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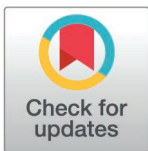
RESEARCH ARTICLE

Determinants of viral haemorrhagic fever risk in Africa's tropical moist forests: A scoping review of spatial, socio-economic, and environmental factors

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Abstract

Background

Viral haemorrhagic fevers (VHFs) are identified by international health authorities as priorities for research and development, as they pose a threat to global health and economy. VHFs are zoonotic diseases whose acute forms in humans present a haemorrhagic syndrome and shock, with mortality rates of up to 90%. This work aims at synthesizing existing knowledge on spatial and spatially aggregable determinants that support the emergence and maintenance of VHFs in African countries covered by tropical moist forest, to better identify and map areas at risk.

Methodology/principal findings

Using the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA-ScR) guidelines, extension for scoping reviews, we searched the PubMed, Embase, CAB Abstracts, and Scopus databases. English and French peer-reviewed documents were retrieved using Boolean logic and keyword search terms. The analysis of 79 articles published between 1993 and 2023 offers a comprehensive overview of the complex interactions among abiotic, biotic, demographic, socio-economic, cultural, and political risk factors in driving the emergence and maintenance of VHFs in African countries covered by tropical moist forests. Human-to-human transmission is mainly driven by socio-economic, political, and demographic factors, whereas zoonotic spillover is determined by almost all groups of factors, especially those of an anthropogenic nature.

Conclusions/significance

Many questions remain unanswered regarding the epidemiology of VHFs in tropical forests. By elucidating spatially relevant determinants which have already been studied, this review seeks to advance VHFs hotspot predictions, risk mapping for disease surveillance and control systems improvement.

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Data availability statement: The research protocol that supports the findings of this study are publicly available from the Open Science Framework repository and can be found at the following link <https://osf.io/p6x8d/>. All relevant data are within the manuscript and its [Supporting information](#) files.

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Author summary

Viral haemorrhagic fevers (VHFs) represent a significant burden to public health and local economies due to their ability to cause unpredictable and widespread epidemics. To maximize early detection and rapid diagnosis of their occurrence, surveillance efforts should target areas where circulation is most likely. However, identifying such hotspots of potential emergence is a major challenge. The ecological conditions leading to VHF outbreaks are shaped by complex interactions between the virus, its vertebrate hosts, arthropod vectors, abiotic and human environments that are often poorly understood. Here, we systematically reviewed spatially relevant risk factors associated with the emergence and maintenance of VHFs in the tropical moist forest of Africa. These include mosquito-borne zoonoses (Rift Valley fever, dengue, yellow fever), tick-borne zoonosis (Crimean-Congo haemorrhagic fever), zoonoses transmitted by direct contact (Ebola Virus Disease, Marburg Virus Disease, and Lassa Fever). Analysis of all the documents considered reveals that the invasion of humans on nature is the main risk factor incriminated in spillover events of VHFs. This work provides baseline information for the identification of regions and habitats that have suitable environmental and human conditions for emergence and maintenance, useful for forecasting and targeted surveillance programs.

1. Introduction

Infectious diseases are continuously emerging, and most known human pathogens are zoonoses (infections in animals that are transmitted to humans) or of zoonotic origin [1]. Zoonoses are a growing threat to global health, global economy and security [2–4]. Viral haemorrhagic fevers (VHFs) are a group of acute zoonotic diseases with high mortality and morbidity rates that infect both humans and animals [5]. VHFs are caused by 4 families of viruses (*Arenaviridae*, *Bunyaviridae*, *Filoviridae*, and *Flaviviridae*) [6]. These diseases are endemic in some parts of the world and can cause serious outbreaks. VHFs such as Ebola Virus Disease (EVD), Lassa Fever (LF), Rift Valley Fever (RVF), or Marburg Virus Disease (MVD) are highly contagious and have the potential to become pandemics with a loss of many lives. From 1976 to 2023, the Democratic Republic of the Congo (DRC) has experienced 15 EVD outbreaks [7]. EVD outbreaks also occurred in the Republic of Congo in 2001–2003, 2005 and in Gabon in 1994–1997, 2001–2002 [8,9]. MVD outbreaks affected DRC from 1998 to 2000 and Gabon in 2023 [10]. VHFs viruses pose severe threats to both human and animal health due to their very high morbidity and mortality rates, human-to-human transmission and the potential to be aerosolized and used as bioweapons [11]. VHFs share common features in terms of virus structure, clinical manifestations and epidemiological characteristics, with case fatality rates up to 90% [12].

In a systemic framework of interactions between pathogens, hosts and their shared environment, the term “risk factor” refer to agents or environmental variables that influence a given health phenomenon, where risk is the probability of occurrence of that health event [13]. This study focuses on spatially relevant determinants. These include spatial risk factors which refer specifically to those that determine the environmental, socio-economic and socio-political context of the milieu in which the disease occurs or spreads. Most are factors with spatially referenced (geolocatable) data, but “spatial risk factors” also include determinants that, while not strictly spatial, are spatially aggregable and relevant for disease mapping (e.g. education level, gross per capita income).

Spatial patterns in the distribution of zoonotic diseases are regularly observed. Environmental factors (climate, vegetation, landscape characteristics, etc.), as well as human factors (socio-economical, socio-political, socio-environmental) influence the characteristics of the various agents, their behaviour and their relations. Spatial and temporal variations in health outcomes are therefore the result of these interactions [14]. This has led several authors to try to understand the reasons why the risk is higher in some areas than in others [8,15,16]. However, to date, spatially relevant determinants shaping outbreak patterns of VHF are still not fully identified and understood [17].

The tropical and subtropical moist broadleaf forest ecoregion is the predominant biome in the central region of Africa [18,19]. It has witnessed numerous outbreaks of VHF epidemics such as EVD, MVD, yellow fever (YF), dengue and LF [20,21], with the total number of cases between 2013 and 2023 shown in Fig 1. Cases of RVF and Crimean-Congo haemorrhagic fever (CCHF) have been observed, but no epidemics or epizootics have yet been recorded [22–24]. The factors contributing to zoonotic epidemics in this region are rarely studied due to a lack of human, material, and financial resources [20]. Whilst many high-income countries have

