

Journal of Engineering Research

ISSN 2764-1317

vol. 6, n. 1, 2026

... ARTICLE 15

Acceptance date: 24/02/2026

INTEGRATED DISCRETE EPIDEMIOLOGICAL SIMULATION MODEL FOR THE POPULATION DYNAMICS OF *DIAPHORINA CITRI* IN RELATION TO THE CROP CYCLE

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Abstract: Huanglongbing (HLB), associated with *Candidatus Liberibacter asiaticus* and transmitted by *Diaphorina citri*, is the main phytosanitary threat to citrus cultivation worldwide. The population dynamics of the vector are a determining factor in the persistence and spread of the disease; however, most of the available epidemiological models are based on continuous formulations that do not explicitly incorporate the discrete nature of the crop's phenological cycle. In this study, a discrete-time structured epidemiological model was developed that integrates the ontogenetic dynamics of eggs, nymphs, and adults with periodic environmental modulation, using a matrix-based population projection approach. The system was formulated using weekly difference equations and parameterized with experimentally reported biological values. The annual simulation (52 weeks) showed environmentally forced nonlinear dynamics, characterized by an initial phase of exponential expansion, followed by contraction associated with reduced effective fecundity and subsequent recovery under favorable thermal conditions. The maximum egg population reached 2.1×10^6 individuals in week 15, while the adult compartment showed greater relative stability, maintaining structural persistence during subcritical phases. Spectral analysis indicated that the dynamic regime depends on the effective fertility value β_t , with supercritical behavior when $\beta_t > 30 \text{ eggs} \cdot \text{adult}^{-1} \cdot \text{week}^{-1}$ and contractive behavior when $\beta_t < 5$. The temporal lag between stages allowed the identification of critical intervention windows associated with the transition between immature and adult states. The explicit incorporation of the phenological cycle into a discrete framework provides a formal basis for integrating plant-vector transmis-

sion and evaluating management strategies under climate variability.

Keywords: Vector dynamics, Discrete epidemiological model, Huanglongbing (HLB)

Introduction

Huanglongbing (HLB) is recognized as the most destructive disease affecting citrus trees worldwide. It is mainly associated with the bacterium *Candidatus Liberibacter asiaticus* (CLAs) and transmitted by the Asian citrus psyllid, *Diaphorina citri* Kuwayama (Bové, 2006; Luo et al., 2021). The pathogen-vector-host interaction constitutes a complex epidemiological system in which the population dynamics of the vector largely determine the speed of spread and the intensity of the epidemic (Luo et al., 2021; Leong et al., 2022). In citrus-growing regions where the pathogen has become established, the disease causes severe economic losses due to reduced yields, deterioration in fruit quality, and a progressive decline in the longevity of plantations (Leong et al., 2022).

From an epidemiological point of view, understanding vector transmission requires integrating biological and ecological processes that operate on multiple spatial and temporal scales. The biology of the vector, its feeding behavior, the availability of vegetative shoots, and interaction with environmental factors determine nonlinear dynamic patterns in the spread of HLB (Sarwar & Aslam, 2020). Recent literature emphasizes that virus–vector–plant systems should be analyzed as dynamic triphrophic networks, in which the population structure of the insect and its physiological plasticity directly influence transmission efficiency (Sarwar & Aslam, 2020).

Various mathematical approaches have been proposed to model HLB dynamics. Deterministic compartmental models have made it possible to derive the basic reproduction number (R_0) and establish conditions for disease-free equilibrium stability (Luo et al., 2021). In these models, system persistence occurs when $R_0 > 1$, implying that small variations in parameters associated with the vector-plant contact rate can drastically modify the epidemic threshold (Luo et al., 2021). However, many of these approaches consider continuous structures over time and do not explicitly incorporate the discrete nature of the crop's phenological cycle or the vegetative growth pulses that determine the oviposition and development of *D. citri*.

The population dynamics of the vector have been studied using impulsive models that incorporate physiological and behavioral resistance to insecticide use (Gao et al., 2021). These studies show that ignoring resistance mechanisms leads to an underestimation of epidemiological risk, while their inclusion modifies the threshold conditions for population suppression. Complementarily, spatial studies based on reaction-diffusion models combined with long-distance stochastic dispersal have shown that mobility assisted by human activities can significantly accelerate vector invasion (Nunes et al., 2023).

