Including Host Availability and Climate Change Impacts on the Global Risk Area of Carpomya pardalina (Diptera: Tephritidae)

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Fruit flies are a well-known invasive species, and climate-based risk modeling is used to inform risk analysis of these pests. However, such research tends to focus on already well-known invasive species. This paper illustrates that appropriate risk modeling can also provide valuable insights for flies which are not yet “on the radar.” Carpomya pardalina is a locally important cucurbit-infesting fruit fly of western and central Asia, but it may present a risk to other temperate countries where melons are grown. MaxEnt models were used to map the risk area for this species under historical and future climate conditions averaged from three global climate models under two shared socio-economic pathways in 2030 and 2070 from higher climate sensitivity models based on the upcoming 2021 IPCC sixth assessment report. The results showed that a total of 47.64% of the world’s land mass is climatically suitable for the fly; it could establish widely around the globe both under current and future climates with host availability. Our MaxEnt modeling highlights particularly that Western China, Russia, and other European countries should pay attention to this currently lesser-known melon fly and the melons exported from the present countries. The current and expanding melon trade could offer direct invasion pathways to those regions. While this study offers specific risk information on C. pardalina, it also illustrates the value of applying climate-based distribution modeling to species with limited geographic distributions.

Keywords: Carpomya pardalina, MaxEnt, potential geographical distribution, climate change, host availability management

INTRODUCTION

Climate change and biological invasion are two interlinked global challenges. Invasive species can cause far-reaching ecological and economic impacts in invaded regions (Mack et al., 2000; Cook et al., 2007; Hulme, 2009), while climate change can assist invasive species by increasing their probability of establishing if areas which are currently environmentally unsuitable become more suitable (Early et al., 2016; Hulme, 2017). This is particularly true for insects, which depend on local environmental conditions for survival and development within their thermal limits (McGeoch et al., 2010; Cornelissen et al., 2019). Because of the negative impacts pest insects have on agriculture, and their well-documented invasiveness (Bradshaw et al., 2016), studies on the impacts of climate change on the distribution of agricultural insects is considered a fundamental aspect of assessing the
Carpomya pardalina but currently unknown risk to other regions where melons are restricted geographic distribution, the fly constitutes a potential et al., 2006; Baris and Cobanoglu, 2013). While currently with a
of 5–15 cm, and prefers the first 6 cm of soil (Stonehouse et al., 2006; Baris et al., 2016). Generally, the pest causes crop losses
around 10–25%, but crop losses of up to 100% can occur (Toyzhigitova et al., 2019). A total of 34 occurrence points of
C. pardalina were identified across the following countries: Afghanistan, India, Iran, Iraq, Jordan, Kazakhstan, Kyrgyzstan,
Lebanon, Pakistan, Syria, Tajikistan, Turkmenistan, Uzbekistan, Armenia, Azerbaijan, Cyprus, Georgia, central and southern
Russia, Turkey, and Ukraine (Supplementary Table 1 and Figure 1A). The occurrence data were assigned to 9 km x 9 km
climate data grids in ArcGIS 10.2 (ESRI Inc., Redlands, CA, United States) to reduce spatial autocorrelation and sample bias.
Climate data were accessed from the WorldClim website2 version 2.1. Historical (near current) climate data included
19 bioclimatic variables with a spatial resolution at 5 arc-min (9 km at the equator) which were the average monthly climate
data for minimum, mean, and maximum temperature and precipitation for the period 1970–2000 (Fick and Hijmans, 2017).
Multicollinearity among climate variables could hinder species-environment relationships analysis (Heikkinen et al., 2006).
Principal component analysis (PCA) and correlation analysis were conducted in IBM SPSS Statistics version 222 to select a set
of variables with Pearson correlation coefficients having absolute values < 0.8 that were uncorrected and eco-physiologically
relevant for modeling (Qin et al., 2019).

