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Vectorborne diseases in West Africa: geographic distribution and geospatial characteristics

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This paper provides an overview of the methods in which geographic information systems (GIS) and remote sensing (RS) technology have been used to visualise and analyse data related to vectorborne diseases (VBD) in West Africa and to discuss the potential for these approaches to be routinely included in future studies of VBDs. GIS/RS studies of diseases that are associated with a specific geographic landscape were reviewed, including malaria, human African trypanosomiasis, leishmaniasis, lymphatic filariasis, *Loa loa* filariasis, onchocerciasis, Rift Valley fever, dengue, yellow fever, borreliosis, rickettsioses, Buruli ulcer and Q fever. RS data and powerful spatial modelling methods improve our understanding of how environmental factors affect the vectors and transmission of VBDs. There is great potential for the use of GIS/RS technologies in the surveillance, prevention and control of vectorborne and other infectious diseases in West Africa.

Keywords: Epidemiology, Vectorborne diseases, Spatial analysis, Geographic information systems, Remote sensing, West Africa

Introduction

Vectorborne diseases (VBD) place a terrible and unacceptable public health burden on developing countries. Specifically, 7 of the 10 diseases targeted by the WHO Special Programme for Research and Training in Tropical Diseases, and 7 of the 17 diseases classified as neglected tropical diseases (NTD) by WHO, are transmitted by arthropods.[1,2] VBDs play a particularly important role in West Africa because many of them are endemic to the region, and the burden of VBDs continues to be very heavy.

This review addresses a broad range of VBDs (Table 1) and vectors (Table 2) that are prevalent in West Africa (Benin, Burkina Faso, Cape Verde, Côte d'Ivoire, The Gambia, Ghana, Guinea, Guinea-Bissau, Liberia, Mali, Niger, Nigeria, Senegal, Sierra Leone, Togo). The data for this review were collected by searching the National Center for Biotechnology Information (NCBI) PubMed database and the reference lists of relevant articles. The criteria for inclusion in the study were relaxed for the references related to geographic information systems (GIS) and remote sensing (RS) applications used to study VBDs in West Africa (see the review of selected studies in Supplementary Table 1).

GIS and RS technology have opened new avenues for evaluating digital map data generated by earth-observing satellite sensors and for conducting analyses of spatial and temporal environments.[3] It is well known that the distribution of tropical VBDs is particularly sensitive to climatic and environmental factors because of the vulnerability of vectors, intermediate hosts and free-living stages. The concept of spatial focality of VBDs has been observed and discussed for many years.[4]

Numerous reviews have broadly addressed the use of GIS/RS technologies and spatial and space-time modelling approaches in the field of VBDs.[5,6] However, the potential for such technologies and methodologies to be used for the prevention, surveillance and control of tropical VBDs is a critically important issue that has not yet received the attention it deserves. Adapting mapping and modelling techniques for resource-constrained, disease-endemic environments must play a role in the next frontier of research on VBDs.[7]

Our team specifically studies VBDs in West Africa,[8,9] and the aims of this review were to study the geographical distribution of VBDs in West Africa; to provide an overview of the methods in which mapping and spatial and space-time modelling approaches have been used to visualise and analyse vector and epidemiological data; and to discuss the potential for these approaches to be further developed in future studies.

Geographic distribution of vectorborne diseases in West Africa

Malaria

Most of the papers on VBDs in West Africa focus on malaria (15/40; Supplementary Table 1). Malaria is an infectious disease caused by parasites of the genus *Plasmodium*, transmitted to humans through the bites of infected female mosquitoes of the genus *Anopheles*. Malaria is a major public health problem,

Table 1. Selected vectorborne diseases in West Africa

Disease	Pathogen	Reservoir	Vector
Protozoal			
Malaria	*Plasmodium falciparum, P. vivax, P. ovale, P. malariae*	Humans	Mosquitoes (*Anopheles gambiae* s.l., *An. funestus*)
Human African trypanosomiasis	*Trypanosoma brucei gambiense*	Humans, some wild and domestic mammals	Tsetse flies (*Glossina palpalis* s.l., *G. tachinoides*)
Leishmaniasis	*Leishmania* genus	Mammals	Phlebotomus (*Phlebotomus* spp.), *Sergentomyia* (*Spelaeomyia*) *darlingi*
Helminthic			
Lymphatic filariasis	*Wuchereria bancrofti*	Humans	Mosquitoes (*Anopheles* spp.)
Loa loa filariasis (loiasis)	*Loa loa*	Humans, wild mammals	Tabanid flies (*Chrysops* spp.)
Onchocerciasis ('river blindness')	*Onchocerca volvulus*	Humans	Black flies (*Simulium* genus)
Viral			
Rift Valley fever	Rift Valley fever virus	Wild and domestic mammals	Mosquitoes (*Aedes* spp., *Culex* spp.)
Dengue	Dengue virus	Humans	Mosquitoes (*Aedes* spp.)
Chikungunya fever	Chikungunya virus	Primates, humans	Mosquitoes (*Aedes* spp.)
Crimean–Congo haemorrhagic fever	Crimean–Congo haemorrhagic fever virus	Domestic and wild animals	Ticks (*Hyalomma* genus, *Amblyomma variegatum*)
Yellow fever	Yellow fever virus	Primates, humans	Mosquitoes (*Aedes* spp.)
Bacterial			
Mediterranean spotted fever	*Rickettsia conorii*	Wild and domestic mammals	Ticks (*Rhipicephalus evertsi*)
African tick-bite fever	*Rickettsia africae*	Wild and domestic mammals	Ticks (*Amblyomma variegatum, Rhipicephalus evertsi*)
Tickborne relapsing fever	*Borrelia crocidurae*	Rodents	Ticks (*Ornithodoros sonrai*)
Rickettsia felis infection	*Rickettsia felis*	Unknown	Fleas (*Ctenocephalides felis* and others)
Trench fever	*Bartonella quintana*	Humans	Lice (*Pediculus humanus humanus*)
Louseborne relapsing fever	*Borrelia recurrentis*	Humans	Lice (*Pediculus humanus humanus*)
Epidemic typhus	*Rickettsia prowazekii*	Humans	Lice (*Pediculus humanus humanus*)
Buruli ulcer	*Mycobacterium ulcerans*	Unknown	
Q fever	*Coxiella burnetii*	Mammals, birds and arthropods	Ticks[a]

[a]Possibility of transmission of Q fever by tick was not studied.

with more than 200 million cases and causing up to 1 million deaths each year. People in endemic areas with symptomatic and asymptomatic malaria are reservoirs for the infection. Malaria is endemic in all countries in West Africa, but the burden it imposes depends upon the scale of malaria control efforts in the country (Figure 1).[10]

