the prevalence of AAT in wild carnivores, which helps to preserve biodiversity and the integrity of ecosystems by managing these species in their native environment.

Keywords: *Prevalence, AAT, carnivores, tsetse fly disease, Health*

Introduction

A group of wasting disease known as Animal Trypanosomiasis or Trypanosomoses are brought on by single-celled parasitic protozoans belonging to the genus *Trypanosoma* (order Kinetoplastida) (Giordani *et al.*, 2016). Trypanosomiasis among African animals Tsetse fly disease (also referred to as tsetse disease) or African animal nagana is a transmissible disease that can affect both humans and animals (Steverding, 2008). It is one of the most common hemoparasitic illness affecting wildlife (Nantulya, 1990).

Trypanosoma vivax, *Trypanosoma congolense*, *Trypanosoma brucei*, *Trypanosoma simiae* and *Trypanosoma suis* are the many species of single-celled organisms responsible for a variety of parasitic disorders known as African Animal Trypanosomiasis or "Nagana." The bloodsucking tsetse fly Diptera (genus *Glossina*) is the cycle vector of AAT. Certain trypanosome species, including *T. vivax*, may also be actively spread via other biting flies, like *Tabanus* and *Stomoxys* species. AAT influence camels,

hogs, horses and mules, ruminants and meat eaters, but animal trypanosomiasis poses the greatest threat to rural farmers who raise livestock in sub-Saharan Africa (Diall *et al.*, 2017).

T. congolense, *T. vivax*, and *T. brucei* spp. cause AAT. Different kinds of the disease are caused by two subspecies of *T. brucei*. Whereas *T. b. rhodesiense* typically produces a more acute infection and *T. b. gambiense* causes chronic infections. The parasites first appear in the blood, lymph, and peripheral organs in the first stage. In the second stage, they go to the central nervous system and cause serious neurological diseases. If therapy is not received, the disease is fatal (Büscher *et al.*, 2017).

Trypanosoma brucei is a single-celled parasite that infects tsetse flies, is the cause of human African trypanosomiasis (HAT), commonly referred to as sleeping sickness (Büscher *et al.*, 2017). There are three subspecies of it: *T. b. brucei* in animals, *T. b. gambiense* and *T. b. rhodesiense* in human beings (Jamonneau *et al.*, 2019). *Trypanosoma brucei gambiense* is parasite that lives in a variety of environments including forests, mangroves, and savannah of West and Central Africa. It is also found in a variety of animal hosts most notably pigs. *Trypanosoma brucei rhodesiense* acts like a normal zoonotic parasite, primarily infecting cattle and wild mammals before occasionally spreading to people and only found in savannah regions of Eastern and Southern Africa (Steinmann *et al.*, 2015).

Trypanosoma congolense is found in the bloodstreams of mammals (Gibson *et al.*, 2017). It is the tiny parasite that is found in the bloodstream of ill goat, sheep and oxen (Gibson, 2003). *Trypanosoma cruzi* is found in Latin America and spread by the faeces of triatomine insects. It has a wide variety of natural hosts including armadillos, the raccoon, rabbits, native pigs, mice, and marsupial species. It also has a domesticated reservoir that includes dogs, cats, pigs, sheep, goats, cattle, and horses (Desquesnes *et al.*, 2022). *Trypanosoma vivax* is known to be transmitted non-tsetse in some areas of Africa, including Ethiopia, Chad, and Sudan (Desquesnes *et al.*, 2022). It lives and completes its brief life cycle in the proboscis of the insect. Because of its distinct behavior the parasite can be mechanically spread by other flies that feed on blood. (Giordani *et al.*, 2016)

Trypanosoma simiae belongs to Nannomonas subgenus and causes fatal infections in pigs and result in death within one or two days after symptoms. Other domestic animals are also susceptible to this disease (Kasozi *et al.*, 2022). *Trypanosoma suis* is a little-known parasite in Tanzania that was initially identified by Ochmann in 1905 as causing severe trypanosomiasis in pigs' farms in Tanzania (Hutchinson and Gibson, 2015).

Some of these species of *Trypanosoma* are zoonotic. Zoonotic diseases are infectious illnesses that can spread

from humans to vertebrate mammals through pathogenic agents such as bacteria, fungi, viruses, and prions. Zoonotic disease outbreaks are estimated to result in two billion cases of illness and more than two million fatalities annually, with far-reaching implications for public health. (Green *et al.*, 2020) There are two types of the disease. The parasite *Trypanosoma brucei gambiense* is the cause of the one prevalent in West and Central Africa, whereas *Trypanosoma brucei rhodesiense* is the cause of the other one prevalent in East and Southern Africa (Dickie *et al.*, 2020).

