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Review

A Narrative Overview of Canine Babesiosis in Africa

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Abstract

Canine babesiosis is a vector-borne disease of dogs with a worldwide distribution, presenting varying clinical signs depending on the host, parasite strain and climatic factors. Beyond companionship, dog meat serves as delicacy and is also used for zootherapy in some African communities. In this study, we collated and analyzed molecular biology-based diagnostic data on *Babesia* species of dogs in Africa in order to elucidate the epidemiological factors of the disease on the continent. Four *Babesia* species—*B. rossi*, *B. vogeli*, *B. gibsoni* and *B. canis*—were detected in Africa based on the results from 40 studies that involved the screening of 9435 dog blood samples from 83 study locations. *Babesia rossi* was the most commonly reported (aggregate detection rate = 7.7%) and was detected in samples from all the African regions except northern Africa. *Babesia vogeli* was the second most commonly reported (aggregate detection = 4.8%) and was detected in all of the African sub-regions. There were few reports of *B. gibsoni* (0.6%) in the southern and western African regions, and a single case of *B. canis* in an untraveled Nigerian dog. So far, there were no reports of *Babesia coco*, *Babesia conradae* or *Babesia vulpes* (*Babesia annae*, *Babesia* microti-like) in any of the African countries that have been confirmed by a molecular method. This study presents a synopsis of canine babesiosis in Africa, and provides an overview of common clinical signs, etiologies and risk factors that will serve as a quick guide to veterinarians to achieve timely tentative diagnosis.

Keywords: dog; *Babesia* species; clinical signs; risk factors; Africa

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1. Introduction

Canine babesiosis caused by parasites of the genus *Babesia* (Apicomplexa: Babesiidae) is primarily transmitted by ixodid ticks and occasionally through non-vectorial routes and affects dogs across the globe, leading to varying clinical manifestations depending on the host, parasite and ecological factors [1,2]. Currently, there are at least four large (*B. canis*, *B. rossi*, *B. vogeli*, *B. coco*) and three small (*B. gibsoni*, *B. conradae* and *B. vulpes*) *Babesia* species that infect dogs globally [1,3]. Findings from natural or experimental studies have ascribed varying pathogenicity to the different *Babesia* species [4–6]. However, under clinical condition, similar disease features are manifested broadly across the genus, suggesting that there might be a complex interplay between several intrinsic and extrinsic factors which ultimately determine the severity of the disease [7–9].

Dogs play a vital role in socio-cultural and economic life in many societies in Africa. Apart from being renowned human companions, they have been trained to perform several tasks such as hunting, herding, security, sports, etc., with psychological and economic benefits to man [10]. Furthermore, in some communities in Africa, besides being considered a delicacy, dog meat is also used for zootherapy [11]. Additionally, dog breeding is a lucrative business in some communities in Africa, providing employment and a source of income. This has led to importation of foreign breed of dogs to meet special needs or specific purposes [12]. However, disease conditions like babesiosis constitute a serious threat to the survival of the imported dogs due to immunological naivety [13,14]. Therefore, understanding the epidemiology of canine babesiosis in the local context is desirable as it will serve as a guide to clinicians in achieving prompt diagnosis and to institute appropriate therapeutic measures.

Molecular biology-based diagnostic methods are being increasingly used in Africa for research, and sometimes to aid in the diagnosis and treatment of canine babesiosis. These methodologies are reputed to provide superior results compared to microscopy due to their capacity to distinguishing between *Babesia* spp. [1–3]. Therefore, the purpose of this synopsis is to provide a concise overview of canine babesiosis in Africa in relation to the occurrence, etiologies, clinical features and risk factors of the disease and to suggest areas for further studies.

2. Materials and Methods

To generate the data used in this study we performed a literature search on molecular studies of canine babesiosis in Africa using public databases: PubMed, Google Scholar, Science Direct, African Journals Online (AJOL), CABI, Web of Sciences, and SCOPUS using the combination of the following terms: "canine babesiosis" or "*Babesia rossi*" or "*Babesia vogeli*" or "*Babesia gibsoni*" or "*Babesia* canis" and "Africa" or "specific country name" with no date restrictions to obtained information on the *Babesia* species infecting dogs in Africa. Full-text articles and abstracts were reviewed and those with clearly described methodology and extractable results were considered eligible. We included original studies with samples sourced in Africa that reported at least one of the following outcomes: (a) prevalence studies of *Babesia* species using molecular biology-based methods and (b) case reports of *Babesia* species using molecular identification methods. Non-original articles such as editorials, commentaries or studies without sufficient methodological detail were excluded. Available literature published in the English language up to 5 February 2025 was included in the study. Records retrieved from multiple databases were de-duplicated prior to screening, and when multiple publications appeared to describe the same dataset, the most comprehensive report was retained to avoid duplication. The data were extracted, tabulated and used to plot distribution maps and identify the risk factors of canine babesiosis in Africa. Given the heterogeneity in study designs, outcomes, and reporting standards, a narrative synthesis approach was adopted to develop this synopsis.

