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Variability of Degree-Day Model Parameters for *Jacobiasca lybica* (Hemiptera: Cicadellidae)[1]

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ABSTRACT *Jacobiasca lybica* (Bergevin) (Hemiptera: Cicadellidae) is a major pest of grapevines in Europe and a secondary pest of citruses in Morocco. Accurate forecasting of its population dynamics is essential for minimizing crop losses, optimizing pest control interventions, and reducing unnecessary insecticide applications. However, existing degree-day (DD) models often fail to capture intra-seasonal variability, overlapping generations, and phenological shifts driven by environmental factors. This study aimed to evaluate the variability of parameters in degree-day models describing the population peaks of *J. lybica* populations. Field observations were collected from 2017 to 2021 in the Moulouya region of Morocco, and degree-days were calculated using the minimal theoretical 280 DD of the pest. Two candidate functions, Bragg and Beta, were tested for their best-of-fit to the observed population peaks. The Bragg function showed superior overall performance, with the fully flexible model (M5), which is able to optimize peak height, position, and width, providing the best fit in most years (e.g., 2021: $R^2 = 0.86$, RMSE = 22.1). However, a simpler variant (M4), optimizing only peak height and position, outperformed M5 in certain years (e.g., 2017: $R^2 = 0.994$). These findings support the application of Bragg-type models for capturing intra- and inter-annual variations in pest phenology and highlight their potential utility in integrated pest management programs.

KEY WORDS Population forecast, Beta function, Bragg function, population peak, integrated pest management

Predicting the seasonal activity of insect pests is crucial for effective pest management. As poikilothermic organisms, insects require the accumulation of a specific amount of heat to complete their life cycles. This relationship forms the basis of the degree-day (DD) modeling approach, which is widely used to forecast pest development and optimize control timing in both theoretical and applied entomology (Damos & Savopoulou-Soultani 2012, Zhang 2002, De Jong & Van der Have 2009).

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Degree-day models estimate the accumulation of thermal units above a species-specific developmental threshold, assuming a relatively constant development rate under given temperature conditions. These models are widely used and cost effective in integrated pest management because they help time chemical application optimally and reduce application frequency and waste (Eizenberg et al. 2005). However, DD models can fail to capture intra-seasonal variabilities, such as multiple or overlapping generations, irregular peak timings, and interactions with environmental factors other than temperature (Lischke et al. 1997a,b, Frouz et al. 2002, Son & Lewis 2005, Stauffer & Whitman 1997, Chown & Nicolson 2004). One strategy to address these limitations is to fit flexible mathematical functions to observed population peaks, allowing more accurate modeling of insect population fluctuations over time (Damos & Savopoulou-Soultani 2012, Regniere et al. 2012).

Gaussian and logistic curves are widely used to model seasonal peaks in population dynamics, especially in insect and plant phenology, due to their simplicity and flexibility (Schoolfield et al. 1981, Damos & Savopoulou-Soultani 2012). However, these models may sometimes fail to capture complex phenological patterns when multiple generations overlap or when population fluctuations are highly variable. In contrast, Bragg-type functions are symmetric, peak-centered models originally derived from signal processing and designed to represent periodic or quasi-periodic patterns more accurately (Macnaughton 2023). De la Calleja et al. (2016) demonstrated potential usefulness of Bragg function by incorporating Bragg-Williams approximation in modeling prey–predator biological associations. This work represents one of the few studies exploring the ecological applicability of Bragg-inspired approaches. The key strength of Bragg-type functions lies in their biologically interpretable parameters, peak height (abundance), peak position (timing), and peak width (duration), which enable more precise modeling of phenological patterns (De la Calleja et al. 2016, Macnaughton 2023). Furthermore, since Bragg-type models require fewer parameters than Beta functions, they often provide greater robustness when working with sparse or noisy ecological data (Burnham & Anderson 2002). This makes them particularly promising for forecasting insect population dynamics and identifying intra- and inter-annual variability in pest phenology.

Jacobiasca lybica (Bergevin) (Hemiptera: Cicadellidae) is an economically significant pest of grapevines in Europe (Lentini et al. 2000, Pavan et al. 2000, Delrio et al. 2001, Alma 2002, Tsolakis 2003), and a secondary pest of citrus in Morocco (Mazih 2015, Khfif et al. 2022, 2023). Damage caused by *J. lybica* is primarily due to nymphal feeding, which leads to chlorosis, shoot desiccation, and blemishes on citrus or grapevine leaves (Carle & Moutous 1965, Moore 2013). Although adults also feed, their mobility tends to result in more dispersed damage. Research indicates that densities as low as 0.5–1 nymph per leaf during mid-summer can induce visible symptoms and reduce fruit quality and soluble solids (Delrio et al. 2001). Economic threshold specific to *J. lybica* is not well established. Therefore, growers are advised to monitor nymph density weekly or rely on degree-day models to time insecticide applicationss before damage threshold is exceeded. Insecticides remain common management tools, but the drawbacks of this management strategy, such as resistance development and environmental harm, have led to growing interest in ecological forecasting tools to reduce numbers of insecticide sprays (Daane & Costello 2000, Bentley et al. 2007, Weintraub & Wilson 2010).