If there is a brief gap between the two meals to allow parasites to multiply in the insect mouthpart, tsetse flies can mechanically disseminate trypanosomes throughout mammals by beginning a blood meal on one infected host and finishing it on another (Bilal^{a,b} *et al.*, 2024). Many domestic ungulates may harbour *T. b. brucei* however the condition is more severe in horses, dogs, and camels. In regions where multiple trypanosome species are present, cattle infections with mixed infections are common, and contemporary genetic techniques facilitate easier speciation. Numerous wild animal species in Africa are known to harbour at least one trypanosome species, making them potential reservoirs for highly contagious trypanosomes that can infect humans and livestock (Kasozi *et al.*, 2022).

African trypanosomiasis is predicted to result in annual losses in agricultural gross domestic product of USD 4.7 billion, that has had a significant negative impact on agriculture and economic development in affected nations. About 37% of Zambia's land area is home to tsetse flies, and the reported cases of African animal trypanosomiasis (AAT) in cattle varies by region with estimates ranging from 1% to 90% (Afzal, M & Ali, U at el.,2024) The current Zambian government strategy of protecting natural resources and establishing state-protected National Parks and Game Management Areas has resulted in an increase in the population of tsetse flies, which spread the disease, and an expansion of wildlife populations that act as long-term reservoirs for African trypanosomiasis (Mulenga *et al.*, 2020; Bilal *et al.*, 2021).

Protozoans such as *Trypanosoma brucei gambiense* and *Trypanosoma brucei rhodesiense* can produce parasitic infections that are extremely dangerous to billions of people globally. The need for new drugs especially those made from plants, is growing as there are no effective immunisations and pharmaceutical resistance is increasing. Millions of people in Mexico, America and the United States of American Chagas disease and African trypanosomiasis, both of which are caused by *T.cruzi* and lack a vaccine or clinical research (Panda and Luyten, 2018).

Several species, including *T. brucei*, *T. congolense*, *T. equiperdum*, *T. evansi*, *T. simiae*, *T. suis*, and *T. vivax*, belongs to the genus *Trypanosoma* and cause diseases termed as trypanosomoses in a variety of animal hosts,

including humans. Trypanosome outbreaks are common in Asia, Latin America, and Africa. Cattle, dromedary camels, goats, sheep, pigs, dogs, horses, donkeys, both domesticated and wild buffalo, warthogs, hippopotamus, reedbuck, waterbuck, antelope, giraffes, rhinoceroses, rodents, pangolins, primates, reptiles, and various wild ungulates and carnivores have all been reported to be carriers of *Trypanosoma vivax* (Fetene *et al.*, 2021; Sajjad *et al.*, 2024).

The animal disease surra is caused by *T. brucei evansi* and has an impact on a variety of mammals from various geographic locations. Cattle, camels, horses, and buffalos are the most affected species, although other animals, including wildlife, are also susceptible. Widespread throughout Africa, Asia, and Latin America, surra is spread non-cyclically by tabanids, other insects, vampire bats, and predators (Magri *et al.*, 2021).

Wild animals are susceptible to trypanosomiasis especially lions because of the disease's intricate link to the host's immune system. *T. b. gambiense* and *T. b. rhodesiense*, two infecting trypanosome subspecies can evade immune responses, while people living in HAT-endemic regions build defences against trypanosome species. The illness affects both health and survival as it advances through two stages. It can have a typical duration of up to three years and be either acute or chronic (Venturelli *et al.*, 2022).

T. b. brucei, the trypanosome subspecies that infects animals, is not very important economically for the cattle sector. However, because of its spread and effects on the economy, *T. equiperdum* is a significant threat. *T. equiperdum* is sexually transmitted and can result in large economic losses in several different parts of the world, unlike other fly borne trypanosomes. Although the immune system of mammals may regulate parasitemia to some extent, both innate and adaptive responses cannot offer total immunity against infection. Apolipoprotein L1 and other distinct innate immune pathways are essential for defence against trypanosome diseases like HAT. To counteract APOL1's effects, *T. b. gambiense* and *T. b. rhodesiense* have developed defence mechanisms. Furthermore, many Africans have mutations in APOL1 that provide resistance to *T. b. rhodesiense* infections, but they also raise the risk of chronic kidney disease (Pays *et al.*, 2023; Noor *et al.*, 2024).

