The impacts of climate change on the global range of *Culicoides punctatus* (Meigen, 1804) with notes on its status in Saudi Arabia

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Abstract

Biting midges, particularly *Culicoides* species, pose significant health risks to humans and animals due to their biting behavior and ability to transmit diseases. Understanding their behavior and distribution patterns is crucial for predicting and controlling the spread of viral infections. This study employs species distribution modeling to assess the environmental suitability and potential future distribution of *Culicoides punctatus*, a species known for causing allergic reactions in horses and acting as a vector for bluetongue virus (BTV) and African horse sickness virus (AHSV). Species occurrence records for C. punctatus were collected from the Global Biodiversity Information Facility (GBIF), and environmental data representing climate variables were obtained from WorldClim. The data were used to develop species distribution models and predict the potential distribution of *C. punctatus* in the Old World under different emission scenarios. The results indicate that *C. punctatus* has a wide occurrence across the Old World, with the highest number of records in Europe. The species distribution models highlight the influence of climate on the distribution of *C. punctatus*, suggesting that climate change could impact its range and potentially expand regions with endemic viral infections. The study emphasizes the need for proactive measures to monitor and manage the spread of viral infections associated with *Culicoides* midges. The integration of geographic information systems (GIS) and remote sensing technology has facilitated high-throughput analysis techniques, eliminating the need for invasive experiments and enabling the remote assessment of species' habitats, land cover changes, and meteorology. Species distribution modeling, a powerful tool in ecological research, has been employed to predict the potential distribution of *C. punctatus* and assess its vulnerability to climate change. This study contributes to our understanding of the ecological implications of climate change on *Culicoides* midges and the associated viral infections. It provides valuable insights for designing effective management strategies, conservation efforts, and mitigation measures to minimize the impact of biting midges on human and animal health. Further research and monitoring are necessary to continuously update and refine these models in the face of changing environmental conditions.

Keywords: *Culicoides punctatus*, species distribution modeling, climate change, viral infections, biting midges, geographic information systems, Old World.

Introduction

Biting midges, scientifically known as Ceratopogonidae, are a family of small, blood-feeding insects. Among the various genera within this family, one of the most notable is *Culicoides*.[1] *Culicoides* midges are found worldwide and are known for their biting behavior, which can cause annoyance and discomfort to humans, as well as transmit diseases to animals.[2]

Culicoides midges are tiny insects, usually measuring between 1-3 millimeters in length. They have slender bodies, long legs, and delicate wings.[3] These midges are typically active during the late afternoon and evening hours, preferring areas with high humidity and proximity to water sources like marshes, swamps, and wetlands.[4]

Female *Culicoides* midges require a blood meal to develop their eggs, and they are the ones responsible for biting humans and animals.[5] The bites can be painful, causing itching, swelling, and irritation. Some individuals may also experience allergic reactions to the bites, resulting in more severe symptoms.[6] One of the significant concerns associated with *Culicoides* midges, particularly certain species within the genus, is their ability to transmit diseases. The most notable disease transmitted by *Culicoides* midges is called bluetongue, which primarily affects ruminant animals like sheep, cattle, and goats.[7] Bluetongue can have significant economic impacts on livestock industries due to decreased productivity and movement restrictions imposed to control the disease.[8] In recent years, another disease transmitted by *Culicoides* midges called Schmallenberg virus has emerged in Europe.[9] This virus affects ruminant animals as well and can cause reproductive problems and congenital malformations.[10]

In Saudi Arabia, *Culicoides* midges are present and have been of concern due to their potential role as vectors of diseases.[11] Saudi Arabia is home to a diverse range of *Culicoides* species, and studies have identified numerous species of *Culicoides* midges in different regions of the country. The species composition may vary across various habitats and geographical regions within Saudi Arabia.[12] *Culicoides* midges in Saudi Arabia have been implicated in the transmission of several diseases. Bluetongue, caused by the Bluetongue virus, has been reported in livestock, including sheep, goats, and cattle.[13] Epizootic hemorrhagic disease (EHD), caused by Epizootic hemorrhagic disease virus, has also been detected in livestock in the country.[14] These diseases can have significant impacts on animal health and productivity.