Many efforts have been made to collect and centralise existing entomological, parasitological and epidemiological data in Africa. Nevertheless, a high degree of uncertainty still exists regarding the annual number of malaria cases and their geographic distribution.[11] A summary of the environmental satellite data that are available for studying malaria can be found in the review of Machault et al.[12] The Mapping Malaria Risk in Africa (MARA/ARMA) project was established for developing malaria risk maps on the scale of the entire continent.[13] More recently, the Malaria Atlas Project (MAP) was born with the objective of gathering worldwide parasite prevalence data and making them freely available on the internet (http://www.map.ox.ac.uk/).[14]

Human African trypanosomiasis

The aetiological agent of human African trypanosomiasis (HAT), also known as sleeping sickness, is protozoa of the species *Trypanosoma brucei gambiense* that are transmitted by tsetse flies (*Glossina* spp.). In West Africa, humans are the main reservoir for *T.b. gambiense*. Animals play a less important role, but pigs and some wild animal species have been reported as reservoirs.[15] In West Africa, HAT has been reported in Guinea, Côte d'Ivoire and Nigeria and is also endemic to several other countries (Figure 2). Control of sleeping sickness has always been closely related to

Table 2. Selected vectors of the human vectorborne diseases in West Africa

Vector	Disease
Mosquitoes	
Anopheles spp.	Lymphatic filariasis[a]
An. gambiae s.l.	Malaria
Aedes spp.	Rift Valley fever
	Dengue
	Yellow fever
	Chikungunya fever
Culex spp.	Rift Valley fever
Phlebotomus	
Phlebotomus spp.	Leishmaniasis
Sergentomyia (*Spelaeomyia*) *darlingi*	Leishmaniasis
Tsetse flies	
Glossina palpalis s.l.	Human African trypanosomiasis
G. tachinoides	Human African trypanosomiasis
Tabanid flies	
Chrysops spp.	*Loa loa* filariasis (loiasis)
Black flies	
Simulium spp.	Onchocerciasis ('river blindness')
Ticks	
Rhipicephalus evertsi	Mediterranean spotted fever
	African tick-bite fever
Amblyomma variegatum	African tick-bite fever
	Crimean–Congo haemorrhagic fever
Ornithodoros sonrai	Tickborne relapsing fever
Ornithodoros moubata	Tickborne relapsing fever
Hyalomma spp.	Crimean–Congo haemorrhagic fever
Lice	
Pediculus humanus humanus	Trench fever
	Louseborne relapsing fever
	Epidemic typhus
Fleas	
Ctenocephalides felis and others	*Rickettsia felis* infection[b]

[a]*Anopheles* is a primary vector of lymphatic filariasis in Africa.
[b]Fleas are considered as vectors of *R. felis* worldwide.

disease mapping. The Atlas of HAT is the most prominent attempt at disease control, research and advocacy.[16]

Leishmaniasis

Leishmaniasis refers to a group of VBDs that are caused by more than 20 species of the protozoan genus *Leishmania*, ranging from localized skin ulcers to lethal systemic disease. Leishmaniasis is considered one of the 'most neglected diseases' because limited resources are invested in its diagnosis, treatment and control, and it is strongly associated with poverty.[17] Humans are infected via the bite of phlebotomine sandflies (*Phlebotomus* spp.). The leishmaniases can be classified into two epidemiological entities according to the type of transmission: anthroponotic, if humans are the sole reservoir involved in transmission (and the sole source for vector infection); or zoonotic, if at least one mammalian reservoir is involved.[18] Although there are no major geographic foci of leishmaniasis in West Africa, the cutaneous forms of leishmaniasis have been reported in 11 of 15 countries in the region (Figure 3). In recent studies, the seroprevalence of specific antibodies against *L. infantum* (the agent of visceral leishmaniasis) in the human population was determined in Senegal. Larger-scale studies with application of GIS/RS technologies are now required to define the distribution of *L. infantum* in West Africa and an identification of its potential vector.[19]

Filariasis

Lymphatic filariasis (LF) is a vectorborne parasitic infectious disease caused by *Wuchereria bancrofti*, which is endemic in the tropics, including in sub-Saharan Africa. It is transmitted to humans by infected mosquitoes. In West Africa, the mosquito *An. gambiae* s.l. is a vector of LF and malaria caused by *P. falciparum*. Humans are the only reservoir host of the LF parasite in Africa.[20] Onchocerciasis (or 'river blindness') is a parasitic disease caused by the filarial parasitic nematode *Onchocerca volvulus*. It is transmitted through the bites of infected *Simulium* (black fly) vectors, which breed in fast-flowing streams and rivers.[21] Control of onchocerciasis in sub-Saharan Africa is overseen by the African Programme for Onchocerciasis Control (APOC).[22] *Loa loa* filariasis (loiasis) is a NTD caused by the filarial parasite *Loa loa*. It is an African disease restricted to the equatorial rainforest regions of Central and West Africa.[23] The insect vectors of *L. loa* are flies of the genus *Chrysops*. Humans are the primary reservoir for *L. loa*. LF, loiasis and onchocerciasis are endemic in many countries of West Africa (Figure 4).

Rift Valley fever

Rift Valley fever (RVF) is an arthropodborne viral disease that primarily causes epizootics of abortion and high mortality rates in domestic animals, but it can also infect humans. The RVF virus is mainly transmitted by mosquitoes of the *Aedes* and *Culex* genera to a wide range of animals, from rodents to camels, which are the natural reservoirs for RVF. Although mosquitoes may transmit the RVF virus to humans, human infections result from contact with infected animals.[24] A large RVF epidemic occurred in 1987 in southern Mauritania and northern Senegal. However, all of the countries in West Africa are at risk of RVF (Figure 5).[25]