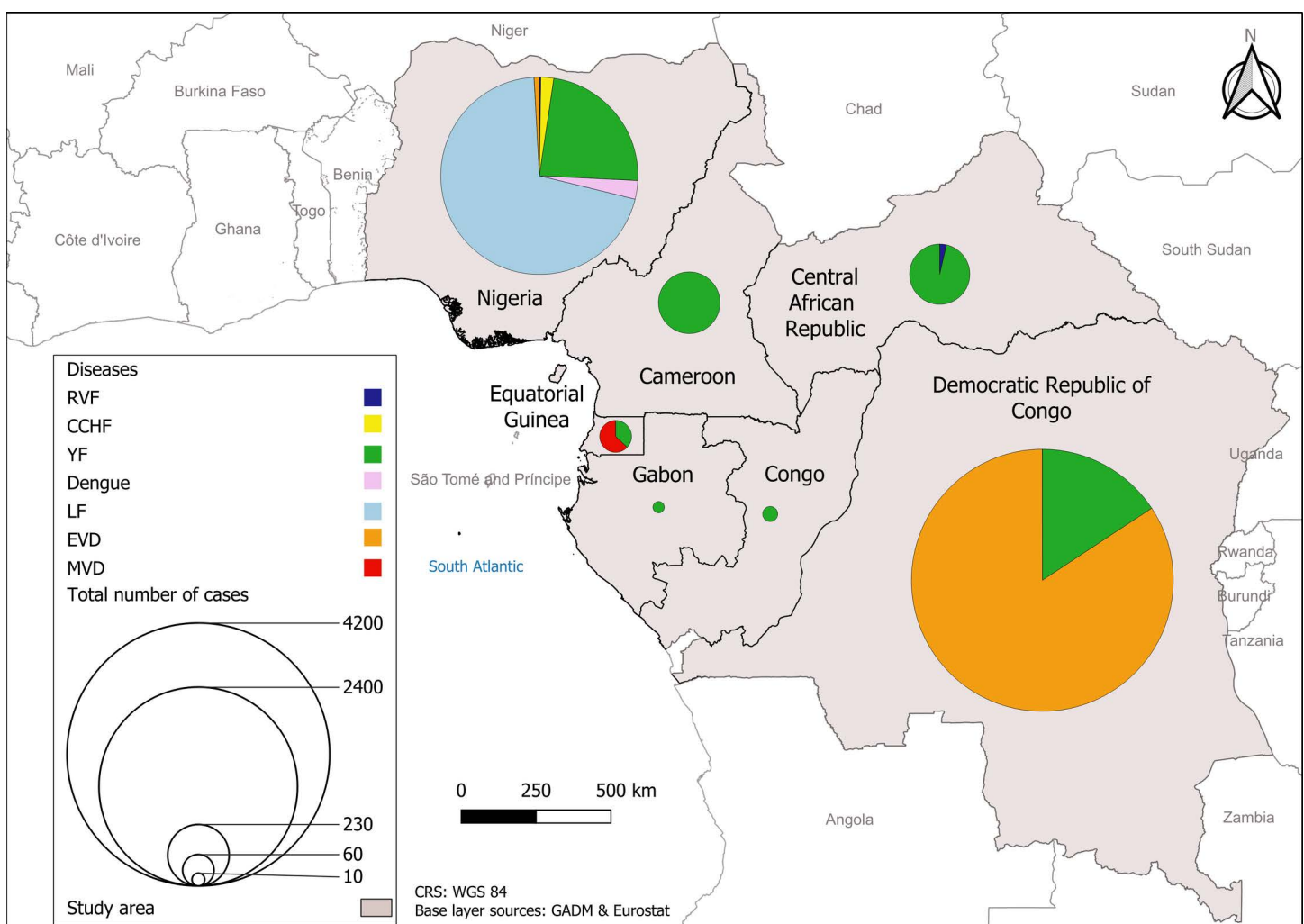


Fig 1. Total number of clinical cases of each VHF in the study area over the 2013–2023 period. Data sources vary by country and disease and are detailed in S1 Table. Direct link to the base layers of the map (the country border shape): <https://ec.europa.eu/eurostat/web/gisco/geodata/administrative-units>.

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successfully reduced or eradicated some zoonotic diseases, the heaviest burden of zoonotic diseases now often falls on low and middle-income countries, such as sub-Saharan African countries [25], who historically have the poorest health infrastructure and are most dependent on livestock for their livelihoods [2,25]. Because of its rich biodiversity, the tropical moist broadleaf forest in the central region of Africa is one of the regions where outbreaks of emerging infectious diseases (including VHF) are most expected to occur [2]. The emergence of novel zoonotic pathogens can even generate super pathogens with surprisingly efficient spread strategies.

In order to predict and prevent the occurrence of such diseases, it is relevant to identify and understand the mechanism of their occurrence by investigating their risk factors [26], which can be further used to create risk maps that are powerful tools for targeting decisions and epidemiologic surveillance in resource-limited settings [27,28]. Reviews play an important role in evidence synthesis [29] but, to our knowledge, no one has reviewed the spatial risk factors for VHF in this African biome [27,28]. The present study aims to assess the current status of knowledge on spatially relevant risk factors responsible for the emergence and maintenance of VHF in the tropical and subtropical moist broadleaf forest in the central region of Africa, and to identify critical research gaps to better understand and prevent future epidemics. “Emergence” refers to the appearance of a disease in a population, or to a rapid increase in the incidence or geographic extent of a disease [1]. “Maintenance” is the ability of a pathogen to survive in an ecosystem over a long period [30].

2. Methods

A scoping review was conducted following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA-ScR) guidelines, extension for scoping reviews [31].

2.1. Study area

This review focused on the seven countries covered by the tropical and subtropical moist broadleaf forest ecoregion in the central region of Africa (Fig 2), based on the map of Battistella [18]. The study area is hereafter referred to as “African tropical moist forest”.

2.2. Identification

Key concepts linked to the research question were highlighted: “risk factor”, “viral haemorrhagic fevers” and “Central Africa”. All possible word variations of each concept (synonyms and related terms) and Medical Subject Headings (MeSH) terms as appropriate were recorded (in English and in French) and validated by a librarian and an expert. Systematic search on published scientific articles related to spatial and spatially aggregable determinants of VHF was conducted using Medline/PubMed, Embase, CAB Abstracts and Scopus databases. Some online journal platforms such as Science Direct, SpringerLink, Wiley Online Library were also consulted. Search queries combining all relevant terms with Boolean operators (AND/OR) were applied in these databases (see S2 Table for examples of search queries applied in PubMed and Scopus). Forward reference search of included studies was also conducted using Google Scholar to identify other research that has referenced any relevant paper. The literature search was undertaken from October 2023 to March 2024. Zotero software version 6.0.30 was used to manage references and remove duplicates.

2.3. Screening

We excluded papers that were not peer-reviewed, and that were not in English or French [32]. No period restriction was applied. Inclusion criteria referred to at least one of the following

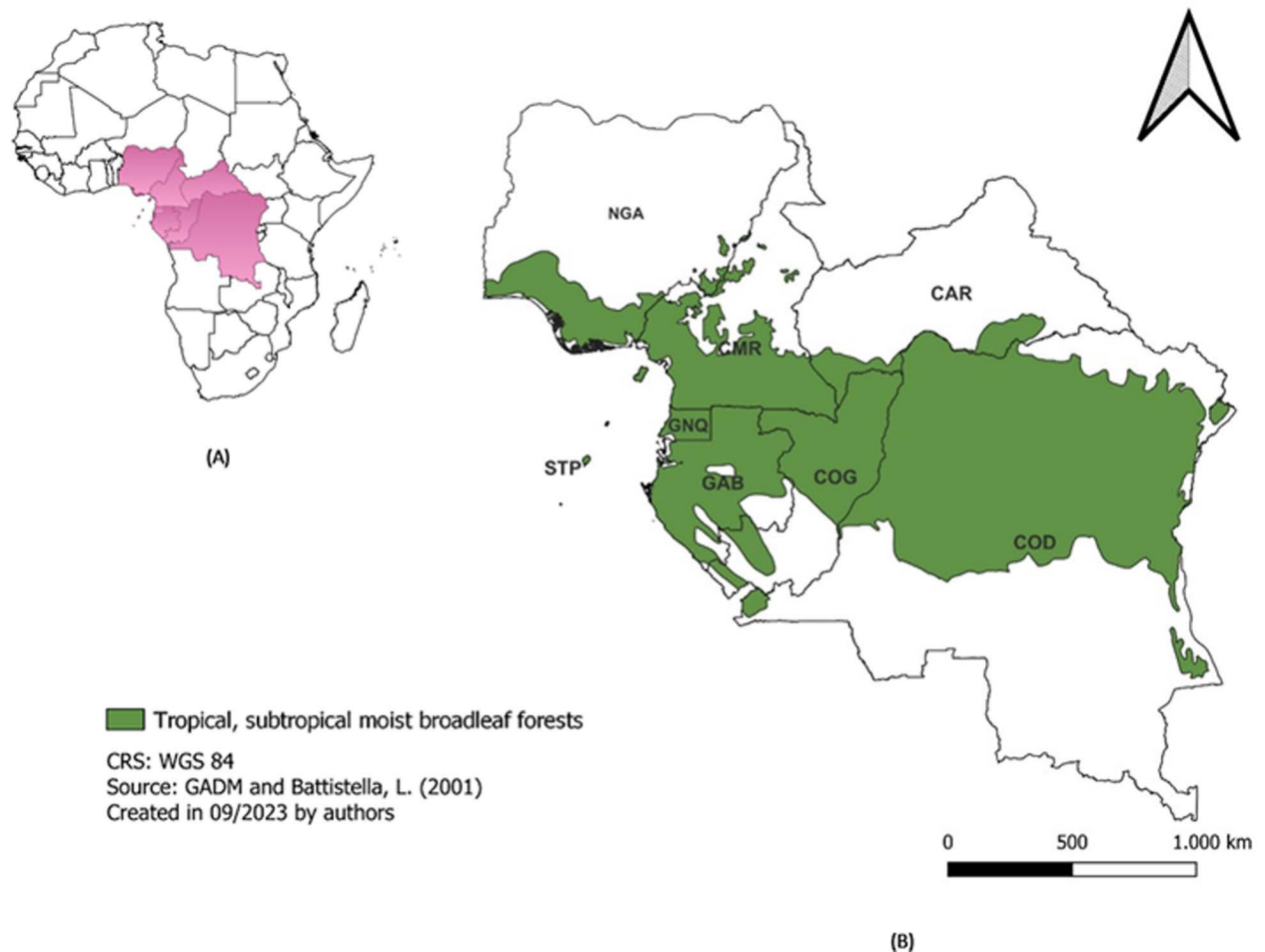


Fig 2. Study area. A) Location of the study area in Africa and B) Countries involved in the study. NGA = Nigeria; CMR = Cameroon; CAR = Central African Republic; GNQ = Equatorial Guinea; GAB = Gabon; COG = Republic of Congo; COD = Democratic Republic of Congo. Direct links to the base layers of the map (the country border shape): <https://gadm.org/> and to the biome map <https://africa-knowledge-platform.ec.europa.eu/dataset/biomes>.

