



HAL
open science

Development and Assessment of a Geographic Knowledge-Based Model for Mapping Suitable Areas for Rift Valley Fever Transmission in Eastern Africa

Annelise Tran, Carlène Trevennec, Julius Lutwama, Joseph Sserugga, Marie Gély, Claudia Pittiglio, Julio Pinto, Véronique Chevalier

► To cite this version:

Annelise Tran, Carlène Trevennec, Julius Lutwama, Joseph Sserugga, Marie Gély, et al.. Development and Assessment of a Geographic Knowledge-Based Model for Mapping Suitable Areas for Rift Valley Fever Transmission in Eastern Africa. PLoS Neglected Tropical Diseases, 2016, 10 (9), pp.e0004999. <10.1371/journal.pntd.0004999>. <hal-04432656>

HAL Id: hal-04432656

<https://hal.inrae.fr/hal-04432656v1>

Submitted on 1 Oct 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons CC BY 4.0 - Attribution - International License

RESEARCH ARTICLE

Development and Assessment of a Geographic Knowledge-Based Model for Mapping Suitable Areas for Rift Valley Fever Transmission in Eastern Africa

Annelise Tran^{1,2*}, Carlène Trevenec³, Julius Lutwama⁴, Joseph Sserugga⁵, Marie Gély⁶, Claudia Pittiglio³, Julio Pinto³, Véronique Chevalier⁶

1 CIRAD, UPR AGIRs, Ste-Clotilde, Reunion Island, **2** CIRAD, UMR TETIS, Ste-Clotilde, Reunion Island, **3** Food and Agriculture Organization of the United Nations, Rome, Italy, **4** Uganda Virus Research Institute, Entebbe, Uganda, **5** Uganda Ministry of Agriculture, Animal Industry and Fisheries, Entebbe, Uganda, **6** CIRAD, UPR AGIRs, Montpellier, France

* annelise.tran@cirad.fr



 OPEN ACCESS

Citation: Tran A, Trevenec C, Lutwama J, Sserugga J, Gély M, Pittiglio C, et al. (2016) Development and Assessment of a Geographic Knowledge-Based Model for Mapping Suitable Areas for Rift Valley Fever Transmission in Eastern Africa. *PLoS Negl Trop Dis* 10(9): e0004999. doi:10.1371/journal.pntd.0004999

Editor: Archie C. A. Clements, University of Queensland, AUSTRALIA

Received: March 1, 2016

Accepted: August 22, 2016

Published: September 15, 2016

Copyright: © 2016 Tran et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Data Availability Statement: All relevant data are within the paper and its Supporting Information files.

Funding: This study was funded by Food and Agriculture Organization's One Health initiative project/GLEWS component for risk analysis and modeling through integration of disease, environment and food safety data. FAO staff (CT, JP) have been involved in study design, data collection, decision to publish and preparation of the manuscript.

Abstract

Rift Valley fever (RVF), a mosquito-borne disease affecting ruminants and humans, is one of the most important viral zoonoses in Africa. The objective of the present study was to develop a geographic knowledge-based method to map the areas suitable for RVF amplification and RVF spread in four East African countries, namely, Kenya, Tanzania, Uganda and Ethiopia, and to assess the predictive accuracy of the model using livestock outbreak data from Kenya and Tanzania. Risk factors and their relative importance regarding RVF amplification and spread were identified from a literature review. A numerical weight was calculated for each risk factor using an analytical hierarchy process. The corresponding geographic data were collected, standardized and combined based on a weighted linear combination to produce maps of the suitability for RVF transmission. The accuracy of the resulting maps was assessed using RVF outbreak locations in livestock reported in Kenya and Tanzania between 1998 and 2012 and the ROC curve analysis. Our results confirmed the capacity of the geographic information system-based multi-criteria evaluation method to synthesize available scientific knowledge and to accurately map (AUC = 0.786; 95% CI [0.730–0.842]) the spatial heterogeneity of RVF suitability in East Africa. This approach provides users with a straightforward and easy update of the maps according to data availability or the further development of scientific knowledge.

Author Summary

Rift Valley fever (RVF) is a zoonotic disease affecting ruminants and humans. It occurs mostly in Africa, causing human deaths and important economic losses in the livestock sector. The RVF virus (RVFV) is transmitted from ruminant to ruminant by mosquitoes. Different climatic, environmental, and socio-economic factors may impact the

Competing Interests: The authors have declared that no competing interests exist.

transmission of the virus. Our work uses all current available knowledge on the epidemiology of the disease and geographic data to map areas suitable for RVFV. The study area includes four East African countries: Kenya, Tanzania, Uganda, three countries which have been historically affected by RVF, and Ethiopia, where the disease has never been reported but which shares borders with infected countries. The resulting maps are compared with the locations of outbreaks reported in livestock. Our results demonstrate the capacity of the spatial multi-criteria evaluation method to map with accuracy the areas suitable for RVF occurrence. Thus, the method we developed provides users with risk maps that could be used for early warning detection and implementation of control measures.

Introduction

Caused by a Phlebovirus (Bunyaviridae) that affects both humans and livestock, Rift Valley fever (RVF) is considered to be one of the most important viral zoonoses in Africa. The RVF virus (RVFV) is transmitted from ruminant to ruminant by mosquitoes [1]. Although never demonstrated, there is field, serological and virological evidence of transmission without any use of vectors [2], suggesting an alternative transmission of the RVFV between ruminants through direct contact. Humans become infected mainly through direct contact with ruminant viremic fluids, such as blood or abortion products, but also through mosquito bites.

Although in the majority of human cases RVF infection is asymptomatic or causes mild illness, severe forms are characterized by retinitis, encephalitis or hemorrhagic fever. In ruminants, RVF infection causes abortion storms in groups or flocks of pregnant females and acute deaths in newborns [3]. Both health and economic impacts can be greatly reduced when control measures, such as vaccination, insecticide spraying and dissemination of information, are quickly implemented. The delay between case detection and control measure implementation depends on, among other factors, the efficiency of surveillance networks; therefore, an accurate definition of at-risk areas needs to be monitored along with other factors.

RVF virus circulation has been reported in several eco-climatic areas: arid in western Africa and the Arabic Peninsula [4, 5]; sub-humid in East Africa [6, 7]; wet forests in central Africa [8]; dam and irrigated agricultural land under hot climatic conditions in Egypt, Mauritania and Sudan [9–11]; and humid highlands in Madagascar [2, 12].

Depending on the areas of concern, different risk factors have been identified, either for transmission, spread or human and/or livestock occurrence. Potential mosquito vectors of the RVFV belong to the genera *Aedes*, *Anopheles*, *Culex*, *Eretmapodites* and *Mansonia*. The majority of the factors driving mosquito vector presence and abundance, thus driving the risk of RVF transmission, are related to climate, water and landscape. The *Aedes* genus is mostly associated with temporary water bodies such as flooded area, temporary pond, puddles, and rice fields. *Culex* and *Anopheles* mosquito breeding areas are diverse and could be temporary (rice fields, swamps) or permanent (lakes, ponds) bodies of water. Stagnant and permanent water bodies are the habitats of *Eretmapodites* and *Mansonia*, respectively [13].

In fact, the presence of temporary water bodies and floodplains are outbreak risk factors for RVF in semi-arid areas in eastern Africa, the Arabian Peninsula and western Africa [4]. In eastern and southern Africa, the risk of RVFV infection has been shown to vary as a function of rainfall, temperature, and a remotely sensed vegetation index (NDVI: normalized difference vegetation index) [14, 15]. Artificial water bodies, such as dams and irrigated rice fields, are also known to be associated with the high abundance of RVFV vectors in western Africa [4]. In

addition to eco-climatic factors, cattle density has been identified as a risk factor for transmission of the RVFV [6, 16]. Habitat, gender, profession, and contact with ruminants and ruminant products have also been identified as risk factors of RVF occurrence in humans [17].

The Horn of Africa has been historically affected by RVF [18]. However, the occurrence of RVF has never been reported in Ethiopia, which shares borders with infected countries, namely, Kenya [6], northern Somalia [19], and Sudan [20]. In Uganda, although no outbreak in humans or animals were reported until 2016, a recent serological survey revealed that RVFV was endemic in goats in four districts [21].

In Kenya and Tanzania, where RVF is endemic, historical knowledge indicates that ‘dambos’ are areas at risk of RVF [22]. Moreover, recent eco-epidemiological studies identified the main environmental risk factors for RVF, which has allowed for health targeted surveillance by health authorities [6, 14, 23]. However, the application of these models to regions outside of the study area of interest may lead to incorrect inferences. Moreover, information related to the suitability of both Ethiopia and Uganda ecosystems for the transmission of the RVFV are scarce. Given this lack of information, pragmatic approaches must be developed to provide risk maps that could be used for early warning detection and implementation of control measures.

Spatial multi-criteria evaluation (MCE) is a rapid and pragmatic knowledge-based method adapted for mapping disease suitability in the absence of large epidemiological datasets. Defined as ‘a process that transforms and combines geographical data and value judgments (expert and bibliographic knowledge, including uncertainties, subjective and qualitative information) to obtain appropriate and useful information for decision making’ [24], this method has been used to map suitable areas for RVF transmission in Africa, on a continental scale [25] and in Senegal [26], and in the European countries of Spain [27] and Italy [28]. However, the predicted maps could not be validated for European countries which are disease-free regions, while in Senegal the validation could only be performed in a qualitative way [26]. Moreover, in these studies, only the ‘amplification step’, defined as the local transmission of the RVFV to its hosts by mosquito vectors, was considered and did not account for the possible transportation of the virus from a primary outbreak to secondary foci in a ‘spread step’. This process may involve different risk factors than those of the amplification step, such as animal trade [12, 29].

The goal of the present study was to adapt a geographic knowledge-based method [25] to identify suitable areas for RVF amplification and spread in four Eastern African countries, namely, Kenya, Tanzania, Uganda and Ethiopia, and to assess the predictive accuracy of the model using livestock outbreak data from Kenya and Tanzania.

Materials and Methods

Epidemiological definitions

Under suitable conditions and after the introduction or low-level transmission of a given pathogen, the pathogen can be locally transmitted to a ‘primary’ host through direct or vectorial transmission and then transferred from the primary infectious host to several secondary hosts; this is the “amplification” process [30]. Therefore, ‘spread’ is defined as the transportation of the pathogen from the primary outbreak to secondary foci. In this study, ‘suitability’ is defined as the ability of a habitat to support either the amplification or the spread of RVF. Amplification is a necessary condition for primary RVF occurrence. Both amplification and spread are needed for secondary outbreaks.

