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Estimating the Optimal Control Areas of Two Classical Biocontrol Agents Against the Fall Armyworm Based on Hotspot Matching Analysis

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Abstract: *Spodoptera frugiperda*, the fall armyworm (FAW), is a widespread and polyphagous crop pest, causing serious crop yield losses worldwide, especially maize and other cereals. Biological control (biocontrol) is considered as the generally safer and more environmentally benign strategies compared to chemical insecticides in managing FAW. *Chelonus insularis* and *Eiphosoma laphygmae* are two promising classical biocontrol parasitoids against FAW. However, the optimal control areas for FAW with the two parasitoids in its invasive ranges remain unclear. This study is first time to integrate species distribution models and hotspot analysis to estimate the optimal areas for controlling FAW with these two parasitoids worldwide. Key variables influencing distribution include human influence index, temperature, and precipitation. The optimal control areas of FAW with *C. insularis* and *E. laphygmae* are in most of sub-Saharan Africa, Mediterranean regions, eastern, southern, and southeastern Asia, and Oceania. These areas are expected to expand to high-latitude areas under changing climatic conditions. Niche comparisons indicated that the FAW and *C. insularis* niches were closely aligned. *Chelonus insularis* and *E. laphygmae* are potentially effective against FAW in Africa, Asia, and Oceania. Our findings offer insights into the strategic use of the two parasitoids against FAW worldwide.

Keywords: fall armyworm; classical biocontrol; parasitoids; climate match; hotspot

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1. Introduction

Crop pests cause severe economic losses and threaten global food security by reducing key crop yield and quality [1,2]. Biological invasions exacerbate the effects of crop pests on crop yield, economic losses, and food security [3,4]. *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae), commonly known as the fall armyworm (FAW), is a highly destructive, migratory, and invasive pest of the order Lepidoptera, originally native to America [5] FAW feeds on more than 350 host plants (primarily Poaceae), causing considerable crop yield losses (e.g., maize, sorghum, and rice) [6,7]. FAW was first observed and officially reported in West Africa in 2016, and rapidly spread to almost all areas of sub-Saharan Africa in 2018 [8], causing unprecedented economic damage to African maize production. A previous study revealed that economic losses in maize yield caused by FAW were between US $2.5–6.3 billion across 12 countries in Africa in 2017 [9]. FAW has successfully invaded Asia since 2018, including India, Myanmar, China, and Sri Lanka in

2019, thereby causing serious maize yield losses. Until 2023, FAW covered more than 130 countries and regions, posing a significant threat to food security worldwide. This indicates the urgent need to develop a sustainable and safe control strategy for the management of their invasive range.

Chemical insecticides have been frequently used to control FAW populations in agricultural production since 1940 because the control effect can be achieved in the short term [10]. However, the overuse of chemical insecticides has led to the rapid development of insecticide-resistant FAW populations [5]. Among the FAW management strategies, biological control (biocontrol) measures are considered the most effective, sustainable, and environmentally benign [11,12]. FAW has various natural enemies in its native range, including parasitoids, predators, and parasitic nematodes. Parasitoids are frequently used as biocontrol agents for FAW [13,14]. Several classical biocontrol programs were developed in the 20th century that introduced native parasitoids to control FAW populations in invasive or native ranges where parasitoids were absent [5]. However, selecting classical biocontrol agents for FAW must include a potential risk assessment of the introduced agents (particularly their effect on non-target hosts) and an estimation of climate matching areas of the agents against FAW. Climate mismatch between classical biocontrol agents and target species is frequently considered a limiting factor to the agent's population establishment and successful control of target species populations [15,16].

Climate matching approaches (e.g., niche modelling and theory), including species distribution models (SDMs) and niche similarity analysis approaches, can estimate climate matching areas and compare the niche similarity of classical biocontrol agents against target invasive species, assessing the agents' potential for introduction and control in the target invasive species' fundamental niche [17]. SDMs have been frequently used to investigate the climate matching of classical biocontrol agents against invasive species, such as the evaluation of climate matching for three parasitoids against the invasive pest *Sirex noctilio* Fabricius (Hymenoptera: Siricidae), using MaxEnt [18], and six biocontrol agents against the invasive plant *Ambrosia artemisiifolia* L. (Asterales: Asteraceae), using four single SDMs [19]. The hotspot analysis approach can identify spatial clusters of significantly high values, which can be used to estimate the significantly high climatic suitability areas of classical biocontrol agents, thereby identifying the optimal control areas for target invasive species. Hotspot areas of climatic suitability for classical biocontrol agents can further increase the establishment and persistence of populations that persist in the invasive ranges of the target invasive species. Niche similarity analysis approaches, such as the *n*-dimensional hypervolume concept, have been frequently used to compare the species niches [20,21], and could also be used to analyze the niche similarity between classical biocontrol agents and target invasive species, thereby assessing their potential for introduction.

Chelonus insularis (Cresson) (Hymenoptera: Braconidae) (i.e., egg-larval parasitoid) and *Eiphosoma laphygmae* (Costa Lima) (Hymenoptera: Ichneumonidae) [22] are native to the Americas and are considered promising biocontrol agents [23,24]. *Chelonus insularis* can lay eggs within the egg masses of FAW, affecting the FAW larvae until the fourth instar stage [25]. *Eiphosoma laphygmae* can attack the larval development of FAW, leading to their death [26]. Previous studies revealed that *C. insularis* and *E. laphygmae* emerged as prominent FAW parasitoids in the natural field environment, and played a critical role in contributing to FAW mortality [23]. However, the climate matching areas and niche similarity of *C. insularis* and *E. laphygmae* against FAW remain unclear in the native and invasive ranges, resulting in uncertainty regarding the introduction and selection of the release areas of the two parasitoids.