Dengue and yellow fever

Dengue fever is a viral infectious tropical disease. The mosquito *Ae. aegypti* is the primary vector of the dengue virus, and humans are the most common reservoir. Dengue is a widespread disease in the subtropics and tropics, but in Africa the burden of the disease is poorly understood.[7] In West Africa, sylvatic
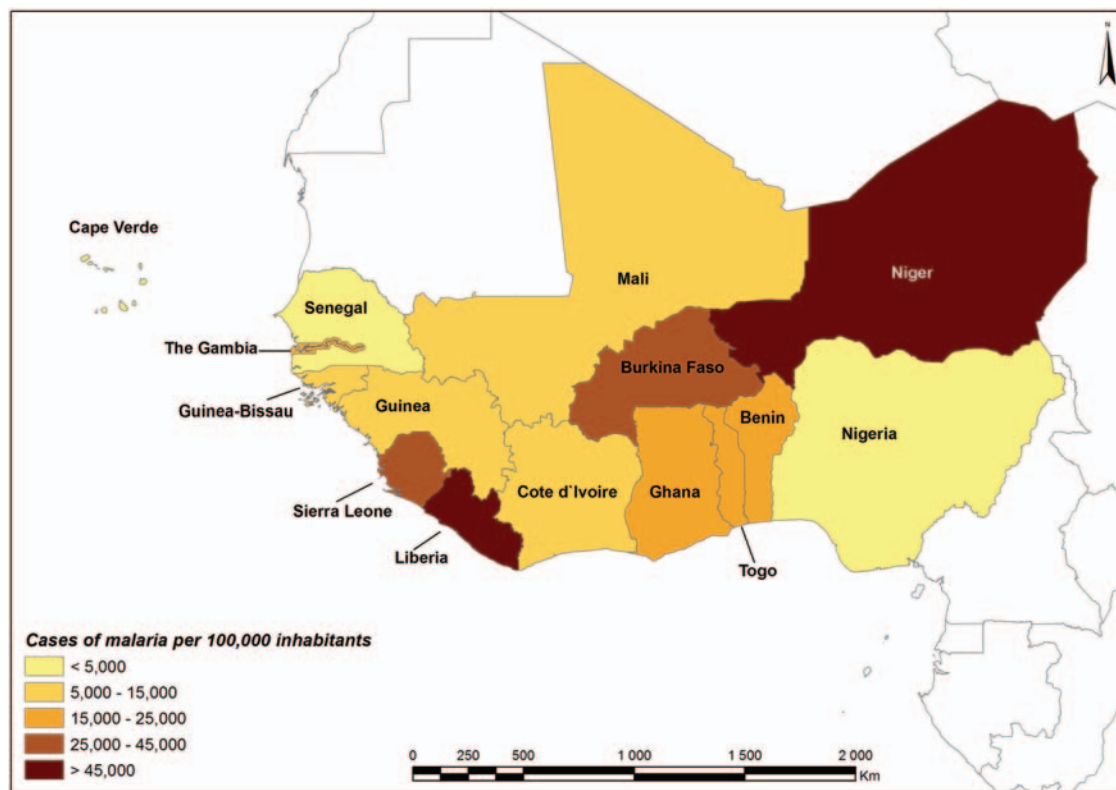
Figure 1. Cases of malaria per 100 000 inhabitants in West African countries in 2010 or latest available year (data from the WHO, retrieved from http://www.who.int).

circulation of the dengue virus is the predominant form of circulation (with lower primates as the main reservoir).[26] Evidence regarding circulation of the dengue virus was obtained from 11 countries in the region, although the mosquito vectors are present throughout West Africa (Figure 6).

Yellow fever (YF) is an acute viral haemorrhagic disease transmitted in West Africa by infected *Aedes* spp. mosquitoes. Up to 50% of severely affected persons who do not receive treatment die from YF, and there is no cure. The YF virus circulates both in urban and sylvatic settings, involving several vertebrate species. In the sylvatic cycle, mosquitoes act as the main vectors and monkeys act as the primary hosts. In the urban cycle, the virus is transmitted between human beings and mosquitoes (predominately *Ae. aegypti*). In Africa, transmission of the virus can also occur in an intermediate cycle between human beings or non-human primates and *Aedes* spp. mosquitoes that breed in tree holes on the savannah.[27] Vertical transmission also occurs within the mosquito population and may play an important role in maintaining the sylvatic cycle.[28] In West Africa, YF is holoendemic in all countries except in the Sahara Desert regions of Mali and Niger (Figure 7).[27]

Crimean–Congo haemorrhagic fever

Crimean–Congo haemorrhagic fever is a viral tickborne disease. The virus causes severe illness throughout the world, including West Africa. Its distribution closely matches that of its main arthropod vector, ixodid ticks belonging to the genus *Hyalomma*.

Human infection occurs through tick bites, contact with infected livestock or nosocomial transmission.[29] In West Africa, enzootic circulation of the Crimean–Congo haemorrhagic fever virus has been shown in serological surveys of cattle, but only sporadic human cases have been reported (Figure 8).[30]

Borrelioses

In West Africa, tickborne relapsing fever (TBRF) is caused by *Borrelia crocidurae*. Studies in Senegal indicate that TBRF is, after malaria, the most common cause of outpatient visits to a rural dispensary. Investigations found that the vector tick (*Ornithodoros sonrai*) was present in villages in Senegal, Mauritania and Mali with high infection rates. Rodents and insectivores are the reservoirs of *B. crocidurae* in West Africa.[31] Unfortunately, no attempts have been made to perform a spatial analysis of TBRF prevalence in West Africa.

