

# Cotton production areas are at high risk of invasion by *Amrasca biguttula* (Ishida) (Cicadellidae: Hemiptera): potential distribution under climate change

Abdelmutalab AG Azrag,<sup>a\*</sup> Saliou Niassy,<sup>b</sup> Adin Y Bloukounon-Goubalan,<sup>c</sup> Elfatih M Abdel-Rahman,<sup>a</sup> Henri EZ Tonnang<sup>a,d</sup> and Samira A Mohamed<sup>a</sup>



## Abstract

**BACKGROUND:** The cotton jassid, *Amrasca biguttula*, a dangerous and polyphagous pest, has recently invaded the Middle East, Africa and South America, raising concerns about the future of cotton and other food crops including okra, eggplant and potato. However, its potential distribution remains largely unknown, posing a challenge in developing effective phytosanitary strategies. We used an ensemble model of six machine-learning algorithms including random forest, maxent, support vector machines, classification and regression tree, generalized linear model and boosted regression trees to forecast the potential distribution of *A. biguttula* in the present and future using presence records of the pest and bioclimatic predictors. The accuracy of these algorithms was assessed based on the area under the curve (AUC), correlation (COR), deviance and true skill statistic (TSS).

**RESULTS:** All algorithms showed good performance in forecasting the distribution of *A. biguttula* (AUC  $\geq$  0.91, COR  $\geq$  0.72, TSS  $\geq$  0.77 and deviance  $\leq$  0.65). Mean temperature of wettest quarter, mean temperature of driest quarter and precipitation of the wettest month were the key variables that contributed to predicting *A. biguttula* occurrence. Projection of the model showed that cotton production areas in Asia, sub-Saharan Africa, and South America are at threat of invasion by *A. biguttula* under the current climatic scenario. Additionally, range expansion for *A. biguttula* is projected in the future in sub-Saharan Africa, South America and China, indicating a suitable ecological niche for *A. biguttula* to thrive.

**CONCLUSION:** Our results provide early warning and decision-making information that can guide efforts to prevent this pest's further spread and invasion into new areas.

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Supporting information may be found in the online version of this article.

**Keywords:** invasive species; species distribution; cotton jassid; ecological niche modelling; global warming

## 1 INTRODUCTION

The jassid, *Amrasca biguttula* (Ishida) (Cicadellidae: Hemiptera), commonly known as cotton jassid or Indian cotton leafhopper, is a polyphagous pest from Asia. It attacks several species of malvaceous crops, especially cotton, *Gossypium* spp. and okra *Abelmoschus esculentus*, causing serious economic losses.<sup>1,2</sup> *Amrasca biguttula* also attacks solanaceous crops such as eggplant, *Solanum melongena* and potato, *Solanum tuberosum*, and other legume crops.<sup>3</sup> This pest feeds on the underside of the leaves, inducing upward curling along the edges, which results in a crinkled appearance.<sup>2</sup> Severe infestation of *A. biguttula* also results in dried leaf that crumbles when crushed, damaged leaf edges and stunted growth.<sup>1,2</sup> Furthermore, *A. biguttula* produces honeydew, which induces the growth of mould, decreasing the plant's photosynthesis and resulting in significant yield loss. In India, *A.*

*biguttula* infestation in cotton caused between 40% and 60% yield reduction,<sup>4,5</sup> whereas on okra, a loss of  $\leq$ 88% was recorded.<sup>6</sup>

\* Correspondence to: AAG Azrag, International Centre of Insect Physiology and Ecology (icipe) Nairobi, Kenya, E-mail: [agazrag@yahoo.com](mailto:agazrag@yahoo.com); [agesmalla@icipe.org](mailto:agesmalla@icipe.org) (Azrag)

a International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya

b African Union Inter-African Phytosanitary Council (AU-IAPSC), Yaoundé, Cameroon

c Food and Agriculture Organization, Rome, Italy

d University of KwaZulu-Natal, School of Agricultural, Earth, and Environmental Sciences, Pietermaritzburg, South Africa

Recently, *A. biguttula* has progressively expanded its geographical distribution to other regions, including West Africa<sup>7,8</sup> and South America.<sup>9</sup> Climate creates a favourable environment for the pest to establish in new regions and is the primary driver of its expansion. Also, biotic factors that have contributed to the successful establishment of *A. biguttula* in new regions include the availability of suitable host plants for feeding and reproduction. The lack of inefficient natural enemies, such as predators, and parasitoids in newly invaded areas, also have allowed the pest population to grow unchecked. Additionally, global trade and movement of agricultural products might have inadvertently facilitated the spread of *A. biguttula*, enabling it to establish itself in new areas. The invasion of *A. biguttula* in countries such as Côte d'Ivoire, Mali, Burkina Faso, Senegal and Togo, has led to significant yield losses between 10% and 50% in cotton and okra.<sup>7</sup> Losses as a result of *A. biguttula* on cotton in the 2022/2023 season were estimated at over West African CFA franc (XOF) 34 billion in Côte d'Ivoire,<sup>8</sup> and XOF 65 billion in Burkina Faso, highlighting the significant economic impact of this pest on the agricultural industry. Likewise, Mali and Senegal have reported substantial infestations, which have resulted in a decrease in cotton productivity and economic losses.<sup>10</sup> Although it has been 3 years since its detection in West Africa, *A. biguttula* continues to spread in the region as the pest was reported in 2024 in Cameroon<sup>7</sup> and Nigeria.<sup>11</sup> Beyond Africa, *A. biguttula* also was reported in 2023 in Puerto Rico, South America,<sup>9</sup> and in 2024 in Barbados, south-eastern Caribbean Sea,<sup>12</sup> indicating the expansion of this pest to new regions.

Climatic variables such as precipitation and increased temperature significantly impact the survival and reproduction of insects, leading to changes in population dynamics.<sup>13</sup> For instance, higher temperatures have been shown to shorten the life cycle of insects, leading to multiple generations within a single growing season.<sup>14,15</sup> Additionally, rising temperatures and shifting precipitation patterns would create more favourable conditions for many insect species, resulting in the expansion of their geographical ranges.<sup>15,16</sup> However, extreme temperature increases may directly harm some insect species by exceeding their thermal tolerance limits, leading to physiological stress, reduced fecundity, and increased mortality.<sup>17,18</sup> These negative effects could result in localized declines of certain pests, especially those adapted to cooler climates. Also, higher temperatures may alter the timing of pest life cycles, causing pests to emerge earlier or later than their host plants' growth stages, potentially reducing the pests' food availability and reproductive success.<sup>17,18</sup> Climate change could aggravate the invasion risk of *A. biguttula* by altering its potential geographical range and increasing its population density. This has already been experienced by the recent introduction and establishment of *A. biguttula* in West Africa, the Middle East and South America.<sup>7–9</sup>

Following the recent invasion of *A. biguttula*, there is a growing outcry from the cotton and vegetable sectors in Africa, Southeast Asia and South America. There is an urgent need for integrated pest management approaches that are flexible and responsive to its spread and abundance. This includes the development of early warning systems and improved monitoring techniques that safeguard the invasion risk of *A. biguttula*. However, there is limited knowledge about the bioecology of *A. biguttula*; in particular, its potential distribution in the context of climate change remains largely unknown. This knowledge gap presents a significant challenge for developing effective management strategies and

phytosanitary measures to control its spread to new areas. Therefore, predicting shifts in the invasion of *A. biguttula* under present and future climatic scenarios is important for better management strategies and safeguarding its spread into new agricultural territories.