Identification of risk factors from bibliographic review

Following the spatial multi-criteria evaluation (MCE) methodology that has been detailed elsewhere [25, 31], we first identified the amplification and spread risk factors of RVF through a

literature review. PubMed and ISI Web of Knowledge were searched for articles published from 1980 to 2014 using the search terms “rift valley fever” AND (separately) “model” or “spatial”, or “risk factors” or “analysis” using the “all fields” option to allow for the retrieval of articles in which the search terms appeared in the titles, abstracts, or keywords. Inclusion criteria were reviews and/or articles using expert knowledge, and/or statistical and mathematical modelling approaches to model RVF risk to ruminants or humans. A total of 62 references were thus included.

In [Table 1](#), we listed the factors associated with the risks of amplification and spread of RVF according to the published literature review. Only risk factors that could be mapped were selected for the risk mapping process. The following risk factors were thus included:

Sheep, goat and cattle densities. Assuming the existence of direct transmission, an increase in domestic ruminant density is expected to increase the number of potentially infectious contacts that a susceptible individual experiences over a given time; therefore, there is a greater risk of amplification. Because infectious ruminants may travel after being sold, ruminant density was also considered as a factor of spread [[16](#), [32](#)].

Markets and trade. The role of ruminant trade in RVFV dissemination was previously documented [[19](#), [29](#), [32–34](#)]; increased densities of markets, roads and railways are expected to be associated with increased ruminant trade and thus related to a high risk of RVF spread.

Wildlife. A detailed literature review of the role of a wild mammal reservoir in the epidemiologic cycle of RVFV concluded that buffaloes and other wild ruminants could contribute to the amplification and spread of the disease in southern and eastern Africa [[35–39](#)]. The proximity of wildlife national parks and the existence of domestic and wild ruminants with

Table 1. Risk factors associated with the amplification and spread of Rift Valley fever in livestock populations as identified by the published literature review.

	Risk factor ^a [proxy ^b]	Reference
Individual level	Species	[4 , 40–43]
	Age	[12 , 16 , 29 , 44 , 45 , 46]
Production systems	Sheep, goat and cattle densities* [Water bodies as zones of increased contact among animals]*	[16 , 32]
Markets and trade	Proximity to animal markets*	[12 , 29]
	Ruminant trade [roads, railways]*	[19 , 32–34 , 47 , 48]
	Traditional and commercial practices	[12 , 29]
	Festival periods	[32 , 49 , 50]
Wildlife	Presence of wild ruminants [proximity to conservation areas]*	[35–39]
Vector populations and landscape variables	<i>Aedes</i> , <i>Culex</i> , <i>Mansonia</i> and <i>Anopheles</i> genera [Elevation* and landform*, land cover*, soil type*]	[6 , 7 , 12 , 16 , 46 , 51–73]
Climate	Season	[14 , 22 , 32 , 71 , 74 , 75 , 76]
Surveillance	Quarantine, surveillance system efficiency/sensitivity (protective factors)	[14 , 50 , 74 , 77]

^a Risk factors included in the present study (= risk factors for which spatial data or proxies were available) are indicated by an asterisk

^b If the data corresponding to an identified risk factor was not available, a proxy (= variable assumed to resemble the risk factor) was used

doi:10.1371/journal.pntd.0004999.t001

overlapping home ranges could thus be associated with increased risk of RVF amplification and spread.

Vector populations and landscape variables. RVF occurrence is expected to be strongly associated with the distribution and the abundance of the RVFV vector populations [14, 22]. Environmental variables (land cover, elevation, landform, soil type) have been shown to be associated with increased incidence of RVF in humans in Kenya and were hypothesized to provide optimal vector habitat at each life stage, thus reflecting suitable conditions for the densities of RVFV vectors [6]. Moreover, due to the limited active flying capacities of mosquito vectors, a shorter distance from water bodies is expected to be associated with an increase in the risk of amplification (vector-borne transmission is associated with permanent and temporal water bodies providing breeding sites for the RVFV vectors, such as ‘dambos’ in Kenya [22]) and spread (increased contact among animals that share rivers, lakes or ponds as sources of drinking water).

Generation of standardized geographical layers for each risk factor

A search was conducted to obtain digital geographical data for each identified risk factor (Table 1). The different sources of the data that were used and their main characteristics are provided in S1 File and S1 Table. The data were imported into a geographic information system (GIS) and processed to produce standardized spatial risk factor layers, namely a mosquito index (reflecting the suitability for RVF mosquito vectors), sheep density, goat density, cattle density, proximity to markets, road density, railways density, proximity to water bodies, proximity to wildlife national parks (software: ESRI ArcMap and ArcMap Spatial Analyst Extension, Redlands, CA, USA). At the end of the process, each image layer was raster-based, with pixel dimensions of 300 m x 300 m. The scale of all spatial risk factor layers was continuous, ranging from 0 (completely unsuitable) to 1 (completely suitable). The different sources of the data used and the calculation method of the standardized geographical layers are provided in S1 File. The resulting maps for the risk factor layers are presented in S1 Fig.

Generation of weights for each risk factor

We assumed that the weight of each risk factor in the amplification and spread processes were not equivalent. For example, small ruminants are known to be more susceptible than cattle for the transmission of the RVFV [42] and, therefore, more prone to play a more important role during the amplification phase than the latter. Markets are aggregation points where ruminant herds meet and have potential contact with each other before returning back to their living area; markets are, therefore, more important for spread than roads that may be used by herders for travelling. Based on the literature review and our own expertise, we ranked RVF risk factors for virus amplification and spread according to their putative relative importance in both processes [78]. Factors were compared two at a time: 1) We first specified whether risk factor A was more or less important than risk factor B; and 2) We specified the degree of importance of factor A regarding factor B on a nine-point scale using the Saaty scale (factor A can be extremely more important, very strongly more important, strongly more important, moderately more important, equally important, moderately less important, strongly less important, very strongly less important or extremely less important than factor B), resulting in a pair-wise comparison matrix. A numerical weight was then derived for each risk factor from the pair-wise comparison matrix [79]. We calculated pair-wise comparison matrices separately for amplification and spread, considering the vector distribution being much more important in the amplification process than in the virus spread phase.

Combination of the risk factors and creation of suitability maps

Then, three different maps were generated, considering two distinct groups of risk factors and their associated weights for the amplification and spread steps.

Assuming that vector presence is a necessary condition for RVF amplification, the suitability of areas for RVF amplification was calculated for each raster cell as the product of the mosquito index map (computed as described in [S1 File](#)) and a weighted linear combination (WLC) of each of the standardized geographical risk factor layers associated with RVF amplification using its corresponding weight. Regarding the spread process, the raster maps for RVF risk factors associated with RVF spread were combined by computing a WLC with their corresponding weights.

The suitability maps for amplification and spread were then combined to create two different suitability maps for RVF occurrence. First, the values of suitability indices for amplification and spread were recoded in three classes (low/medium/high suitability) using a quantile discretization. These two recoded maps were then merged into a primary synthetic RVF suitability map with nine classes corresponding to all possible combination of amplification suitability (low/medium/high) and spread suitability (low/medium/high). Second, the areas with the highest risk (suitability estimates greater than 0.1, i.e., in the 90th percentile) of RVF amplification were selected. The Euclidean distance between these areas was calculated and transformed into a 'proximity to RVF amplification areas' index, which assumed a sigmoid-shaped decreasing relationship between 0 and 100 km and negligible risk thereafter. Finally, suitability estimates for RVF occurrence, combining the spread and amplification processes, were computed as the product of the suitability estimates for RVF spread and the proximity to RVF amplification areas index, resulting in a second synthetic RVF suitability map expressed as a continuous suitability index.

Sensitivity and uncertainty analyses

A sensitivity analysis (SA) was conducted to assess the sensitivity of the method to the expert choices. To determine the effect of a change in the weights applied to each risk factor, a range of weight values to explore was defined by adding and subtracting 25% from the original weights. Ten weight values within this range were tested (+/-5%, +/- 10%, +/-15%, +/-20% and +/-25%). Each of the newly calculated weights was incorporated into the modelling process, while other factor weights were proportionally decreased or increased such that the sum of the weights equaled 1. For each combination of weights obtained, maps of suitability indices for RVF amplification, spread and occurrence were calculated, and a total of 169 suitability maps for RVF occurrence were generated. Based on these different realizations, the contribution of the different risk factor weights to model output variance was calculated for each country (see [S2 File](#) for details).

Finally, an uncertainty surface was produced. It represented the standard deviation of the different suitability maps resulting from the change in weights [80].

Validation

RVF outbreaks in livestock reported in Kenya and Tanzania between 1998 and 2012 were collected to assess the consistency of RVF suitability map (Source: FAO EMPRES-i database: <http://empres-i.fao.org>). A total of 145 outbreaks were located using geographic coordinates ([Fig 1](#)).

Then, 150 locations of disease 'pseudoabsence' data were randomly generated in these two countries, under the condition of being 25 km from another 'pseudoabsence' or outbreak location. The value of the quantitative suitability estimates for RVF occurrence was extracted for

