Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 26 December 2022 doi:10.20944/preprints202212.0487.v1

Disclaimer/Publisher's Note: The statements, opinions, and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions, or products referred to in the content.

Article

INFLUENCE OF CLIMATIC VARIABLES ON INCIDENCE OF WHITEFLY-TRANSMITTED BEGOMOVIRUS IN SOYBEAN AND BEAN CROPS IN NORTHEN ARGENTINA

Pablo Reyna [1], Franco Suarez [1,2], Mónica Balzarini [1,2] and Patricia Rodriguez Pardina [1*]

1 Unidad Ejecutora UFYMA - INTA-CONICET
2 Facultad Ciencias Agropecuarias, Universidad Nacional de Córdoba
* Correspondence: rodriguez.patricia@inta.gob.ar

Abstract:. Over the last 20 years, begomoviruses have emerged as devastating pathogens, limiting the production of different crops worldwide. Weather conditions increase vector populations, with negative effects on crop production. In this work we evaluated the relationship between the incidence of begomovirus and climatic conditions before and during the crop cycle. Soybean and bean fields from the northwest (NW) of Argentina were monitored for 14 years and classified as moderate (≤50%) and severe (> 50%) according to the relative incidence. Two hundred bio-meteorological variables were constructed, summarizing meteorological data in 10-day periods from June to March of each crop year. The studied variables included temperature, precipitation, relative humidity, wind (speed and direction), pressure, cloudiness and visibility. For bean, high maximum winter temperatures, low spring humidity and precipitation 10 days before planting correlated with severe incidence. In soybeans, high late winter and pre-planting temperatures, and low spring precipitations were found to be good predictors of high incidence of begomovirus presence. The results suggest that temperature and pre-sowing precipitations can be used to predict incidence status [predictive accuracy: 82% (bean) and 75% (soybean)]. Thus, these variables can be incorporated in early warning systems for crop management decision-making to reduce the virus impact on bean and soybean crops.

Keywords: Pathosystem, Viral diseases, Weather, Predictive model

1. Introduction

Viral diseases are one of several factors that can affect the yield of legume and grain crops. In Argentina, the most important viral disease in these crops is that caused by begomoviruses. Estimated losses in grain production due to begomoviruses can vary from 40 to 100% depending on the crop, incidence, planting date and cultivar. Begomoviruses are small, circular, single-stranded DNA viruses (family *Geminiviridae*; genus *Begomovirus*) that infect a wide range of crops in the tropics and subtropics. Epidemics caused by re-emerging and newly emerging geminiviruses are becoming frequent, even in regions that were earlier free from these viruses [1]. The incidence and severity of the diseases caused by begomoviruses have increased considerably in the last two decades. Several crops, such as bean, soybean, tomato, cotton and cassava, are infected with begomoviruses worldwide [2].

More than 50 begomoviruses have been detected infecting bean and soybean crops, with bean golden mosaic virus, sida micrantha mosaic virus, tomato severe rugose virus, and mungbean yellow mosaic India virus having been found in both crops [3–5], In Argentina, eight different begomoviruses were identified: bean golden mosaic virus (BGMV), tomato yellow spot virus (ToYSV), soybean blistering mosaic virus (SbBMV), tomato mottle wrinkle virus (ToMoWrV), sida golden mosaic Brazil virus (SiGMBRV), tomato yellow vein streak virus (ToYVSV), euphorbia mosaic virus (EuMV), and bean bushy stunt virus (BbsV) The first three species were detected in both bean and soybean

© 2022 by the author(s). Distributed under a Creative Commons CC BY license.

crops, whereas ToMoWrV, SiGMBRV, ToYVSV and BBSV were found only in bean and EuMV only in soybean crops [6].

Begomoviruses are transmitted by the whitefly *Bemisia tabaci* (Gennadius) (*Hemiptera*: *Aleyrodidae*); the presence of whitefly is essential for the occurrence of begomovirus outbreaks, since the greater the whitefly populations, the greater the incidence of viruses and the damage they cause [7]. Recent studies suggest that the complex of the whitefly *B. tabaci* comprises at least 40 genetically distinct cryptic species [8–10], three of which have been lately detected in soybean (New world 2-NW2), bean (NW2, Middle East Asia-Minor 1-MEAM-1 and Mediterranean- MED), tomato (MED) and melon (MEAM-1) in Argentina [11,12]. The increase in the damage caused by *B. tabaci* in the last years is due to several factors, including changes in cropping practices, increased worldwide germplasm exchange and intensive use of insecticides [1]. The appearance of whitefly 'B' biotype contributed to the emergence and spread of begomovirus diseases, along with other factors, such as genomic recombination and human activities. Weather conditions can heavily impact whitefly populations, favoring the spread of begomovirus diseases and limiting crop production.

