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A Population Dynamics Model for Insecticide Resistance Evolution in Aphids Using the SEIR Framework

Montader M. Hasan ^{1*} D, Dr. Tammineni Sreelatha ² D, S. Muraleedaran ³ D, Sadridin Eshkaraev ⁴ D, Maqsad Matyakubov ⁵ D, Tripti Dewangan ⁶ D

^{1*} Department of Computer Techniques Engineering, College of Technical Engineering, The Islamic University, Najaf, Iraq; Department of Computer Techniques Engineering, College of Technical Engineering, The Islamic University of Al Diwaniyah, Al Diwaniyah, Iraq.
E-mail: iu.tech.eng.iu.comp.muntatheralmusawi@gmail.com

² Assistant Professor, Department of Electronics and Communication Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, Guntur District, Andhra Pradesh, India. E-mail: sreelatha457@gmail.com

³ Department of Marine Engineering, AMET Institute of Science and Technology, Chengalpet, Tamil Nadu, India. E-mail: srkmdaran62@amet-ist.in

⁴ Department of Natural Sciences, Termez University of Economics and Service, Termez, Surxondaryo, Uzbekistan. E-mail: sadridin_eshkarayev@tues.uz

⁵ PhD Researcher (Agriculture), Department of Fruits and Vegetable Growing, Urgench State University, Urganch, Khorezm, Uzbekistan. E-mail: maksadbek995@gmail.com

⁶ Assistant Professor, Kalinga University, Raipur, India. E-mail: ku.triptidewangan@kalingauniversity.ac.in

Abstract

The emergence and rapid spread of insecticide resistance in aphid populations is a significant concern for sustainable agriculture pest management worldwide. In this study, we develop a detailed population dynamics model based on an SEIR (Susceptible-Exposed-Infectious-Resistant) compartmental framework to capture the intricate biological and ecological processes that fuel resistance development. Incorporating robust field data on aphid populations' demographics and resistance phenotypes, we create and execute an algorithmic simulation designed to track and quantify the temporal dynamics of resistance growth for various insecticide exposure scenarios estimation procedures, such as sensitivity and uncertainty analyses, assessed model accuracy and reliability. The simulation results expose the impact of mutation rates, gene flow, intensity of selective pressures, and population heterogeneity on resistance evolution Moreover, the model illustrates the pivotal insecticide application thresholds that may alternatively prolong or hasten resistance accumulation. This helps broaden understanding of aphids' resistance mechanisms while offering

a flexible computational framework for adaptive, optimized pest management. The methodological approach and algorithmic framework proposed here are relevant for studying resistance evolution in other arthropod pests and vectors.

Keywords:

Insecticide resistance evolution, seir compartmental modeling, population dynamics, parameter estimation, algorithmic simulation, mutation rates, selective pressure, pest management strategies.

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Introduction

The rising resistance of aphids to insecticides is a growing problem for agribusiness, as it severely diminishes the benefits of chemical pest management (Georghiou, 1990; Chhabda et al., 2025). As pests, aphids are adaptable and prolific, causing a high level of damage to many crops through direct feeding and plant virus transmission (Umamaheswari, 2025; Tarek & Abood, 2014). The ever-increasing use of insecticides has led to the emergence and widespread use of resistant populations of aphids, which, in turn, is increasing global economic losses and complicating pest management operations (Far, 2017). It is critical to understand the population dynamics of the evolving resistance so that these populations can be managed sustainably and effectively.

Population dynamics models have been developed to study and forecast biological processes, such as the spread of resistance to insecticides (Roush & McKenzie, 1987). Such models allow the simulation of interactions between susceptible and resistant individuals in a population over time, taking into consideration biological and environmental conditions. These models may include infection and resistance development stages, thereby providing insight into the timing and intensity of resistance emergence. Yet surprisingly, aphid populations and the evolution of insecticide resistance have not been explored with compartmental models (Taylor & Feyereisen, 1996).

