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[Ayman Ahmed](#)*, [Emmanuel Edwar Siddig](#), [Nouh Saad Mohamed](#)*

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Review

Arthropod-Borne Parasitic Diseases in Africa: Prevalence, Diversity, and the Risk of Re-Emergence

Ayman Ahmed ^{1,2,3,4,*}, Emmanuel Edwar Siddig ^{1,5} and Nouh Saad Mohamed ¹

¹ Pan-Africa One Health Institute (PAOHI), Kigali 11KG St 203, Rwanda

² Institute of Endemic diseases, University of Khartoum, Khartoum, Sudan

³ Swiss Tropical and Public Health Institute (Swiss TPH), Allschwil, Switzerland

⁴ University of Basel, Petersplatz 1, Basel, Switzerland

⁵ Faculty of Medical Laboratory Sciences, University of Khartoum, Khartoum, Sudan

* Correspondence: ayman.ame.ahmed@gmail.com ; Tel.: +249123456789

Abstract: Vector-borne parasitic diseases represent a critical public health challenge in Africa, disproportionately impacting vulnerable populations and linking human, animal, and environmental health through the One Health framework. In this review we explore the epidemiology of these diseases, particularly those that are underreported and highlight the complex transmission dynamics involving domestic and wild animal hosts. Climate change, urbanization, and deforestation exacerbate the emergence and reemergence of arthropod-borne parasitic diseases like malaria, leishmaniasis, and trypanosomiasis, complicating control and disease elimination efforts. Despite progress in managing certain diseases, gaps in surveillance and funding hinder effective responses, allowing many arthropod zoonotic parasitic infections to persist unnoticed. The increased interactions between humans and wildlife, driven by environmental changes, heighten the risk of spillover events. Leveraging comprehensive data on disease prevalence, distribution, and vector ecology, coupled with a One Health approach, is essential for developing adaptive surveillance systems and sustainable control strategies. This review emphasizes the urgent need for interdisciplinary collaboration among medical professionals, veterinarians, ecologists, and policymakers to effectively address the challenges posed by vector-borne parasitic diseases in Africa, ensuring improved health outcomes for both humans and animals.

Keywords: arthropod-borne parasitic diseases; vulnerable populations; zoonotic infections; One Health; Africa

1. Introduction

Vector borne parasitic diseases remain a significant public health challenge in Africa, disproportionately affecting vulnerable populations and posing threats to both human and animal health [1]. These diseases, caused by a range of protozoan, helminthic, and ectoparasitic organisms, are often underreported and neglected in disease surveillance programs [2]. Despite global efforts to eliminate some of these infections, their persistence, reemergence, and spread in different regions of Africa highlight the complexity of their transmission dynamics. This review aims to shed light on the epidemiology of vector borne parasitic diseases in Africa, emphasizing underreported conditions and addressing the role of animal hosts in the transmission cycle within the One Health framework.

The One Health approach recognizes the intricate link between human health, animal health, and environmental factors in disease transmission. Given the increasing frequency of climate change effects, shifting ecological landscapes, and growing human and animal population movement, zoonotic parasitic diseases are emerging in new geographical locations, making their control even more challenging [1]. Factors such as deforestation, agricultural expansion, urbanization, and trade-related animal movement contribute to the changing epidemiology of these infections.

Understanding and addressing these factors holistically is crucial for developing sustainable disease control and prevention strategies.

While some zoonotic parasitic diseases receive global attention, many remain neglected and lack sufficient epidemiological data. This review highlights the necessity of a comprehensive examination of these diseases, particularly those that remain underreported in Africa. The scarcity of surveillance data and limited research funding contribute to the knowledge gap surrounding these diseases, delaying timely interventions and control measures [3]. Vector borne parasitic diseases such as malaria, leishmaniasis, trypanosomiasis, lymphatic filariasis, among others, often go unnoticed in countries where the disease is not officially recognized to be endemic or also due to misdiagnosis, lack of awareness, or inadequate healthcare infrastructure in such settings [4]. Additionally, the role of domestic and wild animals as reservoirs of parasitic infections is frequently underestimated although many efforts were made in the fight of vector borne diseases such as leishmaniasis, livestock, companion animals, and wildlife serve as crucial reservoirs for these parasites, often maintaining transmission cycles that eventually spill over into human populations [5,6]. Addressing these diseases requires an integrated approach involving veterinarians, medical professionals, ecologists, and policymakers to establish effective surveillance and control programs.

Although some zoonotic parasitic diseases have been successfully controlled or eliminated in specific regions, changing environmental and socio-economic factors facilitate their resurgence. The history of parasitic disease elimination in Africa demonstrates that the absence of continuous monitoring and control measures can lead to the reintroduction of these infections. For example, trypanosomiasis, which remains endemic in African regions, has been documented to reappear in previously controlled areas due to ecological changes and population displacement [7].

Climate change further exacerbates this issue by altering parasite-host dynamics [8]. Rising temperatures, changes in rainfall patterns, and extreme weather events influence the distribution of vector and intermediate host populations, expanding the geographical range of parasitic infections. For instance, the transmission dynamics of vector-borne parasitic diseases such as leishmaniasis and trypanosomiasis are shifting due to changes in the habitats of sandflies and tsetse flies, respectively [8]. Additionally, the expansion of agricultural activities and human settlements into wildlife-rich regions increases the likelihood of human exposure to novel zoonotic parasites [8,9].

Furthermore, international and regional trade, along with human migration, contribute to the introduction of parasitic infections into new locations. The movement of infected livestock across borders facilitates the spread of diseases. Additionally, the displacement of human populations due to conflicts or economic opportunities leads to the movement of individuals from endemic to non-endemic regions, potentially introducing infections to previously unaffected populations [10].

The need for a renewed focus on zoonotic parasitic diseases in Africa cannot be overstated. While efforts have been made to control and eliminate certain parasitic infections, the evolving interplay of environmental, economic, and social factors continues to challenge disease eradication. This review underscores the importance of adopting a One Health approach that integrates human, animal, and environmental health perspectives to tackle these diseases effectively. By addressing underreported parasitic diseases, improving disease surveillance, and mitigating factors leading to reintroduction and reemergence, public health systems can be better equipped to control the burden of zoonotic parasitic infections in Africa.

In this review, we will discuss arthropod-borne parasitic diseases affecting humans and animals in Africa, which require blood-feeding arthropod vectors for transmission. An exception is the fruit fly, which transmits Thelaziasis by feeding on animal tears.

2. Overview on Arthropod-Borne Parasitic Diseases in Africa

Arthropod-borne parasitic diseases pose a significant public health and veterinary burden across Africa, affecting both humans and animals. These diseases are transmitted by vectors such as mosquitoes, ticks, sandflies, blackflies, and tsetse flies, facilitating the spread of parasites that's causing diseases malaria, trypanosomiasis, leishmaniasis, babesiosis, thelaziasis and filariasis

diseases; such as lymphatic filariasis, onchocerciasis, mansonellosis, and elaeophorosis (Table 1). The epidemiology and distribution of these diseases are influenced across Africa by many factors including climatic factors, vector ecology, socio-economic conditions, and human-animal interactions. Many of these infections are underreported due to limited surveillance and diagnostic capacity, particularly in rural and resource-limited areas.

Table 1. List of countries where records of occurrence of arthropod-borne parasitic diseases and their associated vector type(s).

Arthropod-borne parasitic diseases	Vector type	Countries with record of occurrence
Malaria	Mosquito	Algeria, Djibouti, Angola, Burundi, Benin, Botswana, Burkina Faso, Cabo Verde, Cameroon, Central African Republic (CAR), Chad, Republic of the Congo, Comoros, Côte d'Ivoire, Democratic Republic of the Congo (DRC), Egypt, Equatorial Guinea, Eritrea, Eswatini, Ethiopia, Gabon, Ghana, Guinea, Guinea-Bissau, Kenya, Liberia, Libya, Madagascar, Malawi, Mali, Mauritania, Mauritius, Morocco, Mozambique, Namibia, Niger, Nigeria, Rwanda, São Tomé and Príncipe, Senegal, Seychelles, Sierra Leone, Somalia, South Africa, South Sudan, Sudan, Tanzania, The Gambia, Togo, Tunisia, Uganda, Zambia, and Zimbabwe.
Trypanosomiasis	Tsetse fly	Algeria, Angola, Burundi, Benin, Botswana, Burkina Faso, Cameroon, CAR, Chad, Republic of the Congo, Côte d'Ivoire, DRC, Egypt, Equatorial Guinea, Eritrea, Ethiopia, Gabon, Ghana, Guinea, Kenya, Liberia, Libya, Madagascar, Malawi, Mali, Mauritania, Mauritius, Morocco, Mozambique, Niger, Nigeria, Rwanda, São Tomé and Príncipe, Senegal, Sierra Leone, Somalia, South Africa, South Sudan, Sudan, Tanzania, The Gambia, Togo, Tunisia, Uganda, Zambia, and Zimbabwe.
Leishmaniasis	Sandfly	Algeria, Djibouti, Angola, Burundi, Burkina Faso, Cameroon, CAR, Chad, Republic of the Congo, Côte d'Ivoire, DRC, Egypt, Equatorial Guinea, Eritrea, Ethiopia, Gabon, Ghana, Guinea, Guinea-Bissau, Kenya, Libya, Madagascar, Malawi, Mali, Mauritania, Morocco, Mozambique, Namibia, Niger, Nigeria, Senegal, Somalia, South Africa, South Sudan, Sudan, Tanzania, The Gambia, Togo, Tunisia, Uganda, Zambia, and Zimbabwe.
Babesiosis	Ticks	Algeria, Angola, Burundi, Benin, Botswana, Burkina Faso, Cabo Verde, Cameroon, Chad, Comoros, Côte d'Ivoire, DRC, Egypt, Equatorial Guinea, Eritrea, Eswatini, Ethiopia, Gabon, Ghana, Guinea, Kenya, Lesotho, Libya, Madagascar, Malawi, Mali, Mauritius, Morocco, Mozambique, Namibia, Nigeria, Rwanda, Senegal, Somalia, South Africa, South