Rickettsioses

Following malaria, tickborne rickettsioses are one of the most common causes of systemic febrile illness among travellers from developed countries, but little is known about their prevalence in indigenous populations, especially in West Africa.[32] There is a high incidence (4.4%) of *Rickettsia felis* in Senegal.[33] A case of Mediterranean spotted fever was described in Senegal, and its agent *R. conorii* was found in the ticks *Rhipicephalus evertsi evertsi*.[8] There is a plethora of serological studies
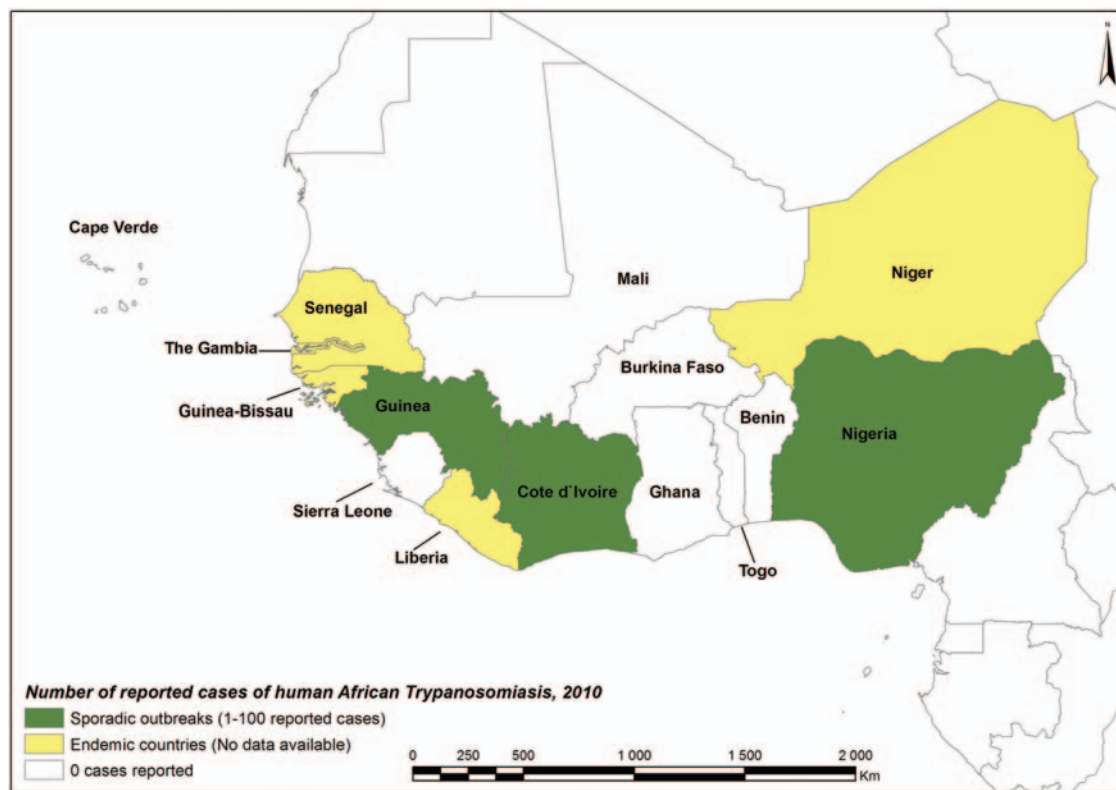
Figure 2. Geographic distribution of human African trypanosomiasis (*Trypanosoma brucei gambiense*) in West African countries in 2010 (data from the WHO, retrieved from http://www.who.int).

of the prevalence of rickettsioses and entomological studies of ticks for *Rickettsia* spp. Although attempts to map the geographic distribution of rickettsioses in Africa have been made, they simply displayed infected sites or counties with reported cases as points, without conducting any geostatistical analyses.[8,34] Thus, the spatial aspects of borrelial and rickettsial VBDs in West Africa have not received the attention they deserve.

Buruli ulcer

Buruli ulcer (BU) disease, caused by *Mycobacterium ulcerans*, is an emerging infectious disease in many tropical and subtropical countries. The exact mode of transmission of this disease remains unclear. Although vectors and modes of transmission remain unknown, it has been hypothesized that transmission of BU disease is associated with human activities in and around aquatic environments (the role of water bugs has been discussed) and that characteristics of the landscape play a role in the spread of BU disease.[35] In West Africa, Côte d'Ivoire, Ghana and Benin are the countries that are particularly affected by BU disease (Figure 9).

Q fever

In West Africa, Q fever has a wide distribution, which has been shown repeatedly in human serological studies and studies of reservoirs (domestic animals).[36] It was reported that the main

vector of TBRF, the soft tick *O. sonrai*, also harboured *Coxiella burnetii*.[37] The possibility that this tick transmits Q fever was not studied, but some species of tick may play a role in the transmission of Q fever.

Geographic information systems and remote sensing for spatial analysis of vector distribution

The geographic distribution of VBDs depends on the distribution of their vectors, environmental factors and climatic factors. Vectors depend on specific abiotic conditions, and advances in RS and mapping of variations in abiotic conditions have stimulated efforts to create risk maps for VBDs.[5,38] This spatial concordance of environmental variables and vector distribution is often used to estimate the current distribution of vectors in unstudied areas.

There have been many studies of the entomological inoculation rate and parasite prevalence, vector density and breeding sites, and risk mapping and modelling in West Africa related to the *Anopheles* mosquito. The distribution of *Anopheles* spp., which are the major vectors of LF and malaria in West Africa, was studied in relation to normalised difference vegetation index (NDVI) values.[39] Several studies were dedicated to investigating the risk factors for malaria and identifying the potential *Anopheles* mosquito breeding sites in urban environments in Côte d'Ivoire and Senegal.[40,41] In Burkina Faso and The
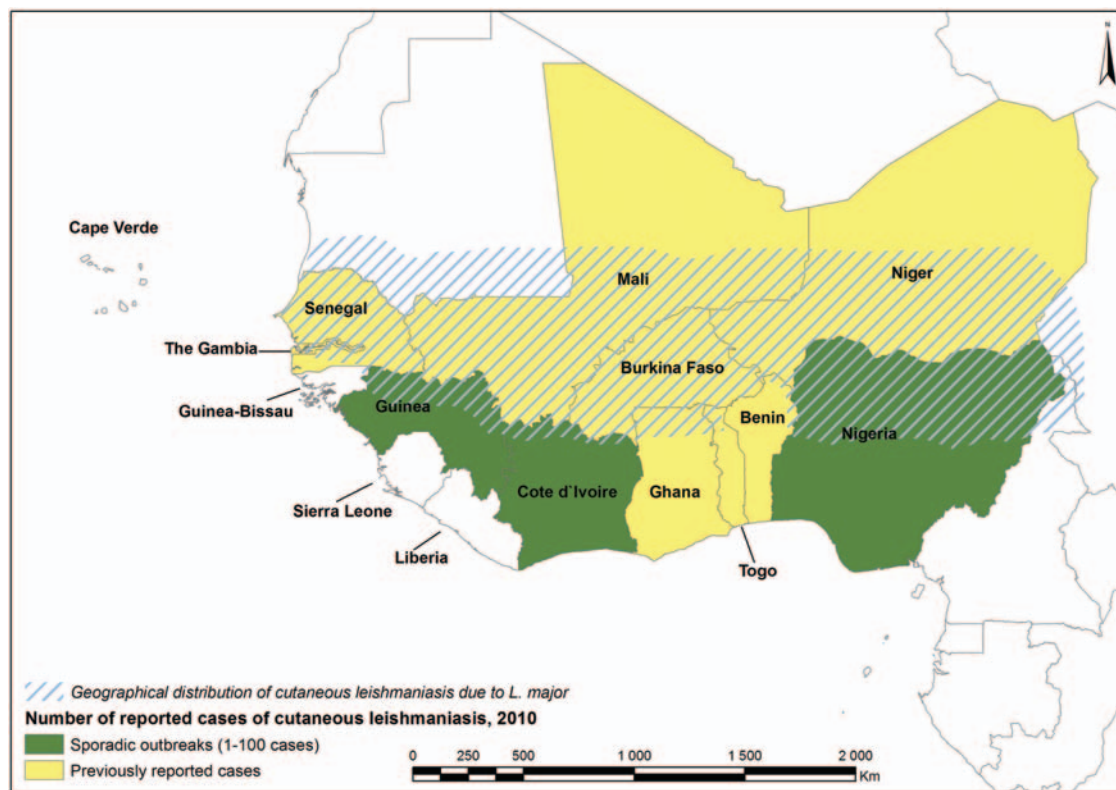
Figure 3. Geographic distribution of cutaneous leishmaniasis in West African countries in 2010 (data from the WHO, retrieved from http://www.who.int).

