Climate Influence on Emerging Risk Areas for Rift Valley Fever Epidemics in Tanzania

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Abstract. Rift Valley Fever (RVF) is a climate-related arboviral infection of animals and humans. Climate is thought to represent a threat toward emerging risk areas for RVF epidemics globally. The objective of this study was to evaluate influence of climate on distribution of suitable breeding habitats for *Culex pipiens* complex, potential mosquito vector responsible for transmission and distribution of disease epidemics risk areas in Tanzania. We used ecological niche models to estimate potential distribution of disease risk areas based on vectors and disease co-occurrence data approach. Climatic variables for the current and future scenarios were used as model inputs. Changes in mosquito vectors' habitat suitability in relation to disease risk areas were estimated. We used partial receiver operating characteristic and the area under the curves approach to evaluate model predictive performance and significance. Habitat suitability for *Cx. pipiens* complex indicated broad-scale potential for change and shift in the distribution of the vectors and disease for both 2020 and 2050 climatic scenarios. Risk areas indicated more intensification in the areas surrounding Lake Victoria and northeastern part of the country through 2050 climate scenario. Models show higher probability of emerging risk areas spreading toward the western parts of Tanzania from northeastern areas and decrease in the southern part of the country. Results presented here identified sites for consideration to guide surveillance and control interventions to reduce risk of RVF disease epidemics in Tanzania. A collaborative approach is recommended to develop and adapt climate-related disease control and prevention strategies.

BACKGROUND

Climate change projection reports in Tanzania indicate future increases in average annual temperatures from 1 to 3°C above the baseline, increase in precipitations, and intensification of extreme events such as floods and droughts by the 2050s.^{1,2} Climate change is expected to have impacts on the distribution of suitable conditions for breeding of mosquito vectors responsible for transmission and maintenance of Rift Valley Fever virus (RVFV).³ Climate is thought to represent a threat to emergence of new risk areas for RVF epidemics worldwide.^{4–6} These changes may play a major role to catalyze the emergence of RVF epidemic risk areas. Climate change is likely to affect human health from food insecurity and malnutrition to potential increase in malaria⁷ and some other climate-sensitive vector-borne diseases such as RVF.^{1,8–10} Other studies indicate that climate change influences dynamics and spatiotemporal distribution of *Aedes vexans* density, based on the total rainfall amount and ponds emergence in some areas of west Africa.¹¹

RVFV uses vectors such as mosquitoes and other arthropods for infection transfer to animals and humans.^{12,13} The virus persists throughout the inter-epidemic period (IEP) in the eggs of the floodwater *Aedes* mosquitoes for several years in dry conditions. This vertical transmission provides an explanation for the persistence of the virus through the IEP. Changes in weather conditions determine the emergence of the infected mosquito populations and the amplification of the virus.¹⁴ *Culex pipiens* complex is a prominent RVF-associated mosquito vector located in many RVF-endemic areas. *Cx. pipiens* complex is the main vector recorded in Ngorongoro District in Tanzania where RVF epidemics have been recurring.¹⁵ It was recorded as main vector during epidemics in different parts of Africa such as Egypt¹⁶ and South Africa.¹⁷

Cx. pipiens complex has been demonstrated in the laboratory to be capable of transmitting the virus; laboratory-established colonies from Tahiti exhibited the highest disseminated infection when infected with two strains of RVFV, the virulent ZH548 and the avirulent Clone 13.^{18,19} Vector competence tests indicate that *Cx. pipiens* is an important mosquito species for RVFV transmission.^{20,21}

Ecological niche models (ENMs) provide useful tools to assess risk of emergence and re-emergence of potential RVF epidemic hotspots due to changing climate and weather conditions. ENMs use combination of environmental-climatic factors such as temperature, precipitation, elevation, and derived-normalized difference vegetation index to predict climate change effects on disease vectors distribution.^{22,23} In Tanzania, few studies have already been done to identify potential risk areas in relation to RVF²⁴ using ENMs. There is still inadequate information on linkages of local environmental and future climatic conditions in determination of potential epidemic risk areas. Hence, we use ENMs such as Maximum Entropy Species Distribution Modeling (MaxEnt)²⁵ for *Cx. pipiens* complex to evaluate potential for emerging disease epidemics areas in response to climate change based on modeled current and future climate scenarios for 2020 and 2050.²⁶ Findings provide information to guide future surveillance efforts in geographic areas with high potential for RVF epidemics.

