Will Global Climate Change Favor the Kissing bug (Triatoma infestans)?

Küresel iklim Değişikliği Öpücük Böceğinin (Triatoma infestans) Yararına Mı Olacak?

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Öz

Öpücük böceği olarak bilinen *Triatoma infestans*, Güney Amerika'da Chagas hastalığının başlıca sebeplerinden biridir. Bu türün salgıladığı parazit nedeniyle Dünya Sağlık Örgütü tarafından çok sayıda koruma çalışması yapılmıştır. Ancak koruma çalışmalarının modelleme tabanlı ve yeterli düzeyde olmadığı tespit edilmiştir. Bu çalışma, küresel ölçekte değişen iklim koşullarının öpücük böceği üzerindeki etkilerini belirlemek amacıyla yürütülmüştür. Modelleme yöntemi olarak MaxEnt, iklim değişkenleri olarak ise Chelsa V2.1 tercih edilmiştir. Öpücük böceği, günümüz modeli eğitim/test veri seti AUC değerleri 0,867/0,866 olmasıyla "iyi" model kategorisindedir. Modele katkı sağlayan değişkenlerin sırasıyla yıllık ortalama sıcaklık, mevsimsel sıcaklık, yağış mevsimselliği, engebelilik ve yükseklik olduğu tespit edilmiştir. Mevcut modele katkıda bulunan değişken değer sonuçlarına göre, 2100 yılı için Chelsa iklim zarfı modelleri simüle edilmiştir. Sonuç olarak öpücük böceğinin yayılışının 2100 yılına kadar farklı iklim zarfı modellerine göre genişlediği belirlenmiştir. Bu çalışma, öpücük böceğinin 2100 yılına kadar yayılmasıyla Chagas hastalığından kaynaklanan ciddi sağlık sorunlarının ortaya çıkacağına dair alarmlar vermektedir.

Anahtar Kelimeler: Böcek, Chagas hastalığı, Chelsa iklim, Habitat uygunluk

Abstract

Triatoma infestans, known as the kissing bug, is one of the main causes of Chagas disease in the South America. Due to the parasite secreted by this species, many protection studies have been carried out by the World Health Organization. However, it has been determined that the conservation efforts are not model-based and at a sufficient level. This study was carried out to determine the effects of changing climate conditions on the kissing bug on a global scale. MaxEnt was preferred as the modelling method and Chelsa V2.1. was preferred as the climate variables. Kissing bug is in the "good" model category with AUC values of 0.867/0.866 on the training/test dataset of current model. According to the variable value results contributing to the present model, the Chelsa climate envelope models for the year 2100 were simulated. As a result, it has been determined that the distribution of the kissing bug will expand according to different climate envelope models by the year 2100. This study raises alarms that serious health problems from Chagas disease will emerge in 2100 due to the expansion of the kissing bug.

Keywords: Insecta, Chagas disease, Chelsa climate, Habitat suitability

1. Introduction

Triatoma infestans, belonging to the Triatominae (Hemiptera: Reduviidae) family of the Insect class of the Animal kingdom, are generally known as triatomines or kissing bug (Lorenzo and Lazzari, 1999; Lazzari, 2021). The oldest wild population distribution of *Triatoma infestans* is assumed to be the subtropical and dry Cambodian forests of Argentina, Paraguay and Bolivia (Usinger et al., 1966; Schofield, 1988; Noireau, 2009). Today, this insect species is generally distributed in the Andean valley in South America. In this context, because of genome size and rDNA focused studies, it has been proven that *Triatoma infestans* is distributed in the Andean valley (Dujardin et al., 1998; Bargues et al., 2006). *Triatoma infestans*, known as kissing bug, live in bird nests, rocky areas, rotten trees and caves where bats live in this region. In addition, it is possible to encounter kissing bugs in chicken coops, rodent nests and dog kennels in their geography. Thus, in South America, kissing bugs have been identified as a symbol of poverty (homes with dirt floors and no windows) (Zeledon and Rabinovich, 1981; Gürtler et al., 1999; Cohen and Gurtler, 2001). Being an invasive species, they have a nasty habit of entering people's homes in these areas, and kissing bugs are the most common vector of Chagas disease in the Americas (Dias et al., 2002).

Although its name may seem harmless, the "kissing bug" is a type of insect whose bite can be dangerous, even fatal to humans. Because this insect is a carrier of the protozoan parasite Trypanosoma cruzi, which causes Chagas disease (Buarque et al., 2013; Elliot et al., 2015; Paranaiba et al., 2019). Thanks to the parasite it provides, it starts with swelling of people's eyelids, fever and pain, then causes malnutrition, heart diseases and even heart failure. In this context, Chagas disease, which is spread by the kissing bug, has been reported to cause more deaths in America than all other parasitic diseases (WHO, 2003). However, little is known about the epidemiology of transmission of Chagas disease in the South America (Strasen et al., 2014).

Since 1991, it has been one of the leading subjects of conservation efforts to eliminate Chagas disease caused by the kissing bug (Vassena et al., 2000). Later, in 2002, a control program was initiated due to the death of a baby due to Chagas disease in an urban community. The control program has focused on urban centers and their surroundings, where people live densely, rather than the rural areas of South America. Despite the application of insecticide to densely populated areas, it has been noted that new measures may be needed to reduce the size of the kissing bug population and prevent the epidemics it causes (Levy et al., 2006). In this context, it has been stated that temperature and relative humidity affect the habitat preference of the kissing bug, the vector of Chagas disease (Lorenzo and Lazzari, 1999).