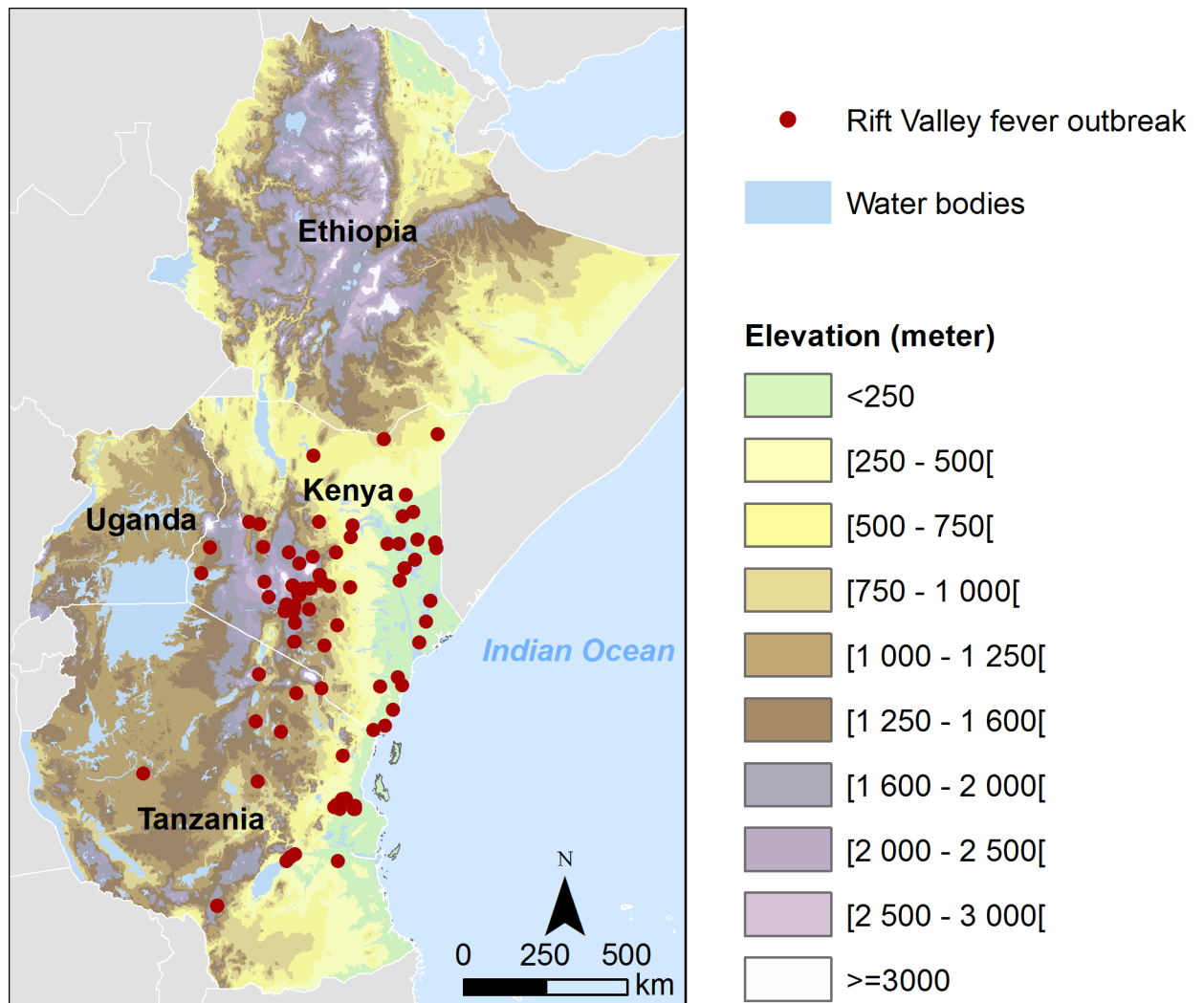


Fig 1. Location of Rift Valley fever outbreaks in livestock reported in Kenya and Tanzania between 1998 and 2012.

doi:10.1371/journal.pntd.0004999.g001

each ‘presence’ or ‘pseudoabsence’ location and the AUC (area under curve) of the ROC curve [81], and the sensitivity and specificity were calculated to evaluate the quality of the suitability map.

Results

Weights of RVFV amplification and spread risk factors

The resulting weights of risk factors for RVFV amplification and spread are presented in Table 2 (see S1 and S2 Tables for the details of the pair-wise comparison matrices).

Regarding amplification, we assumed that the mosquito index was the most important factor, and a necessary condition for RVFV amplification. Then, small ruminant densities were identified as important factors, followed by (in descending order) cattle density, proximity to markets that are aggregation points for animals, proximity to roads, water bodies and railways, and proximity to wildlife parks.

Table 2. Risk factor weights calculated using the analytical hierarchy process, regarding RVFV amplification and spread processes.

Risk factor	Weight RVF amplification	Weight RVF spread
Mosquito index		0.025
Sheep density	0.288	0.204
Goat density	0.288	0.204
Cattle density	0.203	0.144
Proximity to markets	0.080	0.175
Density of roads	0.042	0.062
Proximity to water bodies	0.034	0.062
Density of railways	0.034	0.062
Proximity to wildlife national parks	0.031	0.062

doi:10.1371/journal.pntd.0004999.t002

Regarding spread, we considered that viremic hosts were the most important means of virus dissemination and that markets were, again, an aggregation point for people and their herds. The proximity to roads and water bodies were also important factors because they allow for trade movements. Finally, proximity to wildlife national parks and the mosquito index were factors of low influence in the spread process.

Suitability maps for RVF amplification, spread and occurrence

[Fig 2](#) presents the different maps produced from the MCE process: a map of suitability for RVF virus amplification ([Fig 2a](#)), a map of suitability for RVF spread ([Fig 2b](#)) and a final map of suitability for RVF occurrence in domestic ruminants ([Fig 2c](#)) (maps of all standardized risk factors are provided in [S1 Fig](#)).

According to the results of the MCE, areas suitable for RVF amplification were located in the low elevation areas of Kenya (the eastern coast, the northeastern portion that borders Ethiopia and Somaliland, and, to a lesser extent, the northwest region bordering Uganda), Tanzania (northeastern portion) and Ethiopia (in the Northwest and Southwest). Uganda presented a very low suitability for RVF amplification in domestic ruminants.

In addition, the suitability map for RVF spread in domestic ruminants ([Fig 2b](#)) showed a different pattern, identifying the highlands of Ethiopia, Kenya, and Uganda as areas favorable to RVF spread. In Tanzania, areas suitable for RVF spread were located in the northern part of the country.

The combination of the ‘amplification’ and ‘spread’ maps resulted in two final synthetic maps of the areas suitable for RVF occurrence in domestic ruminants that were complementary ([Fig 2c and 2d](#)). According to the map that highlights the different categories of amplification/spread combinations ([Fig 2c](#)), the majority of eastern Kenya was identified as highly suitable for RVF occurrence, with a medium-to-high suitability for RVF amplification combined with medium-to-high suitability for RVF spread. This pattern was also observed in northeastern Tanzania and southwestern Ethiopia. Areas with medium suitability for both RVF amplification and spread, such as northwestern Tanzania, or areas with low amplification suitability but high spread suitability, such as western Kenya, the majority of Uganda and the Ethiopian highlands, were identified as suitable for RVF occurrence. This first map also highlighted areas with low suitability for RVF occurrence (low suitability for amplification and spread), such as eastern Ethiopia and central Tanzania. Taking into account the proximity of the areas with the highest suitability for RVF amplification, the second synthetic RVF suitability map ([Fig 2d](#)) highlighted the different patterns of the areas suitable for RVF occurrence: the

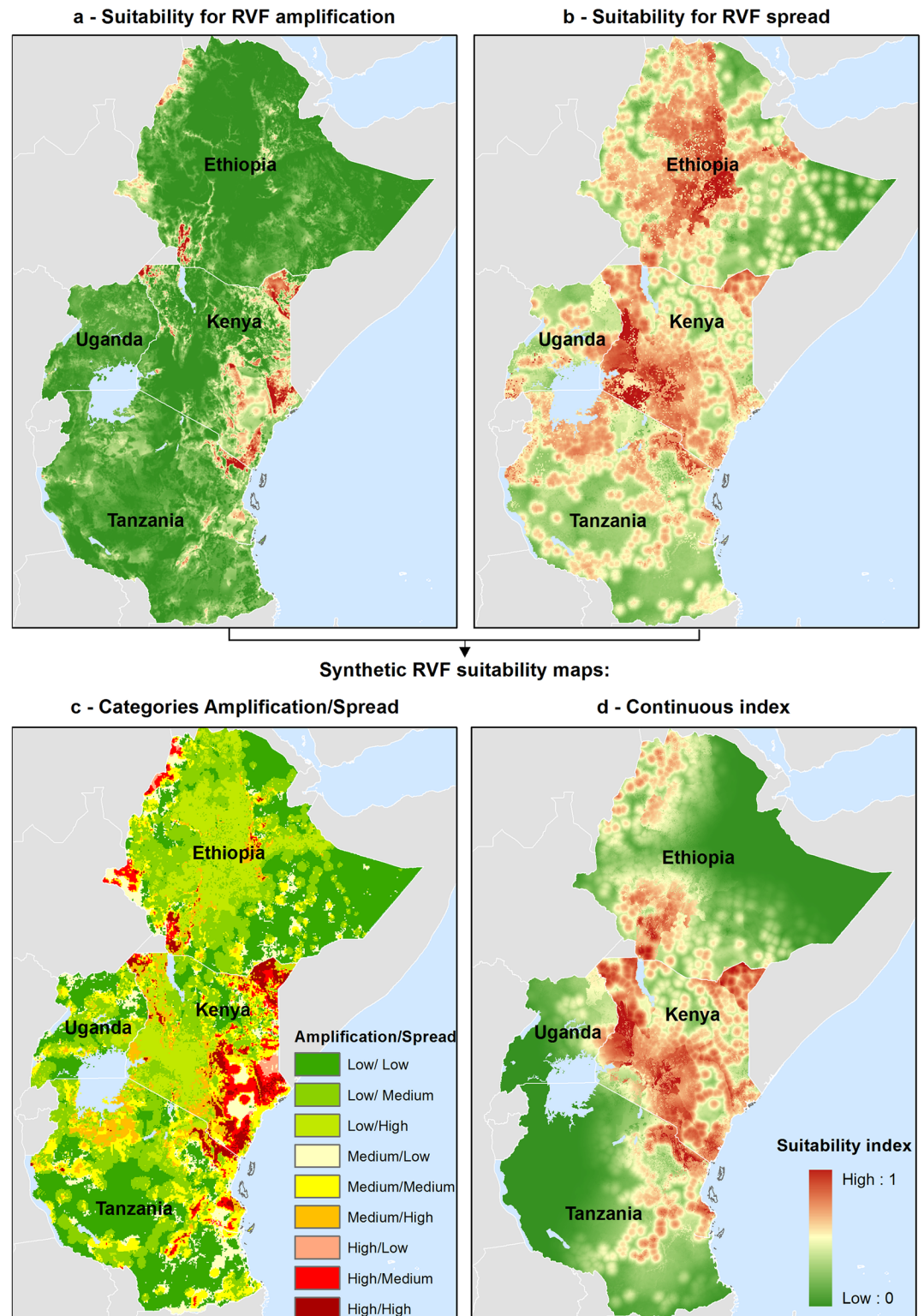


Fig 2. Suitability maps for RVF amplification (a) and spread (b) are combined to produce a synthetic suitability map for RVF occurrence in livestock with nine classes corresponding to all possible combinations of amplification suitability (low/medium/high) and spread suitability (low/medium/high) (c) and a second synthetic RVF suitability map expressed as a continuous suitability index (d).

doi:10.1371/journal.pntd.0004999.g002

majority of Kenya was identified as suitable; however, in the three other countries, the areas suitable for RVF occurrence were smaller than those shown in Fig 2c.