Gambia, potential *Anopheles* breeding sites were mapped at the village level using satellite imagery.[42,43]

A critically important review regarding the potential for GIS/RS technologies and methodologies to be used for the prevention, surveillance and control of the mosquito *Ae. aegypti*, the dengue virus vector, can be found in an article by Eisen et al.[7] In Senegal, a clear association between the amount of rainfall, the abundance of vectors and the prevalence of RVF has been demonstrated.[44] In another study in Senegal, the average total monthly rainfall from December to February was the most important spatial predictor of the risk of RVF.[45]

GIS and RS techniques are promising and powerful tools for describing tsetse distribution because thermal data appeared to be the most useful predictor variable, followed by indices of vegetation and rainfall.[46] Recently, a study demonstrated the potential of high-resolution images for mapping the habitat of *Glossina* on a local scale as well as in larger areas.[47]

Applications of GIS/RS have been summarised, with examples of studies on various vectors, such as the malaria vector *Anopheles*, the arbovirus vector culicine mosquitoes (*Aedes* spp. and *Culex* spp.), the leishmaniasis vector *Phlebotomus* sandflies, the trypanosomiasis vector tsetse and the loiasis vector *Chrysops* in a review by Thomson and Connor.[48]

Previous studies have used multivariate analyses to estimate the spatial prevalence of particular tick species and to make inferences about different environmental variables that determine their distribution in Africa.[49,50] Another approach to predicting tick distribution was established using a set of methods in

which the author concluded that, on average, climatic variables are better predictors of tick distribution than vegetation-related variables, and the key to describing tick distribution is the covariance of temperature and rainfall.[51]

It should be taken into account that risk mapping based on vectors has serious limitations. Primarily, disease risk or incidence is most closely correlated with the abundance of pathogen-infected vectors, rather than simply the presence of vectors or the total abundance of vectors.[52]

Perspectives of application of geographic information systems/remote sensing technologies for studying vectorborne diseases, remaining challenges and conclusion

GIS facilitate comparisons between disease patterns and environmental data, while RS technologies can use high-resolution satellite data to provide estimates of variables such as temperature, vegetation and humidity.[53] During the past two decades, satellite RS technology has shown promising results in assessing the risk of various VBDs at different spatial scales. Satellite-based imagery is characterised by its spatial, spectral and temporal resolution. Despite some limited attempts to apply RS to epidemiology, the methods have not yet demonstrated their expected potential. GIS/RS technologies are undoubtedly a valuable source of information for epidemiologists. GIS/RS technologies should not be overestimated and it is necessary to take all of
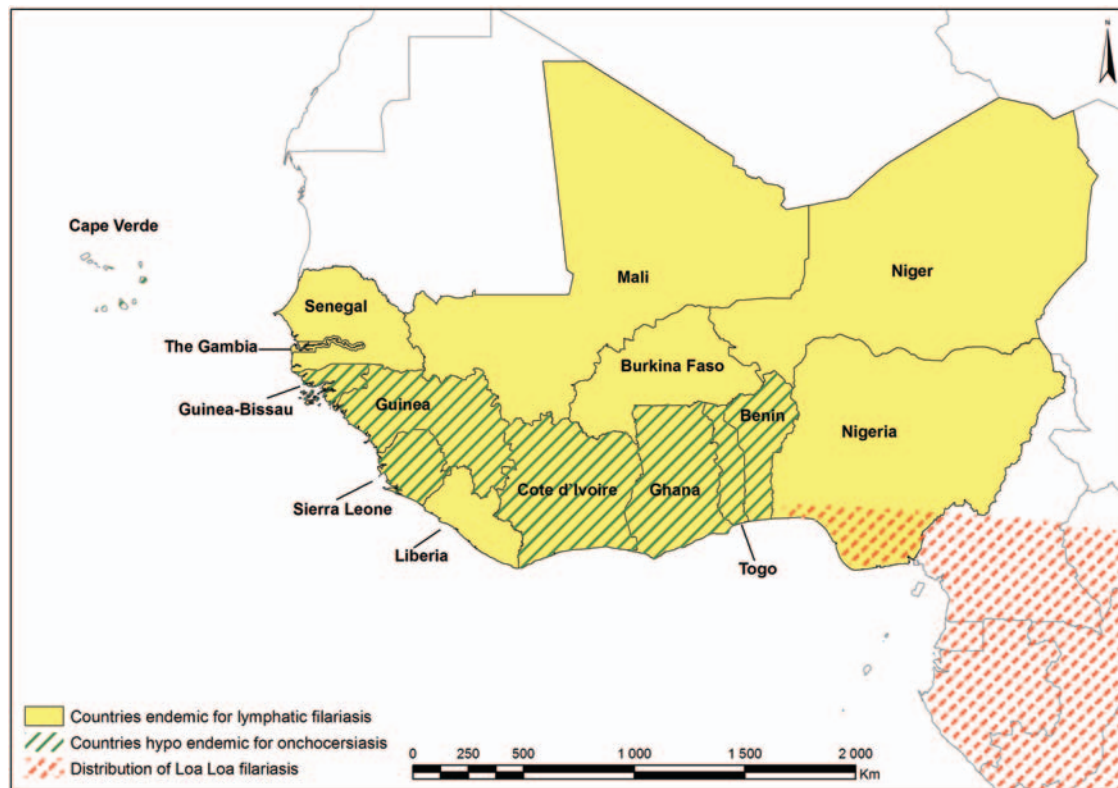
Figure 4. Geographic distribution of lymphatic filariasis, *Loa loa* filariasis (loiasis) and onchocerciasis in West African countries (data from the WHO, retrieved from http://www.who.int).
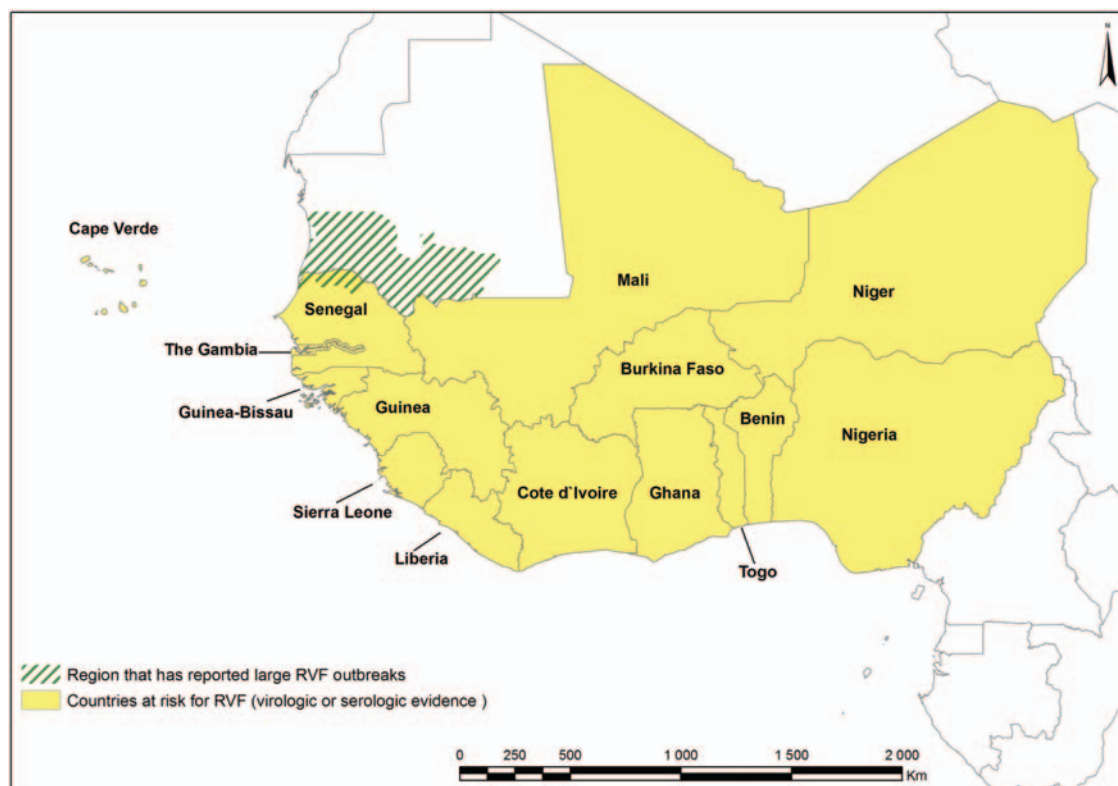