Common bean (*Phaseolus vulgaris* L) is one of the most important legumes for direct consumption worldwide, and a source of protein for millions of people, especially in Latin America, Africa and the Caribbean [13], In Argentina, dry bean production in 2019 reached 578,713 tons in a cultivated area of 419,927 ha [14]. Argentina is the world's leading exporter of Alubia bean and fourth of black, red and cranberry bean varieties, with exports accounting for 90% of the country production. Bean is grown in the north-western (NW) region of Argentina, with Salta province being the main producer, followed by the provinces of Jujuy, Tucumán, Santiago del Estero, Catamarca and north of Córdoba. The climate in the NW region is humid subtropical with a dry season (monsoon regime), with rainfall ranging from 900 to more than 2,000 mm a year.

Argentina is also the world's third largest producer [14] of soybean (*Glycine max* (L) Merr), a legume native to China used as animal feed and for oil and biodiesel production. Soybean production in Argentina is limited by the 20 °C isoline in January, which is the limit for thermal insufficiency. Soybean is grown mainly in the Pampas region, but the cultivated area is extending to NW lands. A large portion of Argentine bean and soybean crop regions presents probability of occurrence of begomovirus diseases. In this work, we investigate the relationship between the level of incidence of begomoviruses in bean and soybean crops in the Argentine NW region, where temperatures are relatively high and drought is more frequent than in the Pampas. We hypothesized that the relative incidence of begomoviruses in bean and soybean cropped in the NW of Argentina could respond to the influence of the weather conditions during the pre-planting period on the vector populations.

2. Materials and Methods

2.1. Plant sampling and analysis

To assess the relative incidence of begomoviruses on soybean and bean crops, plots located in the NW region of Argentina (65.63 "and 60.44" W, and 31.34" and 22.49"S), were monitored during 14 years. During this period, more than 2000 symptomatic bean and 1400 soybean samples were collected and maintained at -20° C until virus analysis. All samples were tested with a general probe that detects all begomovirus species, according to the protocol previously described by [15].

2.2. Obtaining biometeorological variables

Data from several climatic variables were extracted using the library "Climate" in R [16] and associated with each sampled field. The extracted climatic variables were: Average temperature (AVT), Maximum temperature (MXT), Minimum temperature (MNT), Average Dew point temperature (TdAV), Average Humidity (AVH), Minimum average humidity (MNH), Maximum average humidity (MXH), Wind direction (WDR), Wind Intensity (WIn), Atmospheric pressure (ATP), Total precipitation (TPP), Total cloudiness (TCl), low cloudiness (lCl) and Visibility (VIS). To build bio-meteorological variables, data

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 26 December 2022 doi:10.20944/preprints202212.0487.v1

were summarized (by adding up precipitation values and averaging other variables) by10-day periods spanning the period before and during the crop cycle (from June to March). The total bio-meteorological variables (p=200) results from multiplying the number of climatic variables by the number of 10-day periods explored in each growing season.

Each biometeorological variable was denoted with a code consisting of three letters and the number of the month. Data collected over two 10-day periods (20 days) were identified using an underscore with the numbers 1 or 2 to indicate the first or the second 20-day period of the month, respectively. For example, ATP9 = atmospheric pressure of September, ATP9_1 = atmospheric pressure of the first 20 days of September. When 10-day subperiods were considered, they were indicated with the letter *d* plus a number corresponding to the 10-day period starting on the crop planting date, e.g., MXT_d1 = maximum temperature of 10-day period 1, or first 10 days after sowing. A protocol to clean spatial data [17] comprising homologation of spatial coordinates and removal of outliers was applied to the climatic datasets.

2.2.1. Dataset of begomovirus in bean crop

The dataset of begomovirus in bean consisted of n=2014 records of begomovirus presence or absence obtained between 2001 and 2018 in NW Argentina. These data were used to calculate the relative incidence of begomovirus by adding up the positive samples for a geographic point and dividing by the sample size. This procedure resulted in 156 geographic points with disease and climatic data that were further used to explore the climate-incidence relationship (Figure 1). Geographic points with data from a bean plot were classified into plots with moderate (<=50%) or severe (>50%) incidence.

2.2.2. Dataset of begomovirus in soybean crop

The soybean dataset included n=1395 records collected between 2000 and 2018. Relative incidence was calculated as in bean; 96 geographic points were generated for the analysis of the climate-disease relationship (Figure 1). The climatic variables were obtained for the period between the mid-September and mid-March. Pre-planting winter months were also considered, with a period of 10 days to summarize the climate data. These variables were then expressed in months; the climatic variables were also obtained for every 15 days for September, October and November.