Diseases can spread to humans and wild animals through wildlife farms, especially those that raise non-domesticated species for commercial gain. African lions are raised and bred on commercial farms in South Africa for a variety of purposes, such as hunting trophy, active tourism, and the export of bones for traditional medical items. There are chances for zoonotic sharing because of the lions and humans' high degree of direct connection. Infectious diseases like as trichinosis, filariasis, sarcoptic mange, pentastomiasis,

echinococcosis, taeniasis, hepatozoonosis, anthrax, and babesiosis have been known to move from wild populations to captivity. The prevalence of lion-human contact and the risk of zoonotic disease transmission are increased by South Africa's extensive and intense breeding facilities (Green *et al.*, 2020).

The family Trypanosomatidae is made up of a variety of protozoan parasites, some of which can infect more than one species of host. This family contains important human pathogens such as several species of *Trypanosoma* and *Leishmania*, which cause infections spread by insect vectors. Exploring endemic host-parasite interactions in Chile is intriguing due to its distinct biogeographic features and high endemism. But little is known about how trypanosomatids infect local species of vertebrates in Chile, particularly considering the arrival of foreign animals that bring with them their own parasite fauna. *Trypanosoma cruzi*, the most researched trypanosomatid in Chile, infects both native and foreign mammals using triatomine vectors; however, thorough assessments of *T. cruzi* infection in mammals as well as other trypanosomatids that may be present are absent. (Correa *et al.*, 2020)

Companion animals are essential for the upkeep and dissemination of parasites, both zoonotic and veterinary. Their ranges have grown due to urbanisation and environmental changes, which has aided in the spread of parasites. However, it can be difficult to detect parasites because of their elusiveness and protected status. There are restrictions on the use of diagnostic procedures such as serological testing, macroscopic inspection, and molecular tools, and environmental conditions might affect the quality of samples (Rojas *et al.*, 2024).

In the southern United States, the illness *T. cruzi*, which affects wild mammals, is harming conservation and peri domestic animals because of interaction with infected vectors. Studies on wildlife populations may not fully account for its effects but reports of Chagas disease in a rising number of exotic and zoo animals have implications for conservation and relocation initiatives. Making a diagnosis is difficult, and the list of illnesses could not fully reflect real cases (Busselman and Hamer, 2022).

Because of their restricted area and declining number, lions are the focus of African conservation efforts. For conservation attempts to be successful, it is essential to comprehend the natural surroundings of lions. By looking into lion habitat preferences and discovering common features in various circumstances, researchers may assess habitat suitability and direct conservation activities. In doing so, ecological variety is preserved (Sargent *et al.*, 2022).

The ability of wild animals to suppress the growth of fatal African trypanosomes, which serves as the reservoir host for these parasites, is known as trypanotolerance. Trypanosomiasis is usually moderate in

nature, but in captive populations breakouts can be lethal. Infested areas are primarily transmitted by tsetse flies, although there are alternative methods of transmission as well, including transmission through mechanical means via different biting flies and oral transmission by contaminated animals. The degree of infection varies according to environmental factors and pressure levels; coexistence is observed in independent wild animals but is interrupted by conditions such as famine, drought, and imprisonment. Trypanosomiasis in captive and wild mammals is still little understood, despite its significance for conservation initiatives. This calls for more research and documenting of the clinico-pathology and processes of the parasitic infection (Mbaya *et al.*, 2009).

Carnivores can contract trypanosomiasis by eating contaminated meat. The exposure of wildlife to trypanosomiasis is influenced by its diet, particularly wild Bovidae. Browsers are more vulnerable, but semi-browsers are more sensitive to attacks (Ali, U & Vungarala, S, *et al.*, 2024) Because of the lush forest, animals with greater infection rates include kudus, bushbucks, elands, and waterbucks. Wildlife hosts throughout the day are more susceptible, and incidences of infection are impacted by the movement of large animals (Kasozi *et al.*, 2021).

African animal trypanosomiasis (AAT) is a disease that affects wild carnivore populations worldwide. The study aims to determine how common AAT is, how it affects wildlife health and conservation, what factors influence the disease's spread among wild carnivore species, how effective present management, diagnosis, and detection methods are, and what steps can be taken for preventing and controlling it to lessen its negative effects on wildlife.

