A MULTIPLE MODEL APPROACH FOR FUTURE POTENTIAL DISTRIBUTION OF HLB: SOUTH AMERICA CASE STUDY

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Abstract

The objective of this work was to estimate the potential geographical distribution of HLB in South America, under historical climate records and future climate change scenarios, based on climatic conditions at the sites where HLB has been established in South America. Different spatial modeling algorithms were used. Climate change estimates of the Fifth IPCC Assessment Report, by the 2050s and 2070s, were considered. Results of assessed models differed significantly in the estimation of areas with greater climatic risk for the establishment of HLB in South America. According to the estimates of the fifth IPCC report, the effects of climate change would determine that in future, high-risk areas for HLB establishment would be displaced towards the southwest of the areas considered riskier nowadays. Even individual models do not present a clear pattern for HLB establishment and distribution, the integration of the results generated by different algorithms in a consensus model, can provide additional information for phytosanitary decision making.
Key words: *Climate Change, HLB, invasive species, Phytosanitary risk, distribution model.*
JEL Codes: *Q16, Q54, O54*

1. Introduction

Huanglongbing or HLB, is considered the most serious disease of the citruses at a global level, due to the losses it causes in production and the fruit quality, and a marked reduction of the infected plants longevity (Hall *et al.* 2008). It is a vascular disease, limited to the phloem, caused by the bacterium *Candidatus Liberibacter* ssp.; *Trioza erytreae* and *Diaphorina citri* (Hemiptera: Psyllidae) being the vectors of greater economic importance at a global level (Lee

et al. 2015). Not only it is important because effective methods for its control are unknown and it has caused serious economic damage to the countries where it was detected, but also due to its rapid spread in many of the citrus growing areas worldwide, especially in the American continent, causing big losses in short time (Gottwald, 2010). It was estimated that worldwide the disease caused the loss of more than 60 million trees (10 million in Brazil alone), causing total crop losses in countries like South Africa (Santivañez *et al.*, 2013).

For this reason, the Plant Health Committee of the Southern Cone (COSAVE) has elaborated a Regional Containment Plan of HLB, in order to avoid the spread of the pest towards free disease areas in the region, by strengthening of a set of national phytosanitary actions, locally coordinated. The elaboration of pest risk analysis protocols and specific surveillance is a pre-border prevention practice that is commonly adopted by National Organization of Phytosanitary Protection (ONPF). It is in the frame of these activities of official phytosanitary prevention, where the Species Potential Distribution Models (SDMs) could provide an efficient methodological support for the quantification of possible environmental risk scenarios for planting and pest under analysis, in historical scenarios as well as in climate change (Mateo *et al.*, 2011). However, few spatially explicit models have been developed until now to assess risk for this pest in South America at orchard level (Gasparoto *et al.*, 2018), whereas there are some available approximations to predict the potential establishment of HLB in North America (Gutierrez & Ponti, 2013; Torres-Pacheco *et al.*, 2013; Narouei-Khandan *et al.*, 2016).

Climatic factors determine the phenology of citruses, population dynamics of HLB, and their vectors (Shimwela *et al.*, 2019). However, there is a close correlation between the increase of infection rates of citruses with HLB and the presence of big populations of their vectors (Lee *et al.*, 2015). Population dynamics of *D. citri* is influenced by the sprouts availability, the temperature conditions, and the humidity of the environment (Hall *et al.*, 2013). Low temperatures in winter cause a high mortality of the psyllid populations (Hall *et al.*, 2011). The populations' survival rises when the environment relative humidity increases but the intense rainfall can mechanically sweep nymphs increasing the population mortality (Patt & Sétamou, 2010; Shimwela *et al.*, 2019).

Despite the uncertainty about possible impacts of the climate change on the behavior of the agricultural pests, different authors estimate that these would be able to respond better to climatic changes than the agricultural plantings and the native species communities. Consequently, climatic change could potentially create suitable conditions for the occurrence of a greater number of biological invasions, as well as an increase in the severity of the damages caused by the agricultural pests and/or forest (Bellard *et al.*, 2012; Pautasso *et al.*, 2012; Shimwela *et al.*, 2019).

The objective of this study is to estimate the potential geographical distribution of HLB in South America, based on the comparison between the climatic conditions of disease free areas and the historical climate records of the main areas where HLB has established in Brazil. It is also expected to evaluate the influence that climate change could produce as future potential geographical distribution of this disease.