The present study integrated the ensemble model, hotspot analysis approach, and *n*-dimensional hypervolumes to assess the potential for the introduction of *C. insularis* and *E. laphygmae* and to provide insight into the selection of classical biocontrol agents for FAW worldwide. Specifically, our objectives were: (1) to identify the important environmental variables affecting the potential distribution of FAW and the two parasitoids; (2) to estimate the climate and hotspot matching areas of the two parasitoids against FAW under current climate conditions, thereby identifying the optimal control areas for FAW; (3) to demonstrate how climate change affects the optimal control areas for FAW involving the two parasitoids; (4) to compare the niche similarity of the two parasitoids against FAW.

2. Materials and Methods

2.1. Occurrence Records and Environmental Variables Data

Global occurrence records for FAW and the two parasitoids were compiled from commonly used online databases and previous literature (see Appendix A for detailed information). Potential sampling bias and the presence of record redundancy significantly affect the accuracy of model predictions [27]. Consequently, occurrence records with erroneous coordinates (such as the geographic centers of countries or capital cities) were eliminated. ENMTools package version 1.0 was selected to remove duplicate occurrence records and screen the records of each study species by randomly selecting one occurrence record in each 2.5 arc-minutes resolution grid cell [28].

The environmental variables that potentially affected the distribution patterns of FAW and the two parasitoids comprised 19 bioclimatic variables and the human influence index (HII). Current (1970–2000) and future bioclimatic variables (2021–2040, hereafter 2030s) at the global scale were compiled from the WorldClim database at a resolution of 2.5 arc-minutes, including three shared socioeconomic pathways, including SSP1-2.6, SSP2-4.5, and SSP5-8.5, based on the BCC-CSM2-MR global circulation model. The global-scale HII was obtained from the Global Human Influence Index (Geographic) v2 database (1995–2004) [29]. The HII for future climatic conditions (2030s) is not yet available. Consequently, we assumed that the HII would not change worldwide until the 2030s, following previous studies. To avoid the effect of the collinearity between two environmental variables on model performance, we used ENMTools to analyze their pairwise Spearman's correlations [28]. Seven less correlated environmental variables ($|r| < 0.8$) were retained to calibrate the SDMs (bio2, bio5, bio6, bio12, bio14, bio15, and HII) (Figure S1).

2.2. Climate and Hotspot Matching Analysis

To eliminate the uncertainty of extrapolation from different single models, we selected an ensemble model measure to estimate the climate matching areas between FAW and two parasitoids based on the four single models (including generalized additive model, generalized linear model, maximum entropy model, and random forest) in the ENMTML package [30]. The pseudo-absence records were randomly generated for each model with the ratio of 0.5 presence-absence from the background areas that were created as a 300 km buffer zone around the occurrences of each study species. For each study species, we selected the 5-fold cross-validation approach to calibrate the individual SDMs, that is, 80% for calibration and 20% for evaluation. We then evaluated model performance using the values of the Sorensen similarity index, area under the ROC curve (AUC) and true skill statistics (TSS) [30–32]. We selected to ensemble the final model using the mean weight approach with Sørensen index, thereby obtaining the final potential global suitable probability distribution for each study species. Based on the lowest-presence threshold (LPT), the ensemble model results for each species were converted into binary maps (including unsuitable and suitable areas) [33]. Spatial analysis tools were then used to obtain global climate matching areas between FAW and the two parasitoids. Finally, we selected the optimized hotspot analysis approach to produce a map of statistically significant hotspots using Getis-Ord Gi* statistical analysis in the potentially globally suitable areas for the two parasitoids. The optimal control areas for FAW were determined by identifying the hotspots of the two parasitoids that fell above the 90% confidence interval of the significance test. These hotspots should also overlap with potentially suitable areas of the FAW.

2.3. Niche Similarity and N-Dimensional Hypervolume Between FAW and Two Parasitoids

We estimated the niche similarity and multidimensional hypervolumes of FAW and two parasitoids using the "hypervolume" package [34]. First, the temperature (including bio2, bio5, and bio6) and HII variables were normalized using a z-score transformation. We then selected the Gaussian kernel density estimation approach to generate multidimensional hypervolumes of the FAW and the two parasitoids [34]. The bandwidth of each variable axis was used as a cross-validation method for the optimization calculations. Finally, the hypervolumes of FAW and two parasitoids' niches were compared using both a similarity index (Sørensen) and a hypervolume distance (centroid distance) metric [35].

3. Results

3.1. Ensemble Model Outperforms Single Models in Predicting Distribution of FAW and Two Parasitoids

Based on the 9407 occurrence records of FAW, and 231 (*C. insularis*) and 82 (*E. laphygmae*) of two parasitoids globally (Figure 1) and the environmental data (including five bioclimatic variables and a human influence index variable), the five single SDMs and an ensemble model with ensemble forecasting approach were constructed in biomod2 platform to estimate the climate matching areas of two parasitoids against FAW.