		Sudan, Sudan, Tanzania, The Gambia, Tunisia, Uganda, Zambia, and Zimbabwe.
Theileriosis	Ticks	Algeria, Angola, Benin, Botswana, Burkina Faso, Burundi, Cameroon, CAR, Chad, Comoros, Côte d'Ivoire, DRC, Egypt, Eritrea, Ethiopia, Gabon, Ghana, Guinea, Guinea-Bissau, Kenya, Libya, Madagascar, Malawi, Mali, Mauritania, Morocco, Mozambique, Namibia, Niger, Nigeria, Republic of Congo, Rwanda, São Tomé and Príncipe, Senegal, Sierra Leone, Somalia, South Africa, South Sudan, Sudan, Eswatini, Tanzania, The Gambia, Togo, Tunisia, Uganda, Zambia, and Zimbabwe.
Onchocerciasis	Black fly	Angola, Somalia, Burkina Faso, CAR, Burundi, Benin, Cameroon, Chad, Republic of the Congo, Côte d'Ivoire, DRC, Egypt, Equatorial Guinea, Ethiopia, Gabon, Ghana, Guinea, Guinea-Bissau, Kenya, Liberia, Malawi, Mali, Mozambique, Niger, Nigeria, Rwanda, Senegal, Sierra Leone, South Africa, South Sudan, Sudan, Tanzania, Togo, Tunisia, Uganda, Zambia, and Zimbabwe.
Lymphatic Filariasis	Mosquito	Angola, Burundi, Benin, Botswana, Burkina Faso, Cabo Verde, Cameroon, CAR, Chad, Republic of the Congo, Comoros, Côte d'Ivoire, DRC, Egypt, Equatorial Guinea, Eritrea, Ethiopia, Gabon, Ghana, Guinea, Guinea-Bissau, Kenya, Liberia, Madagascar, Malawi, Mali, Mauritius, Mozambique, Niger, Nigeria, Rwanda, São Tomé and Príncipe, Senegal, Seychelles, Sierra Leone, South Sudan, Sudan, Tanzania, The Gambia, Togo, Uganda, Zambia, and Zimbabwe.
Loiasis	Deer fly	Angola, Benin, Cameroon, CAR, Chad, Republic of the Congo, DRC, Equatorial Guinea, Ethiopia, Gabon, Ghana, Guinea, Malawi, Nigeria, Rwanda, South Sudan, Uganda, Zambia, and Morocco.
Mansonellosis	Midges and blackfly	Angola, Burundi, Benin, Burkina Faso, Cameroon, CAR, Chad, Republic of the Congo, Côte d'Ivoire, DRC, Egypt, Equatorial Guinea, Ethiopia, Gabon, Ghana, Guinea, Guinea-Bissau, Kenya, Liberia, Malawi, Mali, Mozambique, Niger, Nigeria, Rwanda, São Tomé and Príncipe, Senegal, Sierra Leone, South Sudan, Sudan, Tanzania, The Gambia, Togo, Uganda, Zambia, and Zimbabwe.
Canine Heartworm Disease	Mosquito	Egypt, Tunisia, Nigeria, South Africa, Zimbabwe, Mozambique, Tanzania, Malawi, Botswana, Namibia, Zambia, Cape Verde, Morocco, Sao Tome and Principe,

		Chad, Kenya, Senegal, Gabon, Sierra Leone, Côte d'Ivoire, and Algeria.
Seteriasis	Mosquito	Burkina Faso, The Gambia, Egypt, Nigeria, Kenya, Ethiopia, Namibia, South Africa, Zimbabwe, Tanzania, CAR, Chad, Cameroon, Senegal, Guinea Bissau, Côte d'Ivoire, Somalia, and Morocco.
Acanthocheilonemiasis	Fleas, Lice, and Ticks	Kenya, Nigeria, Egypt, South Africa, Namibia, Botswana, Mozambique, Zambia, Uganda, and Côte d'Ivoire.
Litomosoides species	Mites	South Africa and Madagascar.
Thelaziasis	Fruit fly	Zambia, Senegal, Ethiopia, Kenya, Nigeria, Egypt, DRC, Tanzania, Namibia, and Uganda.
Elaeophorosis	Horsefly	Tanzania and Republic of Congo.
<i>Anthemosoma garnhami</i> infection	Ticks	Zimbabwe, Ethiopia, and Namibia.

2.1. Human and Non-Human Primate Malaria

Malaria remains a major public health challenge in Africa, with the World Health Organization (WHO) African Region bearing the highest global burden of cases and deaths [11]. The disease is caused by *Plasmodium* parasites, with *Plasmodium falciparum* being the most severe species, often leading to life-threatening complications. Malaria is transmitted through the bite of an infected female *Anopheles* mosquito, which ingests the parasite from an infected person and later spreads it to others [12]. The impact is particularly devastating for children, as malaria contributes significantly to child mortality and impairs cognitive development. Pregnant women are also at high risk, facing complications such as low birth weight, premature delivery, and maternal death [13]. The highest malaria burden is found in sub-Saharan Africa, where warm temperatures, high rainfall, and stagnant water create ideal conditions for mosquito breeding. Socioeconomic factors, including poverty, limited healthcare access, and inadequate vector control, further sustain malaria transmission. Despite progress in controlling the disease through insecticide-treated bed nets (ITNs), indoor residual spraying (IRS), and antimalarial treatments, malaria remains a leading cause of morbidity and mortality [11].

While malaria control efforts have made significant progress in several African countries, imported malaria remains a concern. Imported malaria refers to infections acquired in endemic regions but diagnosed in non-endemic areas, often due to international travel or migration. This poses a challenge in countries where malaria transmission has been eliminated or significantly reduced, as travelers, expatriates, and refugees from endemic regions may reintroduce the parasite. Some African countries, including Libya [14,15], Egypt [16], Morocco [17,18], Tunisia [19], Cabo Verde [20], Mauritius [21], Seychelles [22], and more recently Algeria [23], which is on the WHO roadmap for malaria-free certification, continue to report malaria cases. The presence of malaria vectors in these regions raises concerns about potential re-establishment of local transmission, emphasizing the need for ongoing surveillance, rapid diagnosis, and preventive measures [24].

The increasing prevalence of zoonotic malaria, particularly *P. knowlesi*, has become a growing global concern. Reports of *P. knowlesi* infections have been documented primarily in Southeast Asia and, more recently, in regions of South America [25–27]. The expanding geographical range of this parasite underscores the urgent need for continuous surveillance and research to understand its transmission dynamics and potential impact on public health and malaria control efforts.

In Africa, non-human primates (NHPs) harbor a diverse range of *Plasmodium* species, many of which were previously thought to be exclusive to wildlife but are now recognized as potential

zoonotic threats. Among these malaria parasites are *P. reichenowi*, *P. gaboni*, *P. georgesi*, *P. gonderi*, and *P. petersi*. Additionally, a newly identified malaria parasite, *Plasmodium* sp. DAJ-2004, has recently been reported in Africa, further expanding the known diversity of *Plasmodium* species in primates [28–32]. With increasing deforestation, habitat fragmentation, and landscape modifications in many African regions, the risk of cross-species transmission from NHPs to humans is heightened. These environmental changes facilitate closer interactions between humans and wildlife, providing greater opportunities for spillover events of malaria parasites [33,34].

Several *Plasmodium* species that infect NHPs in Africa, including *P. vivax*, *P. malariae*, and *P. ovale*, were historically infecting both humans and non-human parasites. However, recent studies suggest that these species can be transmitted between humans and NHPs, posing a significant challenge for malaria control and eradication efforts [35].

Among the *Plasmodium* species infecting African NHPs, *P. schwezi* has been identified in chimpanzees and gorillas, while *P. cynomolgi* and *P. inui* are known to infect other primate species. *P. cynomolgi*, in particular, has gained attention due to its ability to cause infections in humans, raising concerns about its potential to establish itself as an emerging zoonotic malaria parasite [36]. The increasing reports of zoonotic malaria cases highlight the need for improved diagnostic tools, as well as enhanced surveillance programs, to detect and monitor such infections in both human and animal populations.