The goals are to review the literature that has already been written about the prevalence and distribution of AAT in different wild carnivore species, to gather field data and samples to use diagnostic tools to assess AAT prevalence to analyze spatial and temporal patterns of AAT occurrence in relation to environmental factors, to investigate the effects on mortality, reproduction, and population dynamics, to investigate the role of wild carnivores as reservoir hosts, to determine knowledge gap.

Material and Methods

Study Design

Relevant documents were found by searching the ScienceDirect and PubMed (NCBI) databases. PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) criteria were followed in the conduct

of this investigation to guarantee that every relevant piece of information was included in the review.

Search Strategy

A literature search was conducted using AJOL, PubMed Cross Ref, Research gate, and Google Scholar. 385 published publications on AAT and tsetse infections were subjected to meta-analysis. Eligibility was determined by study type, location, prevalence of tsetse species, overall distribution, lion /tsetse diagnosis method, and year of sampling. We visually searched through the reference lists of pertinent papers to find any studies that were missing.

Data inclusion

There were 132 studies in all. Every document released from 1990 to 2024 in English language was considered. Required parameters were searched out separately using some keywords like Prevalence, Trypanosom*, Control, tsetse, Glossina, Wild Carnivore, lion, AAT, and Primates. The published and unpublished literature, reports, and organization websites from pertinent institutions were then added to these data.

These sources included Google Scholar, the websites of the organizations, the references of the publications that were identified, and the key informants. This review was centred on AAT Prevalence and control. Nevertheless, in regions where cattle serve as a reservoir for HAT, a few Tsetse and Trypanosomiasis control actions that target both AAT and HAT were also included. Tanzania, south and west Africa, Brazil, Luangwa and Zambia, sub-Saharan Africa countries data was taken.

Data Quality

Peer-reviewed publications were given a particular significance when assessing the quality of the papers. The literature, surveillance reports from Google Scholar and other data sources follow an organized strategy to data collection, analysis, and interpretation, offering valuable insights into the global epidemiology, historical background, and regional dynamics of African trypanosomiasis in lion populations. Those articles whose relevance was not clear from the abstract alone were read full and concern piece of information collected from it. Articles that satisfied all above qualifying requirements were eventually included (Afzal *et al.*, 2021).

For African Animal Trypanosomiasis (also known as "Nagana") and American Animal Trypanosomiasis (also known as "Chagas") we gathered previously published peer-reviewed articles and extracted pertinent data pertaining to AAT control and program-specific data, including outcome metrics. I investigated

geographical variations of African trypanosomiasis in lion populations, as well as historical perspectives and worldwide epidemiology.

Data on global epidemiology were gathered from a variety of sources such as databases, government publications, and peer-reviewed publications. Studies with an emphasis on prevalence rates, geographic distribution, and related risk factors were chosen for inclusion in the review process due to their significance to lion populations. The global distribution of diseases was analyzed and visualized using descriptive statistics and spatial analytic techniques. Through the classification of areas according to geographical and ecological parameters, regional variations were investigated.

Results and Discussion

Trypanosoma vivax

There are 39 African and Latin American nations where *T. vivax*, an African parasite, has been detected, together with 47 mammalian host species. *T. vivax* prevalence in tropical Africa varies from 5 to 15%, frequently accounting for as much as 50% of total trypanosome prevalence. *T. vivax* was identified in malnourished cattle for the first time in South America in French Guiana. Reports of the disease were then received from Venezuela, Guadeloupe, Martinique, Colombia, Suriname, Panama, Guyana, and Brazil. In some parts of South America, including the Venezuelan Llanos, the Brazilian Amazonia's lowlands, and the Pantanal wetlands of Bolivia and Brazil, *T. vivax* is endemic. *T. vivax* has been detected in Colombia. Cattle in Uganda have been shown to have a mixed *T. vivax* and *T. congolense* infection. Only cases of *T. vivax* in cattle and water buffalo have been reported in Central America. Cattle in Uganda have been shown to have a mixed *T. vivax* and *T. congolense* infection (Kapo *et al.*, 2023).



Fig.1. *Trypanosoma vivax* Global distribution across the World (Kapo *et al.*, 2023).

Trypanosoma brucei

Cattle are linked in new areas and local outbreaks of sleeping sickness, which is primarily spread by domestic and wild animals. Via wild animal reservoirs, sporadic transmission to hunters and game park visitors happens. Although instances of foreign travel are uncommon, they do occasionally happen in the US. In 2020, fewer than 600 instances of sleeping sickness in Africa were documented, primarily due to *Trypanosoma brucei gambiense*. The identification of *T. b. gambiense* and *T. b. rhodesiense* in livestock species emphasises how crucial it is to include them in the fight against sleeping sickness (Kapo *et al.*, 2023).