In the Moulouya region of Morocco, where *J. lybica* exhibits several population peaks per season driven by temperature and other environmental variables (Khfif et al. 2023), accurate forecasting of its seasonal dynamics remains challenging. Conventional degree-day models are often limited in their ability to capture intra-seasonal variability, overlapping generations, and inter-annual phenological shifts caused by environmental factors. To address these gaps, we evaluated the potential of incorporating Bragg-type and Beta-type mathematical functions to improve the predictive accuracy of degree-day models for *J. lybica*.

Materials and Methods

Study area and data collection. Field data on the population dynamics of adult *J. lybica* were collected between 2017 and 2021 in the Moulouya region of northeastern Morocco. The study site was located within the Couteaux de Saïdia Domain (35°01′45.7″N, 2°24′04.3″W; elevation 55 m), encompassing adjacent citrus orchards, vineyards, and windbreaks in Berkane Province. Daily meteorological data, including temperature and humidity, were recorded from 2017 to 2021 using a weather station (GP2 Data Logger; Delta-T Devices Ltd., Cambridge, UK) located approximately 5 km from the experimental plots at the National Institute for Agricultural Research (INRA) - Qualipole of Berkane.

During 2017 and 2018, the monitored area included a 2-ha citrus orchard planted with 40-y-old 'Berkane' clementine (*Citrus* × *clementina* Hort. ex Tanaka; Rutaceae) trees and a 1.8-ha vineyard (Guyot system) of 8-y-old *Vitis vinifera* cv. Carignan (Vitaceae). These plots were contiguous and separated by a windbreak composed of *Acacia karroo* Hayne (Fabaceae) and *Cupressus sempervirens* L. (Cupressaceae). In 2019–2021, an additional 2-ha vineyard of 8-y-old *V. vinifera* cv. Syrah was included. All plots were maintained under similar agronomic practices, including drip irrigation adjusted seasonally.

Five yellow sticky traps (15 × 10 cm) were deployed per habitat (citrus orchard, Carignan and Syrah vineyards, and windbreak trees). Within each habitat, traps were evenly spaced at approximately 20 m intervals to ensure representative sampling coverage. Placement was standardized by positioning traps on trees without prior selection based on known infestation levels to avoid bias, although trap locations were chosen to ensure homogeneous coverage across the plot. For windbreak trees, three traps were placed on *C. sempervirens* and two on *A. karroo*, following the same spacing. Traps were installed at a height of approximately 0.5 m in grapevines and 1.5 m in citrus and windbreak trees, always facing southeast. Traps were replaced weekly from late March to mid-August in 2017, from early April to late August in 2018, and from mid-March to early September in 2019. Due to constraints imposed during the COVID-19 pandemic, sampling in 2020 was conducted from early July to late December. Sampling resumed from mid-April to early September 2021.

Weekly trap catches were counted under stereomicroscopes at INRA - Qualipole of Berkane. For each year, the average number of adults per week was calculated using total catches across all traps. The final sample sizes (number of trap observations per year) were 330 in 2017, 315 in 2018, 500 in 2019, 480 in 2020, and 420 in 2021.

Degree-days calculation. Degree-day (DD) accumulation for *J. lybica* was calculated using the single-sine method, based on *J. lybica*'s lower developmental threshold of 10°C, as previously reported by Langham (2019). Daily DD values were estimated as the difference between the mean daily temperature and the threshold, using the following formula:

$$\mathrm{DD}_{\mathrm{daily}} = \max(0,\ \frac{\mathrm{T}_{\max} + \mathrm{T}_{\min}}{2} - 10),$$

where $\mathrm{T}_{\max}$ and $\mathrm{T}_{\min}$ are the daily maximum and minimum air temperatures, respectively. When the mean daily temperature was below the developmental threshold, the daily DD value was set to zero.

Degree-day accumulation started on 1 January of each year and continued throughout the monitoring period. A theoretical cumulative threshold of 280 DD was used to approximate the development time from egg to adult emergence for *J. lybica* (Langham 2019). This threshold also served as a reference for standardizing population peak curves.

Determination of the optimal smoothing curve. To identify the candidate theoretical models best describing the phenological development of *J. lybica*, we first constructed an average development curve based on observed adult abundance. This process began by selecting representative population dynamics from 14 typical seasonal curves, each corresponding to a distinct year. These curves were extracted by identifying clear population peaks within each season.