Sensitivity and uncertainty analysis

The uncertainty of the surface-based model produced by the data for the four countries showed that the predictions of the location of suitable areas for RVF occurrence in livestock were robust, meaning that they remained stable when varying the risk factor weights in the ‘amplification’ and ‘spread’ steps. Indeed, the maximum standard deviation (STD) of the suitability maps for RVF occurrence was less than 0.1. The results highlighted a spatial heterogeneity in uncertainty, with higher uncertainty in the western parts of Ethiopia and Kenya (S2 Fig).

The sensitivity analysis showed that the variation in the suitability index was explained by four factors for the amplification step and by seven factors for spread (Fig 3). The most sensitive parameters for the amplification step were the sheep density and the proximity to markets, wildlife national parks, and water bodies. Regarding the spread step, the most sensitive parameters were the cattle and goat densities, the density of roads and railways, and the proximity to national parks and water bodies. The importance of these sensitive parameters varied among the four countries, particularly the importance of the livestock densities (cattle, sheep and goats) (Fig 3).

Map validation

The ROC AUC associated with the suitability map for RVF occurrence in Kenya and Tanzania showed a good fitting (AUC = 0.786; 95% CI [0.730–0.842]) (Fig 4a), demonstrating the capacity of the model to distinguish ‘presence’ from ‘absence’ locations with good predictive accuracy (Fig 4b). With a cut-off point of 0.3 maximizing both sensitivity and specificity, the sensitivity was 0.74, and the specificity was 0.75. A total of 74% (107 out of 145) of the RVF outbreak locations were mapped in at-risk areas, which were defined as the areas with a suitability index for RVF occurrence greater than 0.3, the cut-off point value maximizing sensitivity and specificity (Fig 5b).

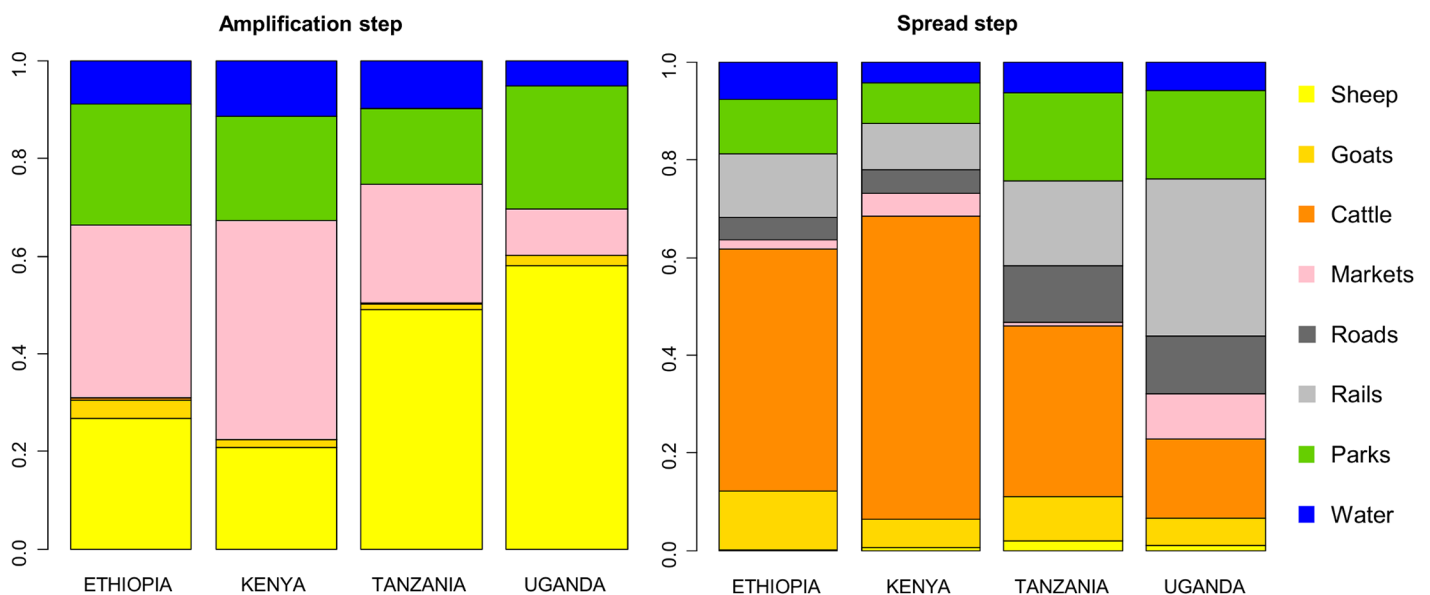


Fig 3. Contribution of the different risk factor weights to model output variance.

doi:10.1371/journal.pntd.0004999.g003

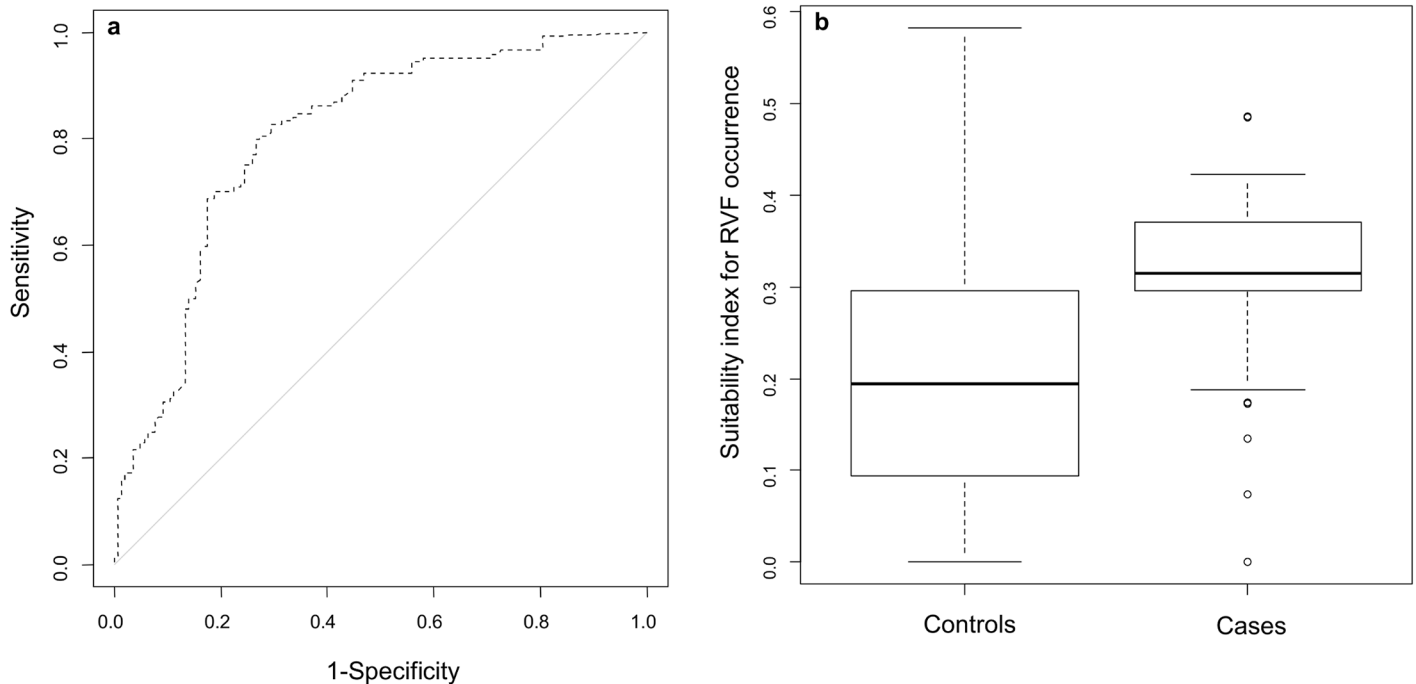


Fig 4. Assessment of the suitability index for RVF occurrence in livestock in Kenya and Tanzania. a) ROC curve. b) Box-plot showing RVF occurrence suitability index values for cases (RVF outbreak locations) and controls (random ‘pseudoabsence’ locations). Box-plots show median values (solid horizontal line), 50th percentile values (box-plot outline), 90th percentile values (whiskers), and outlier values (open circles).

doi:10.1371/journal.pntd.0004999.g004

Discussion

Many regions from Kenya and Tanzania were previously and heavily affected by RVF outbreaks [6, 82]. However, some areas may be at-risk without having experienced outbreaks in past years. The identification of these areas is essential for implementing risk-based surveillance and reducing the impact of RVF human and animal outbreaks in the coming years. Until 2016, Uganda and Ethiopia remained free from outbreaks, but their geographical locations as well as the livestock exchanges they have with their neighbors make these two countries highly vulnerable to the disease.

In this context, the implementation of the GIS-based MCE method for RVF risk mapping appeared to be a very efficient method to map suitability areas for the amplification and spread of the virus based on freely available geographic data. To our knowledge, this is the first study aiming to produce regional suitability maps for RVF using MCE methodology combined with outbreak dataset validation.

Validation of the suitability map using disease presence and background data randomly generated produced good results according to the ROC AUC method (AUC = 0.786). However, the use of randomly generated ‘pseudoabsence locations’ may be controversial; indeed, the absence of reported outbreaks is not an evidence of absence of pathogen transmission. The results of regional serological surveys may give a more precise evaluation of the RVF suitability map.