3. Prevalence of Babesia Species in Africa

Overall, data on canine babesiosis obtained by molecular biology-based methods was available from 19 African countries. The information was generated from the results of over 40 studies in which 9435 blood samples from 83 study areas were screened for *Babesia* spp. DNA in either research survey studies or case reports (Figure 1, Table 1). These results were obtained using molecular biology techniques to detect the DNA of *Babesia* spp. in dog blood samples. The studies employed highly sensitive and specific methods such as the Reverse Line Blot Hybridization (RLB), Polymerase Chain Reaction (PCR) and a targeted next generation sequencing (tNGS) to amplify and sequence the conserved region

of 18S rRNA gene of *Babesia* spp. These techniques have high sensitivity and specificity compared to the classical diagnostic methods that are popular in most veterinary practices in African. The 18S rRNA gene is highly conserved among *Babesia* species and is reputed as a valuable target for the screening of samples to detect the presences of *Babesia* species DNA. Furthermore, the analyses of the nucleotide sequences provided additional confirmation of the specific *Babesia* spp. through phylogenetic analysis. However, in rare cases the identity of the infecting *Babesia* could not be resolved, either due to poor quality sequence data, or possibly a novel variant that does not have matching sequences in the public databases. In such instances, the isolates were referred to as *Babesia* sp. Three of such cases, one of each reported in Angola, South Africa and Nigeria were excluded from the final dataset used for the analyses in this study.

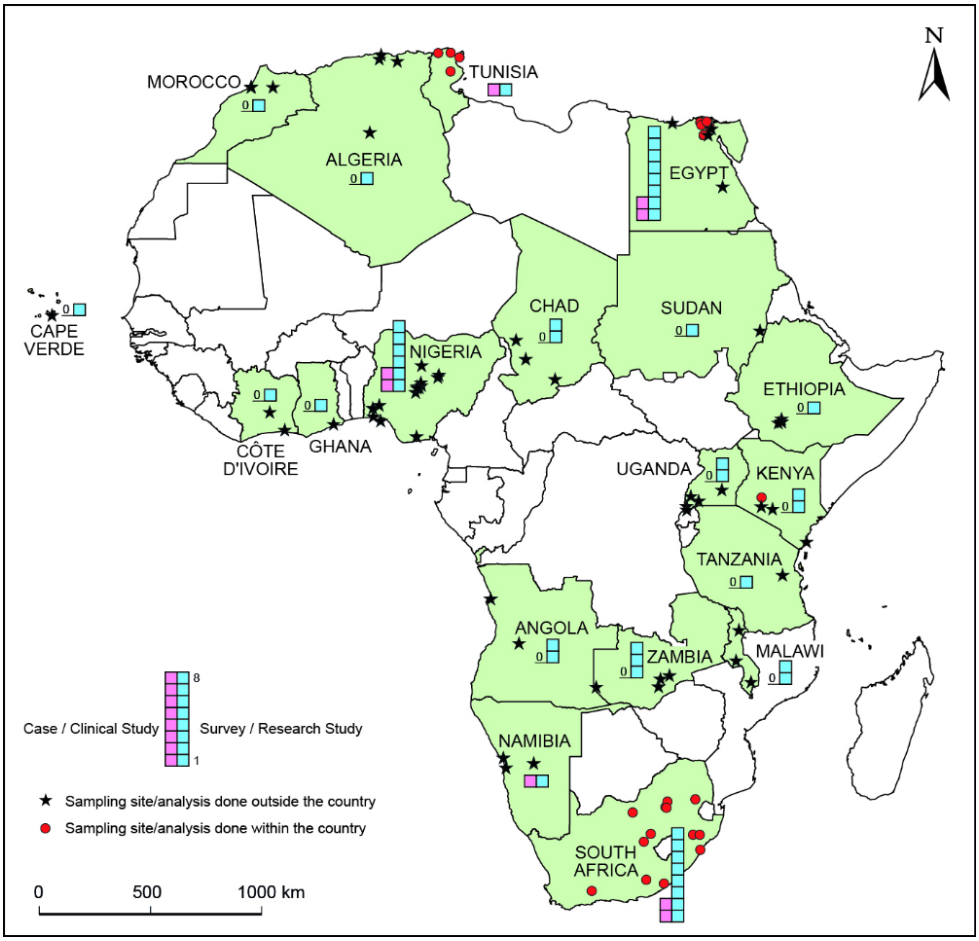

Figure 1. Sampling and study locations (green) and type of study on canine babesiosis in Africa.

