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ARTHROPODS AND MEDICAL ENTOMOLOGY - REVIEW

Using ecological niche models to describe the geographical distribution of the myiasis-causing *Cochliomyia hominivorax* (Diptera: Calliphoridae) in southern South America

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Abstract

In southern South America, namely Argentina and Chile, *Cochliomyia hominivorax* (Coquerel) is the main myiasic agent on humans and domestic animals. The distribution pattern of the species is poorly known and the southern limit of its geographic distribution is unclear. The aims of this study are to elucidate the basic environmental factors associated with occurrence of this myiasic species, evaluation of models constructed on the basis of occurrence data based on adult specimen records to predict geographic occurrence of myiasis, evaluation of unsurveyed sites of high potential of occurrence of the species, and recognition and prioritization of areas that need medical control and specific prophylaxis practices related to this pest. The maximum entropy modeling system (Maxent) was used. Maps of potential distribution of *C. hominivorax* were produced using two different datasets, models obtained with all localities known for the species (combining medical data and taxonomic data) and only-taxonomic models (excluding medical data). The results obtained include an updated compilation of occurrence of the species in Argentina and Chile. Predictive models obtained in this work indicated that large areas of central-eastern territory of Argentina has the potential for *C. hominivorax* occurrence, probably reaching the parallel 42° S as is indicated by the complete datasets. Only-taxonomic models fail to predict those myiasic cases occurring in the nearer areas of the Andean chains. The main variables associated with the distribution of *C. hominivorax* were, alternatively, isothermality or minimum temperature of the coldest month. These results provide a new analytical resource of high potential for the prevention of myiasis and to supports further epidemiological studies.

Keywords Myiasis · *Cochliomyia hominivorax* · Screwworm fly · Distribution · Ecological niche models

Introduction

Myiasis describes the infestation of tissues of a vertebrate host with dipteran larvae. In the case of domestic animals and humans, this infestation by maggots is frequently associated with neglected wounds, known as traumatic myiases (Hall and Wall 1995). The screwworm fly, *Cochliomyia hominivorax* (Coquerel) is an obligatory parasite of wild and domestic animals and humans, whose larval instars complete their development in living tissues. During the infestation, the larval stages of this pest-species cause serious injuries and can lead to host death. These characteristics provide this species with a high economic and sanitary impact (CABI 2018).

Due to its considerable economic and medical importance, *C. hominivorax* has been the subject of intense research into many aspects of its behavioral ecology (Brenner 1984; Thomas and Mangan 1989; Thomas 1991; Mayer and Atzeni 1993), habitat preference (Brenner 1985; Mangan and Thomas 1989), and morphology (Leite and Guevara 1993; Leite 1995) among several other topics. However, little is known in terms of the basic environmental factors associated with its

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occurrence, and the species has received little attention in preventive studies and risk evaluations at a geographic scale in the neotropics.

The original geographic distribution of this myiasic agent ranges from the southern USA to Argentina and Chile (James 1947; Hall and Wall 1995). However, control programs have eradicated this pest from North America but the screwworm fly is still an important pest in South America. At the southern extreme of its distribution in South America, namely Argentina and Chile, *C. hominivorax* is the main myiasic agent on humans and domestic animals, with higher infestation prevalence in comparison to other fly species according to the few existing medical and veterinary reports (e.g., Mazza 1939; Mariluis et al. 1994; Visciarelli et al. 2007). In such cases, however, the screwworm was recorded from few localities in Argentina (see Mariluis and Mulieri 2003; Fresia et al. 2013) and Chile (Dear 1985), and the available literature is unclear and ambiguous regarding the southern limits of its geographic distribution. As argued by Del Ponte (1958), *C. hominivorax* can reach 45° S, whereas other works have fixed the southernmost ranges at 30° S, approximately (e.g., Boero and Morini 1965).