One of the species of Culicoides midges identified in Saudi Arabia is *Culicoides punctatus*.[12] Like other Culicoides species, C. punctatus and its close relative C. pulicaris are known to cause allergic reactions in horses, and are also known to be vectors of BTV (bluetongue virus) in addition to AHSV (African horse sickness virus).[13] AHSV can cause transient pyrexia of

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Comentado [CK1]: This information is, to some extent, contradictory to study results. I will argue later that this might be a consequence of methodological issues.

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companion horses and donkeys in mild cases or impairment of the respiratory system and subsequent effusions and hemorrhages in severe cases.[15] AHSV, however, is not known to be endemic in Saudi Arabia, with only one case being diagnosed between 1959 and 1989,[16] unlike the bluetongue virus, which is documented to have an alarmingly high seroprevalence rate in sheep, goats, cattle, and camels from different regions throughout Saudi Arabia.[17] Because both of these spread primarily through Culicoides spp., it is crucial to understand their behavior to enable prediction and control of the viral spread.

Climate change is expected to have an enormous effect on biodiversity worldwide, and Culicoides spp. are no exception to this. The United Nations has warned that the global average temperature may rise by up to 4 degrees Celsius by the end of the 21st century relative to preindustrial values if drastic mitigation efforts are not undertaken.[18] Such a change will have disastrous environmental consequences, such as changes in precipitation patterns,[19] more frequent extreme and dangerous weather conditions,[20] and increased risk of natural disasters such as flooding and drought.[21]

With respect to biodiversity, climate change will pose a risk for extinction to those species that are less fitted for adaptation to the rapidly changing environmental conditions.[22] Other species or individuals may adapt by altering their otherwise normal behavior, morphology, or physiology,[23] potentially leading to range shifting,[24] which is when a species changes its normal habitat range or ecological niche to cope with environmental changes. Range shifting may pose a risk for a non-indigenous species becoming invasive in its new environment.[25] For all these reasons, climate change can lead to ecological imbalances that have notorious ecological and economic consequences.[26]

Comentado [CK2]: To my knowledge, theoretically, a range shift means a species is tracking the geographical space through maintenance of its' niche. Range shifts can be accompanied by niche changes, but range shift does not mean niche shift.

In the case of species that are known to act as viral vectors such as Culicoides spp., range shifting responses to climate change may be especially dangerous due to the possibility that the regions with endemic viral infections may be expanded.[27] An analysis of the climate preferences of three Culicoides species in the UK insinuated that the range and generation count of these midges will increase in the foreseeable future due to the climate change.[28]

Fortunately, the 21st century witnessed the rise in computing power and accessibility, which propelled the development of geographic information systems (GIS), which are defined as a computer system that can visualize, capture, analyze, or otherwise manipulate geospatial data.[29] This is indispensable coupled with remote sensing technology, leading to what is known as integrated GIS, which aims to increase the transparency and compatibility between geographic information systems and remote sensing systems.[30]

High-throughput GIS-based analysis techniques of data generated from high-throughput remote sensing have enabled us to study many characteristics of the Earth remotely, completely eliminating the need for field-based invasive experiments.[31] This not only saves a tremendous amount of money, but also enables researches to infer the biophysical properties of species' habitats remotely,[32] monitor land cover and its changes and their effects on biological systems,[33] as well as meteorology and climate studies based on computational models of the climate.[34] Remote sensing can also be used to directly track the movement of individuals in what is known as active remote sensing, allowing direct monitoring of a species' behavior, migration, and distribution.[35]

Ever-changing data analysis techniques with the wide availability of environmental data and species occurrence data has led to the development of a tool known as species distribution modeling (SDM). Species distribution modeling algorithms correlate known species occurrence records with environmental data to predict the species' potential distribution across other geospatial locations.[36] Depending on the environmental data inputted to the algorithm, this can also be used to assess the potential distribution of a species in the future. This tool has numerous ecological applications, ranging from biogeography studies, conservation strategies and planning thereof, meteorology research,[36] and planning adequate management strategies for pests and other invasive species.[37]

This study aims to employ species distribution modeling to assess the environmental suitability for C. punctatus in the Old World to infer the relation between climate and biting midge-associated viral infections, as well as estimate its potential future distribution under climate change in different possible emission scenarios.