Climatic variables such as temperature and precipitation affect the habitat preference and distribution of many insect species, as well as the kissing bug (Lorenzo and Lazzari, 1999; Stange and Ayres, 2010; Andrew and Hill, 2017; Pureswaran et al., 2018). Changing climate conditions on a global scale cause the habitats of some insect species to shrink, fragment or even disappear (Raven and Wagner, 2021). At the same time, climate change has a direct or indirect effect on the distribution of wild animal species (Acarer, 2024a; Acarer, 2024b; Acarer, 2024c; Acarer and Mert, 2024). Although global climate models are so effective on natural ecosystems, no study has been found that reveals the habitat preference of the kissing bug under the influence of global climate models. Chelsa (Climatology at High Resolution for the Earth's Land Surface Areas) climate models are generally preferred in studies aiming to reveal the effects of global climate change on insect and wild animal species (Dubos et al., 2023; Sbaraglia et al., 2023). Chelsa climate models with high resolution (~1 km) are important for researchers, scientists and decision makers who want to analyze climatic changes in detail (Karger et al., 2017; Karger et al., 2021; Karger et al., 2023). In this context, species distribution modeling and mapping come to the fore to reveal the effects of climate change on insect and wild animal species (Özkan, 2012).

Species distribution models are an increasing method of determining and mapping current and potential distribution areas with presence-absent and only presence data of target species on a regional or global scale (Miller, 2010; Johnson et al., 2012; Morera-Pujol et al., 2023; Cushman et al., 2024). Species distribution models are also an effective method for the management of species at risk of biological invasion (Jiménez-

Valverde et al., 2011; Özdemir, 2024). Species distribution models provide a rapid assessment of species distribution, which can help identify unoccupied areas and understand the formation and spreading processes of highly competitive species (Zimmermann et al., 2010). While there are many methods for species distribution modeling (Özdemir et al., 2024), one of these methods is Maximum Entropy (MaxEnt). MaxEnt software is a method of estimating species distribution based on the principle of entropy. MaxEnt software uses only the variance data of species and environmental variables as inputs and estimates the probability of species distribution under changing environmental conditions by maximizing entropy. Compared to other types of distribution modeling and mapping methods that work only with presence data, more accurate and reliable results are obtained in the MaxEnt software (Phillips, 2005; Phillips and Dudík, 2008; Elith et al., 2011; Merow et al., 2013; Phillips et al., 2017).

Considering this information, this study aimed to determine the current and future potential distribution of the kissing bug, an invasive and deadly insect species, under global climate change. For this purpose, Maximum Entropy software, which is frequently preferred in wildlife species distribution modeling, and UKESM1-0-LL/ SSP126, SSP 370 and SSP 585 climate envelope models of Chelsa V2.1 for the year 2100 were preferred to reveal the effects of global climate change. In this context, variables contributing to the current habitat suitability modeling of the kissing bug were determined and simulated in the climate envelope models for the year 2100.

2. Materials and Methods

2.1. Study area and Kissing bug data collection

Triatoma infestans, also known as kissing bugs, are described as creatures that generally move from one place to another by flying or walking (Abrahan et al., 2011). Although it has been distributed in wide geographical areas around the world since the past, the kissing bug’s distribution in South America has generally been limited (Klotz et al., 2014). Therefore, it is important to know how the changing climate conditions will affect the kissing bug in the South America. Because global climate change generally causes the habitats of plant, wild animal and insect species to fragment, shrink or disappear (Mert and Yalçınkaya, 2016; Ertuğrul et al., 2017; Mert and Kıraç, 2017; Acarer, 2024d, Acarer, 2024e). In this context, the South America region constitutes the study area to determine how the distribution of the kissing bug will be affected compared to other wild animals in the world. The South America is classified into eight major geomorphological regions. The most important of these regions is the Andean mountains along the west coast of South America. The Andean Mountain region has a volcanic and seismic structure, and the largest volcanic mountains in the world are in this region (Camiz et al., 2017). South America is also located in a geographical location where various climate types are likely to be seen (Garreaud et al., 2009). Thanks to its diverse geomorphological structure and different climate types, South America is home to a variety of wild animal and insect species (Pinto et al., 2008; Alves and Alves, 2011; Schowalter, 2022). Kissing bug, one of the insect species, has a wide distribution area in South America. To fill the gap in the literature or to improve existing knowledge to determine the changing climate conditions on the kissing bug distributed in South America, the presence data of the target species was obtained from the Global Biodiversity Information Facility (GBIF) data infrastructure (GBIF, 2024). Kissing bug presence data obtained from the GBIF database, which provides open access to living species on Earth, has been resized by introducing the “WGS_1984_Mercator” coordinate system according to the South America regional borders. Data regarding the spatial distribution of presence data for 4006 number of kissing bugs (*Triatoma infestans*) within the boundaries of the study area are shown in red (Figure 1).