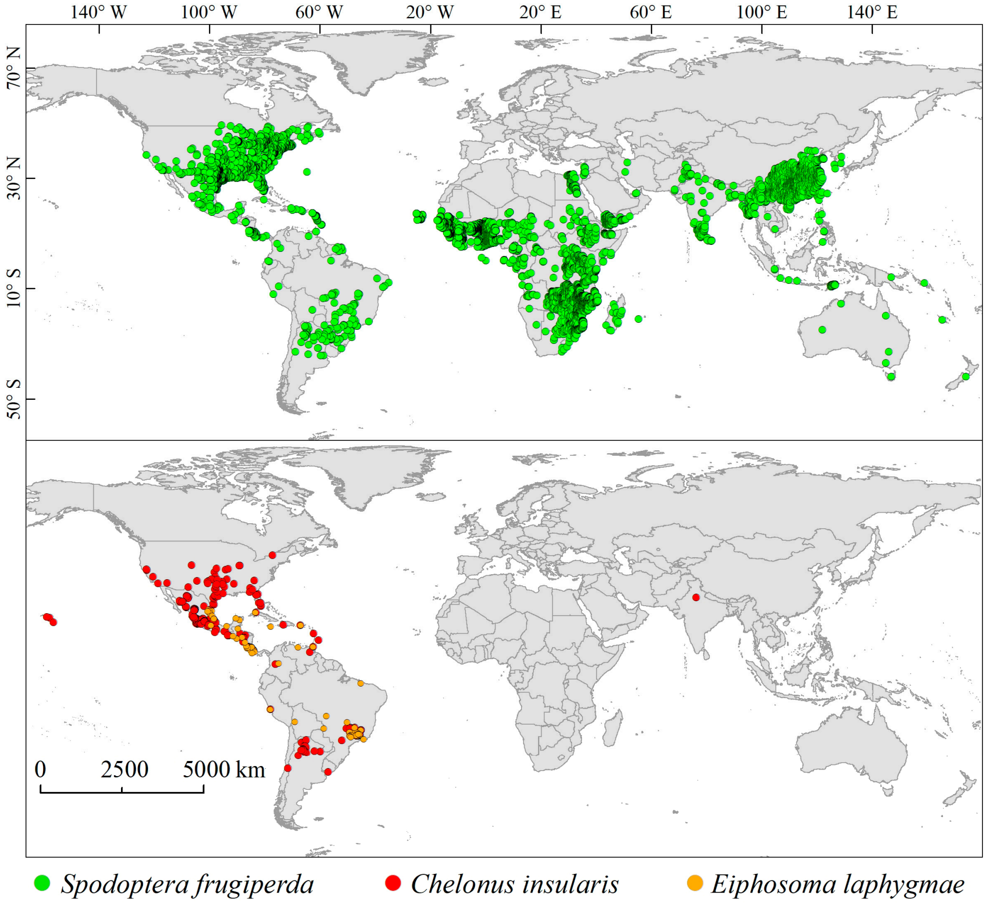

Figure 1. Global occurrence records of the fall armyworm (*Spodoptera frugiperda*) and two parasitoids (*Chelonus insularis* and *Eiphosoma laphygmae*).

We calculated the model performance using the Sørensen similarity index, AUC and TSS values (Figure 2a–c). Based on the results of the model evaluation for FAW and the two parasitoids, the ensemble model performance showed high predictive performance using ensemble models (median Sørensen similarity index value = 0.91, range = 0.88–0.92; median TSS value = 0.87, range = 0.83–0.87; median AUC value = 0.96, range = 0.93–0.97), which indicated that the prediction performance of the potential distribution of FAW and the two parasitoids with EM was reliable. The contributions of bioclimatic and HII variables to FAW and the two parasitoids are shown in Figure 2d. The high-ranking environmental variables for FAW and the two parasitoids were HII, bio5, and bio6, which had a significant impact on the distribution patterns of FAW and the two parasitoids.

