

Research Article

Current and future potential distribution of maize chlorotic mottle virus and risk of maize lethal necrosis disease in Africa

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Abstract: Maize Lethal Necrosis (MLN), caused by the synergistic effect of *maize chlorotic mottle virus* (MCMV; Tombusviridae: Machlomovirus) and any potyvirus, has the potential to devastate maize production across Africa. Since the first report in Kenya in 2011, MLN has spread to Tanzania, Uganda, Rwanda, and probably other surrounding countries. To understand the spatiotemporal distribution of MCMV and MLN risk in Africa, we developed ecological niche models using a genetic algorithm (GARP). Model inputs included climatic data (temperature and rainfall) and known detections of MCMV and MLN across Africa. Model performances were more statistically significant ($p < 0.05$) than random expectations, with Receivership Operating Curves (ROC) / Area Under Curve (AUC) scores above 86% and Kappa values above 0.936. Field observations generally confirmed model predictions. MCMV and MLN-positive incidences across the region corresponded to a variety of temperature and precipitation regimes in the semi-arid and sub-humid tropical sectors of central and eastern Africa. Ethiopia, Tanzania, and Democratic Republic of Congo have the potential to lose 662,974, 625,690 and 615,940 km² potential maize landmass, respectively. In terms of proportional loss of national maize production area, Rwanda, Burundi, and Swaziland have the potential to lose each 100%, and Uganda 88.1%. Future projections indicate smaller potential areas (-18% and -24% by 2020 and 2050, respectively) but climates consistent with current MCMV distributions and MLN risk are predicted even into the future. In conclusion, MLN risk in Africa is high, hence the need for better allocation of resources in management of MLN, with special emphasis on eastern and central Africa, which are and will remain hotspots for these problems in the future.

Keywords: Africa, Climate change, GARP, Hotspots, Maize, MCMV, MLN

Introduction

Maize *Zea mays* L. is the most important cereal crop in sub-Saharan Africa (SSA), covering over 25 x 10⁶ ha, largely in smallholder systems (Smale *et al.*, 2011). However, yields are often

not optimal, so the region imports about 7 x 10⁶ tons per annum (28%) of the maize required to cover deficits in production (Deininger and Byerlee, 2011). The deficit is partly a result of pest and disease burden, among which, Maize Lethal Necrosis (MLN) disease now figures importantly. Complete maize production losses attributed to MLN have been reported (CIMMYT, 2012).

In Kenya alone, by early 2012, MLN disease had affected 26,000 ha of maize,

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amounting to US\$ 52 m in losses to the country (MDRAT, 2012). In Tanzania, eight of the twenty major maize-growing regions are affected, and have been quarantined, while in Uganda, eight districts have been affected so far (IPPC, 2014). Some efforts are currently being devised to control or eradicate *maize chlorotic mottle virus* (MCMV) and MLN in Africa, including establishing local maize-free periods to eliminate virus reservoirs, identifying and encouraging the use of cultivars with resistance to either MCMV or the potyviruses, and strengthening the phytosanitary systems (Miano *et al.*, 2013).

MLN is caused by the synergistic effect of two viruses including *maize chlorotic mottle virus* (MCMV) (Tombusviridae: Machlomovirus) and any Potyviridae (i.e., either *maize dwarf mosaic virus*, MDMV; *Sugarcane Mottle Virus*, SCMV or *Wheat Streak Mosaic Virus*, WSMV). Niblett and Claflin (1978) described MLN as maize infection with MCMV and WSMV. In the USA, MCMV is transmitted by at least six species of chrysomelid beetles, including the western corn rootworm, *Diabrotica virgifera virgifera* LeConte, whereas in Hawaii, the corn thrips, *Frankliniella williamsi* Hood (Thysanoptera: Thripidae) has been identified to be the main vector (Nault *et al.*, 1981; Jiang *et al.*, 1992; Cabanas *et al.*, 2013).

Globally, MLN incidence dates back to 1973 in Peru, and to 1976 in Kansas, in the USA (Castillo and Hebert, 1974; Niblett and Claflin, 1978). The two early detections gave rise to two viral serotypes: MCMV-P (Castillo and Hebert, 1974) and MCMV-K, respectively (Niblett and Claflin, 1978). MCMV incidence was confirmed in Hawaii in 1990 (Jiang *et al.*, 1992 and China in 2010 (Xie *et al.*, 2011). Indeed MCMV is the most widespread corn virus in the Hawaiian Islands. Records of MCMV also exist for Argentina (Teyssandier *et al.*, 1983) and Mexico (Carrera-Martinez *et al.*, 1989).

In Africa, however, the disease seems to be a recent arrival. The first report of MCMV and

MLN was in September 2011 at lower elevations (1900 masl) in the Longisa division of Bomet county, southern Rift Valley of Kenya; the disease later spread to the Narok south and north and Naivasha districts (Wangai *et al.*, 2012). Subsequently, the disease was detected in Tanzania (CIMMYT, 2012; Makumbi and Wangai, 2013; Miano *et al.*, 2013), Uganda (IPPC, 2014), and Rwanda (Adams *et al.*, 2014); and some unconfirmed records exist from South Sudan. Given poor phytosanitary systems, porous borders, and poor regulatory regimes in the ECA region, the disease is likely to spread broadly to all countries bordering Kenya (FSNWG, 2012).