Figure 1. Kissing bug (Triatoma infestans) presence data map in South America

2.2. Creation of base maps of environmental and climate (Chelsa) variables

After obtaining available data on the target species from field studies or reliable websites on a global scale for species distribution modelling, environmental and climatic base maps that the species may prefer must be prepared. To produce digital base maps, a digital elevation model covering the study area with a pixel size of ~1 km (30 arc seconds) was first obtained from the website https://www.usgs.gov/. The coordinate system suitable for the obtained digital elevation model was introduced and resized. Slope, slope classes, aspect, aspect classes, elevation and elevation class base maps of the study area were produced with the help of ArcMap 10.8 software, based on the digital elevation model dimensioned according to the study boundaries (Tekeş and Cürebal, 2019). In addition, ruggedness index, roughness index, temperature index, temperature index

(McCune), landform position index, topographic position index, compound topographic index and hill shade index base maps, which may be effective on the kissing bug distribution, were produced. Thus, continuous and categorical digital base maps that can influence the distribution of the kissing bug were produced.

Chelsa V2.1 climate data, which is frequently preferred in wildlife studies to determine the climatic variables (Özdemir et al., 2020) that may have an effect on the distribution of the kissing bug, an invasive species, was obtained from the internet address https://chelsa-climate.org/. Chelsa V2.1 climate data has a high resolution of 30 arc seconds, or ~1 km pixel value. Chelsa climate data includes 19 climate variables from bio1 to bio19 for current and future (2100) years. There are different climate envelope models (GFDL-ESM4, IPSLCM6A-LR, MPI-ESM1-2- HR, MRI-ESM2-0, UKESM1-0-LL) based on the temperature and precipitation values of these climate variables (Karger et al., 2017; Karger et al., 2023). From these climate data available on a global scale, the base maps of the kissing bug for different scenarios (UKESM1-0-LL/ SSP126, SSP 370 and SSP 585) for current and future have been optimized according to the study area. As a result, 19 Chelsa climate data for current and future year (2100) that may have an impact on the kissing bug have been produced. The name, code, scale, unit, offset and conversion method of scale values of the 19 Chelsa climate data produced are given below (Table 1.)

Table 1. Chelsa climate variables name, code, scale, unit, offset chart

Name	Code	Scale	Unit	Offset
Annual mean temperature	**bio1**	0.1	^{0}C	-273.15
Mean diurnal range	**bio2**	0.1	^{0}C	0
Isothermality	**bio3**	0.1	^{0}C	0
Temperature seasonality	**bio4**	0.1	^{0}C/100	0
Max temperature of warmest month	**bio5**	0.1	^{0}C	-273.15
Min temperature of coldest month	**bio6**	0.1	^{0}C	-273.15
Temperature annual range	**bio7**	0.1	^{0}C	
Mean temperature of wettest quarter	**bio8**	0.1	^{0}C	-273.15
Mean temperature of driest quarter	**bio9**	0.1	^{0}C	-273.15
Mean temperature of warmest quarter	**bio10**	0.1	^{0}C	-273.15
Mean temperature of coldest quarter	**bio11**	0.1	^{0}C	-273.15
Annual precipitation	**bio12**	0.1	Kg m^{-2} year^{-1}	0
Precipitation of wettest month	**bio13**	0.1	Kg m^{-2} month^{-1}	0
Precipitation of driest month	**bio14**	0.1	Kg m^{-2} month^{-1}	0
Precipitation seasonality	**bio15**	0.1	Kg m^{-2}	0
Precipitation of wettest quarter	**bio16**	0.1	Kg m^{-2} month^{-1}	0
Precipitation of driest quarter	**bio17**	0.1	Kg m^{-2} month^{-1}	0
Precipitation of warmest quarter	**bio18**	0.1	Kg m^{-2} month^{-1}	0
Precipitation of coldest quarter	**bio19**	0.1	Kg m^{-2} month^{-1}	0

***The data presented in the CHELSA database contains values converted using scale and offset values. This conversion is done by multiplying the value by the scale value and adding it to the offset value. For example, the value of 2800 for bio5 corresponds to (2800 x 0.1) + (-273.15) = 6.85 °C.

2.3. Kissing bug habitat suitability modelling and mapping

In studies on wildlife ecology and management, one of the methods that estimate suitable and unsuitable habitats for the dependent variable based on only the presence data of the target species is Maximum Entropy (*MaxEnt*). MaxEnt calculates probability density with two different analyses for estimating suitable areas to determine target species distribution. First, MaxEnt characterizes the variable values belonging to the areas where the target species is only presence data. Secondly, it calculates the probability suitability within the habitat by creating different plan points belonging only to the presence data in its background. By calculating the difference between these two probabilities, it reveals the relative area-based suitability of the target species presence data. Finally, it produces a habitat suitability map for the entire area by determining the suitable habitats for the entire area according to the variable values (Phillips, 2005; Phillips and Dudík, 2008; Elith et al., 2011; Merow et al., 2013; Phillips et al., 2013; Acarer, 2024f; Acarer, 2024g; Acarer, 2024h).