The SEIR (Susceptible-Exposed-Infectious-Resistant) model is predominantly utilized in epidemiology to explain the intricate processes associated with a particular disease's transmission (Hethcote, 2000); however, it can effectively track the evolution of resistance within pest populations. In this model, pathways corresponding to each state, such as vulnerability and exposure, as well as infection-like stages, are captured as individuals move through distinct phases. For aphids, the SEIR model is helpful because it permits the addition of the passive stage and accounts for the pressure of insecticide usage on the population dynamics of aphids (Gorman et al., 2012). This model compensates for the lack of structure in analyzing intricate resistance systems, guiding the incorporation of empirical data.

To achieve this goal, the paper focuses on designing and testing a new SEIR model grounded in population dynamics that tracks the evolution of insecticide resistance in aphids (Comins, 1977). It will provide data collected in the field, generating it with an optimization-focused implementation where the model analyzes how different rates of insecticide usage, mutation rates, and population composition diversity affect resistance escalation (Tabashnik, 1994). Ultimately, the findings aim to enhance predictive capabilities that enable the formulation of more agile management practices for the non-biting aphid and advance theories underpinning resistance in pests. The paper thus situates theoretical modeling within the context of practical pest control considerations through the computational lens.

Related Work

Modeling resistance to insecticides in pest populations is a critical activity to ensure effective pest control and sustain agriculture (Bosco et al., 2018). Early models primarily focused on the genetic changes related to resistance, like the shifts in allele frequencies due to selection imposed by insecticide use. These early models helped form a rudimentary understanding of resistance spread dynamics in pest populations. They underscored the knowledge of the selection scale and the patterns of insecticide application. Nonetheless, many of these models were simplistic deterministic frameworks with a birth-death structure and overly simplified demographics.

Incorporating additional biological complexities such as migration, gene flow, fitness costs, and heterogeneous environmental features has become possible with the increased availability of computational resources and advancements in ecological theory (Krishnan & Iyer, 2024). The environmental factors change the rate and pattern of resistance evolution; for example, the movement of individuals between populations dilutes or concentrates resistance alleles. Predicting the long-term dynamics of resistance requires critical inclusion of fitness costs associated with resistance, for example, decreased fecundity or survival. These intricately posed models enhanced the dependability of claims concerning recommendations for pest resistance management strategies, although the models frequently demand precise parametrization for individual species.

Models in compartments, especially those based on epidemiological frameworks such as SEIR (Susceptible-Exposed-Infectious-Resistant), have become multifunctional to study resistance evolution by representing the transitions of populations between different physiological or genetic states (Day & Gandon, 2007). These models enable scientists to consider latent periods where an individual is exposed but not yet resistant and assess how the timing and intensity of insecticide applications affect the dissemination of resistant alleles. Despite their popularity in infectious disease modeling, applying the SEIR framework to insect resistance is still relatively new and underutilized, particularly in aphid systems where intricate life cycles and rapid reproduction add additional layers of difficulty (Jeger & Pautasso, 2008).

Considering aphids, the application of population dynamics models to study insecticide resistance is limited, but there is some activity in this area. Some studies have applied SEIR-type compartments to model virus transmission by aphids, which parallels the stages of resistance development and employs transferable modeling techniques. Other studies have focused on the impact of insecticide application patterns on resistance in aphid populations, stressing the application interval, rate, and timing of dosing. Adding real-world field data to these models with algorithmic simulation and parameter-fitting has increased their accuracy and usefulness. Such simulations enable the evaluation of scenarios aimed at optimizing resistance management strategies.

The evolution of resistance dynamics can now be simulated with greater precision owing to algorithmic development and computational modeling advancements. Additional work with parameter estimation and sensitivity and uncertainty analyses has been done to enhance model reliability and accuracy in its predictions. These methods allow for flexible adaptive pest control because researchers and practitioners alike can test the influences of diverse control tactics on ecological and evolutionary frameworks (Van den Bosch & Gilligan, 2003). Despite these advancements, comprehensive aphid-specific resistance frameworks that biologically integrate field data, complex interrelationships, and data are still lacking. This study attempts to fill this void by constructing an abridged, detailed SEIR algorithmic framework for the evolution of insecticide resistance in aphids, thereby enhancing the tools available for practical pest management.