In comparison to necrophagous Calliphoridae, *C. hominivorax* is relatively poorly sampled (Cardona López et al. 1994; Coronado and Kowalski 2009) and consequently, the species is scarcely documented in biological collections of museums. The paucity of detailed records on geographic distributions of this primary-myiasis agent has been a major limiting factor for modeling areas of potential distribution and, consequently, risk-areas associated with this species. The availability of tools for ecological niche modeling (ENM) has made possible development of high-resolution maps of potential distribution for arthropods of medical and veterinary importance (e.g., Foley et al. 2008; Almeida et al. 2013). In the case of *C. hominivorax*, there are recent studies using such models of distribution, focusing on the phylogeographics of the species, describing the mode and time of divergence of the regional groups of *C. hominivorax* on a continental scale to construct hypotheses of population divergence (Fresia et al. 2013, 2014). There is no distribution model devoted to accurately describing the potential distribution of this myiasis-causing species in southern South America.

Labels of voucher specimens deposited in scientific collections probably constitute the largest primary biodiversity data. Although biological information available in this format is generally biased, natural history museums are crucial resources for biological information of poorly known taxa, particularly given the development ENM approach (Reutter et al. 2003; Gaubert et al. 2006). For instance, such a model uses presence data only and is a useful tool in cases with a small number of occurrence records. (Pearson et al. 2007). Hence, modeling the spatial distributions of parasitic flies on human and domestic animal is crucial to understanding the environmental determinants of myiasis as well as for guiding the planning of control programs and prevention.

In an attempt to refine information on the geographical distribution of the screwworm fly in southern South America, a revision aimed at collecting available data of this species in natural history museums, in addition to bibliographical sources (taxonomic works and myiasis reports), was developed. The following goals are associated with this data collection effort and modeling obtained through ENM: (1) generation of updated maps of the screwworm fly's current and potential distribution, (2) description of basic environmental factors and its influence associated with the occurrence of this myiasic species, (3) evaluation of models constructed on the basis of occurrence data based on adult specimen records to predict geographic occurrence of myiasis, (4) evaluation of unsurveyed sites of high potential of occurrence of the species, and (5) recognition and prioritization of areas that need medical control and specific prophylaxis practices related to this pest.

Materials and methods

Species occurrence data

All available records of *C. hominivorax* from southern South America (i.e., Argentina and Chile) were used. The occurrence database was compiled from literature and material deposited in museum collections: "Instituto-Fundación Miguel Lillo" (IFML) (Tucumán, Argentina); Museo Argentino de Ciencias Naturales "Bernardino Rivadavia" (MACN); and Museo de La Plata (MLP) (Table 1). Localities that remained unrecognizable or imprecise were not taken into account for models. Data recovered were classified in two categories: (1) *medical data*: based in human myiasis cases obtained from literature (e.g., case reports) or (2) *taxonomic data*: associated with adult specimens recovered from museums or taxonomic literature (Table 1). In the case of medical data, the georeferences are ascribed to the origin of the patients affected with myiasis wounds whenever these data are available from the original publications.

Variables

A total of 19 bioclimatic variables with a spatial resolution of 2.5 arcmin (approximately 5 km^2) were used to construct the models. These data are available from the WorldClim Version 2 database (Fick and Hijmans 2017) and were derived by interpolation of climate station records from 1970 to 2000 to represent biologically significant information that may influence the distribution of a species. These environmental variables included 19 climatic layers.

Table 1 Records of *Cochliomyia hominivorax* from Argentina and Chile, obtained from museums and bibliographic sources

