EISSN: 2707-0425

East African Journal of Science, Technology and Innovation, Vol. 7 (Special Issue 1): January 2026

Predicting the current and future suitable habitats of cassava and cassava brown streak disease in Africa

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Abstract

Cassava (*Manihot esculenta*) is among the most important staple crops globally. In sub-Saharan Africa, it is cultivated mainly by subsistence farmers who depend directly on it for their socio-economic welfare. However, its yield in some regions has been threatened by several diseases, especially the Cassava brown streak disease (CBSD). Changes in climatic conditions enhance the risk of the disease spreading to other planting regions. This work aimed to identify, characterize and map the current and potential future suitable habitats for cassava and cassava brown streak disease in Africa using species distribution models (SDMs). We obtained occurrence data for cassava in Africa from the Global Biodiversity Information Facility (GBIF), and cassava brown streak disease occurrences from published literature. We used an ensemble of four species distribution models (SDMs), together with environmental covariates to characterize the current and future distribution of cassava and CBSD in Africa. Our results identified isothermality (Bio03, relative importance: 31.6%) as the highest contributor to the current distribution of cassava, while cassava cassava-harvested area (CHA, 14.6%) contributed the most to the current distribution of CBSD outbreaks. The geographic distributions of these target species are also expected to shift under climate projection scenarios for two mid-century periods. Using the most recent climate scenarios from the Coupled Model Intercomparison Project (CMIP6) for the mid-term (2041-2060) and long-term (2061-2080) in Africa, our study highlights suitable habitats for cassava, as well as one of its economically important diseases (CBSD). For cassava, about 54.6% (16.2 million km^2) of the continent is currently suitable for cassava production. These suitable habitats (i.e., suitability above 0.2) were predicted to be located predominantly in Sub-Saharan Africa. On the other hand, approximately 33.7% of Africa's land area (10.2 million km^2) is currently at risk of CBSD spread. Based on our findings we propose that improved cassava varieties tolerant to CBSD should be deployed in all cassava production regions.

Key words: *Cassava; cassava harvested area; cassava brown streak disease; climate change; food security*

Cite as: Sikazwe *et al.* (2026). Predicting the current and future suitable habitats of cassava and cassava brown streak disease in Africa. *East African Journal of Science, Technology and Innovation 7 (Special Issue 1).*

Received: 10/03/25
Accepted: 09/12/25
Published: 15/01/26

Introduction

Manihot esculenta Crantz (Cassava) from Latin America (Brazil) was introduced to sub-Saharan Africa by Portuguese traders and has increasingly become a major source of calories for over 800 million people worldwide (FAO, 2013). Africa contributes at least 56% of the World's total cassava production (FAOSTAT, 2021), and cassava is the second most important staple food crop in sub-Saharan Africa (Tomlinson *et al*., 2018). Cassava's popularity emanates from its adaptability and capacity to provide acceptable yields under marginal farming conditions and limited water availability. However, various abiotic stressors (temperature and rainfall) and biotic stressors (pests and pathogens) can greatly affect the plant's physiology and growth (Jones and Barbetti, 2015) and consequently, threaten the Sustainable Development Goal of 'Zero hunger' and socio-economic benefits to millions of resource-limited farmers across Africa. It is therefore imperative to assess the current and future suitability of cassava and its biotic stressors under a changing climate.

Cassava exhibits an array of responses to different climate variables. Temperature, for example, affects various stages of cassava's growth and development, including sprouting, leaf formation, leaf size, and storage root formation. The optimum growth of each stage is reached at an optimum temperature range of 25–35^{o}C (El-Sharkawy, 2004). Sprouting is faster at a soil temperature of about 28–30^{o}C. However, sprouting is arrested at temperatures above 37^{o}C and below 17^{o}C (El-Sharkawy, 2004). This partly explains its current cultivation niches, which are predominantly distributed across most tropical and sub-tropical regions. Nevertheless, cassava is a resilient crop and can be cultivated under variable rain-fed conditions, where annual rainfall exceeds 600 mm, like in the semi-arid tropical regions (S.M. DE TAFUR, 1997), and in regions with over 1000 mm of annual rainfall, like in the sub-humid and humid tropical regions (Pellet and El-Sharkawy, 1997). Excessive rainfall, however, can result in flooding and yield losses (IPCC, 2021).

Cassava production in Africa is also significantly constrained by Cassava brown streak disease (CBSD), caused mainly by the cassava brown streak virus and its Ugandan variant, which are both members of the family *Potyviridae* and genus *Ipomovirus* (Winter *et al*., 2010). Interestingly, to date and the best of our knowledge, CBSD is confined to Africa only. For over 70 years, the disease was distributed only along the East African coast (Tomlinson *et al*., 2018). Earlier reports indicated that altitudes greater than 1000m above sea level (masl) were unfavourable for the survival of the disease (Nichols, 1950). Cold temperatures were also believed to enhance symptom severity and lead to the death of infected plants through die-back, starting from the shoot tip (Jeremiah *et al*., 2015). However, from 2004, CBSD outbreaks were reported in regions of Uganda and other parts of East and Central Africa above 1000 masl (Alicai *et al*., 2007). The CBSD outbreaks above the previous attitudinal ceiling (i.e., <1000 masl) were associated with an elevated vector population, whitefly *Bemisia tabaci,* in these regions. Whiteflies have become better adapted to conditions prevalent in cassava-growing zones of the Great Lakes region (800 to 1,500 masl) (Jeremiah *et al*., 2015).

Cassava brown streak viruses can be introduced into cassava plantations in two ways: through immigrating infectious whiteflies and/or through the use of infected cuttings (Donnelly *et al*., 2020). The former is a more important secondary spread within the farm (i.e., for short-distance movement) whereas the latter is more important for both the short and long-distance spread of the viruses. Indeed, the use or sharing of infected planting materials for establishing a new field, especially for vertically transmitted plant diseases, plays a significant role in the dispersal of pathogens. This is especially important when the extent of using infected materials is commonly practiced at places where the abundance of infected whiteflies is low. This also may introduce pathogens to other distant countries where the viruses are currently absent. Also, the network over which the farms are connected will then facilitate pathogen dispersal and needs to be considered when attempting to control or contain the disease (McQuaid *et al*., 2017).

Species distribution models (SDM) are a powerful tool for understanding factors that drive species distribution in a geographic region (Mudereri *et al.*, 2021). They offer a means to study the projected impact of climate change on the geographic distribution of plants, pathogens, and pests. The model generates categories of climate suitability and matches these to geographical regions (Ramos et al., 2018). A few SDMs have been developed for predicting the geographic range of cassava and whiteflies (Campo *et al.*, 2011; Jarvis *et al.*, 2012). In particular, Campo *et al.* (2011) used the Maximum Entropy (Maxent) algorithm in the SDM to evaluate the global distribution of four key biotic constraints: whiteflies, cassava green mites, cassava mosaic disease (CMD) and CBSD; they identified parts of Brazil, the Americas, Africa's rift valley, the southern tip of India, and much of Southeast Asia as potential hotspots for cassava pests and disease outbreaks. Using the EcoCrop model and 24 Global Circulation Models (GCMs) to project into the future climate, Jarvis *et al.* (2012) examined the impact of climate change on cassava in Africa and reported -3.7% to +17.5% changes in climate suitability across the continent. How these anticipated changes will affect the suitability of cassava, and CBSD, as well as their interactions, has not been quantified.