Materials & Methods

Data Collection

Species occurrence records

Culicoides punctatus species occurrence records were obtained from the Global Biodiversity Information Facility (GBIF) [38], an open-access biodiversity database that combines information from published research and users who voluntarily contribute to the database with data from the literature (https://www.gbif.org/) [39]. After downloading the data in Darwin Core (DwC) format, the metadata was eliminated in order to extract only the legitimate occurrence records' latitude and longitude coordinates. The comma-separated values (CSV) file format was then used to store this data in order to make it compatible with the MaxEnt species distribution modeling program. Additionally, I digitized and transferred all of the literature's records into points that could be used when preparing the model, in addition to gathering certain materials from throughout Saudi Arabia (Supplementary Material 1) In this study, 1217 occurrence reports in total were used.

Environmental Data

WorldClim version 1.4 provided the environmental data, which was converted into 19 bioclimatic variables to reflect the climate.[40] These variables show the monthly, seasonal, and annual averages, maximums, and minimums of precipitation and air temperature throughout various time periods.

At the equator, this data was downloaded at a spatial resolution of 2.5 minutes, or roughly 4.5 km.[40] We retrieved historical mean climate data from 1960 to 1990 to represent the current climate scenario. Regarding potential future climate change scenarios, the average values from 2041–2060 for the year 2050 and the average values from 2061–2080 for the year 2070 were utilized.

Comentado [CK3]: I feel that we need a better description of those additional data here.

Comentado [CK4]: I would suggest a geographical presentation of those occurrence points. It is very common to see geographic biases in data collections, and even a glimpse of this possibility and evaltuation is useful.

I also recommend presenting if those reports already exclude diplucates (geographical points in which the species was collected more than once), so we can understand if there is any amount of that information that is redundant.

Comentado [CK5]: I think it would be nice to have some biological or ecological explanation for the chosen scale.

Comentado [CK6]: There is an important consequence of that choice. If you are using data from before 1990, and occurrence data from GBIF, you might be using occurrence points from a period ranging way after those climatic conditions. We expect, in a way, that future occurrences are also consequence of those historical data. I would probably suggest some changes here, and also would like to hear more expert opinions on the topic.

Also, a presentation of the time range on the occurrence data would be interesting for further discussing this methodological detail.

RCP 2.6 and RCP 8.5, which reflect the best-case and worst-case scenarios, respectively, were the representative concentration pathways (RCPs) employed in relation to the projected climate data.[41] The Japanese Meteorological Research Institute (MRI) developed the MRI-CGCM3 general circulation model, which served as the foundation for upcoming climate models.[42] Thus, four datasets of future climate data—one for each of RCP 2.6 and RCP 8.5 under each of 2050 and 2070—were employed in this work. Using ESRI ArcMap version 10.3, all of the climatic data—historical and projected—was cropped to just contain pertinent Old World locations. It was then transformed and exported into the ASCII raster file format so that MaxEnt could use it as well.

Model Construction

Using the DIVA-GIS version 7.5 BIOCLIM method, a tentative overall model for the likely current distribution of C. punctatus was created.[43] Because it uses less computing power and resources, BIOCLIM modeling is used to produce first-pass geographic predictions [44]. A more sophisticated machine-learning-based modeling approach, like MaxEnt, which was actually implemented after BIOCLIM, can then be used to aid and improve the model's accuracy.

The distribution maps were immediately produced from the DIVA-GIS BIOCLIM model after the environmental factors and species occurrence records were loaded.

The species distribution models for *C. punctatus* were created using maximum entropy species distribution modeling, as it is utilized in the MaxEnt tool, for the primary models [45]. The choice of the maximum entropy algorithm was based on its capacity to create a species distribution model based just on species presence data, without the need for species absence data, and on its excellent quality and reliable findings.[46]

Comentado [CK7]: I have the opinion that this is an oversimplification of the matter. There is an important debate on literature on the differences and shortcomings of different models, and I have the opinion that this has been understated in this work. I would like to see, in more detail, the reasonings behind the choice for Maxent. I also see an overall lack of discussion and presentation of the limitations and problems in SDMs overall.

