

Serological dynamics of viral-vector-borne zoonoses in domestic and wild animals in a context of tropical forest habitat transformation, Southern Cameroon

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Abstract

Rift Valley Fever (RVF) and Crimean-Congo Hemorrhagic Fever (CCHF) are emerging zoonotic pathogens causing severe impacts on human health. The goal of this study was to use animal host populations to monitor the circulation of those pathogens in a forest region in Southern Cameroon. From 2017 to 2026, a total of 769 plasma samples were collected from five domestic animal species (cattle, sheep, goats, pigs and dogs) and two wild species (*Cercopithecus cephus* and *Philantomba monticola*) across twelve villages in the study area. Serological testing using commercial ELISA tests revealed an overall seroprevalence of RVF antibodies of 8.2% (63/769). With the exception of sheep, these antibodies were detected in all animal populations with significant variations across species and villages. The overall seroprevalence of antibodies against CCHF virus was 7.4%, detected only in cattle and sheep, with rates of 45.4% and 14.8%, respectively. These findings provide, for the first-time, baseline data on two arboviruses in a forest area of Southern Cameroon undergoing habitat transformation, suggesting a natural endemic circulation of RVF. The limited circulation of CCHF in sheep and cattle highlights a risk of introduction of CCHF virus from other area through livestock trade and justifies further monitoring efforts of sentinel animal hosts.

Introduction

The emergence of zoonotic diseases is associated with a range of underlying causal factors including habitat destruction [1, 2]. Mostly caused by anthropogenic pressure due to human population growth, land-use change and overexploitation of natural forest resources, deforestation can significantly modify natural habitats, promote contact between animals and humans, and also disrupt vector ecology and wildlife host behaviour [3].

In Central Africa, anthropic pressure is a primary driver of deforestation and forest degradation [4], mostly due to implantation of small and large-scale agriculture, timber extraction [5], and localized population displacement [6]. Moreover, it is anticipated that the 5-fold population growth expected by 2100 in Central Africa will lead to a significant increase of food and resource demands from logging, mining, and agricultural sectors and will lead to a significant higher impact in the environment [7]. Several forest areas are experiencing significant changes as a result of the commercial exploitation of natural resources and biodiversity loss [8]. Such developmental initiatives attract human populations and trigger huge socio-economic and environmental changes, that can easily have an impact on habitat transformation and potential consequences in factors affecting the emergence of infectious diseases. A potential direct consequence is often an increase in the demand for animal protein which can lead to overexploitation of wildlife resources by hunting [9]. However, although less documented, this demand can also generate the introduction of livestock into previously forested areas, providing new animal host populations which can generate new epidemiological pathways for emerging diseases. Nevertheless, these contexts of change and their potential influence on vector borne diseases remain poorly documented. This is the case for the Rift Valley Fever (RVF) and Crimean-Congo Hemorrhagic Fever (CCHF) which are classified as emerging vector-borne zoonotic diseases capable of causing epidemic outbreaks [10, 11].

RVF is an acute viral zoonosis affecting domestic ruminants and humans [12, 13]. The virus is mainly transmitted through mosquitoes of the *Aedes* and *Culex* genera, or through direct contact with body fluids

from infected animals [14]. RVF driven abortion outbreaks represent a significant public health risk which is listed as a priority human disease by the World Health Organization [15]. Widely spread across Africa countries, the outbreaks of RVF induces a major impact to livestock production such as abortions in gravid females and mortality estimated to 5–60% among young animals [12, 16–18]. Preventing such outbreaks requires to identify risky transmission zones by detecting antibodies against RVF virus in either human or livestock.

Crimean-Congo hemorrhagic fever (CCHF), caused by a Nairovirus, constitutes another major aboviral threat for human health prioritized by WHO (2024). Transmitted by bites of hard tick-mainly from *Hyalomma* ticks but also other species [19], the role of those vectors in the maintenance and transmission of this virus remains unclear in the African context [20]. It circulates between hard ticks and other vertebrate hosts, including wild and domestic animals [21, 22]. Inducing high fatality rate ranging from 10% to 40% in human [23], animals are asymptomatic carriers, making them silent amplifying hosts of the virus and tick populations that can serve as sentinel animals for its surveillance in endemic areas [21]. Detecting antibodies against CCHF virus in animal populations is an efficient tool to monitor the circulation of the virus and identify areas with a higher risk of transmission [24].

Previous studies in Cameroon have documented human exposure to RVF and CCHF viruses, alongside the presence of their main vectors (*Hyalomma* spp. for CCHF; *Aedes* and *Culex* for RVF) [25–28]. Nevertheless, epidemiological data on RVFV and CCHF virus infections in animals remain scarce and poorly documented. This is particularly relevant in tropical forest habitats which have been insufficiently investigated in terms of the ecology and epidemiology of emerging infectious diseases [29]. In such context characterized by a rapid landscape anthropization, seasonal and transboundary livestock movements and intensified human/animal interactions, generating baseline data on the circulation of RVF and CCHF viruses is crucial for future comparative analysis but also to anticipate more effective prevention and control strategies to mitigate the emergence of these viral infectious diseases.

The present study intended to assess, the level of habitat transformation in the Campo forested zone of south Cameroon since the beginning of the century, and the potential influence of these ecological changes in the seroprevalence of antibodies against RVF and CCHF viruses in animals host populations during the last decade.