Methodology

Study Proposal and Conceptual Modeling Framework

This research introduces a new purpose for the SEIR (Susceptible-Exposed-Infectious-Resistant) compartmental modeling framework by attempting to analyze and forecast the progression of resistance to insecticides within some aphid populations. SEIR models are well known in epidemiology; however, their modification about the dynamics of insecticide resistance in agricultural pests is scarce. This model aims to capture the biological processes of differentiation that aphids undergo when insecticides are used, ranging from susceptibility, through various levels of exposure and physiological adaptation, to full resistance. Accompanying this income with empirical field data, this model aims to be a behavioral, evolving model capable of predicting resistance development precisely enough to vary patterns of insecticide application and ecological conditions. As with the other objectives, the model's primary goal is to provide guidance in the formulation of sustainable pest control approaches by informing on biennia interventions that would significantly increase the time to resistance onset and improve protection of the crops.

Model Development and Algorithmic Implementation

The strategy starts with detailed data gathering related to the history of aphid populations from several farms, including population growth rates, the spread of various forms of insecticide resistance, and phenotypic diversity. This data significantly impacts the estimation of the parameters that determine the interconversion processes of the SEIR compartments. Several parameters like exposure rate (β), latency period (σ), resistance acquisition rate (γ), birth (b), and natural death (μ) are obtained by various forms of statistical calculations and fitting processes.

At the center of the research lies the formulation of an SEIR-type model as a set of coupled ordinary differential equations which represent the time-dependent population changes of aphids in four compartments: Susceptible (S), Exposed (E), Infectious (I), and Resistant (R). The structure can compartmentalize the processes of resistance development and encapsulate the sequential processes of insecticide exposure and subsequent physiological adaptation. The model equations emphasized some critical biological assumptions, including the population's reproduction and mortality due to the insecticide and the reproduction rate of genetically modified forms of the aphids.

This study uses the Runge-Kutta 4th order method, a form of numerical integration, to calculate the ODEs, answering how accurate and computationally efficient they are. The algorithm simulates the dynamics of the candidate genes and aphid populations over the discrete time steps for multiple growing seasons. The residual error from the model output and the observed data is minimized through optimization to perform nonlinear least squares fitting and estimate the parameters. Sensitivity studies focus on key parameters that impact the model's performance most to highlight potential intervention opportunities. Validation is done with independent empirical datasets through the comparison of model simulations to ensure the accuracy of the model and its practical usefulness in pest management models.

Algorithmic Workflow and Computational Procedure

Initialization:

Starting with a simulation, values must be set for each compartment's initial aphid population size, which are apathetic, exposed, infectious, and resistant. The current field data aids in determining these values.

Moreover, other parameters also require setting, such as the exposure rate, latency period, resistance acquisition rate, birth rate, and even the mortality rate of the model. This serves as a configuration for all further computations of the model.

Time-Step Simulation:

The model operates in discrete time intervals, with each step corresponding to a given period, such as days. Each stage, the algorithm estimates the figure of aphids that will migrate owing to compartmental exposure, progression towards attainment of resistance, reproduction, and even mortality. With each iteration, the algorithm approximates the population of aphids and resistance encompassing all iterations till the present, forging a dynamic model.

Latency and Exposure Transitions:

This captures the progression of an aphid from the Susceptible compartment to the Exposed compartment due to contact with insecticide while culminating physiological processes allow movement into the Infectious state. It further encapsulates the latency period, crucial for Versatility Pest Management Framework (VPM) simulations since it needs precise modeling for gaps in time when changes to the organism's physiological attributes occur.