Future climate conditions were assessed with global climate model (GCM) data downscaled from Coupled Model
Intercomparison Projects (CMIP) 6 (World Climate Research Programme)4 with WorldClim v2.1 as the baseline climate. The
2013 IPCC fifth assessment report (AR5) featured climate models from CMIP5, while the upcoming 2021 IPCC sixth
assessment report (AR6) will feature the new state-of-the-art CMIP6 models. The (CMIP) 6 models used in our study have
notably higher climate sensitivity than models in CMIP5, and

MATERIALS AND METHODS

Occurrence Data and Climate Data

The species occurrence data of C. pardalina were obtained from the EPPO Global Database (EPPO)1 and literature (Akkaya and
Uygur, 1999; Stonehouse et al., 2006; Pavlov, 2012; Baris et al., 2016; Toyzhigitova et al., 2019). The occurrence data were assigned to 9 km x 9 km climate data grids in ArcGIS 10.2 (ESRI Inc., Redlands, CA, United States) to reduce spatial autocorrelation and sample bias.

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1https://gd.eppo.int/taxon/CARYPA/distribution
2http://worldclim.org/
3https://www.ibm.com/support/docview.wss?uid=swg21646821
4https://www.wcrp-climate.org/wgcm-cmip/wgcm-cmip6

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Contribute to the projections of greater warming in this century (around 0.4°C warmer than similar scenarios run in CMIP5) (Eyring et al., 2016; Hausfather, 2019), which is why we chose them. To reduce the uncertainties arising from different global climate model (GCM) projections (Guisan et al., 2013), we selected three GCMS: BCC-CSM2-MR (BCC), IPSL-CM6A-LR (IP), and MIROC-ES2L (MI), estimated for 2030 (average for 2021–2040) and 2070 (average for 2061–2080) to offer a wide range of temperature and rainfall changes. Data editing and conversion were conducted in ArcGIS 10.2.

The models were each run under two shared socio-economic pathways (SSPs) updated from the IPCC fifth assessment report (AR5): the first SSP was a scenario with very high greenhouse gas emissions (SSP5-8.5), and the second SSP was a stringent mitigation scenario (SSP1-2.6).

Host data were downloaded from FAOSTAT. Four items including watermelons; pumpkins, squash, and gourds; melons, other (including cantaloupes); and cucumbers and gherkins. The production for each country and export quantity for the present countries were averaged for the last 5 years (2015–2019).

MaxEnt Modeling

The potential geographical distribution of C. pardalina under historical and projected future climate scenarios was conducted in MaxEnt (v3.4.4) with presence-only data (Phillips et al., 2006). In this study, models were calibrated using 25% random test percentage, 5,000 maximum iterations, the 10 percentile training presence threshold rule, and 10 replicates under the subsample run type following Young et al. (2011) and Qin et al. (2019). Fifty-thousand randomly chosen background points in areas of C. pardalina current occurrence were selected, as recommended in MaxEnt studies that are carried out on a global scale (Rank et al., 2020). The MaxEnt “fade-by-clamping” option was used to eliminate extrapolations outside of the environmental range (Owens et al., 2013; Rank et al., 2020). ENMeval, an R package, was used to avoid overfitting and improve the performance of MaxEnt by tuning the regularization multiplier (RM) and feature types (Muscarella et al., 2014; Wei et al., 2020). The feature combinations (FC) included linear (L), quadratic (Q), product (P), threshold (T), and hinge (H). The RM values were set from 0.5 to 4 with increments of 0.5. “Checkerboard2” was used to calculate the Akaike information criterion (AICc) values. The lowest delta AICc values corresponding to RM = 0.5 and FC = LQ were applied to the final model (Supplementary Figure 1).