Of note is that, although the samples originated from Africa, the analyses were mostly conducted outside the continent, except for studies conducted in South Africa and some in Tunisia and Egypt (Figure 1). This can be attributed to the lack of availability of modern diagnostic facilities in most veterinary settings in African countries. The results obtained by PCR and nucleotide sequence analysis showed that four *Babesia* species—*B. rossi*, *B. vogeli*, *B. gibsoni*, and *B. canis*—were detected in dogs in Africa in 1241 out of 9435 samples analyzed (Table 2).

Table 1. Studies reporting *Babesia* spp. in dogs in Africa using molecular biology-based diagnostic methods.

Country/Study Location	Sample Size	Study Type	Health Status/Clinical Signs	*Babesia* Species Detected	Risk Factors	Diagnostic Method	Reference
Angola: Luanda	103	Research	Anorexia, weight loss, icterus, fever, tick infestation, anemia, dehydration, enlarged lymph node	*B. vogeli*, *B. gibsoni*,	Breed	PCR and sequencing	Cardoso et al., 2016 [15]
Tchicala-Tcholoanga. Huambo provine (Mbave, Sede, Sambo and Samboto)	85	Research	Apparently healthy	*B. vogeli*, *B. rossi*	Ticks	PCR-RLB	Sili et al., 2021 [16]
Algeria: Kabylia	227	Research	fever, anorexia, lymphadenopathy, body weight loss, lethargy	*B. vogeli*	Age (Juveniles), sex (females)	PCR and sequencing	Medkour et al., 2020a [17]
Egypt: Giza and Cairo	13	Clinical study	Fever, anorexia, anemia, ticks, enlarged Lymph node	*B. vogeli*	Breed, age	Seminested PCR	Salem & Farag, 2014 [18]
Giza and Cairo	208	Research	Ticks, anemia, emaciation, jaundice, hemoglobinuria	*B. vogeli*	None	Microscopy, PCR & sequencing	Hegab et al., 2022 [19]
Giza, Kafr El Sheik, Qalyubia and Gharbia	275	Research	unspecified	*B. vogeli*	Sex, age, breed, ticks and housing type	PCR & sequencing	Selim et al., 2022 [20]
Sharkiato and Dakahlia	75	Clinical study	Anorexia, fever, weakness, pale mucosa, ticks, hemoglobinuria	*B. vogeli*	Age, tick infestation, Breed	Microscopy and PCR	El-Neshwy et al., 2020 [21]
Cairo	203	Research	NA	*B. vogeli*	none	PCR and sequencing	Abdullah et al., 2021 [22]
Giza	116	Research	Anorexia, weakness, ticks, fleas	*B. vogeli*	NA	PCR and sequencing	Izenour et al., 2022 [23]
Luxor	100	Research	Anemia, ticks, diarrhea, emaciation,	*B. vogeli*	Ticks	PCR and sequencing	Mahmoud et al., 2024 [24]
Cairo and Giza	800	Research	fever, emaciation, jaundice, and red urine.		Age, sex	Microscopy, PCR and sequencing	Khalifa et al., 2025 [25]
Sharkia	49	Research	fever, dehydration, icterus, weakness, anorexia, pale mucosa and red urine	*B. vogeli*	Ticks	RT-HRM PCR and sequencing	Gad et al., 2023 [26]
Malawi: Muzuzu, Lilongwe and Blantyre	209	Research	Anemia, haematuria, enlarged lymph node, ticks	*B. rossi*, *B. vogeli*	Sex, local breed, ticks	PCR and sequencing	Chatanga et al., 2021 [27]
Morocco: Rabat-Sale', Fes and Sale'	144	Research	Ticks	*B. vogeli*	NA	PCR and sequencing	Zahri et al.,2025 [28]
Cape Verde: Praia	130	Research	Apparently normal	*B. vogeli*	NA	PCR and sequencing	Gotsch et al., 2009 [29]
Chad: Moyen Chari	428	Research	Apparently healthy	*B. vogeli*	NA	PCR and sequencing	Haynes et al., 2024 [30]
Mayo Kebbi est, Chari Baguirmi south	1202	Research	Apparently healthy	*B. vogeli*	NA	tNGS	Daniel et al., 2025 [31]