Fig.2. *Trypanosoma brucei* geographical distribution across the world

Trypanosoma congolense

Primarily present in African cattle, *T. congolense* is a parasite that causes illnesses in animals. It is a major contributor to serious and even deadly diseases in household animals, especially dogs. Less virulent strains induce persistent infections, while more virulent strains cause acute illnesses with significant fatality rates. Africa is home to several *T. congolense* species, including savannah, woodland, Tsavo, and Kilifi. There is evidence of travel-related infections in dogs, which implies that African dogs might be trypanotolerant. The *Glossina morsitans* tsetse fly is thought to be common in African cattle, which could aid in the transmission of *T. congolense* infection.



Fig.3. *Trypanosoma congolense* global distribution across the world (Kapo *et al.*, 2023).

Trypanosoma evansi

T. evansi is the causative agent of Surra, a noncyclic parasitic disease that afflicts animals and results in a considerable death and morbidity rate. It is indigenous to Africa, the Middle and Far East, Asia, Mexico, Central and South America, and Europe. It is spread by tabanids, flies, vampire bats, or predators. The area north of Senegal to Kenya, which includes nations like Mauritania, Morocco, Algeria, Tunisia, Libya, Egypt, Sudan, Eritrea, and Ethiopia, is home to *T. evansi*. With occasional reports of epizootics from Argentina to Panama, it has spread throughout South America. *T. evansi* has recently been brought to France and Spain, where it is frequently found to cause mixed infections in household animals (Kapo *et al.*, 2023)



Fig.4. *Trypanosoma evansi* global distribution across all over the World (Kapo *et al.*, 2023).

Trypanosoma cruzi

Trypanosoma cruzi is the cause of Chagas disease, a serious international health concern that affects about 8 million individuals in 21 Latin American nations. The majority of cases of the disease are found in impoverished rural areas of Central and South America, where vectors are the main means of transmission. Although enzootic cycles of *T. cruzi* transmission have been found in a few southern states in the US, the proportion of locally acquired infections is still quite low. There are anywhere from 45,000 to 67,000 instances of Chagas disease in Spain alone, and there may be over 100,000 cases across the continent. Pets, including house cats and dogs, can serve as markers for infections in local populations of triatomines or in humans. Through recurrent contacts with infected vectors, wild animal species, including ocelots, raccoons, opossums, and rodents, are important players in the enzootic transmission of the parasite. *T. cruzi* may be traced to a larger family of trypanosomes that were first found in bats (Kapo *et al.*, 2023).



Fig.5. Chagas disease's pattern of distribution in humans and animals, with light blue signifying non-endemic countries and dark blue suggesting endemic countries.

The frequency of AAT in Nigeria for 60 years. The analysis of variance's Tukey multiple pairwise comparison test reveals no discernible variation in the prevalence reports between decades ($F(5, 68) = 1.616$, $P = 0.1676$, $r^2 = 10.6\%$) (Fig. 6)