Model performance was evaluated by area under receiver operating characteristic (ROC) curves with (AUC) values averaged over the replicated runs. AUC values range from 0 to 1: models with an AUC value of 0.5 represent a model with discrimination ability no better than random, AUC values from 0.7 to 0.9 indicate satisfactory to moderate model performance, and values > 0.9 indicated high performance (Swets, 1988; Pearce and Ferrier, 2006; Peterson et al., 2008). It should be noted that the AUC calculated by MaxEnt can be overestimated, i.e., not present the “true” AUC, if background data used by the model are not an accurate reflection of true absences. Moreover, AUC weighs omission and commission errors equally, which should,
Relative contributions of the selected bioclimatic variables to the model distribution of *C. pardalina* were conducted for variable selection. In PCA, the first four principal components explained 90.033% of the total variance with the first and fourth components mainly attributed to temperature (bio1, bio5, bio6, bio8, bio10, bio11) and the second and third attributed to precipitation (bio12, bio13, bio14, bio16, bio17). The Eigen vector with the highest explanatory value from each of the first four principal components (to avoid correlation between variables) were selected for MaxEnt modeling (Table 1). Finally, bio1 (annual mean temperature), bio8 (mean temperature of wettest quarter), and bio16 (precipitation of wettest quarter) positively related and bio14 (precipitation of driest month) negatively related were selected for modeling.

**RESULTS**

**Bioclimatic Variables Selection**

Principal component analysis and correlation analysis of 19 bioclimatic variables were conducted for variable selection. In PCA, the first four principal components explained 90.033% of the total variance with the first and fourth components mainly attributed to temperature (bio1, bio5, bio6, bio8, bio10, bio11) and the second and third attributed to precipitation (bio12, bio13, bio14, bio16, bio17). The Eigen vector with the highest explanatory value from each of the first four principal components (to avoid correlation between variables) were selected for MaxEnt modeling (Table 1). Finally, bio1 (annual mean temperature), bio8 (mean temperature of wettest quarter), and bio16 (precipitation of wettest quarter) positively related and bio14 (precipitation of driest month) negatively related were selected for modeling.

**Model Performance and Variable Contributions**

The averaged AUC value over 10 replicates was 0.930, and the mean value for partial AUC at 0.05 over 1000 replicates was 0.9257608 ($p < 0.001$), indicating a good performance of the MaxEnt models for predicting the risk area of *C. pardalina* (Figure 2A and Supplementary Figure 2). A “fixed cumulative value 5 Cloglog threshold” value of 0.08 was obtained. The Jackknife test indicated that the environmental variable with the highest gain when used in isolation was bio1 (annual mean temperature) which also decreased the gain the most when it was omitted (Figure 2B). Therefore, bio1 appeared to have the most useful information by itself and the most information that was not present in the other variables. The estimation of relative contributions of the selected bioclimatic variables to the MaxEnt model were 65.5% (bio1, annual mean temperature), 25.5% (bio8, mean temperature of wettest quarter), 6.5% (bio14, precipitation of driest month), and 2.5% (bio16, precipitation of wettest quarter).

**Potential Geographical Distribution Under Historical Climate Including Host Availability**

The MaxEnt-predicted potential geographical distribution of *C. pardalina* under near-current climate conditions (1970–2000) is shown in Figure 1A. We categorized risk areas into four levels: negligible risk (0.00–0.08), low risk (0.08–0.23), medium risk (0.23–0.62), and high risk (0.62–1.00) considering the MaxEnt plots of this species (Supplementary Figure 3), Jenks Natural Breaks Classification, and “Fixed cumulative value 5 Cloglog threshold.” Under near-current climate conditions, it was predicted that *C. pardalina* could potentially establish in Asia, Africa, North America, South America, Europe, and Oceania in ArcGIS 10.2. The host production for each country was classified and showed using ArcGIS 10.2. The host export quantity for the present countries was displayed in Origin Lab after logarithm.