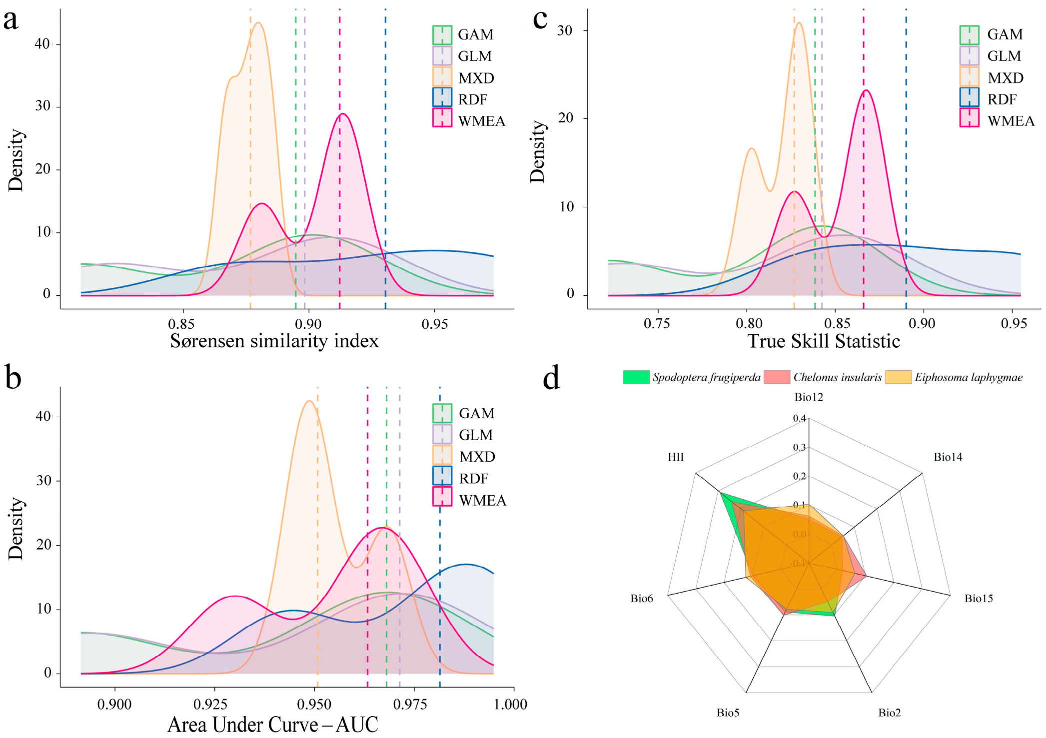

Figure 2. The Sørensen similarity index (**a**), area under the receiver operating characteristic curve (AUC) (**b**) and the true skill statistics (TSS) (**c**) for Generalized Additive Models (GAM), Generalized Linear Models (GLM), Generalized Boosting Regression (GBM), Maximum Entropy (MXD), Random Forests (RDF), Neural Network (NET), and the contribution values of environmental variables of *Spodoptera frugiperda* and two parasitoids (**d**).

3.2. Optimal Control Areas for FAW Using Two Parasitoids Across Continents

Potentially suitable areas for FAW and *C. insularis* were widely distributed across six continents, while those for the *E. laphygmae* were primarily distributed in America, Africa, and Asia (Figure S2).

Climate matching areas between FAW and *C. insularis* (outside of America) were primarily distributed in Europe, Africa, Asia, and Oceania. Hotspot matching areas between FAW and *C. insularis* (outside of America) were primarily distributed in most of sub-Saharan Africa, Mediterranean regions, eastern, southern, and southeastern Asia, and Oceania. The optimal control areas for FAW with *C. insularis* were 2299.59 × 10^4 km^2, accounting for 43.33% of the total potentially suitable areas of FAW globally (Figure 3).

Climate matching areas between FAW and *E. laphygmae* were primarily distributed in Africa and Asia. The hotspot matching areas between FAW and *E. laphygmae* (outside of America) were primarily distributed in western, central, eastern and southern Africa, and southern, southeastern, and eastern Asia. The optimal control areas for FAW with *E. laphygmae* were 1469.96 × 10^4 km^2, accounting for 27.7% of the total potentially suitable areas of FAW globally (Figure 4).

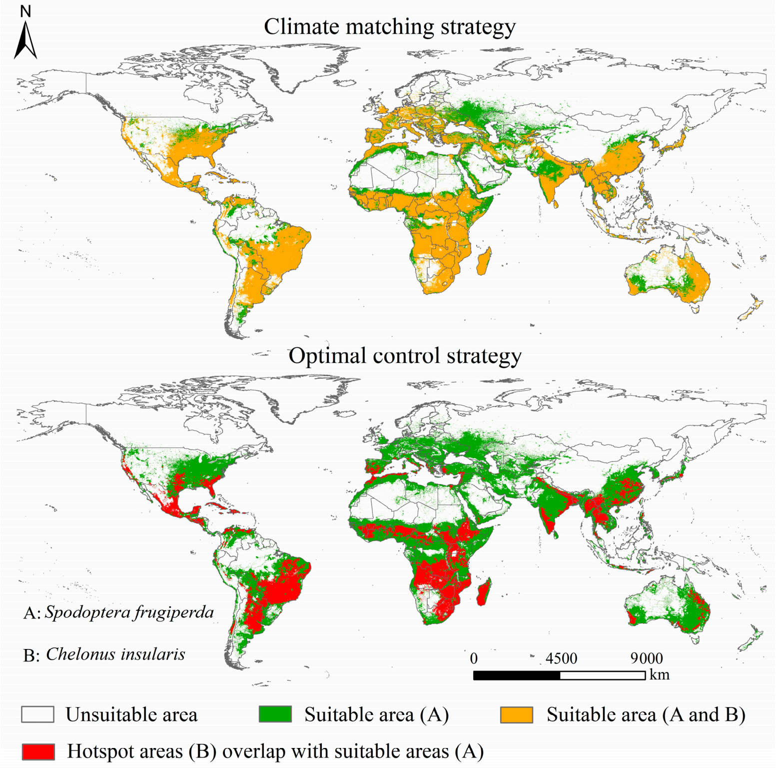

Figure 3. Climate and hotspot matching areas between *Spodoptera frugiperda* and *Chelonus insularis* under current climate conditions.