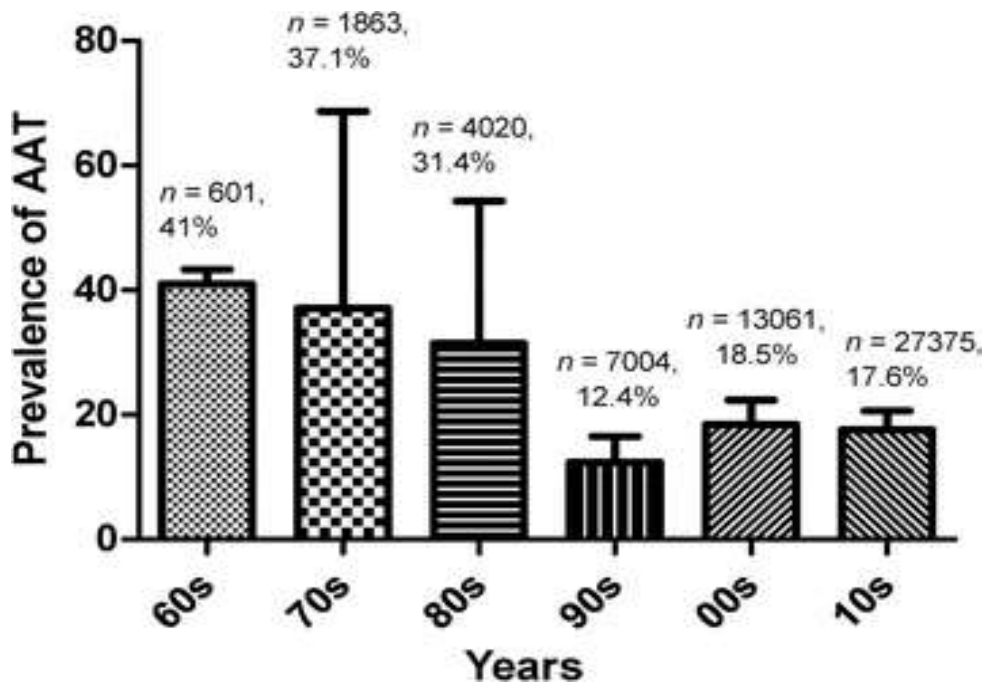


Fig 6. Prevalence of African Animal Trypanosomiasis in South Africa

T. vivax is the most phylogenetically different species of African trypanosome. Different isolates exhibit varying degrees of pathogenicity in cattle; in certain instances, they cause acute hemorrhagic infections, while in others, they cause chronic, subclinical infections. Though *T. vivax*, also known as *T. congolense*, has traditionally been thought to stay within the host's vascular system, certain strains may, particularly in late infections, also reach extravascular locations (such as lymph nodes, the eyes, and the cerebrospinal fluid), where they may cause direct harm to tissue and where they are more difficult to treat with medication Cortez *et al.*, (2006)

Trypanosomiasis prevalence and taxonomic categories of wildlife hosts are correlated. It is highly prevalent in wildlife hosts belonging to the bovine group in *T. vivax* and *T. congolense*. Their grazing habits expose them to biting flies such as tsetse, which is thought to be the source of infection (Fig. 7). Both wildlife hosts from the suidae family and those belonging to the Pantherinae group have an extremely high rate of mixed trypanosome infections (Kasozi *et al.*, 2021).