To enable comparison and aggregation across years, the selected curves were normalized in both the x- and y-axes. The x-axis normalization involved centering each curve on its peak and restricting the window to 280 DD on either side. For the y-axis, adult abundance values were transformed into relative percentages, where the maximum value (i.e., the peak) of each curve was set to 100%.

The 14 normalized curves were then superimposed using a common peak-centered x-axis, allowing direct comparison of their temporal profiles. A smoothing spline was applied to the resulting composite data to generate an average development curve. This smoothed curve represented the general phenological trend of *J. lybica* adult abundance and served as the empirical basis for evaluating the adequacy of candidate theoretical models. All data processing and smoothing procedures were conducted in R (R Core Team 2021), with time-series interpolation and gap-filling handled via the "zoo" package (Zeileis & Grothendieck 2005).

Selection of model. To identify the most appropriate theoretical functions describing the phenological dynamics of *J. lybica*, we fitted the smoothing spline curve (derived from normalized peak data) using nonlinear least squares (NLS) models implemented via the "nls()" function in R (R Core Team 2021). Two candidate functions were selected: the Bragg and the Beta function. Both models were initially evaluated against the synthetic average development curve derived from observed data, followed by their application to selected individual peak events.

The Bragg function was chosen for its symmetric shape and parsimonious parameterization, making it less prone to overfitting, an advantage when working with sparse or noisy data (Burnham & Anderson 2002, Macnaughton 2023).

This function, derived from signal processing, is conceptually similar to a Gaussian curve, featuring interpretable parameters such as peak height (d), position (e), and slope at inflection points (b, related to peak width). The Bragg function was fitted using "NLS.bragg.3()" from the "aomisc" package (Macnaughton 2023), with the formulation: $\mathrm{Y} = \mathrm{d} \times \exp^{[-\mathrm{b}(\mathrm{X}-\mathrm{e})^2]}$, where d is the peak height (maximum abundance), e is the location (position in DD), b relates inversely to the width of the curve and X is the accumulated degree-days (DD).

Conversely, the Beta function is an asymmetric distribution capable of modeling processes constrained by lower and upper bounds. It was included because it accommodates biological phenomena with known developmental thresholds (Schoolfield et al. 1981, Damos & Savopoulou-Soultani 2012). The model was fitted using the "NLS.beta()" self-starter in the "aomisc" package (Macnaughton 2023) and has the following form: $\mathrm{Y} = \mathrm{d}\left[\left(\frac{\mathrm{X}-\mathrm{X_b}}{\mathrm{X_0}-\mathrm{X_b}}\right)\left(\frac{\mathrm{X_c}-\mathrm{X}}{\mathrm{X_c}-\mathrm{X_0}}\right)^{\frac{\mathrm{X_c}-\mathrm{X_0}}{\mathrm{X_0}-\mathrm{X_b}}}\right]^{\mathrm{b}}$ for $\mathrm{X_b} < \mathrm{X} < \mathrm{X_c}$, where d is the maximum level for the expected response y, which is the high of peak, $\mathrm{X_b}$ is the minimum threshold levels at x-axis (degree-days), $\mathrm{X_c}$ is the maximum threshold levels at x-axis, $\mathrm{X_0}$ is the degree-day value at the maximum expected response d, and b is the shape parameter, which is the width of peak.

Models fitness and optimization. Given the visually superior fit of the Bragg function to the observed population peaks, showing clearer peak shapes and better alignment with data trends (Figure 3), it was adopted for additional statistical analyses. Individual peaks for each year from 2017 to 2021 were modeled using Bragg-type functions with degree-days as the predictor variable. By summing predicted Bragg curves, we could replicate realistic scenarios in which population peaks overlap, representing potential overlapping generations of *J. lybica*.

To explore model sensitivity and improve predictive accuracy, we implemented five nested Bragg-based models (M1 to M5), each with increasing flexibility in parameter optimization:

- M1: Baseline model with fixed peak height (d), position (e), and width ($\mathrm{b} = 0.0000385$);
- M2: Optimized peak height (d), with fixed (e) and (b);
- M3: Optimized peak position (e), with fixed (d) and (b);
- M4: Jointly optimized height (d) and position (e), with fixed (b); and
- M5: Fully optimized model with all three parameters (d, e, and b) independently estimated.

Optimization was conducted via the general-purpose "optim()" function in R (R Core Team 2021) by minimizing residual sum of squares between observed and predicted values. For M5, width coefficients (b) were estimated using pseudo-linear regression derived from the linearized Bragg form: $\log\left(\frac{\mathrm{y}}{\mathrm{d}}\right) = -\mathrm{b}(\mathrm{x}-\mathrm{e})^2$. This transformation allowed estimation of b via the slope in a regression of log-transformed pseudo-responses.