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conditions: (1) the application of spatial analysis or mapping; (2) studies on ecological variables that may promote VHF introduction, maintenance and circulation, including variables related to climate, land use/cover, soil characteristics, vegetation, topography, demographic, socio-economic and animal/vector hosts and reservoir; (3) papers that concerned one or more of the 7 countries of interest.

2.4. Selection process

The selection process started with the removal of duplicates (Fig 3). Titles and abstracts of documents were then screened and kept or not based on inclusion/exclusion criteria. The next step was a full reading of the articles and only papers relating to the countries of interest were finally selected for qualitative analysis ($n = 69$). In addition, ten other articles of interest were added from the reference list of the selected papers. The search strategy and the included papers were peer reviewed by an expert.

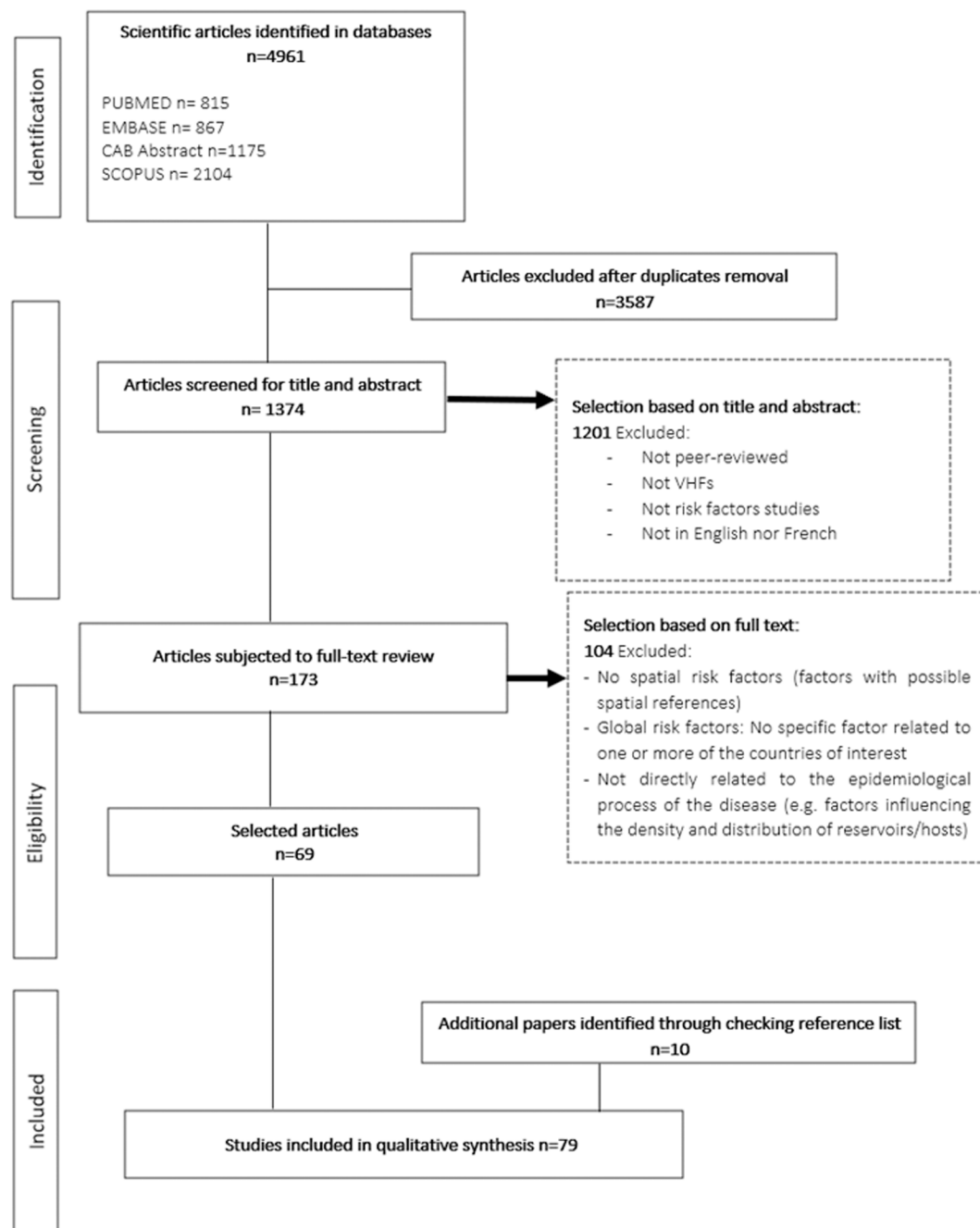


Fig 3. Flow of the literature search through the different phases of the scoping review.

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2.5. Data extraction

First, we extracted the relevant data contained in each selected article using an Excel spreadsheet extraction form (S3 Table). We focused on risk factors linked to characteristics that could have a spatial reference and to spatially aggregable determinants that can be aggregated by administrative units. A factor was considered as spatial if one or more of the following conditions were fulfilled: (i) the factor was explicitly described as a spatial one; (ii) it has been

involved in studies that analysed disease distribution data with the aim to characterize their spatial or temporal pattern, to identify spatial predictors associated with disease presence, or to map disease risk; (iii) it has been considered in previous studies as being spatially correlated with other phenomena (e.g. urban development, traffic accident); (iv) the existence of spatial dependency between individual characteristics and the possibility to aggregate those data by spatial units, such as demographic or socio-economic information provided by censuses. We focused on geographically referenced risk factors that can be mapped using geographic information system (GIS) techniques.

For each selected article, we extracted the title, the authors, the year of publication, the country(ies) under study, the VHF concerned, the methodological design, the epidemiological processes and spatially relevant variables studied, and a summary of the main results. For each variable, we extracted information on its association with epidemiological processes, the nature and significance of the relationship, and its availability. All these analyses (paper gathering, visualization, items highlighting and data selection within each paper) were performed in Zotero software. The data extraction form was subjected to a pilot extraction performed on 4 of the selected articles (pre-test). Data were extracted by one independent reviewer (ISK) and a second reviewer (CL) checked data extraction for accuracy.

2.6. Data synthesis

A thematic content analysis was carried out to classify risk factors into themes and sub-themes by affinity. In line with the holistic One Health approach, which seeks to unite the environmental, animal and human dimensions of health, we have sought to identify and group risk factors according to these broad subdivisions. More specifically, the sentences and figures extracted from the selected articles were then aggregated according to whether they related to one or other of the three risk factor categories (environmental, animal or human). Within each category, factors were then grouped according to whether they belong to one or other of the themes or sub-themes referring to climatic factors, land cover, topography, vectors, domestic and wild fauna, or human factors. This type of organization provides a cross-sectional overview of the spatial risk factors common to certain countries, certain diseases and certain epidemiological processes. This division into themes and sub-themes seemed to be useful for gaining a detailed view of how each factor acts alone and interacts with other elements of the system. Information on the associations between spatial variables and epidemiological processes made it possible to establish the confirmed or assumed status of each risk factor identified (S4 Table). A risk factor was considered as confirmed when it was possible to establish its association with disease occurrence risk, statistically quantify the strength of the association, and establish a significance level (p-value or % of the model explained). Otherwise, it is presumed or assumed. Descriptive statistics were conducted to describe the proportion of papers mentioning each risk factor category, and the proportion of paper per study type. Summary tables reporting the characteristics and results of each paper were produced. The research protocol was freely deposited on the Open Science Framework on 08 March 2024 and can be found at the following link <https://osf.io/p6x8d/>.

3. Results

A large part of the 79 selected papers (see contextual summary and characteristics of each of these papers in S5 Table) were reviews (31%), followed by cross-sectional studies (27%) and spatial modelling studies (21%). These articles were published over the 1993–2023 period. They concerned mainly Nigeria (48%), DRC (29%) and Cameroon (27%).

Most of the VHFs under review are vector-borne (RVF, dengue, YF, CCHF), while the others are directly transmitted (EVD, LF and MVD). The papers reviewed focused mainly on EVD (36%) and RVF (28%), while LF (10%) and MVD (8%) were the least studied diseases.

Risk factors identified in the literature relate to emergence and maintenance processes. Various terms have been aggregated, especially incidence, occurrence, exposure, infection, and distribution. Both emergence and maintenance are influenced by the three types of disease transmission: animal to human transmission (also known as zoonotic spillover), interhuman transmission and animal to animal transmission. [Table 1](#) shows very clearly that human-to-human transmission is mainly driven by demographic and socio-economic factors, whereas zoonotic spillovers are determined by almost all groups of factors, especially those related to human activities and behaviours. Emergence and maintenance of VHFs are the result of a complex interaction between environmental and human factors, as well as factors linked to animal hosts and vectors ([Fig 4](#)). These various factors, classified by categories, have been reviewed and detailed as follows.