This mapping produced by the MaxEnt method has the feature of reaching the most accurate, reliable and high explanatory margin results. In addition, the MaxEnt method helps reveal factors such as human impact and climate change, as well as both continuous and categorical variables. Moreover, MaxEnt helps with the simulation process to reveal the impact of changing climate conditions on a global scale on future wildlife species (Elith et al., 2011; Phillips et al., 2013). In this context, the most up-to-date and new version of MaxEnt version 3.4.4, was preferred to determine the current habitats of the kissing bug and compare it with future Chelsa climate scenarios

As in species distribution modelling, the accuracy of the model and mapping outputs produced with the MaxEnt method must be checked. This check is performed with 2 different methods such as Area Under the Receiver Operating Characteristic Curve (AUC) and Jackknife graphs contribution and value results. In addition, two different methods are preferred for checking the AUC. To check the AUC, the first step is to have the training data set of the obtained model higher than the test data set. Another is that if the model is a training data set, it is important that the difference between the test data set and the AUC values is at the lowest. Baldwin (2009) classified the models developed on wildlife species according to the AUC values of the training and test data sets as 0.9< AUC “very good”, 0.7< AUC <0.89 “good” and AUC <0.69 “uninformative”. In the Jackknife graph, care should be taken to ensure that the individual contribution of the variables contributing to the formation of the species distribution model does not exceed the entire contribution of the other variables contributing to the model (Phillips and Dudík, 2008; Merow et al., 2013; Phillips et al., 2013).

3. Result

Before proceeding to kissing bug modeling and mapping, statistical analysis was performed on the base maps produced within the study area boundary. Because the reason why the base maps created for species distribution models have close values to each other causes multicollinearity problems in the modeling phase (Süel, 2018). To eliminate this multicollinearity problem, Pearson correlation analysis was applied between global climate variables specified in literature studies. According to the results of the Pearson correlation analysis applied to Chelsa climate variables, it was determined that there was a high correlation (r>0.8) between climatic variables (Özdemir et al., 2020). Therefore, factor analysis was applied to determine the best representative variables of the study area and the distribution of kissing bugs among climate variables. According to the Factor Analysis results, it was determined that the cumulative value of the model of the 4 climate variables that would best represent the distribution of kissing bugs was 97.24% and the variance was 10.8%. These variables were determined as annual mean temperature (bio1: 0.896), precipitation of coldest quarter (bio19: 0.872), precipitation seasonality (bio15: 0.865) and temperature seasonality (bio4: 0.841), respectively. Later, it was examined whether there was a high correlation between these variables and other base maps with other categorical and continuous data. A total of 33 variables produced at the beginning of the study were subjected to statistical analysis and it was decided to proceed to the modeling phase with 18 variables. For the kissing bug habitat suitability modeling studies, a total of 24 different models were produced with 4006 target species data and 18 environmental variables. To obtain the best model, it was repeated until at least two variables remained that contributed to the models. As a result, the 21st model was selected as the best model with a training data set AUC of 0.867 and a test data set AUC of 0.866 (Figure 2A). According to Baldwin (2009), the model is in the “good model” category with an average AUC value of 0.865 (Figure 2B).

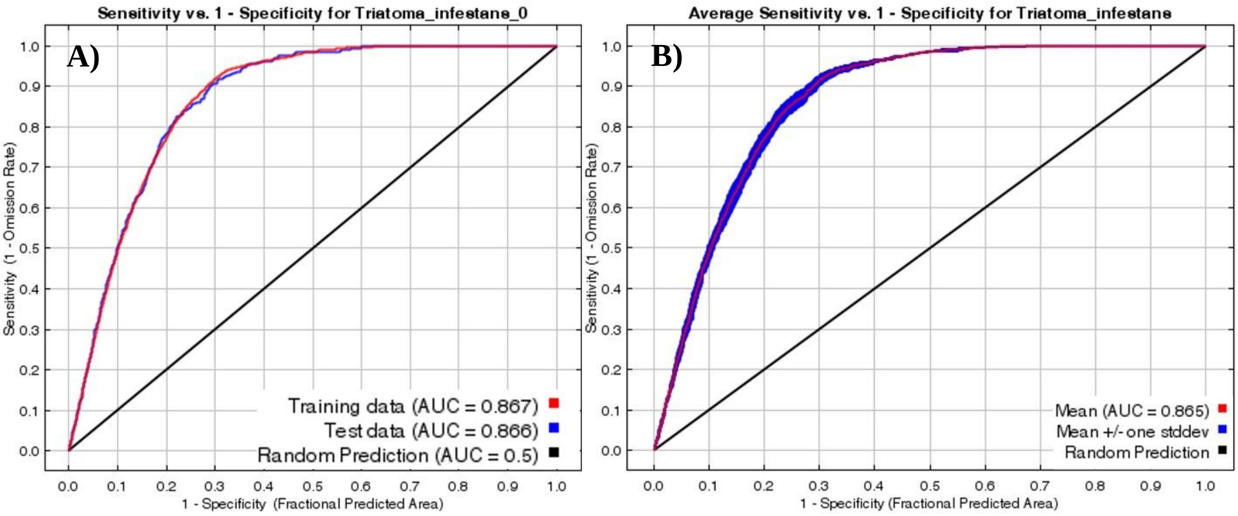

Figure 2. Kissing bug habitat suitability model, A) training data set AUC and test data set AUC value B) average AUC value

It is necessary to determine the variables that contribute to the current distribution model of the kissing bug, which is in the “good model” category. In this context, the Jackknife graph, which shows the variables that contribute to the formation of the model, should be examined. According to the Jackknife AUC graph of the kissing bug habitat suitability model, it has been determined that the annual mean temperature (bio1), temperature seasonality (bio4), precipitation seasonality (bio15), roughness and elevation variables contribute to the formation of the model (Figure 3). The area shown with a blue in the jackknife graph indicates the contribution of that variable to the formation of the model only when it is present.