Material and Methods

Study site

The Campo Sub-Division is located in the South Region of Cameroon and belong to the tropical humid forest of the Congo basin, characterized by a typical maritime equatorial climate with four seasons. This area lies along the Atlantic coast and extends along the Ntem River, which constitutes the Cameroonian and Equatorial Guinean border. It has a dense hydrographic network with several rivers, swampy areas and marshes which offer favourable conditions for the development of many pathogen vectors such as tse-tse flies, mosquitos and *Culicinea* [27, 30, 31]. Sharing borders with the Campo Ma'an National Park, the Campo Sub-Division is made up of several villages located along the coast and the roads. Fishing, picking, hunting agriculture and

small-scale livestock farming are the main activities practiced by inhabitants of this area. Known since 1932 as a Wildlife Reserve, part of the Campo Sub-Division officially became the Campo-Ma'an National Park through decree No. 2000/004/PM of the 06 January, 2000 [32]. Beyond its high wildlife diversity [33], a wide variety of plant taxa [34] are also described in the area. Since the last two decades, deep socioeconomic and environmental mutations have occurred in the area, including human population growth, transboundary population movements between Cameroon and Equatorial Guinea [31, 35], forest clearance for agriculture framing, installation of logging companies, and more recently the clearance of 6500 ha of forest (on the 60,000ha expected), for industrial palm grove (Fig. 1). Furthermore, the preservation of the wildlife biodiversity in the Campo Ma'an National Park that share borders with villages of the Campo subdivision has stimulated domestic livestock farming to reduce hunting activities. For this study, samples were collected in 12 villages of the Campo subdivision (Fig. 1).

Assessment of habitat transformation

To quantify forest cover dynamics in the study area, annual forest cover data for the period 2000–2025 were extracted from the Tropical Moist Forest (TMF) dataset [36], developed by the Joint Research Centre (JRC) using time series of Landsat 7, 8, and 9 imageries at a 30 m resolution, based on the analysis of valid (cloud-free) pixel observations describing landscape extent, disturbance (degradation and deforestation), and forest regeneration. For each year, annual TMF forest cover data were downloaded to analyze the site's change dynamics. Preprocessing steps, including geometric and radiometric correction, cloud and shadow masking, and temporal segmentation, were performed by the JRC as part of the TMF annual production workflow. The TMF product has an overall accuracy of 91.4% and was validated using 5000 reference sample points. Finally, land cover type change between 2000 and 2025 was calculated and expressed in km².

Livestock population data

The animal population in Campo has increased in recent years, largely driven by increased local food demand. Based on our observations during field trips, we estimate that 50 to 100 cattle are regularly introduced every year into the area for a short fattening period of approximately three months prior to slaughter, some individuals are kept for several months for breeding purposes. In addition, driven by local development NGO initiatives seeking to increase the availability of animal protein to curb hunting pressure and conserve wildlife, pig farming has expanded significantly in the study area. Moreover, local residents also traditionally breed sheep and goats locally. During each field survey, any animal that spent at least one month in villages of the Campo subdivision prior to sampling date were selected and included in the study upon owner's agreement.

Sample collection

Blood sample collection and plasma preparation

Between 2017 and 2026 (excluding the COVID-19 period of 2020–2021), seven (7) field surveys (July 2017, November 2019, January 2022, August 2023, April 2024, April 2025 and January 2026) were conducted. Before field surveys, a sensitization step was conducted, where the objectives of the study were explained to the local administrative and traditional authorities as well as to local veterinarian and inhabitants of different villages. Village, species, reported origin, sex, and sampling-site coordinates were recorded for each selected animal.

All blood sampling procedures for livestock, small ruminants, pigs, and dogs were performed on conscious animals without the administration of anesthetic or sedative agents, thereby eliminating potential physiological or metabolic confounding factors associated with chemical restraint. To ensure animal welfare and minimize stress, all subjects were handled gently by trained personnel using physical restraint techniques specific to each species. Specifically, blood samples from livestock and small ruminants were collected via jugular venipuncture while animals were held in standard farm chutes or stanchions. Pigs were sampled via the cranial vena cava or auricular vein utilizing low-stress physical restraint, and dogs were sampled via cephalic venipuncture while resting on a standard treatment surface. All collection procedures were completed within a brief duration (less than one minute per animal).

Approximately 5 mL of blood was collected into EDTA tubes from the jugular vein of cattle, pigs, sheep, and goats and from the saphenous vein of dogs. Wildlife blood was collected by cardiac puncture. Blood sample tubes were carefully labelled and stored at 4°C in an electric cooler before being transported to the laboratory where plasma was immediately separated. After blood sample collection, anthelmintic drugs and vitamins were administered to domestic animals following veterinarian's advice.

Plasmas were obtained by centrifugation of each blood tube at 3000 rpm for 10 min. Thereafter, 500 µl of plasma were collected from each tube and transferred into 1.5 ml sterile micro-tubes that were subsequently stored at -20°C until use. A total of 769 plasmas samples were collected during the surveys. Those included 733 samples from 5 domestic animal taxa (108 cattle, 388 pigs, 54 sheep, 94 goats, 89 dogs) and 36 samples from wildlife (7 from *Cercopithecus cephus* and 29 from *Philantomba monticola*) (Fig. 2). These wildlife species are abundant and considered of least concern by the IUCN and Cameroon National legislation and therefore, their hunting is permitted.

Vector collection and identification

During the January 2026 survey, three cattle herds from two villages Mintom and Trinitas (Camvert) were inspected for tick collection. Approximately 50% of the cattle in each herd were randomly selected, resulting in a total of 51 animals examined. Tick inspection was performed systematically on the head, ears, neck, back, dewlap, abdomen, limbs, and tail. Ticks were removed with forceps, preserved in 70% ethanol, and transported to the Molecular Parasitology and Entomology Sub-Unit, University of Dschang. Once in the laboratory, after observation with a stereomicroscope (40X magnification), each tick was morphological identified using taxonomic keys as described by Walker *et al.* (2003) [37]. However, RVF mosquito vectors were not investigated in the present study.