Numerous cases of NHP malaria have been reported across various African countries, including Cameroon, Sierra Leone, Gabon, the DRC, Kenya, the Republic of the Congo, Uganda, and Madagascar [37,38]. Notably, *Plasmodium* species such as *P. adleri*, *P. billcollinsi*, *P. blacklocki*, *P. praefalciparum*, *P. gaboni*, and *P. reichenowi* have been identified in these regions. Some of these species are suspected to be capable of infecting humans directly or acting as reservoirs that facilitate the maintenance of malaria transmission cycles in nature. This complexity further complicates malaria eradication strategies, as non-human reservoirs may continuously reintroduce parasites into human populations [39].

2.2. Human and Animal Trypanosomiasis

Trypanosomiasis, commonly known as sleeping sickness in humans and nagana in animals, is a parasitic disease caused by protozoan parasites of the genus *Trypanosoma*. It is transmitted by the tsetse fly (*Glossina* spp.) and poses a major health and economic burden in Africa [40]. The disease is caused by several *Trypanosoma* species, which infect both humans and animals. Human African trypanosomiasis (HAT) is primarily caused by two subspecies of *Trypanosoma brucei*: *T. b. gambiense*, which causes chronic sleeping sickness in West and Central Africa, and *T. b. rhodesiense*, which causes an acute form of the disease in East and Southern Africa [41]. Initial symptoms among human include fever, headaches, muscle aches, and swollen lymph nodes. As the disease progresses, it affects the central nervous system (CNS), causing confusion, sleep disturbances, and coma if left untreated. *T. b. gambiense* accounts for over 95% of reported cases and can persist undetected for years. While *T. b. rhodesiense* is more virulent, with rapid disease progression [42]. The early symptoms of the disease include fever, headaches, muscle aches, and swollen lymph nodes. As the disease progresses, it affects the CNS, leading to confusion, sleep disturbances, and coma if left untreated. *T. b. gambiense* accounts for over 95% of reported cases and can persist undetected for years, while *T. b. rhodesiense* progresses more rapidly, often leading to severe illness within weeks [43]. Although their geographical distribution is assertions in certain regions in Africa, their existence in newly unreported regions is confirmed [44].

On the other hand, animal trypanosomiasis, commonly known as nagana, affects livestock and wild animals, leading to significant economic losses [45]. Several *Trypanosoma* species contribute to nagana, including *T. congolense* [46], *T. vivax* [47], *T. godfreyi* [48], *T. simiae* [49], *T. brucei* [50], *T. lewisi* [51], *T. simiae* [52], *T. suis* [53], *T. theileri* [54], *T. uniforme* [55], *T. equiperdum*, and *T. evansi* [56]. Symptoms in infected animals include fever, anemia, weight loss, reduced fertility, and lethargy.

Dairy cattle may experience decreased milk production, while high mortality rates further impact the livestock industry.

Although significant progress has been made in controlling trypanosomiasis, it remains a major economic and public health challenge. Countries with documented cases of the disease among animals and/or humans in Africa include Algeria [57–59], Angola [60], Burundi [61], Benin [62,63], Botswana [64], Burkina Faso [65], Cameroon [66,67], CAR [68,69], Chad [70,71], Republic of the Congo [72], Côte d’Ivoire [73], DRC [74,75], Egypt [76,77], Equatorial Guinea [78,79], Eritrea [80,81], Ethiopia [82,83], Gabon [84,85], Ghana [86,87], Guinea [88], Kenya [89,90], Liberia [91–93], Libya [94], Madagascar [95,96], Malawi [97–99], Mali [100,101], Mauritania [102], Mauritius [103], Morocco [104], Mozambique [97,105], Namibia [106], Niger [107], Nigeria [108,109], Rwanda [110,111], São Tomé and Príncipe [112,113], Senegal [114–116], Sierra Leone [117,118], Somalia [119], South Africa [120], South Sudan [121,122], Sudan [123], Tanzania [99,124], The Gambia [125,126], Togo [116,127,128], Tunisia [129,130], Uganda [99,131], Zambia [99,132], and Zimbabwe [133,134] (Figure 1). These reports highlight the possibility of disease re-emergence in both humans and animals, particularly in areas where tsetse fly populations remain active. Some countries have not reported cases of the disease, but given the presence of the vector in those regions, extensive surveillance and improving diagnostic capacity are necessary to prevent potential outbreaks.

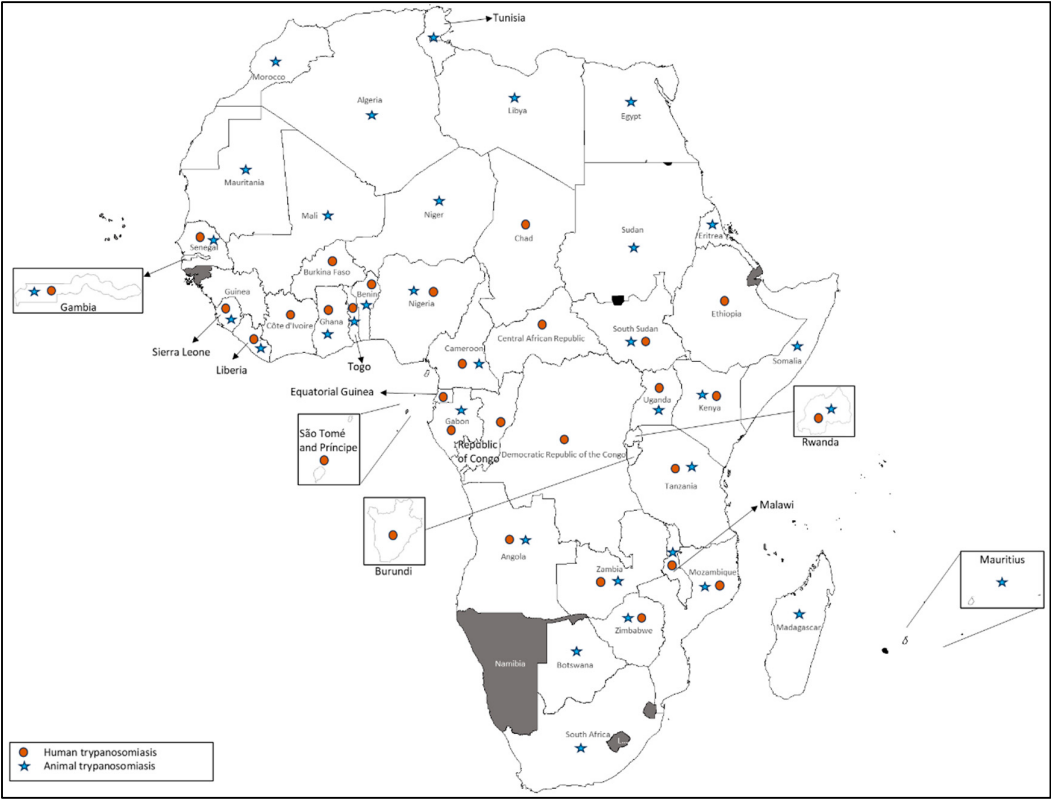


Figure 1. Map of Africa showing countries where animals or human trypanosomiasis disease records of occurrence has been documented. Countries highlighted in grey color indicate unavailable data about trypanosomiasis among human or animals.

2.3. Human and Canine Leishmaniasis

Leishmaniasis is mainly transmitted through the bite of infected sand flies of the *Phlebotomus* or *Lutzomyia* spp, however, there are also uncommon routes including blood transfusion, transplacental, or venereal [135]. Leishmaniasis has several forms including vesical or also known as kala-azar, cutaneous also called Spundia or oriental sore, and mucocutaneous leishmaniasis also known as

Spundia. The visceral one may progress and form a dermatological form of the disease called post kala azar dermal leishmaniasis [136–139]. Visceral leishmaniasis (VL) is a potentially fatal infectious disease. The disease primarily affects the internal organs, particularly the spleen, liver, and bone marrow. If left untreated, it can lead to severe complications and even death [136]. Human and/or animal VL cases have been reported from many parts of Africa, including Algeria [140,141], Djibouti [142], Angola [143], Burkina Faso [141,144], Cameroon [141], CAR [145], Chad [141], Côte d'Ivoire [146], DRC [141], Egypt [141], Eritrea [141], Ethiopia [147], Gabon [148], Kenya [141], Libya [141], Mauritania [141], Morocco [141], Niger [141], Senegal [141], Somalia [149], South Sudan [150], Sudan [151], Tanzania [141], The Gambia [152], Togo [153], Tunisia [141], Uganda [141], and Zambia [154,155] (Figure 2).