Model validation and rationale for chosen tests. To evaluate model performance, we used three standard metrics widely applied in phenological and ecological modeling:

- Coefficient of determination (R^2) to measure the proportion of variance explained by the model;
- Root Mean Square Error (RMSE) to quantify prediction error; and
- Residual Sum of Squares (RSS) to evaluate overall model fit.

These metrics were selected because they provide complementary insights into goodness-of-fit and predictive accuracy (Burnham & Anderson 2002, Regniere et al. 2012). In addition, we visually inspected the fitted curves against observed data for each year to confirm that the predicted phenological peaks aligned with field observations. Model validation was further supported by comparing predictions against independent subsets of data excluded during initial fitting. This combined approach ensured that the selected model was not only statistically optimal but also biologically consistent with observed seasonal patterns.

Results and Discussion

Determination of the optimal smoothing curve and model selection. The selection and evaluation of candidate models began with the construction of a synthetic average curve from normalized population peaks observed across 5 y (Figure 1). To address variability in peak widths across seasons, we applied both smoothing splines and loess fitting. The resulting loess-smoothed curve displayed a unimodal and nearly symmetrical profile, reflecting a consistent seasonal emergence pattern for *J. lybica* adults. This curve served as a benchmark for evaluating the suitability of two theoretical functions: the Bragg and Beta models.

Initial visual inspection revealed that the Beta function provided a closer fit to the average loess curve. This is expected because the Beta distribution accommodates asymmetrical shapes and incorporates both lower and upper bounds (minimum and maximum thresholds), which align with biological limits of insect development (Schoolfield et al. 1981, Damos & Savopoulou-Soultani 2012). However, when applied to discrete annual peaks (Figure 2), the Bragg function consistently outperformed the Beta function. The superior performance of the Bragg model is attributed to its symmetric formulation, fewer parameters, and greater robustness in datasets with low resolution or overlapping generational events (Lischke et al. 1997b, Son & Lewis 2005).

These findings emphasize the importance of selecting function forms that match not only the mean trend but also the underlying biological and sampling structure. While the Beta model offers flexibility, it is more susceptible to overfitting, especially under sparse or noisy conditions. Conversely, the Bragg function provides stable and interpretable fits across a range of phenological patterns, making it well-suited for field-based pest modeling.

Our results revealed a clear interannual variability in the phenology and abundance of *J. lybica,* with earlier and higher population peaks observed in 2018 and 2020 compared to 2017, 2019, and 2021. These differences are likely influenced by climatic conditions, particularly spring temperature patterns, which directly affect nymphal development rates and adult emergence. In warmer years, accelerated development resulted in earlier peaks, whereas cooler springs delayed population growth and reduced overall abundance. In addition,

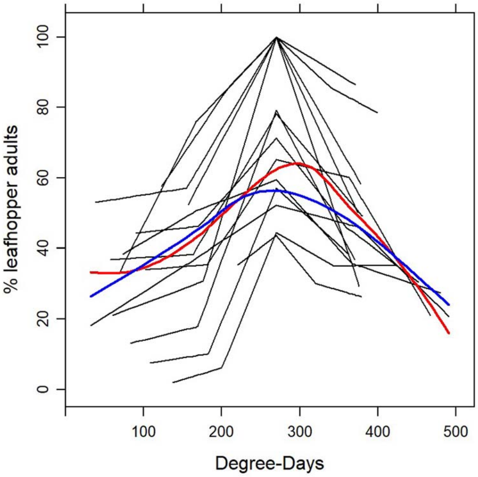

Fig. 1. Leafhopper peaks selected for all years with smoother (red) and LOESS (blue) curves.

variations in host plant phenology, such as budburst and leaf expansion, may have contributed to shifts in peak timing by modifying the availability of suitable feeding sites. Finally, differences in vineyard management practices (e.g., irrigation, pruning, and pesticide applications) may have amplified spatial and temporal variability among habitats and years. These findings emphasize the complex

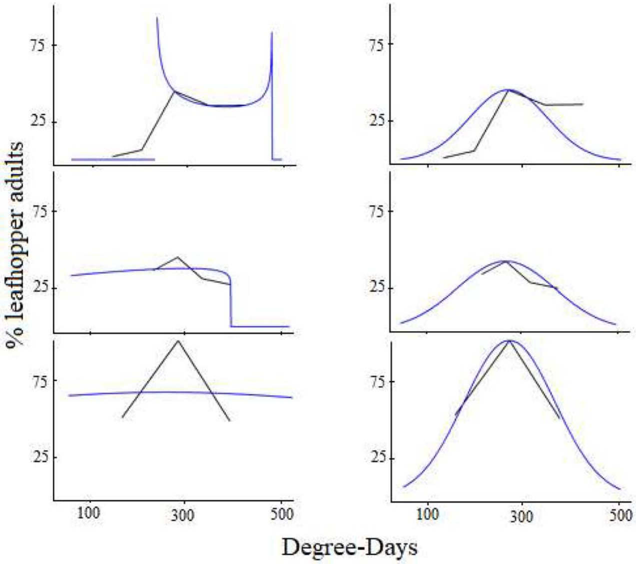

Fig. 2. Example of some peaks selected (black) fitted with Beta function (blue) in left and Bragg function (blue) in right.