Currently, environmental conditions favoring MLN emergence remain poorly understood, making design of temporal and spatially explicit mitigation and response strategies difficult. Further, livelihoods of smallholder farmers in SSA are greatly challenged by variable and uncertain climate that could exacerbate agricultural pests and diseases (Ojwang *et al.*, 2010). It is not yet clear how MLN will interact with these projected climate variabilities in Africa. Ecological niche modeling (ENM) tools, which relate known occurrences of biological phenomena (such as disease emergence) to environmental characteristics of landscapes, may offer insights into such knowledge challenges (Lopez-Gardenas *et al.*, 2005; Peterson *et al.*, 2007; Sandoval-Ruiz *et al.*, 2008; Liria and Navarro, 2010; Sarkar *et al.*, 2010; Mak *et al.*, 2010). The approach involves algorithms that discover associations between point occurrence data and sets of digital maps summarizing environmental and ecological dimensions that may or may not be important in limiting geographic distributions or suitability (Peterson and Vieglais, 2001; Peterson and Shaw, 2003; Peterson *et al.*, 2005). These associations constitute an approximation to fundamental ecological niches and hence provide a basis for understanding many ecological and geographic phenomena related to geographic suitability.

The premise for these approaches is that knowing suitable environmental conditions for key disease elements (in this case, the virus), one identifies the areas at risk of emergence (Lopez-Cardenas *et al.*, 2005; Peterson *et al.*, 2007; Sarkar *et al.*, 2010). Hence, we applied ENM to estimate the ecological niche of MCMV, and characterize potential risk areas of MLN across Africa. This approach has potential to provide invaluable insights into spatial and temporal MLN disease dynamics across Africa, including in the face of climate change. This information is important in planning operational aspects of responsive and preemptive management strategies for MLN disease across Africa.

Materials and Methods

MLN Incidence Point Data

Current distributional data (Fig. 1) were gathered through extensive literature review, personal consultation and incidence detections across Eastern and Central Africa. Important literature sources were FSNWG (2012), MDRAT (2012), Wangai *et al.*, (2012), IPPC (2014), Miano *et al.*, (2013), and RAB (2013). In some cases incidence data were georeferenced by hand from East African maps to approximately 1 km precision. All occurrence data were verified, georeferenced to the nearest 0.001° and organized in Excel 2010 (Microsoft Corp., Redman, WA) spreadsheets for analysis (Peterson *et al.*, 2002).

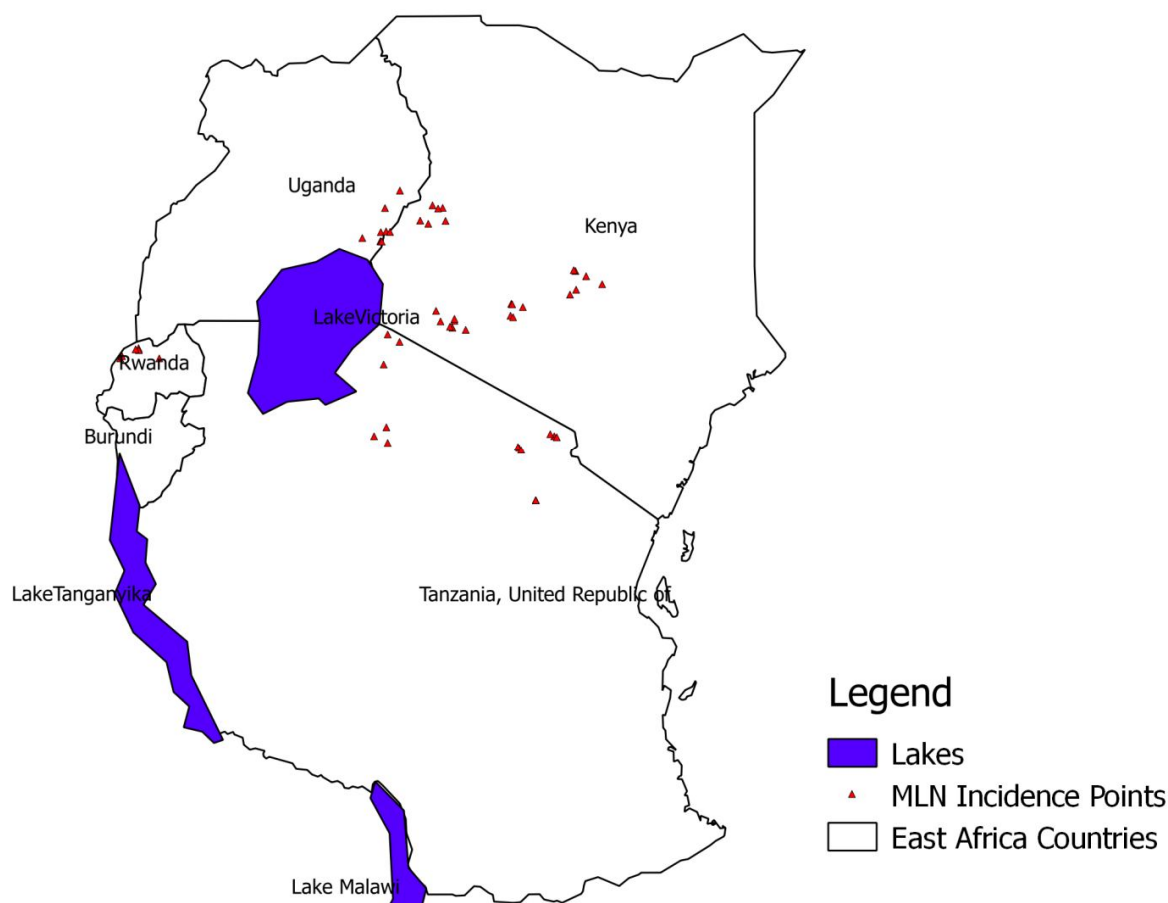


Figure 1 Map of East Africa indicating known Maize Lethal Necrosis (MLN) disease incidence data.