2. Materials and Methods

Suitable environment for potential establishment of HLB in free disease areas in South America was performed by means of different Species Potential Distribution Models (SDMs), considering the monthly meteorological statistics of different climatic scenarios. Firstly, a historical climatic scenario was assessed, considering monthly meteorological data of maximum, minimum temperature and precipitation, and bioclimatic variables statistics from

the series 1950-2000 (Hijmans *et al*., 2005; Fick & Hijmans, 2017). Secondly, different scenarios of climate change proposed by the Fifth Assessment Report of *Intergovernmental Panel on Climate Change* (IPCC5), by the decades 2050 [2041-2060 average] and 2070 [2061-2080 average], were evaluated. Three global climate models (GCMs), [GFDL-ESM2G, GISS-E2-R and HadGEM2-ES] for two representative concentration pathways (RCPs), [2.6 and 4.5], were considered (Collins *et al*. 2011).

The different SDMs assessed were: *Generalized linear model* (GLM), *Maximum Entropy* (MAXENT), *Support Vector Machine* (SVM), *Back propagation artificial neural network* (BP-ANN). *Principal component analysis* (PCA), was performed by means of Robertson's *et al., 2001* methodology. Conceptually, it was used the conceptual approach proposed by Moschini & Heit (2015), who have delimited agroclimatic risk zones for *D. citri* in the main citrus regions of Argentina, by climate comparison with a site where epidemiological conditions for the establishment of *D. citri* were highly predisposing. In this study, San Pablo State and some districts of Paraná States and Minas Gerais in Brazil were considered as prediction site, due that in this area South America, the epidemiological conditions for the establishment and spread of HLB and *D. citri* were highly suitable during the past decade (Gasparoto *et al*. 2018; Lopes *et al*. 2009).

From this area, 450 points from cells that had a Normalized Difference Vegetation Index greater to 0.3 in all the months of the year were randomly obtained (Heit *et al*., 2013; Nasa, 2018). Average and standard deviation values of climatic variables associated prediction dataset were obtained, in order to standardize with this set of variables the twelve future climate scenarios. Since the use of high number of components can result in overadjustment of the output models, and the consequently a loss of generalization Mateo *et al*. (2011), principal component analysis was used as a pre-analytical technique for modeling the species potential distribution. Principal component analyses with a time series orientation by mean monthly maximum temperature, mean monthly minimum temperature, and mean monthly precipitation were made. Over 19 bioclimatic variables, PCA were performed with a spatial orientation. In T-mode, every image of the series is considered as a variable and the analysis searches spatial patterns recurrent in time. In S-mode, every pixel is considered as a variable and the analysis searches temporary patterns recurrent on the space. T-mode PCA input variables were tested independently of bioclimatic variables. The resolution of climatic variables used as input of the models was 4 km and cartographic projection South America Albers Equal Area Conic was used.

For those SDMs that required pseudo-absences data a mask was created to delimit those areas where, climatic risk of the establishment of HLB, could be considered *a priori*, as low. Citeria suggested by Zhu in 2006, who proposed that a mean monthly minimum temperature of 6.4º can be used as a limiting factor of the geographical distribution of *D. citri*. was used. The classes of land cover of bare soil of the Global Land Cover Map for 2009 (Arino *et al*., 2012) were selected in order to create a mask of those areas where neither the citrus plants nor the alternate hosts of the *D. citri* could develop. From these masks 400 random points were generated, which were incorporated to the analysis as pseudo-absences (Tognelli *et al*., 2009). Kappa statistics of the resulting layers were calculated against a matrix of the areas with presence of HLB and *D. citri* in Brazil.

For each SDM, pixels of each category, between 0 and 1, were counted. Analysis of variance and Tuckey test of the surfaces with climatic similarity index higher than 0.5 or 0.9 were performed (α: 0.05). Agreement output model resulting of combination of SDMs, RCPs and input variables to SDMs was estimated based on fuzzy classification of pixel values with climatic similarity index higher than 0.9, in each of the assessed models (Narouei-Khandan *et al*., 2016). Thus, the Agreement Risk Index (Ag*RI*) has values that range from 0: low risk and

lack of repeatability among scenarios, to 1: maximum risk and similarity among scenarios estimations. For the information management, software QGIS 2.12, IDRISI Selva and Infostat were used.

3. Results

Five potential distribution models assessed: Principal component analysis (PCA), Generalized linear model (GLM), Maximum Entropy (MAX-ETP), Support Vector Machine (SVM) and Back propagation artificial neural network (BP-ANN), estimated different climatic risk areas in relation to the spatial pattern, in surface estimated by category and in the spatial distribution itself (See Table 1 and 2).