Ecological niche and phenological modelling have been intensively employed to forecast the climate suitability for many insect species in light of global warming.<sup>16,19,20</sup> Phenological modelling is a deductive technique that relies on the life-cycle attributes of insect species, interpret environmental conditions in terms of survival rates, reproductive success and population growth.<sup>21,22</sup> This response is then integrated with climatic variables to identify areas that are conducive to pest establishment.<sup>13,19</sup>

By contrast, ecological niche modelling is an inductive approach that uses species locality data (presence/absence). It is adaptable enough to take into account a wide range of abiotic elements for prediction, including environmental variables.<sup>23</sup> This method employs statistical or machine learning algorithms to correlate species presence records with environmental factors, making it widely used for predicting habitat suitability.<sup>23,24</sup> However, to improve prediction accuracy, an ensemble modelling approach that combines multiple models has been introduced in ecological niche modelling. This approach enhances the robustness and reliability of predictions.<sup>25</sup> It mitigates the biases and limitations inherent in individual models, providing a more comprehensive and accurate representation of potential outcomes.<sup>25</sup> Therefore, this study utilized an ensemble modelling technique to forecast the potential distribution of *A. biguttula* under both present and future climate change scenarios.

## 2 METHODOLOGY

### 2.1 Presence records

*Amrasca biguttula*'s presence records used in this study were obtained from the scientific literature. These records were supplemented by data from online databases, namely the Global Biodiversity Information Facility,<sup>26</sup> Centre for Agriculture and Bioscience International<sup>27</sup> and iNaturalist (<https://www.inaturalist.org/>). Over 848 records were obtained from these sources (Supporting Information S1). This dataset was filtered using the `SPThin` package v0.2.0<sup>28</sup> in the R environment in order to remove any points that were duplicated.<sup>29</sup> To reduce the spatial autocorrelation, we thinned these records using the same R package and retained only one point within 5 km<sup>2</sup>.<sup>29</sup> This process resulted in 398 records that were utilized for modelling the potential distribution of *A. biguttula*.

### 2.2 Bioclimatic variables

We utilized 19 bioclimatic factors and elevation from WorldClim<sup>30</sup> to forecast the distribution of *A. biguttula* in the present climatic scenario (Table 1). The aforementioned variables, produced from temperature and rainfall data, were extensively utilized in previous studies to model suitable areas for numerous species.<sup>16,31,32</sup> Additionally, some studies have demonstrated that these variables provide sufficient results when used in species distribution modelling without incorporating other climatological variables.<sup>32–34</sup> To forecast the suitable habitat of *A. biguttula* in the future, we used simulated data for the years 2061–2080 under the SSP2-4.5 climate scenario. These future data represent 20-year averages of monthly values (2061–2080),<sup>30</sup> reflecting both near-term and long-term climatic conditions. The SSP2-4.5 is a

**Table 1.** Bioclimatic variables used to forecast the distribution of *Amrasca biguttula*. The uncorrelated variables in bold are the ones utilized in the final modelling process to predict the potential distribution of *A. biguttula*

Bioclimatic variables	Unit
Bio1: Annual mean temperature	°C
<b>Bio2: Mean diurnal range [mean of monthly (max temp – min temp)]</b>	°C
<b>Bio3: Isothermality (Bio2/Bio7) (× 100)</b>	°C
Bio4: Temperature seasonality (standard deviation ×100)	°C
Bio5: Max temperature of the warmest month	°C
Bio6: Min temperature of the coldest month	°C
Bio7: Temperature annual range (Bio 5 - Bio 6)	°C
<b>Bio8: Mean temperature of the wettest quarter</b>	°C
<b>Bio9: Mean temperature of the driest quarter</b>	°C
Bio10: Mean temperature of the warmest quarter	°C
Bio11: Mean temperature of the coldest quarter	°C
Bio12: Annual precipitation	mm
<b>Bio13: Precipitation of the wettest month</b>	mm
<b>Bio14: Precipitation of driest month</b>	mm
<b>Bio15: Precipitation seasonality (coefficient of variation)</b>	mm
Bio16: Precipitation of the wettest quarter	mm
Bio17: Precipitation of the driest quarter	mm
<b>Bio18: Precipitation of the warmest quarter</b>	mm
<b>Bio19: Precipitation of the coldest quarter</b>	mm
<b>Elevation</b>	masl

moderate scenario that assumes continued economic development and technological progress but with some level of climate policy and efforts to mitigate greenhouse gas emissions.<sup>35</sup>

### 2.3 Selection of the variables

Owing to the multicollinearity that exists amongst the bioclimatic variables, the selection of the variables in species distribution modelling is an essential step that significantly impacts the accuracy and reliability of the model predictions. In other words, variable selection is necessary because correlated predictor variables can have a detrimental effect on the performance of the model, potentially resulting in overfitting. In this study, two distinct criteria were employed, namely the variance inflation factor (VIF) and Pearson correlation, to guide the selection process of the variables. The VIF quantifies and estimates whether the variance is inflated as a consequence of the presence of multicollinearity among the predictors. Variables with a VIF > 10 indicate significant multicollinearity and thus were excluded during model-fitting. By contrast, Pearson correlation evaluates multicollinearity by examining the correlation coefficient  $|r|$ . Predictors exhibiting a correlation value of  $|r| \geq 0.7$  also were omitted in the modelling process, as they indicate a high level of correlation.

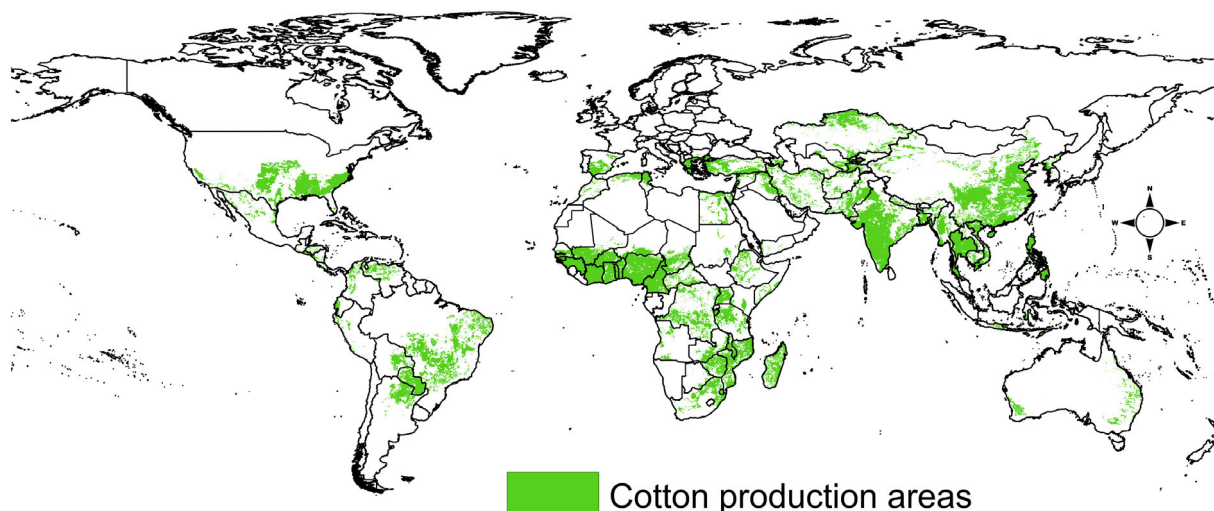
### 2.4 Modelling approach

We utilized machine learning algorithms embedded in the *SDM* package<sup>36</sup> in R to model the potential distribution of *A. biguttula*. The *SDM* package utilizes object-oriented, extendable and repeatable methods to combine multiple machine learning algorithms into a single platform system.<sup>36</sup> Among the 22 modelling methods available in *SDM*, we selected six models based on their