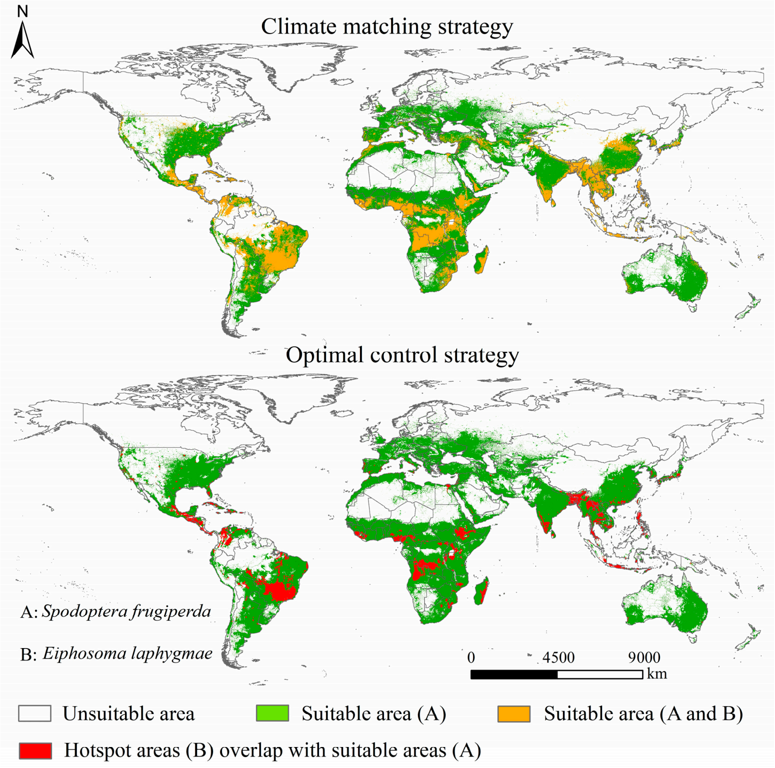

Figure 4. Climate and hotspot matching areas between *Spodoptera frugiperda* and *Eiphosoma laphygmae* under current climate conditions.

3.3. Optimal Control Areas Projected to Expand Toward High-Latitude Areas Under Future Climatic Conditions

The results indicated that the optimal control areas for FAW and the two parasitoids are projected to expand toward higher latitude areas under future climate conditions (2030s) (Figure 5). The optimal control areas for FAW with *C. insularis* (outside of America) are projected to increase in Mediterranean regions, China, and Australia (Figure 5). The increase in optimal control areas for FAW with *C. insularis* under the three future climatic scenarios (2030s), SSP1-2.6, SSP2-4.5, and SSP5-8.5, accounted for 12.04%, 14.02%, and 11.62% of the total optimal control areas for FAW with *C. insularis* under the current climatic conditions, respectively. Under future climatic conditions, it is expected that the optimal control areas for FAW with *E. laphygmae* are projected to increase in Republic of the Congo, South Africa, and China. The increased optimal control areas for FAW with *E. laphygmae* under various climatic scenarios (SSP1-2.6, SSP2-4.5, and SSP5-8.5) of the 2030s accounted for 14.58%, 14.21%, and 15.35% of the total optimal control areas for FAW with *E. laphygmae* under the current climate conditions, respectively.

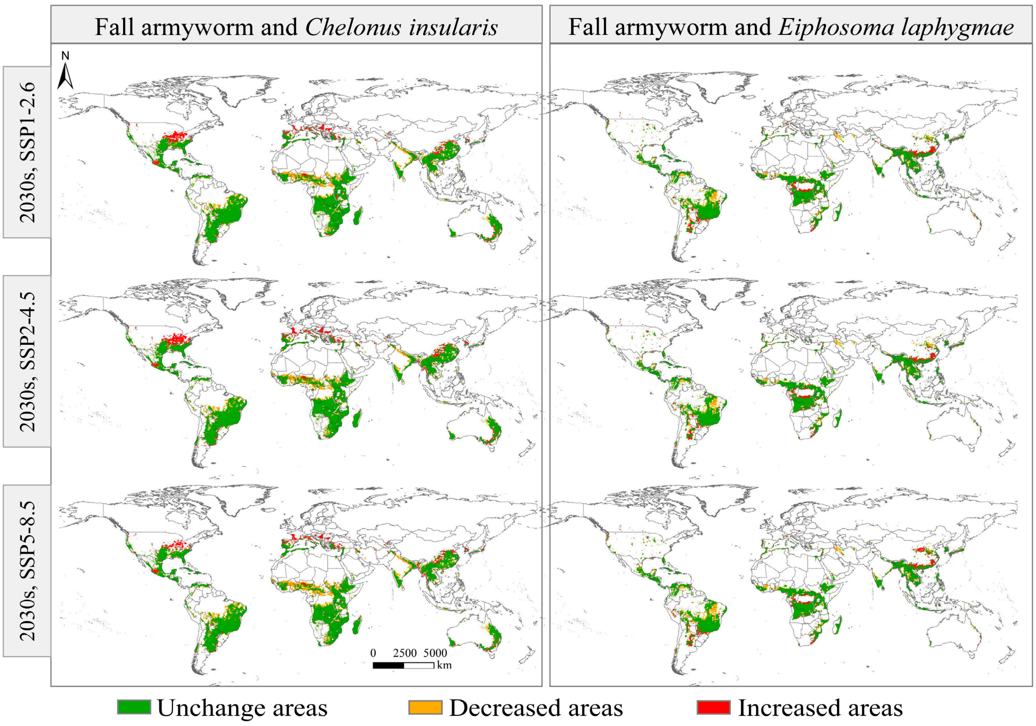

Figure 5. Changes in climate and hotspot matching areas between *Spodoptera frugiperda* and *Chelonus insularis*, and those between *S. frugiperda* and *Eiphosoma laphygmae* under future climatic conditions (2030s).