Environmental variables

Nineteen digital environmental variables were obtained from the WorldClim (2015) dataset at 30th spatial resolution (Hijmans *et al.*, 2005). On the basis of results of multicollinearity tests, and jackknifing procedures for relevancy to MCMV/MLN incidence (Pearson *et al.*, 2007) a subset of 12 bioclimatic variables was used for modeling MLN suitability across Africa: annual mean temperature, isothermality, min temperature of coldest month, temperature annual range, mean temperature of warmest quarter, mean temperature of coldest quarter, precipitation of wettest month, precipitation of driest month, precipitation seasonality, precipitation of wettest quarter, precipitation of warmest quarter, and precipitation of coldest quarter. Current situation was modeled based on the 1950-2000 baseline, while future data layers for 2020 and 2050 were obtained from the IPCC (2015). The future climate variables were derived from the Global Circulation Model ECHAM5 downscaled using the CLM Regional Circulation Model of the Max Planck Institute (<http://cera-www.dkrz.de>). A resolution of 100 × 100 m was then obtained by adding the anomalies between current and future climate conditions, which were downscaled to 1 km² using the change factor methodology to the current baseline data to match the resolution of the current data.

Ecological Niche Modeling

The Genetic Algorithm for Rule-Set Prediction (GARP; Stockwell and Peters (1999), a robust evolutionary computing application within openModeller was used for niche model calibration (Peterson and Shaw, 2003; Tsoar *et al.*, 2007; Terribile *et al.*, 2010). Among diverse ENM platforms, GARP has frequently proven to have better transferability and hence performs better in anticipating occurrences in unsampled regions (Peterson *et al.* 2007). The latter attribute makes it a better option in the present case in which MLN has been detected in the continent only recently. GARP develops a series of decision rules that summarize those factors associated with phenomena by random re-sampling occurrence

points to create training and test data sets in an iterative process of rule selection, evaluation, testing, and incorporation or rejection (Lopez-Cardenas *et al.*, 2005). At each step, predictive accuracy is evaluated based on random subsamples, and change in predictive accuracy from one iteration to the next is used to evaluate whether or not a particular rule should be incorporated into the model. In this way, the program offers relatively more accurate predictions and improved flexibility in choice of predictive environmental/ecological data coverage (Tsoar *et al.*, 2007). In this study we used GARP with the best sets option within openModeller version 1.1.0, which is a complete rewrite of the earlier DesktopGarp code, with improved gene values, atomic rules, heuristic operator parameters and bug fixation (Anderson *et al.*, 2003). The procedure involved: (i) modeling ecological niche requirements based on current MCMV/MLN records across Africa; (ii) testing the accuracy of predictions by splitting available data into calibration (75%) and evaluation (25%) subsets; and (iii) projecting the niche model continent-wide to identify areas potentially vulnerable to MLN incidence. Modeled suitability was divided into three risk strata: low risk; medium risk; and high risk (L'opez-Cardenas *et al.*, 2005). We tested model prediction with the null hypothesis that the observed coincidence between prediction and test points was no better than chance expectations. We used chi-square test (Peterson and Shaw, 2003), the area under the curve in a receiver operating characteristic (ROC) and Kappa analysis (Elith *et al.*, 2006) for model quality assessment. QGIS (Version 2.2.0-Valmiera) was used to integrate and explore model outputs.

To characterize the environmental envelope or niche of MCMV across Africa, climate data were estimated at each MCMV/MLN-positive site in QGIS. Descriptive summaries were made for each variable, and similarities in MCMV environmental preference among all variables were computed using principal component (PC) analysis. Projections of present MCMV/MLN models onto future climate layers estimated long-term future distributions. We developed

detailed comparisons of current and future potential distributions.

Results

MCMV environmental envelope

MCMV virus appears to have the potential to establish viable populations across a wide range of environmental conditions in East Africa (Table 1) as incidences of the virus fall under diverse temperature and precipitation regimes. Annual mean temperature ranged between 11.6 -23.9 °C, and mean temperature of coldest quarter ranged between 9.6-22.2 °C. Similarly, MCMV appears viable under conditions as low as 0 mm (precipitation of driest month) up to 813 mm (precipitation of wettest quarter). Also it showed broad tolerances regarding variability in temperatures (Isothermality) and precipitation (seasonality) (Table 1).

The three principal components (PC) extracted from the twelve-bioclimatic variables explained 85% of overall variance in MCMV environmental distributions (Table 2). Principal component I explained 39% of variance and was significantly negatively correlated with temperature (minimum temperature of coldest

month, mean temperature of coldest quarter, annual mean temperature), PC II was positively correlated with precipitation seasonality, but negatively related with precipitation of coldest quarter, precipitation of driest month, and Isothermality; hence PC II is component that summarizes climate variability. Principal component III was significantly negatively correlated with precipitation of wettest quarter and month. Low-to-medium temperatures (PC I) were associated with higher niche suitability, as with medium-to-high seasonality (PC II) and medium-to-high precipitation (PC III).

MCMV and MLN niche in Africa

Model Performance

On the basis of the different model prediction tests, the MLN ecological niche models developed in this study were highly predictive of MCMV potential distribution and MLN relative risk across Africa. Model performance for current distributions was statistically more significant than random expectations ($P < 0.05$). All ROC AUC test and all Kappa values were above 86% and 0.936, respectively. Consequently, all indications were of very good to excellent model performance (Swets, 1988).