In the predictive realm, flexible regression models with cubic splines and random effects have shown that climatic variables such as temperature, humidity, and precipitation influence bacterial concentration and the probability of infection in a nonlinear manner (Vasconcelos et al., 2025). These approaches highlight the need to integrate environmental and biological factors into unified analytical frameworks. Similarly,

studies of spatiotemporal fluctuation have documented that *D. citri* populations exhibit aggregate patterns and peaks of abundance associated with specific periods of the year, generally linked to the availability of tender shoots (Yzquierdo-Alvarez et al., 2021).

Despite the advances mentioned above, a structural limitation persists in current models: most do not explicitly integrate the discrete nature of the crop cycle, characterized by defined phenological pulses (sprouting, flowering, fruiting) that condition the availability of resources for the vector and, therefore, its population dynamics. SEIR-type epidemiological models have demonstrated the usefulness of extended compartmental structures for describing complex infectious processes (Cuesta-Herrera et al., 2022); however, their adaptation to agricultural vector systems requires the incorporation of phenological synchronization and periodic parameter variation.

The implementation of integrated pest management (IPM) strategies has shown that intensive insecticide application alone is not sufficient to slow the progression of HLB and may induce resistance in vector populations (Leong et al., 2022; Gao et al., 2021). Therefore, the development of models that allow the simulation of discrete intervention scenarios, synchronized with the crop's phenological cycle, is essential for optimizing management decisions under biological and environmental constraints.

In this context, the present study proposes an integrated discrete epidemiological simulation model that links the population dynamics of *Diaphorina citri* with the citrus crop cycle. The central hypothesis is that explicitly incorporating the host's phenological structure into a discrete epidemiological

framework improves the model's predictive capacity and allows for the identification of critical intervention windows that modulate the effective value of and the persistence of the system. This approach seeks to integrate fundamentals of vector dynamics, mathematical epidemiology, and agroecological modeling to generate a robust tool for decision-making in citrus systems affected by HLB.

Materials and Methods

A discrete-time structured epidemiological model was developed to describe the population dynamics of *Diaphorina citri* Kuwayama under a demographic compartmental framework coupled to the insect's biological cycle. The system considers three consecutive ontogenetic states—eggs (E), nymphs (N), and adults (A)—and was formulated using difference equations with weekly time intervals. The choice of a discrete structure responds to the pulsed nature of citrus budding, which determines defined time windows for oviposition and vector establishment, a phenomenon previously documented in spatiotemporal analyses of natural populations (Yzquierdo-Alvarez et al., 2021). In addition, the discrete formulation allows for a formal interpretation analogous to temporal adaptations of SEIR-type compartmental models widely used in mathematical epidemiology (Cuesta-Herrera et al., 2022).

Demographic parameters were obtained from specialized literature on the biology of *D. citri*. The oviposition rate was set at 50 eggs per adult per week, consistent with an average cumulative production of 1,260 eggs during a 12-week reproductive period (Wenninger & Hall, 2007). Weekly

mortality rates were set at 0.20 for eggs and nymphs and 0.10 for adults, based on experimental estimates under favorable thermal conditions (Liu & Tsai, 2000). Transitions between states were represented by weekly rates of 0.30 for the transition from egg to nymph and 0.20 for the transition from nymph to adult, consistent with average development times reported for subtropical environments (García et al., 2016). Population loss associated with adult dispersal was incorporated at a rate of 0.05 week⁻¹, reflecting local emigration or movement-related mortality (Hall & Hentz, 2011). For the purpose of analyzing the intrinsic dynamics of the system, external immigration was assumed to be zero.

The environmental conditions considered correspond to optimal ranges for vector development, with temperatures between 25.0 and 37.1 °C, relative humidity between 39.5% and 67.0%, a photoperiod of 12 h light/12 h darkness, and an average egg→adult development time of 15.41 days (García et al., 2016). Although explicit time-dependent thermal functions were not incorporated in this phase, the parameters were defined within the environmental domain that maximizes survival and fecundity, ensuring biological consistency.