Detection of antibodies against RVF virus and CCHF virus

Following the manufacturer's instructions, antibodies against CCHF virus were detected using a CCHF double-antigen, multispecies ELISA kit (ID Screen; IDvet, Grabels, France) while a Competition Multi-species cELISA, ID Screen® (IDVet Innovative Diagnostics, Grabels, France) was used to detect antibodies against RVF virus. In the case of the RVF test, the diagnostic sensitivity of the IgG kit is 98% and specificity 100 [38], while for CCHF, the test has been validated in multiple animal species with a sensitivity of 99.8% and a specificity of 100% [39].

Statistical analysis

The Pearson's chi-square test (χ^2) was used to assess the differences in infection rates across animal species and villages. When the expected frequencies in contingency tables were below 5, the Fisher's exact test was employed. Statistical analyses were conducted using SPSS version 25, with a significance threshold set at $p < 0.05$.

Results

Habitat degradation in the study area

In 2000, undisturbed tropical rainforest covered 1275.7 km², reflecting a well-conserved state of the forest ecosystem (Fig. 3-a). In 2025, the spatial configuration of forest cover had changed, with undisturbed forest declining to 1157 km², a net decrease of 118.7 km², corresponding to a 9.3% loss of the initial forest cover over 25 years (Fig. 3-b). Over the same period, degraded forest increased ninefold (from 7.3 to 66.8 km²), while deforested areas increased from 2.2 to 58 km². Spatially, the 2025 map revealed that these losses are concentrated along road axes and near settlements. A major deforestation hotspot was identified in the northwestern side of Campo Ma'an National Park periphery, adjacent to the Trinitas (Camvert) area.

Seroprevalence of antibodies against RVF and CCHF according to animal taxa

The overall seroprevalence of antibodies against RVFV was 8.2% (63/769). These were detected in all the sampled species except sheep with significant variations ($p < 0.05$) (Table 1). Cattle showed the highest overall prevalence of 32.4% (35/108) with peaks of 57.7% in 2025 and 47.6% in 2024 (supplementary table 1). This overall seroprevalence was low in other domestic animal taxa: 0.7% in pigs, 8.5% in goats and 5.6% in dogs, (Table 1). The cumulative seroprevalence reported for all the analyzed wildlife was 33.3% (12/36) (Table 1), with *P. monticola* showing the highest seroprevalence rate at 34.4% (10/29), and *C. cephus* showing a rate of 28.5% (2/7). The seroprevalence of RVF showed a significant ($p < 0.0001$) variation over the years, with a gradual increase from 5.5% in 2017 to 17.5% in 2024 and a value of 13.0% in 2026 (supplementary table 1).

The overall seroprevalence of antibodies against CCHF virus was 7.4% (57/769) with a significant difference according to animal species ($p < 0.0001$) (Table 1). Only cattle and sheep had antibodies against CCHF virus during our time of observation. Cattle were the main animal taxon having antibodies against CCHF virus, with an overall seroprevalence of 45.4% (49/108) (Table 1). In sheep, a seroprevalence of 14.8% (8/54) was observed (Table 1). The analysis of samples collected over the years (2017–2026) revealed a significant ($p <$

0.0001) increasing trend in seroprevalence, rising from 1.8% in 2017, to 12.2% in 2025 and to 23.9% in 2026, essentially driven by cattle infection (supplementary table 2).

Table 1
Seroprevalence of antibodies against RVF virus and CCHF virus according to animal taxa

Animal taxa	Total samples	Seroprevalence RVF (%)	IC 95%	Seroprevalence CCHF (%)	IC 95%
Cattle	108	35 (32.4)	23.7–42.1	49 (45.4)	35.8–55.3
Pigs	388	3 (0.7)	0.2–2.2	0 (0.0)	NA
Sheep	54	0 (0.0)	NA	8 (14.8)	6.6–27.1
Goats	94	8 (8.5)	3.7–16.1	0 (0.0)	NA
Dogs	89	5 (5.6)	1.8–12.6	0 (0.0)	NA
Wildlife	36	12 (33.3)	18.6–51.0	0 (0.0)	NA
Total	769	63 (8.2)	6.4–10.4	57 (7.4)	5.7–9.4
IC: confidence interval; NA: Non-Applicable; RVF: Rift Valley Fever; CCHF: Crimean-Congo Hemorrhagic Fever					

Seroprevalence of antibodies against RVF virus and CCHF virus according to villages

Antibodies against RVF virus were found in 75% of the sampled locations while CCHF was less widespread (33.3% of the villages only) (Table 2). In both cases, values in seroprevalence varied significantly depending on the location. In addition, the co-exposure to RVF and CCHF viruses was detected in 14 cattle (12.9%, 14/108) from 3 villages (Itondefang, Trinitas Campo-ville).

Table 2
Seroprevalence of antibodies against RVF virus and CCHF virus according to villages

Villages	Number of total samples analyzed	Seroprevalence RVF (%)	IC 95%	Seroprevalence CCHF (%)	IC 95%
Akak	61	2 (3.3)	0.4–11.3	0 (0.0)	NA
Bouandjo	33	3 (9.1)	1.9–24.3	0 (0.0)	NA
Campo-Ville	222	18 (8.1)	0.0–6.5	9 (4.1)	1.9–7.6
Campo-Beach	84	1 (1.2)	0.0–6.5	1 (1.2)	0.0–6.1
Doumassi	40	0 (0.0)	NA	0 (0.0)	NA
Ipono	59	0 (0.0)	NA	0 (0.0)	NA
Itondefang	73	17 (23.3)	14.2–34.6	13 (17.8)	9.8–28.5
Mabiogo	14	0 (0.0)	NA	0 (0.0)	NA
Mintom	53	3 (5.6)	1.2–15.7	5 (9.4)	3.1–20.7
Nkoelon	39	11 (28.2)	15.0–44.9	0 (0.0)	NA
Tondefon	28	1 (3.6)	0.1–18.3	0 (0.0)	NA
Trinitas (Camvert)	63	7 (11.1)	4.6–21.6	29 (46.0)	33.4–58.9
Total	769	63 (8.2)	6.4–10.4	57 (7.4)	5.7–9.4
IC: confidence interval; NA: Non-Applicable; RVF: Rift Valley Fever; CCHF: Crimean-Congo Hemorrhagic Fever					