Table 1 Descriptive statistics for environmental conditions at 40 locations of known occurrence of *maize chlorotic mottle virus* across East Africa, obtained from digital climatologies (Hijmans *et al.*, 2005).

Climatic variable	Minimum	Maximum	Mean	SD ¹	SEM ²
Annual mean temperature (°C)	11.6	23.9	18.9	3.18	0.50
Mean temperature of warmest quarter (°C)	13.0	25.2	19.9	3.13	0.49
Mean temperature of coldest quarter (°C)	9.6	22.2	17.7	3.35	0.53
Precipitation of wettest month (mm)	118.0	386.0	223.1	70.20	11.10
Precipitation of driest month (mm)	0.0	61.0	28.4	19.10	3.00
Precipitation seasonality (mm)	35.0	121.0	61.0	23.00	3.60
Precipitation of wettest quarter (mm) ³	284.0	813.0	507.2	124.10	19.60
Precipitation of warmest quarter (mm) ³	143.0	587.0	324.5	106.70	16.90
Precipitation of coldest quarter (mm) ³	1.0	474.0	179.6	136.60	21.60
Isothermality	67.0	91.0	80.5	7.10	1.10
Minimum temperature of coldest month (°C)	4.5	16.2	11.2	3.47	0.55
Temperature annual range (°C)	12.3	20.5	16.2	2.04	0.32

¹ SD: Standard Deviation.

² SEM: Standard Error of Mean.

³ A quarter is a period of 3 months.

Table 2 Character loading and percentage of variance explained by principal components summarized by 12 environmental variables at 40 *maize chlorotic mottle virus*-positive localities in East Africa. Variables with highest loadings are indicated in bold.

Climatic variable	PC I	PC II	PC III
Annual mean temperature	-0.896	0.236	-0.359
Mean temperature of warmest quarter	-0.874	0.314	-0.340
Mean temperature of coldest quarter	-0.922	0.099	-0.349
Precipitation of wettest month	0.482	0.199	-0.813
Precipitation of driest month	0.022	-0.792	-0.293
Precipitation seasonality	0.236	0.929	-0.163
Precipitation of wettest quarter	0.399	-0.057	-0.849
Precipitation of warmest quarter	0.793	-0.153	-0.474
Precipitation of coldest quarter	-0.257	-0.838	-0.079
Isothermality	-0.178	-0.742	-0.309
Minimum temperature of coldest month	-0.950	0.092	-0.267
Temperature annual range	0.481	0.344	-0.248
Eigenvalue	4.726	3.099	2.318
Percent of variance explained	39.379	25.829	19.320

Current MCMV ecological niches and MLN risk in Africa

Generally, MCMV and MLN showed a broad potential distribution and risk area across the warm arid, semi arid, and sub-humid tropics of eastern and southern Africa. Most hotspots were located in the humid and sub-humid parts of central and eastern Africa (Fig. 2). Western and southern Africa showed only moderate suitability, while much of North Africa appears to be marginal in risk. The countries with largest modeled suitable habitats for MCMV virus were Ethiopia (662,974 km²), Tanzania (625,690 km²), D. R. Congo (615,940 km²), Angola (361,556 km²), South Africa (298,402 km²) and Madagascar (265,564 km²). However, in terms of proportional potential loss, Rwanda, Burundi, and Swaziland might lose all (100%), and Uganda (88.1%), Tanzania (65.9%), Ethiopia (59.8%), Malawi (53.8%), Madagascar (45.1%), and Kenya (41.1%) have broad swaths of national territory,

potentially inclusive of all or most of the maize production land.

Areas across western and central Kenya; northern and central Tanzania; most of Uganda, Rwanda, and Burundi; southwestern DRC, northern Angola; and the Ethiopian highlands showed very high risk (warmer colors, Fig. 2). Other important risk areas include Madagascar, Swaziland, Botswana, Lesotho, South Africa, and Mozambique. In West Africa, central Cameroon and eastern Nigeria also hold suitable sites, while lower levels of risk are distributed sparsely across Ivory Coast, Ghana, Nigeria, and Guinea.

Modeled future climate change effects

The result of projection of present-day niches to conditions in two future periods (2020 and 2050) to visualize the potential climate change effects on MCMV distributions and MLN risk indicated significant dynamics in suitability (Figs. 3 and 4). Although future areas were slightly smaller, potential

distributional areas agreed closely (Fig. 5). For 2020, Ethiopia (621,010 km²), Tanzania (477,438 km²), DRC (405,028 km²), Angola (237,848 km²), and South Africa (337,870 km²) were projected to present the most suitable environments (Fig. 3). However, by 2050, MCMV is predicted to make significant gains southwards: to Mozambique (536,406 km²), Angola (499,850 km²), Malawi (317,122 km²), Namibia (302,614 km²), Zimbabwe (298,688 km²), and Madagascar (227,344 km²).

