

A Hybrid Artificial Intelligence Model for *Aeneolamia varia* (Hemiptera: Cercopidae) Populations in Sugarcane Crops

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Abstract

Sugarcane spittlebugs are considered important pests in sugarcane crops ranging from the southeastern United States to northern Argentina. To evaluate the effects of climate variables on adult populations of *Aeneolamia varia* (Fabricius) (Hemiptera: Cercopidae), a 3-yr monitoring study was carried out in sugarcane fields at week-long intervals during the rainy season (May to November 2005–2007). The resulting data were analyzed using the univariate Forest-Genetic method. The best predictive model explained 75.8% variability in physiological damage threshold. It predicted that the main climatic factors influencing the adult population would be, in order of importance, evaporation; evapotranspiration by 0.5; evapotranspiration, cloudiness at 2:00 p.m.; average sunshine and relative humidity at 8:00 a.m. The optimization of the predictive model established that the lower and upper limits of the climatic variables produced a threshold in the population development rate of 184 to 267 adult insects under the agroecological conditions of the study area. These results provide a new perspective on decision-making in the preventive management of *A. varia* adults in sugarcane crops.

Key words: pest insect, population management threshold, Random Forest, genetic algorithm

Sugarcane (*Saccharum officinarum* L.) is an important crop in tropical areas, as it has a huge potential to produce sugar, ethanol, biodegradable products, energy, and food for animal production (Heinrichs et al. 2017). However, crop yields can be threatened by biotic factors, such as pests and diseases. In Latin American countries, yield losses have been caused by three spittlebug genera, *Mahanarva* Distant, *Prosapia* Fennah, and *Aeneolamia* Fennah (Hemiptera: Cercopidae), which feed on most of the commercial varieties of sugarcane in Brazil, Venezuela, Mexico, and Colombia (Cuarán et al. 2012). Sugarcane spittlebugs, including *Aeneolamia varia* (Fabricius), are considered important pests in American sugarcane farming because they are widely distributed from the southeastern United States to northern Argentina (Peck 2001, Cuarán et al. 2012). Despite the economic impact of spittlebugs on sugarcane crops, there is still no efficient method of controlling them in the Neotropical region. In addition to chemical control, some biological control strategies—including parasitoid wasps (*Cotesia falivipes* Cameron (Hymenoptera: Braconidae)), entomopathogenic nematodes (*Steinernema* spp. and *Heterorhabditis bacteriophora* (Poinar) (Nematoda: Heterorhabditidae)), and fungus (*Metarhizium anisopliae* (Metchnikoff) Sorokin (Hypocreales: Clavicipitaceae) and *Beauveria bassiana* (Bals.-Criv.) Vuill. (Hypocreales: Clavicipitaceae))—have produced varying levels of success (Rosero-Guerrero et al. 2012, Kassab et al. 2015).

Aeneolamia varia has been reported as the most important insect pest limiting sugar production in the central-west region of Venezuela. However, advances in the development of an efficient management program have been limited due to insufficient knowledge of the effects of climate on population ecology in a sugarcane agroecosystem (Figueredo et al. 2013). Additionally, this cercopid species has developed a crucial mechanism to overcome climate variations through the production of diapause eggs, which are able to synchronize their life cycle with the rainy season (Fontes et al. 1995, Castro et al. 2005). Thus, considering the ability of cercopid species to adapt to their environment, several studies predicting population fluctuations have been carried out. García-García et al. (2006) developed a risk deductive model for *Aeneolamia postica* (Walker) (Hemiptera: Cercopidae), which showed that high temperature and precipitation were the most important factors in a field previously infested with nymphs and utilizing precarious weed control, triggering high densities of *A. postica*. These findings were corroborated by a study using a generalized linear model showing that the number of spittlebug adults increased by 1.92, 1.48, 3–4.5, and 0.051 due to the presence of nymphs, previous infestations, weed coverage, and temperature, respectively (Álvarez et al. 2017).