3.1. Risk index RI > 0.9

Considering the estimations made, using the rcp2.6 projections and the Bioclimatic variables as inputs to the MDEs, no statistically significant differences were observed in the HLB risk area estimated by the different SDMs (F: 0.60, p: 0.6650). Significant differences were observed in the area between future climate scenarios estimated by IPCC (F: 6.17, p: 0.022), showing an average increase of 748,000 km^2, with respect to the estimated areas considering historical scenarios. For the 2070s, a reduction of 181,000 km^2 of the surface is expected, compared to the historical scenario. No interactions were observed between SDMs and IPCC scenarios (F: 0.34, p: 0.8495). See figure 1.
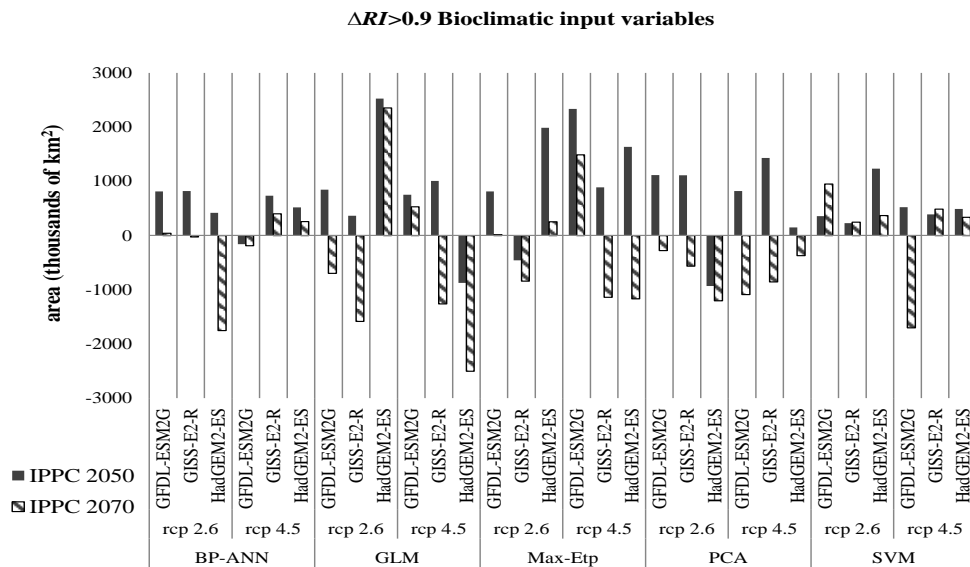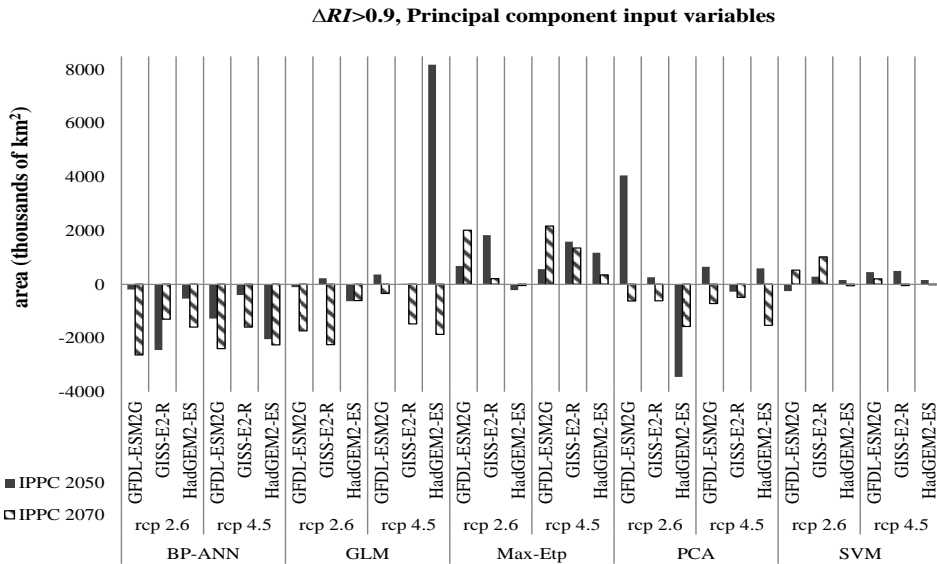
$\triangle RI>0.9$ **Bioclimatic input variables**

Notes: IPCC Global Climate models (GFDL-ESM2G, GISS-E2-R, HadGEM2-ES); representative concentration pathways (RCP: 2.6 and 4.5); Species distribution models: Generalized linear model (GLM), Maximum Entropy (MAXENT), Support Vector Machine (SVM), Back propagation artificial neural network (BP-ANN). Principal component analysis (PCA).

Figure 1 Comparison of the Relative Climatic Risk Surfaces Estimated by Different Bioclimatic Variables and Models.