Whereas, Cutaneous leishmaniasis (CL) infection primarily affects the skin, causing the development of sores or ulcers that can vary in size and appearance. These lesions often leave scars and can cause significant disfigurement and social stigma. CL is endemic in various regions worldwide, in Africa CL has been reported many regions including Algeria [156], Djibouti [157], Angola [158], Burundi [159], Burkina Faso [160], Cameroon [161], CAR [162,163], Chad [164], Republic of the Congo [165], Côte d'Ivoire [166], DRC [167], Egypt [168], Eritrea [169], Ethiopia [170], Ghana [171], Guinea [172], Guinea-Bissau [173], Kenya [174], Libya [175], Malawi [176], Mali [177], Mauritania [178], Morocco [179], Namibia [180], Niger [181], Nigeria [182], Senegal [183], South Africa [184,185], Sudan [186], Tanzania [187], The Gambia [152], Tunisia [188], and Uganda [189] (Figure 2).

Concerning the shared situation of leishmaniasis between animals and human, as well as several animals were considered as a reservoir of the parasite, in some situations the disease also severely threaten animals' life and may also cause significant economic losses. The animal form of the disease is known as canine leishmaniasis [190]. Canine leishmaniasis has been reported among several animals in countries where neither CL or VL human cases is reported such as Zimbabwe while in areas where the diseases is already being reported including Algeria [191], Angola [192], Burkina Faso [193], Cameroon [194], Republic of the Congo [195], Côte d'Ivoire [196], Egypt [197], Eritrea [195], Ethiopia [198], Guinea [199], Kenya [200], Libya [201], Madagascar [202], Malawi [203], Morocco [204,205], Mozambique [206], Niger [195], Nigeria [207], Senegal [208], South Africa [209], South Sudan [210], Sudan [211], The Gambia [212], Tunisia [213], Uganda [214], Zambia [155], and Zimbabwe [215,216] (Figure 2). Animals in these settings including dogs or cattle infected with leishmaniasis might play and considered having significant role in diseases reemergence in such settings where a susceptible vector population exists.

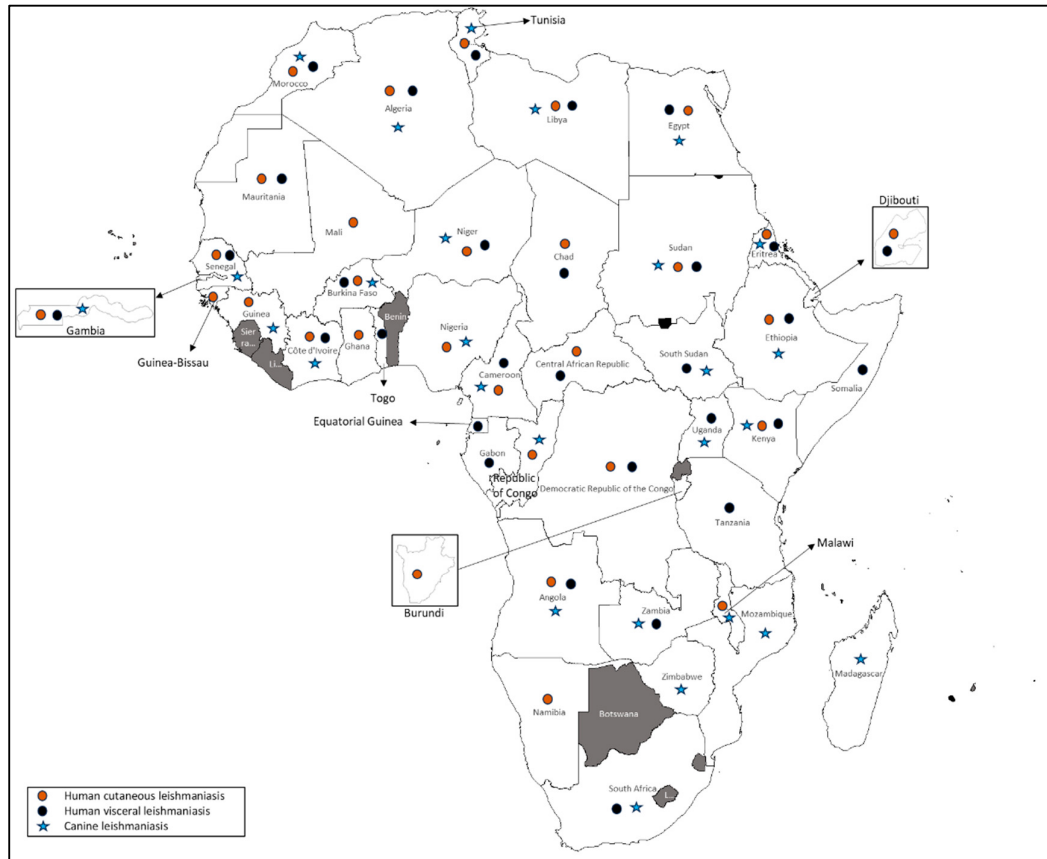


Figure 2. Map of Africa showing countries where human or canine leishmaniasis disease records of occurrence has been documented. Countries highlighted in grey color indicate unavailable data about leishmaniasis among human or animals.

2.4. Human and Animal Babesiosis

Babesiosis is a disease caused by infection with apicomplexan parasites of the genus, *Babesia*. While more than 100 species have been reported, only a few have been identified as causing human infections, including *B. microti* [217], *B. divergens* (also infect cattle) [218], *B. odocoilei* [219], *B. duncani* [220], and a currently un-named strain designated MO-1 [221]. Whereas species causing animal babesiosis includes *B. bovis* [222] and *B. bigemina* [223] in cattles, *B. caballi* [224] in horses, and *B. gibsoni* and *B. canis* in dogs [225], and *B. motasi* in sheep [226]. There are four species of *Babesia* are reported among birds including *B. poeala* [227], *B. peircei* [228], *B. bennetti*, and *B. uriae* [229].

These parasites are primarily transmitted through the bite of infected ticks, particularly *Ixodes scapularis* (the black-legged or deer tick). In rare cases, babesiosis among human can be transmitted through blood transfusions, organ transplants, or from an infected mother to her baby during pregnancy or delivery [230].

The most common cause of babesiosis in humans is *B. microti*, especially in the United States, though other species like *B. divergens* and *B. duncani* have been implicated in specific regions or cases [231]. Symptoms of babesiosis can vary widely. Many individuals are asymptomatic or experience mild symptoms, but others may develop fever, chills, sweats, headaches, fatigue, muscle aches, and hemolytic anemia, which can lead to jaundice and dark urine. In severe cases, the disease can cause complications such as organ failure, low blood pressure, and even death. Severe disease is more likely to occur in individuals with weakened immune systems, those who lack a spleen, the elderly, or those with other underlying health conditions [232].

Diagnosis of babesiosis involves examining blood smears under a microscope to detect the presence of *Babesia* parasites within red blood cells. PCR tests are also used to detect *Babesia* DNA, while serological tests can identify antibodies against the parasite [233]. Treatment typically involves a combination of atovaquone and azithromycin for mild to moderate cases, while severe cases may require clindamycin and quinine. In life-threatening situations, blood exchange transfusions may be necessary to address severe anemia [234].

Babesiosis is geographically distributed in regions where the primary tick vectors are prevalent. Cases of animal babesiosis has been recognized in several regions across Africa including Algeria [235], Angola [236], Burundi [237], Benin [238], Botswana [239], Burkina Faso [240], Cabo Verde [241], Cameroon [242], Chad [243], Comoros [244], Côte d’Ivoire [245], DRC [246], Egypt [247], Equatorial Guinea [248], Eritrea [249], Eswatini [250], Ethiopia [251], Gabon [252,253], Ghana [254], Guinea [255], Kenya [256], Lesotho [257], Libya [258], Madagascar [259], Malawi [260], Mali [261], Mauritius [262], Morocco [263], Mozambique [264], Namibia [265], Nigeria [266], Rwanda [267,268], Senegal [269], Seychelles [270], Somalia [271], South Africa [272,273], South Sudan [274], Sudan [275], Tanzania [276], The Gambia [277], Tunisia [278], Uganda [279], Zambia [280], and Zimbabwe [281] (Figure 3). However, human babesiosis have not been reported in many regions, those reported human cases include Cameroon [282], Egypt [283], Equatorial Guinea [248], Mozambique [284], Nigeria [285], South Africa [286], Tanzania [276], and Ghana [287] (Figure 3). Although, in Tanzania and Ghana the detection was not possible to be confirmed using molecular techniques, the detection was made using serological methods, both studies highlight the possibility of *Babesia* infection circulation among the population, since in Ghana slides positivity was confirmed, but the molecular technique used to confirm the parasite presence relayed on certain species of *Babesia* while this undetected infection could be another *Babesia* species such as the newly emerged MO.1 [287].