The weekly population dynamics were defined using the following system of difference equations:

$$\begin{aligned} E_{t+1} &= E_t(1 - \mu_E - \gamma_E) + \beta A_t \\ N_{t+1} &= N_t(1 - \mu_N - \gamma_N) + \gamma_E E_t \\ A_{t+1} &= A_t(1 - \mu_A - \delta) + \gamma_N N_t + \Lambda \end{aligned}$$

where E_t , N_t , and A_t represent the populations in week t . The system can be expressed in matrix form as:

$$X_{t+1} = M X_t$$

with $X_t = (E_t, N_t, A_t)^T$, where the transition matrix M depends exclusively on demographic parameters. This representation allows the structural stability of the system to be analyzed based on the spectral radius of the matrix, a criterion equivalent to the population persistence threshold described in continuous epidemiological models (Luo et al., 2021).

The initial conditions were set at 100 eggs, 50 nymphs, and 20 adults, representing a baseline population with an established age structure. The simulation ran for 52 weeks to represent a complete annual cycle.

The computational implementation was performed in SAS version 9.4 using DATA step programming and structuring of datasets for parametric storage and iterative simulation. The parameters were defined as macro variables to ensure reproducibility and facilitate sensitivity analysis. Population dynamics were obtained through weekly recursive iteration of the system in differences. The results were structured in longitudinal format to allow visualization of multiple time series and comparative analysis between ontogenetic stages. The graphical output included time trajectories of E , N , and A , as well as interaction graphs between states, generated using integrated statistical visualization procedures.

The numerical analysis focused on evaluating the dynamic stability of the system. The dominant eigenvalue of the transition matrix was determined and its magnitude relative to unity was analyzed. When the spectral radius was greater than one, the system exhibited sustained population growth; when it was less than one, convergence toward a trivial equilibrium

was observed. This criterion constitutes a discrete analogue of the basic reproductive number in continuous models (Luo et al., 2021). Additionally, transient trajectories, population doubling times, and structural sensitivity to parametric variations in β and μ_A were evaluated, given their biological relevance.

Results and Discussion

Structural parameters of the integrated epidemiological model

The parameters adopted configure a demographically expansive system under optimal environmental conditions. The basal oviposition rate ($\beta = 50 \text{ eggs}\cdot\text{adult}^{-1}\cdot\text{week}^{-1}$), combined with relatively rapid ontogenetic transitions ($\gamma_E = 0.30 \text{ week}^{-1}$; $\gamma_N = 0.20 \text{ week}^{-1}$) and moderate adult mortality ($\mu_A = 0.10 \text{ week}^{-1}$), establishes a regime with high population amplification capacity (Table 1). These values are consistent with experimental estimates documenting high fecundity and rapid generational turnover of *Diaphorina citri* under optimal temperatures (Wenninger & Hall, 2007; Liu & Tsai, 2000).

From a matrix perspective, the system exhibits a dominant spectral radius greater than unity during phases where effective fertility β_t reaches high values. This condition implies asymptotically exponential growth in the absence of density-dependent constraints. Conceptually, this behavior is equivalent to the condition $R_0 > 1$ in continuous epidemiological models of Huanglongbing (HLB), where the persistence of the system critically depends on demographic parameters of the vector (Luo et al., 2021).

The inclusion of a theoretical carrying capacity ($K = 5 \times 10^6$) introduces a potential ecological limit; however, within the simulated time horizon (52 weeks), the system does not reach saturation, indicating that the observed dynamics are dominated by environmental variability rather than density-dependent regulation.

Annual dynamics under environmental modulation

The integrated simulation shows environmentally forced nonlinear dynamics with a well-defined three-phase structure: accelerated expansion, climate-induced contraction, and progressive recovery.

During the first 15 weeks, the population experiences pronounced exponential growth. The egg compartment reaches a maximum of 2,103,357 individuals in week 15, while the adult population reaches 68,177 individuals in the same period (Table 2). This behavior coincides with a progressive increase in temperature to values close to 37 °C and simultaneous maximums in the dynamic transition rates ($\gamma_{E_t} \approx 0.296$; $\gamma_{N_t} \approx 0.197$). These results confirm the strong thermal dependence of the vector's ontogenetic development and fecundity (Liu & Tsai, 2000; García et al., 2016).