A no statistically significant increase to the risk area (year 2050) was estimated using the same input variables with a representative concentration pathway 4.5 (f: 1.05, p: 0.4071). By the 2070s, a reduction in the risk area of 452000 km^2, is estimated (F: 11.80, p: 0.0026). There were no interactions between SDMs and IPCC scenarios (F: 0.80, p: 0.5415).

Figure 2 present differences in risk area considering representative concentration pathways 2.6 and Principal component as input variables. No differences in the surface were observed among SDMs (F: 2.30, p: 0.0945), nor between IPCC scenarios (F: 1.35; p: 0,258).

ΔRI>0.9, Principal component input variables

Notes: IPCC Global Climate models (GFDL-ESM2G, GISS-E2-R, HadGEM2-ES); representative concentration pathways (RCP: 2.6 and 4.5); Species distribution models: Generalized linear model (GLM), Maximum Entropy (MAXENT), Support Vector Machine (SVM), Back propagation artificial neural network (BP-ANN). Principal component analysis (PCA).

Figure 2 Comparison of The Relative Climatic Risk Surfaces Estimated by PCA Input Variable.

Taking into account representative concentration pathways 4.5 and Principal component as input variables, statistically significant differences were observed between IPCC scenarios (F: 4.90, p: 0.0386) and among SDMs (F: 3.05, p: 0.0410). There were no interactions between SDMs and IPCC scenarios (F: 1.7, p: 0.1904).

Mean risk area was estimated on 687790 km^2 (year 2050) and a reduction in the risk area of 478,860 km^2 compared to the estimated, by historical scenarios, by the 2070s. The biggest risk area, was estimated by the Maximum Entropy algorithm (average Δ1202850 km^2), which differed significantly from the Back propagation artificial neural network algorithm (average Δ -1661890 km^2).

3.2. Risk index RI>0.5

Considering RI>0.5 estimations using the representative concentration pathway 2.6 projections and Bioclimatic variables as inputs to the MDEs, no statistically significant

differences were observed in the HLB risk area estimated by different IPCC scenarios (F: 0.36, p: 0.557), but statistically significant differences in HLB risk area among SDMs were found (F: 8.6, p: 0.0003). See figure 3.
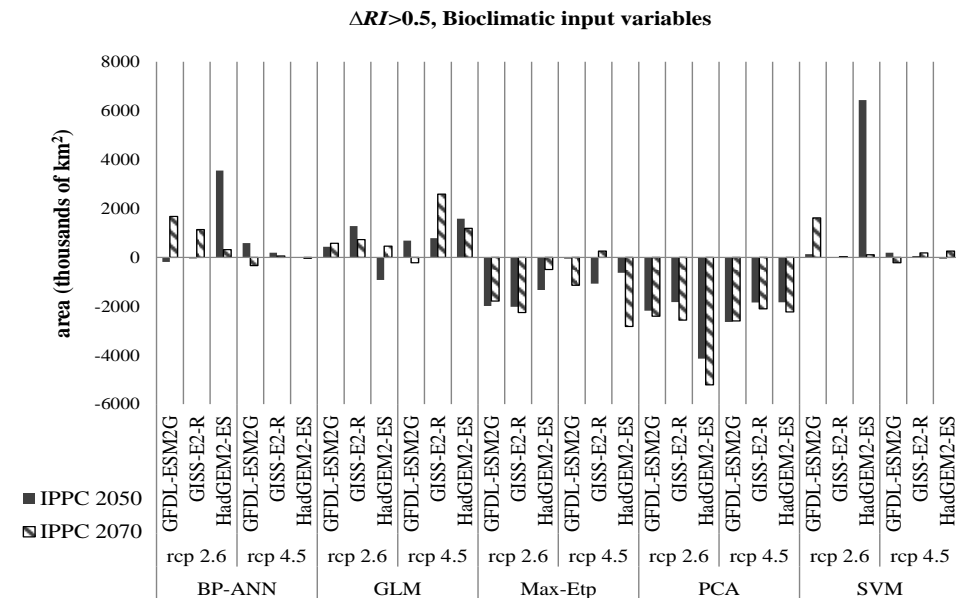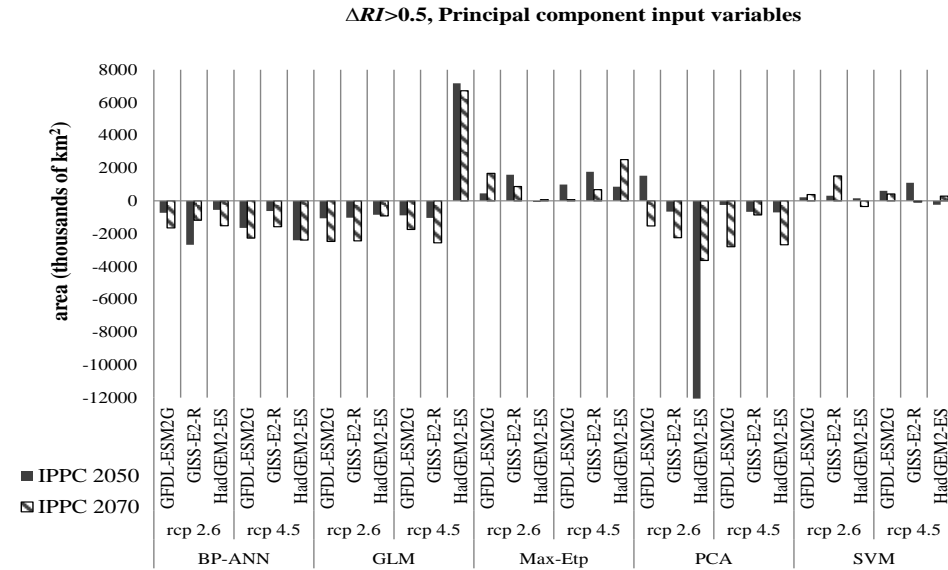