Country	Province/region	Locality	Lat	Long	Specimens	Source
Argentina	Buenos Aires	Arroyo Largo, Paraná Miní	− 34.21	− 58.44	1 m	MACN
	Buenos Aires	Bahía Blanca	− 38.72	− 62.28		*Visciarelli* et al. 2007
	Buenos Aires	Buenos Aires	− 34.61	− 58.44		Mariluis and Mulieri 2003
	Buenos Aires	Estación Lezama	− 35.87	− 57.88		Lyra et al. 2009
	Buenos Aires	Estancia San Claudio	− 35.64	− 61.35	10 m	FAUBA
	Buenos Aires	Guernica	− 34.92	− 58.38		*Menghi* et al. 2010
	Buenos Aires	Hudson	− 34.79	− 58.15		Centeno et al. 2004
	Buenos Aires	La Plata	− 34.91	− 57.94	2 m, 1 f	MLP
	Buenos Aires	Llavallol	− 34.79	− 58.39		Mariluis and Mulieri 2003
	Buenos Aires	Longchamps	−34.86	−58.39		*Menghi* et al. 2010
	Buenos Aires	Martinez de Hoz	− 35.33	− 61.61	5 m	FAUBA
	Buenos Aires	San Antonio de Areco	− 34.24	− 59.47	4 m	FAUBA
	Buenos Aires	San Isidro	− 34.50	− 58.58		Mariluis and Mulieri 2003
	Buenos Aires	Villa Elisa	− 34.84	− 58.10		Mariluis and Mulieri 2003
	Buenos Aires	Zelaya	− 34.37	− 58.89	2 m	MACN
	Chaco	Colonia Benitez	− 27.32	− 58.93		Cardona López et al. 1994
	Chaco	Resistencia	− 27.46	− 59.01	1 f	MACN
	Chaco	Villa Angela	− 27.58	− 60.72		Heizenreder et al. 2009
	Córdoba	Agua de Oro	− 31.07	− 64.30		Mariluis and Mulieri 2003
	Córdoba	Capilla del Monte	− 30.85	− 64.52		Mariluis and Mulieri 2003
	Córdoba	La Para	−30.87	−62.98		Mariluis and Mulieri 2003
	Córdoba	Ongamira	− 30.75	− 64.46	1 m	MACN
	Corrientes	Bella Vista	− 28.50	− 58.83		Mariluis and Mulieri 2003
	Corrientes	Corrientes	− 27.46	− 5878		Dufek et al. 2015
	Corrientes	Esteros del Iberá	− 28.32	− 59.94	2 f	MACN
	Corrientes	Galarza	− 28.10	− 56.68		Dufek et al. 2015
	Corrientes	Ituzaingo	− 27.59	− 56.68	1 f	IFML
	Corrientes	San Nicolás	− 28.18	− 57.45	1 f	Dufek et al. 2015
	Corriente	Santo Tomé	− 28.55	− 56.04	1 m	IFML
	Entre Ríos	Boca Río Mocoretá	− 30.68	− 57.87	2 f	MACN
	Entre Ríos	Pronunciamiento	− 32.34	− 58.43	2 f	MACN
	Formosa	Reserva El Bagual	− 26.22	− 58.86		Mariluis and Mulieri 2003
	Formosa	Las Lomitas	− 24.70	− 60.60		*Mazza and Reyes Oribe* 1939
	Jujuy	La Mendieta	− 24.32	− 64.97		Mariluis and Mulieri 2003
	La Pampa	INTA Anguil	−36.52	−64.02		Suárez 2002
	Mendoza	Agua de las Chilcas	− 32.79	− 68.96		Mazza and Basso 1939
	Mendoza	Chacras de Coria	− 32.97	− 68.88		*Basso* 1939
	Mendoza	Chapanay	− 32.92	− 68.88		*Basso* 1939
	Mendoza	El Vergel	− 32.80	− 68.63		*Basso* 1939
	Mendoza	La Consulta	− 33.74	− 69.12		*Basso* 1939
	Mendoza	Maipú	− 32.97	− 68.78		*Visciarelli* et al. 2003
	Mendoza	Mendoza	− 32.89	− 68.82		*Basso* 1939
	Mendoza	Uspallata	− 32.59	− 69.35		*Basso* 1939
	Misiones	Puerto Iguazú	− 25.60	− 54.57		Mariluis and Mulieri 2003
	Neuquén	Parque Nacional Lanín	?	?	1 m	IFML
	Río Negro	Río Colorado	− 38.99	− 64.09	1 f	MACN
	San Juan	?	?	?		Oliva 2002
	San Luis	Potrero de los Funes	− 33.21	− 66.23	1 m	MACN

Table 1 (continued)

Country	Province/region	Locality	Lat	Long	Specimens	Source
	Santa Fe	Castellanos	− 31.22	− 61.73	1 m	FAUBA
	Santa Fe	El Piquete	− 31.57	− 60.72	1 m	MACN
	Santa Fe	Rafaela	− 31.27	− 61.48		Mariluis and Mulieri 2003
	Tucumán	Los Puestos	− 27.29	− 65.01	1 m	IFML
	Tucumán	Monteros	− 27.17	− 65.50		*Olea* et al. 2014
Chile	Valparaíso	Limache	− 32.99	− 71.27		Dear 1985
	Valparaíso	Valparaíso	− 33.05	− 71.61		Dear 1985
	Metropolitana	Santiago	− 33.46	− 70.64		*Philippi* 1861