METHODS

Data on mosquito vectors occurrence. The data related to the occurrence of potential mosquito vectors responsible for virus transmission were derived from entomological study previously conducted in Ngorongoro District.^{15,27} Both outdoor and indoor surveys were conducted using Centers for Disease Control and Prevention light traps baited with CO₂ sachets and Mosquito Magnets (Mosquito Magnet Cordless Liberty Plus) baited with octenol attractants. Ngorongoro District was purposely selected as source

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of mosquito occurrence data because of its history of RVF epidemics from previously published work.²⁸ The district indicates weather variability and climatic vegetation cover.¹⁵ In Tanzania, severe socio-economic impacts due to epidemic were reported in 1997–1998 and 2006–2007.²⁹ The 2007 epidemic was the most widespread affecting livestock in 11 regions in Tanzania.^{30,31} A total of 16,973 cattle, 20,193 goats, and 12,124 sheep died of the disease, with spontaneous abortions reported in 15,726 cattle, 19,199 goats, and 11,085 sheep.³² Ngorongoro District is a tourist destination as being part of the Serengeti-Mara ecosystem, which represents a unique zone of interaction between livestock, wildlife, and humans with animal migration. According to the 2012 Tanzania National Population and Housing Census, the population at risk of infection in Ngorongoro District was 174,278.³³

Bioclimatic data. The occurrence of mosquito vectors within habitats is controlled by similar bioclimatic predictors at a given location. Bioclimatic environmental predictors derived from the monthly temperature and rainfall values were used as inputs into the model. Three bioclimatic datasets with a spatial resolution of ~1 km were downloaded from <http://www.worldclim.org/bioclim.htm>; these include the dataset for the past 50 years (1950–2000), which was considered to give the current scenario. For the next 50 years (2001–2050), the dataset was considered to give the likely future climatic conditions, with two scenarios considerations as 2020 and 2050.²⁶ Future projections are based on the current expulsion rates of greenhouse gases, chiefly carbon dioxide (CO₂), assuming that the CO₂ concentration in the atmosphere shall be doubled by 2050.^{1,2} Considering the importance of climatic data downgrading,³⁴ climatic data used in this modeling experiment were downscaled as previously described.²⁶ Nineteen bioclimatic variables were tested, but 13 were used as predictors for *Cx. pipiens* complex distributions for all predicted climatic scenarios. Variables were chosen based on their relevance to mosquito vector distributions and after several jackknifing procedures inbuilt within maxEnt software for exchanging labels on data points when performing permutation tests. Each time the model runs, one variable is removed and then the model tested to check if the removed variable had any significance as previously described.^{24,35,36} Contributions of each

variable to our prediction results were determined by iteration of the algorithm during regularization procedure and by random permutation as shown in Table 1.

Ecological niche modeling. We used MaxEnt version 3.3.1 to develop ENMs for mosquito species distribution in relation to disease records. The dataset for all scenarios was split into training-to-testing ratio of 3:1. We used default settings for MaxEnt except that we specified a random seed with 50% of points set aside for model evaluation and the regularization multiplier factor to reduce overfitting due to many bioclimatic variables. Modifying the regularization multiplier helped to generate risk maps that can be extrapolated to a larger countrywide scale. Because presence-only data originated from Ngorongoro District where RVF has previously been reported, we adjusted the regularization multiplier such that results of predicted models could be extrapolated to the whole country to identify other high-risk unsampled areas as to the main purpose of ENMs. We used a minimum training threshold to convert raw model outputs into actual distributional estimates. The predicted distributions of risk areas are assessed by estimating the probability at maximum entropy based on assumption of uniform probability.^{25,37} Predicted areas were identified as risky because of probability estimates on potential occurrence of infected *Cx. pipiens* complex in the area.