accuracy in predicting the distribution of *A. biguttula*. These models include random forest (RF),<sup>37</sup> generalized linear model (GLM),<sup>38</sup> maximum entropy (Maxent),<sup>39</sup> classification and regression trees (CART),<sup>40</sup> support vector machines (SVM)<sup>41</sup> and boosted regression trees (BRT).<sup>42</sup> Because we used presence data, 1000 pseudo-absence records were produced by employing the function *sdmData* in *SDM*, which was integrated with the presence records for prediction. The maximum iterations were fixed to 5000, and the data were split into 70% for model training and 30% for model accuracy assessment, with 10 replicates. We utilized the default settings in *SDM* package for all tested algorithms to ensure a fair comparison of the outputs while minimizing bias and preventing overfitting. The *SDM* package provides a cohesive and standardized framework for handling species distribution data and modelling techniques, offering a unified interface for fitting different models.<sup>36</sup> Given the variations in the model output, we applied the ensemble approach (weighted average of the six models) by utilizing the 'ensemble' function embedded in *SDM*<sup>36</sup> to project the distribution of *A. biguttula* in the present and future. The ensemble approach exhibits better predictive performance than the output of an individual model, thereby enhancing the overall accuracy and reliability of the predictions.<sup>36</sup> We first predicted the suitable habitat for *A. biguttula* without considering specific crop cultivation areas, as the pest is polyphagous and attacks a wide range of crops. In the second step, we used the cotton crop layer (Fig. 1) provided by the MapSPAM data centre (<https://mapspam.info/data/>)<sup>43</sup> to clip the predicted risk of *A. biguttula* in cotton production areas from the original output.

### 2.5 Model evaluation and accuracy

In order to assess the models' accuracy, we employed the random data-splitting method available in *SDM*. We set the automation to independently and randomly select 70% of the samples to calibrate the models, while 30% was utilized to validate model performance with 10-fold cross-validation replicates. We utilized six evaluation metrics, including the area under the curve (AUC) of the receiver operating curves (ROC), correlation (COR), true skill statistics (TSS), sensitivity, specificity and deviance to evaluate model accuracy.<sup>44</sup> The ROC curve represents the trade-off between the specificity and sensitivity of the model, whereas the AUC measures the overall performance of the model with values near zero (0) indicating poor prediction and values near one (1) signifying the perfect model prediction. The COR metric measures the relationship between observed data and model predictions. It evaluates how well the predicted presence of a species aligns with the actual observed presence or absence records.<sup>45</sup> The TSS is a metric that assesses both the specificity and sensitivity of the algorithm, taking into account omission and commission errors.<sup>44</sup> The TSS ranges from -1 to 1, with the value 1 indicating that the model has correctly identified all presence and absence records without any errors.<sup>44</sup> The discrepancy between the calibrated value and the estimated value is known as deviance and it quantifies the proportion of the variability in the observed data that the model explains. It evaluates how closely the models' predictions match the actual observations.<sup>46</sup> According to Swets,<sup>47</sup> the model's performance is ranked based on AUC discriminatory power from excellent to fail. This is known as Swets rank, which ranks the models' performance as excellent ( $\geq 0.90$ ), good (0.80–0.89), fair (0.70–0.79), poor (0.60–0.69) or (v) fail ( $\leq 0.59$ ).



**Figure 1.** Cotton production areas.

### 3 RESULTS

#### 3.1 Selection of variables

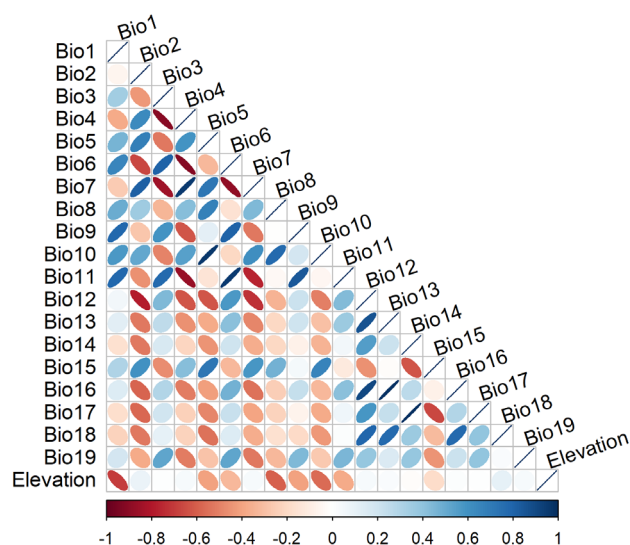
Pearson correlation coefficients and VIP revealed 10 uncorrelated variables amongst the 20 variables obtained for modelling (Fig. 2; Table 1). The selected predictors utilized to model the distribution of *A. biguttula* include Bio2, Bio3, Bio8, Bio9, Bio13, Bio14, Bio15, Bio18, Bio19 and elevation (Table 1). The VIF values for these variables were 3.66, 3.17, 2.68, 4.21, 8.01, 2.23, 6.82, 6.75, 2.02 and 2.46, respectively. These variables also had a correlation value of  $|r| < 0.7$  (Fig. 2), testifying to their eligibility in modelling the distribution of *A. biguttula*.

#### 3.2 Model performance and accuracy

The independent and random split of the data into 70% for calibration and 30% for validating the model performance revealed high accuracy for all models (Table 1). The 10-fold replicates (light blue lines) of the receiver operating characteristic (ROC) in each algorithm demonstrated that the predictions across replications were relatively consistent (Fig. 3). The AUC threshold-independent statistics of the ROC showed that all models were 'excellent' in their performance, with AUC values in the range 0.91–0.98 (Fig. 3; Table 2). By contrast, the TSS threshold-dependent statistics showed a varied performance of the models, with rankings ranging from 'fair' to 'excellent' with TSS values varying from 0.77 to 0.90 (Table 2). Nevertheless, the random forest (RF) algorithm achieved 'excellent' performance in both cases (AUC = 0.98 and TSS = 0.90). The correlation metric also showed a high correlation between the observed and estimated values  $|r| \geq 0.72$  (Table 2). The deviance between the measured and assessed values was relatively low for all models, indicating the high accuracy of the selected algorithms.