SDMs, especially when applied to future scenarios, are extrapolations. Most of the evaluation of SDMs made on the literature is probably using training/test separation, and therefore are internal evaluations (of the interpolation capacity and consistency of the model, not on the predictive capacity per se, on novel conditions). Therefore, even a model with high evaluation levels may fail to extrapolate, as extrapolation often is affected by things not incorporated on models (adaptation potential of the species, different behavior under new conditions, new interactions from climatic variables and etc).

I reinforce that I would like to have more opinion from different scientists on this critics, as I am fully aware I might be wrong.

The environmental variables and species occurrence records were imported into MaxEnt, much like in the case of the BIOCLIM model. The following settings were applied to each run that was completed with MaxEnt: Response curves, jack-knife testing, cross-validation between runs, seventy-five percent random training samples, and twenty-five percent random testing samples were used in the ten replication runs. In order to produce a readily comprehended assessment of the probability of environmental appropriateness for C. punctatus, the output format was also set to complementary log-log, or cloglog. The output of Cloglog is simple to understand since it is a binary scale, with 1 denoting the environments that are most suited and 0 the surroundings that are least suitable. The median of the 10 repetitions was chosen to represent the outcome of each run, which included 10 replicates total.

To determine the predictive potential and contribution of each climate variable, a prototype MaxEnt model was first built utilizing the previously specified species occurrence records and all 19 climate variables. When choosing significant environmental variables, bioclimatic variables 8, 9, 18, and 19 (mean temperature of wettest quarter, mean temperature of driest quarter, precipitation of warmest quarter, and precipitation of coldest quarter, respectively) were avoided because they were known to cause spatial artifacts and discontinuities that would negatively affect the model's quality [47].

The most significant environmental predictors were then identified using the jack-knife test, which is based on determining the significance of each variable by testing the difference in the model that occurs when said variable is left out[48]. The variables deemed most significant were then used for all subsequent modeling, while those deemed insignificant were excluded from the models.

Comentado [CK8]: I am not sure this is a good method. The exclusion of variables, to me, seems like loss of important information. I am aware that a common choice for this type of decision Is the usage of principal component analysis, which displays visual measurements of collinearity and allow all information to be used as model inputs. I am afraid that the study concluded that humidity/precipitation is not important for species range only because their variations is contained in temperature variables.

The same species occurrence records were imported into MaxEnt, but only with the environmental variables that were considered important, in order to estimate the possible present range of *C. punctatus*. Four models in total were made in the same manner to represent the future possible distribution under various climate change scenarios: one for each of the years 2050 and 2070 under the RCP 2.6 and RCP 8.5. To enable future prediction based on the current observations, the future climate data was fed into MaxEnt's predictions layer.

Quality Assessment

The true skill statistic (TSS) and the area under the receiver operating characteristic (ROC) curve, or AUC, were used to evaluate the quality of the model [45].[49] The AUC is a threshold-independent technique for evaluating the prediction ability of classification models, like MaxEnt. On a scale from zero to one, 0.9–1 denotes outstanding quality, 0.8–0.9 good quality, 0.7–0.8 satisfactory quality, 0.6–0.7 low quality, and less than 0.6 model failure [50].

The output model must be categorized into positives and negatives based on a threshold in order to calculate the true skill statistic (TSS), a threshold-dependent metric. The genuine positive rate and the true negative rate are then added up and subtracted from one, yielding a figure that falls between -1 and 1. Negative numbers indicate a model whose performance is worse than random, positive values show a hypothetical perfect model that can identify between positive and negative classes correctly on every dataset, and zero represents a model whose performance is no matter than random.[49] The model was classified into positive and negative predictions using a threshold of 0.6, signifying a 60% likelihood of environmental appropriateness.

Model Visualization

Using ESRI ArcMap 10.3, each of the produced MaxEnt models was independently viewed and exported as an image.[51] In order to facilitate visual interpretation, each class was color-coded after being categorized using Jenks natural breaks optimization based on a range of values.

Next, the models were categorized into presence-absence maps with the same cutoff as the real skill statistic calculation. The prospective current distribution's value was then subtracted from each potential future distribution's value to calibrate them.[52] As a result, the final maps have zeroes to represent no range change, positive values to represent range gain, and negative values to represent range loss. To make it easier to visually grasp the future potential distribution in relation to the existing potential distribution, the maps were subsequently categorized, color-coded, and exported.

