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ORIGINAL ARTICLE

Spatio-temporal risk assessment models for *Lobesia botrana* in uncolonized winegrowing areas

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Abstract

The objective of this work was to generate a series of equations to describe the voltinism of *Lobesia botrana* in the quarantine area of the main winemaking area of Argentina, Mendoza. To do this we considered an average climate scenario and extrapolated these equations to other winegrowing areas at risk of being invaded. A grid of 4 km^2 was used to generate statistics on *L. botrana* captures and the mean temperature accumulation for the pixel. Four sets of logistic regression were constructed using the percentage of accumulated trap catches/grid/week and the degree-day accumulation above 7°C, from 1st July. By means of a habitat model, an extrapolation of the phenological model generated to other Argentine winemaking areas was evaluated. According to our results, it can be expected that 50% of male adult emergence for the first flight occurs at 248.79 ± 4 degree-days (*DD*), in the second flight at 860.18 ± 4.1 *DD*, while in the third and the fourth flights, 1671.34 ± 5.8 *DD* and 2335.64 ± 4.3 *DD*, respectively. Subsequent climatic comparison determined that climatic conditions of uncolonized areas of Cuyo Region have a similar suitability index to the quarantine area used to adjust the phenological model. The upper valley of Río Negro and Neuquén are environmentally similar. Valleys of the northwestern region of Argentina showed lower average suitability index and greater variability among SI estimated by the algorithm considered. The combination of two models for the estimation of adult emergence time and potential distribution, can provide greater certainties in decision-making and risk assessment of invasive species.

Keywords: distribution, invasion risk, *Lobesia*, modeling, viticulture

Introduction

Argentine viticulture occupies a privileged place among the producing areas of the world for its agroclimatic advantages. Wine production is strongly concentrated in the Cuyo region, mainly in Mendoza province, although it is also important for the regional economies of the northwestern provinces and to a lesser extent for the Patagonian provinces. Historically the phytosanitary status of Argentinean vineyards was considered an absolute privilege, since there was no pest that caused significant losses in crop yield and quality (Armendáriz *et al.* 2009). However, in March 2010, the National Health Service and Food Quality of Argentina (SENASA), confirmed the detection of *Lobesia botrana* (Lepidoptera: Tortricidae) in the department of Maipú, Mendoza (González 2010). Since it is considered to be the main pest of vineyards in the Mediterranean basin and Asia Minor (Andreadis *et al.* 2005), a National Program for its eradication was developed. The area was quarantined by Resolution SENASA 122/2010 and a protocol of prevention of *L. botrana* dispersion was set in other winegrowing areas of the country.

Identifying the potential risk of exotic species establishment is a key component of any quarantine pest risk surveillance system and is required in all countries which adhere to the International Plant Protection Convention (IPPC). In this regard, species distribution models could become a valuable auxiliary tool for decision making to deal with potential biological invasion (Hlasny and Livingston 2008). Their different methodological approaches have been described and compared in several bibliographic reviews (Venette *et al.* 2010; Zimmermann *et al.* 2010; Mateo *et al.* 2011).

Regarding phenological models, several empirical approaches have been used to estimate the population dynamics of *L. botrana* in areas where it is endemic. They mainly focus on tactical decision support in integrated pest management (Martín Vertedor *et al.* 2010). Studies in a pest risk analysis framework are limited. It is known that the number of annual generations of *L botrana* could be modulated by environmental factors, where temperature plays a predominant role. Within certain limits of temperature tolerance, other environmental factors can influence pest phenology such as photoperiod, altitude above sea level, wind, precipitation regime, vineyard cultivar and crop phenology (Sutherst 2003). For that reason, it is expected that this pest will have different population dynamics in different winegrowing areas. In this context, the objective of this work was to find equations that describe the voltinism of *L. botrana* in the quarantine area of Mendoza under an average climate scenario and to determine environmental similarities between the quarantined area and other Argentine wine regions not invaded by *L. botrana* in order to extrapolate these equations.