Emerging risk areas at climate change scenario. Generated data from different climate scenarios for mosquito species were processed to produce difference between present and future raster files. To show where areas become newly suitable and an area where conditions stop being suitable, raster map calculator tool in QGIS version 2.2 (Valmiera, Latvia) was used to subtract one from the other scenario. Raster map calculator allows performing manipulations, analysis, and maps generation on the basis of existing raster pixel values written to a new raster layer with a supported format. Results generated were further explored using free tools provided by the Tanzania Biodiversity Information portal at <http://www.tanbif.or.tz> or <http://tanbif.etibioinformatics.nl>.

Model performance evaluation. Partial ROC/AUC software implementation (<https://kuscholarworks.ku.edu/handle/1808/10059>) was used to evaluate model predictive performance.³⁸ Our choice for this approach to model evaluation was based on no absence data to characterize commission

TABLE 1
Contribution of bioclimatic variables used in the species ecological niche model

Bioclimatic variable	Current scenario		2020 Climate scenario		2050 Climate scenario	
	Percent contribution	Permutation importance	Percent contribution	Permutation importance	Percent contribution	Permutation importance
BIO10	29.1	0	28.9	0	29.5	0
BIO11	15.7	30	22.8	35.6	13.9	78.8
BIO3	18.4	10.5	16.4	0.8	21.7	3.3
BIO12	16.2	16.3	10.9	0.5	12.5	6.9
BIO2	1.1	0.3	6.4	4	7.8	11.1
BIO1	3.3	0	4.8	0	5.9	0
BIO17	3.4	15	3.8	30.8	0	0
BIO14	7.5	18	3.7	26.5	0	0
BIO8	2.6	0	0	0	8.7	0
BIO15	0	0	1.5	0	0	0
BIO4	0.4	0.5	0.7	1.8	0	0
BIO6	1.6	0	0	0	0	0
BIO13	0.6	9.4	0	0	0	0

BIO10 = mean temperature of warmest quarter; BIO11 = mean temperature of coldest quarter; BIO3 = isothermality; BIO12 = annual precipitation; BIO2 = mean diurnal range; BIO1 = annual mean temperature; BIO17 = precipitation of driest quarter; BIO14 = precipitation of driest month; BIO8 = mean temperature of wettest quarter; BIO15 = precipitation seasonality; BIO4 = temperature seasonality; BIO6 = min temperature of coldest month; BIO13 = precipitation of wettest month.

errors. Many previous models used ROC approaches, which require both absence and presence data²⁵ and which present numerous other problems.³⁹ Due to lack of absence data, and with more than twenty occurrence records in this study, partial ROC/AUC provides the best alternative approach to jackknifing, which also does not require absence data but when small sample of presence data is used.³⁵ Bootstrapping methods were used to test significance of model performance.³⁸ AUC ratios were determined using proportion area predicted present in the x axis and sensitivity (commission error) in the y axis. Thousand subsets of points were generated to specify the number of iterations during partial ROC/AUC ratio calculations. Frequency distribution of partial AUC ratios with respect to 1.0 (random performance) was generated. For any good model prediction, the frequency distribution of AUC ratios is above 1.³⁸

RESULTS

Variable importance and model performance. Jackknife approach to determine the importance of variables and their percentage contributions shows that the mean temperature of warmest quarter (BIO-10), mean temperature of coldest quarter (BIO-11), isothermality (BIO-3), and annual precipitation (BIO-12) were most important for all climatic scenarios (Table 1). Application of the partial ROC/AUC ratio shows that model predictive performance was statistically significantly better than random prediction ($P < 0.05$). The program generated the partial ROC/AUC ratios ranging from 1.003 to 1.256 at the given 1 – omission threshold of 0.95 using accepted omission error of 5% to the AUC at 50% for random prediction to specify the percentage of testing points that are included in each of the random subsets. The predicted maps show that the probability of the presence of *Cx. pipiens* complex in relation to disease appears to be high to medium across the country. Generally, the probability of the vector presence suitability appears to be high around the areas previously experienced RVF epidemics.

FIGURE 1. Predicted potential distributions of disease epidemic risk areas based on distribution of *Culex pipiens* complex in Tanzania for the current climate scenario. Increasing intensity of red color indicates higher risk suitability. This figure appears in color at www.ajtmh.org.