Climate change has prompted the agricultural sector to optimize pest management. So-called ‘smart agriculture’, which is based on the use of experimental data for the implementation of

intelligent algorithms through data mining methods, enables the development of statistical tools to address some agricultural problems in a dynamic environment (Issad et al. 2019). More recently, alternative modeling strategies based on artificial intelligence (AI) systems, such as hybrid models, have been proposed. These models are based on the integration of various AI algorithms, and work to explore the full potential of each of them (Chen et al. 2008). Thus, the univariate Forest-Genetic method results from the combination of the Random Forest and GAs as an alternative and complementary methodology to optimize the predictive modeling of phenomena from experimental designs (Villa-Murillo et al. 2016). Hybrid models have been developed and applied effectively in various areas of human development, such as education, industry, health, information technology, transportation, economics, state security and microbiology (Deeb and Jimenez 2003, Azizi 2017, Zheng et al. 2017, Panch et al. 2018), although thus far they still have limited applications in studies focusing on the population ecology of insect pests. In this study, optimal climate parameters producing greater effects on the population dynamics of *A. varia* adults were identified, quantified and modeled using the univariate Forest-Genetic method. This information provides new perspectives to help design an Integrated Pest Management Program for *A. varia* in sugarcane fields.

Materials and Methods

Study Area

Aeneolomia varia sampling was conducted in a 0.48 ha sugarcane plot in the Experimental Station Yaritagua, Peña municipality, Yaracuy state, Venezuela (10°02'N, 69°07'W, at 308 m asl). This agroecological zone is characterized as a tropical dry forest climate, according to Holdridge (1967), with a unimodal rainfall pattern from May to October.

Sampling

Sugarcane fields planted with the cultivar CR87-339 were surveyed. Samples of *A. varia* were collected from 6-mo-old plants over three crop cycles during the rainy period, lasting from May 11 to 2 November 2005 (plant-cane); May 11 to 2 November 2006 (second-year ratoon); and May 10 to 1 November 2007 (3-yr ratoon).

The spittlebug population was monitored through 30 permanent equidistant stations established in the field. Adults were captured with yellow traps installed 1.20 m above the ground between two sowing threads (Salazar et al. 1983). Each yellow trap consisted of a yellow plate (23 cm in diameter) covered with a transparent plastic bag (thickness 0.10 mm) and impregnated with diluted glue (1:1; glue:gasoline) on both sides.

During each cycle, the adult population was monitored weekly for a total of 26 evaluations. Relative density was calculated every week for the total number of adults (TotalAd) captured on both sides of each yellow trap between 08:00 a.m. and 12:00 p.m. at each of the permanent monitoring stations. The data were used to estimate population dynamics. Insect control measures were not used during sampling times so as not to affect population dynamics.

Climatological variables were recorded concomitantly: weekly rainfall (WkRain); mean rainfall (MeanRain); minimum temperature (MinTemp); mean temperature (MeanTemp); maximum temperature (MaxTemp); mean insolation (MeanInsol); relative humidity at 8:00 a.m. (RelHum8am); relative humidity at 2:00 p.m. (RelHum2pm); evaporation (Evapor); cloudiness at 8:00 a.m. (Cloudy8am); cloudiness at 2:00 p.m. (Cloudy2pm); evapotranspiration (ET); and

evapotranspiration by 0.5 (ET0.5) (Source: Station Weather Station 0113). Additionally, the Aridity index (Ariindex), degree days of weekly development (DegDayWD) and degree days of accumulated weekly development (DegDayAccWD) were calculated as follows:

$$\text{Ariindex} = \frac{\text{Mean rainfall}}{\text{Potential Evapotranspiration}}$$

$$\text{DegDayWD} = \frac{\text{Max temp} + \text{min temp}}{2} - \text{Base temp}(24^\circ\text{C})$$

$$\text{DegDayAccWD} = \sum \frac{\text{Max Temp} + \text{min temp}}{2} - \text{Base Temp} (24^\circ\text{C})$$

Statistical Analysis

Population data and climatic variables from the three study periods were subjected to the univariate Forest-Genetic method (Villa-Murillo et al. 2016), in which optimum predictive modeling is performed in three phases: data normalization, modeling (identification of an objective function) and optimization of the parameter levels for the established model.