Materials and Methods

Voltinism model

A regional approach for *L. botrana* flight activity was evaluated using male catches data, obtained from the official phytosanitary surveillance system in the quarantined area of Mendoza (Argentina). Captures were followed during three campaigns (2011–2014). The data were preprocessed in the grid structure before their integration into regression equations. Approximately 1000 traps were installed before the emergence of the first adult (late August) and remained in the field till the end of the production season (April). A total of 506 traps were used for this study since they met the requirement of having presence data sustained over time. Weekly statistics of catches were taken in association with maximum and minimum temperature values, all through a homogeneous 2 km polygon grid.

Voltinism of *L. botrana* males was simulated based on the occurrence of a maximum of four non-overlapping flights between early September and late March. A pre-selection of traps to be incorporated into grid statistic was conducted according to the methodology proposed by Damos and Savopoulou-Soultani (2012). Sixty grids with recurrent trap catches were used as input for non-linear regression models and for their subsequent validation, they incorporated data from the 506 pheromone traps selected.

Mean daily records of maximum and minimum air temperature (°C), from the period 1991–2014, were interpolated at a spatial resolution of 2 km. Records from 124 weather stations of the National Weather Service (SMN) and the National Institute of Agricultural Technology (INTA) were used. A digital terrain model of the Shuttle Radar Topography Mission (SRTM) was used as external drift variable for Kriging algorithm (Aalto *et al.* 2013). These raster layers were validated by generalized cross-validation (Haylock *et al.* 2008).

A widespread problem in the interpolation of meteorological data in a mountainous area like this is the lack of weather stations at high altitude sites. Some regional studies have supplemented missing observations at high altitudes with information from remote sensors (Stahl *et al.* 2006). This study supplemented this data deficiency with surface temperature values of 30 randomly selected points along the Andean mountain range. For this, we used monthly averages (2008–2012) from the information generated by the National Oceanic and Atmospheric Administration's (NOAA) meteorological satellite.

Degree-days accumulation (*DD*) for each selected grid from 1 September to 30 March, were calculated according to the simple sine method. The minimum temperature threshold for development of 7°C was considered for any of the developmental stages of *L. botrana* (Gallardo *et al.* 2009).

Weibull regression models were constructed using the percentage of accumulated trap catches as the dependent variable (as values between 0 and 1) and degree-days accumulated above the minimum temperature threshold for development as the independent variable, for each flight period. The following non-linear regression models were used:

$$\mathrm{CAPT}:\ 1-\exp\left(\frac{-DD}{\lambda}\right)^{K},$$

where: CAPT – the cumulative percentage of captured moths, *DD* – the sum of degree-days reached on the date of trap checking. Parameters λ and K were calculated by the non-linear regression models using the professional version of Infostat software (Di Rienzo *et al*. 2013).

A validation of the reference model was performed through the cross-validated correlation coefficient (R^{2*}). For this, data from 15 grids (randomly selected) were used for the external validation of the model (Dos Santos and Porta Nova 2007). Residual values calculated with both data sets were compared by means of the Kolmogorov-Smirnov test. The intrinsic variability of the raster of mean daily maximum and minimum temperature was evaluated through the estimation of the root mean square error (*RMSE*) of each pixel in the study area, from 1 September to 31 March (Ali and Abustan 2014):

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n}(X_{\text{obs},\,i} - X_{\text{model},\,i})^2}{n}},$$

where: $X_{\text{obs},\ i}$ – value observed in the pixel/moment *i*; $X_{\text{model},\ i}$ – value modeled in the pixel/moment *i*; *n* – calendar day.

Habitat modelling

In order to determine environmental similarities betweenthe quarantined area and other Argentine wine regions not invaded by *L. botrana*, different algorithms for Species Distribution Models (SDMs) were evaluated. Principal Component Analysis (PCA), Generalized Linear Model (GLM), Maximum Entropy (MAXENT), Support Vector Machine (SVM), and Back Propagation Artificial Neural Network (BP-ANN) were determined.