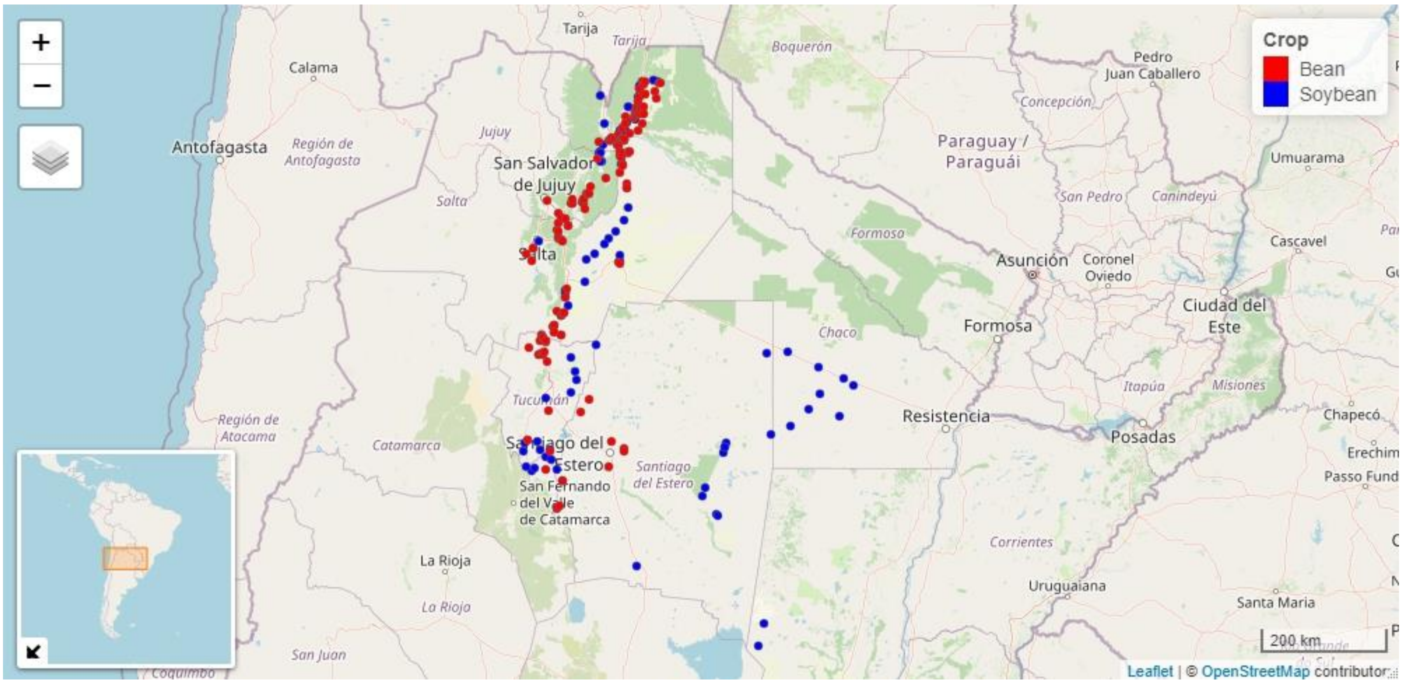


Figure 1. Geographic points with begomovirus incidence in bean (red, n = 156) and soybean (blue, n = 96) crops in NW Argentina

2.3. *Statistical analyses*

The biometeorological variables used for modeling relative incidence were obtained using the Boruta machine learning algorithm [18]. This wrapping method was implemented with another ML algorithm (Random Forest[19]) as a regression method. Random forest can capture non-linear relationships and interactions among variables to quantify the importance of each variable in incidence prediction. To fit predictive models, the climatic variables with importance exceeding a given threshold (>10%) were retained. The Boruta algorithm was applied using the package *Boruta* [18] of the software R [20], with the begomovirus incidence categories as dependent variable.

Finally, a logistic regression [21] was performed for each pathosystem to explain the categories of begomovirus incidence as a function of the selected biometeorological variables. When the value predicted by the model was >0.5, incidence was predicted as severe. To further reduce the number of variables in the predictive modeling, a stepwise variable selection method was applied along with the logistic regression model fitting using the variables indicated by the Boruta algorithm as important or tentative. The logistic regression model was fitted with the function *train, method glm* of the package caret [22] in the software R [20].

2.4. *Model assesement*

Different metrics were calculated to evaluate the accuracy of the prediction obtained with the logistic regression model fitted using the selected biometeorological variables. These metrics were calculated using the function *confusionMatrix* of the package caret in R. The sensitivity of the predicted model (i.e. percentage of positive predictive values or of severe incidence that are classified as severe) as well as the specificity (i.e. percentage of values with moderate incidence that are classified as of moderate incidence) were evaluated [23]. The ROC (Receiver Operating Characteristics) curves were used to determine the model discriminant capacity [24]; the curves were calculated using the function *accuracy* of the package rfUtilities [25].