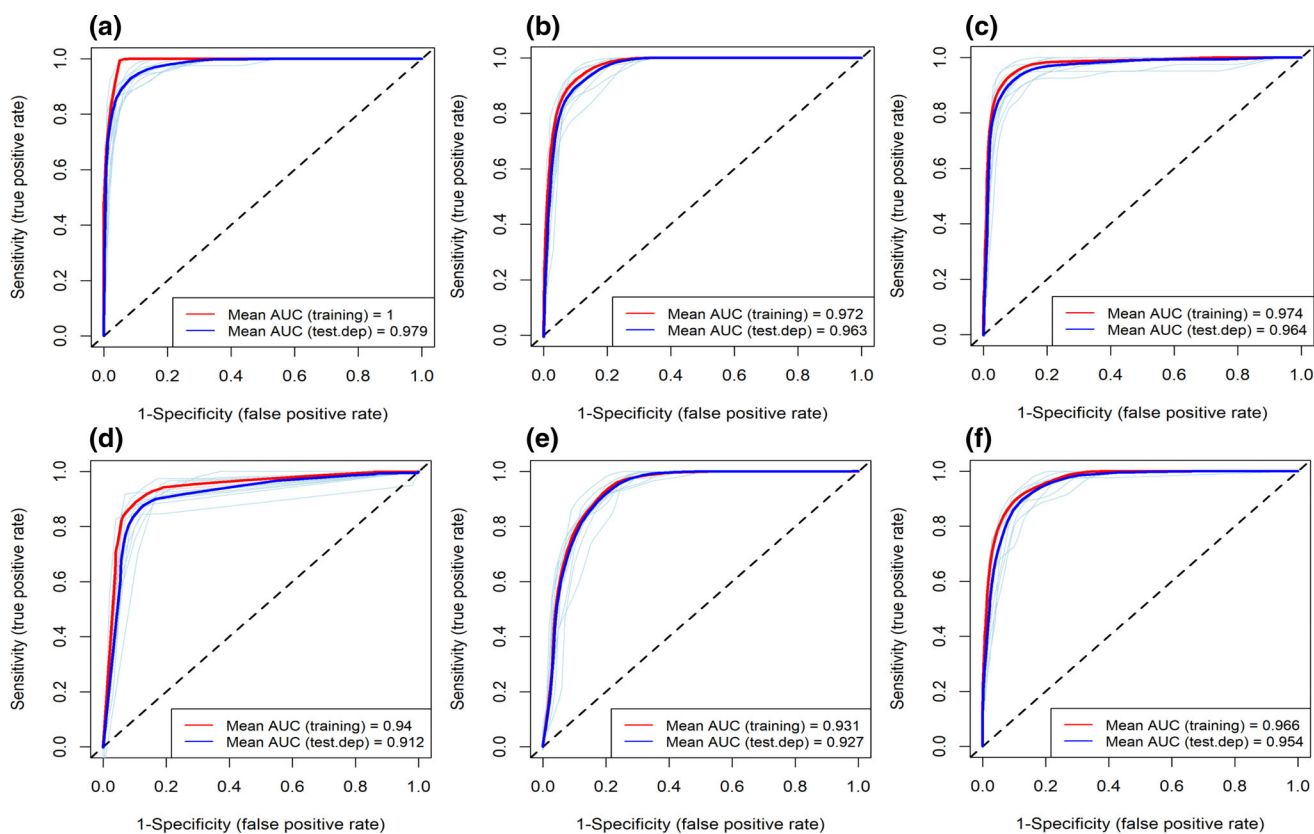
#### 3.3 Contribution and importance of variables

The importance of the 10 selected predictors in forecasting the distribution of *A. biguttula* by each model is presented in Fig. 4. For the RF algorithm, Bio8, Bio13 and Bio9 were the key three top predictors [Fig. 4(a)], contributing by 15.3, 8.4 and 7.8%, respectively. The same three variables were selected by the maxent algorithm as top predictors in forecasting the distribution of *A. biguttula* [Fig. 4(b)], with a contribution of 45.6, 25% and 19%, respectively, for Bio9, Bio8 and Bio13. However, all of the



**Figure 2.** Collinearity matrix of all variables used in predicting the potential distribution of *Amrasca biguttula*. Blue ellipse indicates positive correlations among the variables, and red ellipse indicates negative correlations. Darker shades of these colours represent a high correlation between the variables, whereas lighter shades represent a low correlation.

environmental predictors contributed relatively to the performance of the SVM algorithm, with the exception of Bio14 and Bio19, which had the lowest contributions, with 5.8 and 5.4%, respectively [Fig. 4(c)]. The CART algorithm identified Bio8 (58%), Bio13 (29.7%) and elevation (12.6%) as the top environmental predictors [Fig. 4(d)]. In the GLM model, Bio8 and Bio9 were the key variables that had the highest contribution in forecasting the distribution of *A. biguttula* [Fig. 4(c)]. However, for BRT, the predictor that granted the greatest contribution to the performance of the algorithm was Bio8, which contributed 58%, followed by Bio13, which contributed 14% [Fig. 4(d)]. The combination of all six algorithms in an ensemble model revealed that Bio8, Bio9 and Bio13 had the highest influence in forecasting the distribution of *A. biguttula*, with contributions of 28%, 12.3% and 8.3%, respectively (Fig. 5).



**Figure 3.** Receiver operating curves (ROCs) of the six machine learning algorithms selected to forecast the potential distribution of the *Amrasca biguttula* with (a) RF, (b) maxent, (c) SVM, (d) CART, (e) GLM and (f) BRT.

**Table 2.** Four evaluation metrics used to assess the accuracy of the six machine learning algorithms used to predict the potential distribution of *Amrasca biguttula*: the area under the curve (AUC), correlation (COR), true skill statistic (TSS), and the explained deviance (deviance)

Model name	AUC	COR	TSS	Deviance	Sensitivity	Specificity	Swets rank
Random forest (RF)	0.98	0.87	0.90	0.36	0.91	0.92	Excellent
Maximum entropy (maxent)	0.96	0.80	0.83	0.49	0.89	0.90	Good
Support vector machines (SVM)	0.96	0.85	0.86	0.42	0.92	0.92	Good
Classification and regression trees (CART)	0.91	0.75	0.78	0.65	0.89	0.89	Fair
Generalised linear models (GLM)	0.93	0.72	0.77	0.60	0.86	0.85	Fair
Boosted regression trees (BRT)	0.95	0.78	0.81	0.59	0.89	0.88	Good

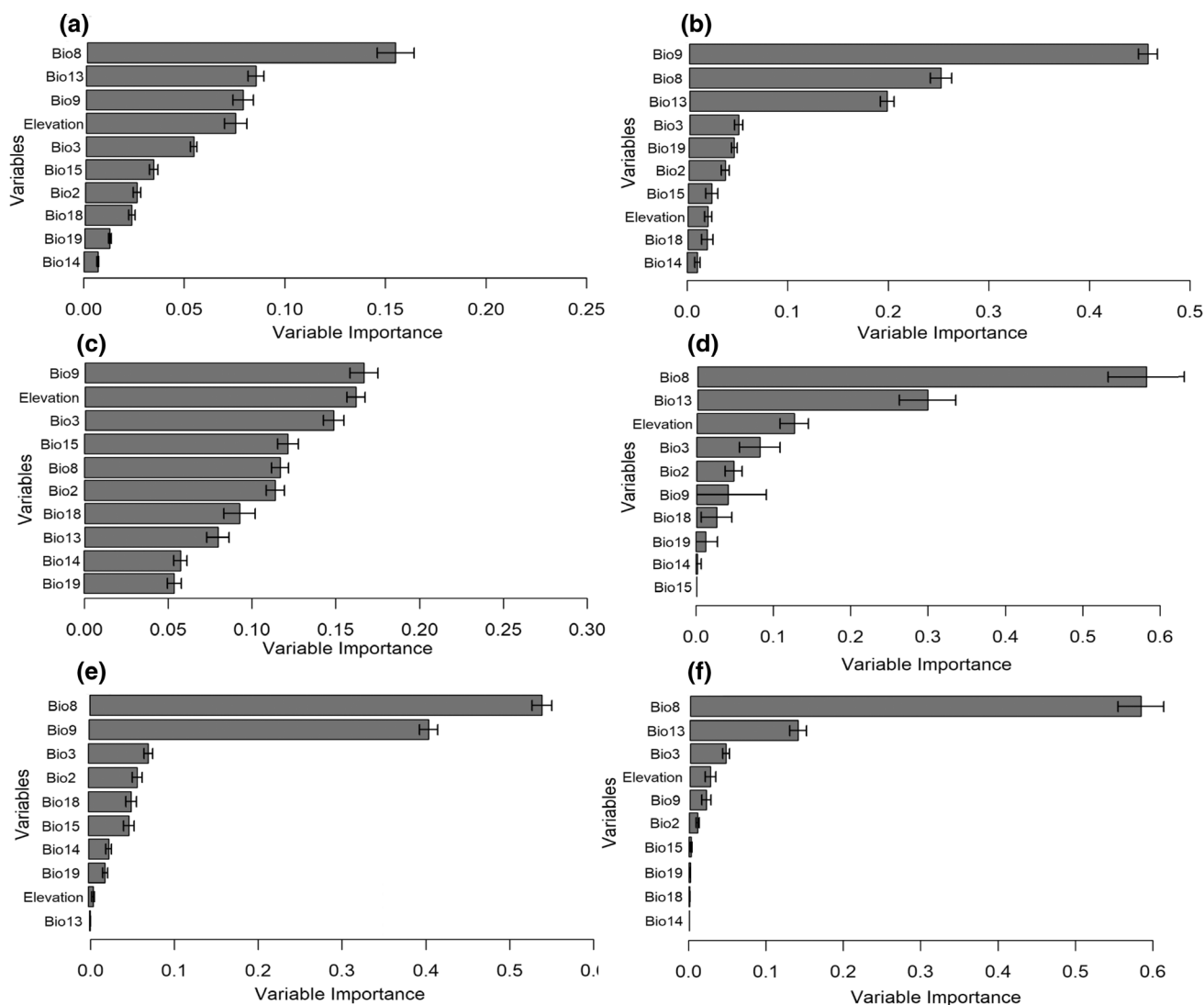
### 3.4 Potential distribution of *A. biguttula* under current and future climatic scenarios