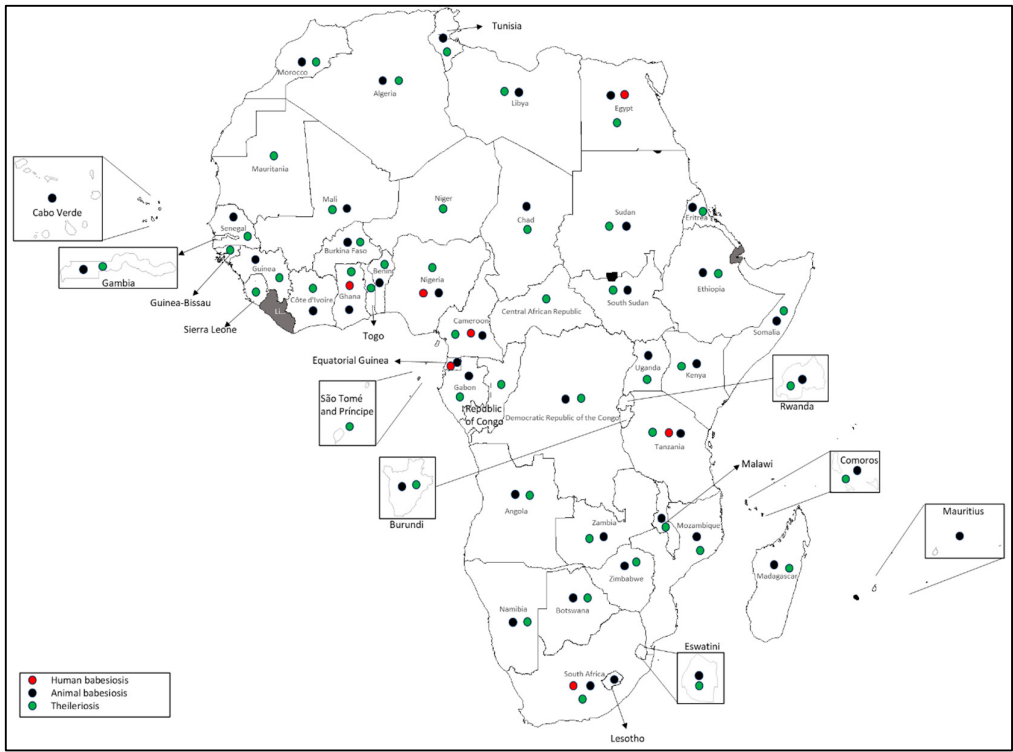


Figure 3. Map of Africa showing countries where human babesiosis or animal babesiosis/theileriosis disease records of occurrence has been documented. Countries highlighted in grey color indicate unavailable data about human babesiosis or animal babesiosis/theileriosis.

2.5. Theileriosis

Theileriosis, caused by protozoan parasites of the genus *Theileria*, is one of the most significant vector-borne diseases among animals in Africa, especially in regions with extensive cattle farming. The disease is transmitted by ticks, primarily *Rhipicephalus* and *Ixodes* species, which serve as the vector for *Theileria* parasites [288]. The most notable forms of the disease in Africa are caused by *T. parva*, the etiological agent of East Coast Fever (ECF), and *T. annulata*, which causes Tropical Theileriosis (TT). East Coast Fever, in particular, is a devastating disease for cattle, with symptoms including fever, swollen lymph nodes, coughing, and severe weight loss. Without prompt treatment, ECF can be fatal, making it a significant cause of livestock mortality in sub-Saharan Africa [289].

In Africa, Theileriosis has a major economic impact due to livestock deaths and the costs associated with treatment and control measures. It is especially problematic in East and Central Africa, where pastoralist communities rely heavily on cattle for food, income, and social status [290,291]. The disease can also affect the productivity of livestock by reducing milk yield, fertility, and overall health. In some regions, the economic losses are compounded by the cost of controlling tick populations, using acaricides, and implementing vaccination programs, which can be expensive and sometimes ineffective due to resistance [292]. Furthermore, the presence of Theileriosis hampers livestock trade across borders, as some countries impose quarantine measures or require proof of vaccination before cattle can be moved [291].

The spread of Theileriosis is closely linked to the distribution of tick populations, which thrive in tropical and subtropical climates, making Africa highly susceptible to the disease. Changes in land use, such as deforestation, and the movement of livestock for trade or migration have exacerbated the spread of ticks and *Theileria* parasites [293]. Climate change, with rising temperatures and shifting rainfall patterns, also influences tick populations, potentially expanding the range of Theileriosis [293]. In response, efforts to control the disease in Africa include tick control strategies, vaccination programs, and ongoing research into better diagnostic and treatment methods. However, these efforts face challenges related to infrastructure, resources, and the variability of tick resistance to treatments [294]. Thus, Theileriosis remains a significant challenge to livestock health and productivity in Africa, and continued efforts are needed to mitigate its impact.

The presence of *Theileria* species in Africa has been documented in many regions including Algeria [295], Angola [296], Benin [297], Botswana [298], Burkina Faso [297], Burundi [299], Cameroon [300], CAR [301], Chad [301], Comoros [302], Côte d'Ivoire [245], DRC [303], Egypt [304], Eritrea [305], Ethiopia [306], Gabon [307], Ghana [308], Guinea [309], Guinea-Bissau [310], Kenya [311], Libya [304], Madagascar [312], Malawi [304], Mali [313], Mauritania [314], Morocco [304], Mozambique [304], Namibia [315], Niger [316], Nigeria [317], Republic of Congo [318], Rwanda [304], São Tomé and Príncipe [319], Senegal [320], Sierra Leone [321], Somalia [271], South Africa [322], South Sudan [304], Sudan [323], Eswatini [250], Tanzania [304], The Gambia [277], Togo [324], Tunisia [304], Uganda [325], Zambia [304], and Zimbabwe [304] (Figure 3).

2.6. Filarial Diseases

2.6.1. Human and Animal Onchocerciasis

Onchocerciasis is a disease infecting both human and animals through the bite of infected black fly of the genus *Simulium*. There are many species of *Onchocerca* reported making onchocerciasis among animals, including *O. boehmi*, *O. dewittei dewittei*, *O. dewittei japonica*, *O. dukei*, *O. eberhardi*, *O. fasciata*, *O. flexuosa*, *O. gutturosa*, *O. jakutensis*, *O. lupi*, *O. ochengi*, *O. ramachandrini*, *O. reticulata*, *O. skrjabini*, *Onchocerca* spp. type I, *O. suzukii*, and *O. takaokai* [326]. *O. volvulus* is the species which causes onchocerciasis mainly among human, also known as river blindness, however *O. lupi* which causes ocular onchocerciasis in dogs also been reported causing ocular onchocerciasis among human [327]. Other *Onchocerca* species mainly infecting animals but also identified in humans are *O. dewittei japonica* [328], *O. jakutensis* [329], *O. gutturosa* [330], and *O. cervicalis* [331]. Animal reservoir of *O. volvulus* was suspected as the enlands (*Taurotragus oryx pattersonianus*) which detected to have nodules containing an *Onchocerca* species that morphologically identical to *O. volvulus* [332].

Meanwhile in a study conducted by Van Den Beughe et al., among eastern Congo gorillas (*Gorilla beringei*), they identified *O. volvulus* in the skin nodules of several gorillas [333].

Onchocerciasis can cause severe itching, disfiguring skin conditions, and visual impairment, including permanent blindness. The disease primarily affects people living in rural areas near rivers and streams in sub-Saharan Africa and parts of Latin America. Treatment for onchocerciasis typically involves medications to kill the adult worms and prevent the development of new larvae. Mass drug administration campaigns are often used to control the spread of the disease in endemic areas [334].

In Africa, in several region, onchocerciasis has been reported among human or animal including Angola [335], Burundi [335], Benin [336], Burkina Faso [337,338], Cameroon [339,340], CAR [335], Chad [335], Republic of the Congo [333,335], Côte d'Ivoire [341], DRC [342], Egypt [343], Equatorial Guinea [335], Ethiopia [335], Gabon [335], Ghana [336,344], Guinea [345], Guinea-Bissau [346], Kenya [335], Liberia [335], Malawi [347], Mali [348], Mozambique [349], Niger, Nigeria [350,351], Rwanda [335], Senegal [352], Sierra Leone [353], Somalia [354], South Africa [355], South Sudan [356], Sudan [332,357], Tanzania [358], Togo [336,359], Tunisia [360,361], Uganda [362,363], Zambia [364], and Zimbabwe [365] (Figure 4).