Here, we use historical climate data (from worldclim.org) that represent different rainfall and temperature regimes to explain the current distribution of cassava and CBSD in Africa. To explore the potential future distributions, we use climate projections from the phase-6 "BCC-CSM2-MR" GCM of the Coupled Model Intercomparison Project (CMIP 6), together with two scenarios of its Shared Socio-economic Pathway (SSP126 and SSP585) for the year 2050 (average for 2041 to 2060) and year 2070 (average for 2061 to 2080). These climate scenarios show that annual temperatures and precipitations are expected to shift considerably in the future decades (Almazroui *et al.*, 2020). For model fitting, we collate occurrence records of each species from the Global Biodiversity Information Facility (GBIF) and published literature. Our dataset does not allow us to distinguish between the two viral species of the disease (the cassava brown streak virus and Ugandan cassava brown streak virus), and we thus refer to them collectively as CBSD. We use an ensemble of four SDM methods for model fitting, including boosted regression trees (BRT), maximum entropy (Maxent), generalized additive model (gam), and multivariate adaptive regression splines (mars). The results highlight important factors responsible for the current distributions of cassava and CBSD. Suitable habitats for cassava cultivation and those at risk of invasion by CBSD are mapped, to guide policy and adaptation planning for governments, private organizations, and farmers.

Materials and methods

Occurrence data collection

We obtained occurrence data in Africa from the Global Biodiversity Information Facility (GBIF), including 1,422 records for cassava (accessed 14 June 2021, doi.org/10.15468/dl.98jqqy). For quality assurance, we excluded records without geolocation and only kept unique records to avoid duplication. The occurrence records of CBSD were integrated from published literature (Alicai *et al.*, 2019), GBIF, and country-wide surveys from the Cassava Diagnostic Project (CDP) in East Africa (accessed 21 November 2021 via AgShare.Today). The CDP involved seven countries, namely Tanzania, Kenya, Uganda, Rwanda, Mozambique, Malawi, and Zambia, following a published sampling protocol (Alicai *et al.*, 2019). Through the Tanzania Agricultural Research Institute (TARI), we only accessed data from Tanzania and Uganda, which included CDP surveys from the National Crops Resources Research Institute (NaCRRI, Uganda) between 2004 and 2017. The data collection protocol is described in (Alicai *et al.*, 2019). In these surveys, cassava fields were randomly selected along motorable roads at intervals of 7–10 km and up to 20 km, depending on the density of cassava plants. A farmer was identified and asked for consent to survey the field at each location. Fields with crops between 3–6 months after planting were selected for the surveys, as CBSD foliar symptoms become apparent at this stage and before leaf shedding. Field location coordinates were collected using handheld GPS devices. In each field, 30 plants of the predominant variety were surveyed along two diagonal transects in an X-shape, with 15 representative plants in each transect. Each sampled plant was scored for severity of foliar and stem symptoms on a 1–5 scale, where 1 indicates no visible symptoms and 5 corresponds to pronounced/extensive vein yellowing, chlorotic blotches on leaves or severe lesions, streaks on stems, or defoliation and die-back (Alicai *et al.*, 2019).

Environmental covariates

The extent of our current study is Africa, the second-largest continent in both area and human population, stretching 30.4 million km^2 in land area with six distinct climate zones: the equatorial, humid tropical, tropical, semi-desert (Sahalian), Mediterranean, and desert (Beck *et al.*, 2018). North Africa has an arid desert climate characterized by high temperatures and little precipitation. Equatorial West and Central Africa have a monsoon climate characterized by high temperatures, soaring humidity, and heavy seasonal rains. East Africa is characterized by dry and rainy seasons, while the southern part of Africa is generally more temperate (Nicholson, 2017). For the current climate, we used the 19 interpolated bioclimatic variables of 1970-2000 from the WorldClim database (worldclim.org) at a 10-min (~340 km^2) resolution (Table 1). We also included other biologically relevant predictors, including cassava harvested area (CHA), elevation (elev) and seven measures of soil quality (sq1-7) (Table 1). The CHA is an essential determinant of disease presence, and we used a standardized, high-quality, representative cassava map from Szyniszewska (2020), accessible via the Figshare repository (10.6084/m9.figshare.9745118). Elevation data was downloaded from the digital elevation model (DEM) of the shuttle radar topographic mission (srtm.csi.cgiar.org), available at approximately 90 m pixel size with a vertical error of less than 16 m. Although cassava is a resilient crop, adaptable to diverse and poor soils, the quality of soils substantially improves the crop's productivity. We used seven key soil qualities that are important for crop production: nutrient availability, nutrient retention capacity, rooting conditions, oxygen availability to roots, excess salts, toxicities, and workability, denoted as sq1 to sq7, respectively, from the FAO soils portal (fao.org/soils-portal) at a 30 arc-sec (about 1 km^2) resolution (FAO and IIASA, 2000).

To assess the potential future distributions of cassava and the CBSD outbreaks, we used the "BCC-CSM2-MR" climate model developed by the Beijing Climate Center of the China Meteorological Administration. We used predictions from this model under two SSPs (SSP1-2.6 and SSP5-8.5) for the year 2050 (mid-century average for 2041-2060) and year 2070 (near late twenty-first-century average for 2061-2080). The SSP1-2.6 scenario is part of the "sustainability" SSP1 socio-economic family, representing the best case where the best policies are implemented. Conversely, the SSP5-8.5 scenario represents the worst-case scenario with high fossil fuel consumption throughout the 21st century and without climate mitigation policies (Meinshausen *et al.*, 2020), resulting in global warming ranging from a low of 3.1°C to a high of 5.1°C by 2100.

Table 1.

A list of environmental data layers used for characterization of cassava, cassava brown streak disease (CBSD) in Africa and the percent contribution of each variable.

Code	Variable description	Unit
Bio01	Annual Mean Temperature	°C
Bio02	Mean Diurnal Range	°C
Bio03	Isothermality	°C
Bio04	Temperature Seasonality	°C

Code	Variable description	Unit
Bio05	Max Temperature of Warmest Month	^{o}C
Bio06	Min Temperature of Coldest Month	^{o}C
Bio07	Temperature Annual Range	^{o}C
Bio08	Mean Temperature of Wettest Quarter	^{o}C
Bio09	Mean Temperature of Driest Quarter	^{o}C
Bio010	Mean Temperature of Warmest Quarter	^{o}C
Bio011	Mean Temperature of Coldest Quarter	^{o}C
Bio012	Annual Precipitation	mm
Bio013	Precipitation of Wettest Month	mm
Bio014	Precipitation of Driest Month	mm
Bio015	Precipitation Seasonality	mm
Bio016	Precipitation of Wettest Quarter	mm
Bio017	Precipitation of Driest Quarter	mm
Bio018	Precipitation of Warmest Quarter	mm
Bio019	Precipitation of Coldest Quarter	mm
sq1	Nutrient availability	-
Sq2	Nutrient retention capacity	-
Sq3	Rooting conditions	-
Sq4	Oxygen availability to roots	-
Sq5	Excess salts	-
Sq6	Toxicity	-
Sq7	Workability	-
Elev	Elevation; Ground height above sea level	m
CHA	Cassava harvested area	km^2

Species distribution modelling

Before building the SDM, out of 28 predictors we selected a subset according to the variance inflation factor (VIF) to avoid a high level of collinearity that increases the uncertainty in model parameters and decreases the efficiency and power of model predictions (De Marco and Nóbrega, 2018; Naimi and Araújo, 2016). We calculated the VIFs of all predictors using the "usdm" R-package and excluded the one with the greatest VIF sequentially till all remaining predictors have VIFs <10 (Naimi and Araújo, 2016). As a result, 15 predictors were selected for cassava and 10 predictors for CBSD.