Overall, the suitable areas for *A. biguttula* establishment under the current climatic scenario are largely confined within South and Southeast Asia, Australia, sub-Saharan Africa, and South and Central America [Fig. 6(a)]. Future predictions also showed these regions to be highly suitable for *A. biguttula* to establish with an increase in suitable areas as a result of climate change [Fig. 6(b)].

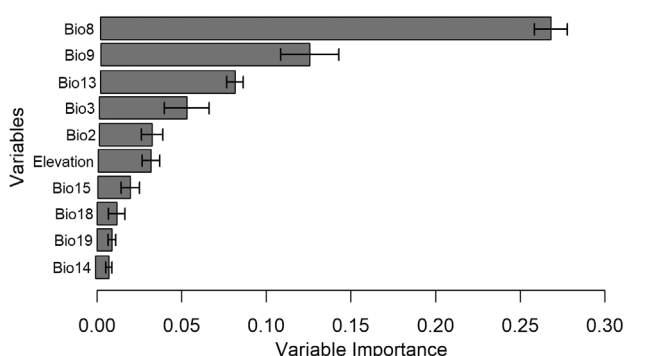
### 3.5 Potential distribution of *A. biguttula* in cotton production areas

In the current scenario, the ensemble model (weighted average of the six algorithms) predicted high climate suitability for *A. biguttula* to thrive in cotton production areas in many countries across the world [Fig. 7(a)]. In Asia, a high invasion risk by *A.*

*biguttula* is predicted in India, Pakistan, Bangladesh, Myanmar (Burma), Thailand, Cambodia, Vietnam and southern China [Fig. 7(a)]. In Africa, the model predicted cotton production areas in all of West and Central Africa including the countries Côte d'Ivoire, Benin, Mali, Burkina Faso, Nigeria, Ghana, Cameroon, Chad, Equatorial Guinea, The Gambia, Guinea, Guinea-Bissau, Liberia, Niger, Senegal, Togo and Sierra Leone to be at threat of invasion by *A. biguttula*. Also, cotton production areas in East and southern African countries, including Tanzania, Somalia, Mozambique, Malawi, Madagascar, and some parts of Zimbabwe and South Africa, are highly threatened by *A. biguttula* invasion under current climatic conditions [Fig. 7(a)]. However, low-to-moderate risk of invasion is predicted by the model for Sudan, Ethiopia, Kenya, Uganda, Zambia, the Democratic Republic of Congo and Burundi. Likewise, medium-to-high risk is



**Figure 4.** Relative variable importance in forecasting the distribution of *Amrasca biguttula* using six machine learning algorithms with (a) RF, (b) maxent, (c) SVM, (d) CART, (e) GLM and (f) BRT.



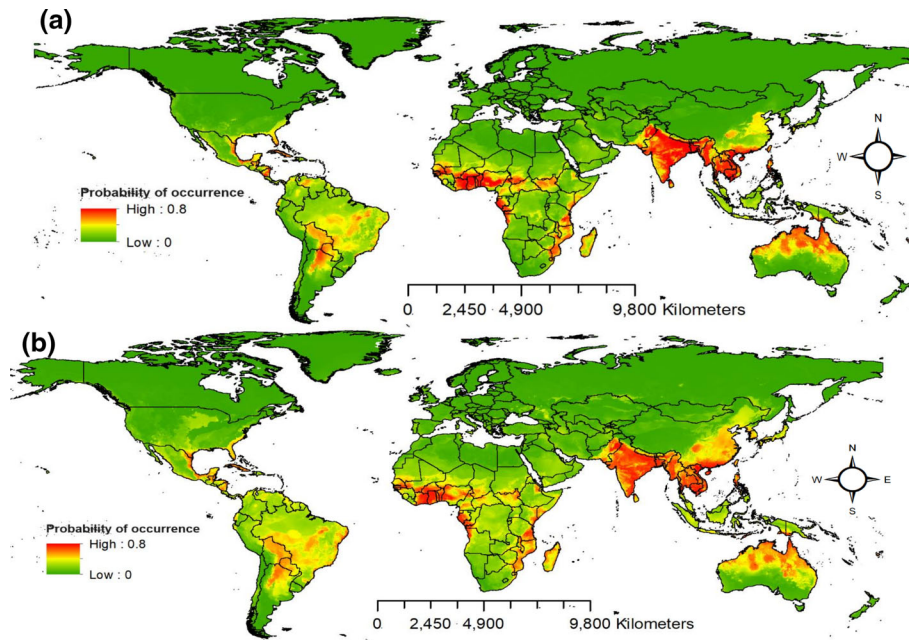
**Figure 5.** Relative variable importance in forecasting the distribution of *Amrasca biguttula* using an ensemble modelling approach (weighted average of six machine learning algorithms: RF, maxent, SVM, CART, GLM and BRT).

predicted by the model for South America: Brazil, Paraguay, Argentina, Venezuela, Colombia, Central America countries, and the USA [Fig. 7(a)].