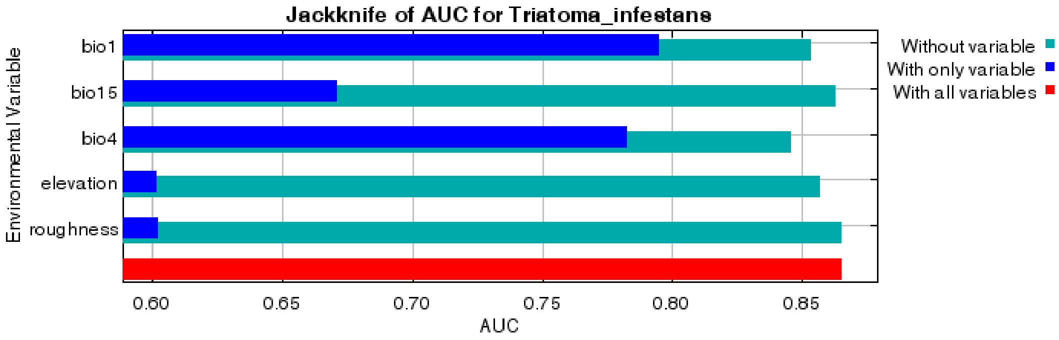

Figure 3. Kissing bug habitat suitability model Jackknife graph

Marginal responder graph of the variables contributing to the jackknife plot of the kissing bug habitat suitability model are shown below. However, when evaluating the climate variable graphs in these graphs, their real values should be evaluated according to the transformations specified in the Chelsa climate variables graph (according to Table 1). Based on this situation, according to the annual mean temperature (bio1) variable, which contributes the most to the current model, areas where the annual mean temperature is approximately 12.85 °C to 16.85 °C have been identified as suitable areas for species distribution. It has been determined that the average annual temperature values within the study area are above or below these values and have a negative effect on species distribution (Figure 4A). According to the temperature seasonality (bio4) variable that contributes to the formation of the model, areas between 3.5 °C and 6 °C have a positive effect on species distribution, while areas before or after these values have a negative effect (Figure 4B). According to the precipitation seasonality (bio15) variable, it was determined that the distribution of the kissing bug was high in the areas receiving 620 mm to 1350 mm of rainfall within the area (Figure 4C). However, for the kissing bug, high or moderately rugged areas have been found to have a negative effect on species distribution (Figure

4D). Finally, when the altitude variable that makes the least contribution to the current habitat suitability model of the kissing bug is examined, it has been determined that the target species has a positive effect on the species distribution in areas with an altitude of 200 meters to 3800 meters. It has been determined that the probability of seeing the kissing bug is low in areas before or after these altitude values (Figure 4E).