Sources referred to human myiasis reports (medical data) are indicated in italic. *f*, female; *m*, male

Unknown locality or georeference are indicated with question marks

Models

The inclusion of too many of these climate variables may cause "over-fitting" problems, as many represent similar and highly correlated dimensions of climate. To avoid over-fitting models, we removed highly correlated variables prior to analysis. We calculated the Pearson product-moment correlation coefficient (r) in a pair-wise fashion for all 20 bioclimatic variables for all locality records. A single variable from a pair of highly correlated variables ($r > 0.70$) was selected according to the estimated percent contribution of each environmental variable to the model including all variables (full model). We discarded the variable that contributed least to this full model. The resultant model includes the following variables: mean diurnal range (BIO2), isothermality (BIO3), temperature seasonality (BIO4), mean temperature of the wettest quarter (BIO8), precipitation of driest month (BIO14), and precipitation of the warmest quarter (BIO18) (model 1). Alternatively, we perform a second model by using the set of climate variables selected in the previous work of Fresia et al. (2013): mean diurnal range (BIO2), maximum temperature of the warmest month (BIO5), minimum temperature of the coldest month (BIO6), mean temperature of the wettest quarter (BIO8), precipitation seasonality (BIO15), precipitation of the warmest quarter (BIO18), and precipitation of the coldest quarter (BIO19) (model 2).

Models were produced with a maximum entropy approach and were generated with the software Maxent v3.3 (Phillips et al. 2006; Phillips and Dudik 2008). This presence-only ENM-method is a good-performing tool which is commonly applied to model potential distributions of species (Elith et al. 2006). Default settings were used to run the models. Ten replicates were made using the subsample option, and setting a random test percentage of 20% of the input localities set aside for model testing. Models fit were evaluated by mean of the area under the curve (AUC) of the receiver operating characteristic (ROC) plot (Phillips et al. 2006). The AUC ranges from 0 to 1; an AUC < 0.5 indicates poor performing; an AUC > 0.75 indicates a very good fit.

Maps of potential distribution of *C. hominivorax* were produced using two different datasets applied to models 1 and 2. Complete-data models (CDM) were obtained with all localities known for the species (combining medical data + taxonomic data). On the other hand, only-taxonomic models (excluding medical data) (OTM) were performed to test whether its restricted dataset is a good predictor of myiasis occurrence.

To obtain a contextualized map of potential distribution of *C. hominivorax* at the southern portion of South America, 63 existing records for the rest of the countries of South America were included in each of the models (data not showed in maps). These data were obtained from Fresia et al. (2013).

The study of Fresia et al. (2014) indicated that phylogeographic patterns of *C. hominivorax* are very coincident with general patterns of ancient human movements in the Americas, suggesting that humans might have played a crucial role in shaping the distribution and population structure of *C. hominivorax*. In addition, as occur with other blow fly species, intercontinental spread mediated by human activities is well documented (Chermette 1989; Lindquist et al. 1992). Our models were calibrated in a large study region that included the entire geographical range of the species, including the invaded areas of Northern Africa (Lindquist et al. 1992). Using random sites across global scale implies the species could have dispersed anywhere across the continents, and the whole continents considered available for sampling. This is usually questionable because the oceanic areas or other unsuitable areas are likely barriers to dispersal of the focus species (Anderson and Raza 2010; Elith et al. 2011). Because human dispersion is applicable for this case, such barrier assumptions are a priori discarded for modeling and eventually for detecting potential areas to being invaded by human facilitation. However, it is recognized that such "landscape of interest" (the area used for background sampling) here adopted significantly affects the results of distribution models, producing overfitting to conditions found near the occupied localities as is pointed out by Anderson and Raza (2010).