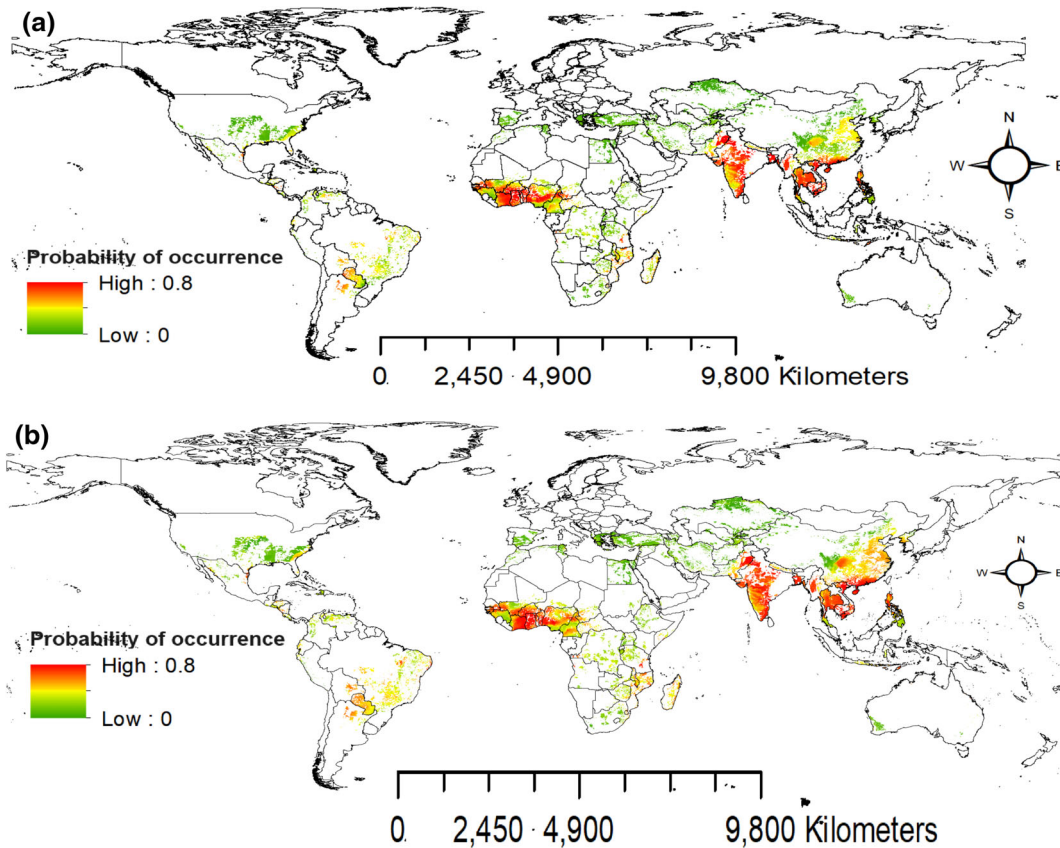
Under future climatic conditions (years 2061–2080), the risk of invasion by *A. biguttula* will rise in cotton production areas across the world, particularly in sub-Saharan Africa and South America [Fig. 7(b)]. Although a slight contraction is expected in some West African countries and India (Fig. 8), these areas will remain optimal for *A. biguttula* to occur [Fig. 7(b)]. As a consequence of climate change, range expansion for *A. biguttula* is expected in cotton production areas in sub-Saharan Africa, South America, some parts of China and the USA (Fig. 8).

**3.6 Variable response**

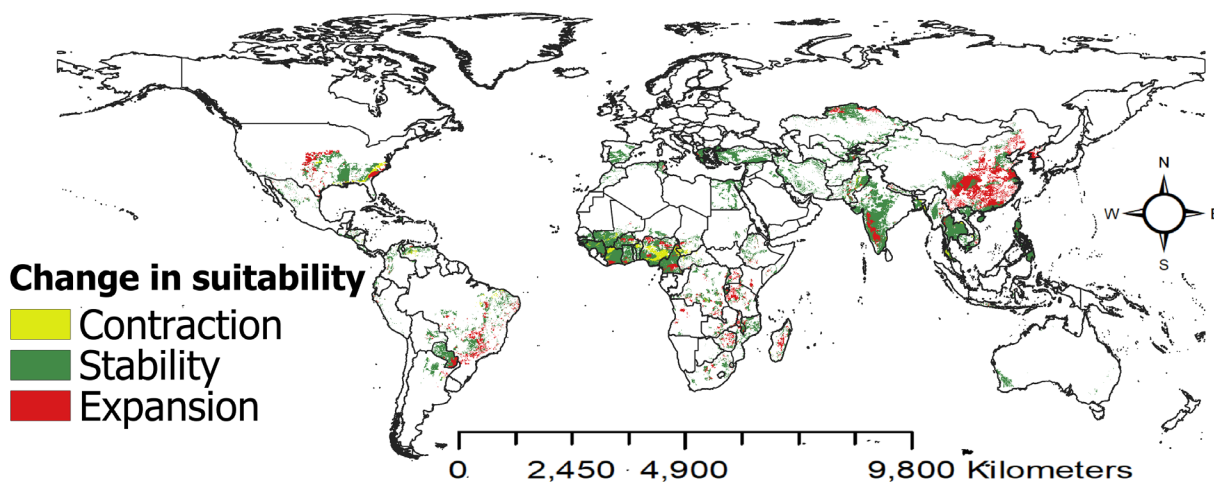
The occurrence of *A. biguttula* in the function of the 10 predictor variables is presented in Fig. 9. The probability of *A. biguttula* distribution shrinks with an increase in Bio2 and Bio3. Nevertheless, increases in Bio8 and Bio9 between 0 and 40 °C, lead to an increase in the probability of occurrence for *A. biguttula* (Fig. 9). Also, the precipitation variables influenced the potential distribution of *A. biguttula* where the highest probability occurs when Bio13 reaches ≈400 mm, with no precipitation occurring in the driest month (Bio14 = 0). The response curve also showed



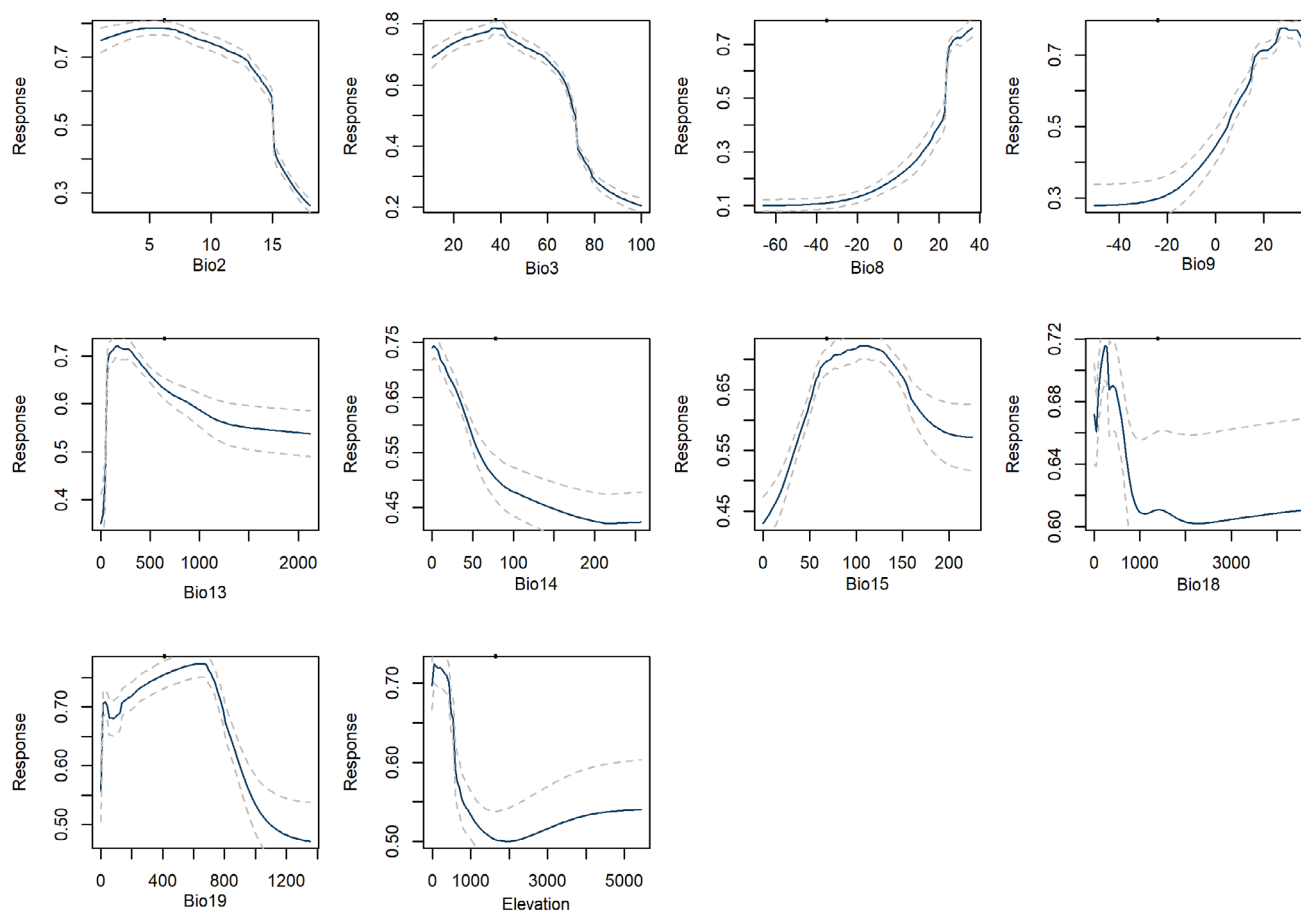
**Figure 6.** Overall potential distribution of *Amrasca biguttula* under (a) current and (b) future climatic scenarios predicted using an ensemble model (weighted average of six machine learning algorithms: RF, maxent, SVM, CART, GLM and BRT).