Tick samples distribution per species and villages

A total of 559 Ixodidae ticks were collected from 51 cattle. All the 559 collected specimens belonged to the genus *Rhipicephalus* (Table 3). *Rhipicephalus decoloratus* was the most abundant species accounting for 47.6%, followed by *R. annulatus* (32.6%) (Table 3). A significant difference ($\chi^2 = 191.7$, $P = < 0.0001$) was observed between villages, a higher number of ticks being collected in cattle from Trinitas (Camvert) compared to those from Mintom (Table 3).

Table 3
Distribution of *Ripicephalus* species per villages

Species	Sex		Villages		
	N. of ticks collected (%)	N. of Female	N. of Male	N. in Mintom (%)	N. in Trinitas (Camvert) (%)
R. decoloratus	266 (47.6)	229	37	38 (14.3)	228 (85.7)
R. annulatus	182 (32.6)	156	26	23 (12.6)	159 (87.4)
R. microplus	109 (19.5)	88	21	16 (14.7)	93 (85.3)
R. sanguineus	2 (0.3)	2	0	0 (0.0%)	2 (100)
Total	559 (100)	475	84	77 (13.8)	482 (86.2)

Discussion

Although since several decades the central African region is being subjected to deep socio-environmental changes that are recognized as key factors influencing the transmission of emerging pathogens, this association remains poorly investigated, particularly in tropical forest habitats in Central Africa. Moreover, despite the fact that animal serological values are a good tool to understand transmission dynamics and infer potential zoonotic risks, epidemiological data on sentinel animal populations from tropical forest areas remains limited. This study was designed to explore the potential environmental impact of anthropization in the circulation of RVF virus and CCHF virus in local domestic and wild animal populations. This information could be used to anticipate potential disease risks related to the circulation of RVF virus or CCHF virus among rural populations living in a tropical forest habitat exposed to habitat changes. Both arboviruses constitute significant threats to both human and animal health and are classified among priority zoonotic diseases by the Cameroonian national program for the prevention and fight against emerging and re-emerging zoonoses [40, 41].

Our assessment of habitat status indicated a considerable level of forest cover loss; reaching 60 Km² in our study area. This is consistent with similar dynamics described at the scale of the Congo Basin, where forest degradation and conversion have been accelerated over the past two decades [42]. Spatially, the 2025 map reveals that these losses are concentrated along road axes and around human settlements. This pattern of peripheral deforestation is characteristic of pioneer fronts, where the opening of tracks facilitates the penetration of human activities into forested areas [43]. A massive deforestation hotspot was identified in the northwestern side of Campo Ma'an National Park, linked to the agro-industrial oil palm exploitation activities of a national company. This finding confirms the major impact of cash crop expansion on tropical deforestation in sub-Saharan Africa, corroborating the work of previous authors [43, 44]. Although our study did not directly quantify this impact, such a considerable surface of forest habitat clearance, is likely to induce a considerable disturbance in wildlife populations from the area. Discussions with local communities

suggested that crop damages from elephants and human-wildlife conflicts have increased in the last two years, suggesting a considerable perturbation and behavioral change in wildlife populations. Our study intended to document the circulation of two vector borne zoonoses in this context of tropical forest habitat transformation.

The overall observed seroprevalence of antibodies against RVFV reported in this study during the last decade (8.2%) varied significantly between years, villages and species, with cattle exhibiting the highest cumulative seroprevalence compared to other domestic and wild taxa. The higher seroprevalence in domestic cattle can be indicative of a preference of RVF vectors for this bovid host populations, as observed in other studies [45]. However, since cattle population in our study area come from other Cameroon regions and only present for a few weeks, our observations are not necessarily the result of a local exposure to the virus. If some of these cattle came infected with RVF, they could play some role in the transmission and spread of the disease. Nevertheless, the fact that antibodies were present in the majority of sampled species since 2017, suggests a regular and widespread circulation of RVF virus in our study area. The lower seroprevalence values of RVF virus antibodies observed in other domestic animals (pigs, goats, and dogs) provide useful baseline information on the levels of exposure of pigs or dogs to RVF virus in tropical forest areas [29]. The fact that no sheep were found positive to RVF virus antibodies suggests that this species might be less exposed to mosquito bites. However, our results showing a seroprevalence of RVF virus antibodies of 8.5% in goats that share the same environment with sheep indicate some potential difference in host susceptibility to this virus. This is also consistent with the low levels of exposure reported for this host in neighboring Gabon [29].

The overall detected seroprevalence of RVF virus antibodies in our analyzed sample of wildlife was 33.3%. Although these antibodies RVF have been previously reported in *P. monticola*, [29] our results reported their first detection in *C. cebus* [46]. Despite the fact that our sample size for this species was low ($n = 7$), detected prevalence values of 28% call for further surveillance efforts in wildlife species to monitor the potential influence of anthropogenic activities such as livestock introductions. Though the yearly sample sizes for different animal species were heterogeneous, our results suggest an endemicity of the study area for RVF with probably low circulation of RVF virus among a diversity of resident wild and domestic hosts. It is worth noting that the seroprevalence values are just an indicator of the level of exposure that is potentially influenced by several factors such as sample size, age, time of exposure, proximity to water sources. In our case, these space and time variations could be potentially explained by local differences in vector ecology, particularly regarding the density and seasonal dynamics of *Aedes* and *Culex* mosquito populations [14, 27, 47].