3.4. Niche Comparison and Suitable Range of Environmental Variables

Here, we selected multidimensional hypervolumes to quantify the niches of the FAW and the two parasitoids (Figure 6). Our findings revealed that the niches between FAW and *C. insularis* were more similar (Sørensen similarity index = 0.52) than those between FAW and *E. laphygmae* (Sørensen similarity index = 0.34) (Table 1). The centroid distance between FAW and *C. insularis* was shorter (1.17) than that between FAW and *E. laphygmae* (1.27) (Table 1).

The suitable ranges of the environmental variables for FAW and the two parasitoids were heterogeneous (Figure 7). Concerning temperature variables, *C. insularis* was better suited to a higher mean diurnal range (bio2) than FAW and *E. laphygmae*. The FAW was better suited to a higher maximum temperature in the warmest month (bio5) than *C. insularis* and *E. laphygmae*. Conversely, *E. laphygmae* was better suited to a higher minimum temperature in the coldest month (bio6) than *C. insularis* and FAW. Regarding the precipitation variables, *E. laphygmae* was better suited to higher annual precipitation (bio12) than *C. insularis* and FAW. *Eiphosoma laphygmae* was better suited to higher precipitation during the driest month (bio14) than FAW and *C. insularis*. *Chelonus insularis* and FAW were better suited to higher precipitation seasonality (bio15) than *E. laphygmae*. Both FAW and two parasitoids demonstrated high suitability to areas with high human influence index (HII).

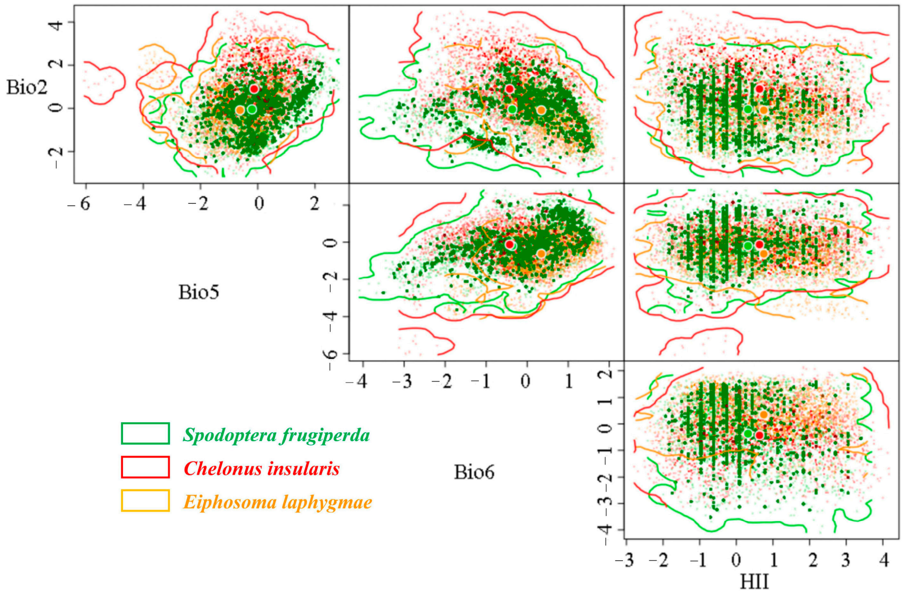

Figure 6. The multidimensional hypervolumes of niches for fall armyworm (*Spodoptera frugiperda*) and two parasitoids (*Chelonus insularis* and *Eiphosoma laphygmae*).

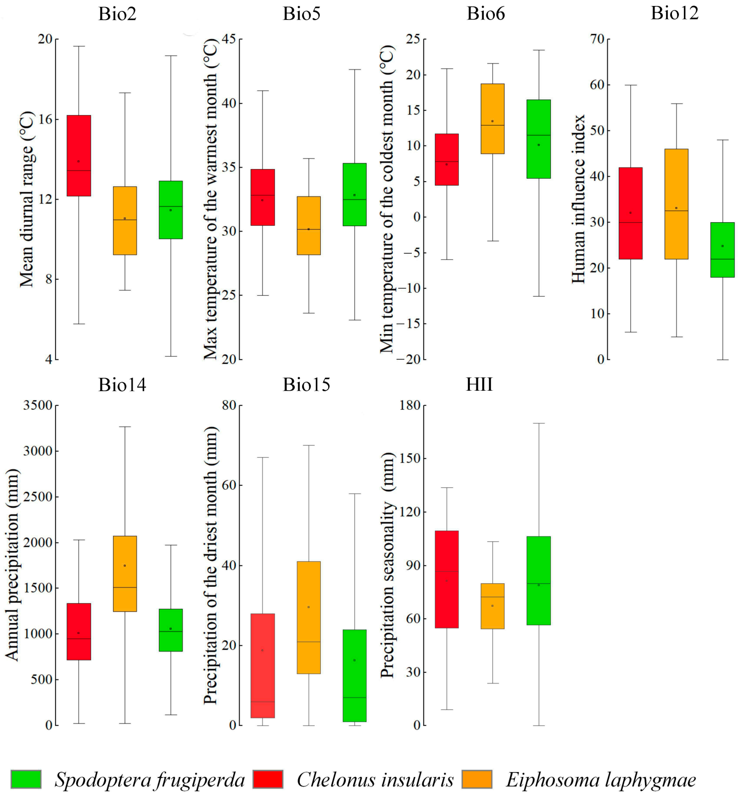

Figure 7. Suitable ranges of various environmental variables for *Spodoptera frugiperda* and two parasitoids (*Chelonus insularis* and *Eiphosoma laphygmae*).