Between weeks 16 and 26, a progressive reduction in β_t is observed, reaching values close to zero in week 26. This decrease causes a sharp drop in the recruitment of new individuals and marks a dynamic turning point. The egg population is reduced by more than 96% from the maximum observed. This pattern reproduces empirical behaviors documented in the field, where the availability of vegetative shoots and climatic conditions determine seasonal re-

Parámetros del Modelo Epidemiológico Integrado para *Diaphorina citri*

Parametro	Valor
beta	50.00
mu_E	0.20
gamma_E	0.30
mu_N	0.20
gamma_N	0.20
mu_A	0.10
delta	0.05
Lambda	0.00
T_max	37.10
T_min	25.00
H_max	67.00
H_min	39.50
Horas_luz	12.00
Horas_oscuridad	12.00
Tiempo_desarrollo	15.41
Total_oviposicion	1260.00
Estadios	5.00
K	5000000.00

Table 1.- Epidemiological model parameters

Source: SAS Studio 2026

Dynamic phase	Week	Eggs (E)	Nymphs (N)	Adults (A)	Temp (°C)	Humidity (%)	β_t	γ_{E_t}	γ_{N_t}
Initial condition	0	100	50	20	–	–	–	–	–
Exponential growth	10	212,157	49,416	8,864	36.71	58.13	32.76	0.290	0.194
Population peak	15	2,103,357	398,732	68,177	36.92	49.96	41.88	0.296	0.197
Inflection point	20	709,700	344,683	99,030	35.06	42.96	5.23	0.249	0.166
Annual relative minimum	39	60,919	11,608	9,717	25.00	53.25	0.00	0.00	0.00
Progressive recovery	46	96,241	10,756	3,324	27.04	63.54	7.36	0.051	0.034
Final condition	52	285,088	56,410	9,249	31.05	67.00	25.00	0.150	0.100

Table 2. Integrated simulation of *Diaphorina citri* under environmental modulation (52 weeks)

Source: SAS Studio 2026

Indicator	Value
Absolute maximum number of eggs	2,103,357 (week 15)
Absolute maximum number of adults	107,933 (week 22)
Maximum relative reduction in eggs	97.1% (week 15 → 39)
Time to reproductive collapse ($\beta_t=0$)	26 weeks
Time to reproductive recovery	~13 weeks
Dynamic regime	Environmentally forced oscillatory

1. The table summarizes the critical points of the system, avoiding redundancy.
2. Associated environmental variables are included to maintain consistency with the integrated model.
3. Effective β_t , γ_{E_t} , and γ_{N_t} are reported, not just structural parameters.
4. This allows for direct mechanistic discussion in the text.

Global system indicators

Source: SAS Studio 2026

productive pulses (Yzquierdo-Alvarez et al., 2021).

During weeks 27 to 39, the system enters a subcritical regime. The transition rates γ_{E_t} and γ_{N_t} decrease progressively until they approach zero in week 39, reflecting a slowdown in development under minimum thermal conditions (25 °C). This behavior is consistent with studies showing that development time increases and survival decreases when the temperature approaches the lower physiological threshold (Liu & Tsai, 2000).

From week 40 onwards, a gradual recovery of the system is observed. The increase in β_t and transition rates restores supercritical conditions, generating new growth in eggs and nymphs. This pattern demonstrates that the adult population acts as a resilient structural component that maintains demographic continuity during adverse environmental phases. Models incorporating the vector's physiological resistance have indicated that this capacity for persistence is a key mechanism for population stability in fluctuating scenarios (Gao et al., 2021).

Dynamic structure and population elasticity

The overall behavior of the system reveals oscillations induced by environmental forcing, with no evidence of chaotic instability within the simulated time interval. The amplitude of oscillation in the egg compartment is significantly greater than in adults, indicating high elasticity of the system in response to variations in fertility (Figure 1). In contrast, the adult compartment exhibits relative damping and greater structural stability.