Selected environmental variables for the SDMs analysis were: *a* – monthly accumulated degree-days (*DD*), from September 1 to March 31, *b* – monthly maximum Normalized Difference Vegetation Index (NDVI), MOD13Q1 16 days (2009–2012), *c* – average monthly precipitation, *d* – monthly average wind speed, both from Spatial interpolation of SMN and INTA meteorological data (1990–2014), *e* – monthly heliophany.

Grids centroids, used to adjust the regression equations, were considered as the reference position for subsequent calculations, hereinafter training sites. As the first step, predictive variables incorporated into the SDMs were pre-processed according to the methodology proposed by Robertson *et al*. (2001) Mean and standard deviation of environmental variables associated with training sites were used to standardize the predictor input variables series. As a second step, a principal component analyses, for temporal monthly series, was done (Mateo *et al*. 2011). Using the PCA analysis in temporal mode, each image in the series was considered as a variable, so the analysis examined for recurrent spatial patterns over time. The incorporation of predictor environmental variables pre-processed by PCA resulted in variables with no autocorrelation (Al Kandari and Jolliffe 2012).

As some models required pseudo-absence data, a mask was generated by delimiting those sites where the climatic risk of *L. botrana* establishment can be considered, *a-priori*, unfavorable (Heit *et al.* 2013). From this mask, 200 aleatory points were incorporated into MDEs as pseudo-absences (Tognelli *et al*. 2009). Probabilistic suitability index (SI), ranging from 0 to 1, was generated. After the generation of correlative models, kappa statistic of the resulting layers against a matrix of training sites was calculated.

Suitability index of each SDMs was aggregated to generate new cartography on the basis of a consensus model (Narouei-Khandan *et al*. 2016). The consensus model was built by the sum of all pixel with a climate suitability index greater than 0.9 from each model evaluated. ∑ EITHER 1 IF (model output ≥0.9) OR 0 OTHERWISE.

In order to get statistics of SI by winemaking regions, the potential distribution of implanted areas was estimated using different sources of information: the National Agricultural Census, Landsat GeoCover ETM (MDA Federal 2004), and 2966 georeferenced pheromone traps of the National Program for the Prevention and Eradication of *L. botrana*.

Theoretical assumptions for MDEs were: a – biotic interactions are not relevant at the regional scale or are constant in time and space, b – the genetic and phenotypic composition of a species is constant in space and time, c – there are no limitations to the spread of the species (Urban *et al*. 2007). Those assumptions are linked to the distribution model itself, not with the voltinism model.

R software (gstat, gdal and automap libraries), QGIS 2.12, IDRISI Selva and Infostat were used for the treatment of the information.

Results

Mean flight activity of *L. botrana,* using male catches, in the official phytosanitary surveillance system in the quarantined area of Mendoza is shown in Figure 1.

Table 1 presents Weibull regressions for accumulated trap catches by grid versus degree-daysaccumulation from 1st September. From these parameters, different prediction equations for *L. botrana* voltinism were constructed. The equations showed high prediction capability, as the mean square error and the coefficient of determination (R^2), were above 91% for all flights. Therefore, it can be deduced that a high proportion of the observed variability in the cumulative percentage of male catches can be explained by the accumulation of *DD* from 1st September. An increased