[Fig 5](#) summarizes the proportion of papers mentioning each risk factor category and shows that land cover and land use risk factors, as well as precipitation and humidity were the most reported for VHFs. The main results are presented below, but the details (particularly the figures of significant associations) are given in [S3](#) and [S4 Tables](#).

3.1. Environmental variables

3.1.1. Climate. Given that most VHFs are arthropod-borne zoonoses, climatic drivers highly influence their transmission patterns [[11,33,63](#)], by affecting host and vector diversity, abundance, genetics and the pathogen infection load in the host and vector [[11](#)].

Table 1. Distribution of factors according to whether they drive a risk of zoonotic spillover, human-to-human transmission, or animal to animal transmission.

Risk factors		Transmission type		
		Zoonotic spillover	Human-to-human	Animal to animal
Climate	Temperature	[15] [26] [30] [33] [34] [35] [36]	[37] [38]	[30] [39]
	Precipitations and humidity	[16] [26] [30] [33] [34] [35] [40] [41] [42] [43] [44]	[20] [24] [33] [37] [38] [76]	[20] [24] [30] [39] [40] [45] [46] [47] [48] [49]
Land cover & land use	Vegetation	[15] [16] [26] [35] [36] [43] [50] [51] [52] [53]	[52]	[30] [46] [47] [48] [51] [54]
	Water bodies, rivers, and streams	[30] [55]		[24] [30] [46] [47] [49]
	Agriculture	[16] [33] [41] [50] [56]		[24] [30] [46] [47] [49] [57]
	Built-up land	[41] [58]	[41] [58] [59]	
Topography		[11] [16] [35] [60]	[38] [60]	[39] [46]
Arthropod vectors		[16] [20] [22] [45] [50] [57] [61] [62]	[33] [59]	[45] [47] [48] [49] [62]
Domestic vertebrate hosts		[15] [45]		[30] [45] [47] [48] [49] [54] [63] [64] [65] [66]
Wildlife		[11] [35] [38] [43] [45] [53] [61] [67] [68]		[30] [39] [45]
Demography and population		[8] [16] [34] [35] [36] [43] [44] [60] [69] [70]	[11] [30] [34] [35] [36] [37] [53] [63] [69] [71] [72]	[30] [46]
Socio-cultural and behavioural risk factors		[16] [20] [23] [34] [35] [36] [38] [40] [43] [53] [60] [61] [63] [64] [67] [69] [73] [74] [75] [76] [77]	[59] [70] [75] [78] [79]	[79]
Socio-economic and political risk factors		[16] [20] [33] [41] [52] [53] [70] [77] [80] [81]	[37] [53] [71] [73] [78] [79] [82] [83]	[59]

References in bold represent articles in which risk factors have been statistically established, while those not in bold represent articles in which they have not yet been.

Lack of evidence	Very few evidence	Limited evidence	Strong evidence
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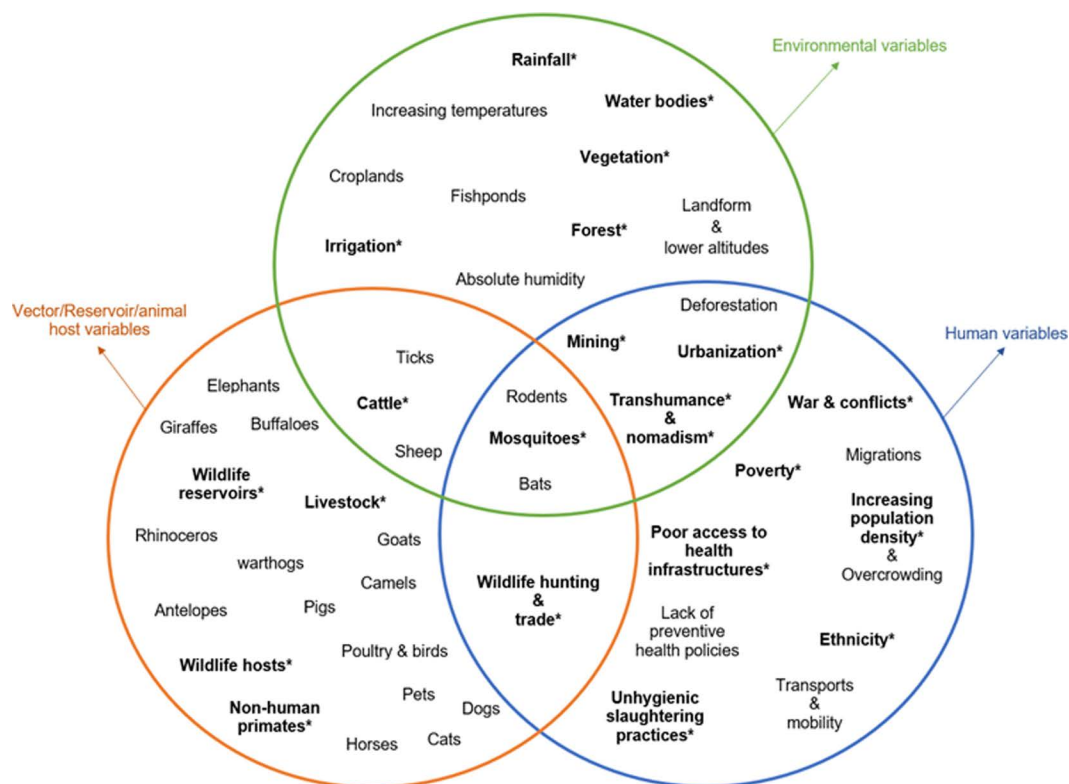


Fig 4. Integrating human, animal and environmental spatially relevant determinants for the emergence and maintenance of VHFs under the One Health approach. Components in bold and marked with an asterisk represent those for which at least 2 statistically significant associations have been demonstrated.

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3.1.1.1. Temperature: Temperature is the most critical factor influencing the risk of VHFs. It affects mosquito reproduction and virus replication [60], impacting breeding site availability, longevity and their competence to microorganisms [20]. In Cameroon, temperature higher than mean temperature range [24.2–25.5 °C] reduce RVF by decreasing seropositivity in cattle [39], while intermediate temperatures promote stable vector populations and RVF maintenance in the African tropical moist forest [30]. *Ae. aegypti* larvae cannot survive below 10 °C and adults below 5 °C, limiting the distribution of diseases transmitted by this vector, like dengue and YF in tropical and sub-tropical regions [84]. Global warming is a likely contributor to the re-emergence of YF virus in endemic and non-endemic areas in Nigeria [33], and alter tick populations [11].

Additionally, temperature is a predictor of EVD outbreaks and MVD [38]. “Temperature Annual Range” and “Mean Diurnal Temperature Range” are key spatial variables determining the distribution of EVD in Africa [34] with small annual temperature ranges being significantly and negatively associated with the areas of high environmental favourability for Ebola virus presence [36].

Land surface temperature significantly predicts MVD zoonotic transmission [26] and had the second most important effect on global CCHF transmission risk to humans [15]. Night-time land surface temperature had an impact on the EVD distribution in an Africa-wide environmental suitability model [35].

3.1.1.2. Precipitations and humidity: Heavy rainfalls is a significant risk factor for mosquito-borne VHF's infection, particularly RVF in cattle and camels in Nigeria [46,85] as