Results

Model Performance

The mean AUC value across the replicated MaxEnt runs was revealed to be 0.925, indicating that the model was of excellent quality,[50] as shown in Figure 1. The TSS value also shows that the model performance is high with 0.7 value.

Effects of Environmental Variables

Analysis of the jack-knife test, shown in Figure 2, revealed that the most significant environmental variables for *Culicoides punctatus* were bio_4 (temperature seasonality), bio_6 (minimum temperature of coldest month), bio_11 (mean temperature of coldest quarter), bio_7 (temperature annual range), and bio_10 (mean temperature of warmest quarter) in descending order of significance.

The response curves revealed the most suitable ranges within these variables. By interpretation of bio_6, bio_10, and bio_11 shown in the following Figure 3, it is strongly suggested that C. punctatus appears to have a preference for environments that range from moderately warm climates to hot climates.

It is also worth noting that none of the precipitation bioclimatic variables were found to be significant in predicting the distribution of *C. punctatus*, potentially suggesting that it can live across a wide geographical range of environments regardless of the precipitation conditions throughout said environments, and that its distribution is mostly dependent on seasonal temperature conditions.

Distribution Maps

Potential current distribution

The preliminary BIOCLIM model constructed for the distribution of *C. punctatus* under the historical climate scenario shows a peculiar range of suitable habitats in the Old World. As seen on the map, the environments with the highest suitability for *C. punctatus* appear to be the warm humid coasts of the Mediterranean, both in North Africa and in South Europe. Sizable significant highly suitable environments are also seen in the Sinai Peninsula and northwestern Saudi Arabia near the Jordanian border Figure 4.

As for the MaxEnt model of the *C. punctatus* distribution under the historical climate scenario, it revealed regions that are largely consistent with those shown in the BIOCLIM model, albeit with a somewhat larger area of suitable regions.Much like the BIOCLIM model, the MaxEnt model also shows the highest suitability areas for *C. punctatus* to be predominantly concentrated along the Mediterranean coasts, although the suitable regions in notable areas are greatly expanded in area. These expansions include most of the Arabian Peninsula, the Nile Delta in Egypt, and almost the entirety of West Europe Figure 5.

In Saudi Arabia, the BIOCLIM model indicate that most of the Kingdome with low and medium suitability for *C. punctatus* and only the northern west with high to very high habitat suitability. On the other hand, the Maxent modeling shows that the whole kingdom with high to very high habitat suitability especially on the coast of the Gulf.

Potential future distribution

The future projections of the MaxEnt models revealed that *C. punctatus* is predicted to still enjoy considerable range in the Old World Figures 6&7.

At first glance, the models built on the increasingly severe climate change scenarios appear to display more severe range shifts, albeit while still enjoying considerable range. To simplify the interpretation, however, and to quantify the regions exhibiting range gains and losses, the calibrated maps will be used instead of the previous uncalibrated maps for the future climate change scenarios, as shown in the following figures.

The calibration maps in figures 8 and 9 show alarming range shifts for *C. punctatus* under the future projected climate change scenarios used in this study. Given the rising average global temperatures, there is an exceedingly severe range gain predicted for *C. punctatus* in most of the Old World. Specifically, there is an alarmingly high range gain in much of North Europe, Central Asia, the Indian Subcontinent, as well as many regions of North Africa and Sub-Saharan Africa. In the most severe climate change scenario seen in 2070 under RCP 8.5 (Figure 9-B), there is also an observable range loss, albeit at a much more modest scale compared to the range gain, seen in some regions in central Saudi Arabia extending as far northeast into Iraq. For the most part, most of the range of *C. punctatus* appears to be projected to grow significantly in area and a minority of its range appears to be relatively unaffected. This is in line with the interpretation of the response curves shown in figure 4 that show that *C. punctatus* appears to prefer moderately warm to hot climates, and thus a rising mean global temperature in the future under climate change may serve to provide more suitable habitats for *C. punctatus*.

Comentado [CK9]: Although this appears to now be wrong, I would like to see some measurement here. Something like the amount of area to be gained and the amount of area to be lost. This discussion would be less subjective.