**Table 1**

| Bioclimatic variables | Principal components |
|-----------------------|----------------------|
|                       | 1       | 2       | 3       | 4       |
| Annual mean temperature (bio1)* | 0.940   | 0.140   | 0.212   | 0.199   |
| Mean diurnal range (bio2) | 0.610   | −0.144  | 0.570   | −0.158  |
| Isothermality (bio3)     | 0.729   | 0.490   | 0.202   | −0.153  |
| Temperature seasonality (bio4) | −0.463  | −0.783  | 0.219   | 0.012   |
| Max temperature of warmest month (bio5) | 0.827   | −0.239  | 0.393   | 0.130   |
| Min temperature of coldest month (bio6) | 0.908   | 0.383   | 0.018   | 0.086   |
| Temperature annual range (bio7) | −0.298  | −0.774  | 0.409   | 0.028   |
| Mean temperature of wettest quarter (bio8)* | 0.215   | 0.202   | −0.084  | 0.885   |
| Mean temperature of driest quarter (bio9) | 0.784   | −0.200  | 0.250   | −0.254  |
| Mean temperature of warmest quarter (bio10) | 0.847   | −0.230  | 0.330   | 0.199   |
| Mean temperature of coldest quarter (bio11) | 0.911   | 0.373   | 0.085   | 0.128   |
| Annual precipitation (bio12) | −0.163  | 0.860   | −0.396  | 0.013   |
| Precipitation of Wettest Month (bio13) | 0.020   | 0.941   | −0.009  | 0.219   |
| Precipitation of driest month (bio14)* | −0.290  | 0.178   | −0.914  | −0.020  |
| Precipitation seasonality (bio15) | 0.595   | 0.467   | 0.578   | 0.084   |
| Precipitation of wettest quarter (bio16)* | 0.006   | 0.944   | −0.023  | 0.191   |
| Precipitation of driest quarter (bio17) | −0.296  | 0.239   | −0.900  | 0.051   |
| Precipitation of warmest quarter (bio18) | −0.252  | 0.437   | −0.624  | 0.536   |
| Precipitation of coldest quarter (bio19) | −0.043  | 0.667   | −0.119  | −0.587  |

*Four uncorrelated variables used in the analysis, values in bold were above 0.8 explaining more variance.

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1.http://shiny.conabio.gob.mx:3838/nichetoolb2/
2.http://www.natureearthdata.com/
west Asia, central Asia, and most parts of China and neighboring countries. European countries, most of Africa except the western part, Congo basin, and the Sahara, southern Australia and New Zealand, the United States, Mexico, and the southern part of South America were also suitable for the species (Figure 1A). Among these areas, central Asia, the coastal Mediterranean, western China, southern Australia, western United States, Chile, and southern Argentina exhibited a relatively high risk for *C. pardalina* establishment.

The extent of the land area that was climatically suitable for *C. pardalina* under near-current climate conditions was quantified for each continent (Table 2). A total of 47.64% of the world's land mass (excluding Antarctica), or $6371.87 \times 10^4$ km$^2$, was climatically suitable. Asia contributed most of the risk area, 31.36% of its total land area, followed by Africa (21.88%), Europe (17.35%), North America (16.40%), South America (8.55%), and Oceania (4.46%) (Table 2).

The average host production (2015–2019) including watermelons; pumpkins, squash, and gourds; melons, other (including cantaloupes); and cucumbers and gherkins for *C. pardalina* from 159 countries are shown on the map (Figure 1B). Almost all the areas predicted to be at risk were also able to offer hosts for *C. pardalina*. The host production was above one million tons in present countries Turkey, India, Russia, Uzbekistan, and Iran and absent countries China, Vietnam, and Brazil. The average host export quantity (2015–2019) from present countries after logarithm is displayed in Figure 1C. Among the 20 present countries of *C. pardalina*, the host export quantity from Iran was 0.78 million tons, followed by Turkey, Jordan, Kazakhstan, and Uzbekistan, where the export quantity was above 0.05 million tons. Among the four items, watermelon export quantity was the highest, up to 0.65 million tons from the 20 countries.
Climate Change Impact on the Potential Geographical Distribution

The potential geographical distribution maps of C. pardalina under a range of possible future climate scenarios for 2030 and 2070 are displayed in Figure 3. The potential range of C. pardalina was predicted to increase in America and Europe, and decrease in Asia, Africa, and Oceania (Figure 3). In Asia, the suitable area expanded in southern and central Russia, but reduced in south China, south Asia, and southeast Asia. In Africa, the risk area decreased notably in southern Africa and the risk severity also declined in northern Africa. In North America, the risk area increased in north-eastern Canada; while in South America at-risk areas decreased in Brazil and Argentina. In Europe, risk areas and threat changed minimally. In Oceania, the risk area retracted to southern temperate Australia (Figure 3 and Table 2).