RVFV persistence is heavily supported by the virus's capacity to survive extended periods within desiccated mosquito eggs, facilitating long-term environmental survival and geographic expansion [14, 48]. Furthermore, animal exposure is likely amplified by livestock mobility, wildlife-livestock interfaces, and proximity to wetland breeding habitats. While cattle movements may introduce imported cases, widespread seropositivity across multiple domestic and wild animal taxa strongly points to active local transmission dynamics within the study area. To our knowledge, Cameroon has never experienced to date human nor animal outbreaks of RVF and this silent circulation of antibodies without clinical manifestation has been reported previously in other areas of Cameroon [28] and other countries in Sub-Saharan Africa [16, 49], including tropical forest habitats [29].

Although the overall seroprevalence of antibodies against CCHF virus of 7.4% recorded over the ten-year period appears low, the value of 45.4% detected in cattle is comparable to the 56.0% reported in the North-West region of Cameroon [50] and significantly higher than the 10.9% reported in cattle from the Centre region [51]. This variation suggests some differences in the exposure or transmission dynamics, likely linked not only to different ecosystems, but also to tick species, their infestation rates, local host densities and livestock management practices. Indeed, values of antibodies against CCHF virus can be very variable depending on ecological settings and livestock practices. Similarly, an increase in local livestock populations could potentially modify the epidemiology of CCHF in our study area by increasing the availability of susceptible hosts and opportunities for virus amplification and transmission. In addition, the higher seroprevalence of antibodies against CCHF virus in cattle compared to other resident species (except for sheep), associated with their local short lifespan (slaughtered after few weeks), suggests that cattle were probably exposed to CCHF virus elsewhere before their arrival to the sampling site. The increasing trend of seroprevalence values observed in this species between 2023 and 2026 suggests a higher number of imported cases. This calls for heightened vigilance regarding the introduction of new pathogens from introduced livestock in tropical forest area, particularly in the context of an increasing demand for animal protein. Conversely, the detection of antibodies against CCHF in resident sheep deserves particular attention and indicates a potential local circulation of the virus in circulating ticks. In the context of vector borne pathogen such as CCHF, it is critical to monitor the presence of emerging tick vectors in the resident animal population, specifically those playing a role in CCHF transmission. As primary vectors of the CCHF virus, the presence of at least three *Hyalomma* tick species (*Hyalomma rufipes*, *Hyalomma truncatum*) has been documented across several regions of the Cameroon [26, 52]. Despite the lower abundance of ticks in the humid southern regions of Cameroon, species of *Amblyomma* and *Rhipicephalus* are commonly reported in these areas [48]. Although *Hyalomma* spp. have not been documented to date in the tropical forest regions of southern Cameroon, other tick genera, including *Rhipicephalus*, *Amblyomma*, and *Dermacentor*, have been reported and may play a role in the transmission of CCHF virus [20].

Given the ecological conditions (humidity and temperature) that are highly favorable for the development of CCHF virus competent vectors, their adaptation and proliferation in forested environments could lead to viral transmission to vertebrate hosts; constituting thus a significant threat for human health [50]. These observations therefore suggest the implementation of prevention and control strategies depending on the regions of Cameroon.

The high seroprevalence observed in cattle compared to other animal taxa is not surprising, as they are among the domestic species most heavily infested with ticks. The detection of antibodies against CCHF virus in local sheep could be explained by their infestation in pastures shared with cattle. This hypothesis is strengthened by results of Gasparine *et al.* (2025) [51] who reported 3.4% of goats with antibodies against CCHF virus in the Central Region of Cameroon where, small ruminants shared grazing lands and resident vectors with cattle. Despite the fact that our sample sizes and the numbers of positive animals were small, the repeated detection of antibodies in eight sheep located in two different villages could indicate a potential local circulation of CCHF virus and this deserves further investigation. As sentinel animals, sheep can serve as early indicators for viral circulation in high-risk areas. In such context, strengthening epidemiological surveillance targeting small ruminants could not only enable early detection of viral emergence, but also help to prevent its spread to other animal species. Moreover, the fact that the exposure to CCHF virus was limited

to two domestic species provides a strategic window for targeted control measures such as the use of acaricides. This control will reduce the risk of transmission to humans.

The detection of antibodies against CCHF virus in absence of its *Hyalomma* ticks, should be interpreted with caution. Indeed, as the sampling was conducted in the heart of the dry season, the environmental conditions characterized by severe water stress and low relative humidity significantly limit the host-seeking activity of these vectors and slow down their development cycle. This temporal bias can mask the presence of *Hyalomma*, which is nonetheless a key vector of the CCHF virus. However, other vectors including *Rhipicephalus* spp, identified in this study, are known to act as vectors CCHF virus transmission in East Africa [53, 54]. Therefore, the hypothesis of local transmission by other *Rhipicephalus* tick species identified in the area remains entirely plausible and should not be ruled out [20]. The hypothesis of potential introduction of CCHF virus and its subsequent local transmission is plausible but requires confirmation by further studies.

Although no wildlife specimens were found positive to antibodies against CCHF virus, the small wildlife sample size analyzed in this study, calls for more sustained monitoring efforts because the presence of livestock has been reported to directly influence virus seroprevalence in sympatric wildlife [22]. Such monitoring is imperative to identify the potential involvement of wildlife species as observed in other regions of the world including Sub-Saharan Africa [22]. In areas, where livestock movements remain restricted and primarily driven by the availability of grazing areas, establishing quarantine points and cattle dipping stations for tick control in residents and newly arrived animals would serve as an effective sanitary barrier to curb the regional expansion of vectors.