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 26 December 2022 doi:10.20944/preprints202212.0487.v1

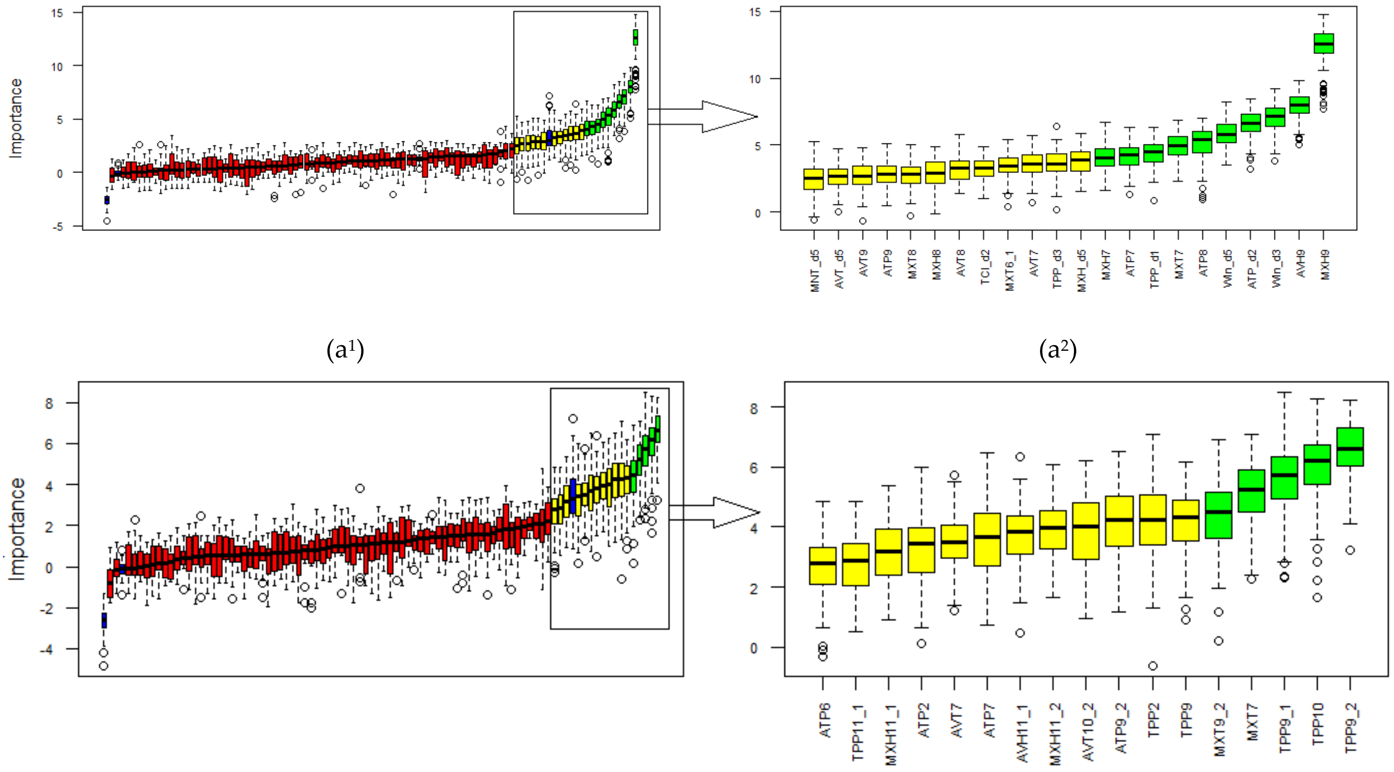
2.5 Validation of predictors

The predictive capacity of the models generated from the logistic regression analysis was tested using cross-validation. This procedure selected 30% of randomly selected records as a validation group. These records were then excluded from the data set used to calibrate the model. This procedure was repeated 30 times, by selecting different random calibration and testing groups. The model fitted for bean was also validated with the dataset of the 2019-2020 crop season; during that period, incidence of begomovirus was monitored in the north of the cropping area in Argentina.

3. Results

3.1. Selection of biometeorological variables

The variable selection procedure for bean identified 10 variables as important and 12 as tentative; the remaining ones were of low importance (Figure 2. (a^{1}) and 2. (a^{2})). For soybean, the Boruta algorithm classified five variables as important and 12 as tentative (Figure 2. (b^{1}) and 2. (b^{2})).



(a^{1}) (a^{2})

(b^{1}) (b^{1})

Figure 2. Classification of variables using the Boruta algorithm. Red: Unimportant variables; Yellow: Tentative variables; Green: Important variables. (a^{1}): General classification for bean. (a^{2}): Tentative and important variables in bean. (b^{1}): General classification for soybean. (b^{2}): Tentative and important variables in soybean.