Figure 5. Geographic distribution of Rift Valley fever (RVF) in West African countries (data from the WHO, retrieved from http://www.who.int).
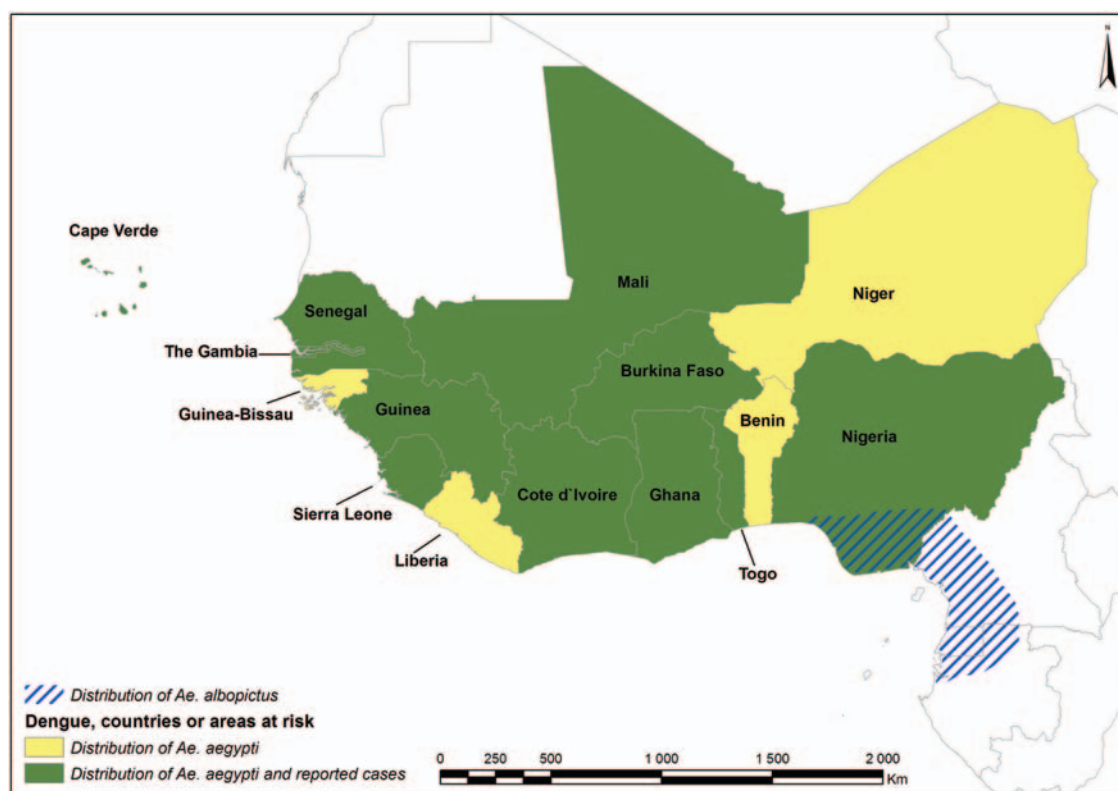
Figure 6. Geographic distribution of dengue in West African countries in 2011 (data from the WHO, retrieved from http://www.who.int).