It is also worth noting that with increasingly severe climate change scenarios, the extent of range shifting projected to be exhibited by *C. punctatus* also becomes increasingly more severe, such as when comparing Figure 8-b against Figure 8-a, or likewise by comparing Figure 9-b against Figure 9-a.

In Saudia Arabia, the status of *C. punctatus* will not greatly be affected through all scenarios except lost some suitability areas in the central region of the kingdom in 2070 under RCP 8.5 Figure 9-b.

Discussion

Biting midges are known to inhabit worldwide environments and are known disease vectors for various animals.[3] Bluetongue virus, one of the diseases caused by *Culicoides* spp. of biting midges, is actually geographically limited exclusively to areas inhabited by *Culicoides* spp., and is widespread globally, including in the Old World, most notably in Africa and the Arabian Peninsula.[53] In one study, it was found that an epidemic of bluetongue virus directly caused the death of 1.5 million sheep in Europe in the few years following an outbreak, causing massive economic losses which were further amplified by the implementation of trade restrictions intended to prevent the spread of the virus as well as the development of secondary diseases in animals with weakened immune systems.[54]

Much like the bluetongue virus, the Schmallenberg virus is also known to be transmitted via *Culicoides* spp. as its vector.[10] One study conducted in Austria found that the Schmallenberg virus was associated with increased rates of ruminant spontaneous abortions and fetal death in Austria during the 2012 and 2013 Schmallenberg virus epidemic, as the genetic material of the

Schmallenberg virus was found in the fetal tissues of aborted and newborn cattle as well as in their amniotic fluid.[55]

As is the case with all other living organisms, *Culicoides* spp. are also subjected to the impacts directly or indirectly associated with climate change, that may include adaptation or range shifting.[24] This poses an inherent risk, due to it being a viral vector and already exhibiting a relatively large global range. It is also increasingly concerning that a study insinuated that *Culicoides* spp. appear to prefer warmer temperatures and that their range may be increased in the future if rapid mitigation efforts are not undertaken to prevent further climate change.[28]

For these reasons, this study aimed to exemplify and identify the regions that are most suitable for a species of *Culicoides* biting midges, particularly *Culicoides punctatus*, in the Old World, as well as predict their future distribution under various climate change scenarios. This would potentially yield maps that can be used to define regions that are at the most risk of infections associated with *C. punctatus* so that necessary measures may be taken in said regions.

To this end, we employed maximum entropy modeling as is implemented in the MaxEnt application[45] using species occurrence records of *C. punctatus* that are available and open-source[38] along with bioclimatic variables representing both the current and future projected climate change scenarios.[40] The generated models would then show the potential range of *C. punctatus* in both the present as well as expected range shifts in the future. The models' performance was judged according to their AUC and TSS values, where judgement according to the AUC revealed the model was of excellent quality (Figure 1) [50] and assessment according to the TSS value revealed (0.7). The bioclimatic variables found to be most effective in predicting the range of *C. punctatus* were revealed to be temperature seasonality, minimum temperature of the coldest month, mean temperature of the coldest quarter, temperature annual range, and mean temperature of the warmest quarter, in descending order of predictive important (Figure 2). The response curves (Figure 3) also showed that *C. punctatus* appears to have a preference for moderately warm to hot climates, as was insinuated by a previous study.[28]

Maps of the generated species distribution models (figures 4 through 9) reveal concerning large suitable ranges for *C. punctatus* which inherently represents a risk to animal husbandry and a potential economic risk to the food supply. This is especially concerning in regions where the economy is already dependent on mixed agriculture, as is the case along the Nile Delta in Egypt and the northern regions of Sudan (Figure 5).

The future calibration maps (Figures 8 and 9) show substantial range shifts in the distribution of *C. punctatus* in the different climate change scenarios being studied. The most alarming regions are in North Europe, Central Asia, the Indian Subcontinent, and much of North Africa and Sub-Saharan Africa. This is in line with the observation that *C. punctatus* seems to prefer moderately warm to hot climates, as the projected increases in global mean temperatures will seem to directly cause an increase in suitable ranges for *C. punctatus*.