3.2. Regression models fitted to predict begomovirus incidence

In the case of bean, the fitted logistic regression [Accuracy: 0.80, Sensitivity: 71%, Specificity: 86%] modeled the logarithm of the chances of severe incidence based on the variables maximum temperature in the first 10-day period of June (MXT6_1), maximum temperature in July (MXT7), mean temperature in July (AVT7), maximum temperature in August (MXT8), mean temperature in August (AVT8), average humidity in September (AVH9), and total precipitations in the first 10-day period (TPP_d1), before sowing date

(Table 1). The Probability of high incidence of begomovirus derived from the fitted model is:

$$Prob(Incidence > 50\%) = \frac{exp^{9.07-0.36\,MXT6\_1+2.14\,MXT7-2.32\,\,AVT7-2.20\,MXT8+3.64\,AVT8+\,-0.42\,AVH9\,-0.015\,TPP\_d1}}{1+\,exp^{9.07-0.36\,MXT6\_1+2.14\,MXT7-2.32\,\,AVT7-2.20\,MXT8+3.64\,AVT8+\,-0.42\,AVH9\,-0.015\,TPP\_d1}} \tag{1}$$

For the begomovirus pathosystem in soybean, the fitted predictive model [Accuracy: 75%, Sensitivity: 72%, Specificity: 89%] included the following climatic variables of high predictive capacity: mean temperatures in the first 20 days of September (AVT9_1), total precipitations in the last 20 days of September (TPP9_2) and mean temperature in the last 20 days of October (AVT10_2) (Table 1). The Probability of high incidence of begomovirus derived from the fitted model is:

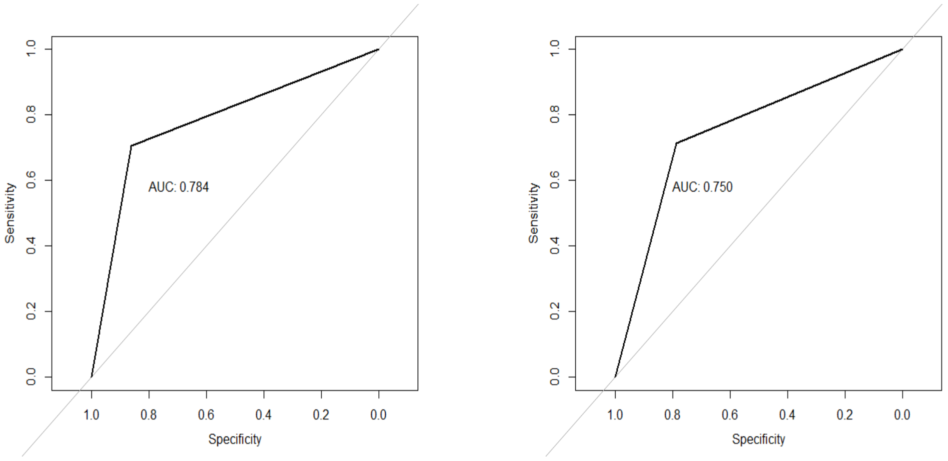
$$Prob(Incidence > 50\%) = \frac{exp^{10.05+0.30\,AVT9\_1-0.16\,TPP9\_2-0.62\,AVT10\_2}}{1+\,exp^{10.05+0.30\,AVT9\_1-0.16\,TPP9\_2-0.62\,AVT10\_2}} \tag{2}$$

Table 1. Regression coefficients that explain the logarithm of the chances of severe incidence of begomovirus in bean and soybean cultivated in NW Argentina.

		Estimate	Std. Error	z value	Pr(>|z|)	
Bean	Intercept	9.0749	10.0292	0.905	0.365545	
	MXT6_1	-0.3599	0.1233	-2.920	0.003506	**
	MXT7	2.1496	0.7224	2.976	0.002925	**
	AVT7	-2.3241	0.6961	-3.338	0.000842	***
	MXT8	-2.1989	0.5513	-3.989	6.64e-05	***
	AVT8	3.6146	0.8607	4.200	2.67e-05	***
	AVH9	-0.4208	0.0998	-4.213	2.52e-05	***
	TPP_d1	-0.0152	0.0071	-2.132	0.033041	*
Soybean	Intercept	10.050	4.918	2.044	0.040994	*
	AVT9_1	0.303	0.123	2.456	0.014043	*
	TPP9_2	-0.160	0.047	-3.376	0.000734	***
	AVT10_2	-0.622	0.231	-2.691	0.007125	**

Meaning of symbols: '***':0; '**': 0.001 '*': 0.05 '.': 0.1 ' ': 1

The associated ROC curves showing good capacity to differentiate sites with high probability of severe incidence from those with high probability of moderate incidence are shown in Figure 3. The bean model was evaluated with 10 new records of begomovirus incidence from the north of Argentina after downloading the climatic variables of the 2019-2020 crop season; classification was correct in 90% of the cases.



(a) (b)

Figure 3. ROC curve and area under the curve (AUC). (a) Bean. (b) Soybean.