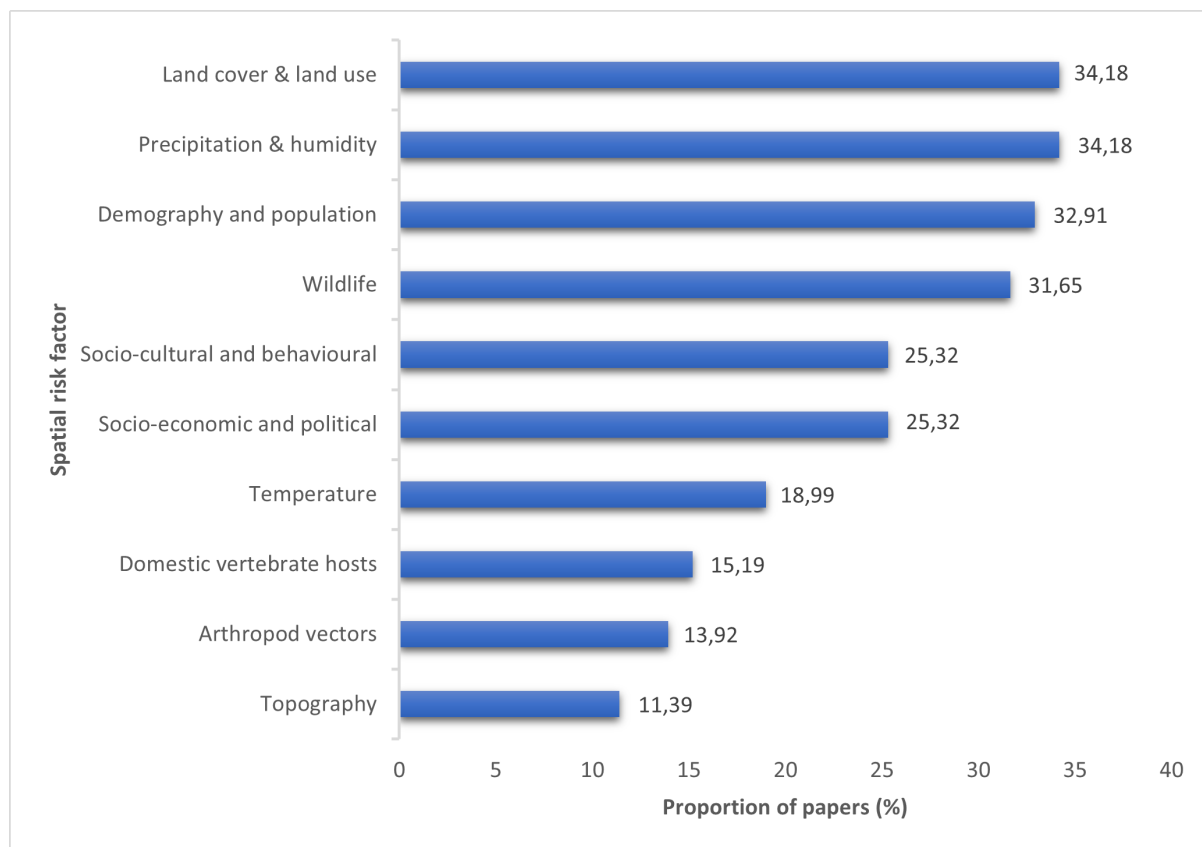


Fig 5. Proportion of papers mentioning each risk factor category.

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well as YF and dengue transmission in Nigeria and Cameroon respectively [33,86]. High rainfall increases RVF occurrence in pastoral cattle herds in Nigeria [47]. In DRC, short periods of heavy rainfall [60] led to multiple flooding events followed by early droughts which increase breeding sites and consequently the density of mosquitoes [20,24,79]. Excessive seasonal rain, especially after drought, significantly contributes to RVF outbreaks in Nigeria [40]. In Cameroon, rare heavy rainfall and flooding are critical entomological risk factors for RVF in cattle [39,45]. An increase in the number of wet months raises the odds of *Ae. albopictus* (primary vector of RVF virus) presence by seven times in Cameroon [87], and intermediate rainfall can establish stable vector populations for RVF maintenance [30]. Increasing rainfall intensity is also a driver for YF re-emergence in Nigeria [33].

Redding et al. [41] found a strong association between LF cases and rainfall in southern Nigeria, with LF peaking in areas with 1500–2000 mm of annual rainfall [42] and declining sharply in the more arid northeast [16]. In Nigeria, it has been shown that the incidence of LF in humans correlates negatively with rainfall [88]. Rodents will forage near humans only when rainfall levels drop [88,89]. Mean monthly rainfall is a key spatial variable influencing EVD distribution and outbreak dynamics in parts of Republic of the Congo and Gabon [34,37,43], with spillover intensity peaking with intermediate rainfall [44].

Absolute humidity also affects the development of VHF vectors, particularly ticks, as it is crucial for their water balance [48]. In Cameroon, higher absolute humidity is positively linked to lower odds of CCHF virus antibody seropositivity in pastoral cattle [48].

Additionally, potential evapotranspiration is important for predicting EVD outbreak and MVD zoonotic transmission [26,38].

3.1.2. Land cover and land use. Around 34.2% of the reviewed papers identified land-use and land cover changes (Fig 5) as favouring factors for VHF in the study area, including RVE, LF and EVD.

3.1.2.1. Vegetation: Vegetation plays an important role in harbouring mosquito breeding sites. Bushy vegetation has been found to significantly influence RVE's emergence in cattle [47] and occurrence in camels of Nigeria [46]. The presence of bush around the house is also a potential factor increasing the risk for LF infection in humans in Nigeria [50,90].

Shrub density is positively associated with CCHF virus antibody seropositivity in pastoral cattle in Cameroon [48]. Tick abundance correlates strongly with tree species composition and shrub cover. Areas with higher proportion of grass and shrub account for almost 62% of predicted CCHF virus emergence or re-emergence in humans, based on global CCHF virus distribution model [15]. The standard deviation of mean EVI (Enhanced Vegetation Index) (8%), and mean EVI (5%) are also critical factors influencing global CCHF transmission risk to humans [15].

Adamu et al. [46] found that RVE occurrence in one-humped camels in Nigeria was significantly associated with mosaic vegetation, corroborated by Linthicum et al. [51] using a vegetation index. Vegetation is also a key determinant in the spatial distribution of MVD [26] and EVD cases [35].

The tropical, subtropical moist broadleaf forest of our 7 countries of interest comprises about 54.9% of the continent's total forest area [91]. Forest cover is a significant covariate in model to produce maps of areas suitable for Ebola virus spillover in the Republic of the Congo and Gabon [43]. In Gabon, high prevalence regions were mainly located within forest ecosystems as it is the primary home of the zoonotic cycle of EVD [35]. This confirmed that the forest, particularly the deep forest, is the environment most at risk for Ebola viral infection in Gabon [36], as it harbours susceptible hosts such as great apes and bats [92]. Forest cover is a spatial variable that also influence other VHF such as the emergence of LF [16] and those which are mosquito driven. In the forest area, the RVE seroprevalence was significantly higher than the savannah area in cattle raised by smallholder farmers in of DRC [54]. Increase RVE virus seroconversion was noted in animals after forest exposure, even far from endemic areas [30]. Moreover, non-human primates, the primary host of dengue virus are abundant in forests, supporting the sylvatic cycle of the disease [52].

3.1.2.2. Water bodies, rivers and streams: Rivers, streams, and water bodies are breeding grounds for mosquitoes [24]. Some mosquito species, including those transmitting RVE, dengue and YF (genus *Aedes* and *Culex*) were abundantly collected from rivers in Ngaoundere, Cameroon [93]. In pastoral herds of Nigeria, the presence of rivers and streams in grazing fields was eleven times more likely to influence RVE occurrence [47,49].

In Cameroon, Ngadvou et al. [93] collected the greatest number of mosquitoes (genus *Aedes* and *Culex*) in gutters and lakes. Children living in stagnant water free environment were less likely to contract dengue in Yaoundé [55]. In the same country, animal access to water bodies significantly influenced seroprevalence of RVE virus in domestic small ruminants, with herd locations along the Benue river posing risks for RVE transmission [24]. A Nigerian study identified water bodies as key factors for camel exposure to RVE virus [46], while surveys across Africa linked proximity to water points with inter-epidemic RVE transmissions [30]. In Cameroon, areas near water banks like Kismatari and Pitoa showed significant RVE antibody seroprevalence in domestic small ruminants [24].

3.1.2.3. Agriculture: Agriculture influences VHF occurrences in two ways: by providing breeding habitats for vectors and by increasing human exposure to vectors, such as *Ae. aegypti*

species [33]. Agricultural practices, like irrigation and fishponds, are linked to increased mosquito abundance and diversity. In Nigeria, dams and irrigated rice fields significantly contribute to emergence and occurrence of RVF in herds [46,47,49]. Serological surveys have identified irrigation as a risk factor for inter-epidemic RVF transmissions and its maintenance in the environment [24,30]. Fishponds serve as breeding sites for mosquitoes, increasing the density of certain species more than natural water bodies [20]. Nomadic pastoral communities in Nigeria have recognized ponds as risk factors for RVF occurrence [49]. In Cameroon, the presence of ponds may also favour sporadic RVF transmission among livestock [57]. Rainfed croplands have been identified as a risk factor for RVF occurrence, and in [46] one-humped camels in Nigeria, they were significantly associated with RVF virus antibodies [46].

Additionally, the destruction of natural habitats for agricultural activities has driven multi-mammate rats (*Mastomys natalensis*) to seek new homes, often invading residential areas and increasing the risk of LF emergence [16] and infection [50].

3.1.2.4. Built-up land: Both occurrence and incidence models of LF in Nigeria show a strong positive association with built-up land [41]. LF is a neglected endemic zoonosis primarily found in rural West African regions [41,50]. Redding et al. [41] observed that LF tends to invade urbanized areas, which may be attributed to increased reporting and medical access or to rodent synanthropy, as urban environments provide favourable conditions for rodents [41]. Additionally, higher population densities in urban areas may facilitate human-to-human transmission and affect the distribution of rodent reservoirs and their interactions with humans [58]. Similarly, seropositivity rates for the dengue virus in Cameroon were higher near major urban centres compared to more remotely located areas, suggesting an association between dengue cases and urban areas [59].

