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Original Article

Estimating the climate change consequences on the potential distribution of *Culex pipiens* L. 1758, to assess the risk of West Nile virus establishment in Chile

Estimando las consecuencias del cambio climático en la distribución potencial de *Culex pipiens* L. 1758 para evaluar el riesgo de establecimiento del virus del Oeste del Nilo en Chile

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ABSTRACT

Climate change affects the dynamics of vector-borne diseases. *Culex pipiens* Linnaeus is the main vector of West Nile fever; a widely distributed arbovirus, it is continuously increasing its distribution. Using a species distribution model, maps of suitable habitats of *Cx. pipiens* were generated for Chile in the current climate and three climate change scenarios, using global and regional georeferenced vector presence records as input, plus bioclimatic variables. Since this virus has not yet arrived in Chile, the purpose of this study is to anticipate potential risk areas and to prevent the establishment and spread of the virus. *Cx. pipiens* is widely distributed in Chile. The suitable habitats in Chile were concentrated mostly from 32° to 35°S, increasing in future scenarios up to 113 % in the northern zone and moving towards the mountains. This species conserves around 90 % of its niche in the future, and shows a reduction of 11.4 % in the severe climate change scenario. It is anticipated that Chile will experience an increase in the environmental suitability for *Cx. pipiens* moving from the Andes to the coastal zone throughout the country, mainly in the center-south. This will raise the risk of local virus transmission if the virus is introduced to the country via diverse routes.

Keywords: Vector-borne diseases, mosquitoes, MaxEnt, species distribution models.

RESUMEN

El cambio climático afecta la dinámica de las enfermedades transmitidas por vectores. *Culex pipiens* Linnaeus es el vector principal de la fiebre del Nilo Occidental, un arbovirus que aumenta continuamente su distribución. Usando un modelo de distribución de especies, se generaron mapas hábitats favorables para *Cx. pipiens* en los escenarios de cambio climático actuales y tres futuros. Se utilizaron registros de presencia de vectores georreferenciados globales y regionales como entrada, más un conjunto de variables bioclimáticas. Dado que este virus aún no ha llegado a Chile, el propósito de este estudio es anticipar áreas de riesgo potencial y prevenir el establecimiento y la propagación del virus. *Cx. pipiens* está ampliamente distribuido en Chile. Las mayores probabilidades de

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presencia en Chile se concentraron principalmente de 32° a 35°S, aumentando en escenarios futuros hasta el 113 % en la zona norte y avanzando hacia la cordillera. Esta especie conserva alrededor del 90 % de su nicho en el futuro y muestra una reducción del 11,4 % en el escenario de cambio climático severo. Se propone que Chile experimentará un aumento en los hábitats favorables para *Cx. pipiens*, el vector clave del WNV, que se moverá desde los Andes a la zona costera en todo el país, principalmente en el centro-sur. Esto producirá un aumento en el riesgo de transmisión del virus local si se introduce en el país a través de diversas rutas.

Palabras clave: Enfermedades transmitidas por vectores, mosquitos, MaxEnt, modelos de distribución de especies.

INTRODUCTION

West Nile Fever is a public health problem in several countries of the world. It is caused by an arbovirus belonging to the family Flaviviridae, genus *Flavivirus* (Brault 2009; Hernández *et al*. 2009; Weaver & Reisen 2010; Paz & Semenza 2013). It is appears as a mild flu and occasionally as a severe neuro-invasive disease, called West Nile encephalitis, that can occur with headache, high fever, neck stiffness, stupor, disorientation, coma, tremors, convulsions, muscle weakness and flaccid paralysis (Pradier *et al*. 2012). Since its identification in 1937, it has been isolated from all continents except Antarctica (Hernández *et al*. 2009; Weaver & Reisen 2010). Its geographical distribution has expanded considerably in the last ten years, probably due to global trade, climate change, ecological factors and the emergence of new viral genotypes (Brault 2009; Weaver & Reisen 2010; Chancey *et al*. 2015). This virus has two cycles of transmission: a primary enzootic cycle that occurs by transmitting the virus through the bite of an adult mosquito to susceptible bird species, resulting in virus amplification (Hernández *et al*. 2009; Paz & Semenza 2013). A secondary cycle involves mosquitoes that feed on the blood of birds and mammals, which behave as bridge vectors that spread infection to equines and humans, among other vertebrates. It has been isolated from species of mosquitoes belonging to 12 different genera (*Aedes* Meigen, *Aedeomyia* Theobald, *Anopheles* Meigen, *Coquillettidia* Dyar, *Culex* Linnaeus, *Culiseta* Felt, *Deinocerites* Theobald, *Mansonia* Blanchard, *Mimomyia* Theobald, *Orthopodomyia* Theobald, *Psorophora* Robineau-Desvoidy and *Uranotaenia* Lynch Arribálzaga). *Culex* is the most important vector genus involved in its maintenance, amplification and transmission. The participation of *Cx. pipiens* L. has been a common factor in the epidemic outbreaks that have occurred in different countries (Hernández *et al*. 2009).