During the normalization phase, a previous preparation of the data set was made to reduce variability. Modeling yielded the predictive model (objective function) for the set of normalized data and their respective variables by means of the Random Forest Algorithm. Finally, during the optimization phase, optimum parameter levels were determined for the response variable according to the objective function. All analyses were programmed and performed using R language (R version 3.5.2; R Core Team 2018) and its auxiliary libraries randomForest, rpart, rpart.plot, ggplot2, and dplyr.

Results and Discussion

The results of the univariate Forest-Genetic method were as follows.

Normalization Phase

Following Villa-Murillo et al. (2016), data normalization was performed using the function below.

$$f_2(x) = \begin{cases} 0 & x = 0 \\ \frac{1}{1 + \exp(-x')} & \text{othercases} \end{cases} \quad \text{with } x' = \frac{(x - \text{Min})}{\text{Max} - \text{Min}}$$

Modeling Phase

The climate variables with the greatest effect on the developmental rate of adult spittlebug populations were identified by establishing an objective function through the Random Forest algorithm (PRED-RF) as follows:

$$\begin{aligned} \text{TotalAd} \sim & \text{WkRain} + \text{MeanRain} + \text{MinTemp} \\ & + \text{MeanTemp} + \text{MaxTemp} + \text{MeanInsol} \\ & + \text{RelHum8am} + \text{RelHum2pm} + \text{Evapor} + \text{Cloudy8am} \\ & + \text{Cloudy2pm} + \text{ET} + \text{ET0.5} + \text{AriIndex} + \text{DegDayWD} + \text{Week} \end{aligned} \quad (1)$$

After the model was adjusted, a root mean square error (RMSE) = 0.001985308 model accounted for 75.8% of the variability among 1,000 trees. Those values are considered quite

acceptable not only for predictive purposes, but also for estimation and optimization during the subsequent phase.

The importance of climatic variables in modeling the adult spittlebug population was established using the mean square error (MSE) (Fig. 1). Thus, evaporation (Evapor), evapotranspiration by 0.5 (ET0.5), and Evapotranspiration (ET) were shown to have the greatest effect on the occurrence and population increase of *A. varia*, followed in order of importance by Cloudy2pm, MeanInsol, RelHum8am, MeanRain, DegDayWD, WkRain and MeanTemp, respectively. Based on the results, predictive variables with the greatest influence on the initial model shown in equation 1 were selected as the main climatic factors that positively affect the population development rate of *A. varia*. Consequently, the resulting model was established as follows.

$$\begin{aligned} \text{TotalAd} \sim & \text{Evapor} + \text{ET0.5} + \text{ET} + \text{Cloudy2pm} \\ & + \text{MeanInsol} + \text{RelHum8am} + \text{MeanRain} \\ & + \text{DegDayWD} + \text{WkRain} + \text{MeanTemp} \end{aligned} \quad (2)$$

Optimization Phase

The model optimization process was initiated after elements of the selected Genetic Algorithm (GA) were defined as follows:

GA Elements

Initial population: a random sample of 100 chromosomes was generated according to the structure defined in the established model (equation 2); their responses were estimated and expressed according

to the initial scale of the study. This constituted the initial population of the GA.