Future niche losses and gains

MCMV was projected to retract somewhat under future conditions losing 18% and 24% net potential distribution area by 2020 and

2050, respectively (Fig. 5). Under both future climate change projections, MCMV and MLN are predicted to see improvement in some areas, but worsening conditions in others (Fig. 5). Potential geographic range contractions were projected for D.R. Congo (-298,818 km²), Angola (-154,986 km²), Ethiopia (-126,568 km²), Tanzania (-125,840 km²), Madagascar (-103,584 km²), Cameroon (-70,018 km²), Zimbabwe (-58,266 km²), Central African Republic (-49,556 km²), Congo (-33,488 km²) and Zambia (-31,098 km²). On the other side, niche area gains were predicted for Mozambique (69,862 km²), Sudan (28,080 km²), Somalia (10,894 km²), South Africa (4,212 km²), Senegal (2,860 km²), Lesotho (2,574 km²) and Gabon (2,522 km²) (Fig. 6).

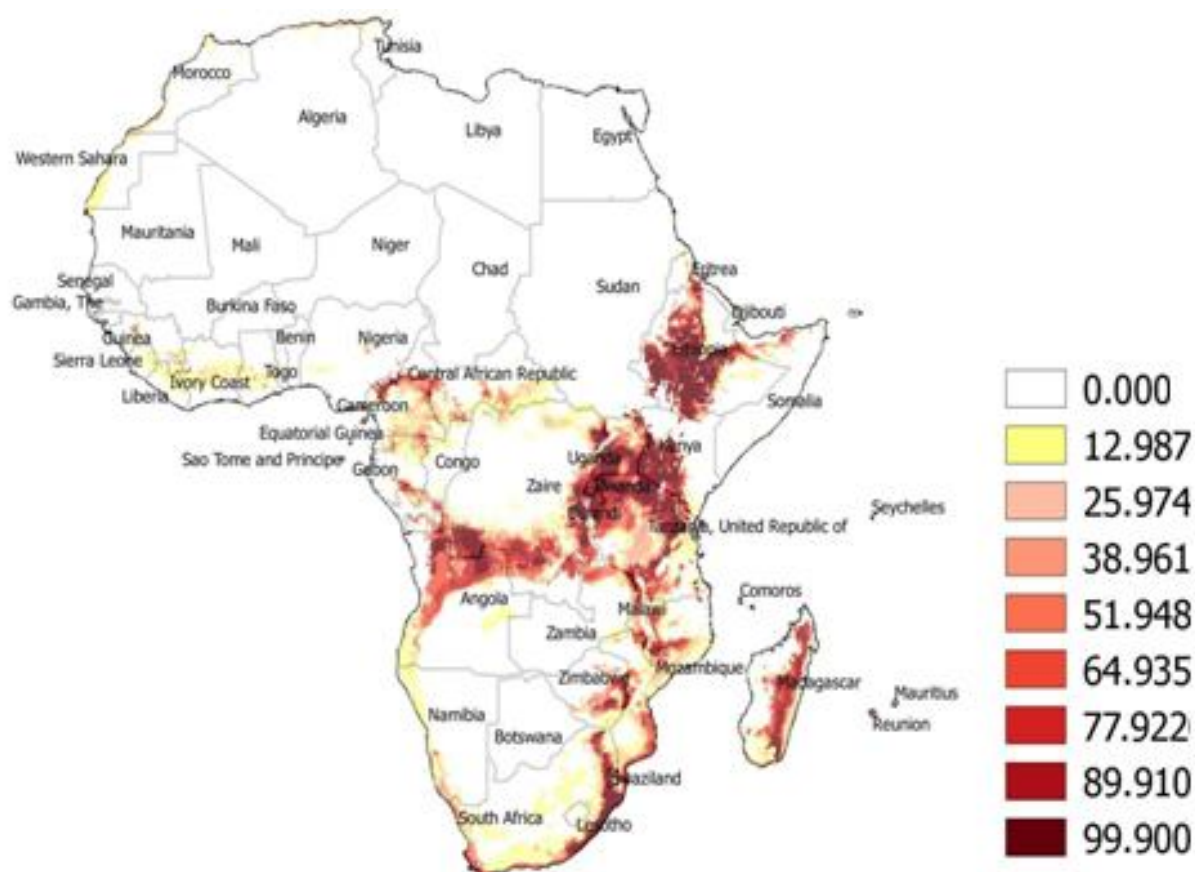


Figure 2 GARP model outputs for suitability for *maize chlorotic mottle virus* and potential risk of Maize Lethal Necrosis (MLN) disease across Africa. Warmer colors indicate higher suitability and risk.