Nevertheless, 74% of the reported RVF outbreaks in livestock were located in areas with the highest predicted suitability for RVF occurrence (Fig 5b). Interestingly our MCE-based model performed better than other predictive models based purely on climatic anomalies and previously validated with human outbreaks [14]. These models, which showed the highest accuracy

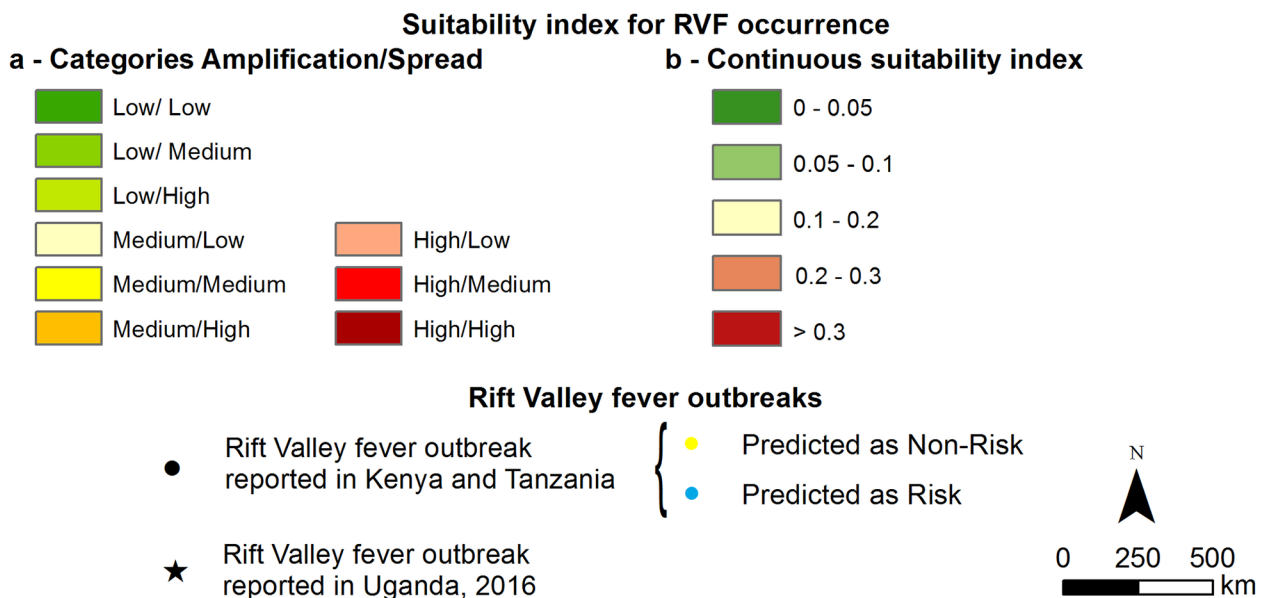
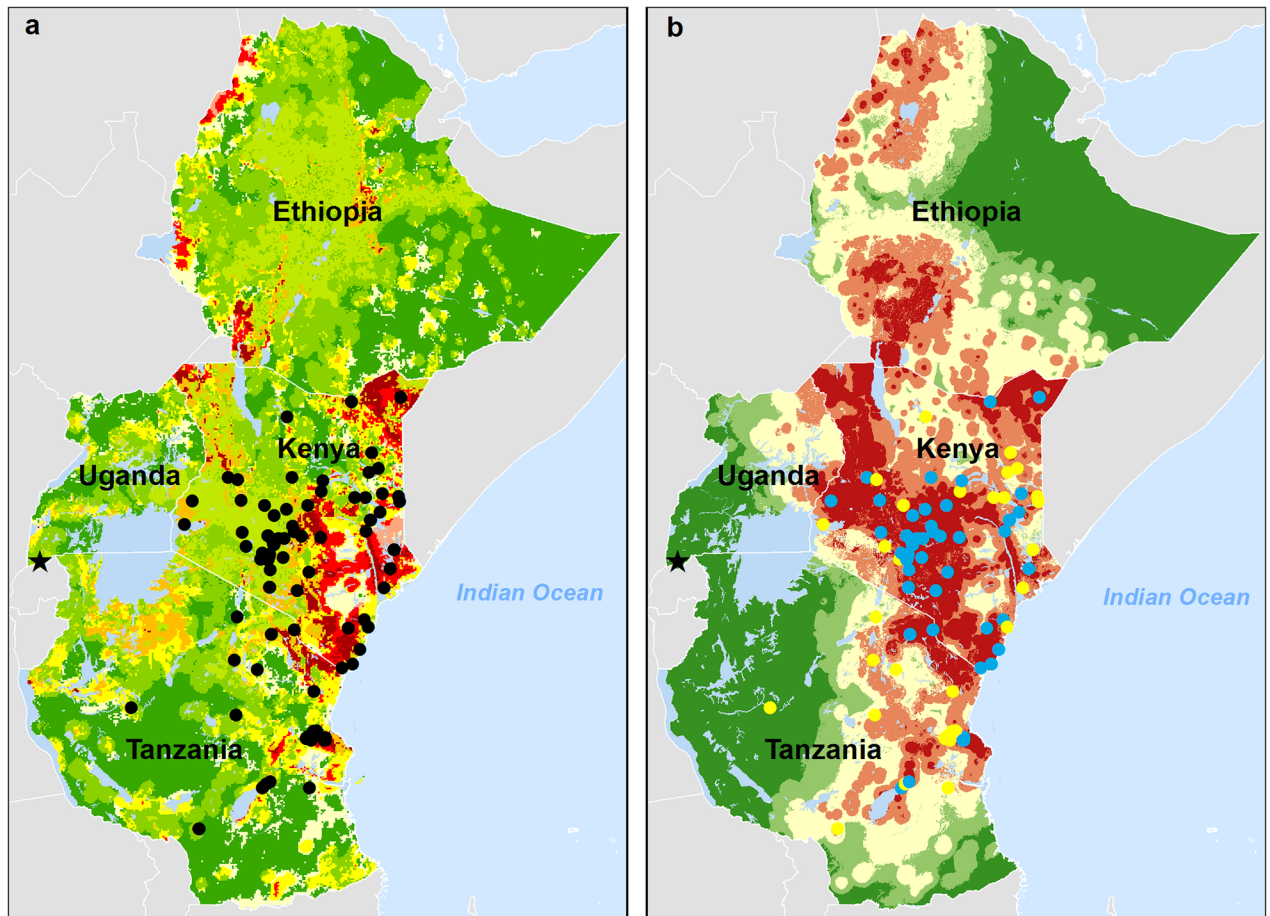


Fig 5. Suitability maps for RVF occurrence and the locations of RVF outbreaks in livestock: a) Combination of amplification and spread suitability categories; b) continuous suitability index. Blue dots indicate the outbreak locations that were identified in the RVF at-risk areas. Yellow dots indicate outbreak locations not considered to be at-risk.

doi:10.1371/journal.pntd.0004999.g005

in the Eastern African region, included 65% of the human case locations in predicted at-risk areas. Two human cases of RVF have been reported in early March 2016 in the Kabale District, southwestern Uganda [83]. The outbreak occurred in an area that was identified by our model as poorly suitable for RVF amplification but highly suitable for RVF spread (Fig 5a). This result is highly consistent with the socio-economic and ecological environment of Kabale district. Indeed, Kabale is an important commercial center with six animal markets, a situation associated with a higher risk for RVF spread according to our assumptions. Being outside of the ‘potential epizootic area mask’ [14], this area is not predicted by the climate-based model [83]. Despite the strong 2015–2016 El Niño phenomenon and the associated abnormal rainy season in East Africa, no substantial climatic anomalies were observed in the Kabale area during the 2016 epidemics. Differently from the southeastern and central districts in Uganda and neighboring countries, such as Kenya and Tanzania, both cumulative precipitation as well as NDVI values were lower than or equal to average in Kabale area during the period September 2015 to February 2016, except for short periods in October and December 2015. We therefore hypothesize a little role of vector-borne transmission in the Kabale outbreak.

Thus, our results highlighted the importance of taking into account livestock data and the factor of animal trade in addition to environmental factors to develop predictive maps of RVF occurrence. Moreover, these maps increase the confidence level for the approach applied to RVF free-areas [27, 28].

Indeed, the MCE approach we applied to four countries of eastern Africa was very similar to previous modelling studies that used the same approach in different geographic contexts [25–28]. All of these studies considered two main categories of risk factors: on the one hand, those related to domestic ruminant densities, and on the other hand, those related to vector presence (*i.e.*, vector distributions or proxies of vector distributions, such as temperature, elevation, rainfall, and proximity to aquatic areas). One of the distinctive features of our study was the ability to distinguish RVF amplification and spread steps in the modelling process, thus considering risk factors related to animal trade and movements (markets, roads and railways). Moreover, the hypothesized role of wildlife reservoirs in the amplification and spread of RVF was considered.

Identifying areas of low amplification with high spread suitability and vice versa (Fig 5a) was expected because these two epidemiological phenomena imply different mechanisms: vector and host densities favor local amplification, whereas animal movements favor the long-range spread of the disease. From a control perspective, surveillance strategies should be adapted; active surveillance in sentinel herds would be relevant in amplification areas that act as virus sources for areas that are not at risk of amplification, and analysis of the trade network and the existing links between amplification areas and other regions could be used as an early warning tool to protect spread areas from viremic ruminant introduction in case of primary foci.

However, the limits of our method must be noted. First, in the absence of homogeneous information on RVFV vector abundance and distribution in our study area, we used environmental variables to map a vector index reflecting the suitability of locations for the presence of RVF vectors. These variables were identified through a study performed in Kenya; this study may not be perfectly relevant for the three other countries because this vector suitability map needs to be validated by landscape-targeted mosquito trappings in each country. Among mosquito species vectors recorded in the countries of concern, several were demonstrated to be competent in the lab [42]. However, even if competency measures were to provide elements to infer the potential role of a given mosquito species in RVF outbreaks, these measures are not sufficient to definitely incriminate the species. Indeed, mosquito abundance and foraging

behavior are major elements that also shape the epidemiology of arboviruses. Better knowledge of these entomological characteristics should be considered to improve the vector index map.

Second, the spatial scale chosen for mapping the suitable areas for disease transmission has a great impact on the produced maps due to the spatial resolution of the data used to calculate the risk factors and the choice of the risk factors included to map suitability areas for pathogen transmission. Moreover, the weight attributed to each risk factor may differ between regional and national scales. In this study, we provided regional maps of suitability for RVF; however, maps produced on a national scale with higher spatial resolution, derived from risk factors and weights discussed with experts of each country (with particular attention paid to the most sensitive weights identified by the SA), would be more accurate and useful for surveillance and control purposes. Moreover, the threshold used to define the areas highly suitable for virus amplification (90th percentile threshold considering the whole study area) may introduce a bias in suitability predictions. This threshold value should be adapted for each country to provide better predictions at the national level.

Lastly, limitations of the produced map are related to the availability of data used as risk factors and their quality. For instance, due to a lack of geographic data on the locations of veterinary services and surveillance networks within each country, this information was not taken into account in our model, although both are key factors for the control of animal diseases—the spread intensity and magnitude from primary foci depending on the detection delay and, thus, on the efficiencies of veterinary and surveillance services. Moreover, the immunological status of ruminant populations induced by previous virus circulation episodes or vaccination campaigns were not taken into account although they are important factors, as demonstrated in South Africa in 2010 [84]. Additional information on how landscape features and socio-economic factors impact domestic and wild ruminant movements may also be important to refine the cost distance calculations of markets, water and wildlife park proximity indices.