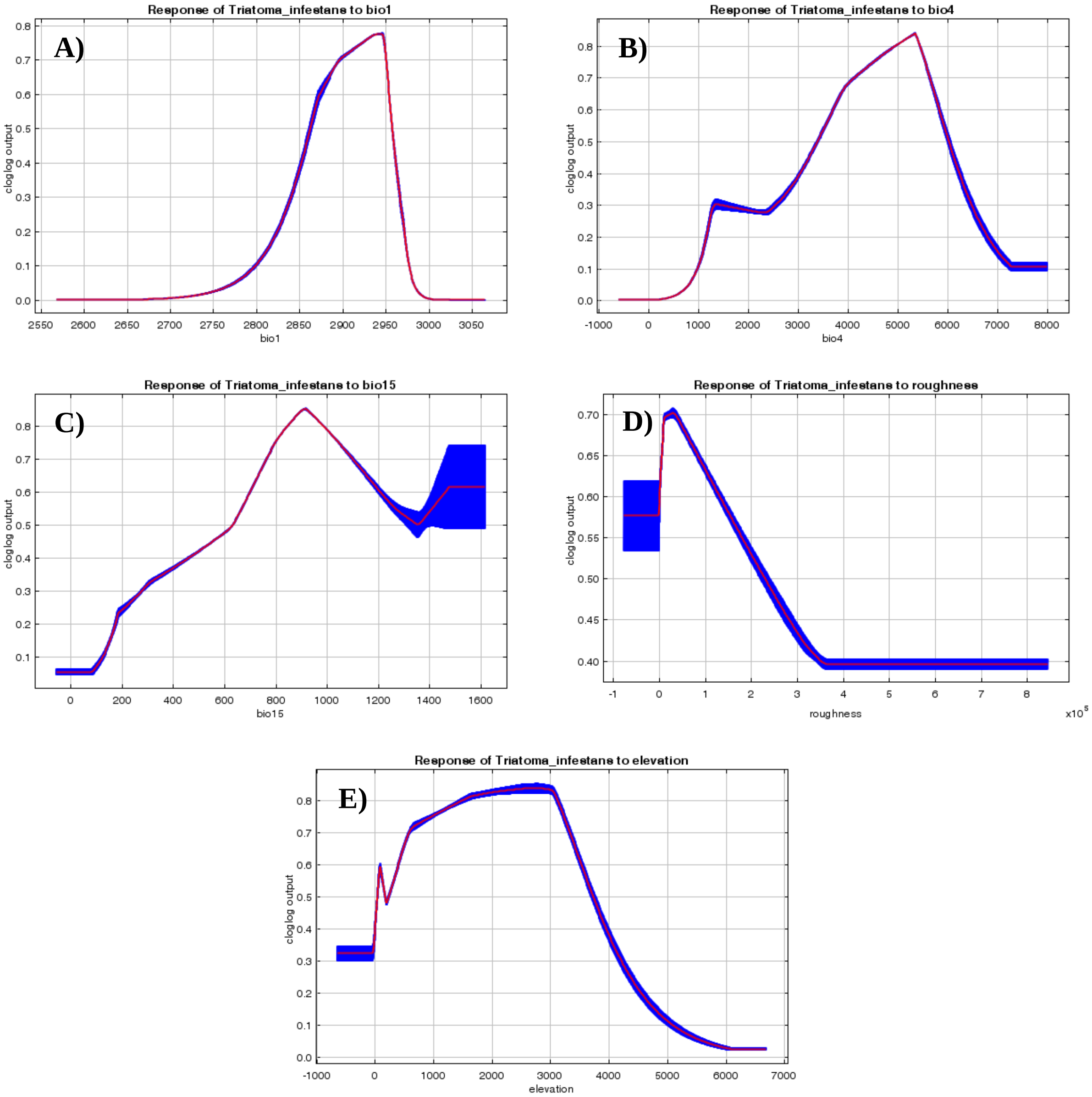

Figure 4. Contributing to the kissing bug habitat suitability modelling A) annual mean temperature (bio1) graph, B) temperature seasonality (bio4) graph, C) precipitation seasonality (bio15) graph, D) roughness index graph E) elevation graph

Habitat suitability mapping was presented according to the variable values contributing to the kissing bug's current model (Figure 5). According to this mapping, the kissing bug, which is distributed in the South America region, heavily prefers the northern region of Argentina's country. It has also been determined that the northern part of Chile, which is an extension of the Andean Mountains, has high habitat suitability. Moreover, it has been determined that there is a high probability of it being found as a colony in the southern part of the country of Bolivia. In addition, although habitat suitability has been found in the western region of the Paraguayan country borders, this probability is low. As a result, it was determined in which countries the species distribution is generally in current habitat suitability mapping within the country borders of Argentina, Bolivia, Chile and Paraguay. Based on this, numerical and model-based mapping of the countries where the kissing bug is distributed has been presented for today's habitat suitability mapping.