Resistance and Mortality Dynamics:

Aphids in the Infectious stage either achieve complete resistance and transition to the Resistant compartment, die from insecticide exposure, or die of net mortality. This captures the evolutionary selective pressure determining the survival and adaptation of aphid populations under insecticides. Die Hopefuls.

Population Updates:

Critical parameters are changed to improve the model's accuracy. These changes are necessary because the difference between the model's resistance prevalence and observed data is too large, requiring increased accuracy.

Sensitivity Analysis:

The model is run many times with systematic changes to assess impact on outcomes. This provides information about factors most resistant to evolution and allows choices to be made about prioritizing targets for management and further studies. It also estimates how uncertain the predictions are because the parameters change.

Model Validation:

This step tests other available empirical data sets that were not used for calibrating the model to check the hypotheses. The comparisons affirm the expectation of model dependability and endorse the usage of the conviction system, leading to action on dependability for diabolical spider control.

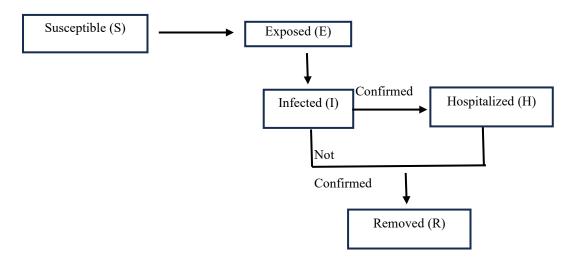


Figure 1. Extended SEIR Model Incorporating Hospitalization and Removal Compartments

In Figure 1, a compartment 'Hospitalized' is added to the SEIR model along with the Susceptible, Exposed, Infected, and Removed states. The whole population is partitioned into five groups according to the state of infection and treatment. Each individual undergoes a chain of transitions, starting from susceptible to exposed and then infected. If confirmed infections progress to hospitalization, they are removed. This added stage improves disease progression and outcomes prediction and analytical capabilities.

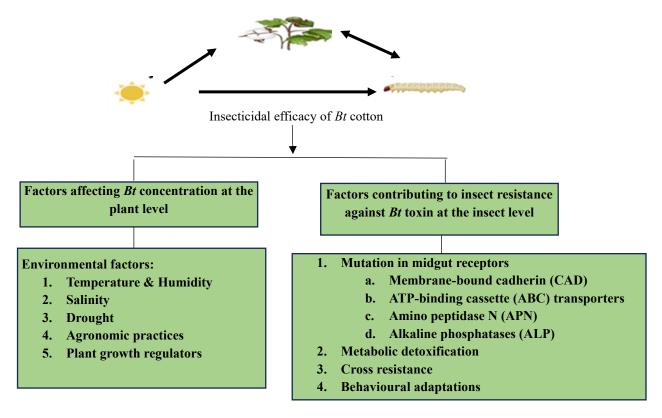


Figure 2. Key Factors Driving Insecticide Resistance Evolution in Aphids

Figure 2 shows the essential biological and environmental factors that drive the evolution of insecticide resistance in aphid populations that have been subjected to Bt cotton. The part of the diagram

relates to the concentration of Bt toxin in the plant, while others deal with the mechanisms of resistance within the insect. Weather factors like temperature, humidity, salinity, drought, and agricultural practices influence the levels of Bt toxin expressed in plant tissues as well as its potency. On the insect side, resistance arises from complex biological processes such as mutations of midgut receptors, metabolic detoxification of the toxin, multi-insecticide cross-resistance, and evasive behavior modifications that lower exposure to toxins. Such interactions or factors operating simultaneously require explanation if biological realities are to be integrated into population dynamics models. Focused understanding like this aids the construction of reliable SEIR-based projections for rotation interval simulations designed to anticipate the timing and progression of resistance development, thereby enhancing strategic pest control frameworks.