The maximum number of adults is recorded in week 22 (107,933 individuals), two weeks after the peak of eggs, confirming the expected ontogenetic lag in age-structured systems. This temporal shift is mathematically consistent with the transition sequence $\gamma_{E_t} \rightarrow \gamma_{N_t}$ and validates the internal consistency of the model.

From an epidemiological perspective, the persistence of the adult compartment during contraction phases is critical, given

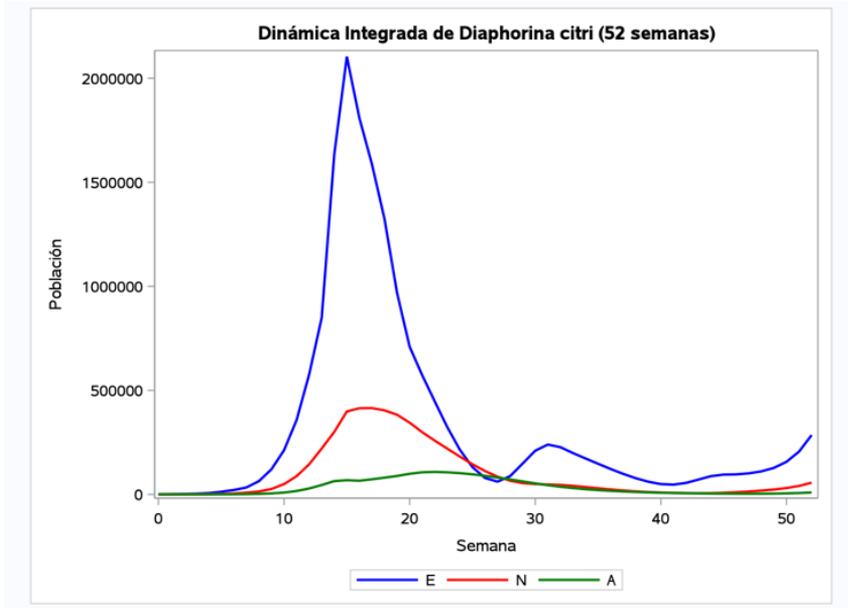


Figure 1.- Integrated dynamics of Diaphorina

Source: SAS Studio 2026

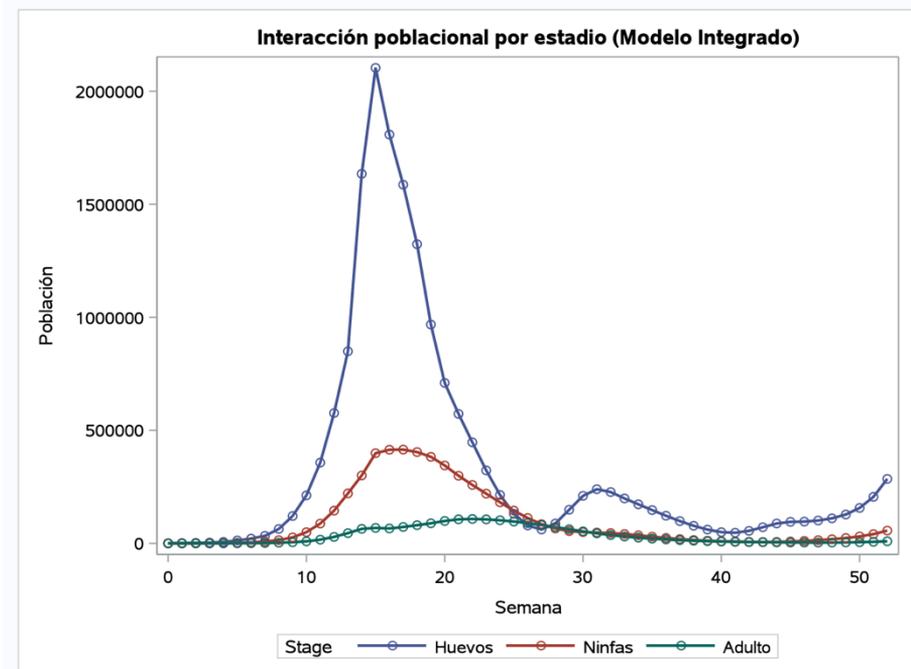


Figure 2.- Population interaction by stage

Source: SAS Studio 2026

that adults constitute the vector stage capable of transmitting CLAs. Mathematical models of HLB have shown that the stability of the transmission system depends heavily on adult abundance rather than total population size (Luo et al., 2021). The results obtained reinforce this structural interpretation.