We developed the SDM using the "sdm" package (Naimi and Araújo, 2016) in the R platform (R version 4.0.5 Development Core Team, 2021). The sdm package provides an object-oriented, reproducible, and extensible platform, capable of handling an ensemble of models. The models are classified based on the nature of data used i.e., presence-only vs presence-background data (Elith *et al.*, 2006). As the species occurrence data consists of presence-only records, we randomly added 1000 pseudo-absences throughout the study area (Thuiller *et al.*, 2013). Variable importance is a metric used to determine the contribution of predictor variables in explaining the species distribution (Naimi and Araújo, 2016). In the "sdm" package, this is handled using the "getVarImp" function. To assess model performance, we used the conventional metrics of the area under the Receiver Operator Characteristic (ROC) curve (AUC), which measures the discriminatory ability of each model. AUC is a threshold-independent performance measure that reflects the probability of a randomly chosen presence site ranking above a background site. The AUC value is usually divided into five levels: 0–0.6 (fail), 0.6–0.7 (poor), 0.7–0.8 (fair), 0.8–0.9 (good), and 0.9–1 (excellent). In this study, the models with AUC outputs in the range (Guan et al., 2021) of 0.97 <AUC<1 were selected for further analysis. A fivefold cross-validation technique with five repetitions was used to assess the model performance (Thuiller *et al.*, 2013). Specifically, models were calibrated on a random sample of 80% of the occurrence data and evaluated on the remaining 20% (Ramos *et al.*, 2018, 2019). As such, we used an ensemble of four species distribution models (SDMs) for predicting the current and future suitable habitats for cassava and cassava brown streak disease.

Model selection and performance

Of the 28 predictors, different sets were selected after eliminating the effect of multicollinearity. For Cassava, 15 predictors (Bio02-04, 08, 13-15, 18-19; Sq1-5, 7) were selected for modelling potential distributions and 10 were selected for modelling CBSD (Bio02-03; 08, 11-14, 18-19; and CHA). The ensemble of four models produced, on average, an AUC of 98.0% for cassava and 99.5% for CBSD. The average of these four models was used for mapping the current and future suitability habitats of targeted species (**Table 2**).

Table 3

The ensemble models used for predicting habitat suitability for cassava and cassava brown streak disease. A single star in the data type column indicates that the model uses presence-background (pb) data whereas double stars show that the model uses presence-only (p**) data.*

Method	Model class/description	Data type	AUC
BRT	machine learning; boosted decision trees	pb*	0.985
MAXENT	machine learning; maximum entropy	pb*	0.983
SVM	machine learning; support vector machine	pb*	0.976
MARS	regression; multivariate adaptive regression splines	pb*	0.976

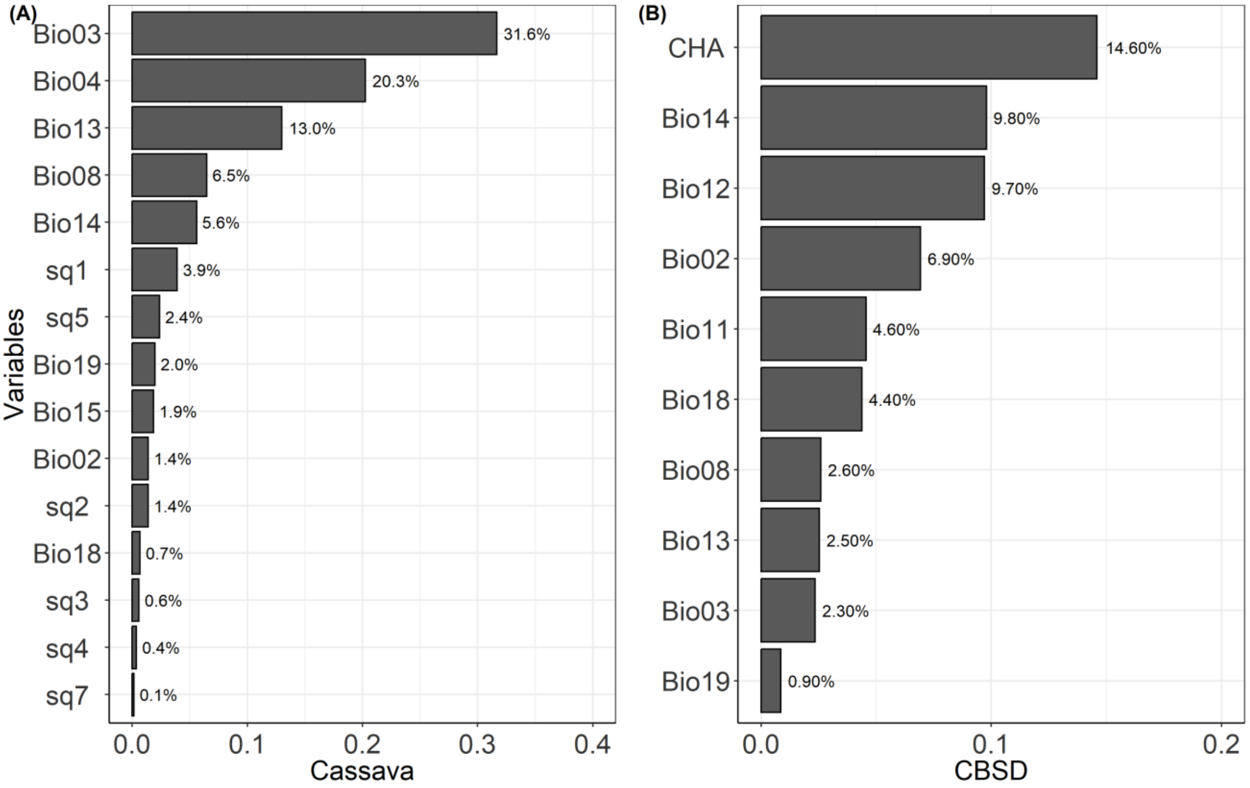
Results

Contribution of predictors on the distributions of cassava and CBSD

For cassava, isothermality (Bio03, relative importance: 31.6%), temperature seasonality (Bio04, 20.3%), precipitation of wettest month (Bio13, 13.0%), and mean temperature of wettest quarter (Bio08, 6.5%) were the top predictors explaining the observed distribution (Figure 1A). In contrast, cassava harvested area (CHA, 14.6%), precipitation of driest month (Bio14, 9.6%), annual precipitation (Bio12, 9.7%) and mean diurnal range (Bio02, 6.9%) were largely responsible for the distribution of CBSD outbreaks (Figure 1B).