Culex species are ornithophilic and anthropophilic, and cosmopolitan in the case of *Cx. pipiens* (Maciá et al. 1997; Salazar & Moncada 2004; Harbach 2011). They are important transmitters of several arboviruses, dirofilariasis and avian malaria (Bueno Marí *et al*. 2008). Nine species have been recorded in Chile: *Cx. acharistus* Root, *Cx. annuliventris* Blanchard, *Cx. apicinus* Philippi, *Cx. articularis* Philippi, *Cx. curvibrachius* Angulo, *Cx. dolosus* Lynch Arribálzaga, *Cx. plicatus* Olivares, *Cx. pipiens* and *Cx. quinquefasciatus* Say, distributed throughout practically all the national territory (González & Mac-Lean 2008). It is difficult to determine the species *Cx. pipiens*; *Cx. molestus* has been mentioned as a physiological variant of *Cx. pipiens* and is currently recognized as one of the more than 30 synonyms of *Cx. pipiens*. This variant is not present in Chile (Harbach 2012). *Cx. quinquefasciatus* is a valid species, which together with *Cx. pipiens*, *Cx. australicus*, and *Cx. globocoxitus* are part of the "pipiens subgroup" within the "pipiens Group". The morphological separation between *Cx. quinquefasciatus* and *Cx. pipiens* is complicated; they are very similar morphologically, especially the adults.

Cx. pipiens has a particularly broad global distribution, which in the Americas ranges from 45° N to 40° S, while in some areas of Europe it reaches up to 63° N. It has also been cited for eastern and southern Africa and different areas of Australia, as well as Asia. *Cx. pipiens* has been collected in an extensive area of Chile that includes cities from Arica (18° 28′ S) to Frutillar (41° 07′ S) (González & Rada 2015). However, studies of the natural history and distribution of Culicidae in Chile are fragmented and incomplete, disregarding relevant aspects of taxonomy, biology and knowledge of the immature forms of the species and their association with adults, which could hinder proper treatment and combat if diseases transmitted by these mosquitoes arrive (González *et al*. 2005; González *et al*. 2017; Carvajal & Faundez 2018). Recently the distributions of *Aedes aegypti* and *Cx. quinquefasciatus*

were analyzed as potential vectors of the Zika virus, showing that *C. quinquefasciatus* had a more temperate distribution up to 42° (Alaniz *et al.* 2019) while the risk involving *A. aegypti* is concentrated mainly in tropical latitudes to 35° in both hemispheres. There are other studies of distribution in changing climates in *A. aegypti* and *Cx. quinquefasciatus* (Samy et al. 2016; Kamal et al. 2018) and others that emphasize local and anthropogenic factors such as vegetation and urbanization in the distribution of mosquitos (Sallam et al. 2016; 2017; Wiese et al. 2019).

Since climate has a key influence on the biology, physiology and abundance of mosquito vectors, which are very sensitive to climatic conditions at many stages of their life cycle (Pradier et al., 2012), it is important to know the niche and distribution of *Cx. pipiens* in different current and future scenarios with climate change with the purpose of planning the health management practices to control and prevent the expansion of this species.

The objectives of this study were to estimate the effects of climate change on the potential distribution of *Cx. pipiens*, in current climatic conditions and under three contrasting scenarios of climate change, in order to identify better the risk zones for the possible future establishment of WNV transmission in Chile.