Table 1. Coefficient of determination (R^2), residual sum of squares (RSS) and root mean square error (RMSE) for each model per year.

Year	Model	R^2	RMSE	RSS
2017	M1	0.977	12.47	2644
2017	M2	0.985	10.12	1740
2017	M3	0.99	8.34	1182
2017	M4	0.994	6.34	683
2017	M5	0.943	19.56	6505
2018	M1	0.526	2.95	199.75
2018	M2	0.681	2.42	134.51
2018	M3	0.736	2.2	111.35
2018	M4	0.768	2.06	97.88
2018	M5	0.7	2.35	126.59
2019	M1	0.7897	9.34	2092.44
2019	M2	0.8781	7.11	1212.64
2019	M3	0.8576	7.68	1416.74
2019	M4	0.9103	6.1	892.79
2019	M5	0.9117	6.05	878.27
2020	M1	0.637	62.64	94,157.36
2020	M2	0.639	62.43	93,543.66
2020	M3	0.725	54.46	71,194.14
2020	M4	0.739	53.14	67,767.73
2020	M5	0.773	49.52	58,843.3
2021	M1	0.7549	29.13	17,813.75
2021	M2	0.7556	29.08	17,760.85
2021	M3	0.7667	28.41	16,953.62
2021	M4	0.7651	28.51	17,069.47
2021	M5	0.8586	22.12	10,277.62

interplay between climate, host plant dynamics, and management strategies in shaping *J. lybica* population patterns.

Models fitness and year-by-year optimization. To evaluate model performance across different years, we compared five Bragg-based models (M1–M5), each with increasing levels of parameter optimization (peak height, position, and width). The results (Table 1) demonstrate a consistent pattern: models with flexible peak timing (M3) and height (M2) perform better than the baseline (M1), but the best-performing models are M4 and M5, which allow simultaneous or full optimization of all parameters.

In 2017 and 2018, *J. lybica* populations exhibited clearly distinguishable peaks with relatively little overlap (Figures 3 and 4). Under such conditions, M4 (optimized peak height and timing with fixed width) consistently outperformed the other models (e.g., $R^2 = 0.994$ in 2017). Surprisingly, the fully flexible model (M5) did not yield further improvements and in some cases performed less, indicating possible overfitting or instability in estimating width (b) from sparse data. These results are consistent with findings in phenological modeling where too

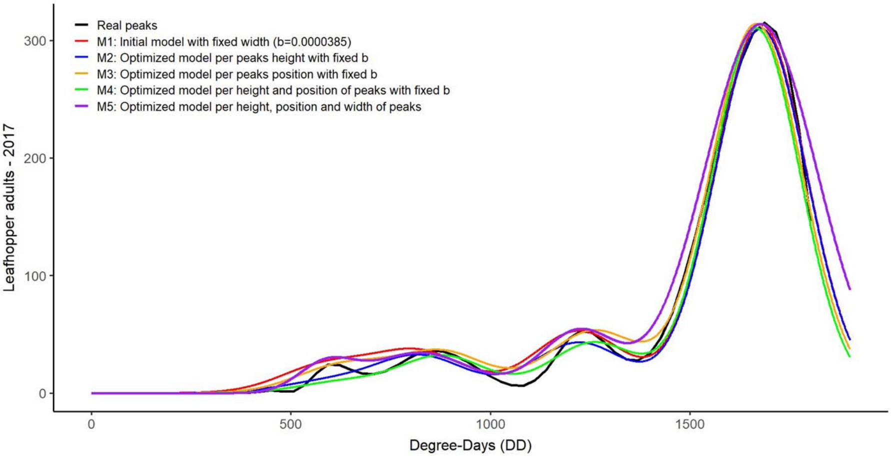

Fig. 3. Degree-Days (DD) initial and optimized models compared to real peaks of *Jacobisca lybica* during 2017.

many free parameters can reduce predictive power (Briere et al. 1999, Regniere et al. 2012).

In 2019, both M4 and M5 provided strong fits ($R^2 = 0.91$–0.91) (Figure 5), indicating that the added flexibility of M5 began to pay off as population peaks became less distinct. This suggests that model complexity should be adapted to the biological context, a principle supported in agroecological modeling (Damos et al. 2018, Guimapi et al. 2020).