FIGURE 2. Predicted potential distributions of disease epidemic risk areas based on distribution of *Culex pipiens* complex in Tanzania for 2020 climate scenario. Increasing intensity of red color indicates higher risk suitability. This figure appears in color at www.ajtmh.org.

Distribution of disease epidemic risk areas. Figure 1 shows that the habitat suitability for *Cx. pipiens* complex in the current scenario coincides with that of the recorded disease epidemic risk areas whereas for the 2020 scenario as indicated in Figure 2 it is found to be apparently spreading. Anticipated high-risk areas are distributed toward the southern parts of Lake Victoria, northeastern parts of Tanzania, indicating more intensification of risks in Tanga regions as well as some areas surrounding Lake Tanganyika and Lake Nyasa. During this 2020 climate scenario, risks seem to disappear in western part of Lake Victoria and central parts of Tanzania as shown in Figure 2. For the 2050 climate scenario, predicted habitat suitability for *Cx. pipiens* complex indicated slightly similar potential

FIGURE 3. Predicted potential distributions of disease epidemic risk areas based on distribution of *Culex pipiens* complex in Tanzania for 2050 climate scenario. Increasing intensity of red color intensification indicates higher risk suitability. This figure appears in color at www.ajtmh.org.

FIGURE 4. Emerging and disappearing predicted potential suitable distribution areas for *Culex pipiens* complex in Tanzania for 2020 climate scenario. Increasing intensity of red and green colors indicates emerging and disappearing suitable risk areas, respectively. This figure appears in color at www.ajtmh.org.

for change as for 2020 but increased intensification and slight shift in the risk distribution toward the western areas of Lake Victoria and with higher risk in the central and northeastern parts, as shown in Figure 3. This scenario indicated areas around Ngorongoro District and Arusha region will continue to remain at relatively high risk through 2050 as shown in Figure 3, but with less emerging new risks as shown in Figure 5. Predicted results of this modeling approach show relatively high association with areas previously recorded with RVF epidemic for both humans and animals.

FIGURE 5. Emerging and disappearing predicted potential suitable distribution areas for *Culex pipiens* complex in Tanzania for 2050 climate scenario. Increasing intensity of red and green colors indicates emerging and disappearing suitable risk areas, respectively. This figure appears in color at www.ajtmh.org.

Emerging disease epidemic risk areas. Figures 3 and 4 show that predicted emerging habitat suitability for *Cx. pipiens* complex and disease risk indicated broadscale potential for change and shift in the distribution of the vectors and disease for both 2020 and 2050 projections. Findings show anticipated emerging risk areas in southern parts of Lake Victoria spreading to eastern parts of Lake Tanganyika while leaving higher emerging risk areas in many parts of Tanga region. Some possible expansions may be expected in parts of Rukwa and Mbeya regions, which are also indicated as potential risk areas. Predicted suitability probability of emerging hotspots for 2050 indicated risk intensification in nearly all parts of the country as indicated in Figures 3 and 4. The anticipated risk seems to disappear only in a few areas in the western parts of Lake Victoria and the whole of southern parts of Tanzania. The phenomenon of a shifting suitability could be visualized from the increased red and green coloration, which seems to cluster around the high and least risk areas, respectively, as shown in Figures 4 and 5.

DISCUSSION

Principal findings. This study presents the unique application of niche-based climate models for prediction of suitable areas for RVF vectors in Tanzania at different climatic scenarios. Findings reflect the distribution of RVF epidemic history based on habitat suitability for *Cx. pipiens* complex, which suggests the continued persistence of RVF epidemic episodes due to changing climate condition. The anticipated potential for distribution risk shift to the eastern parts of Lake Tanganyika and parts of Tanga region for *Cx. pipiens* complex agrees with the actual distribution as previously predicted in the current scenario,²⁴ indicating distribution range limits similar to disease epidemic records. Model projections onto 2050 conditions suggest increases in suitable areas in the northeast of the country. Future climate models scenarios show spread of disease risk from previously dry zones toward wetter zones of the country. This shift in direction to the northeastern regions has also been observed in other vector-borne diseases in temperate regions.⁴⁰