MATERIAL AND METHODS

Presence data

A total of 4694 presence records of the species referred as *Cx. pipiens* L. georeferenced worldwide were obtained from the Global Biodiversity Information Facility database (GBIF, http://www.gbif.org) and 106 from Chile from field sampling and data provided by the Institute of Public Health of Chile. In order to reduce the impact of spatial autocorrelation, a sub-sampling of global presences was obtained, eliminating duplicates and those presences separated by less than 10 km, using R software (version 3.5.1). The total data to calibrate the models included 837 records, of which 50 belong to Chile.

Environmental layers

Bioclimatic variables were obtained from the Wordclim database (http://www.worldclim.org/), with a spatial resolution of 5 arc-minutes (ca. 9 km) for current and future scenarios. We used three different climate change scenarios, from optimistic to pessimistic representative concentration pathways (RCPs): RCP 4.5, RCP 6.0 and RCP 8.5. These were based on 10 global climate models from: Beijing Climate Center, China Meteorological Administration (BCC-CSM1-1) (BC), National Center for Atmospheric Research (CCSM4) (CC), NASA Goddard Institute for Space Studies (GISS-E2-R) (GS), National Institute of Meteorological Research/Korea Meteorological Administration (HadGEM2-AO) (HD), Institut Pierre-Simon Laplace (IPSL-CMSA-LR) (IP), Atmosphere and Ocean Research Institute (The University of Tokyo), National Institute for Environmental Studies, Japan Agency for Marine-Earth Science and Technology (MIROC-ESM-CHEM) (MI), (MIROC5) (MC), (MIROC-ESM) (MR), Meteorological Research Institute (MRI-CGCM3) (MG) and the Norwegian Climate Centre (NorESM1-M) (NO) to 2070 (average for 2061-2080) of global climate models (GCM).

This data set included a total of 19 bioclimatic variables, with temperature and precipitation information. Because the collinearity of variables may lead to over-adjustment in the models (Beaumont *et al.* 2009), using ENMTools 1.4.4 a sub-sample of bioclimatic variables obtained after a Pearson correlation test was selected ($r < 0.70$) (Warren *et al.* 2008). Four bioclimatic variables were selected by this criterion: (bio1) average annual temperature; (bio2) average diurnal temperature range; (bio12) annual precipitation and (bio15) seasonality of precipitation.

Construction of the species distribution models

We used local presence to observe the effects of climate change. MaxEnt software 3.41 was utilized, a method that evaluates the probability of distribution of a species by estimating the probability distribution function of maximum entropy (Philips *et al.* 2006), using only linear, quadratic functions and product characteristics to avoid over-adjustment of the model (Kumar *et al.* 2014). To regulate the excess of parameterization, $\beta = 1$ was used (Phillips and Dudík, 2008). The threshold rule was applied: "10 percentile training presence"; 75 % training data were used and the remaining 25 % were used to check the model generated, with 50 replicates. The number of pseudo-absences used is equivalent to the number of presence records per species multiplied by 10 (Beaumont *et al.* 2009) for global and regional models. We used the PresenceAbsence package of R to choose the best model with the prevalence approach, average probability/suitability, sensitivity-specificity sum maximization approach, the sensitivity-specificity equality approach and the ROC plot-based approach (Liu *et al.* 2005). The pseudo-absences were resampled with ENMTools 1.4.4 with 10 replicates (Barbet-Massin *et al.* 2012).

Distribution stability

To analyze changes in distribution between current and future models, the areas in km^2 were calculated with ArcGIS (10.1) and intersected maps were reclassified with DIVA-GIS with a cutoff threshold of 0.23. A similarity test was performed with

ENMTools 1.4.4; the niche similarity test addresses whether the environmental niche occupied in one range is more similar to the one occupied in the other range than would be expected by chance (Broennimann *et al.* 2012).