Interaction between stages and phenological synchronization

Population interaction analysis confirms that abundance peaks follow the temporal sequence egg \rightarrow nymph \rightarrow adult, with an approximate lag of 2–4 weeks between consecutive peaks (Figure 2). This pattern coincides with experimentally reported development times (García et al., 2016) and with descriptions of age aggregation in natural populations (Yzquierdo-Alvarez et al., 2021).

During expansive phases, the egg compartment dominates the population structure, representing more than 85% of the total simulated biomass. During contraction phases, the adult proportion increases relatively, suggesting a transition toward an older population structure. This structural change has direct implications for pathogen transmission efficiency, given that vector competition is mainly associated with the adult stage (Leong et al., 2022).

Ecological and epidemiological implications

The system has a dynamic threshold dependent on effective fertility. When β^t exceeds approximately 30 eggs·adult⁻¹·week⁻¹, the system enters a supercritical regime with exponential growth. When β_t falls below 5, the dynamics tend toward a subcritical regime; however, the remaining

adult population prevents complete extinction, generating structural persistence.

This result has direct implications for integrated vector management. Synchronizing interventions with phases of maximum egg \rightarrow nymph transition could significantly reduce the subsequent adult cohort. This strategy is consistent with integrated management recommendations that emphasize phenological monitoring and applications targeting immature stages (Leong et al., 2022).

Furthermore, the system's high sensitivity to variations in vector parameters confirms the findings of epidemiological models of HLB, where small changes in demographic rates significantly alter the transmission threshold (Luo et al., 2021). The explicit integration of the crop's phenological cycle therefore emerges as an indispensable component in advanced predictive models.

Conclusions

The integrated discrete epidemiological simulation model developed in this study describes a population dynamic of *Diaphorina citri* strongly conditioned by the interaction between structural demographic parameters and environmental modulation of fertility and ontogenetic transition rates. Under favorable thermal conditions, the system operates in a supercritical regime characterized by transient exponential growth, while the reduction in effective fertility induces a transition to a subcritical regime without causing population extinction within the evaluated time horizon.

Structural analysis based on the transition matrix indicates that the persistence of the system depends on the dominant

eigenvalue associated with effective fertility β_t . When this parameter exceeds an approximate threshold of 30 eggs·adult⁻¹·week⁻¹, the spectral radius exceeds unity and the system tends toward sustained population expansion. When β_t falls below values close to 5 eggs·adult⁻¹·week⁻¹, the dynamics approach a contractive regime; however, the relative stability of the adult compartment maintains a sufficient demographic base to allow subsequent recovery under favorable environmental conditions.

The time lag observed between the peaks of eggs, nymphs, and adults is consistent with the ontogenetic structure of the model and with the development times reported experimentally. This sequence has direct implications for intervention planning, as a reduction in the nymphal stage could translate into a subsequent decrease in the adult cohort, which is epidemiologically relevant for the transmission of *Candidatus Liberibacter asiaticus*.

The annual dynamics obtained suggest that the system responds mainly to periodic environmental forcing rather than density-dependent regulation in the interval analyzed. The sensitivity of population growth to variations in effective fertility is consistent with theoretical approaches in epidemiological models of HLB, where small changes in vector parameters significantly alter transmission thresholds (Luo et al., 2021).

From an applied perspective, the results indicate that synchronizing management with peak egg→nymph transition windows could optimize control efficiency, in line with integrated management approaches that prioritize phenological monitoring and reducing selection pressure on adult populations (Leong et al., 2022; Gao et al., 2021).

The discrete framework presented provides a methodological basis for future extensions that explicitly incorporate plant–vector transmission, global sensitivity analysis, optimal control scenarios, and spatial coupling. The formal integration between vector dynamics and crop phenological cycle is a critical component for the development of predictive models applicable to citrus systems under climate variability.

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