Figure 1

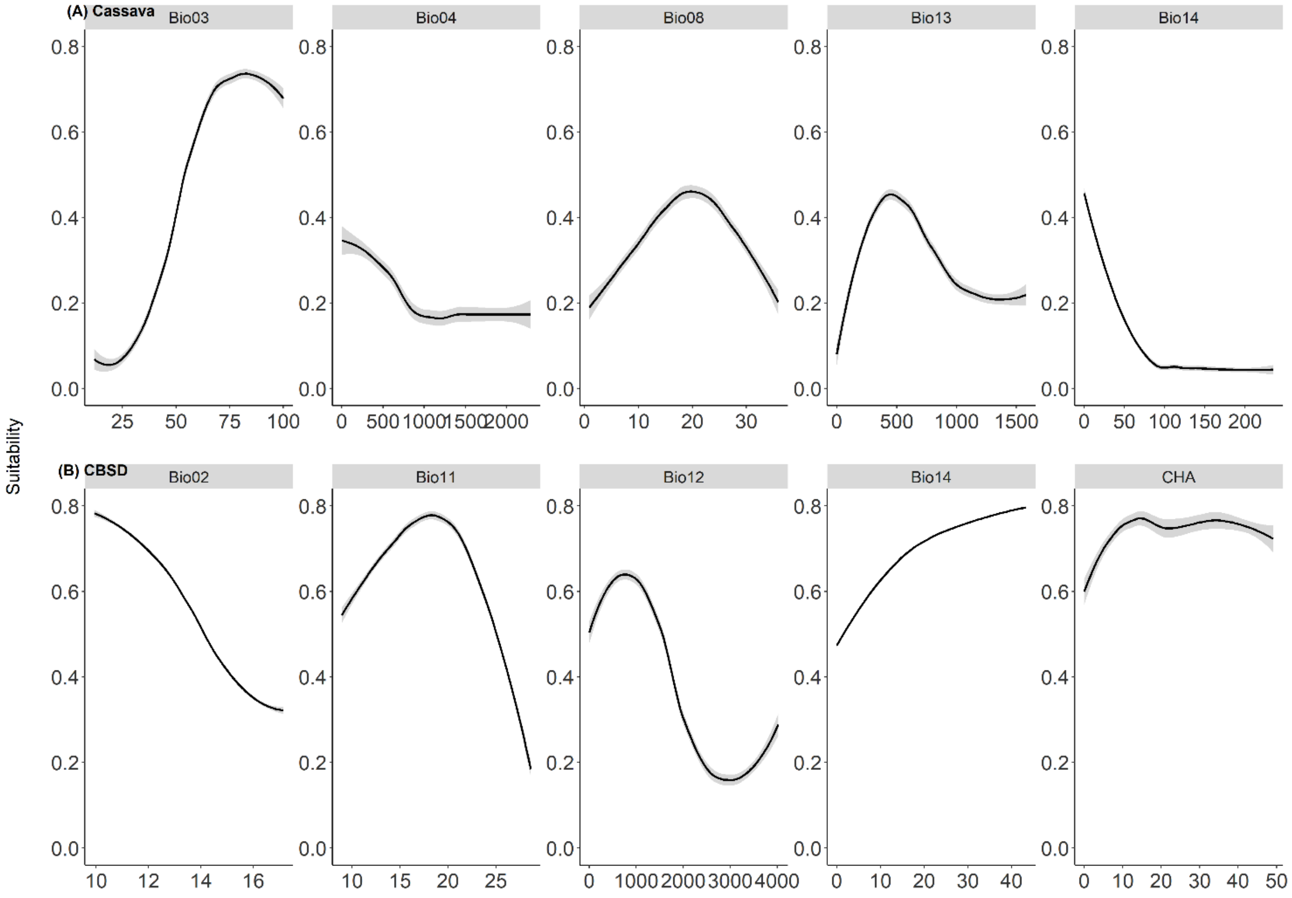
Percent contribution of each variable in the prediction the current distribution of A) Cassava and B) Cassava brown streak disease.



The probability of occurrence responded to different environmental predictors in a nonlinear way (Figure 2). Specifically, for cassava (Figure 2A), the occurrence probability tends to increase with isothermality (Bio03), and precipitation of the wettest month (Bio13), but decline with a mean temperature of the wettest quarter (Bio08). In contrast, cassava harvested area (CHA) and precipitation of the driest month (Bio14) showed a positive relationship with the occurrence probability of CBSD (Figure 2B), while the occurrence probability showed a negative relationship with annual precipitation (Bio12) and mean diurnal range (Bio02).

Figure 2

Response curves for (a) cassava and (b) Cassava brown streak disease showing the probability of occurrences with response to predictor variables.



Current and potential future suitable habitats for cassava in Africa

Cross-validation showed that the predicted range of suitable habitats based on 80% training records is consistent with the observed range from 20% testing records of cassava (Figure 3A), with 54.6% (16.2 million km^2) of the continent suitable for cassava production. These suitable habitats (i.e., suitability above 0.2) were predicted to be located predominantly in Sub-Saharan Africa. The regions with moderate suitability (i.e., 0.4 - 0.6), corresponding to 10.7 million km^2, were also found mainly in Sub-Saharan Africa. Although our data do not contain records from countries such as South Sudan, Sudan, Somalia, Botswana, and Zimbabwe, suitable habitats were predicted in these places. For habitats that are classified as 'very suitable' (suitability above 0.8), a total area of approximately 2.1 million km^2 was identified, predominantly in Coastal Guinea, Sierra Leone, Ivory Coast, Ghana, Togo, Benin, central to southern Nigeria, Cameroon, south-west Central African Republic, southern-western parts of South Sudan, Rwanda and the northern parts of Zambia (Figure 3A-B). Under the two SSP scenarios (SSP1.2-6 and SSP5.8-5) a potential increase of 59.6% and 56.6% in suitable habitats for cassava was projected for the mid-term (2050), predominantly in Sub-Saharan Africa (Figure 3C-D and Table 3). This trend was found to decline slightly towards 2070 (an increase of 57.8% and 55.3% compared to the current distribution). Specifically, highly suitable area (suitability above 0.8) for cassava production is expected to expand, from the East Coast of South Africa to Mozambique, and northern Madagascar (contracted areas are shown in **Table 4**).

Table 4

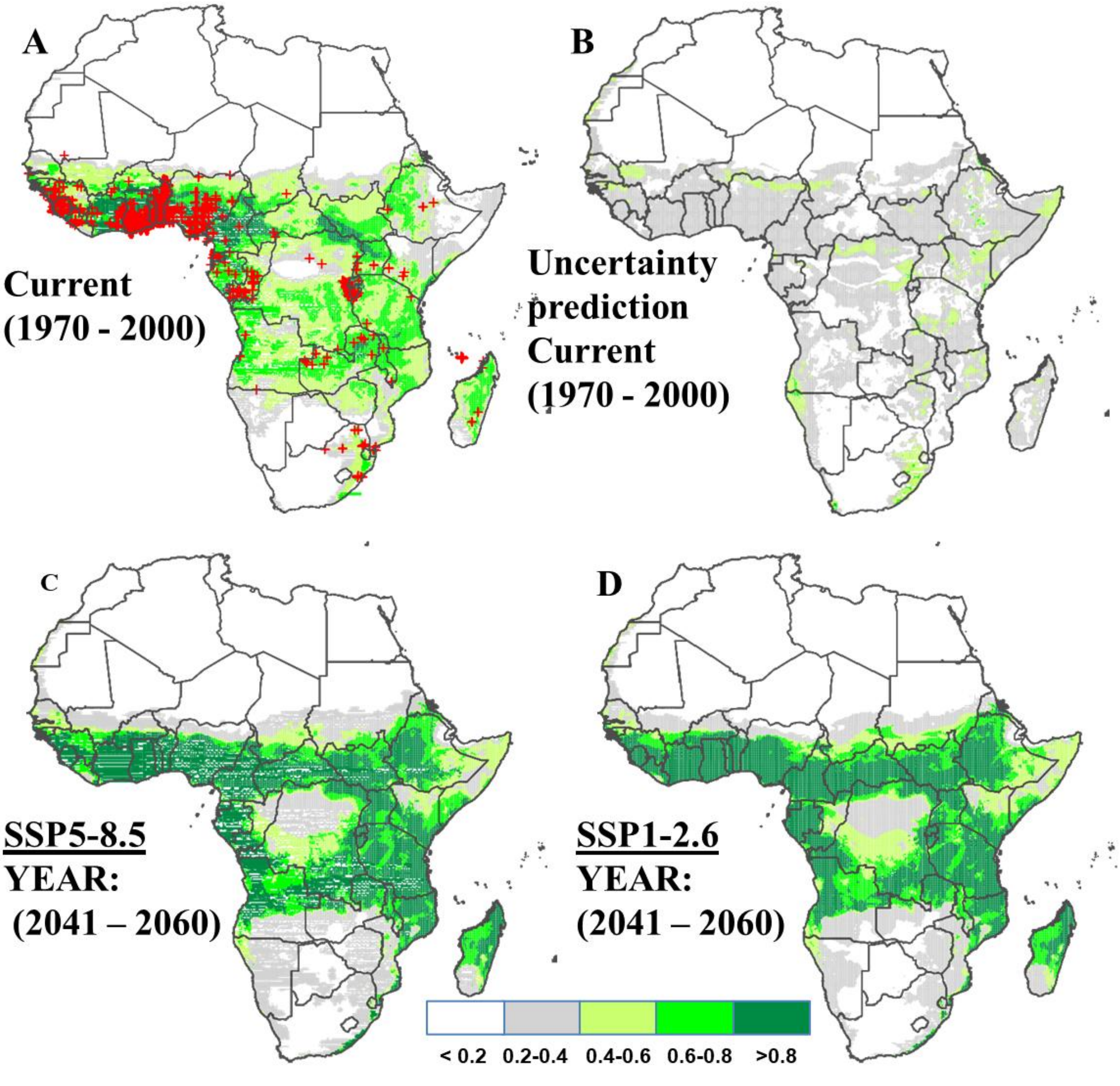
Current and future suitable habitats for (a) Cassava and (b) Cassava brown streak disease (CBSD) as predicted by version 2 of the Beijing Climate Center Climate System Model (BCC-CSM2-MR)