Taxonomic group	Wildlife host (scientific name)	Trypanosome species	References
Bovidae	Waterbuck (<i>Kobus ellipsiprymnus</i>)	<i>T. vivax</i> , <i>T. congolense</i> , <i>T. brucei</i> , <i>T. evansi</i>	(12)
Girafidae	Giraffe (<i>Giraffa camelopardalis</i>)	<i>T. vivax</i> , <i>T. evansi</i> , <i>T. brucei</i>	(12)
Bovidae	African buffalo (<i>Syncerus caffer</i>)	<i>T. b. rhodesiense</i> , <i>T. congolense</i> , <i>T. brucei</i>	(12)
	Bushbuck (<i>Tragelaphus scriptus</i>)	<i>T. b. rhodesiense</i> , <i>T. congolense</i> , <i>T. vivax</i> , <i>T. evansi</i>	(12)
	Greater kudu (<i>Tragelaphus strepsiceros</i>)	<i>T. congolense</i> , <i>T. vivax</i>	(12)
	Red lechwe (<i>Kobus leche</i>)	<i>T. theileri</i>	(18)
	Hartebeest (<i>Alcelaphus buselaphus</i>)	<i>T. godfreyi</i> , <i>T. brucei</i> , <i>T. godfreyi</i>	(18)
	Sable antelope (<i>Hippotragus niger</i>)	<i>T. brucei</i> , <i>T. theileri</i>	(18)
	African buffalo (<i>Syncerus caffer</i>)	<i>T. theileri</i> , <i>T. godfreyi</i>	(18)
	Eland (<i>Taurotragus derbianus</i>)	<i>T. vivax</i> , <i>T. congolense</i> , <i>T. brucei</i>	(12)
	Impala (<i>Impala impala</i>)	<i>T. godfreyi</i> , <i>T. brucei</i>	(18)
Elephantidae	Elephant (<i>Loxodonta africana</i>)	<i>T. vivax</i> , <i>T. congolense</i> , <i>T. evansi</i> , <i>T. elephantis</i>	(19)
Hippopotamidae	Hippopotamus (<i>Hippopotamus amphibius</i>)	<i>T. vivax</i> , <i>T. brucei</i> , <i>T. evansi</i> , <i>T. congolense</i>	(20)
Suidae	Warthog (<i>Phacochoerus africanus</i>)	<i>T. b. rhodesiense</i> , <i>T. vivax</i> , <i>T. congolense</i> , <i>T. evansi</i>	(20)
	Warthog (<i>Phacochoerus africanus</i>)	<i>T. godfreyi</i> , <i>T. brucei</i> , <i>T. simiae</i>	(18)
	Feral pig (<i>Sus scrofa</i>)	<i>T. evansi</i> and <i>T. cruzi</i>	(21)
Pantherinae	Lion (<i>Panthera leo</i>)	<i>T. brucei</i> , <i>T. evansi</i> , <i>T. congolense</i> , <i>T. congolense</i>	(12, 18)
	Leopard (<i>Panthera pardus</i>)	<i>T. brucei</i> , <i>T. congolense</i> , <i>T. evansi</i>	(12)
Equidae	Zebra (<i>Equus quagga boehma</i>)	<i>T. b. rhodesiense</i>	(12)
Cephalophinae	Common duiker (<i>Sylvicapra grimmia</i>)	<i>T. b. rhodesiense</i> , <i>T. vivax</i> , <i>T. congolense</i>	(12)
Aepycerotinae	Impala (<i>Aepyceros melampus</i>)	<i>T. b. rhodesiense</i> , <i>T. congolense</i> , <i>T. evansi</i>	(20)
Rhinocerotidae	Rhino (<i>Diceros bicornis</i>)	<i>T. brucei</i>	(20)
Alcephinae	Wildebeest (<i>Connochaetes taurinus cooksoni</i>)	<i>T. brucei</i> , <i>T. congolense</i> , <i>T. vivax</i>	(20)
	Hartebeest (<i>Alcephalus buselaphus</i>)	<i>T. evansi</i> , <i>T. brucei</i>	(20)
Hyaenidae	Hyena (<i>Hyaena hyaena</i>)	<i>T. evansi</i> , <i>T. congolense</i>	(12)
Cercopithecinae	Vervet monkey (<i>Cercopithecus species</i>)	<i>T. gambiense</i>	(12)
	Baboon (<i>Papio cynocephalus</i>)	<i>T. congolense</i>	(12)
Crocodylinae	Crocodile (<i>Crocodylus niloticus</i>)	<i>T. vivax</i>	(12)
Hippotraginae	Roan antelope (<i>Hippotragus equinus</i>)	<i>T. vivax</i> , <i>T. congolense</i>	(12)
Pteropodidae	Megabat/fruit bat (Chiroptera)	<i>Trypanosoma dionisi</i> , <i>T. cruzi</i>	(22, 23)
Phalangeridae	Brushtail possum (<i>Trichosurus vulpecula</i>)	<i>Trypanosoma</i> spp.	(17)
Muridae	Brush-tailed rabbit-rat (<i>Conilurus penicillatus</i>)	<i>Trypanosoma</i> spp.	(5)
Potoroidae	Brush-tailed bettong (<i>Bettongia penicillata</i>)	<i>T. vegrandis</i> , <i>T. copemani</i>	(24)
Dasyuridae	Northern quoll (<i>Dasyurus hallucatus</i>)	<i>Trypanosoma</i> spp.	(5)
Peramelidae	Northern brown bandicoot (<i>Isodon macrourus</i>)	<i>Trypanosoma</i> spp.	(5)
Phascolarctidae	Koalas (<i>Phascolarctos cinereus</i>)	<i>Trypanosoma inwini</i> , <i>T. copemani</i>	(25)
	Koalas (<i>Phascolarctos cinereus</i>)	<i>T. gilletti</i>	(25)
Cervidae	Marsh deer (<i>Blastocerus dichotomus</i>)	<i>Trypanosoma theileri</i> , <i>T. evansi</i>	(26)
Canidae	African wild dog (<i>Lycaon pictus</i>)	<i>T. godfreyi</i>	(18)
Potoroidae	Boodie (<i>Bettongia lesueur</i>)	<i>Trypanosoma</i> spp.	(27)
Tayassuidae	White-lipped peccary (<i>Tayassu pecari</i>)	<i>Trypanosoma evansi</i> and <i>Trypanosoma cruzi</i>	(21)
Mustelidae	Wild European badger (<i>Meles meles</i>)	<i>Trypanosoma (Megatryparium) pestanae</i>	(28)
Meliphagidae	Regent honeyeater (<i>Anthochaera phrygia</i>)	<i>Trypanosoma thomssbancrofti</i>	(29)