**Figure 7.** Potential distribution of *Amrasca biguttula* in cotton production areas under (a) present and (b) future climatic scenarios predicted using ensemble model (weighted average of six machine learning algorithms: RF, maxent, SVM, CART, GLM and BRT).



**Figure 8.** Potential distribution change of *Amrasca biguttula* showing the difference between the present and future climate change scenarios. Yellow represents a decrease in suitability, green indicates no change between current and future conditions, whereas red indicates an increase in suitability.

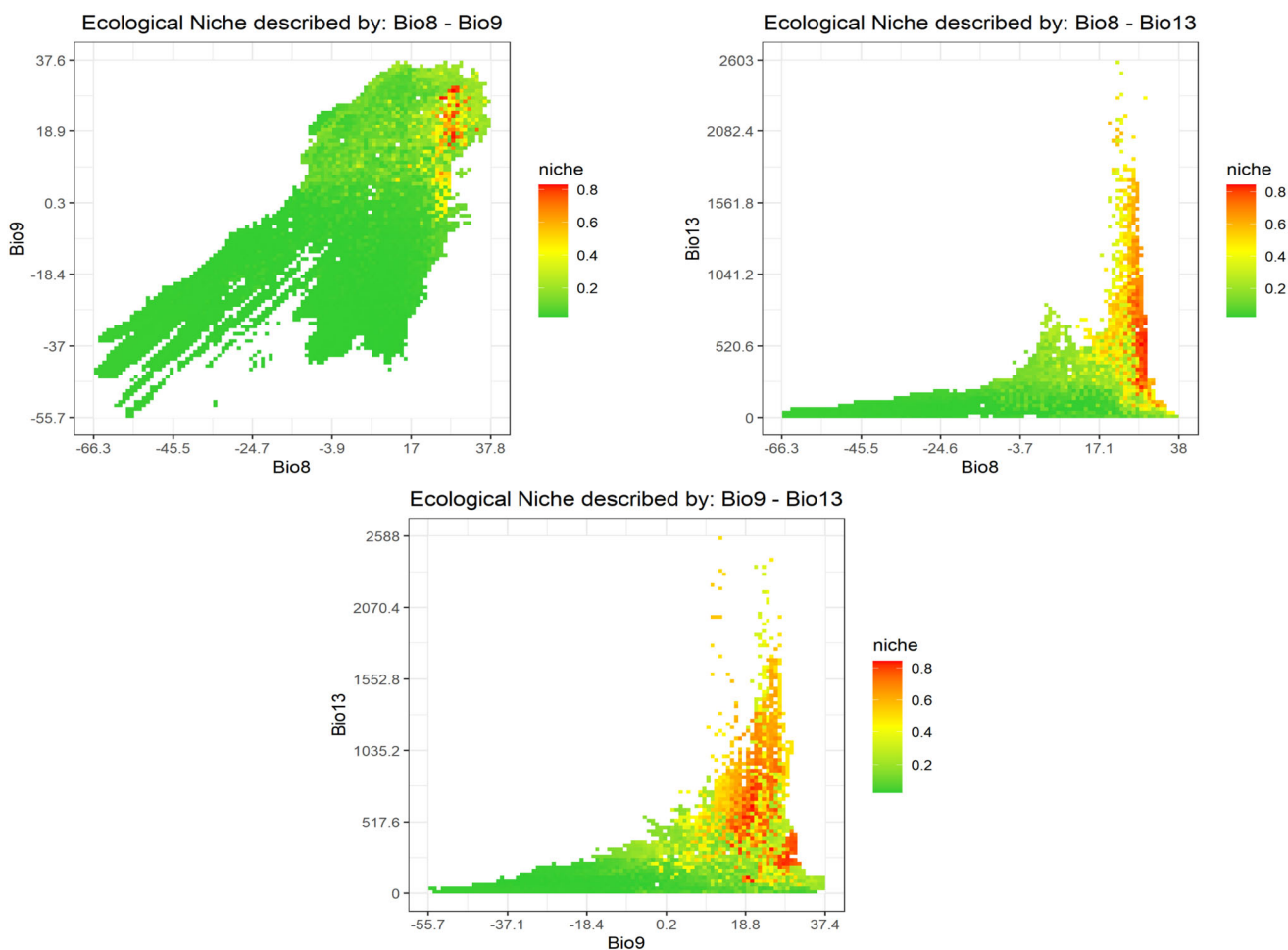


**Figure 9.** Response curves of the selected environmental predictors used to forecast the potential distribution of *Amrasca biguttula* using ensemble modelling (weighted average of six machine learning algorithms: RF, maxent, SVM, CART, GLM and BRT). Blue line is the mean response curve for the six algorithms, and the upper and lower 95% confidence intervals are represented by the grey broken lines above and below, respectively.

that the occurrence of *A. biguttula* is higher at elevations <1000 m above sea level (Fig. 9).

The ecological niche of *A. biguttula* based on the top three contributing variables is illustrated in Fig. 10. The most suitable habitats

for *A. biguttula* are to be found in areas that have Bio8 and Bio9 range between 18 and 35 °C (Fig. 10). Also, areas with precipitation between 0 and 600 mm and temperatures between 18 and 35 °C are considered to be optimal for *A. biguttula* to thrive (Fig. 10).



**Figure 10.** Ecological niche of *Amrasca biguttula* predicted using three top contributing variables: mean temperature of the wettest quarter (Bio8), mean temperature of the driest quarter (Bio9), and precipitation of the wettest month (Bio13).

## 4 DISCUSSION

Rising temperatures as a result of climate change are anticipated to significantly change the geographical distribution of many insect species and facilitate their establishment in new areas.<sup>48,49</sup>

This change raises the possibility of biological invasions by alien species, that could lead to significant crop losses, especially in the agricultural industry.<sup>50,51</sup> This was the case with *Amrasca biguttula*, which recently invaded many countries in South America, Southeast Asia, the Middle East and West Africa.<sup>7–9</sup> Although *A. biguttula* is a significant threat to the economy and food system in many countries, particularly in West and Central Africa, its potential distribution in the present and future scenarios is still unknown, raising the threat of invasion into other uninvaded regions. Therefore, in this study, we projected the global potential distribution of *A. biguttula* under both current and future climatic scenarios using an ensemble model of six ecological niche models.

Although the accuracy of the six models we used in this study was high (AUC  $\geq$  0.91 and TSS  $\geq$  0.77), differences in the output still existed owing to the difference in the computational method of each model algorithm.<sup>52–54</sup> The variations in computational methods by different algorithms usually result in uncertainty thus affecting the reliability and accuracy of the individual model.<sup>25,36</sup> To address this, we used the ensemble method by aggregating

the output of the six algorithms in one model to enhance the robustness and reliability, and maximize the accuracy of the predictions. This approach mitigates the biases and limitations that exist in individual models, thus providing a more comprehensive and accurate representation of potential outcomes.