The modeling phase was based on the Random Forest Algorithm under the scheme of classification and regression trees (CART); thus, each new observation (chromosome) was adjusted to the limits of the corresponding terminal node, which set the limits for the GA optimization process. Following the scheme of the univariate Forest-Genetic method, the fitness function was established by equation 3, defined as an interpolation function between nodes:

$$\hat{y}_{s_i} = \left| \frac{\hat{y}_{m_i}(E_{f_i} - E_{s_i}) - \hat{y}_{f_i}(E_{m_i} - E_{s_i})}{(E_{f_i} - E_{m_i})} \right| \quad (3)$$

where E_{f_i} , E_{m_i} , and E_{s_i} correspond to the values of the Evaporation gene (Evapor) of the i^{th} father, i^{th} mother and i^{th} son, respectively, since Evapor was the variable with the greatest weight, as shown in Table 1 and calculated by equation 4, where it represents the importance of the k^{th} gene in our predictive model.

$$\text{PC} = \frac{I_{x_k}}{\sum_{i=1}^{10} I_{x_k}} \quad (4)$$

Mutational Rate

According to the univariate Forest-Genetic method, the mutational rate was established at 2% (Villa-Murillo et al. 2016).

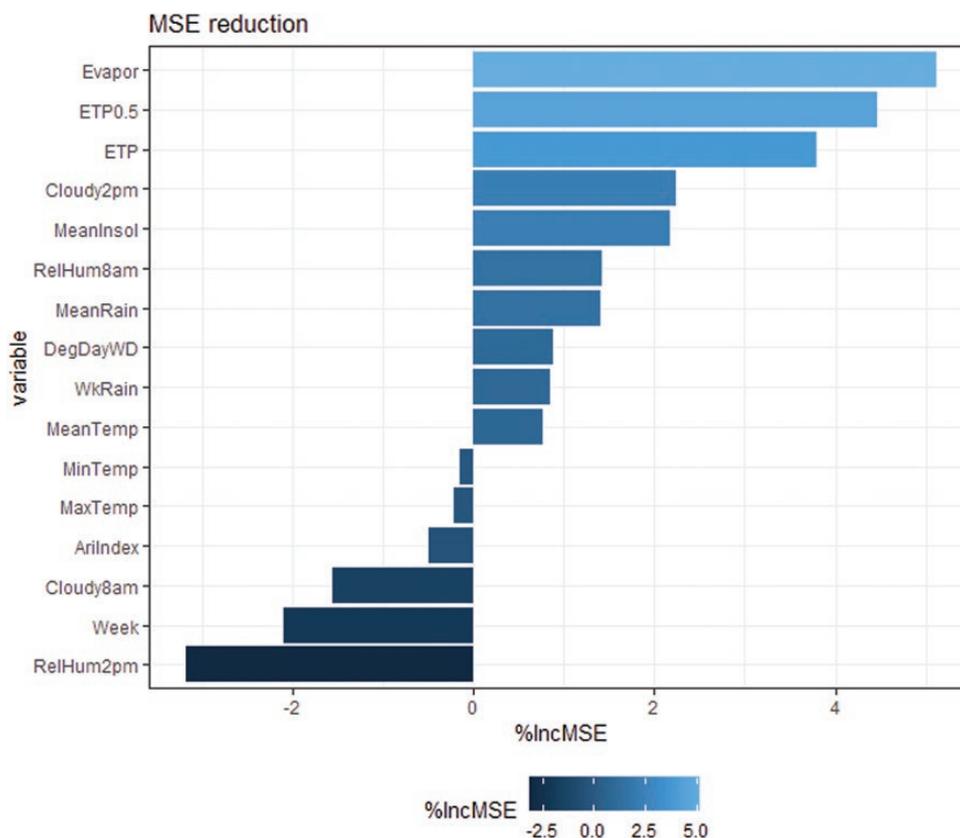


Fig. 1. Climate variables showing greatest influence on the adult population of *Aeneolamia varia* in sugarcane crops, according to (MSE = (RMSE)²).