Setting threshold

Many applications and model evaluations require binary outputs, and thresholds are needed for these transformations. As Maxent produce a continuous prediction, from 0 to 1, a threshold rule is needed to differentiate "suitable" and "not suitable" grid cells. In addition, selecting an appropriate threshold affects result considerably, and in some cases, the same model may have different predictions with different thresholds. There are many approaches to determining thresholds (Liu et al. 2005, 2013). For this work, two alternative thresholds were applied to our obtained models, basically, a criterion sensitive to outliers, and the other more conservative.

First, we chose the lowest predicted value associated to an occurrence data, termed the "least training presence threshold" (LTP). This threshold value is sensitive to outliers and can be either overly restrictive (in cases of few occurrence data) or overly broad (e.g., if occurrence records are incorrectly georeferenced). The alternative threshold used was the "cumulative probability of 10", which rejects 10% of the presence observations (omission of 10%). This restrictive threshold was selected to provide a more conservative interpretation of the distribution.

Results

Records of *C. hominivorax* in Argentina and Chile

The complete dataset of *C. hominivorax* is presented in Table 1 and corresponds to 53 localities for Argentina and 3 for Chile. This result includes 19 new recorded localities (all in Argentina) and 37 previously published records, 14 of which correspond to human myiasis reports (13 in Argentina, 1 in Chile). Data collected include the first records of the species for the following provinces of Argentina: Entre Ríos, Formosa, Neuquén, Río Negro, and San Luis. In the case of references from San Juan (from bibliography) and Neuquén provinces (based on a single male specimen), they are not associated with any precise locality, hence they were not georeferenced (Fig. 1a). Both, the specimen recorded in "Parque Nacional Lanin" (Neuquén province) and the specimen from "Rio Colorado" (Río Negro province), constituted the southernmost objective (specimen-based) records obtained for the species (Table 1).