The total global suitable land mass decreased by 824.59 × 10^4 km^2, or 0.06% under scenario SSP126 (stringent management of greenhouse gas emissions) and 348.58 × 10^4 km^2, or 0.03% under scenario SSP585 (high greenhouse gas emissions) in 2030; and decreased by 528.96 × 10^4 km^2, or 0.04% under scenario SSP126 and 723.94 × 10^4 km^2, or 0.05% of land area under scenario SSP585 in 2070 (Table 2).

**Table 2** Projected risk area globally for Carpomya pardalina under near-current and future (2030 and 2070) climate scenarios expressed as an area (10^4 km^2) and as a percentage of the total area per continent, as predicted by MaxEnt modeling.

| Region          | Near-current (1970–2000) | 2030-ssp126 | 2030-ssp585 | 2070-ssp126 | 2070-ssp585 |
|-----------------|--------------------------|-------------|-------------|-------------|-------------|
| Risk area /10^4 | % Total area             | Risk area /10^4 | % Total area | Risk area /10^4 | % Total area |
| km^2             |                          | km^2         |             | km^2         |             |
| Asia            | 1997.91                  | 31.36        | 1782.92     | 32.14        | 1874.94     | 31.13        |
| Africa          | 1394.17                  | 21.88        | 1009.92     | 18.21        | 1124.02     | 18.66        |
| North America   | 1044.67                  | 16.40        | 1009.80     | 18.20        | 1105.00     | 18.35        |
| Latin America   | 544.57                   | 8.55         | 379.26      | 6.84         | 414.94      | 6.89         |
| Europe          | 1105.59                  | 17.35        | 1138.38     | 20.52        | 1253.08     | 20.80        |
| Oceania         | 284.37                   | 4.46         | 226.40      | 4.08         | 250.72      | 4.16         |
| World^4         | 6371.87                  | 47.64        | 5547.28     | 41.48        | 6023.29     | 45.04        |

SSP5-8.5 refers to a Shared Socio-economic Pathway (SSP) scenario from the IPCC sixth assessment report (AR6) for a scenario with very high greenhouse gas emissions; SSP1-2.6 refers to a second SSP scenario with stringent mitigation of greenhouse gas emissions.

^4The area given for the world excludes Antarctica.

**DISCUSSION**

While currently restricted to central Asia and far eastern Europe, MaxEnt modeling predicts that C. pardalina could establish widely around the globe, both in current and future climates. While invasion pathways for C. pardalina from central Asia to the Americas and Oceania are not obvious, there are very obvious and direct invasion pathways for the fly into Europe and China with host availability.

Within Europe, which imports melons from countries where the fly is already established (Toyzhiyitova et al., 2019), most countries are at risk and Portugal, Spain, France, Italy, and England are at high or medium risk. Melons and other host plants of C. pardalina are widely grown in the EPPO region, in particular in southern Europe and around the Mediterranean Basin which were predicted to be risk areas (EPPO, 2013; Figure 1B). The risk area increased significantly in Russia under climate change which was also a big melon producer and exporter (Figures 1, 3). Carpomya pardalina was formerly, but is not currently, on the EPPO Alert list. Our climate modeling, and the possible transportation of infected melons through trade (Talhuk, 1969; Abdullah et al., 2007), suggests that this fly should be of much greater priority to Europe than is currently the case.

Within Asia, most of China is suitable for this species, while western China is predicted as a medium risk area. Carpomya pardalina is currently absent in China and is a listed quarantine pest. The General Administration of Customs in China has published requests to import melons from Kyrgyzstan in 2018 and Uzbekistan in 2019, for which C. pardalina was on the quarantine pest list of concern. Based on its modeled ability to establish in China and host availability (Figure 1), this quarantine concern is technically justified.