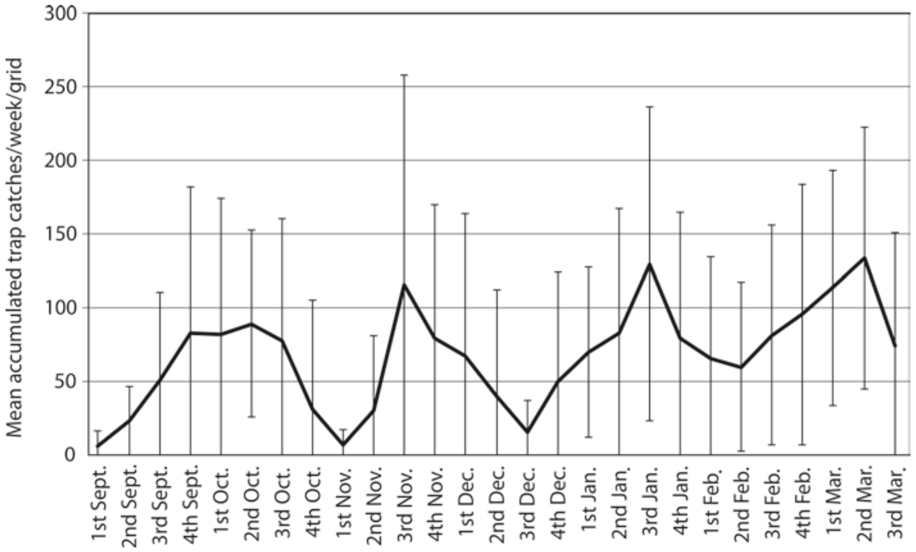

Fig. 1. Cumulative weekly average captures of male butterflies from September through March in the 3-year campaign (2011/12, 2112/13 and 2013/14)

Table 1. Parameters estimated by the regression models to adjust the cumulative catch percentage values per grid, as a function of degree-days

Voltinism	λ	K	RMSE	R^2
1° flight	291.8 ± 3.15	2.3 ± 0.08	0.09	0.92
2° flight	895.7 ± 2.9	9.1 ± 0.33	0.01	0.94
3° flight	1,731.8 ± 4.1	10.3 ± 0.32	0.01	0.91
4° flight	2,400.5 ± 2.91	13.4 ± 0.3	0.01	0.95

λ and K – mean and standard deviation of parameters calculated by non-linear regression; *RMSE* – root mean square error; R^2– correlation coefficient

variation with succeeding generations was observed which could be due to population sizes and because generation overlapping varied considerably between some of the data series.

The intrinsic variability of temperature showed a *RMSE* that averaged 1.45°C for daily maximum temperature and 1.65°C for daily minimum temperature.

There was a good fit between the values obtained experimentally and the predicted equation for *L. botrana* moth phenology for all flights. The cross-validated correlation coefficient (R^{2*}) obtained by the 1st flight was 0.829, by the 2nd flight: 0.857 and by the 3rd and 4th flights 0.804 and 0.793, respectively. Residual values calculated with both sets of data using the Kolmogorov-Smirnov test showed no statistically significant differences for any of the four flights analyzed ($p > 0.05$).

According to these results, it can be expected that 50% of male adult emergence for the first flight occurred at 248.79 ± 4 *DD*, in the second flight at 860.18 ± 4.1 *DD*, while in the third and the fourth flights, when the accumulation of degree-days reached values of 1,671.34 ± 5.8 *DD* and 2,335.64 ± 4.3 *DD*, respectively.

Table 2 shows the average of suitability index (SI) for the main Argentinean viticultural valleys, including five species distribution models: PCA, GLM, MAXENT, SVM, BP-ANN. Estimated SI in northern, central and western oases of Mendoza was greater than 98.3% for all evaluated MDEs. Tulum, Ullum and Zonda Valleys in San Juan showed an average SI greater than 0.9 for all SDMs. The Uco Valley in western Mendoza was characterized by an average index over 0.9 just in the PCA and GLM algorithms, and an average SI higher than 0.79 by BP-ANN, MAXENT and SVM. Southern Mendoza oasis presented an average SI of 0.84 by MAXENT model and greater than 0.9 in the other four models. The upper Río Negro Valley in northern Patagonia was characterized by an average suitability index lower than 0.9 only by the GLM algorithm. Chilecito (La Rioja Province), Calchaquies valleys (Salta and Catamarca Provinces) and Tinogasta (western Catamarca Province) showed average SI lower than 0.9 for all MDEs.