Notes: IPCC Global Climate models (GFDL-ESM2G, GISS-E2-R, HadGEM2-ES); representative concentration pathways (RCP: 2.6 and 4.5); Species distribution models: Generalized linear model (GLM), Maximum Entropy (MAXENT), Support Vector Machine (SVM), Back propagation artificial neural network (BP-ANN). Principal component analysis (PCA).

Figure 3 Comparison of The Relative Climatic Risk Surfaces Greater Than 0.5 (Km2), Estimated by Bioclimatic Input Variables.

The lowest risk area higher than 0.5, was estimated by the Principal component analysis and Maximum Entropy algorithm (average Δ -1645760 to -3054910 km^2), which differed significantly from Support Vector Machine. There were no interactions between SDMs and IPCC scenarios (F: 0.38, p: 0.82). In the same way, using representative concentration pathway 4.5 significant differences in area classified with relative climatic risk index (RI)> 0.5 were observed among SDMs (F: 17.49, p: 0,0001), and no significant differences in output area higher than 0,5 between IPCC scenarios were found (F: 0.61; p: 0,445). The biggest risk area higher than 0.5, was estimated by the Generalized linear model algorithm (average Δ1101940 km^2), which differed significantly from Maximum Entropy algorithm (average Δ -909860 km^2) and PCA algorithm (average Δ -2207590 km^2).

No differences in the surface, classified with relative climatic risk index (RI)> 0.5, were observed among SDMs (F: 2.33, p: 0.0909), nor between IPCC scenarios (F: 0.05; p: 0,832) when estimations were done using the representative concentration pathway 2.6 projections and Principal component variables as inputs to the MDEs (Figure 4). Similarly results were obtained when pathway 4.5 projections was used among SDMs (F: 2.3, p: 0.0946), nor between IPCC scenarios (F: 0.67; p: 0,424).

ΔRI>0.5, Principal component input variables

Notes: IPCC Global Climate models (GFDL-ESM2G, GISS-E2-R, HadGEM2-ES); representative concentration pathways (RCP: 2.6 and 4.5); Species distribution models: Generalized linear model (GLM), Maximum Entropy (MAXENT), Support Vector Machine (SVM), Back propagation artificial neural network (BP-ANN). Principal component analysis (PCA).

Figure 4 Comparison of the Relative Climatic Risk Surfaces Greater Than 0.5 (Km2), Estimated by Principal Component Input Variables.

3.3. Agreement Model Output

Polling all data output and considering the representative concentration pathways 2.6, no differences in the surface classified with relative climatic risk index (RI)> 0.9 were observed among SDMs (F: 1.96, p: 0.114), among global circulation models (F: 0.84, p: 0.437), neither input variables to SDMs (F: 3.51; p: 0.066). No interactions among these variables and climate scenario were observed (p> 0.05), in any case considered. However, area categorized with a relative climatic risk index higher than 0.9 was significantly lower in the scenarios proposed by IPCC for the decade of 2050 than for those proposed by IPCC for 2070 (F: 5.67, p: 0.0207).

Considering the representative concentration pathways 4.5, no differences in the surface classified with relative bioclimatic risk index (RI)> 0.9 were observed among SDMs (F: 0.02; p: 0.97), among global circulation models (F: 0.84, p: 0.43), neither input variables to SDMs (F: 0.04; p: 0.84). No interactions among these variables and climate scenario were observed (p> 0.05), in any case considered. However, difference in area categorized with a relative bioclimatic risk index higher than 0.9, between historic and IPCC 2050 scenario was significantly lower than for those proposed by IPCC for 2070 (F: 5.67, p: 0.0207).