3.1.3. Topography. Higher altitudes have been associated with a significant decrease of the odds of RVF seropositivity in cattle in Cameroon, RVF occurrence in one-humped camel in Nigeria [39,46], and YF seropositivity in DRC [60]. Canelas et al. [87] further confirm that, in Cameroon, lower altitudes are linked to higher odds of *Ae. albopictus* (vector of RVF, YF and dengue) presence. Additionally, elevation is recognized as an environmental covariate driving the outbreaks [38] and cases distribution of EVD [35].

Landforms, such as mountain chains between Nigeria and Cameroon, may function as natural barriers to animal movements, including infected rodents. This could account for the lack of reported LF outbreak in Cameroon, while the neighbouring Nigeria has experienced several large-scale outbreaks [11,16], even if the Lassa virus reservoir and host *M. natalensis* is also found in Cameroon [90].

3.2. Animal distribution and movements

3.2.1. Arthropod vectors. Mosquito vector density and diversity is confirmed as a spatial factor involved in the emergence and maintenance of mosquito-borne arboviruses in Africa [20]. Specific mosquito species are key to maintaining the RVF virus, influencing both enzootic and epizootic cycles [62]. In Nigeria, studies show that pastoralists perceived the presence of mosquitoes as a major risk factor for RVF in cattle [47,49]. Additionally, mean matrix scores indicated that the entry pathway for the RVF agent into the nomadic pastoral herds was primarily through RVF virus-infected mosquitoes [49]. Statistical analysis indicated that the presence of RVF virus-infected mosquitoes in pastoral environments increased the likelihood of RVF occurrence in pastoral herds of Nigeria by eight times [47]. In Cameroon, the presence of primary (*Aedes*) and secondary (*Culex*, *Anopheles*, and *Mansonia*) mosquito vectors poses a risk of RVF transmission to susceptible hosts [45]. Although certain species of mosquito have been associated with the maintenance of the RVF virus in Kenya through

vertical transmission from adult mosquitoes to their progeny via eggs, this transmission mechanism has not been reported in Western and Central Africa [30].

CCHF is transmitted through tick bites (*Hyalomma marginatum*) or direct contact with the body fluids of infected people or livestock [67,94]. Regardless of the region, a higher risk of CCHF virus infection is generally associated with exposure to ticks (either through bites or handling them without gloves) or to animal (particularly among herders, agricultural workers, abattoir staff, veterinarians) [22].

3.2.2. Domestic vertebrate hosts. High cattle density is identified as a risk factor for the occurrence and emergence of RVF in nomadic pastoral herds in Nigeria [47,49]. A stable, dense population of susceptible livestock acts as a major amplification hosts for RVF maintenance in endemic countries [30]. In Cameroon, the presence of various domestic vertebrate hosts (including small ruminants, cattle, dogs, cats, horses, donkeys, and poultry) should be considered when defining RVF risk areas [45]. Additionally, a large serological survey during the 2001–2002 EVD outbreak in Gabon indicated that dogs might be asymptotically infected with Ebola virus, likely due to consuming infected carcasses or contact with body fluids, potentially enabling transmission [63]. While bats and non-human primates are significant in filovirus transmission, other species like pigs and dogs may also be involved [63]. Moreover, sheep appear to be at higher risk for RVF compared to other domestic animals, showing significantly higher seroprevalence [65]. For CCHF, individuals living or working near livestock are considered to be at the highest risk for infection [15].

During the dry season, transhumance addresses seasonal shortages of pasture and water [48]. This practice increases the risk of zoonotic disease transmission, as it brings domestic and wild animals into contact at water source and in pasture, facilitating the spread of viruses like RVF and CCHF [45]. For example, in Cameroon, cattle that participated in transhumance had double the odds of being seropositive for CCHF compared to those that are not involved in the practice [48]. In Nigeria, nomadic pastoral cattle exhibited a higher prevalence of RVF (7.4%) than agro-pastoral animals (3.8%), with animal movements significantly influencing RVF occurrence [47]. Livestock movement could also influence the risk of CCHF virus transmission [64], with potential introduction to a non-endemic area through legal or illegal trade of infected animals or ticks [64].

Contacts between susceptible hosts and mosquitoes at animal watering sites contribute to RVF virus maintenance [30]. An extensive husbandry system significantly influences RVF occurrence in herds while sharing a common water source during nomadic movements was increases the likelihood of RVF occurrence in Nigerian herds in Nigeria by fifty-three times (OR: 24.94, 95% CI: 13.54, 45.93) [66]. In the same region, cattle often graze alongside sheep and goats, which also impacts RVF occurrence in nomadic herds [66]. Sheep are more susceptible to RVF, experiencing more severe clinical outcomes than other ruminants [65,95]. This mixed grazing raises the risk of cross-infection with the RVF virus through infected aerosols [66].

3.2.3. Wildlife. Wildlife plays a crucial role as amplification hosts and reservoirs in the epidemiology of infectious diseases such as EVD, MVD, RVF and CCHF [34]. The presence of wildlife (monkeys, warthogs, rodents, reptiles, etc.) should be considered when defining RVF risk areas [45]. Confirmed wildlife reservoirs for the RVF virus include African buffalos (*Syncerus caffer*), giraffes (*Giraffa camelopardalis*), desert warthogs (*Phacochoerus aethiopicus*), elephants (*Loxodonta africana*), rhinoceroses (*Diceros bicornis*), and possibly bats [30].

3.2.3.1. Rodents: Exposure to rodents has been significantly linked to seropositivity for EVD in DRC [61]. The presence of multimammate rats in/around the houses is the potential risk factor for LF infection [50]. Additionally, rodent species richness serves as a spatial

variable that influences LF emergence events, showing a significant negative association with LF emergence events. This suggests that a dilution effect may apply to the spatial spread of these diseases [16].

3.2.3.2. Bats: Fruit bats are suspected of being reservoirs in the EVD transmission cycle [38]. They may transmit the virus to other wildlife (e.g., duikers, non-human primates) and humans [53]. Modelling studies indicate that the bat distribution significantly impacts EVD distribution and spillover [35,43]. This is supported by Moyon et al. [68], who found that “contact with bats” was significantly associated with Ebola virus antibody detection in blood donors in the Republic of Congo [68]. In DRC, individuals with a bat contact had 1.64 times higher odds of EVD seropositivity compared to those without such contact [96]. Additionally, the Old World rousette fruit bats (*Rousettus spp.*), which serve as reservoirs for Marburg virus and the Ravn virus, contribute to pandemic risk [11].

3.2.3.3. Antelopes and buffalo: Contact between cattle and antelopes increases the risk of cattle becoming seropositive for RVF. While several studies report high seroprevalences in wildlife species, such as various antelopes and buffalo, their epidemiological significance remains unclear [39]. In DRC, exposure to duikers was significantly associated with EVD seropositivity [61].

3.2.3.4. Birds: Birds seem to be resistant to CCHF viral infection but can act as mechanical vectors by transporting infected ticks [94]. Migrating birds provide blood meals for immature ticks, facilitating the spread of infected vectors to remote areas [97].

3.2.3.5. Non-human primates (NHP): In the transmission cycle of the YF virus, NHPs (including chimpanzees, gorilla, and other monkey species) serve as the reservoir hosts of the virus in the forest [33,77]. Besides, NHPs contribute to the sylvan-to-urban spillover of the dengue virus [52]. These wild animals are also affected by Ebola virus, with studies showing serological evidence of exposure in chimpanzees in countries without recorded EVD outbreaks, such as Cameroon [73]. Notably, EVD epidemics in Gabon and Congo have followed significant declines in NHP populations due to EVD infection [98], indicating spillover with the human index cases [99,100]. During human outbreaks, carcasses of western gorillas (*Gorilla gorilla*) and chimpanzees (*Pan troglodytes*) have been discovered in nearby forests. Chimpanzees were identified as the source of an outbreak in Gabon in 1996 [100]. Several studies have found that consumption or contact with NHPs is meaningfully associated with increased odds of Ebola virus seropositivity [101], as well as with MVD transmission [102].

3.3. Human variables

3.3.1. Demography and population. **3.3.1.1. Human population density and growth:** Several studies have shown that population density is a significant factor in the risk of zoonotic EVD transmission. Specifically, it was found that higher population density correlates with spillover risk [8]. A literature review further identified human population density as a key risk factor for *Zaire ebolavirus* spillover [43]. According to Redding et al. [34], human population size has the most significant impact on EVD emergence and epidemic potential in Africa [34]. Furthermore, regions experiencing rising population density are associated with an increased risk of EVD spillover [44].

The spread of dengue is also attributed to population growth [70]. Research has shown that population growth serves as a spatial variable affecting the emergence of LF in Nigeria [16]. In addition, increasing human population may accelerate the risk of EVD transmission in Africa [35].