Fig 7: Taxonomy of Wild Animal hosts and trypanosome species. Modified from Kasozi et al, (2021)

A third of the continent of Africa is afflicted by trypanosomiasis. The Tsetse people live over much of West, Eastern, Central, and Southern Africa. It displays the various tsetse species and subspecies. Tsetse populations need shade (47–49), high relative humidity (75–90%) with a slight saturation deficit, and moderate temperatures (23–25°C). Trypanosomes and Tsetse are not able to survive at temperatures higher than 34.1°C (Kasozi *et al.*, 2021) (Fig. 8)

Subgenus	Glossina species	Glossina subspecies	Country	Wildlife animal spp.	References	
Nemorhina (Palpals)	Glossina palpalis	G. p. palpalis	Nigeria, Angola Cameroon,	Bushbuck, primates, warthogs	(36)	
	G. tachinoides		Nigeria		(37)	
		G. p. gambiense	Gambia, Senegal, Republic of Guinea	Baboons, monkeys, chimps	(39, 40)	
	G. fuscipes	G. f. fuscipes	Uganda, Sudan, Ethiopia, Kenya, DRC	Buffaloes, antelopes	(41)	
		G. f. martini	Uganda, Tanzania, DRC	Buffaloes	(42)	
		G. f. quarzensis	Uganda, Tanzania	Buffaloes, antelopes	(42)	
	G. pallicera	G. p. pallicera	Cameroon, Ivory coast, Liberia	Antelopes	(43–45)	
		G. p. newsteadii	DRC	Lions, leopards	(46)	
	G. tachinoides		Nigeria, Ghana, Cameroon	Buffaloes, lions, buffaloes	(46)	
	G. caliginea		Nigeria, Congo Brazaville	Cheetah, lions, leopards	(46)	
	Glossina (morsitans)	G. morsitans	G. m. morsitans	Nigeria, Uganda, Tanzania, Zambia	Buffaloes, rhinoceros, antelopes	(46)
			G. m. submorsitans	Uganda, Tanzania	Buffaloes, bushbuck, antelopes	(46)
			G. m. centralis	Uganda, Tanzania	Buffaloes, bushbucks, antelopes	(46)
G. swynnertoni			Nigeria, Congo Brazaville	Lions, cheetahs	(46)	
G. longipalpis			Ivory Coast, Senegal, Mali	Buffaloes, lions	(46)	
G. pallipides			Ethiopia, DRC, Uganda, Kenya, Zambia, Tanzania	Buffaloes, lions, antelopes	(46)	
G. austeni			Kenya, Tanzania, Mozambique	Bushbucks, antelopes, lions	(46)	
G. vanhoofi			DRC	Lions	(46)	
G. tabaniformis			Nigeria, DRC	Buffaloes, lions	(46)	
G. severini			DRC	Lions, bushbucks	(46)	
G. schwetzi			Togo, Congo Brazaville	Wild ruminants	(46)	
G. nigrofusca			Ivory Coast, Nigeria, CAR, DRC	Elephants, lions, monkeys	(46)	
G. nashi			Cameroon, Nigeria, Togo	Monkeys, baboons, wild cats	(46)	
G. medicorum			Ghana, Gambia, Nigeria	Lions, buffaloes	(46)	
G. longipennis			Tanzania, Sudan, Kenya	Antelopes, bushbucks, lions	(46)	
G. hanningtoni			Nigeria, Cameroon, Gambia	Bushbucks, buffaloes	(46)	
G. fuscipleuris			CAR, DRC Cameroon	Lions, bushbucks	(46)	
G. brevipalpis		Kenya, DRC, Tanzania	Buffaloes, antelopes	(46)		

Fig 8. Trypanosomiasis-affected wildlife and Tsetse species' geographical distribution. Modified from

(Kasozi *et al.*, 2021)

Conclusion

Prevalence of AAT is high in Nigeria. If concerted efforts are not made, Nigeria may not be able to eradicate trypanosomiasis very soon due to tsetse infection. The incidence of AAT and tsetse infections in Nigeria has been extensively studied using microscopy; however, because of its sensitivity, PCR may provide a higher prevalence. To validate the results of research, study methodology and risk factor assessment are required. It is necessary to conduct additional research to determine how risk factor evaluation for AAT and tsetse infection might account for this difference. Trypanosomiasis and free-living wild animals exist together in their natural environment, physical and somatic stress caused by storms, hunger, intercurrent infections, capturing, transfer, and captivity frequently compromised the animals' natural immunity to the infection.

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