Table 1. *Cont.*

Country/Study Location	Sample Size	Study Type	Health Status/Clinical Signs	*Babesia* Species Detected	Risk Factors	Diagnostic Method	Reference
Cote d'Ivore: Abijan, Yamoussoukro	123	research	Apparently healthy	*B. vogeli*	Ticks	PCR and sequencing	Medkour et al., 2020b [32]
Ghana: Greater Accra	97	Research	Apparently healthy	*B. rossi*	NA	PCR and sequencing	Heylen et al., 2021 [33]
Kenya: Nairobi, Mombasa, Nakuru	143	Research	Shelter dogs with different health condictions	*B. rossi* *B. vogel*	NA	PCR and sequencing	Ngoka et al., 2021 [34]
South Africa: Pretoria/Guateng	1	Case report	Apparently healthy imported from USA	*B. gibsoni*	Breed	PCR-RLB	Matjila et al., 2007 [35]
Zenzele	323	Research		*B. rossi*	Ticks	PCR-RLB	Morters et al., 2020 [36]
Bloemfontein, East London, Durban, Johannesburg, OVAH	336	Research	Note specified	*B. rossi* *B. vogeli*	Breed, age	PCR-RLB	Matjila et al., 2004 [37]
Gauteng, Mpumalanga, KwaZulu Natal, Western Cape	1138	Longitudinal study	Tick, anemia, anorexia	*B. rossi* *B. vogeli*	Ticks, sex, breed	PCR-RLB	Matjila et al., 2008 [38]
OVAH	75	Clinical study	Fever, anorexia, weakness	*B. rossi*	Ticks, breed	PCR-RLB	Shabangu et al., 2021 [39]
Sudan: Barbar El Fugara	78	Research	Ticks	*B. rossi* *B. vogeli*	NA	PCR and sequencing	Oyamada et al., 2005 [40]
Tunisia: Zaga, Sidi Thabet, Sama'a, Bouhajla	332	Research	Ticks	*B. vogeli*	NA	PCR-RLB	M'ghirbi and Bouattour 2008 [41]
Sidi Thabet	99	Clinical studies	Apathy, dehydration, fever, anorexia, weight loss, anemia,	*B. vogeli*	NA	PCR and sequencing	Bouattour et al., 2021 [42]
Uganda: Queen Elizabeth national park, Bwindi impenetrable national park, Mgahinga Gorilla park	38	Research	Ticks, fleas	*B. rossi*	NA	PCR and sequencing	Proboste et al., 2015 [43]
Kampala, Wakiso, Mbarara, Iganga	79	Research	NA	*B. rossi*	NA	PCR and sequencing	Heylen et al., 2021 [33]
Nigeria: Jos	100	Research	Anorexia, fever, pale mucous membranes, rough hair coat, emaciation and weakness	*B. rossi*	Ticks	PCR/RLB	Adamu et al., 2014 [44]
	1	Case report	anorexia, hemoglobinuria, fever, tick infestation and general malaise	*B. canis*, *B. rossi*	Breed	PCR and sequencing	Kamani et al., 2010 [45]
Jos, Port Harcourt, Kaduna	181	Research	Tick infestation, anemia, weakness, pyrexia, anorexia haemoglobinuria.	*B. rossi* *B. vogeli*	Breed, age, ticks	PCR and sequencing	Kamani et al., 2013 [12]
Abeokuta	209	Research	Apparently heathy	*B. rossi*	NA	PCR and sequencing	Takeet et al., 2017 [46]
	104	Research	Apparently healthy	*B. rossi*	NA	PCR and sequencing	Hirata et al., 2022 [47]
	100	Research	Apparently healthy	*B. rossi*	Ticks	PCR and sequencing	Heylen et al., 2021 [33]

Table 1. *Cont.*

Country/Study Location	Sample Size	Study Type	Health Status/Clinical Signs	*Babesia* Species Detected	Risk Factors	Diagnostic Method	Reference
Ibadan	150	Research	Anorexia, apathy, emesis, anemia, splenomegaly, ectoparasitism, diarrhea, fever	*B. rossi*, *B. vogeli*	NA	PCR and sequencing	Gruenberger et al., 2023 [48]
FCT	1	Case report	Anorexia, depression, icterus	*B. vogeli*	NA	PCR and sequencing	Abalaka et al., 2018 [49]
	480	Research	Apparently healthy	*B. vogeli*	Age, season	PCR and sequencing	Obeta et al., 2020 [50]
Nigeria: Not specified	400	Research	Not specified	*B. rossi*, *B. vogeli*	Age, ticks	PCR and sequencing	Sasaki et al., 2007 [51]
Zambia: Shangombo, Mazabuka, Lusaka, Monze	247	Research	NA	*B. rossi*, *B. vogeli*	NA	PCR and sequencing	Qiu et al., 2018 [52]
Lusaka	363	Clinical study	Anorexia, fever, anemia, weakness, ticks, icterus	*B. rossi*, *B. gibsoni*	Ticks, breed, age	Microscopy, PCR	Nalubamba et al., 2015 [53]
Ethiopia: Arba Minch, Chencha, Arba Minch Zuria, Geres	273	Research	asymptomatic	*B. rossi*	Age	PCR and sequencing	Tadesse et al., 2023 [54]
Namibia: Walvisbaai, Hettiesbaai	70	Research	Apparently healthy	Negative	NA	PCR and sequencing	Heylen et al., 2021 [33]