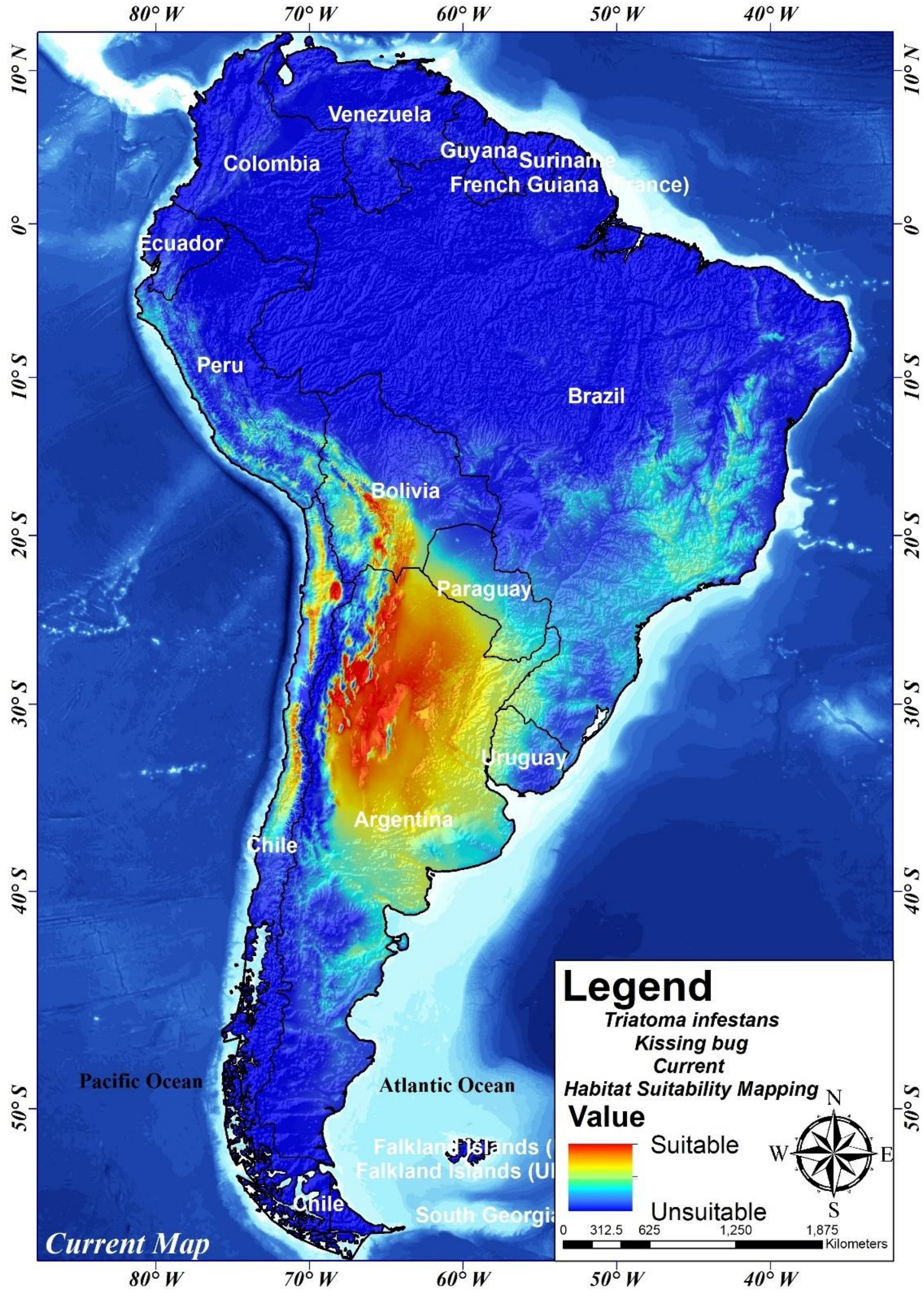

Figure 5. Current habitat suitability mapping of the Kissing bug in South America

The kissing bug was simulated in different scenarios of Chelsa v2.1 for the year 2100, based on the numerical values of the variables contributing to the current model (Figure 6). As a result of the simulation process, habitat suitability maps were revealed according to different scenarios. When these maps are examined, it has been determined that climate change in 2100 supports the distribution of the kissing bug. As a result, it is thought that the point at which the kissing bug's current habitats must be taken under control is the first step in reducing the impact of the Chagas epidemic spread by this species on the world.

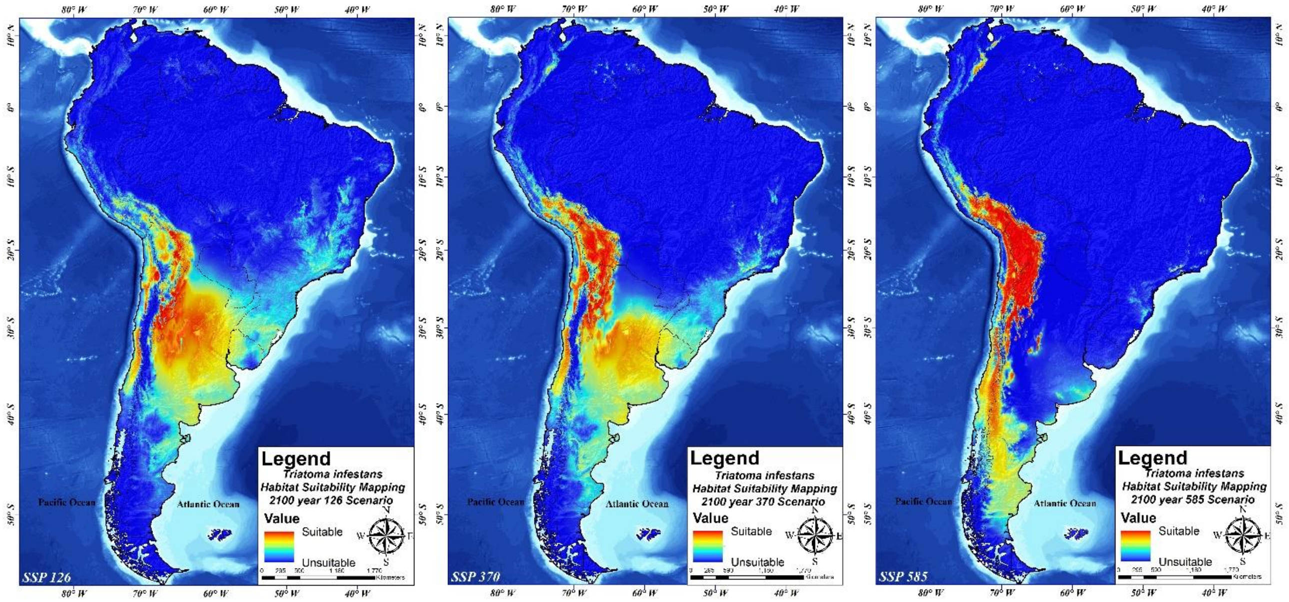

Figure 6. Kissing bug (*Triatoma infestans)* Andean bear habitat suitability mapping year of Chelsa V2.1 2100-year A): SSP1 2.6 scenarios, B) SSP3 7.0 scenarios, C) SSP5 8.5 scenarios

3. Discuss and Conclusion

This study highlights the distribution of kissing bugs in South America under the influence of changing climate conditions on a global scale, with presence data from 4007 locations. Previous studies have shown that both biotic and abiotic variables have positive or negative effects on the distribution of insect and plant species (Galvão and Justi, 2015; Mert and Acarer, 2018; Tekin et al., 2018; Mert and Acarer, 2021; Acarer, 2024b; Picanço et al., 2024). However, the high rainfall in South America and the presence of dense forest cover and a hot and humid environment accelerate the distribution of these plant and insect species and the spread of Chagas disease (Shikanai-Yasuda and Carvalho, 2012; Costa et al., 2014; Ribeiro et al., 2018). It has also been stated that palm trees, which are densely populated in the South America, are a feeding, sheltering and protection area for kissing bugs However, it has been stated that kissing bugs leave their own parasites on these palm trees, which they prefer as feeding, sheltering and protection areas (Picanço et al., 2024). Therefore, this parasite infects other wild animal species that accept the fruits and crowns of palm trees as a feeding preference. Thus, the parasite secreted by the kissing bug continues the cycle of Chagas disease transmission and maintenance within natural ecosystems (Rolandi and Schilman, 2012; Zhang et al., 2018; Margalef-Marrase et al., 2020).