4. Discussion

The main cause of the occurrence of most plant viruses is the anthropogenic introduction of parasites, although severe weather events are also important drivers of disease emergence [26]. Emerging virus diseases, like those caused by geminiviruses in plant systems, is challenging food production in tropical and subtropical areas, where high temperatures and droughts are frequent. Geographic distribution of plant diseases is largely related to the environmental conditions prevailing in the cropping area. These diseases cause economic losses through the reduction of grain quantity and quality, and the increase in production costs from the use of agrochemicals or seeds bred for resistance to pathogens [27–29].

Both pathosystems analyzed in this work include begomovirus, an agent associated with important yield losses in a subtropical area of Argentina, where bean is produced and soybean is increasingly cultivated. The results suggest that maximum winter temperature, relative humidity in September and precipitations 10 days before planting date are variables with high capacity to predict the level of begomovirus incidence in bean crops. Similarly, for soybean, our findings indicate that mean temperatures in September and October, and total of precipitations in the last 20 days of September are the variables that best explained begomovirus incidence, since soybean is commonly planted in September and October in NW Argentina.

It is known that the importance, distribution and incidence of numerous viruses are directly associated with the distribution and population dynamics of the insect vector [11,30,31]. According to [7], for begomovirus, these vector features largely depend on the weather conditions that favor vector reproduction: generally warm temperatures, moderate relative humidity and relatively low to moderate precipitations

In agreement with other works, the models fitted in this work indicate an increase in begomovirus incidence in these crops when pre-planting months are warm. [32] suggest that whitefly populations are affected by extreme low temperatures, low relative humidity (<60 %) and persistent precipitations. It is well known that whiteflies do not adapt to elevations higher than 1000 m asl due to climatic limitations. Temperature is one of the most critical variables for the life development of the insect vector, influencing colonization, behavior and distribution [32]. In general, *B. tabaci* incidence is higher in regions with a dry season of at least 4 months, precipitation records below 80 mm during that season, and a monthly mean temperature of at least 21 °C in the warmest months of the year [33]. As global warming increases, so does the probability of the occurrence of these climatic conditions in bean and soybean subtropical cropping areas, like those in NW Argentina [34].

On average, the vector life cycle ranges between 17 and 27 days, but it can be completed over 12-14 to 43-49 days, depending on warm or cool weather conditions, respectively [35]. The temperature range for development is very wide, with 16 and 24 °C being the most favorable temperatures. Temperatures below 9 °C and above 40 °C are lethal to the insect. Regarding relative humidity, optimum values between 30 and 60% have been reported [36–38]. In the study area, relative humidity ranges between 35 and 65%; values close to the maximum values of that range in spring were negatively associated with virus incidence.

Information about geminivirus and climate is abundant, but few works have performed predictive models of incidence based on climatic conditions, suggesting that the impact of biological correlations on management is underestimated. The models fitted using the begomovirus-climate relationship in this work show high predictive capacity of severe incidence of the virus. Since the variables with greatest contribution are recorded in pre-planting periods, the models could be incorporated to warning systems that also consider other factors, such as crop susceptibility, availability of alternative hosts that allow vector feeding and reproduction, and agronomic management of the affected plots. The inclusion of predictive models in early warning systems for decision making has helped to reduce the risk of virus infection in other crops [39]. Nevertheless, this type of predictive models should be used taking into account that the prediction of the probability of disease development in a crop is characteristic of and exclusive to each pathosystem and can be altered by other factors not included in the model.

5. Conclusions

This work demonstrated that biometeorological variables are correlated with the level of begomovirus incidence in bean and soybean crops. In addition, those variables can be used to generate warning systems that allow producers to implement agronomic practices, such as selection of varieties and planting dates, to reduce the effect of the virus on bean and soybean crops. For bean, high maximum temperatures in winter, low humidity in spring and precipitations 10 days before planting are correlated with severe incidence. In soybean, high temperatures in late winter and before planting, and low precipitations in spring were good predictors of a high incidence of begomovirus presence.

Author Contributions: M.B., F.S., P.R., and P.R.P: Conceptualization, Methodology, F.S. and M.B: Data Analysis, Validation, Visualization; F.S., P.R., M.B. and P.R.P: Writing - review & editing.

Funding: This research was funded by Unidad Ejecutora UFyMA – INTA – CONICET (PUEDD 2019-2023 Nº 22920180100064 CO)

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Acknowledgments: We thank the National Institute of Agricultural Technology (INTA), the National University of Córdoba (UNC) and the National Scientific and Technical Research Council (CONICET) for supporting this research.

Conflicts of Interest: The authors declare no conflict of interest.

References

[1] A. Varma, V.G. Malathi, Emerging geminivirus problems: a serious threat to crop production, Ann. Appl. Biol. 142 (2003) 145–164.

[2] J. Navas-Castillo, E. Fiallo-Olivé, S. Sánchez-Campos, Emerging virus diseases transmitted by whiteflies, Annu. Rev. Phytopathol. 49 (2011) 219–248.