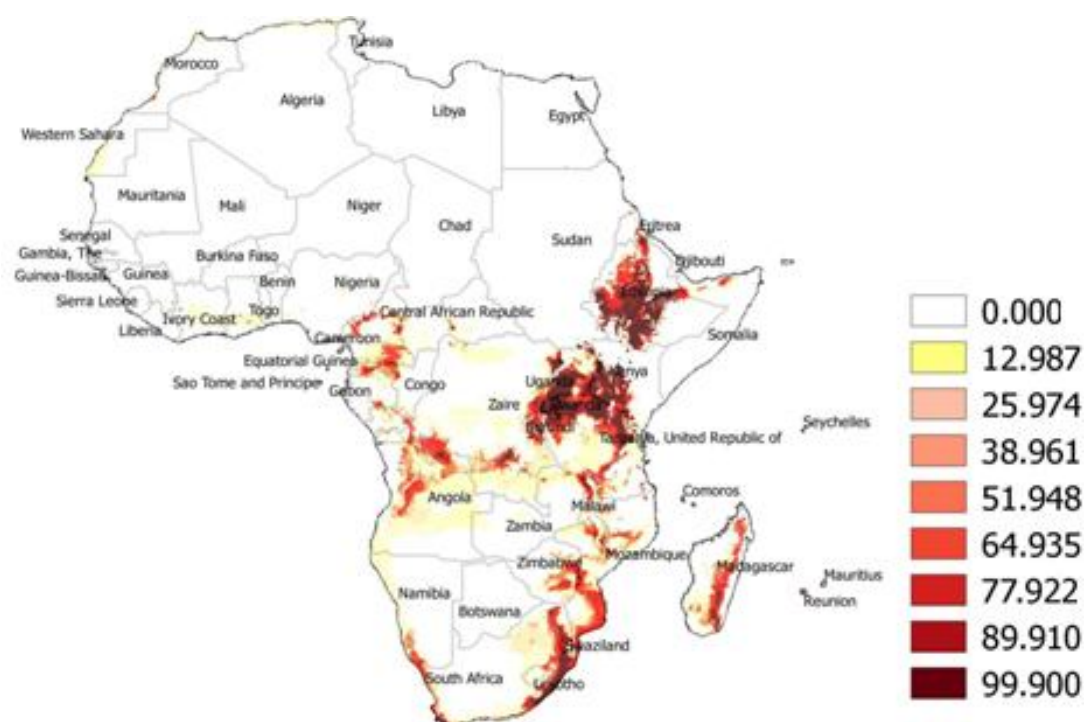


Figure 3 Predicted potential distributions of *maize chlorotic mottle virus* and potential risk of Maize Lethal Necrosis (MLN) disease in 2020 period across Africa. Warmer colors indicate higher suitability and risk.

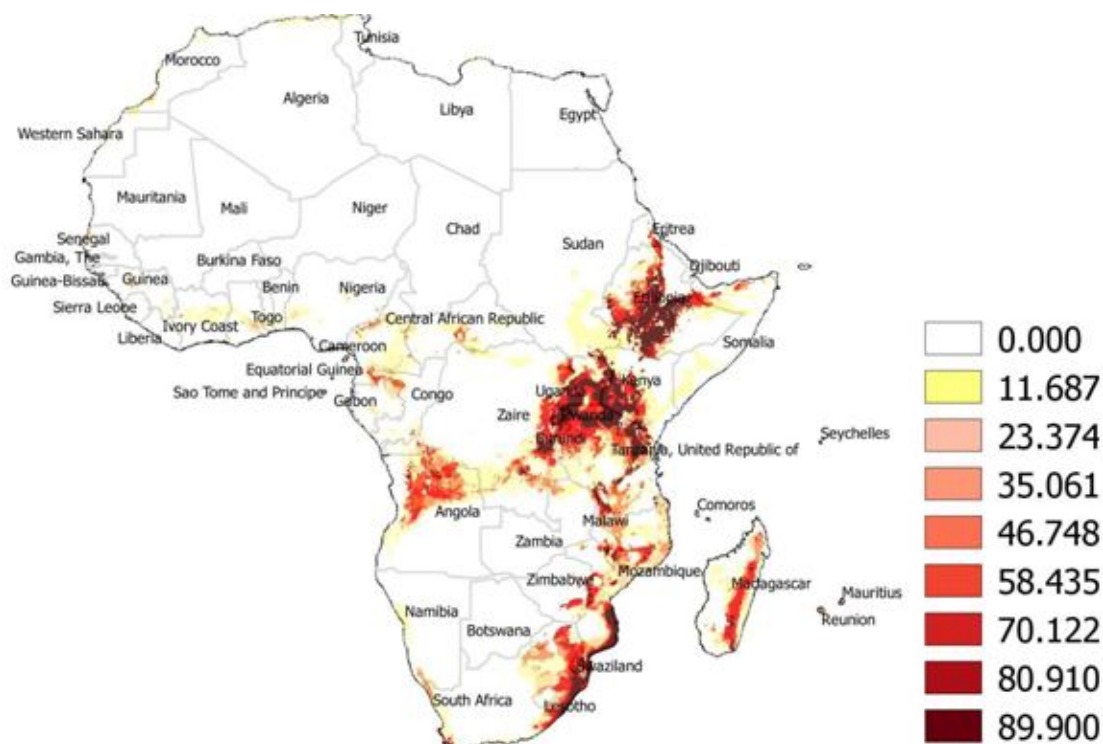


Figure 4 Predicted potential distributions of *maize chlorotic mottle virus* and potential risk of Maize Lethal Necrosis (MLN) disease in 2050 period across Africa. Warmer colors indicate higher suitability and risk.