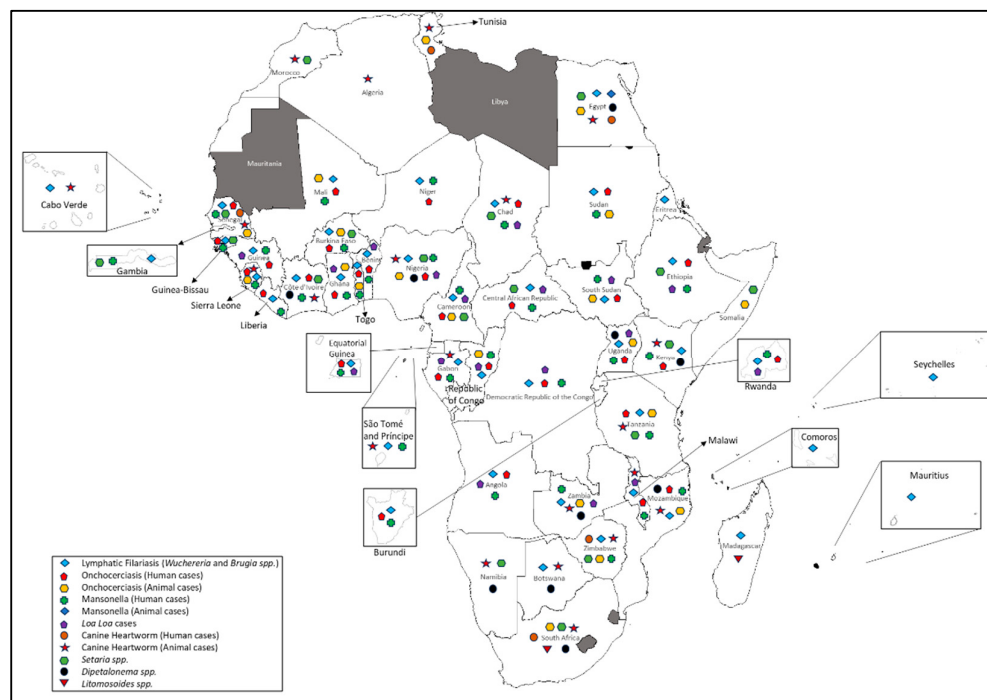


Figure 4. Map of Africa showing countries where filarial diseases records of occurrence has been documented. Countries highlighted in grey color indicate unavailable data about filarial diseases.

2.6.2. Lymphatic Filariasis

Lymphatic Filariasis, commonly known as elephantiasis, is a parasitic disease caused by filarial worms, primarily *Wuchereria bancrofti* and *Brugia spp.* These worms are transmitted to humans through the bites of infected mosquitoes. Once in the body, the worms block the lymphatic vessels, leading to a buildup of fluid and causing swelling in the limbs, genitals, and other body parts. In severe cases, this swelling can become chronic and disfiguring, leading to significant physical and social disabilities. Lymphatic Filariasis is a major public health problem in many tropical and subtropical regions, including parts of Africa. Treatment for Lymphatic Filariasis involves medications to kill the adult worms and microfilariae (immature worms). Mass drug administration campaigns are often used to control the spread of the disease in endemic areas in Africa [366]. In Africa, lymphatic filariasis has been reported from several regions including Angola [367], Burundi

[368], Benin [369], Botswana [370], Burkina Faso [371], Cabo Verde [372], Cameroon [373], CAR [374], Chad [375], Republic of the Congo [376], Comoros [377], Côte d'Ivoire [378], DRC [379], Egypt [380], Equatorial Guinea [381], Eritrea [382], Ethiopia [383], Gabon [381], Ghana [384], Guinea [381], Guinea-Bissau [381], Kenya [381], Liberia [381], Madagascar [385], Malawi [381], Mali [386], Mauritius [387], Mozambique [388], Niger [389], Nigeria [390], Rwanda [368], São Tomé and Príncipe [391], Senegal [392], Seychelles [393], Sierra Leone [394], South Sudan [395], Sudan [396], Tanzania [397], The Gambia [381], Togo [381], Uganda [398], Zambia [399], and Zimbabwe [381] (Figure 4).

2.6.3. Loiasis

Loiasis, also known as African eye worm disease, is a parasitic infection caused by the filarial worm *Loa loa*. It is transmitted to humans through the bites of infected deer flies. Once in the bloodstream, the adult worms can migrate through various tissues, including the subcutaneous tissues, where they can be seen moving under the skin, hence the name “eye worm.” Symptoms of loiasis can include itchy skin, subcutaneous swellings known as Calabar swellings, and in some cases, eye infections [400]. The worms can also migrate to the eyes, causing pain, inflammation, and even vision loss. Loiasis is primarily found in Central and West Africa [400]. Those region reported cases of loiasis in Africa include Angola [401], Benin [401,402], Cameroon [401], CAR [401], Chad [401], Republic of the Congo [401], DRC [401], Equatorial Guinea[401], Ethiopia [403], Gabon [401], Ghana [403,404], Guinea [403], Malawi [403], Nigeria [401], Rwanda [401], South Sudan [401], Uganda [401,403], Zambia [403], and Morocco [405] (Figure 4). Although the later one is historically considered non-endemic, Morocco experience a high rate of *L. loa* cases being imported to the country which eventually might lead to parasite transmission from an infected immigrant to the vector (i.e., Tabanid flies of the genus *Chrysops*) and then to the Moroccan patient, since the patient declared no history of travel within or outside of the country [406,407].

2.6.4. Mansonellosis

Mansonellosis is a neglected filarial disease caused by parasitic nematodes of the genus *Mansonella*, including *M. perstans*, *M. ozzardi*, and *M. streptocerca* [408]. It is transmitted by biting midges (*Culicoides* spp.) and blackflies (*Simulium* spp.), primarily affecting populations in Africa, Central and South America, and the Caribbean [408]. Although often asymptomatic, mansonellosis can cause a range of clinical manifestations, including pruritus, skin rashes, fever, joint pain, and lymphadenopathy. Chronic infections may lead to more severe complications, particularly in immunocompromised individuals [409]. Due to its mild and often nonspecific symptoms, the disease is underreported and poorly studied, contributing to its neglected status. Effective diagnosis relies on microscopic detection of microfilariae in blood or skin samples, though molecular techniques are improving identification. Treatment options remain limited, with ivermectin and albendazole showing variable efficacy, highlighting the need for further research into optimal therapeutic strategies and vector control measures [409]. Cases of mansonellosis that been reported in African countries include Angola [410], Burundi [411], Benin [412], Burkina Faso [413], Cameroon [414], CAR [415], Chad [416], Republic of the Congo [417], Côte d'Ivoire [412], DRC [418], Egypt [419], Equatorial Guinea [420], Ethiopia [421], Gabon [422], Ghana [423], Guinea [412], Guinea-Bissau [424], Kenya [424], Liberia [424], Malawi [425], Mali [426], Mozambique [427], Niger [412], Nigeria [428], Rwanda [411], São Tomé and Príncipe [429], Senegal [430], Sierra Leone [431], South Sudan [396], Sudan [432], Tanzania [433], The Gambia [434], Togo [435], Uganda [436], Zambia [437], and Zimbabwe [438] (Figure 4).

2.6.4. Canine Heartworm Disease

Canine heartworm disease, caused by *Dirofilaria immitis*, is a potentially fatal parasitic disease that primarily affects dogs but can also infect other mammals, including wild canids, felines, and even humans in rare cases [439,440]. This filarial nematode is transmitted through the bite of infected

mosquitoes, which serve as the intermediate hosts. The disease is distributed worldwide but is particularly prevalent in warm, humid regions where mosquito populations thrive [440]. Heartworm infection can cause severe cardiovascular damage. Infected dogs may initially show no clinical signs, but as the worm burden increases, symptoms such as coughing, exercise intolerance, lethargy, and difficulty breathing become evident. In advanced cases, dogs may develop caval syndrome, a life-threatening condition characterized by a large mass of worms obstructing blood flow in the heart. This leads to severe anemia, liver dysfunction, and right-sided heart failure. Without immediate surgical intervention, caval syndrome is often fatal [441].

Prevention is the most effective strategy against heartworm disease, and routine administration of prophylactic medications such as ivermectin, milbemycin, moxidectin, and selamectin is widely recommended. Despite advancements in prevention and treatment, heartworm disease remains a significant global concern, particularly in regions with high mosquito activity [442].

In Africa, countries where human or canine heartworm disease has been reported include Egypt [443–445], Tunisia [278,446], Nigeria [447], South Africa [448,449], Zimbabwe [450], Mozambique [451], Tanzania [452], Malawi [203], Botswana [453], Namibia [453], Zambia [453], Cape Verde [454], Morocco [455], Sao Tome and Principe [456], Chad [457], Kenya [458], Senegal [459], Gabon [460], Sierra Leone [461], Côte d'Ivoire [196], and Algeria [462] (Figure 4).

2.6.5. Other Animal Filarial Diseases

2.6.5.1. *Setaria* Species

Setaria is a genus of filarial nematodes (roundworms) belonging to the family *Onchocercidae*. These parasites primarily infect ungulates such as cattle, horses, deer, and other ruminants. While most *Setaria* species are non-pathogenic in their natural hosts, they can cause significant disease when they infect abnormal hosts, including humans and other animals [463–466].

Setaria species are long, thread-like nematodes that reside in the peritoneal cavity of their definitive hosts. Some species may also be found in the pleural cavity or the CNS. In their normal hosts, *Setaria* worms are usually non-pathogenic and cause little harm. However, in aberrant hosts, they can migrate to unusual sites, leading to severe disease. Certain species, like *S. digitata*, can invade the CNS of horses and cause cerebrospinal nematodiasis, leading to ataxia, paralysis, and death [467]. Some species have been reported in the eyes of humans and animals, causing ocular filariasis [468].