The findings of the seroprevalence of both RVF and CCHF varied among the different villages. However, factors such as differences in animal species composition, sampling years, livestock presence, vector abundance and local environmental conditions can influence variations in pathogen exposure and therefore, may contribute to the observed patterns. Further studies with larger datasets of seropositive animals would be needed to understand the potential influence of different risk factors to the exposure of the targeted pathogens.

Although this study provided evidence of exposure of local animal populations (both domestic and wild) to two arboviruses in the Southern Cameroon, it has some limitations: i) no entomological studies were conducted to search the vectors involved in the transmission of RVF virus; ii) the collection and identification of ticks was only carried out during the last sampling period, which only provides a snapshot of the current circulation of tick species in the region; iii) compared to longitudinal studies crossing several seasons, our cross-sectional study did not enable to appreciate the real diversity and abundance of vector species as well as the variability in the prevalence of vector-borne pathogens that are most often influenced by some bio-climatic differences linked to seasonal variations. Such investigations would have helped to determine the diversity of vectors involved in the transmission of these diseases, notably *Aedes* mosquitoes for RVF and different tick species for CCHF. This is particularly relevant in the context of an increasing introduction and development of livestock production in the area. These data would not only have improved the understanding of vector diversity, but also provided important information on vector density and the proportion of vectors carrying these arboviruses, thereby allowing a more accurate assessment of the actual risk of local

transmission and emergence of these diseases in this forested area under socio-environmental transformation.

Conclusion

Conducted within a context of recent but intense habitat transformation in tropical forest ecosystem of Southern Cameroon, this investigation provides baseline data on the trends of habitat loss combined with epidemiological data on the circulation of emerging viruses in a previously undocumented area of Southern Cameroon. Over the past decade, our long-term survey revealed a regular exposure of domestic and wild animals to RVF virus, suggesting an endemic circulation of this pathogen in the study area. Regarding the case of CCHF, our results do not suggest an endemicity. However, the trade of livestock from other areas of Cameroon could facilitate the introduction of infected ticks with the potential to be maintained by local animal populations in our study area. Despite the absence of any detected clinical cases of RVF or CCHF in animals, these preliminary findings justify the need to continue adequate event-based surveillance and control measures to monitor the dynamics of those viral emerging pathogens, such as awareness campaigns for villagers or animal and human health centers to report unusual deaths or abortions in domestic and wild ruminants or unusual rates of cases of febrile patients.

Declarations

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Author contributions

R.M.N.K. Designed study and the methodology, conducted sample collection, curated the data, performed data analysis and reviewed and edited the manuscript.

G.S. Designed and developed the study, supervised sample collection, provided supervision and wrote the manuscript.

T.T.M.T. Designed and developed the study, sample collection and wrote the manuscript.

J-M.B. Sample collection, reviewed and edited the manuscript

I.V.Y-D. Land Use/Land Cover analysis, reviewed and edited the manuscript

E.M.K.M. Sample collection, reviewed and edited the manuscript

R.M.I.B.D. Sample collection, reviewed and edited the manuscript

I.T. Land Use/Land Cover analysis, reviewed and edited the manuscript

P.C. Land Use/Land Cover analysis, reviewed and edited the manuscript

J-B.N. Local veterinary assistance and sample collection

F.J. Acquired funding, provided general supervision designed methodology, contributed to sample collection and wrote the manuscript.

Competing interests

The authors declare no competing interests.

Consent for publication

Not applicable

Ethical Approval and Consent to Participate

The protocol of this study was approved by the Ocean Divisional Delegation of the Ministry of livestock, fisheries and animals Industries of Cameroon with the reference number Ref N°004/ARA/L11/SP of March 23th, 2023 in accordance with national guidelines. Laboratory procedures were approved by the institutional review board of the Molecular Parasitology and Entomology Subunit of the Department of Biochemistry of the Faculty of Science of the University of Dschang, Cameroon. In addition, our project was approved by the National Ethics Committee for research on human health Cameroon with Ref N°2024/01/1623/CE/CNERSH/SP of the January 17th, 2024. Prior to sampling, informed consent was obtained from all animal owners. All blood sampling procedures for livestock, small ruminants, pigs, and dogs were performed on conscious animals without the administration of anesthetic or sedative agents, thereby eliminating potential physiological or metabolic confounding factors associated with chemical restraint. To ensure animal welfare and minimize stress, all subjects were handled gently by trained personnel using non-invasive physical restraint techniques specific to each species. Specifically, blood samples from livestock and small ruminants were collected via jugular venipuncture while animals were held in standard farm chutes or stanchions. Pigs were sampled via the cranial vena cava or auricular vein utilizing low-stress physical restraint, and dogs were sampled via cephalic venipuncture while resting on a standard treatment surface. All collection procedures were completed within a brief duration (less than one minute per animal). Concerning wildlife including in this study, the sampling was limited to animal that were accidentally met during our field activities because we did not want to encourage hunting activities in these localities. These wildlife species are abundant and considered of least concern by the IUCN and Cameroon National legislation and therefore, their hunting is permitted.

Data availability

All data generated or analyzed during this study are included in this published article.