Figure 5 present the consensus model built, considering climatic similarity indexes higher than 0.9 in the five SDMs, in relation to the historical climatic statistics of South America. Darker greys represent areas expected by a greater number of algorithms and, in consequence, have higher relative values than those areas where there were no consensus between algorithm results.
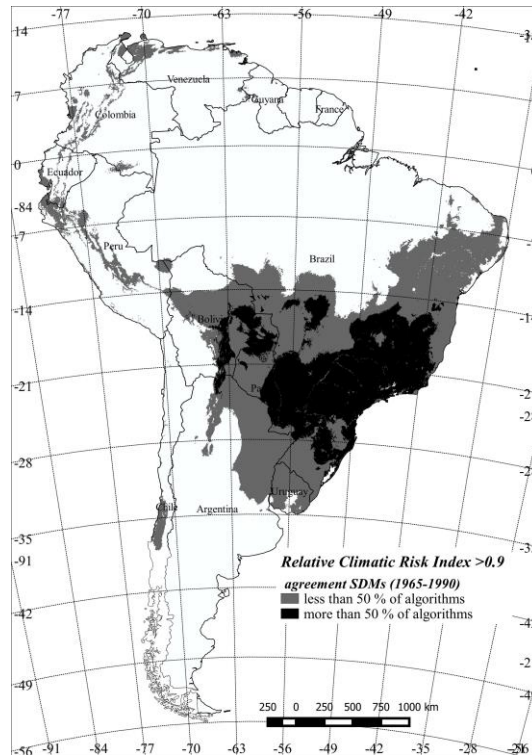
Figure 5 Agreement Output Models Estimate of Climatic Risk of HLB Establishment, Based on Historical Climatic Statistics.

In that sense, higher climatic risk areas would be distributed in southern Brazil, eastern Paraguay, Northeastern Region and eastern area of the Northwestern Region of Argentina, and central and southeastern Bolivia. Central Chile, Uruguay, valleys of central and northwestern Peru, southwestern Ecuador, and northern Venezuela can also be underlined.

It can be observed that, IPCC 2050/2070 distribution model (Fig. 6 to 9, black) areas would be reduced compared with areas estimated form historical climatic data (Fig. 6 to 9, grey).

Representative Concentration Pathway 2.6 scenario for 2050 and 2070 agreement surface with relative climatic risk for HLB >0.9 would be reduced about 420560 km^2 by decade (R²: 0.98) (Fig 6 & 7).

Figure 7 shows Representative Concentration Pathway 4.5 scenario for 2050 and 2070 agreement surface with relative climatic risk for HLB >0.9 would be reduced -333304 km^2 by decade (R²: 0.791).