3.3.1.2. Urbanization: In low- and middle-income countries, demographic growth is associated with poor environmental hygiene and high urbanization levels. This likely favours *Aedes* mosquito productivity and might partly explain the frequent outbreaks of

mosquito-borne zoonoses in the city, like YF [60]. Urbanization also contributes to rural exodus, which has been shown to facilitate the spread of dengue [70].

In Cameroon, urbanization levels can indicate the presence of *Aedes albopictus*. Specifically, a 1% increase in peri-urban area raises the likelihood of this vector's presence by 1.3 times. *Aedes* mosquitoes are known vectors for RVE, YF and dengue. Human exposure to *Ae. aegypti* increases during urban development [33]. Seropositivity rates for dengue and YF, carried by *Ae. aegypti* and *Ae. albopictus*, are higher near major urban centres in Cameroon [59]. In Nigeria, RVE occurrence in one-humped camels is significantly linked to urban areas [46]. LF incidence is positively associated with poverty and urbanization, influencing effective human–rodent contact [41].

Proximity to waste dumpsites is a risk factor for dengue virus infection. Vectors lay eggs in artificial water containers found in homes and waste sites [81]. A significant association between dengue prevalence and residence near waste dumps has been found in Abuja (Nigeria) [81]. Another study confirmed that living near refuse dumps is a significant risk factor for dengue seropositivity [52].

3.3.1.3. Population movements: It is likely that the active and uncontrolled migration of humans [60] and animal population might have played a key role in spreading RVE virus in the DRC. The role of population movement in the emergence and spread of mosquito-borne viruses is highlighted by a recent YF outbreak that began in Angola and spread to the DRC through transboundary trade [60]. The influence of population mobility and transportation on VHF epidemiology was predominant in the dispersal of EVD cases [35,69]. “Human mobility” encompasses a broader range of movements than “migration”, including tourists who do not typically engage in migration [53]. Local and global connectivity played a major role in disease importation in Nigeria, where the first case of EVD was recorded in July 2014 after an infected Liberian-American landed in the densely populated town Lagos [35,53]. Population movements increase the risk of EVD and MVD transmission by rising contacts rates between humans and infected individuals or animals [63]. Porous borders facilitated secondary transmission during the 2014–2016 West Africa EVD outbreak [72]. Countries lacking adequate health screening at entry points experienced introduction and dispersal of arboviral zoonosis like RVE [30] and YF, especially if imported cases reach areas conducive to outbreaks [11]. Proximity of infected individuals to main roads is linked to EVD dispersal [37], with a significant correlation found between Ebola virus locations and distance to roads [36]. In Nigeria, Sokoto and Borno States, which border countries with reported RVE virus infections (Niger, Chad, Cameroon), show relatively higher RVE virus seropositivity rates among residents [23]. These borders are porous and poorly monitored, facilitating the movement of potentially infected domestic ruminants [103].

3.3.2. Socio-cultural and behavioural risk factors. 3.3.2.1. Deforestation and human forest activities: Human encroachment into previously uninhabited areas, through forest fragmentation and habitat destruction, contributes to the spillover of zoonotic pathogens to humans [63], including LF [16,90]. In Cameroon, the increased risk of Ebola virus infection has been linked to logging activities such as clearing and burning [76]. Logged forests provide adequate aeration, humidity, and temperature for mosquito reproduction, enhancing their density and diversity [20]. Intensive deforestation in north-western DRC, Cameroon and CAR has further increased mosquito density and diversity, facilitating the emergence of YF and RVE [60,79].

3.3.2.2. Ethnicity: In 1993, ethnic background, particularly among the Congo basin forest ethnic groups, was identified as a significant factor influencing filovirus antibody activity among the forest communities [75]. Subsequent studies confirmed that ethnic background remains an important risk factor for Ebola virus exposure in many communities, as it shapes

various community behaviours (such as feeding, funerals, and health seeking) among inhabitants, including the Baka Community of the Tropical Rainforest in Cameroon [73]. Specifically, feeding behaviour, particularly the consumption of uncooked fresh bush meat, is a crucial risk factor for Ebola virus exposure [73,76].

3.3.2.3. Water storage: Farmers in the Sudan savannah in Nigeria commonly build small dams to store water at the start of the wet season. In Cameroon, practices such as using temporary walls materials, storing water in containers, keeping old tires in yard, and having uncovered water containers have been independently linked to anti-dengue IgG positivity [104]. These practices create favourable conditions for mosquito breeding, which in turn facilitates the spread of RVF virus and dengue [40,104].

3.3.2.4. Animal slaughtering techniques: People involved in animal slaughtering during events such as Eid-al Adha face risks of infection from VHF s such as CCHF [67] and RVF [74]. High-risk practices, including slaughtering, evisceration, and processing raw meat without protective equipment, as well as using bare mouth to enhance flaying contribute to RVF transmission in abattoirs and slaughterhouses [23]. Significant anthropogenic factors, such as contact with aborted animal tissue, birthing, skinning and/or slaughtering an animal, are significantly associated with RVF infection in Gabon [74]. Abattoirs and slaughterhouses environments may also influence vector dynamics, such as the creation of standing water for mosquito breeding [30]. Additionally, animal handling and slaughtering are noted as risk factors for CCHF virus transmission [67].

3.3.2.5. Wildlife hunting and trade: Cultural practices often linked with poverty, like bushmeat hunting, increase human exposure to wildlife that may harbor several diseases, including EVD [35,69]. In the DRC, hunting, butchering/skinning of bushmeat are significantly associated with human seropositivity for EVD [61]. In CAR, filovirus antibody prevalence among hunter-gatherers is significantly higher than that among farmers who are not in contact with the forest [75].

Lee-Cruz et al. [43] identified anthropogenic factors like bushmeat hunting, trade and consumption as risk factors for *Zaire ebolavirus* spillover. In a spatio-temporal analysis of areas at risk for Ebola virus spillover in Central Africa, hunting areas and bushmeat trade were ranked as the most important risk factors [43].

3.3.3. Socio-economic and political risk factors. **3.3.3.1. Poverty:** Poverty represents a major factor favouring EVD, MVD, LF, and dengue. EVD outbreaks have occurred in rural areas, among geographically isolated populations with poor housing conditions. Poverty-related issues, such as prostitution, violence and sexual exploitation, contribute to the spread of EVD [53,82]. In the tropical rainforest of Cameroon, the Baka community often avoids seeking medical treatment when ill, which drives EVD transmission [73]. Moreover, inadequate infrastructure, such as poor water and sanitation, is assumed to increase EVD transmission [71]. Positive Marburg virus antibodies are significantly associated with mining work in DRC, indicating that local mines may serve as sites of primary infection through exposure to zoonotic reservoirs [80]. In Nigeria, both occurrence and incidence models of LF showed that poverty prevalence was linked to its incidence [41]. Poor housing quality favours close contacts between rodents and humans [90]. Furthermore, gross domestic product per capita is a spatial factor influencing the LF emergence in Nigeria [16]. Socio-economic factors also contribute to the spread of dengue, as *Aedes* mosquito breeding is encouraged by the lack of drinking water and waste collection systems [70].

3.3.3.2. Access to health infrastructures: Insufficient health facilities per unit area and insufficient equipment in existing infrastructures are significant risk factors for disease transmission [105]. Proximity to healthcare facilities has been identified as a driver of EVD transmission within the Baka community in Cameroon [73], and it also affects outbreak

dynamics in countries already experiencing the disease [37,83]. Poor healthcare infrastructure in Western and Central Africa has led to high rates of dengue virus infection from 2009 to 2020 [52]. Diagnostic laboratories enable rapid detection and early interventions in infectious disease outbreak [89] and EVD transmission [105]. However, they can also introduce bias, as incidence rates tend to be higher near these diagnostic laboratories. In Nigeria, for instance, travel time to LF diagnostic laboratory negatively impacted LF incidence in humans [41].

3.3.3.3. War and political instability: Conflict leads to the destruction of health resources and infrastructure, instilling fear, stress, distrust, and causing population displacement [82]. Countries like DRC [71] and Nigeria [89] have a long history of conflicts and insecurity [82]. Internally displaced persons camps can be the original site of an outbreak as closer human contacts and poor hygiene exacerbate the risk of infection. Besides, rebel takeover of certain areas prevents the supply of medical equipment and personnel [71,82]. Research indicates a strong positive association between the number of violent events and EVD cases and deaths in DRC [78]. Furthermore, impacts of socio-political crisis, such as population displacement, may increase the risk of emergence of an RVF epidemic in CAR [79].