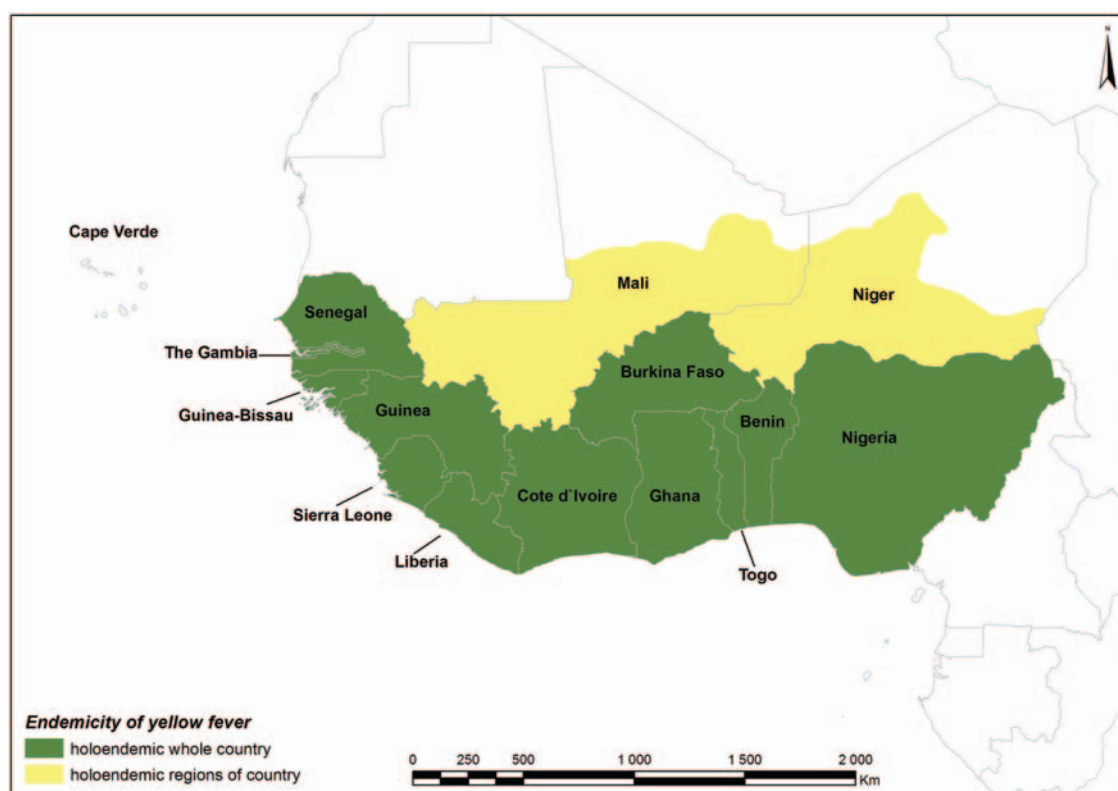**Figure 7.** Geographic distribution of yellow fever in West African countries in 2011 (data from the WHO, retrieved from http://www.who.int).
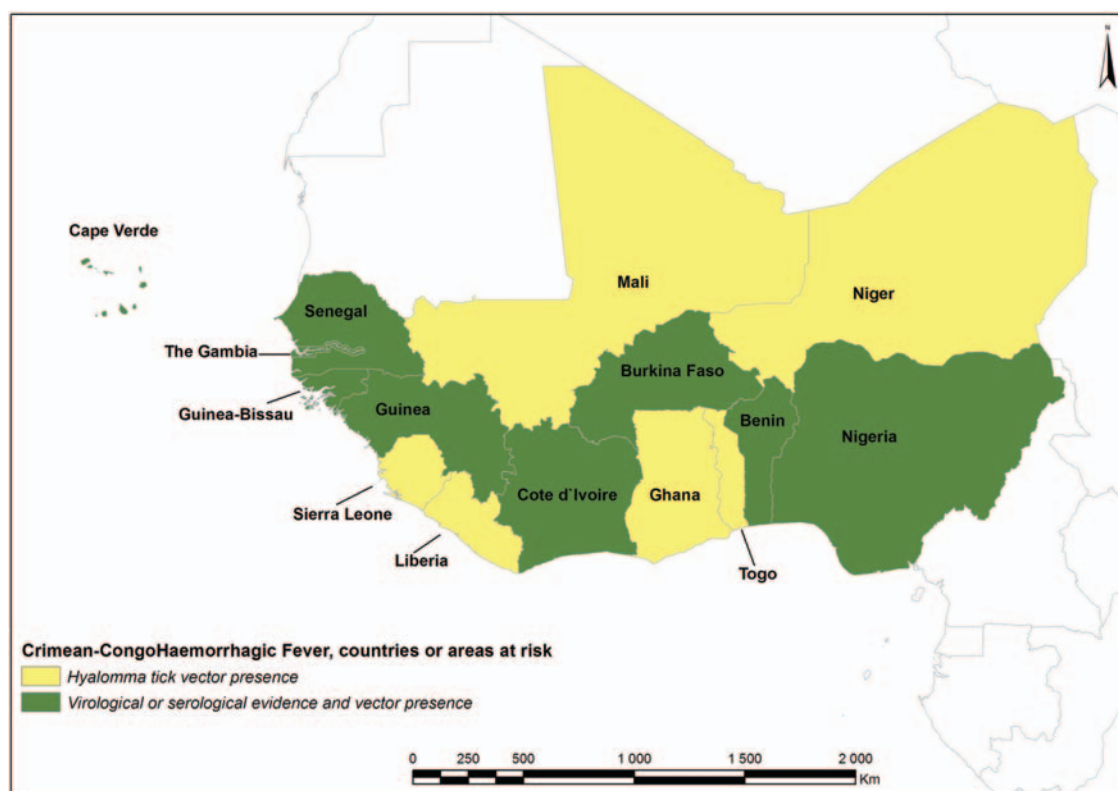
Figure 8. Geographic distribution of Crimean–Congo haemorrhagic fever in West African countries (data from the WHO, retrieved from http://www.who.int).
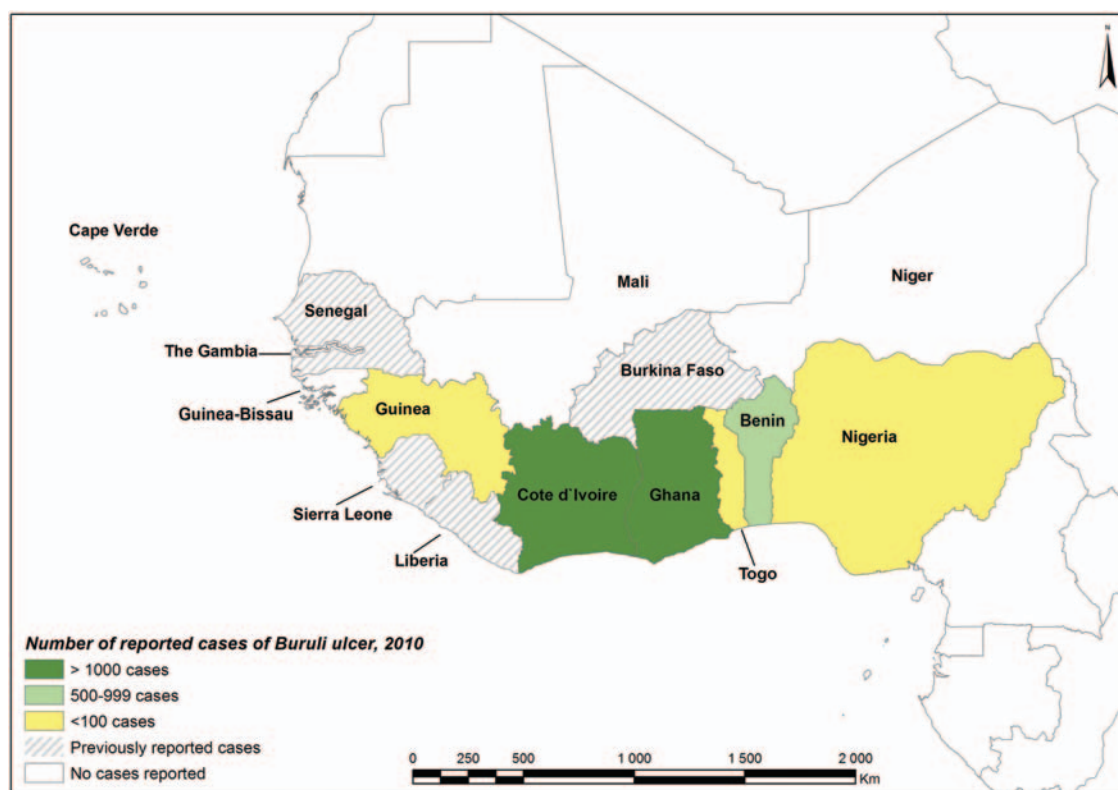