3.1. Etiologies

Babesia rossi, the most virulent of the canine Babesias, was the most frequently reported followed by *B. vogeli*, *B. gibsoni* and *B. canis* (Table 2, Figure 2). Regionally, data were available from four countries in North Africa. In this sub-region, only *B. vogeli*, which is considered the least pathogenic, was detected in 277 of the 2693 blood samples examined. Aggregate reported detection indicated 3.5% in Morocco, 4.5% in Tunisia, 11.4% in Egypt and 13.2% in Algeria (Table 2, Figure 2). In the east African region, data obtained from 1038 blood samples from 18 locations in six countries indicated that *B. rossi* was detected in all the six countries with aggregate detection rates of 1.0, 3.3, 6.4, 7.2, 8.6 and 23.4% in Tanzania, Ethiopia, Sudan, Uganda, Kenya and Malawi, respectively. In addition, *B. vogeli* was detected in 0.8, 2.9 and 2.6% of samples that were examined in Kenya, Malawi and Sudan, respectively (Table 2, Figure 2). Information was available from studies conducted on 2627 blood samples from 22 locations in four southern African countries of Angola, Namibia, South Africa and Zambia. *Babesia rossi* was the most commonly detected species (21.2%) followed by *B. vogeli* (2.8%) and *B. gibsoni* (2.2%). Aggregate detection of *B. rossi* was 16.0, 27.2 and 7.2%, respectively for Angola, South Africa and Zambia. In Namibia, *B. vogeli* was reported in a case report while all 70 samples screened in one study were negative for *Babesia* species (Table 2, Figure 2). In West Africa, data obtained from the analysis of 1447 blood samples collected in 18 locations from four countries showed that *B. rossi*, *B. vogeli* and *B. canis* were detected in 5.3, 4.3 and 0.07%, respectively, of samples analyzed. *Babesia vogeli* was the only species reported in Cape Verde and Cote d' Ivore with aggregate detection rate of 3.8 and 1.6%, respectively, while only *B. rossi* was reported in 1.0% of samples in Ghana (Table 2, Figure 2). The only report of *B. canis* on the continent with available nucleotide sequences was from an untraveled Nigerian dog (Table 1, Figure 2). Data were available for only one central African country, Chad. Information gathered from

the results of the analysis of 1630 samples from four locations using tNGS revealed the presence of only *B. vogeli* in 2.0% of the samples examined (Tables 1 and 2, Figure 2). So far, there were no reported identification of *Babesia coco*, *Babesia conradae* or *Babesia vulpes* (*Babesia annae*, *Babesia* microti-like) in any of the African countries that is confirmed by molecular methods. Although, their putative vector(s) are not definitively known, the non-detection of these pathogens may be related to the absence of their vector(s) on the continent. Another possibility is that they might have been overlooked or misdiagnosed due to non-availability or infrequent use of advanced detection techniques in the routine diagnosis of canine babesiosis in most veterinary practices in Africa. This calls for vigilance and deliberate efforts to probe for their presence on the continent.

Table 2. Aggregate detection of *Babesia* species of dogs in Africa.