RESULTS

All models proved to have excellent predictive performance (AUC > 0.9). The relative contributions of the environmental variables used for the model showed that annual mean temperature variables represent the highest contribution percentages for current and future models (54.6 % at present and 60 %, 60.5 % and 56 % for scenarios RCP4.5, 6.0 and RCP8.5, respectively). According to the jackknife test, the best predictor variable for the distribution of *Cx. pipiens* was annual mean temperature, second was annual precipitation, followed by average daytime temperature range and finally the seasonality of precipitation.

The potential distribution of *Cx. pipiens* in Chile (Figure 1) showed that there is a high probability of presence in the south-central zone of Chile from 32° to 35° S (Figure 1A), increasing in future scenarios (Figure 1 B, C, D). The greatest expansion of the area of 113.84 % (132551 km^2, red color Figure 2) was found in the in the RCP 8.5 scenario, which had the highest probabilities > 0.8, while in the RCP 4.5 scenario it expanded by 94.5 % (110047 km^2, red color, Figure 2A). An increase of 95.5 % (111154 km^2) also occurs in the RCP 6.0 scenario (red color, Figure 2B), mainly in the probabilities > 0.4. The similarity test for present and future climates showed 85 %, 84 % and 77 % in RCP 4.5, 6.0 and 8.5, respectively. Reduction areas (green color, Figure 2) were 1.8, 2.1 and 11.4 % in RCP 4.5, 6.0 and 8.5, respectively.

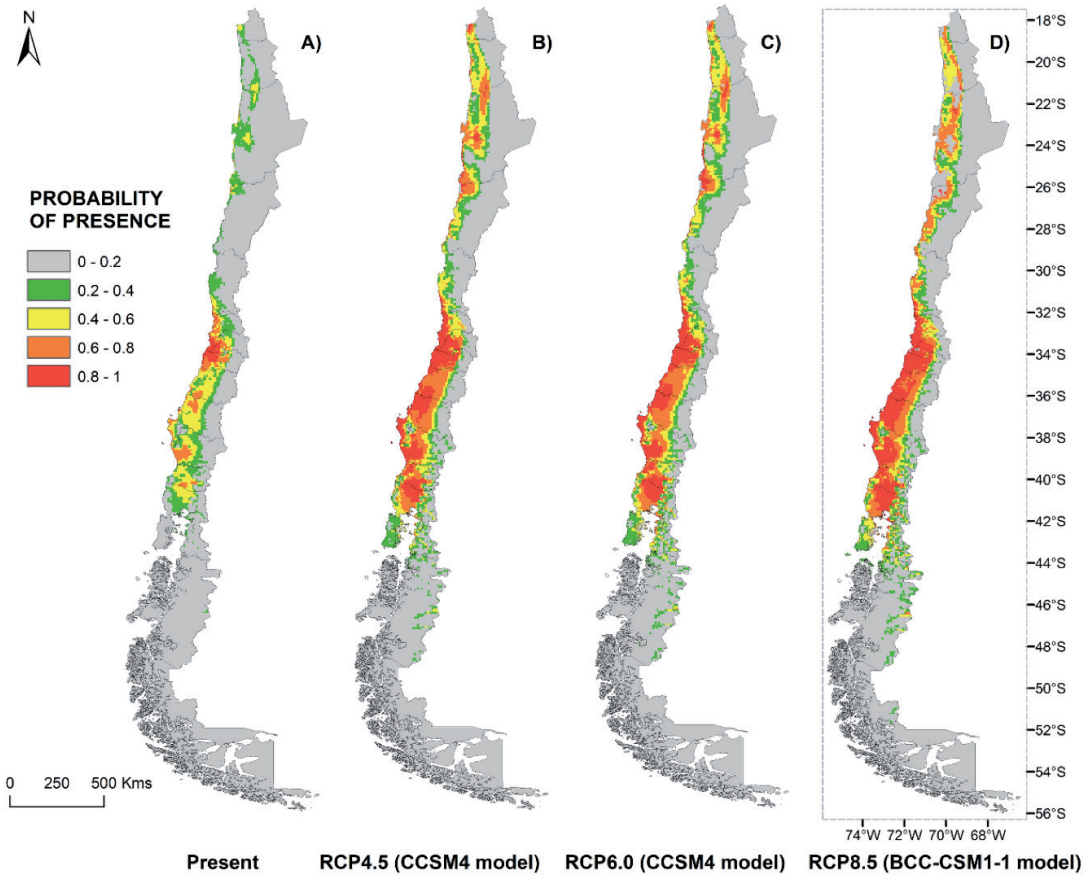

Figure 1. Models of potential distribution of the *Cx. pipiens* group in Chile, current and future according to climate change scenarios. A: Current, B: RCP4.5, C: RCP6.0, D: RCP8.5. / Modelos de distribución potencial del grupo *Cx. pipiens* en Chile, actual y futuro según escenarios de cambio climático. A: actual, B: RCP4.5, C: RCP6.0, D: RCP8.5.