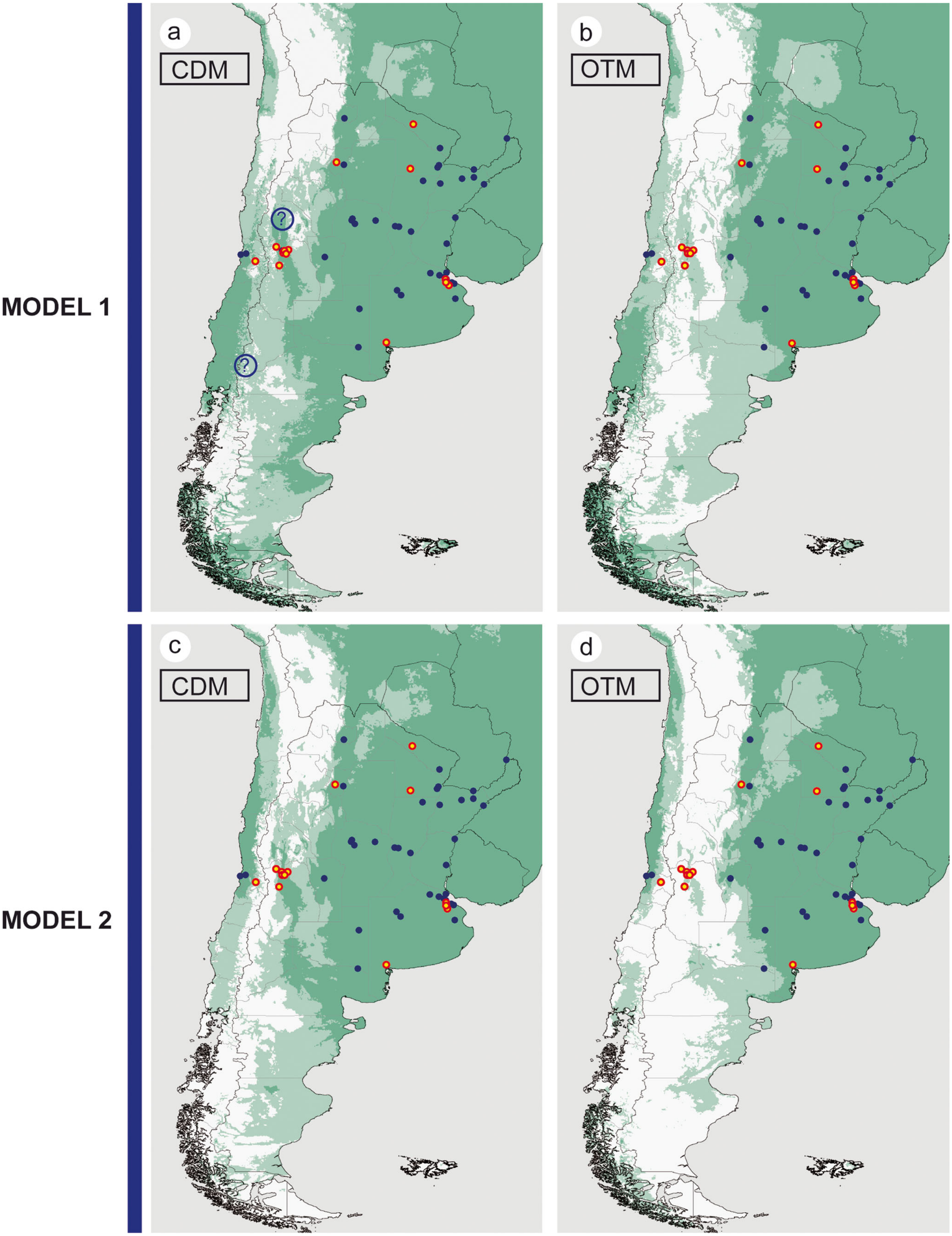
Maxent results

The two environmental datasets used, model 1 and model 2, showed excellent performance in all cases. In the case of complete data models (CDM), the average test AUC of model 1was 0.942, with a standard deviation (SD) of 0.021; and the average test AUC of model 2 was 0.947, with a standard SD of 0.009. In the case of taxonomic data models (excluding myiasis data) (OTM), the average test AUC of model 1was 0.950, with a standard deviation (SD) of 0.012; and the average test AUC of model 2 was 0.944, with a standard SD of 0.016. As is indicated by these results, the AUC values of dataset running under the complete data model 2 showed a slightly better model projection than those of model 1.

Potential range obtained with Maxent indicates that both models, trained on the two datasets, showed the same general pattern of distribution. The four predictions obtained showed larger areas of climatic suitability for the *C. hominivorax* when threshold applied was the least training presence. These enlargements are specially observed toward western and southern areas in Argentina and toward southern and central areas in Chile (Fig. 1a–d). Potential areas defined with the restrictive threshold (cumulative probability of 10) showed more homogeneous results. In all cases, the models defined large continuous distribution in eastern Argentina, with isolated patches of suitability in western Argentina and Chile. All potential distribution obtained for *C. hominivorax* predicted the presence of the species in some Argentinean province with no records currently available, these are Salta, Santiago del Estero, and eastern of Catamarca and La Rioja. However, the predictions provided by the model 1 CDM (Fig. 1a) show a wider distribution of *C. hominivorax* in contrast with the model 2 (Fig. 1c). Model 1 (with both datasets) is covering larger southern and central areas of Chile and Argentina (Fig. 1a–b) in comparison to model 2 (with both datasets) (Fig. 1b–c).

Taxonomic dataset models as predictors of occurrence of myiasis

Only-taxonomic models (OTM) fail to predict those myiasic cases occurring in the nearer areas of the Andean chains; these include the cases myiasis reports documented in western Argentina (Mendoza province) and the single myiasis case of Chile (Fig. 1b, d). Complete data models (CDM) extend the predicted distribution to include the locations referred to these myiasic cases (Fig. 1a, c). However, the performance of models greatly diverges in the predicted areas, especially in Chile and the southern limits of distribution (e.g., 1 CDM indicates suitable regions in southern continental extreme). In fact, the main area where both models overlap is associated with the northeastern Argentina, reaching the north eastern of Chubut province as the southern limit of the species. Conversely, only isolated patches are observed in western Argentina and Chile, indicating poor concordance between models for such areas (Fig. 2).