Setaria spp. causing animal infections have been reported in several regions in Africa including Burkina Faso [469], The Gambia [470], Egypt [471], Nigeria [350], Kenya [472], Ethiopia [473], Namibia [474], South Africa [475], Zimbabwe [476], Tanzania [477], CAR [478], Chad [478], Cameroon [478], Senegal [269], Guinea Bissau [479], Côte-d'Ivoire [480], Morocco [481], and Somalia [482] (Figure 4).

2.6.5.2. *Dipetalonema* and *Acanthocheilonema* Species

Dipetalonema and *Acanthocheilonema* are both genera of filarial nematodes belonging to the family *Onchocercidae* [483]. While they share similarities as vector-borne parasites that infect mammals, including humans and animals, they have key differences in their taxonomy, morphology, host specificity, and transmission. *Dipetalonema* is a genus of filarial nematodes that are primarily parasitic in domestic animals, particularly dogs, and certain wild mammals [483]. These parasites are known to cause a variety of health issues, though they are often less pathogenic compared to other filarial nematodes. The genus *Dipetalonema* is closely related to other filarial nematodes like *Onchocerca*, *Wuchereria*, and *Brugia* spp., but it has distinct characteristics that differentiate it from these better-known parasites [484].

Several *Dipetalonema* species infect a variety of hosts, primarily dogs, but occasionally other animals. Some of the notable species include, *D. reconditum* commonly found in dogs, and *D. gracile* found in a range of wild animals [485–487].

While infections with *Dipetalonema* species are typically mild, the presence of the parasite can still cause some clinical issues. Infected animals may develop small, non-painful nodules under the skin where adult worms reside. These nodules are usually benign and don't result in severe clinical signs.

Although *Dipetalonema* species are primarily of veterinary concern, there is some evidence suggesting that these parasites may have zoonotic potential, though this is rare [488]. Their role in veterinary parasitology is significant for understanding vector-borne filariasis in domestic animals, especially in terms of diagnostic accuracy. Recent research also focuses on understanding the genetic and ecological relationships between *Dipetalonema* species and other filarial nematodes. This knowledge helps in developing more effective diagnostic techniques, improving treatments, and providing better understanding of their transmission dynamics.

Dipetalonema species causing animal infection in Africa has been reported from Kenya [489], Nigeria [490], Egypt [491], South Africa [492], Namibia [493], Botswana [453], Mozambique [451], Zambia [494], Uganda [495], and Côte d'Ivoire [196] (Figure 4).

2.6.5.3. *Litomosoides* Species

Litomosoides is a genus of filarial nematodes belonging to the family *Onchocercidae*, primarily known for infecting various mammals, including rodents and NHPs [496]. Unlike some other filarial nematodes, *Litomosoides* species are less commonly associated with severe disease in their natural hosts but can be of veterinary and research importance. These parasites are most often studied due to their relevance to veterinary medicine, their role in understanding filarial transmission, and their potential zoonotic importance [497].

Several *Litomosoides* species are known to infect different mammalian hosts, including rodents and other wild animals. Some of the most notable species include, *L. carinii* a species primarily found in wild rodents, especially rats, *L. sigmodontis* and *L. parkeri* [498].

This parasite has been found associated with bats in Africa and reported in South Africa [499], and Madagascar [500] (Figure 4).

2.7. *Thelaziasis*

Thelaziasis is a parasitic infection caused by nematodes of the genus *Thelazia*, commonly known as "eyeworms." These parasites primarily affect the eyes and associated tissues of mammals, including humans, causing conjunctivitis, excessive tearing, and ocular discomfort [501]. The disease is transmitted by dipteran flies, which serve as intermediate hosts. There are several species of *Thelazia* infect different hosts, including *T. callipaeda* – the most common species affecting humans, dogs, cats, and other mammals, *T. californiensis* – mainly infects animals, occasionally reported in humans, and *T. gulosa* – primarily affects cattle but has been reported in humans [502,503].

Thelaziasis is found worldwide but is more prevalent in regions where the intermediate fly vectors are abundant. *T. callipaeda* is the most significant species in human infections, with cases reported in China, India, Russia, Europe, and recently in South America [504–506]. The disease is zoonotic, with dogs and other mammals acting as reservoirs. Although the fly transmitting the larvae is not through inoculation, the parasite larvae is mechanically transferred to the host when the fly is feeding on the host tears. The disease mainly characterized by excessive tearing (epiphora), Conjunctivitis, Ocular irritation and rubbing, Photophobia (light sensitivity), and Corneal ulcers and/or Blurred vision in severe infections

While rare in humans, Thelaziasis is emerging as a public health concern due to increased pet travel and global climate changes influencing vector distribution. Veterinarians and public health officials should be aware of its zoonotic potential and implement preventive measures.

Although, cases of human Thelaziasis is mainly reported in Asia [507–509] and Europe [510], in Africa human cases are rare, however, animal Thelaziasis has been reported in Zambia [511], Senegal [512,513], Ethiopia [514], Kenya [515], Nigeria [516], Egypt [517], DRC [518], Namibia [519], Uganda [520], and Tanzania [521] (Figure 5).

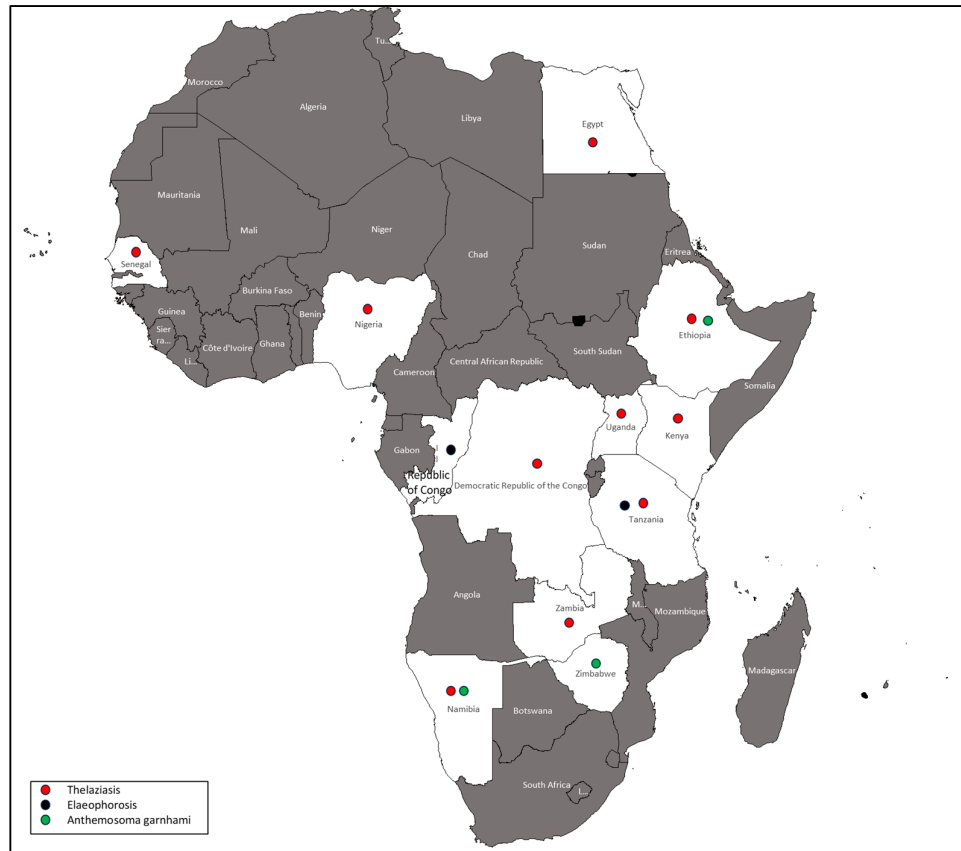


Figure 5. Map of Africa showing countries where Thelaziasis, Elaeophorosis, and *Anthemosoma garnhami* diseases records of occurrence has been documented. Countries highlighted in grey color indicate unavailable data about Thelaziasis, Elaeophorosis, or *Anthemosoma garnhami*.

2.8. Elaeophorosis

Elaeophorosis is a parasitic disease caused by the nematode *Elaeophora* species which live attached to the interior surfaces of major arteries, veins and/or heart chambers in the animal host following inoculation by blood-feeding horse flies [522]. The species of *Elaeophora* have been found in many regions including Africa, Asia, Europe, and North America continents [523–525]. Although the disease has not been reported frequently in Africa, this parasite has been considered as a potential significance contributing factor to the morbidity and mortality in the Minnesota moose population in the USA [522]. Previous reports of this disease in Africa were from Tanzania [358], and Republic of Congo [526] (Figure 5). Although this disease has not been considered as human risk, however, the economic burden placed by this disease cannot be neglected.