Based on the Kappa statistic ranges, suggested by Fauvel *et al.* (2013), all the algorithms achieved a high agreement. Maximum Entropy modelling technique achieved the best relative adjustment,

Table 2. Average and standard deviation of the suitability index in relation to the quarantined area by different models, based on historical climatic statistics

Viticultural area		SI area statistic	Species Distribution Models				
			BP-ANN	GLM	MAXENT	PCA	SVM
Northwest Region	Calchaquies Valleys (Salta)	mean	0.653	0.480	0.798	0.736	0.824
		SD	0.354	0.138	0.237	0.066	0.248
	Tinogasta (Catamarca)	mean	0.813	0.413	0.275	0.812	0.849
		SD	0.306	0.188	0.319	0.074	0.299
	Chilecito (La Rioja)	mean	0.656	0.745	0.755	0.874	0.718
		SD	0.361	0.254	0.287	0.082	0.268
Cuyo Region	Tulum, Ullum and Zonda Valleys (San Juan)	mean	1.000	0.902	0.999	0.958	1.000
		SD	0.005	0.114	0.008	0.009	0.004
	Northern and central oases (Mendoza)	mean	0.994	0.992	0.983	1.000	0.992
		SD	0.010	0.042	0.071	0.001	0.030
	Uco Valley (Mendoza)	mean	0.839	0.947	0.806	0.961	0.791
		SD	0.304	0.096	0.252	0.072	0.295
	Southern oasis (Mendoza)	mean	0.955	0.991	0.840	0.997	0.953
		SD	0.072	0.040	0.194	0.002	0.043
North Patagonian Region	Upper Río Negro Valley (North Patagonia)	mean	0.960	0.787	0.979	0.960	0.962
		SD	0.127	0.206	0.077	0.010	0.117

BP-ANN – Back Propagation Artificial Neural Network; GLM – Generalized Linear Model; MAXENT – Maximum Entropy; PCA – Principal Component Analysis; SVM – Support Vector Machine; SI – suitability index

0.92. Kappa values obtained from PCA were 0.822, GLM: 0.87, BP-ANN: 0.88 and SVM: 0.82.

Figure 2A shows consensus model output, focusing in Cuyo and North Patagonian Regions, based on the sum of climate suitability index greater than 0.9 of each model. According to these results, 93% of the northern and central oases of Mendoza area was categorized with a scoring of five, which represents the maximum similarity scoring, and 6% of the area with a scoring of four. Also, in Mendoza province, 45% of the Uco Valley obtained a score of five, 23% was classified with an additive climate suitability index greater than 0.9 by four models, 12% of the area by three, 8% of the area by two models and 13% by only one model.

The main irrigated areas of San Juan province (the valleys of Tulum, Ullum and Zonda) were classified with an additive model scoring of five in 65% of their surface, and 35.4% of the area with a scoring of four. Upper Rio Negro Valley in North Patagonia was only characterized with a consensus model scoring of five in 35% of its area and 52% was classified with an additive climate suitability index greater than 0.9 by four models.

Figure 2B shows the map resulting from the consensus model for the winemaking areas of northwestern Argentina. In this region, the biggest differences were observed in the consensus model with respect to other winemaking areas of the country. Only 4.3% of the Chilecito area showed concordance among the five algorithms and 13% of the area with a scoring of four. Only 1% of the surface of Tinogasta (Catamarca) valley was classified with a climate suitability index greater than 0.9 by five algorithms. Calchaquíes valleys were classified with a model scoring consensus one, two and three, corresponding to each class, approximately a third of the total area.

Discussion and Conclusions

Although only a small percentage of species introduced into a new area have a significant impact on agricultural, forestry or natural ecosystems, the increased trading volume of goods and services, including plant products from different origins, as well as tourism, have determined that the probability of entry of invasive alien species into the country has increased (Hlasny and Livingston 2008).