In this study, we focused on mapping the areas suitable for RVF amplification and spread; thus, we focused on the spatial dimension of RVF risk. Although transmitted by mosquitoes and probably by direct contact, RVF is a seasonal disease, occurring during or at the end of the rainy season when mosquito abundance is at its highest. Future work should take into account this temporality to provide seasonal suitability maps for RVF transmission in livestock. Coupling climate-based models [14] with the RVF suitability map, which includes livestock and commercial variables, would allow for the development of seasonal suitability maps for RVF transmission in livestock. However, it must be stressed that this requires a good understanding of the drivers of RVF emergence. Indeed, with the exception of Kenya, where a strong association was demonstrated between heavy rainfall events and outbreak occurrence [22], rainfall may not be the only key factor for RVF emergence. Host density, associated with suitable climatic conditions and the introduction of the virus by ruminant trade, probably led to the 2000 outbreak in Yemen [32]. In Madagascar in 2008, no abnormal rainfall was noticed before the outbreak [85]. In Senegal in 2003, an intense transmission was described without any abnormal rainfall [44]. Soti *et al.* (2012) observed that in this region, the rainfall pattern rather than rainfall abundance could be responsible for triggering outbreaks [86]. Therefore, the seasonality of outbreaks should be incorporated in models with caution, depending on the area considered.

Conclusion

The present study confirmed the capacity of GIS-based MCE method to synthesize available scientific knowledge and map with accuracy the spatial heterogeneity of RVF suitability in four countries of East Africa. Moreover, such an approach enables users a straightforward and easy updating of the maps according to data availability or scientific knowledge development to

include more precise geographic data or additional risk factors and to modify the weights of each factor.

Supporting Information

S1 Fig. Standardized risk factors for RVF amplification and spread in Ethiopia, Kenya, Uganda and Tanzania. Values of each risk factor range from zero (low risk: black areas) to one (high risk: white areas).

(TIF)

S2 Fig. Uncertainty map (standard deviation of RVF occurrence suitability maps) for Ethiopia, Kenya, Uganda, and Tanzania.

(TIF)

S1 Table. Details of the Geographic Information Systems manipulations required to convert the collected data into risk factor layers in raster format.

(PDF)

S2 Table. Scaling functions applied to Rift Valley fever risk factor layers.

(PDF)

S3 Table. Correlation matrix for risk factors associated with Rift Valley fever amplification and spread.

(PDF)

S4 Table. Pair-wise comparison matrices of the analytical hierarchy process (AHP) for risk factors associated with Rift Valley fever amplification.

(PDF)

S5 Table. Pair-wise comparison matrix of the analytical hierarchy process (AHP) for risk factors associated with Rift Valley fever spread.

(PDF)

S1 File. Spatial risk factors for Rift Valley fever: Sources of the data used, and calculation of the corresponding standardized geographical layers.

(PDF)

S2 File. Sensitivity analysis.

(PDF)

Acknowledgments

We gratefully thank for their help and fruitful discussions during this study the many diverse staff members from CIRAD, FAO, Royal Veterinary College (UK), the International Livestock Research Institute, the Interafrican Bureau for Animal Resources, the Uganda Veterinary Services, the Uganda Virus Research Institute, the Uganda Vector Control Division, the Uganda Ministry of Agriculture Animal Industry and Fisheries, the Uganda Bureau of Statistics, the Ethiopian National Animal Health Diagnostics and Investigation Center and the Institut de Recherche pour le Développement (France).

Author Contributions

Conceptualization: AT CT JP VC.

Data curation: AT MG.

Formal analysis: AT VC.

Methodology: AT CT VC.

Project administration: CT VC.

Resources: AT CT JL JS MG CP VC.

Software: AT.

Supervision: VC JP.

Validation: AT CT CP JP VC.

Visualization: AT MG.

Writing – original draft: AT VC.

Writing – review & editing: CT JL JS CP.

References

- Wilson ML. Rift Valley fever virus ecology and the epidemiology of disease emergence. *Ann NY Acad Sci.* 1994 Dec 15; 740:169–80. PMID: [7840448](#).
- Nicolas G, Durand B, Tojofaniiry T, Lacote S, Chevalier V, Marianneau P. A three years serological and virological cattle follow-up in Madagascar highlands suggests a non-classical transmission route of Rift Valley Fever virus. *American Journal of Tropical Medicine and Hygiene.* 2014 Dec 23; 90(2):265–6. doi: [10.4269/ajtmh.13-0538](#) PMID: [24366500](#)
- Peyre M, Chevalier V, Abdo-Salem S, Velthuis A, Antoine-Moussiaux N, Thiry E, et al. A Systematic Scoping Study of the Socio-Economic Impact of Rift Valley Fever: Research Gaps and Needs. *Zoonoses Public Health.* 2015 Sep 24; 62(5):309–25. PMID: [25256804](#). doi: [10.1111/zph.12153](#)
- Chevalier V, Pepin M, Plee L, Lancelot R. Rift Valley fever—a threat for Europe? *Euro Surveillance.* 2010 Mar 11; 15(10):1–11. PMID: [20403309](#).
- Jupp PG, Kemp A, Grobbelaar A, Leman P, Burt FJ, Alahmed AM, et al. The 2000 epidemic of Rift Valley fever in Saudi Arabia: mosquito vector studies. *Medical and Veterinary Entomology.* 2002; 16:245–52. PMID: [12243225](#)
- Hightower A, Kinkade C, Nguku PM, Anyangu A, Mutonga D, Omolo J, et al. Relationship of climate, geography, and geology to the incidence of Rift Valley fever in Kenya during the 2006–2007 outbreak. *Am J Trop Med Hyg.* 2012 Feb; 86(2):373–80. PMID: [22302875](#). doi: [10.4269/ajtmh.2012.11-0450](#)
- Sindato C, Karimuribo ED, Pfeiffer DU, Mboera LE, Kivaria F, Dautu G, et al. Spatial and temporal pattern of Rift Valley fever outbreaks in Tanzania; 1930 to 2007. *PLoS One.* 2014; 9(2):e88897. PMID: [24586433](#). Pubmed Central PMCID: 3934866. doi: [10.1371/journal.pone.0088897](#)
- Pourrut X, Nkoghe D, Souris M, Paupy C, Paweska J, Padilla C, et al. Rift Valley fever virus seroprevalence in human rural populations of Gabon. *PLoS Negl Trop Dis.* 2010; 4(7):e763. PMID: [20668541](#). Pubmed Central PMCID: 2910672. doi: [10.1371/journal.pntd.0000763](#)
- Digoutte JP, Peters CJ. General aspects of the 1987 Rift Valley fever epidemic in Mauritania. *Res Virol.* 1989 Jan-Feb; 140(1):27–30. PMID: [2711042](#).
- Meegan JM. The Rift Valley fever epizootic in Egypt 1977–78. 1. Description of the epizootic and virological studies. *Trans Roy Soc Trop Med Hyg.* 1979; 73(6):618–23. PMID: [538803](#).
- Hassan OA, Ahlm C, Sang R, Evander M. The 2007 Rift Valley fever outbreak in Sudan. *PLoS Negl Trop Dis.* 2011 Sep; 5(9):e1229. PMID: [21980543](#). Pubmed Central PMCID: 3181235. doi: [10.1371/journal.pntd.0001229](#)
- Chevalier V, Rakotondrafara T, Jourdan M, Heraud JM, Andriamanivo HR, Durand B, et al. An unexpected recurrent transmission of Rift Valley fever virus in cattle in a temperate and mountainous area of Madagascar. *PLoS Neglected Tropical Diseases.* 2011 Dec; 5(12):e1423. PMID: [22206026](#). doi: [10.1371/journal.pntd.0001423](#)
- Tantely ML, Le Goff G, Boyer S, Fontenille DAdp. An updated checklist of mosquito species (Diptera: Culicidae) from Madagascar. *Parasite.* 2016; 23:20. doi: [10.1051/parasite/2016018](#) PMID: [27101839](#)
- Anyamba A, Linthicum KJ, Small J, Britch SC, Pak E, de La Rocque S, et al. Prediction, assessment of the Rift Valley fever activity in East and Southern Africa 2006–2008 and possible vector control