The most complex phenological patterns emerged in 2020 and 2021, likely influenced by environmental variability and sampling interruptions during the COVID-19 pandemic. In 2020, model M5 yielded the highest R^2 (0.773), outperforming simpler

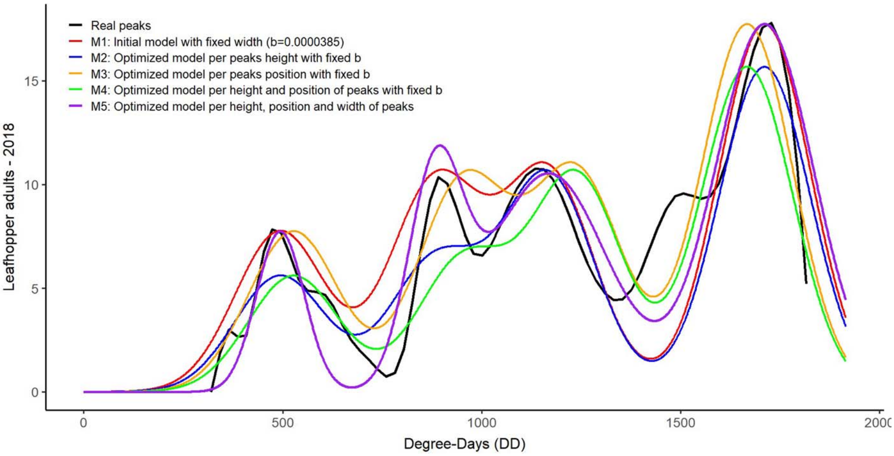

Fig. 4. Degree-Days (DD) initial and optimized models compared to real peaks of *Jacobisca lybica* during 2018.

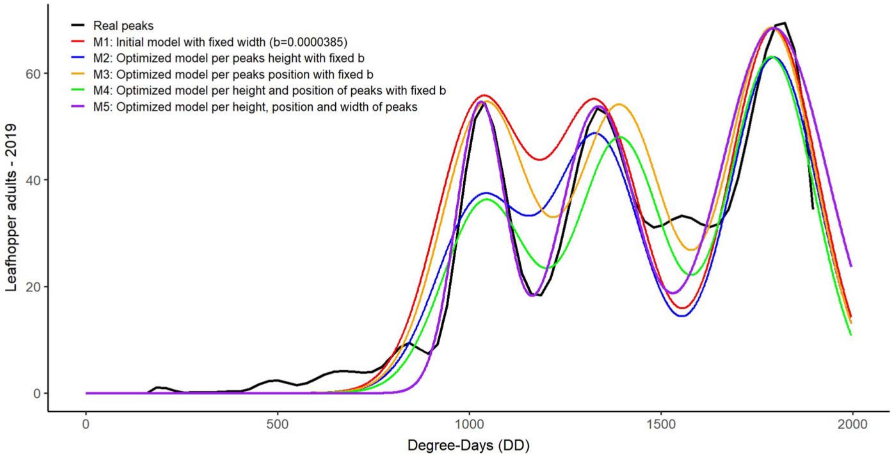

Fig. 5. Degree-Days (DD) initial and optimized models compared to real peaks of *Jacobisca lybica* during 2019.

models by a significant margin (Figure 6). The same was true in 2021, where M5 achieved $R^2 = 0.859$, compared to $R^2 = 0.765$ in M4 (Figure 7). These findings demonstrate that when multiple generations overlap or when environmental noise is high, flexible modeling of peak width becomes essential.

Boxplot analysis of R^2 and RMSE across 5 y demonstrates that sequential optimization of phenological model parameters significantly enhances explanatory power and predictive accuracy (Figure 8). The baseline model (M1), with fixed peak parameters, consistently showed the lowest R^2 and highest RMSE, indicating poor adaptability to inter-annual variation. Incremental optimization of peak height (M2) and position (M3) modestly improved performance, while combined optimization (M4) yielded stronger gains. The fully flexible model (M5), which includes peak width (b), achieved the highest median R^2, lowest RMSE, and least variability, proving most robust across varying ecological conditions. These results underscore the importance of modeling intra-seasonal variability and overlapping generations, especially in warmer years, and support M5's application in pest forecasting and IPM strategies, a phenomenon well-documented in other hemipteran species (Jayasimha et al. 2012, Damos et al. 2018, Bashir et al. 2022).

This aligns with empirical studies showing that higher temperatures compress insect development times, leading to overlapping generations and broader or merged population peaks (Chown & Nicolson 2004, Frouz et al. 2002, De Jong & Van der Have 2009). Our results show an inverse relationship between peak width ($\frac{1}{\sqrt{b}}$) and ambient temperature, confirming that rising temperatures reduce the duration of developmental stages, thus facilitating generational overlap. This temperature–phenology interaction is especially pronounced in poikilothermic organisms such as leafhoppers, whose development rates are strongly dependent on environmental temperature (Trudgill et al. 2005). The mathematic explanation is that the normal function is presented as: $f(x) = \frac{1}{\sqrt{2\pi\sigma^2}}\exp^{\left[\frac{-1}{2\sigma^2}\ (x-m)^2\right]}$ compared to