An international effort has been made by National Plant Protection Organizations (NPPOs) to improve prediction capabilities of the potential distribution of invasive species. Even though there has been an increase in the number of scientific papers published on the subject in the last decade, there is no general consensus on methodological approaches for the realization of species distribution models based on International Standards for Phytosanitary Measures (ISPMs). Therefore, it is not possible to generate

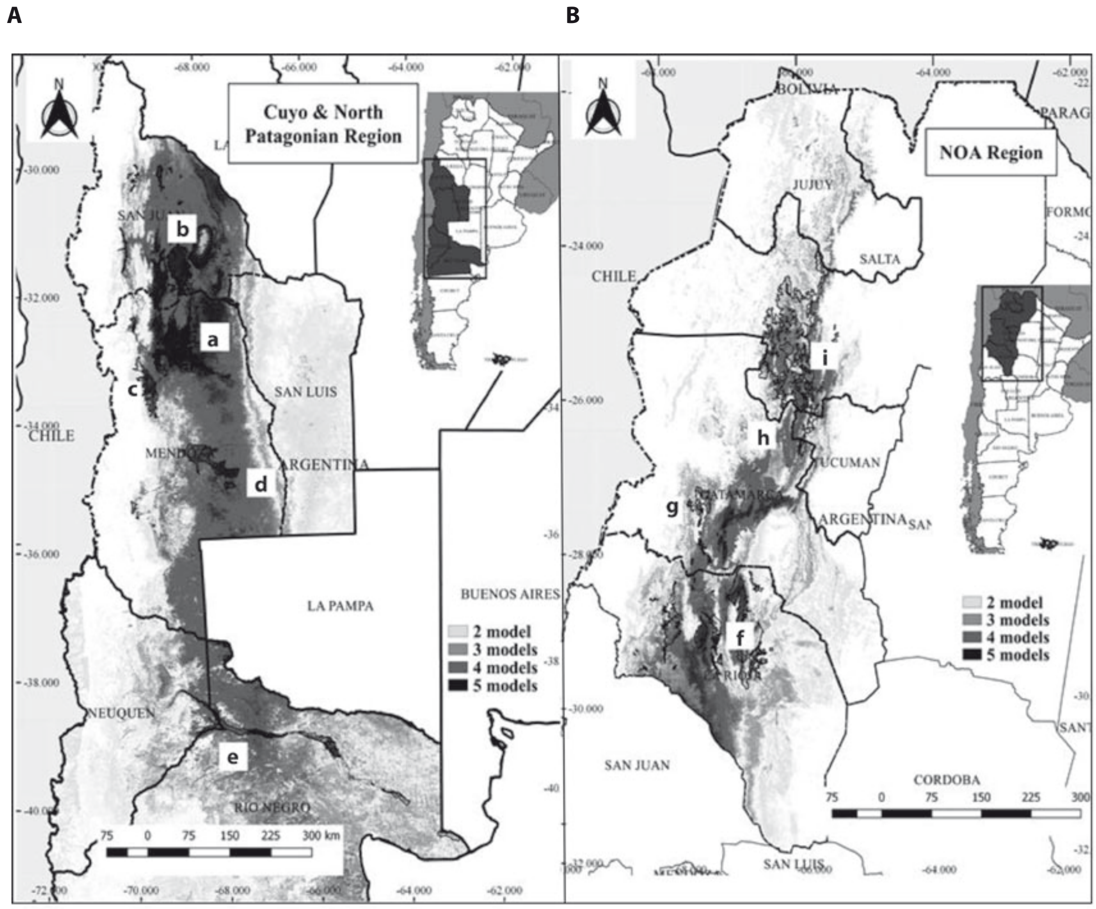

Fig. 2. The consensus model of suitability index: A – Cuyo and North Patagonian Region, B – NOA Region. Model in relation to the quarantined area of Mendoza by different correlative models, based on the sum of climate suitability index greater than 0.9 of each model output evaluated. a – Northern and central oases (Mendoza Province), b – Tulum, Ullum and Zonda Valleys (San Juan Province), c – Uco Valley (Mendoza), d – Southern oasis (Mendoza Province), e – Upper Rio Negro valley (North Patagonia), f – Chilecito (La Rioja Province), g – Tinogasta (Catamarca Province), h – Calchaquies valleys (Catamarca Province), i – Calchaquies valleys (Salta Province)

a single working protocol for the majority of cases addressed by NPPOs.