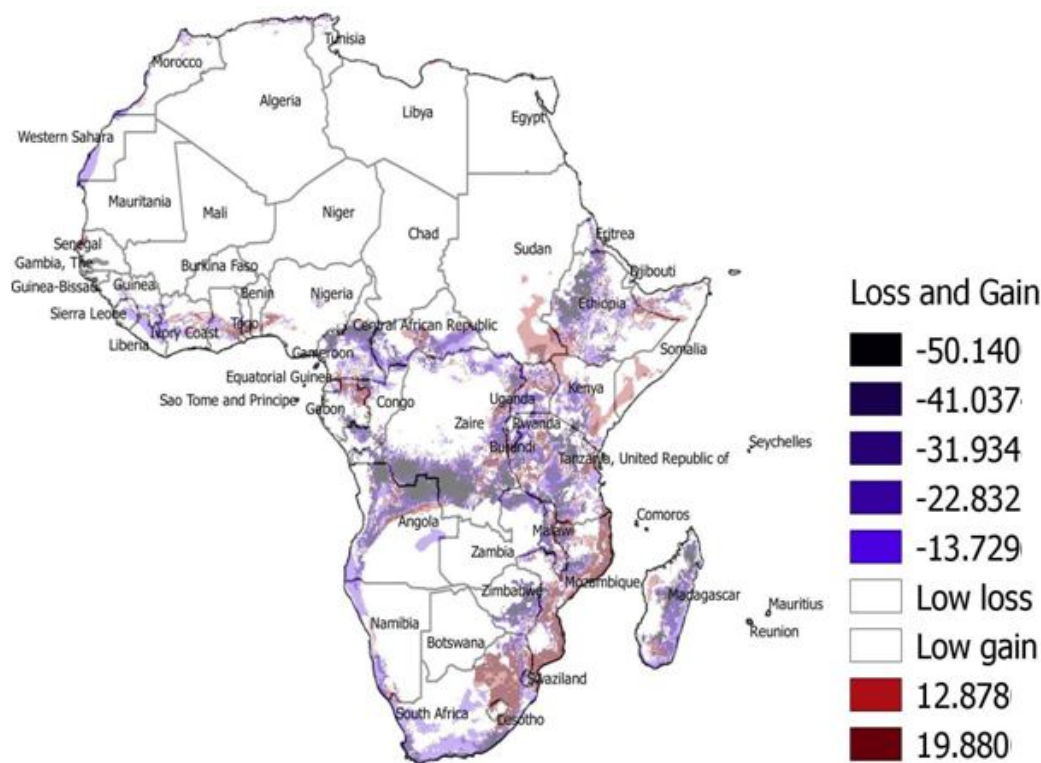


Figure 5 GARP predicted distribution of the fundamental niche of *maize chlorotic mottle virus* and potential risk of Maize Lethal Necrosis (MLN) disease across Africa. Loss and gains were calculated by taking the difference between the 2050 and the present day suitability rasters. Warmer colors indicate higher suitability and risk.

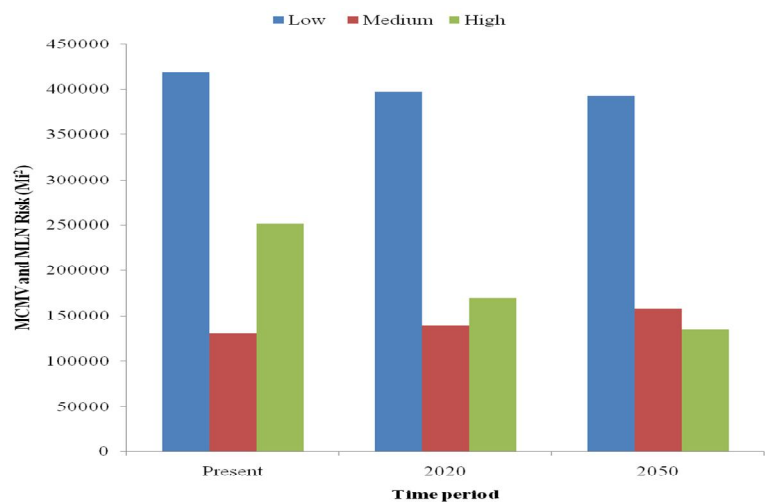


Figure 6 Histogram depicting total area (Square Miles) in Africa suitable for *maize chlorotic mottle virus* (MCMV) and at risk of Maize Lethal Necrosis (MLN) damage presently, in 2020, and in 2050, based on modeled climates for current and future time periods.

Discussion

Our models were robust in identifying the potential distribution of the virus and associated disease risk, as modeled suitability patterns were consistent with independent subsamples of previous records of incidence (Wangai *et al.*, 2012; CIMMYT, 2012; Miano *et al.*, 2013; NARO, 2012; RAB, 2013). This result is very important in and of itself, as it provides the first attempt to understand the landscape ecology and epidemiology of the MCMV and MLN across Africa. Our predicted distributions around Southern Rift Valley, Narok and Naivasha districts in Kenya, in northern Tanzania, and in Rwanda and eastern Uganda are consistent with earlier observations (Wangai *et al.*, 2012; CIMMYT, 2012; Miano *et al.*, 2013; NARO, 2012; RAB, 2013). Our models were also consistent in predicting more marginally suitable areas in eastern Kenya and South Sudan. Our prediction of suitability in eastern D.R Congo has been confirmed by recent laboratory results showing specimens from there as positive for MCMV and MLN (Dr. Lava Kumar IITA personal Communication, April 2014). Incidentally, all of these areas coincide with the major maize production zones in Africa (IFPRI, 2012). These findings are therefore both timely and highly relevant in instituting regional and local-level management strategies in Africa.

Our future predictions showed a moderate decline overall but considerable shifts in risk patterns across Africa as a consequence of climate change. Shifts as a result of climate change have also been noted in other diseases systems (Rogers *et al.*, 2002; Peterson and Shaw, 2003; Lane and Jarvis, 2007; Peterson, 2009). In our case, this result most likely occurs because MCMV has limits to its temperature tolerances; hence, projected changes in climate are likely to lead to shifts in habitat suitability. Of course, increased suitability does not necessarily result in expanded geographic distributions as many other factors (e.g., MCMV vectors, agronomic practices) determine the distribution, in addition to climate (Lafferty, 2009). Therefore, it stands to reason that our predicted net decline in the future

geographic suitability with the predicted climate change is plausible. Mozambique, Sudan, Somalia, South Africa, Senegal, Lesotho, Gabon, and other areas projected to see significant gains in suitable areas have cause for concern; given the severe consequences, even countries projected to see reductions still are at risk. It is important that climate change mitigation and adaptive strategies be put in place to guard against loss of maize produce in the future.