SDMs achieved moderate to substantial levels of agreement when historical scenarios were considered (Fauvel *et al.* 2013), and moderate agreement for IPCC scenarios. No statistically significant differences were observed among SDMs Kappa in future climate scenarios (p>0.05).
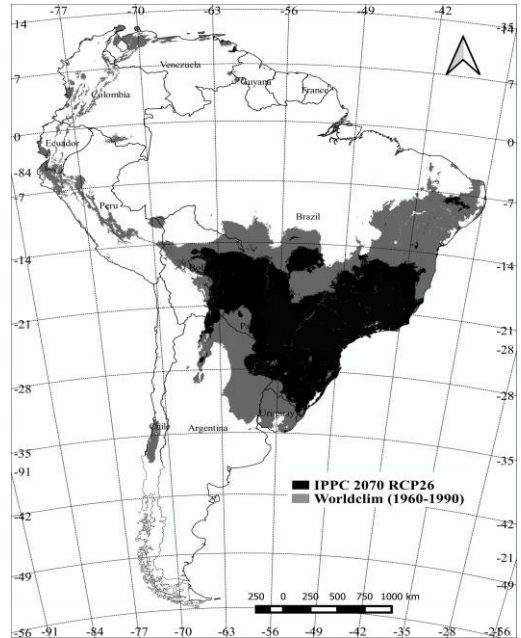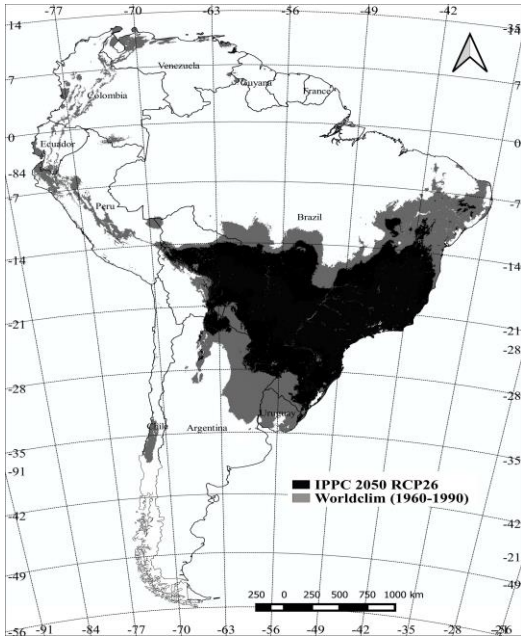
Figure 6 & 7. Variation on Agreement Output Model of Relative Climatic Risk for HLB Establishment, Based on Representative Concentration Pathway 2.6 Scenario For 2050 and 2070.
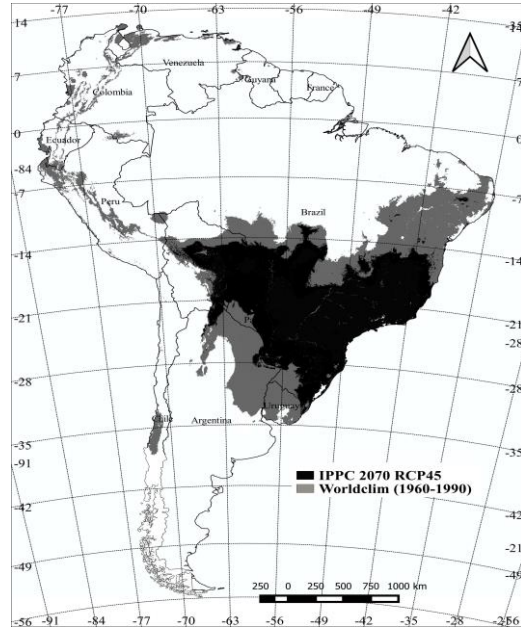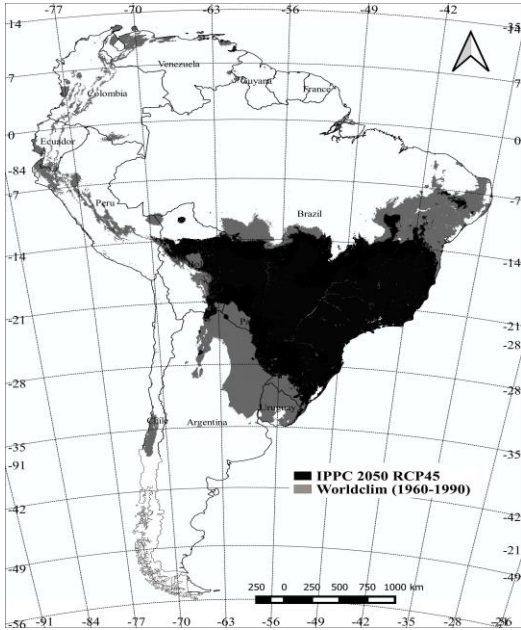

Figure 8 & 9. Variations on Agreement Output Model of Relative Climatic Risk for HLB establishment, Based on Representative Concentration Pathway 4.5 Scenario for 2050 and 2070.

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4. Discussion

The Species Potential Distribution Models have been used to estimate the potential distribution of a pest in the first phase of the biological invasion process, and its results can be useful to support the planning tasks for preventive monitoring or delimiting the free areas and the application of quarantine pest eradication measures (Heit *et al*., 2014; Aurambout *et al*., 2009).

The results found in this study match the potential distribution of HLB obtained by means the algorithms of maximum entropy (MAXENT) by Narouei-Khandan *et al*. (2016), but they differ significantly from the estimated by Support Vector Machines (SVM), which estimated areas of high risk in an important portion of the Amazonas basin.

The delimitation of citrus areas in Argentina, with conditions for HLB establishment, are considerably similar to those determined by Moschini & Heit (2015). This author delimited areas of agroclimatic risk, for presence and abundance of *D. citri,* using an agroclimatic risk index [AIR] that employs daily records of temperature, relative humidity, and precipitation, and compare them to the records in Campinas [Brazil]. Both methodologies identified a greater climatic risk for the development of *D. citri* and HLB establishment, in the central and northeastern portion of Argentinean Mesopotamia and also Northwestern Argentina. Marginal citrus zones of Southern Mesopotamia and north Pampean region are the areas with lower relative climatic risk. Although the climate change scenarios proposed by IPCC5 estimate a gradual rise of the climatic risk of these zones in next decades. Austin (2007) states that different methods, modeling the species potential distribution, can generate different results among themselves, even producing contradictory results. Even when it is not possible to confirm that a specific method has a better performance for all situations, the comparison of the different approaches in the same case, can provide complementary information for phytosanitary decision making (Hirzel & Lay, 2008).