A. Cassava

Scenario	Time	Unsuitable (x10^6 km^2)	Low (x10^{6}km^2)	Moderate (x10^{6}km^2)	Suitable (x10^{6}km^2)	Very Suitable (x10^{6}km^2)
Current	1970-2000	13.6(45%)	3.4 (11%)	5.9 (20%)	4.8 (16%)	2.1 (7%)
SSP 126	2050s	12.0(40%)	5.3 (18%)	2.3 (8%)	3.0 (10%)	7.1 (24%)
	2070s	12.6(42%)	4.7 (16%)	2.4 (8%)	3.0 (10%)	7.2 (24%)
SSP 585	2050s	12.9(43%)	4.5 (15%)	2.5 (8%)	3.1 (10%)	6.8 (23%)
	2070s	13.3(45%)	4.0 (13%)	2.4 (8%)	2.9 (10%)	7.3 (24%)
B. CBSD						
Current	1970-2000	19.8(66%)	4.4(15%)	2.9 (10%)	1.9 (6%)	8.0 (3%)
SSP 126	2050s	13.4(45%)	10.3(35%)	2.9 (10%)	1.9 (6%)	8.0 (3%)
	2070s	13.8(46%)	10.1(34%)	4.6 (8%)	2.2 (4%)	1.5 (8%)
SSP 585	2050s	14.6(49%)	9.8 (33%)	4.8 (8%)	2.0 (4%)	1.3 (6%)
	2070s	15.1(50%)	10.2(34%)	4.9 (8%)	1.8 (3%)	1.0 (5%)

Figure 3

Plots showing (a) the predicted distribution for cassava under the current climate (1970-2000), (b) prediction uncertainty for cassava under the current climate, (c) predicted future suitable habitats for cassava under the SSP1-2.6 scenario and (d) predicted future suitable habitats for cassava under the SSP5-8.5 scenario for the year 2050



Current and potential future suitable habitats for Cassava brown streak disease

The area currently at risk to CBSD spread covers approximately 33.7% of Africa's land area (10.2 million km²; Figure 4A). The countries most vulnerable to this disease include the east coast and Lake zones of Tanzania, Uganda, and Southeast DRC (Table 5). Although no occurrence records were available in western Africa, the ensemble models highlighted suitable conditions in this region, specifically in Ivory Coast, Ghana, Nigeria (highest), and Cameroon, and East Africa emerged as a hotspot for CBSD outbreaks. Under two SSP scenarios (SSP1-2.6 and 5-8.5) CBSD is expected to expand its range to 55% (16.6 million km²) and 56.6% (10.2 million km²) of Africa's land area, respectively, by 2050 (Figure 4 B-C), and this predicted range remains largely unchanged towards 2070, with countries most susceptible including those where the disease is yet to be reported, including Ivory Coast, Ghana, Benin, Nigeria, and Cameroon, all located in West Africa which is key for current cassava production. Other suitable areas were also found in southern Africa, specifically southwestern DRC, northern Angola, northern Zambia, and the eastern shores of Mozambique (**Table 5**).

Table 5

Predicted future change in suitable habitats for (a) Cassava and (b) Cassava brown streak disease (CBSD) using shared social economic pathways (SSPs); SSP1-2.6 and SSP5-8.5 for 2041-2060 and 2061-2080.

A. Cassava				
Scenario	Time	Contraction (x10^{6} km^{2})	Expansion (x10^{6} km^{2})	Unchanged (x10^{6} km^{2})
SSP 126	2050s	4.8 (16.0%)	14.8 (49.2%)	10.4 (34.8%)
	2070s	4.8 (16.2%)	14.6 (49.0%)	10.4 (34.8%)
SSP 585	2050s	5.5 (18.3%)	14.7 (49.1%)	9.7 (32.6%)
	2070s	5.4 (18.0%)	15.4 (51.5%)	9.1 (30.5%)
B. CBSD				
SSP 126	2050s	10.8 (36.3%)	12.8 (42.8%)	6.2 (20.9%)
	2070s	10.9 (36.6%)	12.5 (42.0%)	6.4 (21.4%)
SSP 585	2050s	11.3 (38.0%)	12.0 (40.4%)	6.5 (21.6%)
	2070s	12.0 (40.0%)	11.7 (39.3%)	6.2 (20.7%)