Table 1. Sørensen similarity index and centroid distance metric for fall armyworm (*Spodoptera frugiperda*) and two larval parasitoids (*Chelonus insularis* and *Eiphosoma laphygmae*). Above the diagonal is the Sørensen similarity index, below the diagonal is centroid distance metric.

	S. frugiperda	***C. insularis***	***E. laphygmae***
Spodoptera frugiperda	—	0.52	0.34
Chelonus insularis	1.17	—	0.36
Eiphosoma laphygmae	1	1.27	—

4. Discussion

Classical biocontrol of FAW that introduces parasitoids or other natural enemies from its native range can significantly reduce damage and threats to agricultural ecosystems and food security worldwide [5,12]. This study estimated the climate and hotspot matching areas between FAW and two native parasitoids (*C. insularis* and *E. laphygmae*) worldwide and compared their niches by integrating SDMs, niche concepts, and hotspot analysis into the classical biocontrol strategy for FAW. Our findings can inform the decision-making process for selecting potential optimal control areas for FAW, with the two parasitoids within the invaded ranges of FAW. In addition, our study sheds light on how climate change may affect the optimal control areas for FAW with its two parasitoids.

4.1. Key Environmental Variables and Niche Similarity

Temperature, precipitation, and human activities significantly affected the distribution pattern, development, population density, and survival of FAW and the two parasitoids. The FAW population densities were lower during the dry season than those in the rainy season in in southern Florida and tropical America [36], and the development rate of FAW increased linearly with rising temperatures within the range of 18 to 30 °C [37]. The FAW cannot survive in the extremely low temperatures, indicating that have a great impact on its development and growth, while the minimal temperature allowing the development of all stages of FAW is between 12 and 13 °C [5,38]. Our findings indicate that FAW preferred the regions with higher annual precipitation and minimum temperature of the coldest month, which are key factors affecting its occurrence and distribution. Human activity has had a significant impact on the distribution of FAW and the two parasitoids, with the transport of FAW on direct commercial flights between the Americas and West Africa and their subsequent spread within Africa [39]. In addition, human activities significantly influence the planting patterns for the main hosts, which can indirectly affect the distribution patterns of FAW and the two parasitoids [40].

A previous study found that while being the predominant parasitoid in regions where its host overwinters (Southern Florida and Mexico), *C. insularis* exhibited a low abundance in the northern migratory areas of FAW [41]. *Chelonus insularis* would not be able to overwinter in Georgia and more northerly regions. *Eiphosoma laphygmae* is frequently found in tropical areas and rarely found in subtropical areas [23]. The above findings revealed that the low temperature would have a key role in the distribution of the two parasitoids. Our findings indicated that *C. insularis* and *E. laphygmae* prefer higher minimum temperatures in the coldest month, which greatly impact their potential distribution. Notably, FAW showed a higher tolerance to low temperatures than the two parasitoids, which may explain why the potential distribution of FAW was wider than that of the two parasitoids. Concerning the niche similarity of the two parasitoids and FAW, the niches of *C. insularis* and FAW were more similar compared to *E. laphygmae*. This can be attributed to the wider natural distribution of *C. insularis* in the Americas compared to that of *E. laphygmae* [42].

4.2. Classical Biocontrol Implications for FAW Management

Based on our findings, the optimal control areas for FAW with the two parasitoids were widely distributed in the native ranges (South America and North America), as well as in the invaded ranges (Africa and Asia). *Chelonus insularis* is widely distributed in the

Americas and is the most important parasitoid of FAW in its native range [42]. Our findings indicate that the optimal control areas for FAW with *C. insularis* are widely distributed in southern North America and South America. Optimal control areas for FAW with *C. insularis* are also widespread in most of sub-Saharan Africa, Mediterranean regions, eastern, southeastern Asia, and Oceania. If *C. insularis* had host specificity and a low risk of competition with native parasitoids in the above ranges, it would be a potential release area of *C. insularis* for the classical biocontrol.

Eiphosoma laphygmae is widely distributed in South America north of Argentina [23]. Our findings indicate that the optimal control areas for FAW with *E. laphygmae* are primarily distributed in more than six countries in South America, including Brazil, Colombia, Ecuador, Bolivia, Venezuela, and Peru. *Eiphosoma laphygmae* is absent in the USA and Argentina [43,44], and only a few sampled locations of *E. laphygmae* have been found in Mexico [45] Our findings indicate that Argentina is not the optimal control area for FAW with *E. laphygmae*, and only slightly optimal control areas are distributed in the southern USA and Mexico. *Eiphosoma laphygmae* is a promising biological agent against FAW in Africa and Asia [23]. We found that the optimal control areas for FAW with *E. laphygmae* were distributed in western, central, eastern and southern Africa, and southern, southeastern, and eastern Asia. If *E. laphygmae* had host specificity and a low risk of competition with native parasitoids in the above ranges, it would be a potential release area of *E. laphygmae* for the classical biocontrol of FAW.