[3] M.A. Macedo, T.M. Costa, J.C. Barbosa, J.L. Pereira, M. Michereff-Filho, R.L. Gilbertson, A.K. Inoue-Nagata, A. Bergamin Filho, Temporal and spatial dynamics of begomovirus disease in tomatoes in central Brazil, Plant Pathol. 66 (2017) 529–538.

[4] F.R. Fernandes, A.R.R. Cruz, J.C. Faria, F.M. Zerbini, F.J.L. Aragão, Three distinct begomoviruses associated with soybean in central Brazil, Arch. Virol. 154 (2009) 1567–1570.

[5] A.K. Inoue-Nagata, M.F. Lima, R.L. Gilbertson, A review of geminivirus diseases in vegetables and other crops in Brazil:

current status and approaches for management, Hortic. Bras. 34 (2016) 8–18.

[6] F.J. Morales, G. Varela, V. Ávalos, P. Reyna, I.G. Laguna, P.R. Pardina, Identification, molecular characterization and relative incidence of begomoviruses infecting bean crops in northwestern Argentina: An update, Australas. Plant Pathol. 47 (2018) 343–350. https://doi.org/10.1016/S0065-3527(06)67004-8.

[7] F.J. Morales, History and Current Distribution of Begomoviruses in Latin America, Adv. Virus Res. 67 (2006) 127–162. https://doi.org/10.1016/S0065-3527(06)67004-8.

[8] P. De Barro, M.Z. Ahmed, Genetic networking of the Bemisia tabaci cryptic species complex reveals pattern of biological invasions, PLoS One. 6 (2011) e25579.

[9] M. Shadmany, L.M. Boykin, R. Muhamad, D. Omar, Genetic diversity of Bemisia tabaci (Hemiptera: Aleyrodidae) species complex across Malaysia, J. Econ. Entomol. 112 (2019) 75–84.

[10] J. Xu, P.J. De Barro, S.S. Liu, Reproductive incompatibility among genetic groups of Bemisia tabaci supports the proposition that the whitefly is a cryptic species complex, Bull. Entomol. Res. 100 (2010) 359–366.

[11] V. Alemandri, P. Rodriguez Pardina, E. Argüello Caro, M.F. Mattio, A. Dumón, S.M. Rodriguez, G. Truol, J. Izaurralde, S. García Medina, Incidence of begomoviruses and climatic characterisation of Bemisia tabaci-geminivirus complex in soybean and bean in Argentina, AgriScientia. 29 (2012) 31–39. https://doi.org/10.31047/1668.298x.v29.n1.2797.

[12] V. Alemandri, C.G. Vaghi Medina, A.D. DumÓn, E.B. Argüello Caro, M.F. Mattio, S. Garcia Medina, P.M. López Lambertini, G. Truol, Three members of the Bemisia tabaci (Hemiptera: Aleyrodidae) cryptic species complex occur sympatrically in Argentine horticultural crops, J. Econ. Entomol. 108 (2015) 405–413.

[13] A. Morales-Soto, A. Lamz-Piedra, Genetic improvement methods in the cultivation of common beans (Phaseolus vulgaris L.) against the Bean Yellow Golden Mosaic Virus (BGYMV), Cultiv. Trop. 41 (2020) e10.

[14] F. FAO, Food and agriculture organization of the United Nations, Rome, URL Http//Faostat. Fao. Org. (2019).

[15] P.E. Rodríguez-Pardina, K. Hanada, I.G. Laguna, F.M. Zerbini, D.A. Ducasse, Molecular characterisation and relative incidence of bean- and soybean-infecting begomoviruses in northwestern Argentina, Ann. Appl. Biol. 158 (2011) 69–78. https://doi.org/10.1111/J.1744-7348.2010.00441.X.

[16] B. Czernecki, A. Głogowski, J. Nowosad, Climate: An R package to access free in-situ meteorological and hydrological datasets for environmental assessment, Sustainability. 12 (2020) 394.

[17] A. Vega, M. Córdoba, M. Castro-Franco, M. Balzarini, Protocol for automating error removal from yield maps, Precis. Agric. 20 (2019) 1030–1044. https://doi.org/10.1007/s11119-018-09632-8.

[18] M.B. Kursa, W.R. Rudnicki, M.M.B. Kursa, Package 'Boruta,' (2020).

[19] L. Breiman, Random forests, Mach. Learn. 45 (2001) 5–32. https://doi.org/10.1023/A:1010933404324.

[20] R Core Team, R: A language and environment for statistical computing, R Found. Stat. Comput. (2021). https://www.r-project.org/.

[21] A. Agresti, M. Kateri, Some Remarks on Latent Variable Models in Categorical Data Analysis, Https://Doi.Org/10.1080/03610926.2013.814783. 43 (2014) 801–814. https://doi.org/10.1080/03610926.2013.814783.