Region	Country	No. of Samples	*Babesia* Species (Number) Detected (Aggregate Detection)				Total (%)
			B. vogeli	*B. rossi*	*B. gibsoni*	*B. canis*	
North	Tunisia	332	15 (4.5)	0	0	0	15 (4.5)
	Morocco	144	5 (3.5)	0	0	0	5 (3.5)
	Algeria	227	30 (13.2)	0	0	0	30 (13.2)
	Egypt	1990	227 (11.4)	0	0	0	227 (11.4)
Subtotal		2693	277 (10.3)	0	0	0	277 (10.3)
East	Kenya	244	2 (0.8)	21 (8.6)	0	0	23 (9.4)
	Tanzania	96	0 (0)	1 (1.0)	0	0	1 (1.0)
	Malawi	209	6 (2.9)	49 (23.4)	0	0	54 (25.8)
	Ethiopia	273	0 (0)	9 (3.3)	0	0	9 (3.3)
	Uganda	138	0 (0)	10 (7.2)	0	0	10 (7.2)
	Sudan	78	2 (2.6)	5 (6.4)	0	0	7 (9.0)
Subtotal		1038	10 (0.9)	95 (8.5)	0	0	105 (9.4)
South	Angola	188	26 (13.8)	30 (16.0)	1 (0.5)	0	57 (30.3)
	South Africa	1758	39 (2.2)	478 (27.2)	1 (0.06)	0	518 (29.5)
	Namibia	71	1 (1.4)	0	0	0	1 (1.4)
	Zambia	610	7 (1.1)	47 (7.7)	57 (9.3)	0	111 (18.2)
Subtotal		2627	73 (2.8)	555 (21.2)	59 (2.2)	0	687 (26.2)
West	Cape Verde	130	5 (3.8)	0	0	0	5 (3.8)
	Cote d'Ivore	123	2 (1.6)	0	0	0	2 (1.6)
	Nigeria	1097	56 (5.1)	75 (6.8)	0	1 (0.09)	132(12.0)
	Ghana	97	0	1 (1.0)	0	0	1 (1.0)
Subtotal		1447	63 (4.3)	76 (5.3)	0	1 (0.07)	140 (9.7)
Central	Chad	1630	32 (2.0)	0	0	0	32 (2.0)
Aggregate detection		9435	455 (4.8)	726 (7.7)	59 (0.6)	1 (0.01)	1241 (13.2)

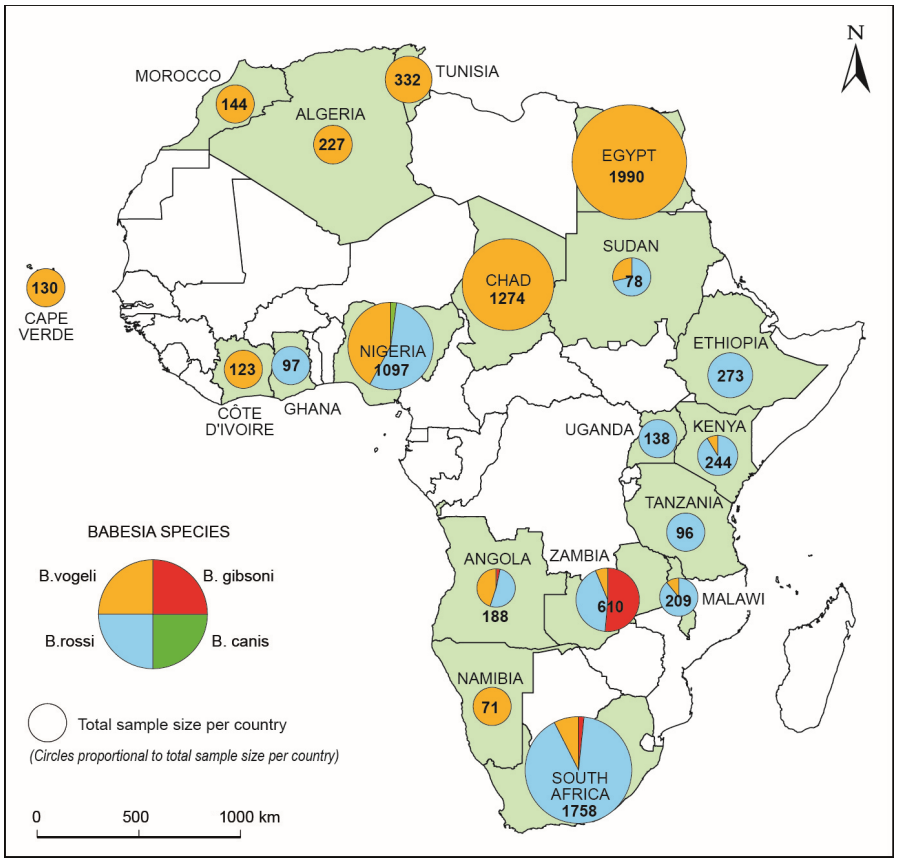

Figure 2. Type and distribution of *Babesia* species infecting dogs in Africa.