Table 1. Weights per variable (gene) of the established model

Climate variable	Weight/variable
Evapor	0.3315
ET0.5	0.2896
ET	0.2454
Cloudy2pm	0.1454
MeanInsol	0.1408
RelHum8am	0.0924
MeanRain	0.0909
Gradodds	0.0569
WkRain	0.0554
MeanTemp	0.0495

Crossing Criterion

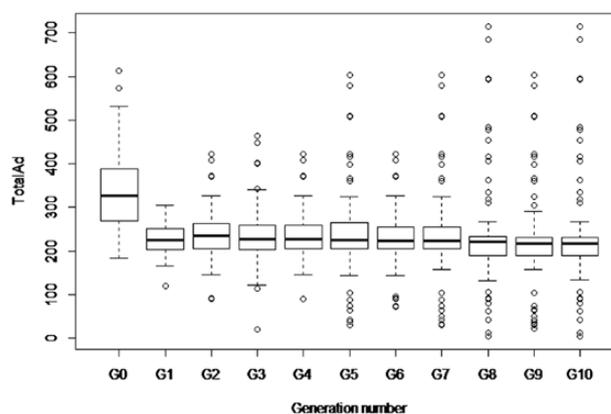
The formation of the following generations was based on a simple one-point weighted crossing, in which weighting corresponded to the allocation of weights among the climatic variables by means of the importance values calculated in Table 1. According to the Forest-Genetic method, this is done to increase the probability of crossing observations (chromosomes) in relation to the most important climate variables.

Optimization criterion:

In this phase, the GA aims to identify those climate parameters yielding the optimal response variable values according to the predetermined quality characteristic. Thus, considering the Physiological Damage Threshold (PDT) of 104 adults accumulated by Taa and estimated by Figueredo et al. (2003), the optimization criterion in the first quartile of our predictive model (184–267) for the TotalAd variable was established. The lower limit (184 adults) indicated the minimum number of spittlebugs required to induce visual symptoms of foliar damage to the sugarcane, while the upper limit (267 adults) indicated the population level required to cause economic damage to the crop. This is known as the Economic Damage Threshold (EDT). Linares (2002) stated that the lower limit indicates the control threshold (CT), that is, the optimum time to perform a management measure to prevent the insect population from reaching the EDT.

The algorithm consisted of applying the corresponding crosses and mutations, starting with generation 0 (G0) as the initial population; then the responses were estimated using the fitness function (equation 3), and a new generation was created by combining the parents' and sons' chromosomes with their corresponding response values. Finally, the optimization criterion was applied to the selection of the 'fittest' individuals, here defined as those belonging to the predetermined threshold, resulting in the first generation (G1). This process continued until the algorithm reached convergence, that is, when individuals tended to be homogeneous in relation to the climate variable values that fell within the corresponding threshold level. Figure 2 shows this convergence using box plots, where the reduction in boxes for each generation and its constant median value from generation 8 (G8) reflects the convergence of the algorithm, leaving out the most heterogeneous individuals (reflected as outliers).

Given the nature of the climate variables, the algorithm established a set of solutions rather than a single vector in the response. In each climate variable, an action interval was established for a response interval in the biological variable TotalAd. Thus, for the predictive model of the *A. varía* population in sugarcane obtained by Random Forest and the optimized model obtained with the GA for the PDT, the environmental variables influencing the TotalAd were defined as shown in Table 2.

**Fig. 2.** Forest-genetic method for the adult stage of *A. varía* in 10 generations of the Genetic Algorithm.**Table 2.** Lower and upper limits of climate variables according to the response variable (TotalAd) of *A. varía* for its agroecological management in sugarcane

Climate variable	Population development thresholds of <i>A. varía</i>	
	Lower limit	Upper limit
Evapor (mm)	6.43	11.18
ET0.5 (mm)	1.97	5.18
ET (mm)	3.13	5.12
Cloudy2pm	0.66	3.80
MeanInsol	3.08	9.89
RHum8am (%)	88.87	97.78
MeanRain (mm)	1.72	18.40
DegDays (°C)	125.7	935
PrecS (mm)	1.93	129.92
MeanTemp (°C)	25.67	28.74
TotalAd (N°)	184	267

Previous studies have demonstrated the effects of climatic parameters, such as rainfall, temperature, and relative humidity, on fluctuations in the *A. varía* population (Castro et al. 2002, García-García et al. 2006). Additionally, studies carried out in Brazil and Mexico reported that evapotranspiration and potential evaporation influenced the adult populations of *Deois flavopicta* (Stal) (Hemiptera: Cercopidae) and *Aeneolamia* spp., respectively (Melo et al. 1984, Álvarez et al. 2017, García-González et al. 2017), which is consistent with the findings in the present study.