Chagas disease, which is transmitted through the bites and faces of kissing bugs, especially in the South America region, is considered a global health problem (Bonney, 2014). It is very interesting that although there has been an increasing epidemic disease in some regional regions of South America recently, current and future habitat suitability modeling of kissing bugs has not been revealed. In this perspective, it has been determined that the model presented in this study has a training data set AUC value 0.867 and a test data set AUC value 0.866. In addition, the average AUC value of the model was found to be 0.865. Based on this, the Baldwin (2009), AUC values that present AUC > 0.90, 0.89-0.7, and 0.69-0.00, are considered excellent, good, and unresponsive, respectively. When the presented model results are compared with the Baldwin (2009), ecological niche model, the model is classified in the “good” model category. The variables contributing to the kissing bug’s current habitat suitability model were determined to be annual mean temperature (bio1), temperature seasonality (bio4), precipitation seasonality (bio15), roughness and elevation.

It has been determined that the areas where the annual average temperature variable and seasonal temperature variables, which contribute to the formation of the kissing bug's current model, increase to a certain level and then decrease are suitable areas for the species. More clearly, this situation is determined that the areas where the annual average temperature difference is approximately 4 °C and the seasonal temperature difference is approximately 2.5 °C are suitable areas for the kissing bug distribution. In this context, it is stated that kissing bugs have significant direct or indirect effects on their biological functions such as reproduction and the transmission ability of the parasites they secrete (Di Luciano, 1983; Roca and Lazzari, 1994; Lorenzo and Lazzari, 1999). At the same time, when the precipitation variable that contributes to the kissing bug's current model is examined, the increase in seasonal precipitation in South America to a certain level is effective on plant species distribution (Alotaibi et al., 2023). The distribution of palm trees, which shelter and protect kissing bugs, is closely related to the amount of precipitation. Because the expansion of palm tree distribution could trigger the spread of Chagas, a disease secreted by the kissing bug (Picanço et al., 2024). Therefore, it is important to evaluate the habitat preferences of kissing bugs distributed in South America together with climate variables such as temperature or precipitation to prevent the Chagas epidemic (Lorenzo and Lazzari, 1999). Moreover, the areas determined to be suitable for the kissing bug in terms of climate are giving alarms for the risks they pose for the end of human life (death) as a disease carrier (WHO, 2024). Because, although Chagas disease has been associated with South America on a global scale, the kissing bug has been identified as suitable for habitat suitability models in Asia and Africa (Bonney, 2014). Thus, it was emphasized that the distribution of the target species will increase according to different climate scenarios for 2040 year and 2080 year and that there is a need for global surveillance of Chagas disease (Picanço et al., 2024). As a result, in this study conducted to determine the effects of global climate change on the kissing bug, the results of the temperature and precipitation variable values contributing to the current model are consistent with the literature.

Environmental variables such as roughness and elevation, which contribute to the kissing bug's current habitat suitability model, have an impact on species distribution. Literature studies indicate that environmental factors will greatly affect the distribution of kissing bugs (Delgado et al., 2013). It was emphasized that in addition to the fact that environmental factors have such an effect on the kissing bug, microclimate variables can be considered to determine the current and potential distribution areas accurately and reliably. In addition, a study was conducted in the South America region to determine the areas infested with kissing bugs. The distance between the infested houses was up to 2000 meters. It was emphasized that the ratio of infested houses to the houses he investigated was 18% and that this infestation was related to environmental variables such as elevation (Delgado et al., 2013). Similarly, it was stated that the roughness and surface temperature of the houses in the area were related to the Chagas disease secreted by the species. As a result, it was determined that the model variable value results obtained in this study, which was conducted to understand the effects of global climate change on the kissing bug, were in the same direction as the literature.

In summary, the environmental and climatic variable value results contributing to the current habitat suitability model of the kissing bug are consistent with the literature. In this context, the current mapping of the kissing bug has been presented. Since the mapping results presented are numerical and model-based, they are quite accurate and reliable. The variables contributing to the formation of the mapping have been simulated using the maxent method based on the Chelsa climate variables of the year 2100. In this direction, it has been determined that the distribution of the kissing bug will expand according to the good, normal and bad scenarios of the year 2100.

As a result, it is recommended to start protection efforts as soon as possible to prevent the number of individuals of the kissing bug, which is an invasive species, and the Chagas virus it secretes. Because kissing bugs can easily feed on humans, wild animals, domestic animals and invertebrates in their habitats. In addition, it is recommended that predator insects should be released into the South America to determine or limit the distribution of kissing bugs, which tend to be light to fly effectively. Finally, this model-based study suggests that although global climate change will have negative effects on the distribution of some wild animal species, it will also mean that the distribution of some insect species will expand.

4. References

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