2.9. Emerging Parasitic Disease

2.9.1. *Anthemosoma garnhami*

Anthemosoma is a genus of parasites of the phylum *Apicomplexa*. There is only one species recognized in this genus - a parasite of mammals [527], the parasite recognized as the African rodent piroplasm. Although Ixodid ticks considered as vectors of piroplasms, however, experiments failed to demonstrate successful transmission. meanwhile, this species was reported to infect immunocompromised patients cause disease similar to malaria [528]. *A. garnhami* is an erythrocytic murine parasite, first described in spiny mice (*Acomys percivali*) in Ethiopia in 1969 [529], The parasite was identified again in rodents in Namibia [530]. Recently, in an HIV-positive man from Zimbabwe who is living in South Africa was treated for several medical conditions with no signs or symptoms

being rolled out, eventually microscopic examination aided with molecular testing detected the presence of *A. garnhami* parasites [528] (Figure 5).

3. Current Knowledge of Prevalence and Diversity of Arthropod-Borne Parasitic Diseases in Africa and Its Implications in One Health

The current knowledge of the prevalence and diversity of arthropod-borne parasitic diseases in Africa provides crucial insights that inform public health strategies, veterinary interventions, and policy-making. Arthropod-borne parasitic diseases, including malaria, leishmaniasis, lymphatic filariasis, trypanosomiasis, onchocerciasis, babesiosis, and mansonellosis, significantly impact human and animal populations, causing high morbidity, economic losses, and hampering socio-economic development [531]. The extensive dataset on their distribution, transmission patterns, and genetic diversity enhances our ability to develop targeted control measures, improve diagnostics, and assess the efficacy of existing interventions.

Understanding the geographical distribution of these diseases is essential in identifying high-risk regions, endemic areas, and potential hotspots of transmission [532]. Many of these parasites are restricted to specific ecological zones where their vectors thrive, such as the *Anopheles* mosquitoes for malaria in tropical and subtropical Africa, the *Glossina* species (tsetse flies) for trypanosomiasis in sub-Saharan regions, and the *Phlebotomus* sandflies for leishmaniasis in arid and semi-arid areas [533–535]. Mapping disease prevalence at national and regional levels allows policymakers and researchers to implement vector control programs tailored to local ecological conditions. This knowledge is particularly vital for combating vector expansion due to climate change, deforestation, and human activities that create new vector habitats.

The integration of current knowledge into vector control strategies is crucial for reducing the transmission of arthropod-borne parasitic diseases. Strategies such as ITNs, IRS, and larval source management have been instrumental in reducing malaria transmission [536]. However, insecticide resistance among mosquito populations poses a growing challenge, emphasizing the need for updated surveillance data on vector resistance patterns [537]. Similarly, the control of tsetse flies through the sterile insect technique (SIT) and trapping methods has contributed to reducing the burden of African trypanosomiasis, but sustained efforts are required to prevent reemergence [538]. For leishmaniasis and onchocerciasis, vector control measures, including insecticide applications and community-directed interventions, have been effective in reducing disease burden in endemic areas [539].

The One Health approach, which integrates human, animal, and environmental health, is essential for addressing the complex epidemiology of arthropod-borne parasitic diseases. Many of these diseases have zoonotic reservoirs, with wildlife and livestock acting as important hosts in transmission cycles [540]. For instance, animal reservoirs of *Leishmania* species contribute to human infections [541], while cattle serve as reservoirs for zoonotic *Trypanosoma* species [542]. Understanding the interplay between human and animal infections is critical for designing sustainable control measures that account for all transmission pathways. Veterinary surveillance and livestock management strategies should be incorporated into public health policies to reduce disease spillover from animals to humans. Additionally, interdisciplinary collaboration among epidemiologists, entomologists, veterinarians, and public health officials strengthens the response to emerging and reemerging threats.

Climate change and environmental modifications are altering the epidemiology of arthropod-borne parasitic diseases, necessitating continuous monitoring and adaptive control strategies. Changes in temperature, humidity, and precipitation patterns influence vector distribution, breeding, and survival rates, potentially leading to the emergence of diseases in previously non-endemic areas. Rising temperatures have been linked to the expansion of malaria vectors into highland regions, while altered rainfall patterns affect the population dynamics of sandflies and tsetse flies. Deforestation, urbanization, and agricultural expansion create new habitats for vectors, increasing human exposure to infected arthropods [543]. Predictive modeling and climate-based risk

assessments are essential tools for anticipating disease outbreaks and implementing proactive control measures before large-scale transmission occurs.

The application of geospatial technologies and big data analytics in disease surveillance has revolutionized the monitoring and control of arthropod-borne parasitic diseases. Geographic Information Systems (GIS), remote sensing, and real-time epidemiological data allow for precise tracking of disease outbreaks, vector movements, and environmental changes affecting transmission dynamics. These tools enable researchers and public health officials to visualize disease patterns, identify emerging hotspots, and allocate resources efficiently [544]. Mobile health (mHealth) applications and community-based reporting systems further enhance disease monitoring by providing real-time data on symptoms, cases, and vector presence [545]. Strengthening disease surveillance systems through technology-driven approaches improves early detection and rapid response efforts.

Public health interventions targeting behavioral and community engagement are fundamental to the success of disease control programs. Community education on preventive measures, early diagnosis, and treatment-seeking behavior is crucial for reducing disease burden [546]. Cultural and socio-economic factors influence health-seeking behaviors, and addressing barriers such as stigma, lack of awareness, and limited healthcare access is necessary for effective disease management. Strengthening healthcare infrastructure, expanding access to diagnostic and treatment facilities, and ensuring the availability of essential medications are vital components of comprehensive disease control efforts. Collaboration with local communities and stakeholders fosters sustainable interventions that align with local contexts and priorities.

The implications of this knowledge within the One Health framework are far-reaching, as arthropod-borne parasitic diseases often affect both human and animal populations. By adopting an integrated approach that considers the interconnectedness of ecosystems, researchers and policymakers can implement more effective disease control measures. Understanding how climate change, land use, and human-animal interactions influence vector populations can help predict and mitigate outbreaks before they escalate.

One Health strategies emphasize the need for collaborative efforts among multiple disciplines, including human medicine, veterinary science, environmental science, and public health. Cross-sectoral cooperation enables the sharing of surveillance data, fostering early detection of disease outbreaks, and implementing coordinated response strategies. This approach is particularly crucial in rural and pastoralist communities, where human and livestock health are closely linked [547].

Zoonotic potential plays a critical role in the persistence and transmission of many arthropod-borne parasitic diseases. For example, certain *Leishmania* species have animal reservoirs, making eradication difficult without a comprehensive approach that includes both human treatment and vector control in animals. Similarly, bovine trypanosomiasis has economic repercussions in agriculture and livestock health, impacting food security and livelihoods [548]. Addressing these concerns through an integrated approach ensures that disease control efforts are sustainable and equitable.

Disease surveillance systems must remain effective even after a disease has been reported as eliminated from a region, as reemergence remains a significant threat. A prime example is African trypanosomiasis, which reemerged in Ethiopia despite efforts to control and eliminate it [549]. Such occurrences underscore the need for continuous monitoring, as factors like climate change, vector migration, and human and animal movements can lead to the resurgence of previously controlled diseases. This review provides comprehensive evidence of diseases recorded and reported in both humans and animals, reinforcing the interconnected nature of human and animal health. The One Health approach is essential in understanding the dynamics of disease transmission, particularly for zoonotic and vector-borne diseases. The emergence of new human infections from traditionally animal-restricted parasites highlights the need for vigilance. For instance, *A. garnhami*, a parasite historically known to infect animals, poses a potential risk to humans if transmitted through vectors [528]. Similarly, *O. lupi*, initially considered an animal parasite, is increasingly recognized as a cause

of human infection [550]. Such examples emphasize that disease surveillance should not only track known pathogens but also identify and assess emerging threats. The risk of human-animal shared diseases is growing due to habitat encroachment, globalization, and climate-driven shifts in vector distributions. Early detection and prompt response to these threats require integrated surveillance systems that combine veterinary, environmental, and human health data. Strengthening these systems is crucial to prevent outbreaks before they escalate into significant public health crises. By continuously monitoring disease patterns, even in regions where a disease is thought to be eliminated, we can mitigate the risks associated with reemergence and novel pathogen spillover.

4. Conclusions

The current knowledge of the prevalence and diversity of arthropod-borne parasitic diseases in Africa is invaluable for shaping public health policies, guiding research priorities, and enhancing disease control strategies. Integrating epidemiological data, genetic studies, vector control measures, climate change adaptation strategies, and technological advancements improves the effectiveness of interventions. A holistic approach that combines human and animal health perspectives, community engagement, and evidence-based policymaking is essential for mitigating the impact of these diseases and safeguarding public health in Africa. Continued investment in research, surveillance, and healthcare infrastructure will be crucial in achieving long-term disease control and elimination goals.

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Abbreviations

The following abbreviations are used in this manuscript:

CAR	Central African Republic
CL	Cutaneous Leishmaniasis
CNS	central nervous system
DRC	Democratic Republic of the Congo
GIS	Geographic Information Systems
HAT	Human African trypanosomiasis
IRS	indoor residual spraying
ITNs	insecticide-treated bed nets
mHealth	Mobile health
NHPs	non-human primates
SIT	sterile insect technique
VL	Visceral Leishmaniasis

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