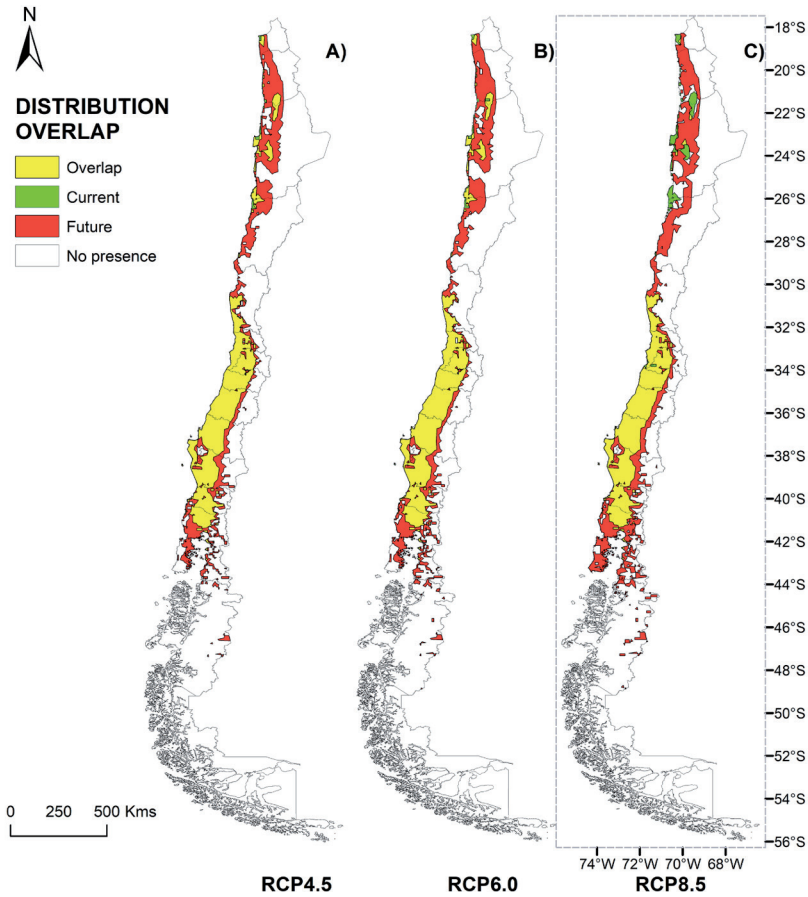

Figure 2. Overlap of current distribution area and different scenarios of climate change of the *Cx. pipiens* group. A: RCP 4.5, B: RCP 6.0, C: RCP 8.5. / Superposición del área de distribución actual y diferentes escenarios de cambio climático del grupo *Cx. pipiens* A: RCP 4.5, B: RCP 6.0, C: RCP 8.5.

DISCUSSION

The potential suitable distribution of *Cx. pipiens* is widespread across the different ecological zones of continental Chile, which is consistent with the ecological preference and empirical geographic distribution of this species, Arica (18° 28′ S) to Frutillar (41° 07′ S) (González & Rada 2015).

This study used bioclimatic variables to predict the distribution of *Cx. pipiens*; the main predictor of the distribution was the mean annual temperature. This agrees with Gardner *et al.* (2012), who found that high average daily temperatures favored the abundance of larvae of the *Cx. pipiens* group, as they develop more rapidly in environments with higher aquatic and environmental temperatures. This is consistent with the microscale analysis performed by Figueroa *et al.* (2016) in three regions of Chile, where the temperature axis was a fundamental axis and positively correlated with the presence of this species. Paaijmans *et al.* (2010) reported that the relationship between mosquito development and temperature is generally one of the keys to understanding the dynamics and current and future distributions of vector-borne diseases. Many models use mean air temperature to estimate larval development times, and therefore adult vector density and/or disease risk.