- strategies. *American Journal of Tropical Medicine and Hygiene*. 2010 Aug; 83(2 Suppl):43–51. PMID: [20682905](#). doi: [10.4269/ajtmh.2010.09-0289](#)
15. Metras R, Jewell C, Porphyre T, Thompson PN, Pfeiffer DU, Collins LM, et al. Risk factors associated with Rift Valley fever epidemics in South Africa in 2008–11. *Scientific reports*. 2015; 5:9492. PMID: [25804974](#). Pubmed Central PMCID: 4372659. doi: [10.1038/srep09492](#)
 16. Heinrich N, Saathoff E, Weller N, Clowes P, Kroidl I, Ntinginya E, et al. High seroprevalence of Rift Valley fever and evidence for endemic circulation in Mbeya region, Tanzania, in a cross-sectional study. *PLoS Negl Trop Dis*. 2012; 6(3):e1557. PMID: [22479657](#). doi: [10.1371/journal.pntd.0001557](#)
 17. Nicholas DE, Jacobsen KH, Waters NM. Risk factors associated with human Rift Valley fever infection: systematic review and meta-analysis. *Tropical medicine & international health: TM & IH*. 2014 Dec; 19(12):1420–9. PMID: [25252137](#).
 18. Nanyingi MO, Munyua P, Kiama SG, Muchemi GM, Thumbi SM, Bitek AO, et al. A systematic review of Rift Valley Fever epidemiology 1931–2014. *Infection ecology & epidemiology*. 2015; 5:28024. PMID: [26234531](#). Pubmed Central PMCID: 4522434.
 19. Soumare B, Tempia S, Cagnolati V, Mohamoud A, Van Huylbroeck G, Berkvens D. Screening for Rift Valley fever infection in northern Somalia: A GIS based survey method to overcome the lack of sampling frame. *Veterinary Microbiology*. 2007 Apr 15; 121(3–4):249–56. ISI:000245797300006. English. PMID: [17257783](#)
 20. Aradaib IE, Erickson BR, Elageb RM, Khristova ML, Carroll SA, Elkhidir IM, et al. Rift Valley fever, Sudan, 2007 and 2010. *Emerg Infect Dis*. 2013 Feb; 19(2):246–53. PMID: [23347790](#). doi: [10.3201/eid1902.120834](#)
 21. Magona JW, Galiwango T, Walubengo J, Mukiibi G. Rift Valley fever in Uganda: Seroprevalence and risk factor surveillance vis-à-vis mosquito vectors, anti-RVF virus IgG and RVF virus neutralizing antibodies in goats. *Small ruminant research*. 2013; 114(1):176–81.
 22. Linthicum KJ, Anyamba A, Tucker C. J., Kelley P. W., Myers M. F., Peters C. J. Climate and satellite indicators to forecast Rift Valley fever epidemics in Kenya. *Science*. 1999 Jul 16; 285(5426):397–400. PMID: [10411500](#).
 23. Munyua PM, Murithi RM, Ithondeka P, Hightower A, Thumbi SM, Anyangu SA, et al. Predictive Factors and Risk Mapping for Rift Valley Fever Epidemics in Kenya. *PLoS One*. 2016; 11(1):e0144570. PMID: [26808021](#). Pubmed Central PMCID: 4726791. doi: [10.1371/journal.pone.0144570](#)
 24. Malczewski J. GIS-based multicriteria decision analysis: a survey of the literature. *Int J Geogr Inf Sci*. 2006 Aug; 20(7):703–26. ISI:000238567200001. English.
 25. Clements AC, Pfeiffer DU, Martin V. Application of knowledge-driven spatial modelling approaches and uncertainty management to a study of Rift Valley fever in Africa. *Int J Health Geogr*. 2006; 5:57. PMID: [17156467](#).
 26. Clements AC, Pfeiffer DU, Martin V, Pittiglio C, Best N, Thiongane Y. Spatial risk assessment of Rift Valley fever in Senegal. *Vector Borne Zoonotic Dis*. 2007 Summer; 7(2):203–16. PMID: [17627440](#).
 27. Sanchez-Vizcaino F, Martinez-Lopez B, Sanchez-Vizcaino JM. Identification of suitable areas for the occurrence of Rift Valley fever outbreaks in Spain using a multiple criteria decision framework. *Vet Microbiol*. 2013 Jul 26; 165(1–2):71–8. PMID: [23602438](#). doi: [10.1016/j.vetmic.2013.03.016](#)
 28. Tran A, Ippoliti C, Balenghien T, Conte A, Gely M, Calistri P, et al. A geographical information system-based multicriteria evaluation to map areas at risk for Rift Valley fever vector-borne transmission in Italy. *Transbound Emerg Dis*. 2013 Nov; 60 Suppl 2:14–23. PMID: [24589097](#). doi: [10.1111/tbed.12156](#)
 29. Nicolas G, Durand B, Duboz R, Rakotondraivo R, Chevalier V. Description and analysis of the cattle trade network in the Madagascar highlands: potential role in the diffusion of Rift Valley fever virus. *Acta Trop*. 2013 Apr; 126(1):19–27. PMID: [23295911](#). doi: [10.1016/j.actatropica.2012.12.013](#)
 30. Weaver SC. Host range, amplification and arboviral disease emergence. *Archives of virology Supplementum*. 2005 (19):33–44. PMID: [16358422](#).
 31. Hongoh V, Hoen AG, Aenishaenslin C, Waaub JP, Belanger D, Michel P. Spatially explicit multi-criteria decision analysis for managing vector-borne diseases. *Int J Health Geogr*. 2011; 10:70. PMID: [22206355](#). doi: [10.1186/1476-072X-10-70](#)
 32. Abdo-Salem S, Tran A, Grosbois V, Gerbier G, Al-Qadasi M, Saeed K, et al. Can environmental and socioeconomic factors explain the recent emergence of Rift Valley fever in Yemen, 2000–2001? *Vector Borne and Zoonotic Diseases*. 2011 Jun; 11(6):773–9. PMID: [21284504](#). doi: [10.1089/vbz.2010.0084](#)
 33. Nicolas G, Chevalier V, Tantely LM, Fontenille D, Durand B. A spatially explicit metapopulation model and cattle trade analysis suggests key determinants for the recurrent circulation of rift valley Fever virus in a pilot area of madagascar highlands. *PLoS Negl Trop Dis*. 2014 Dec; 8(12):e3346. PMID: [25474116](#). Pubmed Central PMCID: 4256285. doi: [10.1371/journal.pntd.0003346](#)

34. Abd El-Rahim IHA, El-Hakim UA, Hussein M. An epizootic of Rift Valley fever in Egypt in 1997. *Rev Sci Tech Off Int Epi.* 1999; 18(3):741–8.
35. LaBeaud AD, Cross PC, Getz WM, Glinka A, King CH. Rift Valley fever virus infection in African buffalo (*Syncerus caffer*) herds in rural South Africa: evidence of interepidemic transmission. *Am J Trop Med Hyg.* 2011 Apr; 84(4):641–6. PMID: [21460024](#). doi: [10.4269/ajtmh.2011.10-0187](#)
36. Beechler BR, Bengis R, Swanepoel R, Paweska JT, Kemp A, van Vuren PJ, et al. Rift valley Fever in Kruger national park: do buffalo play a role in the inter-epidemic circulation of virus? *Transbound Emerg Dis.* 2015 Feb; 62(1):24–32. PMID: [24330522](#). doi: [10.1111/tbed.12197](#)
37. Evans A, Gakuya F, Paweska JT, Rostal M, Akoolo L, Van Vuren PJ, et al. Prevalence of antibodies against Rift Valley fever virus in Kenyan wildlife. *Epidemiol Infect.* 2008 Sep; 136(9):1261–9. PMID: [17988425](#).
38. Olive MM, Goodman SM, Reynes JM. The role of wild mammals in the maintenance of Rift Valley fever virus. *J Wildl Dis.* 2012 Apr; 48(2):241–66. PMID: [22493102](#).
39. Britch SC, Binopal YS, Ruder MG, Kariithi HM, Linthicum KJ, Anyamba A, et al. Rift Valley fever risk map model and seroprevalence in selected wild ungulates and camels from Kenya. *PLoS One.* 2013; 8(6):e66626. PMID: [23840512](#). doi: [10.1371/journal.pone.0066626](#)
40. El Mamy AB, Baba MO, Barry Y, Isselmou K, Dia ML, El Kory MO, et al. Unexpected Rift Valley fever outbreak, northern Mauritania. *Emerg Infect Dis.* 2011 Oct; 17(10):1894–6. PMID: [22000364](#). doi: [10.3201/eid1710.110397](#)
41. Gerdes GH. Rift Valley fever. *Rev Sci Tech OIE.* 2004; 23(2):613–23.
42. Pepin M, Bouloy M, Bird BH, Kemp A, Paweska J. Rift Valley fever virus (Bunyaviridae: Phlebovirus): an update on pathogenesis, molecular epidemiology, vectors, diagnostics and prevention. *Vet Res.* 2010 Nov-Dec; 41(6):61. PMID: [21188836](#).
43. Fafetine J, Neves L, Thompson PN, Paweska JT, Rutten VP, Coetzer JA. Serological evidence of Rift Valley fever virus circulation in sheep and goats in Zambezia Province, Mozambique. *PLoS Negl Trop Dis.* 2013; 7(2):e2065. PMID: [23469300](#). Pubmed Central PMCID: 3585041. doi: [10.1371/journal.pntd.0002065](#)
44. Chevalier V, Lancelot R, Thiongane Y, Sall B, Diaite A, Mondet B. Rift Valley fever in small ruminants, Senegal, 2003. *Emerg Infect Dis.* 2005 Nov; 11(11):1693–700. PMID: [16318720](#).
45. Chevalier V, Thiongane Y, Lancelot R. Endemic transmission of Rift Valley Fever in Senegal. *Transboundary Emerging Diseases.* 2009 Dec; 56(9–10):372–4. PMID: [19548898](#). doi: [10.1111/j.1865-1682.2009.01083.x](#)
46. Lernout T, Cardinale E, Jego M, Despres P, Collet L, Zumbo B, et al. Rift valley fever in humans and animals in Mayotte, an endemic situation? *PLoS One.* 2013; 8(9):e74192. PMID: [24098637](#). Pubmed Central PMCID: 3787064. doi: [10.1371/journal.pone.0074192](#)
47. Carroll SA, Reynes JM, Khristova ML, Andriamandimby SF, Rollin PE, Nichol ST. Genetic evidence for Rift Valley fever outbreaks in Madagascar resulting from virus introductions from the East African mainland rather than enzootic maintenance. *J Virol.* 2011 Jul; 85(13):6162–7. PMID: [21507967](#). Pubmed Central PMCID: 3126502. doi: [10.1128/JVI.00335-11](#)
48. Soumare PO, Freire CC, Faye O, Diallo M, de Oliveira JV, Zanotto PM, et al. Phylogeography of Rift Valley Fever virus in Africa reveals multiple introductions in Senegal and Mauritania. *PLoS One.* 2012; 7(4):e35216. PMID: [22539961](#). doi: [10.1371/journal.pone.0035216](#)
49. Xiao Y, Beier JC, Cantrell RS, Cosner C, DeAngelis DL, Ruan S. Modelling the effects of seasonality and socioeconomic impact on the transmission of rift valley Fever virus. *PLoS Negl Trop Dis.* 2015 Jan; 9(1):e3388. PMID: [25569474](#). Pubmed Central PMCID: 4287488. doi: [10.1371/journal.pntd.0003388](#)
50. Abdo-Salem S, Waret-Szkuta A, Roger F, Olive MM, Saeed K, Chevalier V. Risk assessment of the introduction of Rift Valley fever from the Horn of Africa to Yemen via legal trade of small ruminants. *Trop Anim Health Prod.* 2010 Feb; 43(2):471–80. PMID: [20967567](#). doi: [10.1007/s11250-010-9719-7](#)
51. LaBeaud AD, Sutherland LJ, Muiruri S, Muchiri EM, Gray LR, Zimmerman PA, et al. Arbovirus prevalence in mosquitoes, Kenya. *Emerg Infect Dis.* 2011 Feb; 17(2):233–41. PMID: [21291594](#). doi: [10.3201/eid1702.091666](#)
52. Turell MJ, Linthicum KJ, Patrican LA, Davies FG, Kairo A, Bailey CL. Vector competence of selected African mosquito (Diptera: Culicidae) species for Rift Valley fever virus. *J Med Entomol.* 2008 Jan; 45(1):102–8. PMID: [18283949](#).
53. Turell MJ, Lee JS, Richardson JH, Sang RC, Kioko EN, Agawo MO, et al. Vector competence of Kenyan *Culex zombaensis* and *Culex quinquefasciatus* mosquitoes for Rift Valley fever virus. *J Am Mosq Control Assoc.* 2007 Dec; 23(4):378–82. PMID: [18240513](#).
54. Ahmad K. More deaths from Rift Valley fever in Saudi Arabia and Yemen. *Lancet.* 2000 Oct 21; 356(9239):1422. PMID: [11052595](#).