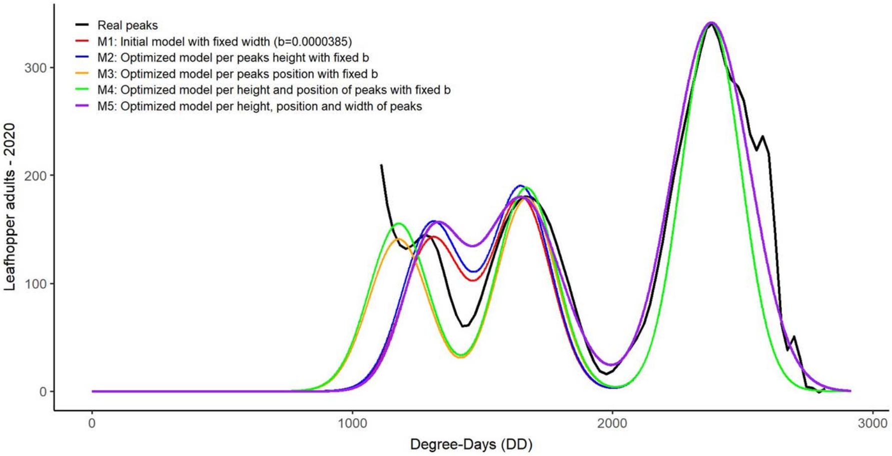

Fig. 6. Degree-Days (DD) initial and optimized models compared to real peaks of *Jacobisca lybica* during 2020.

the Bragg function $Y = \text{d}.\exp^{\left[-\text{b}(X-e)^2\right]}$, which means that b equivalent of $\frac{1}{2\sigma^2}$ and d $= \frac{1}{\sqrt{2\pi\sigma^2}}$, knowing that 95% of the surface of the curve is presented by 2σ and $\sigma = \frac{1}{\sqrt{2\text{b}}}$, we can conclude that by decreasing b, the 95% of the surface of the curve increase, which can explain the presence of overlapping generations.

The biological interpretation of Bragg model parameters provides important insights, that the peak height (d) reflects adult population size or reproductive output, and the peak timing (e) correlates with cumulative degree-days required for emergence, while width (b) is inversely related to the variability in

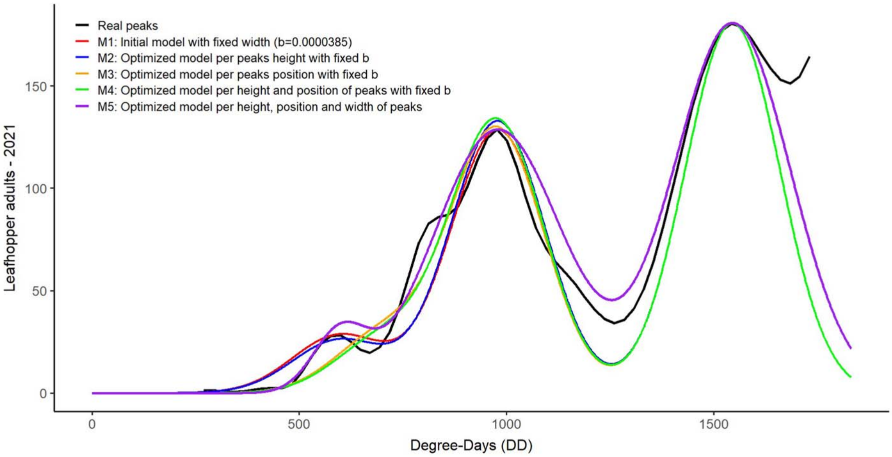

Fig. 7. Degree-Days (DD) initial and optimized models compared to real peaks of *Jacobisca lybica* during 2021.

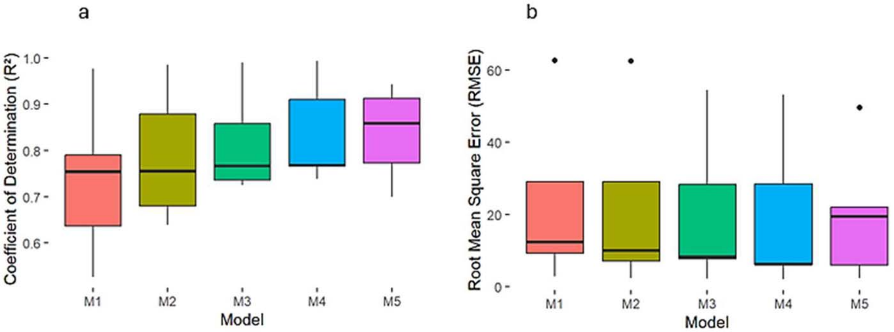

Fig. 8. Model performance R^2 (a) and RMSE (b) across years. The boxes represent the interquartile range (IQR), the horizontal line inside each box indicates the median, and the whiskers extend to 1.5×IQR. Black dots represent outlier RMSE values beyond the whisker range for individual year-model combinations.

emergence time and potentially indicates generational overlap or asynchronous development.