With respect to Chinese domestic quarantine, Xinjiang Province should be of particular concern. Located in western China, Xinjiang has borders with eight countries, including Kazakhstan, Kyrgyzstan, Tajikistan, Afghanistan, Pakistan, and India, all of which are entirely or partially within C. pardalina’s current distribution range. Xinjiang acts as a trade center between China and Central Asia, West Asia, and Europe, and due to its special geographical position suffers extensively from damage caused by invasive species. Ninety-five invasive species were reported from Xinjiang during the last 60 years, with a frequency of 2.88 new invasive species per year since 1990 (Guo et al., 2017). The “one belt, one road” development strategy offers more opportunity for invasive species as the number of China-Europe freight trains entering and exiting Khorgos Port, Xinjiang, already numbering > 4,500 in 2020, increases. With respect to the current study, Xinjiang province is famous for melons, which are the hosts of C. pardalina. Therefore, the surveillance...
and early warning of *C. pardalina* should be strengthened in Xinjiang Province to stop the likely entry and subsequent spread of the fly into China.

Fruit flies are highly invasive organisms and very significant effort goes into risk analysis, quarantine, and phytosanitary treatments in order to minimize their spread (Godefroid et al., 2015; Qin et al., 2015; Hill et al., 2016; Fang et al., 2019). Nevertheless, as demonstrated through the scientific literature and the priorities of national and regional plant protection organizations (as illustrated on their websites), nearly all attention is paid to just a handful of the 250 + tephritids which are known to have pest status. For just one of these lesser flies, *C. pardalina*, our study predicts that risk areas climatically suitable for the fly occur across the globe both currently and under future climate change scenarios with host availability.

Annual mean temperature (bio1) is the most important climatic variable contributing to the current global distribution of *C. pardalina*. Temperature variables contributed more than precipitation indicating temperature may be the driving force for this species. CMIP6 models used in this study project a “well-below 2°C” temperature change under the SSP1-2.6 scenario and a mean warming of 5.0°C this century (Eyring et al., 2016; Hausfather, 2019). Unlike tropical tephritid fruit flies, *C. pardalina* was predicted to not be suitable in southeast Asia and suitable in western Siberia under climate change, suggesting that this species may prefer cool conditions. Developmental temperature and survival threshold for the life cycle of *C. pardalina* needs to be carried out in order to better understand the distribution pattern of this species.

In addition, climatic factors and host availability were considered in the current study. Geographical factors, land use, human factors, and biotic factors will also have influences on the distribution of species (Chen et al., 2020; Liu et al., 2020). MaxEnt is popular among species distribution models (SDMs) to predict suitable habitats for species. There are also regression, machine learning, and classification methods used in other SDMs; model

![FIGURE 3](https://example.com/figure3.jpg)
FIGURE 3 | Potential geographical distribution of Carpomya pardalina in 2030 and 2070 under future climate conditions as predicted by MaxEnt modeling. Mean predicted results are from three global climate models [BCC-CSM2-MR (BCC), IPSL-CM6A-LR (IP), MIROC-ES2L (MI)] which were modeled under (A) 2030-SSP126; (B) 2030-SSP585; (C) 2070-SSP126; and (D) 2070-SSP585. White indicates negligible risk areas, yellow indicates low risk areas, orange indicates medium risk areas, and red indicates high risk areas. SSP5-8.5 refers to a Shared Socio-economic Pathway (SSP) scenario from the IPCC sixth assessment report (AR6) for a scenario with very high greenhouse gas emissions; SSP1-2.6 refers to a second SSP scenario with stringent mitigation of greenhouse gas emissions.

**CONCLUSION**

In conclusion, our MaxEnt modeling highlights particularly that Western China, Russia, and other European countries should pay attention to this currently lesser-known melon fly and the melons exported from the present countries. While currently restricted in its geographic distribution, which likely explains its low international recognition, already existing and growing trade pathways could easily move this fly via melon exports east into China or west into Europe. Besides producing specific recommendations for *C. pardalina*, this study should also be used to alert quarantine agencies of the likely threats posed by other less-known fruit fly species.

**DATA AVAILABILITY STATEMENT**

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

**AUTHOR CONTRIBUTIONS**

YQ and ZL conceived and designed the research. YQ and YZ analyzed the data and wrote the first draft. YQ, YZ, AC, ZZ, and
ZN discussed the idea and reviewed the draft. All authors revised the manuscript and approved the final version.

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**SUPPLEMENTARY MATERIAL**

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fevo.2021.724441/full#supplementary-material

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