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Figures

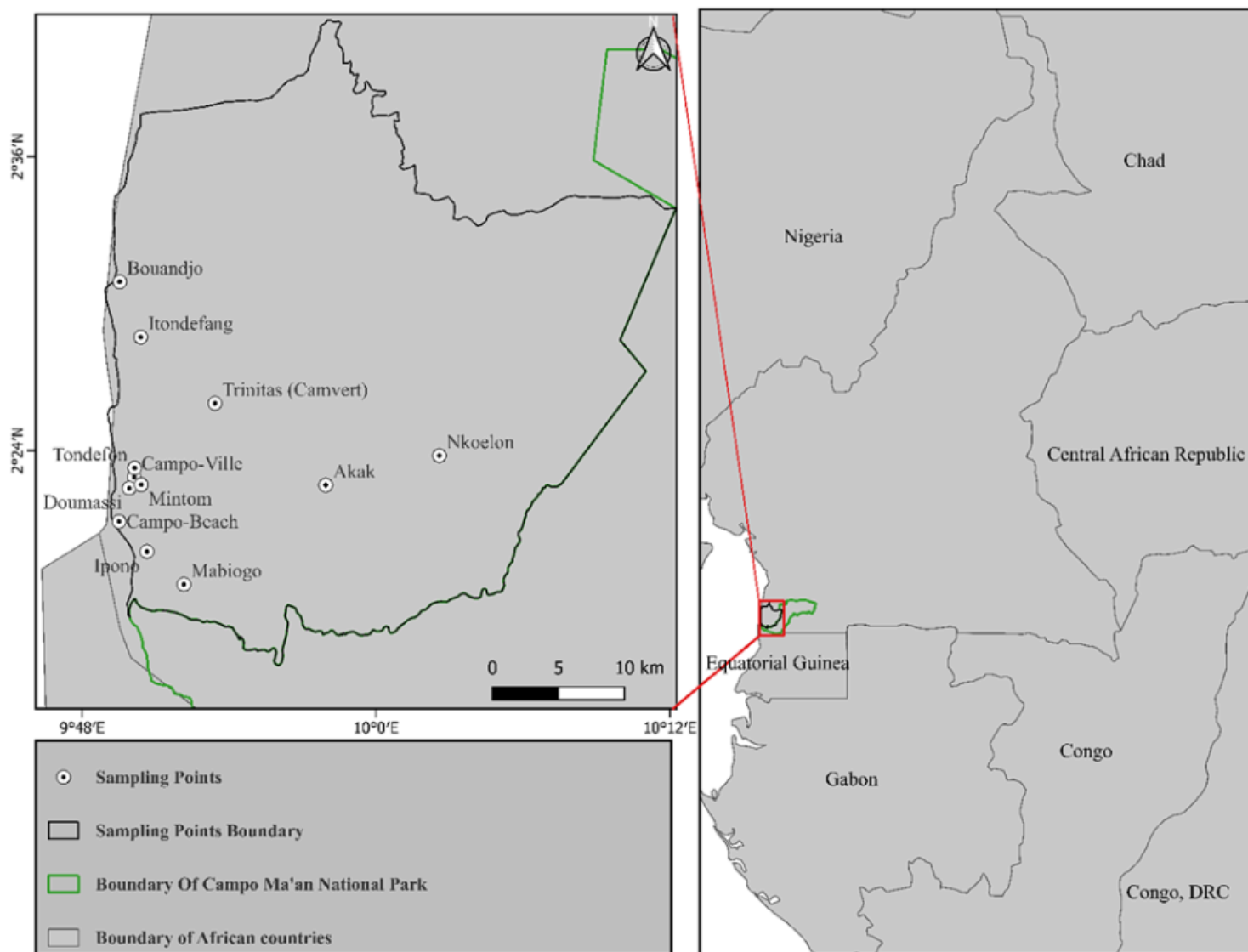


Figure 1

Map showing the location of the study area in Cameroon, adjacent to Campo Ma'an National Park and different villages where animal sampling was implemented