The introduction of parasitoids, such as *E. laphygmae* and *C. insularis* into non-native ecosystems warrants careful consideration due to potential ecological risks, including competition with local species [23]. For instance, the broad host range of *Chelonus* species that have already adapted to FAW indicated that they could parasitize local *Spodoptera* species and interact with other native species in Africa and Asia [46,47]. The risk of competition between native parasitoids and introduced species, such as *E. laphygmae* and *C. insularis*, should be assessed to understand its potential impact on local ecosystems.

Climate change affects the effectiveness of classical biocontrol measures by affecting the distribution and population density of biocontrol agents and target species [48,49]. Our findings indicate that the optimal control areas for FAW with the two parasitoids will expand to high-latitude areas. Increases in temperature in high-latitude areas can decrease the overwintering mortality of biocontrol agents and their target species [50]. The potential suitable areas for biocontrol agents (i.e., *Telenomus remus*, *Trichogramma dendrolimi*, and *Trichogramma chilonis*) of the FAW will expand to high latitude areas in China [51]. Previous studies have reported that potentially suitable areas for FAW will expand in high-latitude areas under climate change [52]. The expansion of optimal control areas for FAW with the two parasitoids under climate change will increase their control effectiveness of introduction and release in high-latitude areas.

5. Conclusions

To better understand the potential biocontrol application of two native parasitoids (*C. insularis* and *E. laphygmae*) against FAW management. We selected the SDMs, *n*-dimensional hypervolumes, and hotspot analysis to estimate the climate and hotspot matching areas and niche similarity of *C. insularis* and *E. laphygmae* against FAW, thereby identifying the optimal areas for FAW with two parasitoids. Our findings indicated that the potential distributions of FAW and the two parasitoids were mainly attributed to HII, bio5, bio6, bio12. The optimal control areas for FAW with the two parasitoids worldwide, which were widely distributed in Africa, Mediterranean regions, Asia, and Oceania, which will expand in high latitude areas under future climate conditions. Prior to the introduction and release the biocontrol gents, the risk of their host specificity and competition with native species also need assess. Our findings provide a theoretical reference for estimate the potential release areas of the two parasitoids against FAW, and also can serve as a reference for screening the classical biocontrol agents and the development of sustainable management strategy for FAW worldwide. The introduction of parasitoids like *E. laphygmae* and *C.*

insularis into Africa and Asia requires careful consideration of their ecological impact, particularly potential competition with native parasitoids, such as those attacking local *Spodoptera* species. Additionally, the host specificity of these parasitoids, including the potential presence of cryptic species, must be investigated to prevent unintended effects on non-target organisms and local biodiversity.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agriculture14122276/s1, Figure S1: Pearson correlation coefficients of retained environmental variables. Figure S2: Potential suitable areas of *Spodoptera frugiperda* (a), *Chelonus insularis* (b), and *Eiphosoma laphygmae* (c) under current climatic conditions.

Author Contributions: Conceptualization, H.Z. and S.Y.; Methodology, H.Z. and S.Y.; Software, H.Z.; Validation, H.Z.; Formal Analysis, H.Z. and S.Y.; Investigation, H.Z. and S.Y.; Resources, H.Z. and S.Y.; Data Curation, H.Z. and S.Y.; Writing—Original Draft Preparation, H.Z. and S.Y.; Writing—Review & Editing, H.Z., S.Y., Y.Z., N.Y., H.L., J.G. and X.X.; Visualization, H.Z.; Supervision, W.L.; Project Administration, W.L.; Funding Acquisition, W.L. All authors have read and agreed to the published version of the manuscript.

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Data Availability Statement: The datasets generated in this study are available from the corresponding author upon request.

Conflicts of Interest: The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A

Data sources for the occurrence records of the fall armyworm (FAW) (Spodoptera frugiperda) and the two native parasitoids *Chelonus insularis* and *Eiphosoma laphygmae*. We collected occurrence records in three steps. First, their accepted scientific names ("*Spodoptera frugiperda* or fall armyworm"; "*Chelonus insularis* or *Chelonus texanus*"; "*Eiphosoma laphygmae*") were selected as the exact search phrases to search for related publications in the Web of Science (https://www.webofscience.com/, accessed 10 March 2023) and China National Knowledge Infrastructure (CNKI, https://www.cnki.net/, accessed 10 March 2023). Because we had no way to distinguish whether *Eiphosoma vitticolle* described in literature published before 2000 was *Eiphosoma laphygmae*, we did not use the occurrence point of *Eiphosoma vitticolle* as the data for *Eiphosoma laphygma*. Second, the occurrence records for FAW and the two native parasitoids were derived from the Barcode of Life Data Systems version 4 (BOLD, http://www.boldsystems.org/, accessed 10 March 2023), and Global Biodiversity Information Facility (GBIF) [53]. the occurrence records for FAW was also obtained from Food Agriculture Organization of the United Nations (https://data.apps.fao.org/catalog/dataset/fall-armyworm-scout-famews-global-latlon, accessed on 20 January 2023). Finally, we obtained 9407, 231, and 82 concurrence records of FAW, *C. insularis* and *E. laphygma*, respectively, were retained to model their potential distribution after the screen of the concurrence records of FAW and the two parasitoids.

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