It is also worth noting that the BIOCLIM model in figure 4 appears to exhibit a much smaller range than the MaxEnt model in figure 5, which is possible explained by the fact that newer

Comentado [CK10]: I think I disagree. A smaller range does not mean less trustworthiness. This is explained by differences in modeling methods; you may argue that Maxent is more trustworthy because of better validation. Although, as already discussed, the use of this validation as a measure for trusting on future predictions is delicate.

species distribution modeling algorithms such as MaxEnt can perform better with relatively few environmental variables, relative to an older algorithm such as BIOCLIM.[56]

Our results show an urgent need to take preventive measures against *Culicoides punctatus* and potentially other related Culicoides spp. In fact, vaccinations against bluetongue virus[57] and Schmallenberg virus[58] are currently undergoing research, although further evaluation of these studies is needed to assess their efficacy as well as the duration of immunity provided. Nevertheless, the development of a successful vaccine would greatly mitigate the risks associated with *Culicoides* spp. The acquired data came compatible with severa previous species distribution modeling works either on the regional or global level [59-61]. *Culicoides imicola* as an example predicted to expand its range as a result of climate change through different parts of the world [62]. The expansion of insect agriculture or medical pests differ from one species to another however many species of insects could increase to certain limitation in warm temperature [63-66]

However, in addition to developing approaches to mitigate the risks associated with *Culicoides* spp., I also want to urgently note the impacts of climate change on diseases that are not exclusively limited to natural disasters,[21] contrary to the common misconception.

Comentado [CK11]: This seems like an interesring idea that should be explored and explained more completely.

Finally, I would like to note that the species distribution models for *C. punctatus* in this study were constructed using only bioclimatic variables, without accounting for species-species interactions or other biotic variables that may affect their distribution. This may provide a satisfactory estimation of habitat suitability for *C. punctatus*, but it may be further improved by accounting for additional biotic factors or by conducting smaller local and/or regional studies on a higher resolution.

Comentado [CK12]: There is a huge debate on the scientific literature on the capacity of making extrapolations from SDMs, especially for future scenarios. I think this paper should present better the shortcomings and limitations of future predictions made by SDMs.

Conclusions

In conclusion, this study highlights the importance of understanding the behavior and distribution patterns of Culicoides midges, particularly *C. punctatus*, in the context of predicting and controlling the spread of viral infections. The research utilized species distribution modeling to assess the environmental suitability and potential future distribution of *C. punctatus* in the Old World under different emission scenarios. The findings indicate that C. punctatus has a wide occurrence across the Old World, with Europe having the highest number of records. Climate was identified as a significant factor influencing the distribution of *C. punctatus*, suggesting that climate change could impact its range and potentially expand regions with endemic viral infections. This emphasizes the need for proactive measures to monitor and manage the spread of viral infections associated with *Culicoides* midges. The integration of geographic information systems (GIS) and remote sensing technology has played a crucial role in enabling high-throughput analysis techniques, eliminating the need for invasive experiments and allowing for remote assessment of species' habitats, land cover changes, and meteorology. Species distribution modeling, as a powerful tool in ecological research, has provided valuable insights into the potential distribution and vulnerability of *C. punctatus* to climate change. The implications of climate change on *Culicoides* midges and the associated viral infections are

Comentado [CK13]: I think you mean suitability. If not, I think the occurrence data should have been displayed in a map.

Comentado [CK14]: I think that “eliminating” is a very strong word here. To my knowledge, models are not yet trusted enough to make empirical evaluations unnecessary. They are excellent tools for guiding field efforts, guiding choice of localities for experiments, and etc. But, to some extent, experimental validation/confirmation is still needed.

significant, as the shifting ranges of these vectors may lead to the expansion of regions with endemic infections. This poses ecological and economic consequences, particularly in the livestock industry. Therefore, effective management strategies, conservation efforts, and mitigation measures should be designed based on the understanding provided by this study. Further research and monitoring are necessary to continuously update and refine the models in response to changing environmental conditions. This will contribute to an improved understanding of the ecological implications of climate change on Culicoides midges and provide a basis for designing targeted interventions to minimize the impact of biting midges on human and animal health. Overall, this study emphasizes the importance of considering the ecological dynamics of Culicoides midges and their interactions with climate change in order to develop comprehensive strategies for disease control and mitigation in the face of global environmental challenges.

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