MODEL 1
a
CDM
?
?
b
OTM
MODEL 2
c
CDM
d
OTM

◀ **Fig. 1** Localities of *C. hominivorax* displayed on the backgrounds of Maxent-created ecological niche models. **a**–**b**, Model 1. **c**–**d** Model 2.Taxonomic data, blue dots; medical data (human myiasis cases), red and yellow dots. Question mark indicated not georreferenced records from San Juan province and Lanin National Park (only included in map a). Model thresholded by "least training presence" are displayed in light green; models thresholded by "cumulative probability of 10" are displayed in dark green. In Figs. **b** and **d** medical data are also included despite they are not part of OTM datasets

Variables

The most informative bioclimatic variables for each model differ (Table 2). For model 1 (CDM and OSM), isothermality (BIO3) appears to be an important variable for constructing the suitability models (Table 2). In contrast, for the model 2 (CDM and OSM), the minimum temperature of the coldest month (BIO6) accounts for most of the information necessary to construct the predicted distribution for the species (Table 2).

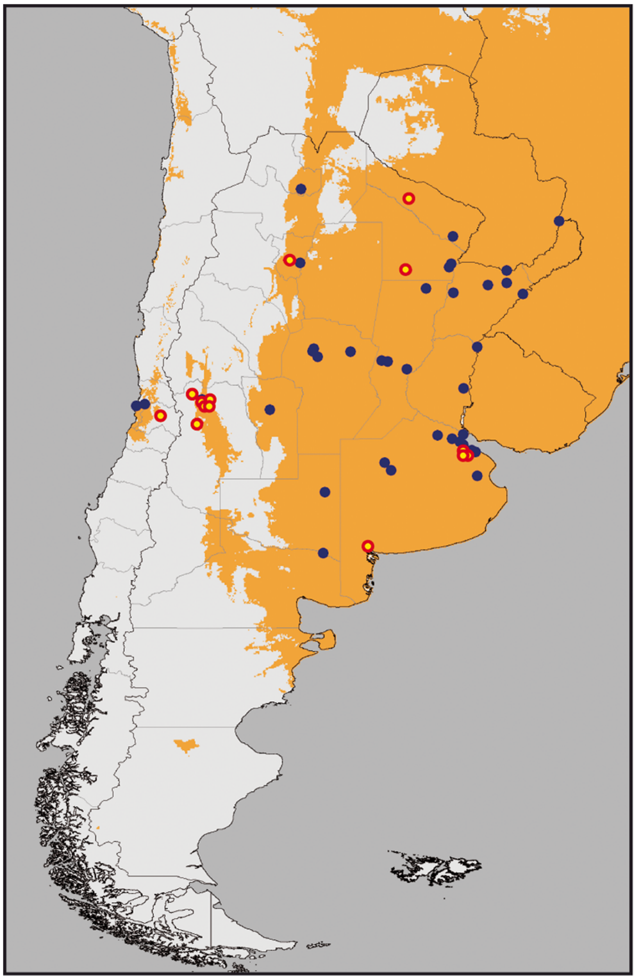


Fig. 2 Overlap between the potential distribution models of *C. hominivorax* obtained with CDM datasets. Taxonomic data, blue dots; medical data (human myiasis cases), red and yellow dots

Discussion

If the species whose potential habitat is being predicted is a pest or disease organism that affects humans, then spatial prediction of its potential distribution gives public health authorities' goals and supports further epidemiological studies (Franklin 2010). Indeed, accurate maps of screwworm habitat would lead to greater monitoring efficiency to delineate strategies for the surveillance of myiasis and earlier control of outbreaks of the species (Phillips et al. 2004). There are few studies summarizing and reporting the field records by localities of *C. hominivorax* including human myiasis cases in southern South America. For myiasis-causing species, little is known of the basic environmental factors associated with their prevalence, and the phenomenon of myiasis has very few well-documented occurrences in Argentina and Chile.

Predictive models obtained in this work indicated that large areas of central-eastern territory of Argentina have the potential for *C. hominivorax* occurrence, probably reaching the parallel 42° S as is indicated by the complete datasets. However, the compiled data are still too scarce to accurately describe the distribution pattern of the screwworm fly in southern temperate areas of South America. For instance, the information obtained from taxonomic sources-based adult specimens (both, directly observed as museum specimens, or indirectly obtained from literature) is not adequate as a surrogate to predict the occurrence of known myiasis cases by this species. Currently, a good modeling of the species can not lack data provided by documented myasis cases, especially in the absence of monitoring programs targeted to adult populations of screwworm (using trappings or sentinel animals), as were applied in other areas (Coppedge et al. 1978; Parker and Welch 1992; Coronado and Kowalski 2009). The occurrence of this species in western Argentina and Chile was not taken into account in a previous model generated by Fresia et al. (2013), whereas the inclusion of such data and the potential distribution obtained for these areas is in the form of isolated patches of suitability, with highly variable patterns between the resultant models. These characteristics may indicate that more efforts are necessary to elucidate subtle patterns of biogeography of this species and the key factors delineating its distribution in southwestern areas of South America.