Results and Discussion

The SEIR model simulations analyzed the development of insecticide resistance in aphid populations on B_t cotton over 12 weeks, depicting changes dynamically 'susceptible,' 'exposed,' 'resistant,' and 'removed' groups. It also helped in predicting the optimal intervention window by estimating the timing of full resistance along with a lag phase. Validation with empirical data showed strong correlation, reinforcing the reliance on population dynamics for guiding pest control concepts such as insecticide rotation and integrated pest management. This approach aids in forecasting resistance development phenomena and facilitates more effective conservation strategies. The model, however, currently lacks consideration of spatial heterogeneity, gene flow, and fitness costs elements that are pivotal to shaping the resistance dynamics. Addressing these in later research will boost the model's precision and relevance in varied agricultural contexts. Overall, the model serves as a powerful tool to understand and manage insecticide resistance in aphids.

$$\frac{dR}{dt} = \beta \times S \times R - \gamma \times R \dots (1)$$

In Equation (1),

- R = number of resistant aphids
- S = number of susceptible aphids
- β = rate at which resistance spreads
- γ = removal rate of resistant aphids (death or control)

The formula captures both the rate of insecticide exposure and the progression towards resistance, thus encapsulating the overall change in the population of resistant aphids with time. This is a simplified model intended to illustrate the developmental dynamics of population resistance mathematically.

Table 1. Daily SEIR-Based Aphid Population Shift Under Bt Cotton Exposure (Day 1–7)

Day	Susceptible (S)	Exposed (E)	Resistant (I)	Removed (R)
1	980	10	5	5
2	950	20	15	15
3	910	30	25	35
4	870	40	40	50
5	820	50	60	70
6	760	60	80	100
7	700	65	100	135

Table 1 Shows the daily changes of the aphid population within the four SEIR compartments for the first 7 days after exposure to Bt cotton. During Day 1 the aphid population is mainly in the susceptible compartment, with very few Exposed or Resistant individuals. Progressing days show the susceptible group experiencing a decline due to greater exposure to the insecticide, while the Exposed and Resistant populations steadily increase. By Day 7, a considerable portion of the population has shifted into the resistant and removed categories. This pattern indicates the early stages of resistance development and underscores the urgent need for responsive control measures in the first week of exposure to avert long-term resistance accumulation.

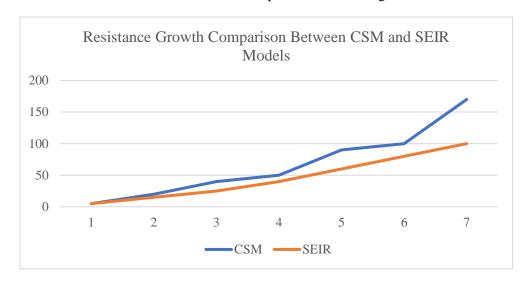


Figure 3. Resistance Growth Comparison Between CSM and SEIR Models

Figure 3 analyzes the development of insecticide resistance in aphids over 7 days with CSM and SEIR modeling. CSM shows resistance growing much faster, reaching 170 resistant aphids by Day 7, whereas the SEIR model shows a slower increase to 100. This displays how the SEIR model can mitigate the delay resistance has through better timed insecticide applications, demonstrating the importance of CSM and population dynamics models in optimizing pest control strategies while prolonging insecticide efficacy.

Conclusion

This research formulated and implemented a population dynamics model using the SEIR approach to study how insecticide resistance evolves in aphid populations. The model accurately captured the development of resistance in response to sustained exposure to insecticides, proving its usefulness for simulating real-world resistance dynamics. The comparative assessment with empirical data and other approaches, particularly noted the SEIR-based approach's advantage in delay of resistance development, thus promoting more environmentally sustainable pest management practices. This model, while useful, could be further strengthened by including spatial distribution, gene flow, and associated fitness costs to improve his forecasting ability. This study highlights the need to integrate population dynamics models into pest management in order to refine the timing of interventions and prolong the potency of insecticides, such as with the use of B_t crops, while also laying the groundwork for tailoring more diverse resistance frameworks for different insect species and resistance models.

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