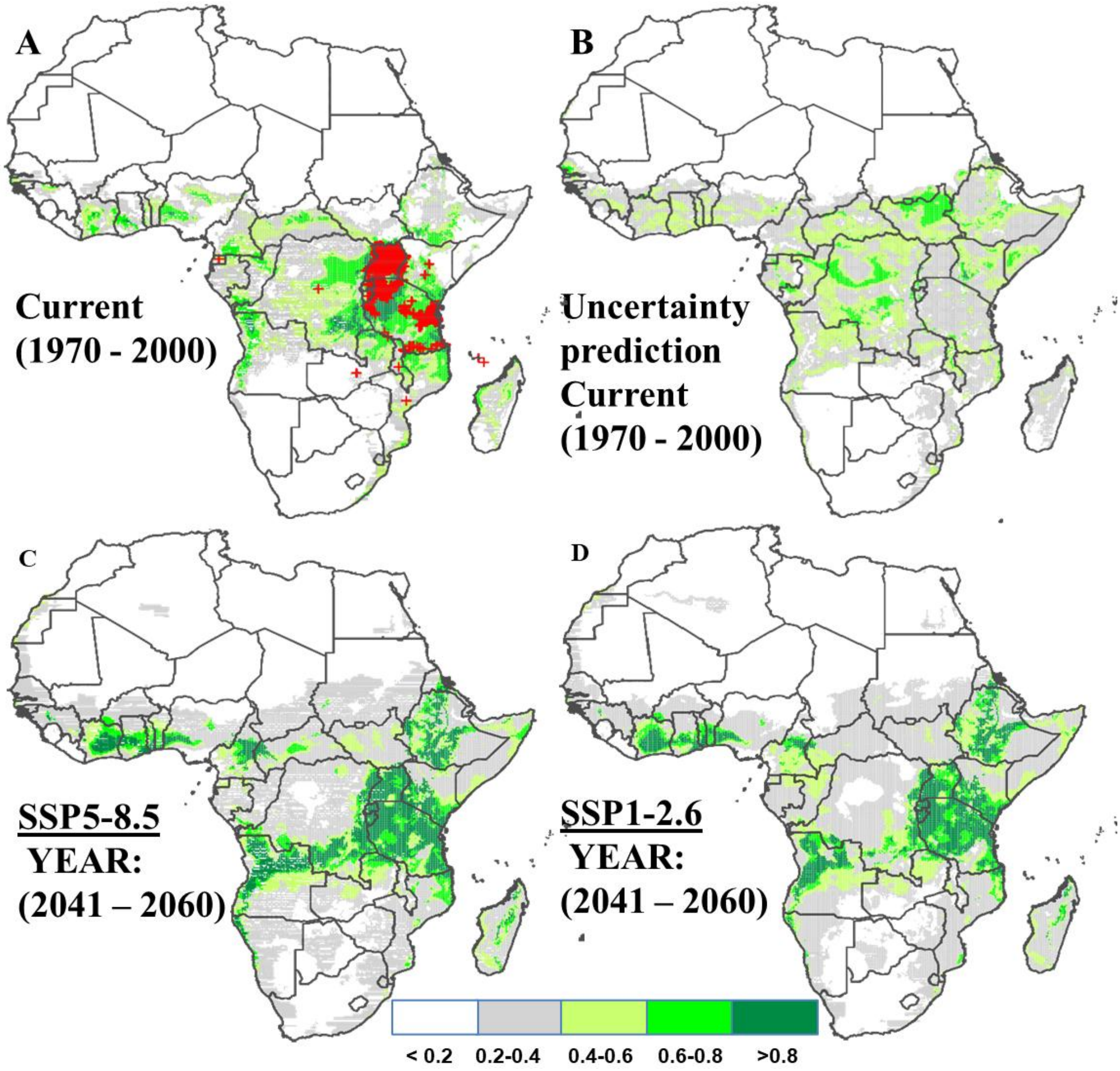
Table 6

African countries by suitability score. Current and potential future regions with suitable and highly suitable areas for Cassava and Cassava brown streak disease in Africa

CLASS	DESCRIPTION	COUNTRIES UNDER THE CURRENT CLIMATE	COUNTRIES UNDER FUTURE CLIMATE
CASSAVA			
0.8 – 1.0	Very suitable	Sierra Leone, Ivory Coast, Ghana, Togo, Benin, Nigeria, Cameron, West Central Republic, and Rwanda	Guinea, Sierra Leone, Ivory Coast, Ghana, Togo, Benin, Nigeria, Cameron, Gabon, Republic of Congo, Central Republic, South Sudan, Ethiopia, Kenya, Uganda, Tanzania, Rwanda, Burundi, Mozambique, Zambia, Angola and Madagascar
0.6 – 0.8	Suitable	Mali, Chad, DR Congo, Angola, Kenya, Tanzania, Ethiopia, Zambia, Malawi, Zimbabwe and Madagascar	Sudan, Somalia, Chad
CBSD			
0.8 – 1.0	Very suitable	Uganda, Tanzania, South DR Congo	Uganda, Tanzania, Kenya, Rwanda, Burundi, South DR Congo, Angola, Ethiopia, Cameron, Nigeria, Ghana, and Ivory Coast
0.6 – 0.8	Suitable	Kenya, Ethiopia, Mozambique, Zambia, Central Republic, Nigeria, Ghana, and Ivory Coast	Mozambique, Somalia, Central Republic and Benin

Figure 4

Plots showing (a) the predicted distribution for CBSD under the current climate (1970-2000), (b) prediction uncertainty for CBSD under the current climate (c) predicted future suitable habitats for CBSD under the SSP1-2.6 scenario and (d) predicted future suitable habitats for CBSD under the SSP5-8.5 scenario for the year 2050



Discussion

Cassava's future and the CBSD threat in Africa

Using the most recent climate scenarios from CMIP6 for the mid-term (2041-2060) and long-term (2061-2080) in Africa, our study provides a comprehensive overview of suitable habitats for cassava, as well as one of its economically important diseases (CBSD). The results indicate that under current conditions, Sub-Saharan Africa remains a hotspot for cassava, its associated virus/disease, and the vector agent (Szyniszewska, 2020; Tomlinson *et al.*, 2018). These results are congruent with the fact that cassava is already widely cultivated in Sub-Saharan Africa, especially western Africa, with Nigeria being the highest producer, producing more than 6 million tons per annum (FAO, 2013, 2020). This is in contrast with the identified high-suitability areas that are largely restricted to Eastern Africa (Tanzania and Uganda). This partially reflects the history that CBSD originated from the Coastlines of Eastern Africa before spreading to Middle Africa despite eradication measures to delimit its spread (Tomlinson *et al.*, 2018). This westward spread of the virus remains of great concern. The SDM ensemble was successful, in terms of model performance (Guan *et al.*, 2021), in reconstructing these patterns for species of interest; it identified new potential suitable habitats for cassava planting and CBSD prevalence in future scenarios, which are informative for local and regional decision-making relating to food security.

Factors of Habitat Suitability

We further found that different predictors are differentially driving the distribution of all three species of interest under current conditions. Only Bio14 (precipitation of the driest month) was, to some extent, driving the distribution of cassava brown streak viruses. For Cassava, we found temperature fluctuations and seasonality to have the strongest influence. Being a drought-tolerant plant, Cassava can survive a wider range of environmental conditions, hence fluctuations, than insects (El-Sharkawy, 2004). The reproductive rate of whitefly is also said to decline with extreme temperatures (Aregbesola *et al.*, 2020). As the host of the virus, the implication is that virus incidences will likely be reduced under unfavourable climate conditions, especially high temperatures (El-Sharkawy, 2004). Such high temperatures and precipitation events reported in Western Africa in this current term (Almazroui *et al.*, 2020; Campo *et al.*, 2011) can explain the low prevalence of the vector and virus in this and other regions depicted by the current distribution.

Future scenarios of cassava planting

With all models and climate scenarios, Sub-Saharan Africa especially will become increasingly suitable for the cultivation of Cassava. This includes even small parts east of southern Africa. This is positive news given the importance and extensive use of Cassava as a food security crop and for biofuel production (Street, 2004). This observation is consistent with other studies, which reported that suitable habitats for Cassava would increase across Africa (Jarvis *et al.*, 2012). However, the above authors also reported that cassava suitability habitats would decrease in Central and West Africa. This contrasts with our findings which depict expansions across a greater proportion of Saharan Africa. A few reasons can be attributed to this discrepancy. Jarvis *et al.* (2012) used future climate information derived from an older phase of the CMIP project (CMIP 3, SRES-A1B emissions scenario). According to the climate modelling community, the CMIP3/CMIP5 over- or under-projects climate changes in certain areas (Brown *et al.*, 2013). Also, it was observed that while CMIP5 models did not capture the observed increase in global mean surface temperature between 1998 and 2013, the historical CMIP6 simulations can reproduce these observed recent temperature increases (Bock *et al.*, 2020). More generally, CMIP6 has a higher ability to reproduce observed large-scale mean surface temperature and precipitation patterns compared to their CMIP3 and CMIP5 counterparts (Bock *et al.*, 2020). Additionally, CMIP6 factors social-economic and policy aspects (Tebaldi *et al.*, 2021; Zelinka *et al.*, 2020). These authors also only used an EcoCrop model, while we used a more robust ensemble of four models.