For applications of niche modeling, it is important to distinguish between fundamental, realized, and climatic niches. The fundamental niche designates the set of all environmental conditions that permit a species to exist (Hutchinson 1957); the realized niche is the portion of the fundamental where the species occurs as a consequence of biotic and abiotic interactions (Wiens et al. 2009), and the climatic niche consists of the set of climatic conditions where the species may occur (Quintero and Wiens 2013). Consequently, when applying ENM, the resultant models that are based on the relationship between climate parameters and species response provide a representation of the climatic niche of

Table 2 Relative contributions (percentage) of the variables to the Maxent models

Variables	Model 1		Model 2	
	CDM	OSM	CDM	OSM
Mean diurnal range (BIO2)	2.6	3.6	5	5.2
Isothermality (BIO3)	56.3	47.3	–	–
Temperature seasonality (BIO4)	6.2	6	–	–
Maximum temperature of the warmest month (BIO5)	–	–	9.3	6.9
Minimum temperature of the coldest month (BIO6)	–	–	52.4	41.2
Mean temperature of the wettest quarter (BIO8)	6	4.9	0.7	0.5
Precipitation of driest month (BIO14)	18	13.7	–	–
Precipitation seasonality (BIO15)	–	–	2.3	2
Precipitation of the warmest quarter (BIO18)	10.8	24.5	23.9	37.6
Precipitation of the coldest quarter (BIO19)	–	–	6.4	6.6

a species (i.e., a subset of the fundamental niche) (Pearson and Dawson 2003). The influence of climatic variables on the occurrence of screwworm fly has been previously documented in other studies (Krafsur et al. 1979; Parker et al. 1993; Orcellet 2005). Our results suggest that variables indicating seasonal temperature fluctuation are the most significant contributors to explain the bioclimatic niche of the species. Climatic model predictions are an important tool and a valid first approach to the potential magnitude and distributional pattern of species, although they should be interpreted carefully because they do not consider important factors other than climatic. In fact, soil temperature and moisture are known factors affecting pupal viability and emergence of screwworm fly (Orcellet 2005). Variables associated with soil characteristics may represent important factors other than climate. In addition, vegetation coverage represents another source of variables which is known to affect *C. hominivorax*, with fly numbers consistently higher in forested habitats (see Mangan and Thomas 1989, Phillips et al. 2004). Given that adults of *C. hominivorax* are associated with forest and the pupal survival depends on such coverage, it would be interesting to incorporate vegetation cover into future analyses to determine if this would refine the habitat suitability models.

Taking into consideration this information, the colonization and, hence, the associated records of the screwworm fly in drier environments, as occur with some Chilean or western-Argentinean records, may have resulted from human-facilitated expansion of the species. Moreover, the presence and persistence of *C. hominivorax* in Mendoza and San Juan probably are associated to productive oasis-lands and its adjacent cities in such dry or arid zones, facilitated by the irrigation and configuration of green spaces and urban or rural forested areas which may support microhabitats and conditions required to maintain populations of the species. The screwworm fly is a good disperser, but its expansion may be aided by transport activities, e.g., population movement or transfer of livestock from one area to another. In Chile, a human-myiasis case which has been identified from immigration coming from Paraguay (Neira et al. 2002) is indicative of this propagule pressure by human activities.

Our work has revealed that the presence of *C. hominivorax* is still not enough surveyed in wide regions from Argentina and Chile. Further explorations and monitoring programs are needed to confirm the presence of adults of *C. hominivorax* at both sides of the Andean chains: i.e., in large areas of western Argentina and specially to establish its southern limit at the western slopes of Andean chains in Chile. Also, ecological niche models here provided can represent a starting point to address an improved system for detecting suitable areas of myiasis-occurrence caused by this species.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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