As temperature increases, insects tend to accumulate degree-days more rapidly, compressing the period between generations and increasing the probability of temporal overlap (Lischke et al. 1997a, Damos & Savopoulou-Soultani 2012). In our study, the lowest b values (widest curves) coincided with high-temperature periods, suggesting thermally driven shifts in voltinism. This phenomenon has been reported in other leafhopper species, including *Empoasca kerri* Pruthi and *Amrasca biguttula* Ishida, where temperature accelerates development while humidity and rainfall modulate abundance and survivability (Jayasimha et al. 2012, Bashir et al. 2022, Rachappa et al. 2016). This thermal responsiveness also complicates control strategies, as overlapping generations reduce the efficacy of time-targeted interventions. Accurate phenological prediction using degree-day models, therefore, becomes critical for optimizing integrated pest management (IPM) timing (Eizenberg et al. 2005, Damos et al. 2018).

Despite its robustness, the Bragg model is constrained by its assumption of symmetry, which may not capture skewed or irregular dynamics observed in field populations influenced by multiple stressors. Additionally, degree-days alone may be insufficient to fully explain population fluctuations. Other environmental variables, such as photoperiod, humidity, and host plant condition, should be incorporated into future models to capture multidimensional drivers of phenology (Guimapi et al. 2020, Ibrahim et al. 2022). Furthermore, overlapping peaks remain a modeling challenge. When generational boundaries blur, fitted models may misinterpret two overlapping cohorts as a single broad emergence, leading to misestimated parameters. Advanced decomposition techniques or mixture models may help disentangle such dynamics.

Recent advances in machine learning (ML) and deep learning offer promising avenues for improving predictive performance. Recurrent neural networks (RNN) and long short-term memory (LSTM) models have been successfully applied to similar time-series ecological data and could be adapted to model *J. lybica* populations with non-linear, high-dimensional environmental inputs (Jian et al. 2007, Ibrahim et al. 2022). However, these techniques often sacrifice interpretability, a key strength of the Bragg model in IPM contexts.

The findings of this study are directly applicable to forecasting *J. lybica* dynamics in Mediterranean citrus and grapevine systems. By capturing intra- and inter-annual variability with biologically interpretable parameters, the Bragg-based degree-day model provides a practical tool for decision support in timing monitoring and control interventions. Its scalability and low data requirements make it particularly valuable in resource-limited settings. Moreover, the modeling framework can be adapted to other multivoltine pests with temperature-driven development, thereby contributing to a broader toolkit for climate-smart pest forecasting.

The modeling of leafhopper adult population peaks using Bragg-type functions across multiple years demonstrates a clear pattern of improving model performance through successive parameter optimizations. The initial model (M1), with fixed peak widths, provides a solid baseline fit ($R^2 \approx 0.63–0.75$), capturing the general shape of the abundance curves. Optimizing peak heights (M2) or peak positions (M3) individually yields modest improvements, with the refinement of peak positions typically offering greater gains than height adjustments alone. Combining height and position optimization (M4) further refines the fit, though with diminishing returns compared to optimizing positions alone. The most substantial enhancement occurs when allowing peak widths to vary independently for each population peak (M5). This model consistently achieves the highest coefficient of determination (R^2 up to $\sim$0.86) and substantially lowers both RMSE and residual sum of squares. This indicates that variability in peak breadths reflects important biological or environmental heterogeneity that fixed-width models cannot capture.

These findings have important implications for the development of broader IPM strategies for *J. lybica* in vineyards and citrus orchards. By integrating degree-day modeling with regular field monitoring, growers can better anticipate phenological peaks and optimize the timing of control measures, thus improving efficiency and reducing unnecessary insecticide applications. Moreover, the pronounced interannual variability observed in this study highlights the need for adaptive management frameworks that can respond to environmental fluctuations. Under scenarios of climate change and increasing drought frequency, shifts in temperature and host plant phenology are expected to alter pest dynamics, potentially leading to earlier and more severe outbreaks. Incorporating predictive models like the Bragg-based framework presented here into climate-resilient IPM programs will be crucial for sustaining vineyard productivity while minimizing ecological and economic impacts.

Fully flexible Bragg-type models, optimizing peak heights, positions, and widths, offer a robust framework for accurately characterizing complex phenological dynamics in leafhopper populations over time. This modeling approach can improve understanding of seasonal patterns and support better predictions of population dynamics in ecological monitoring. This model can be subject to more adjustment, using networks that integrate several parameters for a better understanding of this insect population fluctuation in relationship with parameters studied.

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