[22] M. Kuhn, The caret package.–R Foundation for Statistical Computing, Vienna, Austria, URL Https//Cran. r-Project. Org/Package= Caret. (2012).

[23] M. Carmona, R. Moschini, G. Cazenave, F. Sautua, Relación entre la precipitación registrada en estados reproductivos de la soja y la severidad de Septoria glycines y Cercospora kikuchii, Trop. Plant Pathol. 35 (2010) 71–078. www.sbfito.com.br (accessed August 19, 2021).

[24] J. Aldas Manzano, E. Uriel Jimenez, Análisis multivariante aplicado con R, Ediciones Paraninfo, SA, 2017.

[25] J.S. Evans, M.A. Murphy, Package 'rfUtilities,' (2019).

[26] P.K. Anderson, A.A. Cunningham, N.G. Patel, F.J. Morales, P.R. Epstein, P. Daszak, Emerging infectious diseases of plants: pathogen pollution, climate change and agrotechnology drivers, Trends Ecol. Evol. 19 (2004) 535–544.

[27] O.N. Vizgarra, C. Espeche, S. Mamani, Cultivos De Verano Para El Norte Argentino-Poroto (Phaseolus vulgaris L.): Manejo

Preprints (www.preprints.org) | NOT PEER-REVIEWED | Posted: 26 December 2022 doi:10.20944/preprints202212.0487.v1

del cultivo y recomendaciones, in: 2012.

[28] O.N. Vizgarra, C. Espeche, S. Mamaní Gonzáles, D. Velazquez, L.D. Ploper, Consideraciones generales de la campana de poroto 2012 y resultados de los ensayos evaluados en el Noroeste Argentino., Av. Agroindustrial. 33 (2012) 33:29–34.

[29] O.N. Vizgarra, L.D. Ploper, A.C. Ghio, A. Pérez, TUC 510: nueva variedad de poroto negro (Phaseolus vulgaris L.) con alta tolerancia a las virosis presentes en el noroeste argentino, Rev. Ind. y Agrícola Tucumán. 83 (2006) 39–47.

[30] R.C. Moschini, C. Fortugno, Predicting wheat head blight incidence using models based on meteorological factors in Pergamino, Argentina, Eur. J. Plant Pathol. 102 (1996) 211–218. https://doi.org/10.1007/BF01877959.

[31] E.A. Pozzi, C. Bruno, C.E. Luciani, M.G. Celli, V.C. Conci, M.C. Perotto, Relative incidence of cucurbit viruses and relationship with bio-meteorological variables, Australas. Plant Pathol. 49 (2020) 167–174. https://doi.org/10.1007/S13313-020-00687-8.

[32] R. Krause-Sakate, L.F. Watanabe Maranho, E. Silva Gorayeb, F. Barreto da Silva, D. de Lima Alvarez, V.H. Bello, A.M. Nogueira, B. Rossito de Marchi, E. Vicentin, M.R. Ribeiro-Junior, J. Massaharu Marubayashi, C.A. Rojas-Bertini, C. Muller, R.C. Oliveira de Freitas Bueno, M. Rosales, M. Ghanim, M. Agenor Pavan, Population dynamics of whiteflies and associated viruses in South America: Research progress and perspectives, Insects. 11 (2020) 1–36. https://doi.org/10.3390/insects11120847.

[33] A.B. Heinemann, J. Ramirez-Villegas, T.L.P.O. Souza, A.D. Didonet, J.G. di Stefano, K.J. Boote, A. Jarvis, Drought impact on rainfed common bean production areas in Brazil, Agric. For. Meteorol. 225 (2016) 57–74. https://doi.org/10.1016/j.agrformet.2016.05.010.

[34] IPCC, Ipcc, Clim. Chang. (2014).

[35] R.M.O. Molina, Eficacia de los agrotextiles como método de protección de cultivos, Universidad Almería, 2017.

[36] B. Picó, M.J. Díez, F. Nuez, Viral diseases causing the greatest economics losses to the tomato crop II. The Tomato yellow leaf curly virus - a review, Sci. Hortic. 67 (1996) 151–196.

[37] A. Ghosh, G.P. Rao, V.K. Baranwal, Manual on transmission of plant viruses and phytoplasmas by insect vectors, 2019.

[38] F.J. Morales, P.G. Jones, The ecology and epidemiology of whitefly-transmitted viruses in Latin America, Virus Res. 100 (2004) 57–65. https://doi.org/10.1016/J.VIRUSRES.2003.12.014.

[39] G. March, M. Balzarini, J. Ornaghi, J. Beviacqua, Modelo predictivo de la intensidad de la enfermedad “Mal de Río Cuarto,” Enfermedades Las Plantas. (1995). https://agris.fao.org/agris-search/search.do?recordID=US9563432 (accessed August 3, 2022).