3.2. Clinical Features of Canine Babesiosis in Africa

The frequently reported clinical signs associated canine babesiosis in Africa include anorexia, anemia, weakness, fever and tick infestation (Figure 3). Although there is no comparative evidence for species-specific infections, reported clinical signs appear to be broadly manifested across the genus. Therefore, these signs were not limited to the infection due to a particular *Babesia* species, as they were manifested by dogs in North Africa where only *B. vogeli*, the supposedly mild species, was reported [25,42]. This might be attributed to the fact that natural infections of dogs with babesiosis seldom occur as a single entity, thus complicating the clinical manifestations [17,22,25,28,42]. Furthermore, the severity of the clinical signs varies, with fulminating cases attributed to the virulent *B. rossi* infections. Although there are reports of the detection of the DNA of *B. rossi* in apparently healthy dogs, suggesting that *B. rossi* infection does not always result in fulminating cases [16,33,47], this finding underscores the need for further investigation on the genetic variability in the strains of *B. rossi* circulating in different parts of the world, considering the involvement of different tick vectors. The frequent co-occurrence of tick-borne pathogens infection of dogs in Africa may serve as a classical example of the involvement of multifarious factors that lead to the diverse clinic-pathological findings [30,31]. Similar pattern of weakness, anorexia, fever, and pale mucous membranes have been reported as the main clinical signs of *B. canis* and *B. gibsoni* infections outside of Africa [55]. Indeed, these clinical findings were the key features of canine babesiosis globally [8]. Therefore, it appears that what needs to be considered in the evaluation of canine babesiosis is the intensity of the clinical signs and the demography of infected individuals rather than only the *Babesia* species involved.

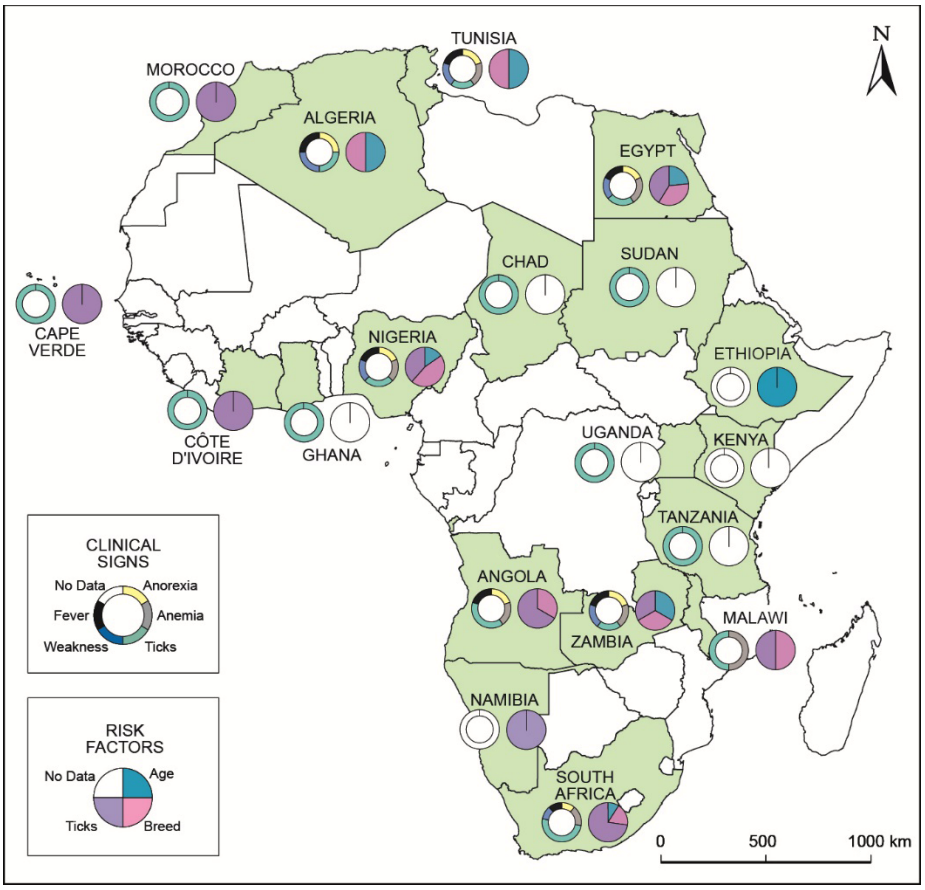

Figure 3. Clinical signs and risk factors of canine babesiosis in Africa.