3.3.3.4. Preventive health policies: Immunization coverage is a crucial spatial factor in the transmission of various VHFs. Re-emergences of diseases like YF in Nigeria and DRC from 2016 to 2019 are partly due to inadequate immunization [29,54]. In Cameroon, YF outbreaks occurred in 1990, 2006, 2007, and 2021, despite the availability of the vaccine. This pattern correlates with vaccination coverage, around 57% in Cameroon in 2022, and 27.2% in Nigeria in 2006, 60.1% in 2010 with a drop of 39% in 2016 [20,77]. The high number of individuals at risk can be linked to low vaccination rates [77].

Table 2 summarizes evidence related to various risk factors for the VHFs studied, indicating areas/diseases needing further investigation to enhance our understanding of these spatially relevant risk factors in African tropical moist forest. It suggests that exploring the effects of climatic and land cover/use variables on the incidence of YF, dengue and MVD would be particularly beneficial.

4. Discussion

This study intended to review our knowledge of the spatially relevant risk factors for the emergence and maintenance of VHFs in the African tropical forest to reduce the burden of VHFs by supporting the development of risk maps and forecasting systems. This facilitates better planning and rational management of resources allocated for prevention policies (e.g. vaccination campaigns) by prioritizing areas prone to the emergence and maintenance of VHFs. We distinguished factors that have been confirmed (validated through statistical associations), and those that have just been assumed. A general overview shows that in most of the 79 reviewed papers, the environmental variables were confirmed by statistical tests, whereas the human variables were often not. This can be attributed to the fact that data on the former are more readily accessible and measurable compared to the latter, making them easier to use in modeling studies. It constitutes a limitation of current spatial models, which rarely include human factors. Furthermore, it emerges that risk factors of occurrence/infection were the most studied while the maintenance/endemicity risk factors were the less encountered. Globally, there is a clear consensus on the ecological conditions favourable to the emergence and maintenance of vector-borne VHFs: indicators of the presence of water and vegetation, average temperature and low altitudes [30,33,48].

Human beings are at the crossroads of pathological dynamics that can be illustrated in two ways. First, poverty (in various forms such as extensive livestock practices, poor access to health infrastructures, poor residential status, uncontrolled animal movements, unhygienic slaughtering techniques, bushmeat hunting, trade, and consumption) along with areas of

Table 2. Summary showing, for each group of risk factors and for each VHF studied, where the evidence is strong and where it is rarer.

Risk factors categories	Ebola virus disease	Marburg virus disease	Lassa fever	Crimean-Congo haemorrhagic fever	Rift Valley fever	Yellow fever	Dengue
Temperature	[26][34][35][37][38]	[26][38]		[15]	[30][33][39][55]	[33]	
Precipitation and humidity	[26][34][35][37][43][44]	[26]	[16][41][42][88][89]	[48]	[30][33][45][47][55][87]	[33]	[55]
Vegetation	[35][36][43][92]	[26]	[16][50][90]	[15][48]	[30][46][47][51][54]		[52][55]
Water bodies					[24][30][46][47][49]		
Agricultural lands			[16][50]		[24][30][46][47][49][57]		
Built-up lands			[41]				
Topography	[35][38]		[11][16]		[39][46]	[60]	
Arthropod Vectors	<i>Not applicable</i>	<i>Not applicable</i>	<i>Not applicable</i>	[22][67][94]	[45][47][49][62]		
Domestic vertebrate hosts	[63]			[15][64]	[30][45][47][49][54][65]		
Wildlife	[35][38][43][53][61][68][73][96][98][99][100][101]	[11][102]	[16][50]	[94][97]	[39][45]	[33][77]	[52]
Demography and population	[8][34][35][36][37][43][44][53][63][69][71][72]		[16]		[23][30]	[11][60]	[70]
Socio-cultural and behavioral	[35][36][43][61][69][73][75][76]	[75]	[16][41][90]	[48][67]	[23][30][40][45][46][66][74][79]	[59][60]	[52][59][70][81][104]
Socio-economic & socio-politic	[37][53][71][73][82][83][78]	[80]	[16][41][90]		[79]	[20][33][70][77]	[52][70]

Class thresholds: Lack of evidence = 0 papers; Very few evidence = 1 paper; Limited evidence = between 2 and 3 papers; Strong evidence = more than 3 papers.

Lack of evidence	Very few evidence	Limited evidence	Strong evidence
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deprived socio-economic status (e.g. rural areas, conflict zones, hard-to-reach regions) are widely cited risk factors. Second, social behaviours and dynamics affect the maintenance of infectious agents through vector, animal and human populations [106]. Consequently, this review shows that in the current era of global change, social and demographic processes combined to ecological aspects typical of the African tropical forest shape the socio-environmental context which foster emergence and maintenance of VHFs in this region.

It is important to emphasize that in our work, we have disaggregated risk factors by taking them separately, to understand the influence of each on the epidemiology of these diseases. However, these factors interact, with feedback, as in a complex system: changes in one factor have consequences (expected or unexpected) for other factors. For example, it appears that anthropogenic factors such as deforestation warm up the climate and cause changes in rainfall patterns leading to conditions of flood or drought.

The synthesis of knowledge generated by epidemiological studies of VHFs aimed to identify gaps in recognized spatially relevant risk factors of these diseases and to identify where future research could be directed. This study highlights the lack of published knowledge on spatially relevant drivers for YF, dengue, CCHF, and MVD in the African tropical forest, unlike EVD

and RVF where evidence is stronger. Most research focuses on Nigeria, with gaps in Equatorial Guinea, likely due to limited resources. Additionally, many identified risk factors have not been thoroughly studied due to a lack of epidemiological data. To address this, local, national, and regional monitoring systems are needed. This data could help clarify the roles of birds in the transmission of CCHF, the role of ponds and wildlife in the transmission of RVF to livestock, and the role of dogs and pigs in filovirus transmission. Given the material and human constraints involved in epidemiological (active) surveillance, alternative strategies such as those based on local expert opinion should be considered. In further studies, it could also be interesting to compare the spatial risk factors identified in the literature with those identified by local stakeholders.

This study has several limitations. First, during data extraction and synthesis phases, a semantic challenge arose because various terms were used by authors to describe the different epidemiological processes, notably: introduction, emergence, re-emergence, transmission, infection, incidence, maintenance, occurrence, exposure, distribution. We decided to group them together in such a way as to best describe two main types of process, namely emergence and maintenance. While this grouping will impact the way results are presented and synthesized, the impact on results and conclusions seems rather limited. Second, in presenting these results, we have chosen to group drivers into three broad categories: environmental, animal and human variables according to the “One health” concept, that aims to more holistically integrate the key factors of these three dimensions influencing emergence of infectious diseases. This is a subjective choice that imposes on readers a certain vision of the arrangement and interactions between all these drivers. There are undoubtedly various ways of representing these factors, which may influence the way the results are presented but which do not affect the main conclusions. Another limitation of this study is that we have probably not been exhaustive in identifying all the existing literature as the search strategy was not applied to all existing bibliographic databases. In addition, we limited our search to peer-reviewed articles written in English and French. Focusing on peer-reviewed articles ensures a certain level of reliability, but also comes with potential selection and information biases. Results and conclusions should therefore not be regarded as universal truths, as there may be other evidence beyond our scope of investigation.

For a deeper investigation of VHF risk factors, which are at the interface between humans, animals, and the environment, using a One Health approach is essential. For example, an integrated surveillance approach that involves local communities such as villagers and hunters [100] and breaks down barriers between countries would be of great help to better predict outbreaks. Risk communication can contribute to the implementation of an effective VHFs prevention and control policy at the animal-environment-human interface. A better understanding of the impact of these factors, their recognition as powerful levers for action, and a greater collaboration with local communities, would help to improve VHF prevention and control.

5. Conclusion

This study provides an overview of the multifaceted factors influencing the emergence and maintenance of VHFs both in humans and in animals in the African tropical forest. Through a scoping review of literature, the analysis underscores the complex interplay of abiotic, biotic, socio-economic, cultural, and political risk factors contributing to the spread of VHFs. The findings highlight the significance of spatially relevant determinants in understanding the dynamics of zoonotic spillovers, interhuman and interanimal transmissions. Importantly, this work lays the groundwork for the development of risk maps aimed at targeting and prioritizing at-risk areas for enhanced surveillance, prevention, and control measures. However, the study also acknowledges the existence of unanswered questions in the spatial epidemiology

of VHFs, especially a lack of evidence regarding MVD, YF and dengue, which emphasizes the need for continued research and collaboration. Ultimately, insights provided by this review have the potential to inform public health strategies and interventions aimed at mitigating the impact of VHFs in Africa and beyond.

Supporting information

S1 Table. Number of cases by VHF in the study area from 2013 to 2023.

(PDF)

S2 Table. Detailed Search strategy.

(PDF)

S3 Table. Data extraction form.

(XLSX)

S4 Table. Extracted data with the confirmed or assumed status of spatial risk factors.

(PDF)

S5 Table. Summary of all articles included in the bibliographic synthesis.

(PDF)

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