The incorporation of the PCA, as a pre-processed predictor, into the models resulted in the introduction of a variable with no autocorrelation (Al-Kandari & Jolliffe, 2012). In addition, the distribution models generated by the gross environmental predictors, generally predict a smaller surface of activity (over adjusted) (Elith & Graham, 2009).

Temperature increase will affect the development of *D. citri* in a direct way, due to the temperature impact on its development rate and, in an indirect way, through the temperature impact over the host plant sprouting cycles. Hotter conditions would have a higher relative impact on the plantation areas of the mild regions, due to the thermal tolerance that the pests present for its development and growth, greatly limited by the occurrence of extreme temperatures, whether cold or hot weather, or in the duration of the adverse term, for example the drought or cold in winter (Jactel *et al*., 2012). In this way, winter seasons which are more benign, could not only increase the survival of the diapause forms, but also it creates longer seasons of growth, thus significantly increasing the potential reproduction of this pest species (Ammunét *et al*., 2012).

Aurambout *et al*. (2009) showed that the seasonal variations in temperature expected before varied climate change scenarios will affect the speed of the development and survival of *D. citri*, simultaneously with a citric host species, Valencia Orange Tree. However, these authors argued that the temperature increase forecasted for the varied scenarios of global warming, would have complex results and especially heterogeneous about the population dynamics and the *D. citri* survival and as a consequence the potential establishment and spread of HLB. For example, the temperature increase during the citruses growing season, would reduce the time [in calendar days], in which *D. citri* would complete its development. This could determine that this pest has a greater number of annual potential generations. In addition, the climate

change will have a significant impact on the date of occurrence of citrus sprouting and its duration. Climate change could also shorten the time needed to lignify sprouts soft tissues, what would reduce the available time for the *D. citri* to reproduce in them, affecting in a significant way the development of the populations of nymphs of this species (Torres-Pacheco *et al*., 2013). Even Shimwela *et al*. (2019) found no spatial relationship between vector populations and HLB-infected trees, they found a tentatively positively correlated with monthly rainfall data and, in a lesser extent, with average minimum temperature as possible divers of HLB distribution.

The development of trade between regions and countries is an increasingly important characteristic of modern agriculture, but along with a great deal of benefits trade carries with it the risk to import exotic plant diseases. Since HLB was found in Florida (United States), citrus production has decreased by 74% (USDA, 2019). From 2004 to 2012, Brazil eradicated around 18 million citrus trees and nowadays, costs related to the HBL vector management is approximately 15% of the cost of citrus production (Adami *et al.*, 2014). The potential establishment of HLB in the citrus-producing regions of Argentina would threaten the assets of 5,300 producers, approximately 120,000 direct jobs, the supply of 529 packing plants and 20 citrus industries (SENASA, 2009). In order to prevent the danger of introducing exotic pets, which can seriously threat social-economic welfare, quarantine activities have generally provided first barrier protection, and since pest eradication programs are often ineffective in practice and highly costly to governments.

In South America, the Plant Health Committee of the Southern Cone (COSAVE) has not developed, until now, any quantitative analysis for the estimation of areas with establishment risk for quarantine pests. The analysis of pest risk performed by the National Organization of Phytosanitary Protection (ONPF), is based on qualitative risk analysis, in which tools derived from geomatics are not used for spatial characterization of the establishment risk of the exotic pests. The nature of the existing interactions among the host plant, HLB, *D. citri*, and the weather is complex and heterogeneous, for this reason the assessment proposed in this study should be considered as a quantitative approach for the estimate of the potential impacts of the climate change on the distribution of quarantine pests at a regional level.

5. Conclusions

By means of different methodological approaches we have identified areas of South America with a climatic risk similar to those where HLB has been established and dispersed rapidly in recent years.

Considering the estimates of the Fifth report of IPCC, the effects of the climate change in the next decades will have complex consequences and especially heterogeneous on the potential establishment and spread of HLB in the free disease areas in South America, however, it would be expected a movement to the areas of greater climatic risk towards southwestern areas with climatic risk nowadays.

The results of the different algorithms used differed among them and as, a consequence, it is not possible to confirm only one method to be the most appropriate to estimate the current and future phytosanitary risk for HLB. However, the integration of the different algorithms in one consensus model can provide complementary information for phytosanitary decision making from the different National Institutions of Plant Protection in South America.

Acknowledgements

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