The potential distribution of *Cx. pipiens* will expand to a large extent in the future because it tends to adapt to optimal climatic conditions for its reproductive cycle (Gardner *et al.* 2012). A slight increase in rainfall in the northern zone of Chile would favor larval stages. Loss of up to 30 % of precipitation in the south-central zone of Chile (IPCC, 2014) could explain the possible distribution increase in this area, because at present excess rain causes immature stages to be washed out (Geery & Holub 1989; Gardner *et al.* 2012; Lebl *et al.* 2013). This increase in the area is mainly in the warm zone of Chile (north-central: 18-32°S) and only a little in the cold zone of the southern Chile (42-44°S). The expansion

of suitable habitats to more southern latitudes found in our study may be due to the ability of *Cx. pipiens* to diapause and therefore extend its distribution to cold areas (Almirón and Brewer 1996). The expansion to warm areas agrees with studies that suggest that warmer conditions are drivers of mosquito abundance (McMichaael et al. 2011). However, in a related species, *Cx. quiquefasciatus*, other studies suggest a delay in the breeding season in areas with hot and dry spring and summer and suitability of occurrence in areas of low temperatures (Samy et al. 2016).

Species distribution models proved to be a good first approach to estimate the current and future potential distribution of the *Cx. pipiens* group in Chile, a species that in the future could be infected by West Nile virus. However, the expansion of the vector is not the only factor for expansion of West Nile virus. It has been shown that the distribution of bird populations, urbanization and agriculture are related to the expansion of this problem (Kilpatrick 2011; Bradley *et al.* 2008; Wiese *et al*. 2019), as well as the underlying sociopolitical issues such as defective public health infrastructure (Gubler 2007) and poverty (Bhakat *et al.* 2014; Hernandez *et al.* 2018) in the regions of its expanse. For example, to understand better the expansion of *Aedes albopictus* into urban places it is important to consider the role of both environmental and neighborhood factors (Wiese et al. 2019). Environmental variables help to explain conditions associated with mosquitoes in suburban/rural areas, while neighborhood factors are better able to explain mosquito habitats in urban places (Wiese et al. 2019). Another study emphasized that the distribution of WNV transmission is dependent on the mosquito vector and its ecological requirements, which vary from one place to another, showing that although precipitation of driest months was the best predicting variable for the density of *Cx. nigripalpus*, the distribution of *Cx. quinquefasciatus* was more related to vegetation. Urbanization and vegetation were also highly relevant in predicting the suitability of this species (Sallam *et al.* 2016).

Limitations to this study are taxonomic, because in some old data the identification of *Cx pipiens* may be doubtful since it is difficult to differentiate from *Cx quinquefasciatus*. Another limitation is that when we consider that the climatic variables are changing, the projection of the niche is conditioned by the local adaptation dilemma *vs*. niche fidelity or conservatism (Wiens *et al.* 2010). Niche conservatism, the tendency of a group to remain in its ancestral environment, is assumed in niche models. However, by contrast in some species dispersion may not be only a demographic response to the opportunity to colonize environments similar to their place of origin but also local adaptation may alter the fundamental niche, particularly when the invasion range is wide enough to encompass a wide spectrum of weather conditions.

The ecological maps produced can contribute meaningfully to the design and planning of mosquito surveillance programs by defining strategic areas for new collections and to control the possible expansion, especially in the case of poorly sampled regions. In this particular case the highest risk zones are currently from 30.5° to 41°S, where the mosquito would remain in the future. The monitoring of their populations should be focused in this zone to evaluate the risk of occurrence of arboviruses, thus optimizing the use of resources, minimizing the effort invested in surveillance and generating important contributions to decision/making and the adoption of preventive measures. The identification of areas potentially inhabited by the WNV vector is crucial for early response and prevention of a prospective epidemic in Chile. These results may be helpful in generating hypotheses and in identifying the appropriate conditions for WNV amplification and transmission if and when introduction occurs.

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