On the other hand, a significant correlation between rainfall and the number of *A. varía* and *D. flavopicta* nymphs has been demonstrated (Melo et al. 1984, Figueredo et al. 2012); however, no correlation has been suggested between precipitation and the number of *A. varía* adults in sugarcane crops. Thus, apart from the abiotic factors mentioned above, the presence of nymphs could account for the increase in adults in the field (Castro et al. 2005). In sugarcane crops approximately 6 mo old, the abundant foliar area increases humidity, which along with the development of secondary roots at the soil surface level affects the development and abundance of spittlebug nymphs.

The climatic variables showing the greatest effect on the population development of *A. varía* adults in sugarcane crops were Evaporation by 0.5, Evapotranspiration, cloudiness at 2:00 p.m., mean isolation, relative humidity at 8:00 a.m. and mean rainfall;

and degree days for weekly development, weekly rainfall and mean temperature, respectively. Previous studies determined that *A. varia* populations increased at rainfall intervals between 36.4 and 112 mm in different ecoregions of Colombia (Castro et al. 2002). In Mexico, García-García et al. (2006) pointed out that temperatures in the range of 26 to 32°C are a determining factor in the development of *Aeneolamia* spp. nymphs and adults, which coincides with the upper limit of the PrecS (129.92 mm) and MeanTemp interval (25.67–28.74°C) established in the agroecological zone in the present study.

The population development thresholds for *A. varia* adults generated by the optimized model provide a key element to predicting the effect of climate variables on the population dynamics of *A. varia* in sugarcane fields, thus offering decision-making tools to apply timely management measures to avoid a potential population increase.

According to Graf et al. (1992), predictive models serve as valuable tools to help us understand pests as an element of the agroecosystem and assess the status of a given pest from a holistic point of view. Moreover, Vasconez et al. (2020) stated that the use of technology enables data acquisition and analysis in agricultural environments, which can help optimize current practices relating to pathogen and disease detection and management.

According to Issad et al. (2019), combining the strengths of different methods confers a greater robustness to the results obtained through data mining and applied to smart agriculture. Thus, the Forest-Genetic method has proven to be an effective tool for a set of complex and high-dimension data, which require flexible and powerful tools for effective statistical analysis (Chen and Ishwaran 2012).

Conclusions

The univariate Forest-Genetic method has been shown to be an alternative tool to improve parameter design through the phases of normalization, modeling, and optimization. It efficiently combines the advantages offered by the Random Forest algorithm in pattern recognition and integrates its measures of importance into the GA's genetic operators (Villa-Murillo et al. 2016). This reduces the variation in products and processes for selecting control factor levels, thus providing the best performance and least sensitivity to noise factors.

The univariate Forest-Genetic method was used for the first time to model pest damage threshold estimation, and it proved to be an adequate tool for predicting the interaction between insect (*A. varia*) and environment (climate), which allows us to introduce a new perspective on agroecological management of the pest insect at different geographical scales. Since agronomic management is staggered in sugarcane cultivation, outbreaks of the various life stages of *A. varia* are commonly observed in the field. Thus, this model allows us to predict the climatic conditions that will lead to higher population levels. In serving as an early warning, it enables us to identify those conditions most favorable to insect populations, and to adopt management tactics to reduce such populations within sugarcane crops.

Author Contributions

L.F. organized and performed field work, contributed to manuscript writing. A.V.-M. performed analytical mathematical work and contributed to manuscript writing. C.V. and Y.C. contributed with the analytical mathematical work and contributed to manuscript writing.

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