The increased cassava suitability habitats reported in this paper also highlights Cassava's ability to withstand climate change relative to other crops like maize, millet, sorghum, banana, and beans (Jarvis *et al.*, 2012; Kotir, 2011). Nevertheless, this does not imply that climate mitigation actions should be ignored in favour of increasing the suitable habitats for Cassava, as our results do not speak to how final agronomic outputs will be affected. Crops are not only affected by temperature but also generally exhibit different responses to increased CO_2 concentration. For Cassava, it is postulated that temperature increases could negatively affect biomass and yields due to poor assimilation (Amuji, 2021). Climate reports indicate that under these shared socio-economic pathway scenarios, temperature levels will already be well above 1.5 ^{o}C and 2 ^{o}C above pre-industrial periods (Osima *et al.*, 2018). These increases are firmly cautioned against in the Paris Agreement on climate change (UNFCCC, 2016).

Increases in suitable habitats for Cassava also correlate positively with increases in CBSD density, as seen in outputs from our future projections. This supports the likelihood of westward spread of the disease, especially along the coastal parts of Western Africa (Bundi *et al.*, 2022). However, the tropical rainforest and monsoon conditions found in the DRC, especially central DRC, and zones along the Sahel belt may continue to have a positive impact in reducing the vulnerability of the region to CBSD. More so, even suitable areas for Cassava would be much reduced in central DRC and along the Sahel hence further limiting disease outbreaks. Adequate pest mitigation measures at international borders, coupled with good farm management strategies, would therefore largely favour a reduced vulnerability to CBSD in these regions. The conclusions from this study corroborate a modelling study (using a different approach) looking at historical climate change in the East Africa region (Kriticos *et al.*, 2020). Indeed, CBSD can be introduced into new areas via planting materials. Using cassava harvested area (CHA) as a covariate we found suitable areas in West Africa where the disease is currently absent. This agrees with other modelling studies evaluating the role of mixed modes of infection in the spread of CBSD. They found that infected planting material through trade was the key long-distance pathogen dispersal mechanism (McQuaid *et al.*, 2017).

Although Africa is one of the largest cassava producers, occurrence records in online repositories do not reflect what is known about cassava production (Szyniszewska *et al.*, 2021). It is reported that less than 4% of the total records published on GBIF pertain to Africa. Another limitation of the current study concerned the resolution of the data. The data used were downloaded at 3o arc-min resolution. This allowed for easier computations yielding the results at a reasonable time. To obtain high-quality figures, a 30-second resolution would be recommended. However, this requires high-performing computers that are currently unavailable. To bridge the gap of data deficit, efforts should be increased to encourage data capturing and sharing to promote more evidence-based studies. Future studies should also focus on how well these cultivars can perform under these climate change conditions under controlled greenhouse conditions to understand if the increased suitability habitats will be commensurate with yield increases.

Conclusion

We have shown in this study using recent climate scenarios that climate change will continue to render the African continent vulnerable to cassava brown streak disease in the mid-century (i.e., by the year 2041-2060). This vulnerability will spread to the coastal parts of Western Africa as cassava-suitable habitats increase. While this increase in cassava-suitable habitats sounds encouraging, the associated risk of disease outbreaks needs to be monitored and potentially mitigated. It, therefore, remains imperative that as the growing areas for Cassava are exploited in the future, more stringent measures should be applied to delimit the occurrence and spread of cassava diseases caused by the brown streak virus.

Recommendations

Based on our findings we propose that improved cassava varieties that are tolerant/resistant to CBSD should be deployed in all cassava production regions. This should be coupled with stricter national and international border controls and quarantine measures on the movement of plant materials to prevent the introduction of the virus to other cassava production regions. Overall, to prevent disease outbreaks and associated costs from yield loss, CBSD-resistant/tolerant varieties should be deployed in areas that are highly suitable for cassava production but where there is a low probability of disease occurrence. There are several cassava varieties with varying levels of resistance (Sheat *et al.*, 2019). However, the most sustainable strategy to control CBSD is using resistant varieties and supplying disease-free planting materials to cassava farmers. Breeding of resistant varieties is achieved using new breeding technologies that require a short breeding period, unlike conventional strategies that require 6 to 8 years before a new variety can be developed (Bizimana *et al.*, 2024). These technologies include marker-assisted selection, genomic selection, transgenesis, genome editing and others that have been developed and applied to cassava. To mitigate actual costs from yield loss, these varieties can also be deployed in suitable areas of cassava production but currently experience high disease outbreaks. Countries that are highly suitable for cassava production include most of West Africa (**Table 5**), where there is currently a low chance of disease incidence. These varieties should be incorporated into farmer-preferred varieties to increase the chances of acceptability. In addition, resources to check for infected cuttings should be invested at the borders of DR Congo with Congo and the Central African Republic. These are the two potential entry borders to West Africa, given that CBSD is already reported to cause substantial yield loss in DR Congo.

Acknowledgements

This work was supported by the African Institute for Mathematical Sciences, with financial support from the Government of Canada, provided through Global Affairs Canada and the International Development Research Centre. CH was supported through the research program 'Advancing Biodiversity Informatics and Ecological Modelling' at the National Institute for Theoretical and Computational Sciences (NITheCS) and the National Research Foundation (NRF grant 89967).

Competing Interest statement

The authors declare that they have no competing interests.

References

Alicai, T., Omongo, C. A., Maruthi, M. N., Hillocks, R., Baguma, Y., Kawuki, R., Bua, A., Otim-Nape, G. W., & Colvin, J. (2007). Re-emergence of Cassava Brown Streak Disease in Uganda. *The American Phytopathological Society*, *91*(1), 24–29.

Almazroui, M., Saeed, F., Saeed, S., Nazrul Islam, M., Ismail, M., Klutse, N. A. B., & Siddiqui, M. H. (2020). Projected Change in Temperature and Precipitation Over Africa from CMIP6. Earth Systems and Environment, 4(3), 455–475.

Beck, H. E., Zimmermann, N. E., McVicar, T. R., Vergopolan, N., Berg, A., & Wood, E. F. (2018). Present and future köppen-geiger climate classification maps at 1-km resolution. Scientific Data, 5, 1–12.

Bizimana, J. P., Ngapout, Y., Nyirakanani, C., Shakir, S., Kanju, E., Legg, J. P., Rukundo, P., Shimelis, H., Nduwumuremyi, A., & Vanderschuren, H. (2024). Breeding strategies for mitigating cassava brown streak disease in Africa. Tropical Plants, 3(1), 0–0.

Bock, L., Lauer, A., Schlund, M., Barreiro, M., Bellouin, N., Jones, C., Meehl, G. A., Predoi, V., Roberts, M. J., & Eyring, V. (2020). Quantifying Progress Across Different CMIP Phases With the ESMValTool. Journal of Geophysical Research: Atmospheres, 125(21), 1–28.

Brown, J. N., Sen Gupta, A., Brown, J. R., Muir, L. C., Risbey, J. S., Whetton, P., Zhang, X., Ganachaud, A., Murphy, B., & Wijffels, S. E. (2013). Implications of CMIP3 model biases and uncertainties for climate projections in the western tropical Pacific. Climatic Change, 119(1), 147–161.

Bundi, M., Kasoma, C., Mbugua, F., Williams, F., & Rwomushana, I. (n.d.). Cassava Brown Streak Disease: An evidence note on impacts and management strategies for Zambia. KNOWLEDGE FOR LIFE.

Campo, B. V. H., Hyman, G., & Bellotti, A. (2011). Threats to cassava production: Known and potential geographic distribution of four key biotic constraints. Food Security, 3(3), 329–345.

Change, U. N. F. C. on C. (1898). The Paris Observatory. Nature, 58(1502), 356.

De Marco, P., & Nóbrega, C. C. (2018). Evaluating collinearity effects on species distribution models: An approach based on virtual species simulation. PLoS ONE, 13(9).