In the present study, Bio8, Bio9 and Bio13 were the most significant climatic variables that contributed to the prediction of *A. biguttula* using an ensemble model. The ecological niche prediction showed that temperature between 18 and 35 °C, is the most favourable condition for *A. biguttula* to occur. This agrees with the report of Patel and Radadia<sup>55</sup> which recorded a significant positive correlation between *A. biguttula* population and temperature within a range between 29 and 37 °C. Similar results also were reported by Rajasekhar et al.,<sup>56</sup> where the population abundance of *A. biguttula* was higher when the maximum temperature ranged between 28 and 34 °C. Generally, many studies have reported that temperature significantly affects the distribution, dispersal and population densities of insects,<sup>13,48</sup> and *A. biguttula* is no exception. Although temperature is a crucial variable, precipitation of the wettest month (Bio13) has a vital role in the occurrence and distribution of *A. biguttula*. The prediction of the model showed that areas with precipitation of 0–600 mm and temperatures of 18–35 °C provide the most favourable niche for *A. biguttula* to occur. This agreed with the results of Janu et al.,<sup>57</sup>

who recorded a high population density of *A. biguttula* in cotton fields when temperature ranged between 20 and 35 °C, with precipitation ranging between 0 and 200 mm. Rainfall can positively influence the abundance of *A. biguttula* at the onset of the precipitation season where the vegetative development of the host plant provides an ideal environment for the pests' development and the population to build up. However, frequent and heavy rainfall can wash *A. biguttula* off the plant leaves, leading to a decline in population abundance. Therefore, our findings demonstrate that the changes in precipitation and temperature are crucial factors in assessing the distribution of *A. biguttula*.

In the present conditions, the distribution of *A. biguttula* predicted by the model was consistent with its known distribution in regions such as India, Pakistan and West African countries where the models projected highly suitable habitats for its establishment. In Africa, cotton production areas in countries such as Guinea, Somalia, Benin, Mozambique, Cameroon, Burkina Faso, Chad, The Gambia, Ghana, Côte d'Ivoire, Guinea-Bissau, Equatorial Guinea, Liberia, Niger, Mali, Senegal, Sierra Leone, Nigeria, Togo, Tanzania, Malawi, Madagascar, Zimbabwe and South Africa were predicted by the model to be optimal for *A. biguttula* to thrive. This has been confirmed by reports of recent invasions of the pest to West and Central Africa, in Nigeria<sup>11</sup> and Cameroon,<sup>7</sup> respectively. This invasion poses a significant threat to neighbouring countries, especially Benin, Gambia, Ghana, Guinea, Guinea-Bissau, Liberia Chad, Niger and the Central African Republic where the pest has yet to arrive. Likewise, the model prediction also showed that eastern and southern African countries are at threat of invasion by *A. biguttula*, where the pest could spread rapidly, if not effectively managed at the borders. Additionally, the recent introduction and establishment of *A. biguttula* in Puerto Rico,<sup>9</sup> and Barbados, southeastern Caribbean Sea,<sup>12</sup> poses a high risk to counties in central and South America at large. Furthermore, the invasion of *A. biguttula* in Iraq in the Middle East,<sup>58</sup> also threatens the entire region where the pest might cause high damage to other alternative hosts such as eggplant, okra and potato.

As mentioned above, *A. biguttula* has a wide host range, including cotton *Gossypium* spp., Hibiscus, *Hibiscus* sp., okra, *Abelmoschus esculentus*, eggplant, *Solanum melongena*, and sunflower, *Helianthus annuus* grown throughout the year in most countries around the world, especially Africa. Crops such as okra and hibiscus are essential food crops that provide essential nutrients (vitamins, minerals, and soluble and nonsoluble fibres), thereby mitigating malnutrition in most parts of Africa. This implies that the broad host range of *A. biguttula* and the movement of infested plant materials within and across borders will be a key driver in the spread of this pest. Therefore, this prediction provides important information for the National Plant Protection Organizations (NPPO) to undertake proactive measures that can intercept the establishment and spread of *A. biguttula* in new regions. These measures incorporate tightening phytosanitary protocols and improving inspection processes at the borders to detect and intercept potential infestations, and continuous surveillance of the pest within the countries for early detection. An understanding of the bioecology of the pest also will help in designing effective and sustainable management options.

Future predictions indicate that the invasion risk of *A. biguttula* will increase, particularly in sub-Saharan Africa and South America. The highest expansion range for *A. biguttula* was projected in eastern and southern Africa, where the environment will

become more suitable for *A. biguttula* in the future scenario in comparison to the present situation. Although the probability of occurrence will decrease in some West African countries, these areas will remain highly suitable for *A. biguttula* to establish in the future, causing devastating damage. Likewise, it is anticipated that climate suitability would increase for *A. biguttula* in South America and China, increasing the threat of invasion in these regions. This underscores the urgent necessity for robust phytosanitary measures and biosecurity restrictions to minimize the invasion of *A. biguttula* invading new countries and protect crop yields and quality, ensure food security, and maintain biodiversity and ecosystem health. Additionally, these measures help safeguard millions of jobs provided along the cotton value chain of countries.

Despite employing an ensemble model (weighted average of six machine learning algorithms) to forecast the distribution of *A. biguttula*, there are some limitations to our study. First, only bioclimatic variables and elevation were considered in this study as predictors to forecast the suitable areas for *A. biguttula* establishment. The study did not take into account important biotic aspects such as natural enemies, such as parasitoids and predators. Nonetheless, using bioclimatic factors to predict the pests' potential distribution and suitable habitats provides valuable information on their ecological niche, aiding in decision-making and the development of suitable management techniques against the pest.<sup>16,32,34</sup> This is particularly critical in light of global warming, as shifting environmental conditions may expand or alter pest distributions, posing new challenges to agricultural production. Another limitation is that a large proportion of the georeferenced points used in this study were mainly from Asia, specifically, India and Pakistan, where the pest is known to exist at the moment. Incorporating additional georeferenced records in the future from newly invaded regions could enhance the accuracy and predictions of the model. Despite these limitations, our findings offer a valuable overview and highlight the invasion risk of *A. biguttula*. The contribution of transboundary movement of infested plant materials on other potential host plants needs to be investigated.

In conclusion, the potential global distribution of *A. biguttula* in cotton production areas has been predicted for the first time in this study. We employed an ensemble model (weighted average of six machine learning algorithms: RF, maxent, SVM, CART, GLM and BRT) to forecast the distribution of this pest. The six accuracy assessment metrics (AUC, COR, deviance, TSS, sensitivity and specificity), were good for all six algorithms, demonstrating their performance in forecasting the habitat suitability of *A. biguttula*. Models output showed that Southeast Asia, sub-Saharan Africa and South America are at high threat of invasion by *A. biguttula* and rising temperatures will increase the suitable regions for the pest to thrive. Our findings have the potential to be utilized as an early warning system, providing critical insights to inform and shape safeguarding policy development against this pest to prevent it from spreading further and invading new regions. Additionally, the results could be useful in the development of effective management techniques for *A. biguttula*. For example, targeted surveillance, early interventions and efficient resource allocation can be implemented in the identified high-risk areas. The results also can support deploying biological control agents in suitable regions to minimise pesticide use. Additionally, incorporating climate change scenarios helps anticipate future risks, ensuring adaptive and proactive pest control measures.

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## DATA AVAILABILITY STATEMENT

The data that supports the findings of this study are available in the supplementary material of this article.

## CONFLICT OF INTEREST

The authors declare that no conflict of interest exists.

## SUPPORTING INFORMATION

Supporting information may be found in the online version of this article.

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