3.3. Risk Factors of Canine Babesiosis in Africa

Risk factors of canine babesiosis as reported by various authors are presented herein. Tick infestation is a common risk factor for canine babesiosis in Africa (Figure 3). This finding agrees with reports from different African countries [24,27,43,50,53]. Indeed, the distribution pattern of *Babesia* species that were detected in the various regions mirrored the recognized occurrence of their tick vectors on the continent [56,57]. Apparently, *B. vogeli* was detected in all the regions and is the only species reported in the North African countries (Figure 2). This aligns with the ubiquitous distribution of *Rhipicephalus linnaei* the reputed vector of *B. vogeli* on the continent. However, the non-detection of this pathogen in some countries in the eastern and western regions could be due to the small sample size or the use of *B. rossi* specific primers as was the case in Tanzania [33]. Surprisingly, despite being juxtaposed between South Africa and Angola where *B. rossi* infection and the *Haemaphysalis* tick vectors are common, there was no report of this pathogen in any of the 71 samples screened in Namibia [33,58]. A recent survey and screening of ticks collected from ruminants and dogs at the Angola-Zambian border, for VBPs did not yield any *Haemaphysalis* tick or *Babesia* species of dogs [52]. Therefore, more studies are needed to determine the true status of this pathogen in Namibia and the sub-region. The western and southern regions record the presence of several *Babesia* species: *B. rossi*, *B. vogeli*, *B. gibsoni* and *B. canis* (Table 1, Figure 2). Various reasons have been advanced to explain the occurrence of *B. gibsoni* and *B. canis* in the absence of their putative vectors in Africa. The *B. gibsoni* detected in a Pit bull terrier pup imported from the USA to South Africa was attributed to pathogen translocation with the host. However, there was no plausible explanation for the case in the Angolan dog. This is similar to the case of *B. canis* infection reported in an untraveled Nigerian dog [15,35,45]. Further studies are needed to clarify the

status of these pathogens in Africa. Indeed, the extensive cross-border human and animal movements in Africa necessitate the conduct of trans-boundary studies tailored along the One Health paradigm in order to evaluate the status of emerging and re-emerging vectors and VBPs of dogs and their public health implications.

The breed of dogs is a significant risk factors for canine babesiosis in some African countries [15,18,20,21,39]. It appears exotic breeds have higher risk of infection than African local breeds. Although the imported exotic breed of dogs in Africa are usually accorded superior level of care than their local counterparts, immunological naivety and environmental factors are perceived disadvantages to their ability to successfully mount resistance against most VBPs infections [14,30]. Furthermore, it appears that the level of care given to a dog plays a greater role in the disease process than the breed, except for instance in the case of *B. gibsoni* where aggressive behavior in a particular breed predisposes to the disease. However, data on dog breed regarding the use of the terms local or exotic breed should be interpreted with caution, as what is referred to as 'local breed' in one country may be an 'exotic breed' in another. Thus, it is recommended where possible, rather than using of general terms like exotic and local breed, researchers should endeavor to identify specific breeds or their crosses when presenting research results.

The age of dogs is considered a risk factor for babesiosis. However, some of the methods adopted for the estimation of the age of dogs are prone to error, especially in studies where the authors relied on information provided by clients. Furthermore, the age grouping categories are imprecise and require standardization. For example, one study used the age category 1–1.5, 2–2.5, 3–3.5 and 4–5, another 0–2, 2–4, 4–6 and >6 and yet others used <1, 1–5 and >5 or < 1 and ≥1 year [17,25,30,50]. Furthermore, some studies used qualitative terms, e.g., young and adults while others used juvenile, adult and old, without specifying their numerical equivalents [28,34]. Obviously, the omission and overlapping of certain age groups or the use of ambiguous terms limits the utility of such data for achieving meaningful comparison. Thus, there is a need for relevant professional bodies to deliberate and advise on how to come up with appropriate guidelines in this regard.

In most studies, the sex of the dog was not found to be a significant risk factor by most of authors. However, some studies have reported the contrary. Thus, propositions on the influence of the sex of the dog on canine babesiosis remains fluid [17,18,32,50,55]. A favored justification for higher prevalence in male dogs is attributed to their tendency to roam about freely especially during mating season, but this cannot be applied solidly for male dogs that are well managed. Therefore, more studies are needed to explicate the role of the sex of dogs on the epidemiology of canine babesiosis in Africa.

3.4. Limitations

The data utilized for the study were extracted from studies published in the English language only, hence inadvertently excluding results published in other languages. The narrative approach adopted in this study limits the robustness of the epidemiological interpretation of the data. Furthermore, variations in study design, heterogeneity of sample populations, diagnostic methods and geographic factors might introduce bias in the results. Also, it was not possible to ascribe specific clinical signs and risk factors to individual *Babesia* sp. since some of the dogs were having multiple VBPs and these were discussed as reported by the authors. Notwithstanding these limitations, this study provides invaluable insights for veterinary practitioners and scientists about the occurrence of canine babesiosis in Africa.

4. Conclusions

Canine babesiosis is prevalent in Africa. Even though *B. rossi* was not detected in the northern region, it was still the most prevalent species reported on the continent. Considering its perceived pathogenicity, veterinarians on the continent should be wary in handling suspected babesiosis cases, especially in area hitherto considered free from this pathogen. Its introduction to a non-endemic area may lead to a devastating condition due to hosts' naivety. Taken together, this study provides up-to-date information on the common epidemiological features of the disease in Africa.

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