Donnelly, R., Sikazwe, G. W., & Gilligan, C. A. (2020). Estimating epidemiological parameters from experiments in vector access to host plants, the method of matching gradients. PLoS Computational Biology, 16(3), 1–15.

Elith, J., H. Graham, C., P. Anderson, R., Dudík, M., Ferrier, S., Guisan, A., J. Hijmans, R., Huettmann, F., R. Leathwick, J., Lehmann, A., Li, J., G. Lohmann, L., A. Loiselle, B., Manion, G., Moritz, C., Nakamura, M., Nakazawa, Y., McC. M. Overton, J., Townsend Peterson, A., … Zimmermann, N. (2006). Novel methods improve prediction of species' distributions from occurrence data. Ecography, 29(2), 129–151.

El-Sharkawy, M. A. (2004). Cassava biology and physiology Cassava: a crop for sustainable agriculture and food security in developing countries. Plant Molecular Biology, 56, 481–501.

FAO. (2013). Save and Grow: Cassava. http://www.fao.org/3/a-i3278e.pdf

FAO, & IIASA. (2000). Global Agro Ecological Zones version 4 (GAEZ v4). Dataset.

FAOSTAT. (2021). FAOStat. FAO, Rome. https://www.fao.org/faostat/en/

Guan, J., Li, M., Ju, X., Lin, J., Wu, J., & Zheng, J. (2021). The potential habitat of desert locusts is contracting: Predictions under climate change scenarios. PeerJ, 9, 1–25.

IPCC. (2021). Climate Change 2021: The Physical Science Basis. Working Group I Contribution to the IPCC Sixth Assessment Report. Climate Change 2021: The Physical Science Basis., 1–16.

Jarvis, A., Ramirez-Villegas, J., Campo, B. V. H., & Navarro-Racines, C. (2012). Is Cassava the Answer to African Climate Change Adaptation? Tropical Plant Biology, 5(1), 9–29.

Jeremiah, S. C., Ndyetabula, I. L., Mkamilo, G. S., Haji, S., Muhanna, M. M., Chuwa, C., Kasele, S., Bouwmeester, H., Ijumba, J. N., & Legg, J. P. (2015). The Dynamics and Environmental Influence on Interactions Between Cassava Brown Streak Disease and the Whitefly, Bemisia tabaci. Phytopathology, 105(January), 1–43.

Jones, R. A. C., & Barbetti, M. J. (2015). Influence of climate change on plant disease infections and epidemics caused by viruses and bacteria Influence of climate change on plant disease infections and epidemics caused by viruses and bacteria. July 2012.

Kotir, J. H. (2011). Climate change and variability in Sub-Saharan Africa: A review of current and future trends and impacts on agriculture and food security. Environment, Development and Sustainability, 13(3), 587–605.

Kriticos, D. J., De Barro, P. J., Yonow, T., Ota, N., & Sutherst, R. W. (2020). The potential geographical distribution and phenology of Bemisia tabaci Middle East/Asia Minor 1, considering irrigation and glasshouse production. Bulletin of Entomological Research, 110(5), 567–576.

McQuaid, C. F., van den Bosch, F., Szyniszewska, A., Alicai, T., Pariyo, A., Chikoti, P. C., & Gilligan, C. A. (2017). Spatial dynamics and control of a crop pathogen with mixed-mode transmission. PLoS Computational Biology, 13(7), 1–18.

Meinshausen, M., Nicholls, Z. R. J., Lewis, J., Gidden, M. J., Vogel, E., Freund, M., Beyerle, U., Gessner, C., Nauels, A., Bauer, N., Canadell, J. G., Daniel, J. S., John, A., Krummel, P. B., Luderer, G., Meinshausen, N., Montzka, S. A., Rayner, P. J., Reimann, S., … Wang, R. H. J. (2020). The shared socio-economic pathway (SSP) greenhouse gas concentrations and their extensions to 2500. Geoscientific Model Development, 13(8), 3571–3605.

Mudereri, B. T., Kimathi, E., Chitata, T., Moshobane, M. C., & Abdel-Rahman, E. M. (2021). Landscape-scale biogeographic distribution analysis of the whitefly, Bemisia tabaci (Gennadius, 1889) in Kenya. International Journal of Tropical Insect Science, 41(2), 1585–1599.

Naimi, B., & Araújo, M. B. (2016). Sdm: A reproducible and extensible R platform for species distribution modelling. Ecography, 39(4), 368–375.

Nicholson, S. E. (2017). Climate and climatic variability of rainfall over eastern Africa. Reviews of Geophysics, 55(3), 590–635.

Pellet, D. M., & El-Sharkawy, M. A. (1997). Cassava varietal response to fertilization: Growth dynamics and implications for cropping sustainability. Experimental Agriculture, 33(3), 353–365.

Ramos, R. S., Kumar, L., Shabani, F., & Picanço, M. C. (2018). Mapping global risk levels of Bemisia tabaci in areas of suitability for open field tomato cultivation under current and future climates. PLoS ONE, 13(6), 1–20.

Sheat, S., Fuerholzner, B., Stein, B., & Winter, S. (2019). Resistance against cassava brown streak viruses from africa in cassava germplasm from South America. Frontiers in Plant Science, 10(May).

DE TAFUR, S.M., M. A. E.S. and F. C. (1997). Photosynthesis and yield performance of.pdf. Photosythetica, 33(2), 249–257.

Street, K. (2004). New challenges in the cassava transformation in Nigeria and Ghana.

Environment and Production Technology Division, International Food Policy Research Institute. Food Policy, 118, 1–118.

Szyniszewska, A. M. (2020). CassavaMap, a fine-resolution disaggregation of cassava production and harvested area in Africa in 2014. Scientific Data, 7(1), 1–5.

Szyniszewska, A. M., Chikoti, P. C., Tembo, M., Mulenga, R., Gilligan, C. A., van den Bosch, F., & McQuaid, C. F. (2021). Smallholder Cassava Planting Material Movement and Grower Behavior in Zambia: Implications for the Management of Cassava Virus Diseases. Phytopathology, 111(11), 1952–1962.

Tebaldi, C., Debeire, K., Eyring, V., Fischer, E., Fyfe, J., Friedlingstein, P., Knutti, R., Lowe, J., O'Neill, B., Sanderson, B., Van Vuuren, D., Riahi, K., Meinshausen, M., Nicholls, Z., Tokarska, K., Hurtt, G., Kriegler, E., Meehl, G., Moss, R., … Ziehn, T. (2021). Climate model projections from the Scenario Model Intercomparison Project (ScenarioMIP) of CMIP6. Earth System Dynamics, 12(1), 253–293.

Thuiller, W., Georges, D., & Engler, R. (2013). biomod2: Ensemble platform for species distribution modeling. R Package Version, 2(7).

Tomlinson, K. R., Bailey, A. M., Alicai, T., Seal, S., & Foster, G. D. (2018). Cassava brown streak disease: historical timeline, current knowledge and future prospects. Molecular Plant Pathology, 19(5), 1282–1294.

Winter, S., Koerbler, M., Stein, B., Pietruszka, A., Paape, M., & Butgereitt, A. (2010). Analysis of cassava brown streak viruses reveals the presence of distinct virus species causing cassava brown streak disease in East Africa. Journal of General Virology, 91(5), 1365–1372.

Zelinka, M. D., Myers, T. A., McCoy, D. T., Po-Chedley, S., Caldwell, P. M., Ceppi, P., Klein, S. A., & Taylor, K. E. (2020). Causes of Higher Climate Sensitivity in CMIP6 Models. Geophysical Research Letters, 47(1), 1–12.