MLN disease records in Africa are quite recent. Therefore there are few peer-reviewed records for the current distribution of the disease. Further, a number of very important factors were not incorporated into the model, including distribution of maize growing regions, alternative hosts, vectors, and the seasonality of maize distribution in the region. Partly, this is due to the fact that some of the factors (alternative hosts for the viruses causing MLN- MCMV and SCMV) are not well described for Africa. We acknowledge that would have helped to increase the robustness of our predictions. For instance, variability in maize seasons and phenology could significantly affect primary host availability, and consequently the incidence of the disease. We did not also consider vector population dynamics, which have been shown to be important in the disease cycle (zu Dohna and Pineda-Krch, 2010).

However, at the continental spatial resolution level, effects of population dynamics are probably not as important as habitat suitability of the vector species (Sarkar *et al.*, 2010). The bioclimatic distribution models employed in this study predominantly predict potential suitability, but not abundance, although epidemiological models usually predict that disease distribution and establishment will depend on the abundance of vector, reservoir and host species (zu Dohna and Pineda-Krch, 2010). In our case, we made the assumption that, beyond a straightforward relationship with probability of occurrence, a species' abundance will also respond to environmental suitability (Sarkar *et al.*, 2010).

The few early records of MLN in Africa used in calibrating our models require that the findings outside Eastern Africa be interpreted with caution, as model sensitivity may decline in areas far from

the current incidence sites (Pearson *et al.*, 2006). In our case, given present lack of records for MCMV and MLN in other parts of Africa (other than Eastern Africa), we made implicit assumptions via pseudo absence sampling (Sarkar *et al.*, 2010). It is possible that MCMV and MLN are spreading west and south and might eventually get there, with implications on the respective area suitability. Further sampling and ground truthing across the continent, as well inclusion of other environmental host constraints would help to improve our knowledge of the range and ecology of MCMV and MLN across Africa.

In conclusion, our findings have provided important views on the distribution and epidemiology of MCMV and MLN across Africa. MLN risk in Africa is high and hence the need for better allocation of resources in management of MLN, with special emphasis on East and Central Africa, which are and will remain hotspots in the future. The methodology piloted in this study has wide range potential applications in integrated pest and disease management (IPDM), especially in planning and instituting regulatory mechanisms. It is hoped that our approach will provide a useful tool for further research and management of the diseases in Africa and lesser-developed nations, as advocated by Hay and Snow (2007).

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پتانسیل پراکنش ویروس پیسک زرد ذرت در حال و آینده و خطر بیماری نکروز کشنده ذرت در آفریقا

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چکیده: نکروز کشنده ذرت (MLN) که به وسیله همافزایی ویروس پیسک زرد ذرت (*maize chlorotic mottle virus* (MCMV; Tombusviridae: Machlomovirus) و هر پوتی ویروس دیگری ایجاد می‌شود، پتانسیل از بین بردن تولید ذرت در قاره آفریقا را دارد. از زمان اولین گزارش این بیماری در کنیا در سال ۲۰۱۱، MLN به تانزانیا، اوگاندا، رواندا و احتمالاً به سایر کشورهای هم‌جوار گسترش یافته است. برای درک توزیع فضایی-زمانی MCMV و خطر MLN در آفریقا، ما مدل‌های کنج اکولوژیکی را با استفاده از الگوریتم ژنتیکی (GARP) بسط دادیم. ورودی‌های مدل شامل داده‌های اقلیمی (دما و بارش) و ردیابی‌های ثبت شده MCMV و MLN در سرتاسر آفریقا بودند. کارایی مدل از لحاظ آماری معنی-دارتر ($p < 0.05$) از انتظارات تصادفی بود، به گونه‌ای که نمرات مربوط به نسبت ROC به AUC بالای ۸۶ درصد و مقدار کاپا (Kappa) بالای ۰/۹۳۶ بود. داده‌های مزرعه عموماً پیش‌بینی‌های مدل را تصدیق نمود. وقایع مثبت و در سرتاسر منطقه در ارتباط به یک سری رژیم‌های دمایی و بارشی در بخش‌های حاره‌ای نیمه‌خشک و نیمه‌مرطوب آفریقای مرکزی و شرقی بودند. اتیوپی، تانزانیا و جمهوری دموکراتیک کنگو به ترتیب پتانسیل از دست دادن ۶۶۹۷۴، ۶۲۵۶۹۰ و ۶۱۵۹۴۰ کیلومتر مربع از زمین‌های کشت ذرت خود را دارند. براساس سهم خسارت وارده به تولید ملی ذرت، رواندا، بروندي و سوازیلند پتانسیل از دست دادن ۱۰۰ و اوگاندا ۸۸/۱ درصد را دارند. تخمین‌های آتی مناطق بالقوه کم-تری را نشان می‌دهد (۱۸- و ۲۴- درصد به ترتیب برای ۲۰۲۰ و ۲۰۵۰) اما داده‌های اقلیمی با پراکنش MCMV انطباق دارد و خطر MLN در آینده نیز پیش‌بینی می‌شود. در نتیجه خطر MLN در آفریقا بالاست و لذا نیاز به تخصیص بهتر منابع در مدیریت MLN با تأکید بر آفریقای شرقی و مرکزی که مراکز اصلی این مشکل در حال و آینده هستند، یک ضرورت است.

واژگان کلیدی: آفریقا، تغییر اقلیم، GARP، هات اسپات، ذرت، MCMV، MLN