Our models indicate higher habitat suitability for *Cx. pipiens* surrounding the Great Rift Valley regions, which suggests that climate change could have a significant influence on emergence of disease epidemic risk in areas. Climate change is likely to cause a shift in the habitat suitability for this vector from lower altitudes to higher altitudes in the future. This shift may in turn force the vectors to migrate toward previously lower disease risk making these areas as potential high disease-risk in the future. It is assumed that the concentration of CO₂ in the atmosphere will double by 2050, leading to an average of 1.5°C increase in temperature, this will lead to the general order of the habitat suitability maintenance and a much greater shift as evident from the less and least suitable area. Also, the peripheral less suitable areas at much lower altitudes increasingly become least suitable. For instance, the less suitable areas at the southern part of Tanzania become least suitable under the 2050 climate scenario.

Findings show that the apparent shift in disease epidemic risk areas is due to the likely changes in precipitation levels

and increases in temperatures with the changing climate, as the global climate gets warmer. In other words, there is an apparent ascend in emerging risk areas from lower altitudes to higher altitudes with respect to climatic conditions of the current and future scenarios, respectively. A reason for this observed trend is that the suitability is strongly influenced by altitude, which determines the micro-climatic conditions at any given location. The climatic conditions of temperature and precipitation, which currently prevail in the suitable habitat range under the current scenario, will likely be attainable only at much higher altitudes in the future. Since climate affects both the physiology of the disease vectors and availability of resources, in the future, species currently occupying the suitable habitat may likely undergo a migratory toward favorable areas to encounter favorable climatic conditions that will be similar to those currently prevailing in the suitable habitat range under the current scenario.

Model projections suggest suitable conditions in the areas surrounding Lake Victoria, Tanganyika, and Nyasa. Therefore, the areas mentioned should be monitored for potential epidemic. New records for epidemic on RVF in areas surrounding Lake Tanganyika in Kigoma region are already available.⁴¹ This could be a consequence of changes in macro- and micro-climatic extremes as a result of climate changes that can directly impact distribution of RVF vectors. Increases in temperature can contribute to disease incidence by reducing pathogen incubation period and expediting vector generation time, larval survival rate, and overall population growth rate.⁸ Also, changes in seasonal precipitation regimes impact life cycles of vectors by changing micro-climate that provide stable and seasonal humidity at egg laying, hatchability of infectious eggs, and larval development sites.⁴ In addition to potential climate change, other factors also present potential increase for future disease risk areas such as ecological imbalanced state as a result of habitat fragmentation, urbanization, land-use changes, and human-imposed species disequilibria, making some other areas especially susceptible to the uncertain effects of global change.

Limitations of the study. In this study, the predicted results are based on distribution of *Cx. pipiens* complex, mosquito vector responsible for disease amplification during epidemics. The main *Aedes* mosquito species responsible for virus maintenance during IEP has never been confirmed; this may limit further application of the study results. Also, used bioclimatic data under the future climate scenarios likely inherited certain level of uncertainty from the modeled climate dataset that was used since the climatic conditions for the future are themselves predictions from the models. Thus, the performance and accuracy assessments shown cannot be prodigious. The results showed that besides the other environmental variables used in the model, the altitude plays a pivotal role on the habitat suitability for *Cx. pipiens* complex. Also, there is an apparent shift in the suitability from lower altitudes to higher altitudes with the changing climate from current through the 2020 and 2050 scenarios of the future modeled climate. Local human activities are concentrated in the habitat range currently suitable for *Cx. pipiens* complex. This overlap puts the disease vectors future survival in higher environmental suitability since many human activities create favorable environmental conditions.

CONCLUSIONS

The predicted distribution presented here shows that *Cx. pipiens* complex, the potential vectors for transmission of RVF, can widely be a cause of concern among disease ecologists, epidemiologists, and vector control professionals in most parts of the country. Climate change conditions show a shift in habitat suitability for vectors while maintaining suitability in areas currently observed as high-risk zones. Under these conditions, it will be necessary to continue studies of the distribution of vectors in the southern part of the country to enhance our understanding of the risk for RVF transmission. A collaborative approach is recommended to develop and adapt control and prevention strategies that will help manage the risk, and reduce the burden of RVF in animals and human populations living within predicted high-risk zones.

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