Figure 9. Geographic distribution of Buruli ulcer in 2010 in West African countries (data from the WHO, retrieved from http://www.who.int).

their advantages and limitations into account. Moreover, VBD interventions have to be identified and recognised as they can confound the relationship between the environment and disease. In the recent malaria indicator surveys in Zambia and Angola, for example, no relationship was observed between remotely sensed data and malaria risk.[54,55]

The typical modelling approach investigates associations between multivariate environmental data and patterns of vector presence or absence for mapping vectors and VBDs. At the first step, simple statistical models could be a good starting point for linking the limited number of environmental variables that can be derived from satellite data. Simple statistical models are restricted because they often fit linear functions between environmental variables and presence/absence data, when it is most likely that such associations are highly complex and non-linear.[20] At the second step, sophisticated process-based models that rely on vector biology as predictors of diseases and their risk should be developed.[56]

Regression models have been widely applied in landscape epidemiology. The type of regression model (logistic, Poisson, linear, etc.) is determined by the type of outcome variable to be predicted (e.g. binary, count, continuous) and environmental variables measured at sampled locations are entered as covariates. The resultant model is then either used to predict the outcome variable at non-sampled locations, based on observed values of the covariates at the prediction locations, or to explain observed patterns of disease on the basis of the model covariates.[57]

Besides regression modelling, there are many other approaches in spatial epidemiology: spatial clustering, discriminant analysis, generalised linear models, generalised additive models, Bayesian estimation methods and others. However, such traditional models require both disease presence and disease absence data. At the same time, there are different 'presence-only' models that could be used when no 'absence data' are available. One of these presence-only machine learning (rule-based) algorithms is an ecological niche modelling algorithm based on maximum entropy (Maxent). This method can be used successfully with very small sample sizes and does not require independence of covariates.[58] Moreover, these advantages could be crucial in Africa where complete surveillance data from all regions are not available.

Basic spatial modelling approaches include interpolation based on spatial dependence in vector or VBD data and extrapolation based on associations between vector or VBD data and environmental or socioeconomic predictor variables. The latter approach can be a powerful tool to gain insights into levels of risk within areas where surveillance data are lacking or unreliable. However, it should be noted that model extrapolation is restricted to areas with ecological and climatic characteristics similar to those of the model development area.[1]

Global strategies for controlling infections in sub-Saharan Africa have focused on the 'big three' diseases, namely AIDS, TB and malaria. Other causes of fever and infection fall into the category of NTDs. In the twenty-first century, it is important to compile a comprehensive list of the infections in sub-Saharan Africa and to study their epidemiology.[59]

Few investigations have addressed the unknown causes of fever in West Africa. The majority of fevers have long been considered to be related to malaria. Recent studies have shown that NTDs are the most frequent causes of fever in both indigenes and travellers. In particular, TBRF due to *B. crocidurae* has been rediscovered,[9,31] and the rickettsiae, including *R. felis,* have been reported.[33] Overall, new pathogens among the rickettsiae were identified in the environment.[8]

The geographic distribution of ticks—vectors of diseases in West Africa—is a neglected area of study. However, applying GIS/RS technologies to the study of *Ixodes* ticks in North America has yielded significant results. For example, the use of geospatial modelling has revealed that high concentrations of *I. pacificus* and *I. scapularis*, which are the key tick vectors of Lyme disease in North America, can be predicted by GIS/RS-based environmental factors related to elevation, slope of the landscape, vegetation type, soil type, temperature and moisture.[60] The same approaches could be used in epidemiological studies of *R. felis* infection, an emerging disease in West Africa.

Today, epidemiologists often use new GIS/RS techniques to study a variety of VBDs. The associations between satellite-derived environmental variables (such as temperature, humidity, elevation, vegetation, rainfall, surface water, land use, land cover type and soil moisture) and vector density are used to identify and characterise vector habitats. A wide variety of RS data, powerful GIS and statistical software packages are available for desktop computing environments, making it affordable and feasible for epidemiologists to experiment with new spatial analysis techniques.[56]

Maps that show the seasonal risk of VBDs will be necessary to monitor the impacts of changes on vector ecology. Using GIS/RS, advanced analytical tools and a landscape ecology approach, these risk maps could play a major role in defining research questions and surveillance needs and in guiding control efforts and field studies.[38]

From the other side, this approach is based on ecological analysis and requires assembling all epidemiologic available data, and moreover it should be supported by fieldwork. The most successful GIS/RS applications to study VBDs in West Africa are either local (country)-level studies using community-based surveillance data or continental (sub-continental)-level studies using published scientific literature data. Cooperation of the epidemiological community could allow enhancing studies of VBDs in West Africa. The most important goal of the application of GIS/RS technologies to the study of VBDs is to reduce the burden of disease by generating information that empowers the public to take protective action and helps public health agencies to effectively allocate their limited prevention, surveillance and control resources. There is great potential to use GIS/RS technologies to improve the surveillance, prevention and control of vector-borne infectious diseases in West Africa.

Supplementary data

Supplementary data are available at *Transactions* Online (http://trstmh.oxfordjournals.org/).

the maps and discussed the content of the review; PR and DR drafted the manuscript. All authors critically revised the manuscript for intellectual content and read and approved the final version. DR is guarantor of the paper.

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