55. Al Qadasi MM, editor Rift Valley fever outbreak in Yemen, September 2000 to February 2001. World Veterinary Congress; 2002; Tunis.
56. Hassan OA, Ahlm C, Sang R, Evander M. The 2007 Rift Valley fever outbreak in Sudan. *PLoS Neglected Tropical Diseases*. 2011 Sep; 5(9):e1229. PMID: [21980543](#). doi: [10.1371/journal.pntd.0001229](#)
57. Tantely ML, Rakotoniaina JC, Tata E, Andrianaivolambo L, Razafindrasata F, Fontenille D, et al. Biology of mosquitoes that are potential vectors of Rift Valley Fever virus in different biotopes of the central highlands of Madagascar. *J Med Entomol*. 2013 May; 50(3):603–10. PMID: [23802456](#).
58. Sang RC, Ahmed O, Faye O, Kelly CL, Yahaya AA, Mmadi I, et al. Entomologic investigations of a chikungunya virus epidemic in the Union of the Comoros, 2005. *Am J Trop Med Hyg*. 2008 Jan; 78(1):77–82. PMID: [18187788](#).
59. Mwaengo D, Lorenzo G, Iglesias J, Warigia M, Sang R, Bishop RP, et al. Detection and identification of Rift Valley fever virus in mosquito vectors by quantitative real-time PCR. *Virus Res*. 2012 Oct; 169(1):137–43. PMID: [22841800](#). doi: [10.1016/j.virusres.2012.07.019](#)
60. Ba Y, Sall AA, Diallo D, Mondo M, Girault L, Dia I, et al. Re-Emergence of Rift Valley Fever Virus in Barkedji (Senegal, West Africa) in 2002–2003: Identification of New Vectors and Epidemiological Implications. *J Am Mosq Control Assoc*. 2012; 28(3):170–8. PMID: [23833896](#)
61. Linthicum KJ, Davies FG, Kairo A, Bailey CL. Rift Valley fever virus (family Bunyaviridae, genus Phlebovirus). Isolations from Diptera collected during an inter-epizootic period in Kenya. *J Hyg*. 1985 Aug; 95(1):197–209. PMID: [2862206](#).
62. Sellers RF, Pedgley DE, Tucker MR. Rift Valley fever, Egypt 1977: disease spread by windborne insect vectors. *Vet Rec*. 1982; 110:73–7. PMID: [7064329](#)
63. Fontenille D, Traore-Lamizana M, Diallo M, Thonnon J, Digoutte JP, Zeller HG. New vectors of Rift Valley fever in west Africa. *Emerging Infectious Diseases*. 1998 Apr-Jun; 4(2):289–93. ISI:000073905300018. English. PMID: [9621201](#)
64. Glancey MM, Anyamba A, Linthicum KJ. Epidemiologic and Environmental Risk Factors of Rift Valley Fever in Southern Africa from 2008 to 2011. *Vector Borne Zoonotic Dis*. 2015 Aug; 15(8):502–11. PMID: [26273812](#). Pubmed Central PMCID: 4545538. doi: [10.1089/vbz.2015.1774](#)
65. Mondet B, Diaite A, Ndione JA, Fall AG, Chevalier V, Lancelot R, et al. Rainfall patterns and population dynamics of *Aedes (Aedimorphus) vexans arabiensis*, Patton 1905 (Diptera: Culicidae), a potential vector of Rift Valley Fever virus in Senegal. *Journal of Vector Ecology*. 2005 Jun; 30(1):102–6. ISI:000230216500014. English. PMID: [16007962](#)
66. Diallo M, Lochouart L, Ba K, Sall AA, Mondo M, Girault L, et al. First isolation of the Rift Valley fever virus from *Culex poicilipes* (Diptera: Culicidae) in nature. *American Journal of Tropical Medicine and Hygiene*. 2000 Jun; 62(6):702–4. ISI:000167937000008. English. PMID: [11304058](#)
67. Diallo M, Nabeth P, Ba K, Sall AA, Ba Y, Mondo M, et al. Mosquito vectors of the 1998–1999 outbreak of Rift Valley Fever and other arboviruses (Bagaza, Sanar, Wesselsbron and West Nile) in Mauritania and Senegal. *Medical and Veterinary Entomology*. 2005 Jun; 19(2):119–26. ISI:000229613200001. English. PMID: [15958020](#)
68. Ratovonjato J, Olive MM, Tantely LM, Andrianaivolambo L, Tata E, Razainirina J, et al. Detection, isolation, and genetic characterization of Rift Valley fever virus from *Anopheles (Anopheles) coustani*, *Anopheles (Anopheles) squamosus*, and *Culex (Culex) antennatus* of the Haute Matsiatra region, Madagascar. *Vector Borne Zoonotic Dis*. 2010 Jun; 11(6):753–9. PMID: [21028960](#). doi: [10.1089/vbz.2010.0031](#)
69. Sang R, Kioko E, Lutomiah J, Warigia M, Ochieng C, O'Guinn M, et al. Rift Valley fever virus epidemic in Kenya, 2006/2007: the entomologic investigations. *Am J Trop Med Hyg*. 2010 Aug; 83(2 Suppl):28–37. PMID: [20682903](#). doi: [10.4269/ajtmh.2010.09-0319](#)
70. Elfadil AA, Hasab-Allah KA, Dafa-Allah OM. Factors associated with Rift valley fever in South West Arabia. *Rev Sci Tech Off Int Epi*. 2006; 25(3):1137–1145.
71. Talla C, Diallo D, Dia I, Ba Y, Ndione JA, Sall AA, et al. Statistical modeling of the abundance of vectors of West African Rift Valley fever in Barkedji, Senegal. *PLoS One*. 2014; 9(12):e114047. PMID: [25437856](#). Pubmed Central PMCID: 4250055. doi: [10.1371/journal.pone.0114047](#)
72. Digoutte JP, Cordellier R, Robin Y, Pajot FX, Geoffroy B. Zinga virus (Ar B 1976), a new arbovirus isolated in central africa. *Ann Microbiol (Paris)*. 1974 Jul-Aug; 125B(1):107–18. PMID: [4157115](#). Le virus zinga (Ar B 1976), nouveau prototype d'arbovirus isole en Republique Centrafricaine.
73. Digoutte JP, Jacobi JC, Robin Y, Gagnard VJ. [Zinga virus infection in man]. *Bull Soc Pathol Exot Filiales*. 1974 Sep-Oct; 67(5):451–7. PMID: [4480466](#). Infection a virus Zinga chez l'homme.

74. Chevalier V, Lancelot R, Thiongane Y, Sall B, Mondet B. Incidence of Rift Valley fever in small ruminants in the Ferlo pastoral system (Senegal) during the 2003 rainy season. *Emerg Inf Dis*. 2005; 11(11):1693–700.
75. Jost CC, Nzietchueng S, Kihu S, Bett B, Njogu G, Swai ES, et al. Epidemiological assessment of the Rift Valley fever outbreak in Kenya and Tanzania in 2006 and 2007. *Am J Trop Med Hyg*. 2010 Aug; 83(2 Suppl):65–72. PMID: [20682908](#). doi: [10.4269/ajtmh.2010.09-0290](#)
76. Anyamba A, Small JL, Britch SC, Tucker CJ, Pak EW, Reynolds CA, et al. Recent weather extremes and impacts on agricultural production and vector-borne disease outbreak patterns. *PLoS One*. 2014; 9(3):e92538. PMID: [24658301](#). Pubmed Central PMCID: 3962414. doi: [10.1371/journal.pone.0092538](#)
77. Jeanmaire EM, Rabenarivahiny R, Biarmann M, Rabibisoa L, Ravaomanana F, Randriamparany T, et al. Prevalence of Rift Valley fever infection in ruminants in Madagascar after the 2008 outbreak. *Vector Borne Zoonotic Dis*. 2011 Apr; 11(4):395–402. PMID: [21395414](#). doi: [10.1089/vbz.2009.0249](#)
78. Horst HS, Huirne RBM, Dijkhuizen AA. Eliciting the relative importance of risk factors concerning contagious animal disease using conjoint analysis: a preliminary study. *Preventive Veterinary Medicine*. 1996; 27:183–95.
79. Saaty TL. How to Make a Decision—the Analytic Hierarchy Process. *European Journal of Operational Research*. 1990 Sep 5; 48(1):9–26. ISI:A1990EG63900003. English.
80. Ligmann-Zielinska A, Jankowski P. Spatially-explicit integrated uncertainty and sensitivity analysis of criteria weights in multicriteria land suitability evaluation. *Environmental Modelling & Software*. 2014; 57:235–47.
81. Park SH, Goo JM, Jo CH. Receiver operating characteristic (ROC) curve: practical review for radiologists. *Korean J Radiol*. 2004 Jan-Mar; 5(1):11–8. PMID: [15064554](#).
82. Mohamed M, Mosha F, Mghamba J, Zaki SR, Shieh WJ, Paweska J, et al. Epidemiologic and clinical aspects of a Rift Valley fever outbreak in humans in Tanzania, 2007. *Am J Trop Med Hyg*. 2010 Aug; 83(2 Suppl):22–7. PMID: [20682902](#). Pubmed Central PMCID: 2913502. doi: [10.4269/ajtmh.2010.09-0318](#)
83. FAO O, WHO. Africa—El Niño and increased risk of Rift Valley fever—Warning to countries. *EMPRES WATCH*. 2015;34.
84. Metras R, Baguelin M, Edmunds WJ, Thompson PN, Kemp A, Pfeiffer DU, et al. Transmission potential of Rift Valley fever virus over the course of the 2010 epidemic in South Africa. *Emerg Infect Dis*. 2013 Jun; 19(6):916–24. PMID: [23735606](#). doi: [10.3201/eid1906.121641](#)
85. Andriamandimby SF, Randrianarivo-Solofoniaina AE, Jeanmaire EM, Ravololomanana L, Razafimanantsoa LT, Rakotojoelinandrasana T, et al. Rift Valley fever during rainy seasons, Madagascar, 2008 and 2009. *Emerging Infectious Diseases*. 2010 Jun; 16(6):963–70. PMID: [20507747](#). doi: [10.3201/eid1606.091266](#)
86. Soti V, Tran A, Degenne P, Chevalier V, Lo Seen D, Thiongane Y, et al. Combining hydrology and mosquito population models to identify the drivers of Rift Valley fever emergence in semi-arid regions of West Africa. *PLoS Negl Trop Dis*. 2012; 6(8):e1795. PMID: [22928055](#). doi: [10.1371/journal.pntd.0001795](#)