The results of this work were focused mainly on species distribution model application to stage 2 of pest risk assessment and the generation of decision tools for phytosanitary surveillance systems (FAO 2015). While prevention strategies used by the national plant protection organizations are mainly based on pre-border risk analysis measures, this study proposes a multiannual weather-driven phenology model for *L. botrana* voltinism, in combination with a species distribution model.

Many deductive models, used to estimate the voltinism of an invasive species in a new environment, usually extrapolate phenological models (constructed from daily climatic data at a specific time and place), to new sites with climatic data from historical statistics. This could determine a low accuracy in estimations, either in the temporal approximation of the event or in the geographical range (Gallardo *et al.* 2009). Models built with a single prediction variable (i.e. temperature) can provide an adequate level of adjustment, but may not consider the negative effects that multiple factors or extreme weather conditions may have on the phenology of the pest (Amo-Salas *et al.* 2011). For that reason, SDMs can provide a useful approach to detect the effects of multiple climatic variables in order to estimate geographical distribution of exotic species, although theyhave only limited explanatory power (Elith and Graham 2009).

Considering that a weather-driven model could show differences when applied to other winemaking regions, and in order to assess the analysis of invasiveness or potential distribution in other viticulture areas at risk, a subsequent climatic comparison determined that climatic conditions of uncolonized areas of Cuyo Region have suitability index similar to the quarantined area used to adjust the phenological model. The upper valleys of Río Negro and Neuquén are environmentally similar. The valleys of the northwestern region of Argentina showed lower average suitability index and greater variability among SI estimated by the algorithm considered. The low suitability index values and the high variability in climatic similarity indexes, estimated for the winegrowing areas of the northwestern region of Argentina with respect to the quarantined area of the province of Mendoza (training sites), do not necessarily imply that these environments are incompatible for the development of *L. botrana* populations. From the point of view of the approach taken in this article a different voltinism is to be expected in these valleys in relation to that observed in the training sites.The recent appearance of this pest in northwestern areas of the country (Cafayate) adequately match our modeled distribution and is well explained by this approximation; three of the five models agree as a highly prone area for *L. botrana* development.

The phenological models can be applied to historical climatic scenarios in order to estimate the probability of occurrence, and the potential number of generations per year in a new environment (Zimmermann *et al.* 2010). There are applications that allow for the inclusion of these approaches into deductive climate models, such as CLIMEX and NAPPFAST, in which the thermal requirements for development are related to georeferenced meteorological data.

Models at the regional scale could have some uncertainty about the accuracy of meteorological information and its correlation with site-specific conditions where adult catch information was obtained. As the availability of meteorological data is a limiting factor for application of the phenological model, the interpolation of temperature can improve model performance in the perspective of wider area pest management strategy (Gilioli *et al.* 2013).

Both kinds of models are prone to intrinsic errors such as: quality of input variables, accuracy in development protocol, system infrastructure limitations, simplified description of the system and of its subsystems (insect density, vine distribution and phenology), or by not considering the effect of important anthropogenic factors e.g. crop management, transport and grape trade by the wine industry (Vennete *et al.* 2010).

The combination of a classical prediction tool, for the estimation of the adult emergence time, and potential distribution modelling, can provide greater certainties in decision-making and risk assessment of invasive species. Considering the variability of SDMs predictions, a consensus modelling framework is an attractive solution as it reduces the predictive uncertainty of single-models (Marmion *et al.* 2009).

In this regard, studies on insect flight patterns are desired to establish warning systems and represent a useful tool for carrying out phytosanitary actions in time, facilitating phytosanitary prevention. In a more strategic, or policy-oriented perspective, simulation of scenarios on a large spatial and temporal scale, based on risk indexes, can be used to assess the effects of this invasive species on climate change scenarios (Gilioli *et al.* 2016).

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