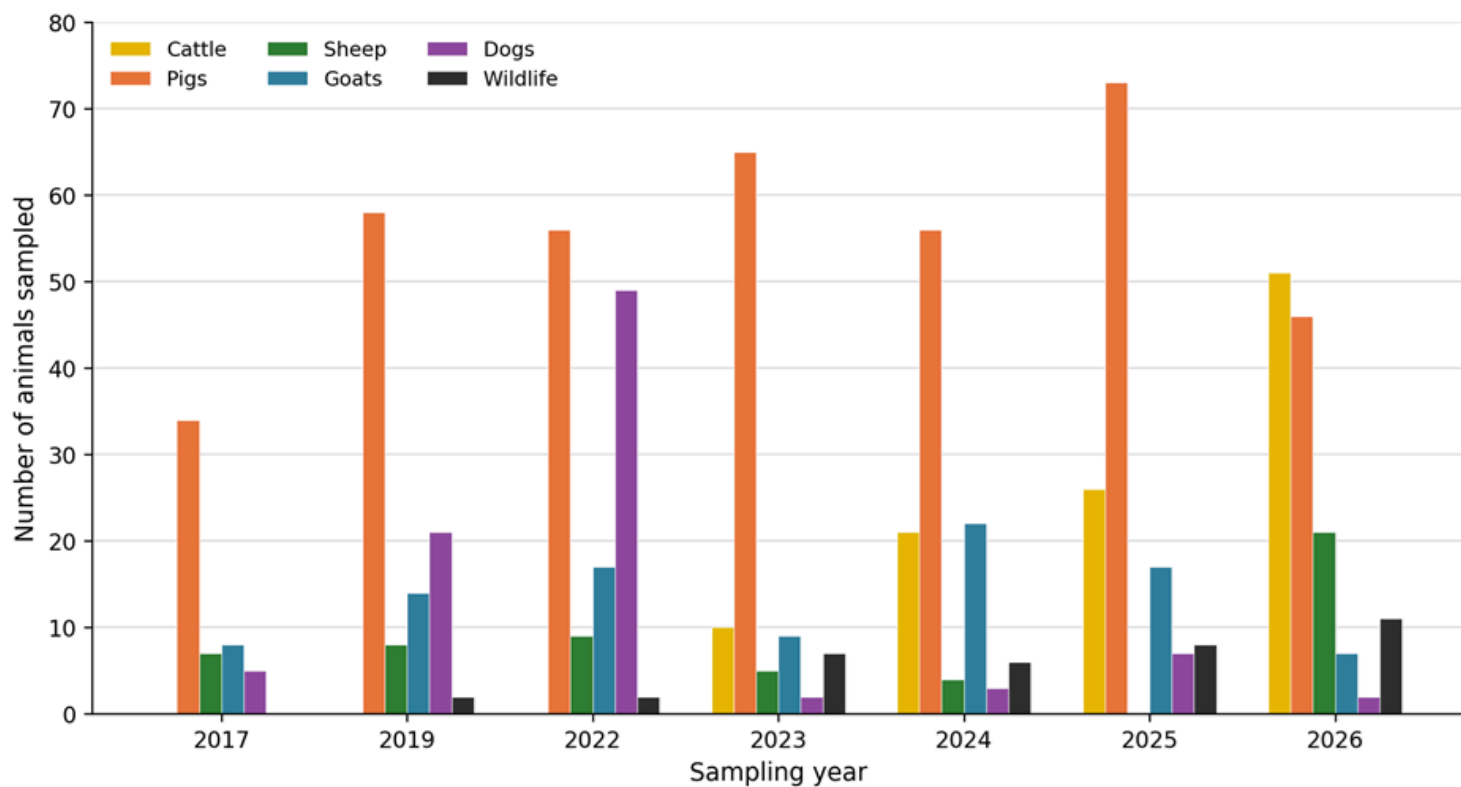


Figure 2

Annual distribution of domestic and wild animals sampled during the seven surveys implemented between 2017 and 2026 in the study area.

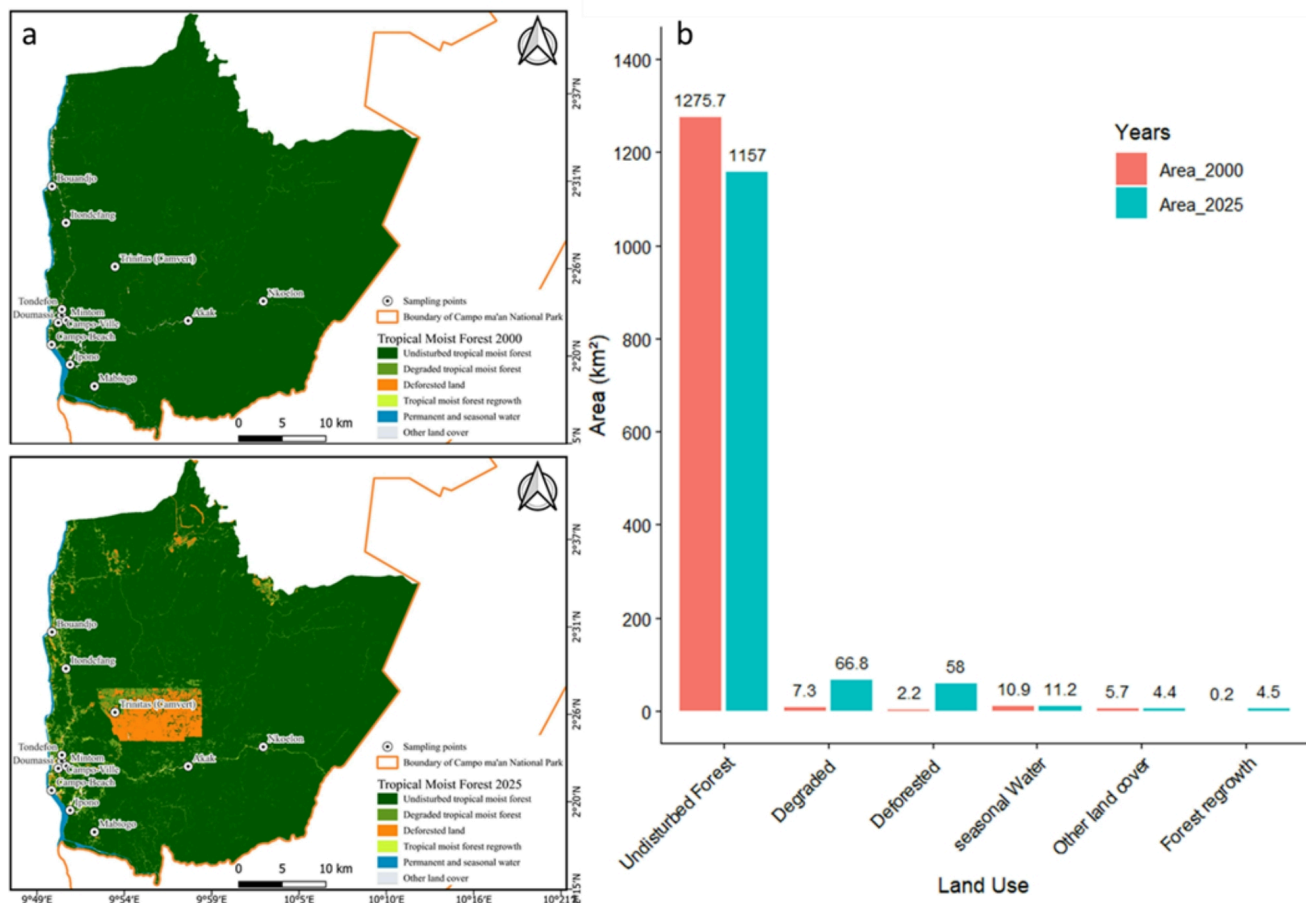


Figure 3

Land cover change between 2000 and 2025: comparative mapping of forest cover (a) and comparative histogram of land cover category areas in km² (b)

Supplementary Files

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- [Supplementarytables12Serologicaldynamicsofviralvectorbornezoonosesindomesticandwildanimals.docx](#)