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AN AGENT-BASED MODEL OF DEFORMED WING VIRUS A AND B CO-INFECTION

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Abstract. The Deformed Wing Virus (DWV) is a major threat to honeybee populations, causing colony collapse disorder and threatening global agriculture and biodiversity. DWV-A and DWV-B, co-infect honeybees, leading to severe outcomes. An agent-based model simulates the interactions between bees, mites, and viruses, incorporating factors like viral transmission rate, pathogenicity, and immune response. The model predicts that the presence of both DWV strains leads to synergistic interactions, resulting in heightened virulence and accelerated colony decline. Furthermore, the findings suggest that targeted interventions, such as mite control and selective breeding for disease-resistant bees, can mitigate the adverse effects of co-infection. This study provides a novel computational framework to explore the multifaceted interactions between DWV strains and their hosts, offering valuable insights into the mechanisms driving colony health and disease resilience. The agent-based approach facilitates the examination of various hypothetical scenarios and intervention strategies, contributing to effective management practices to safeguard honeybee populations. By enhancing our understanding of DWV co-infection dynamics, this research aims to inform policymakers and guide practical efforts to combat the ongoing challenges facing honeybee health, ultimately supporting the sustainability of pollinator-dependent ecosystems and agricultural productivity.

Keywords: Deformed wing virus, Colony collapse disorder, Co-infection, Strains.

1 Introduction

The honeybee, crucial for modern agriculture, provides essential services like pollination, medicine, and nutrition [1]. However, the global decline in honeybee colonies, driven by parasites, threatens agricultural security. The survival of individual bees depends on the colony's population, and varroa mite invasion increases infection prevalence [2,3].

Deformed wing virus (DWV) is a common honeybee virus that causes wing deformities in adult honeybees and affects all life stages [4]. It spreads globally and can be contracted through various routes, including food consumption by workers to varroa mites. Four DWV variants have been reported, with DWV-B being more widespread in Europe and DWV-A in North America. DWV-B has similar or lower virulence in honeybee pupae, but understanding pupal mortality before adulthood is complex [5,6].

The DWV-A and DWV-B variants initially have higher viral loads, but 72 hours after coinfection, DWV-B replicates to higher levels [7]. Superinfection exclusion occurs at the colony level, and DWV-B competes with DWV-A [8]. Varroa mites have developed resistance to synthetic acaricides, making biological control methods effective. Research suggests that African honeybees may be less threatened by pests and diseases due to their resistance, highlighting the importance of understanding resistance mechanisms [9]. Mathematical models have been utilized to study honeybee virus transmission dynamics within and between hives [10,11]. Britton and White's first model used weighted directed graphs, revealing overt infection could occur without mites [12]. Paxton's model analyzed DWV-A and DWV-B variants, emphasizing the relationship between variants [13].

Agent-based modeling (ABM) is a simulation approach to model systems comprising interacting agents. It consists of agents that interact within an environment. Progress suggests that ABM could have far-reaching effects on how researchers use models as electronic laboratories to identify promising research directions [14,18].

Several computational models have been proposed to examine honeybee issues, including the BEEPOP model, which predicts colony growth by considering factors like egg laying, brood development, worker aging, and foraging days [15]. The VARROAPOP model considers the impact of Varroa mite parasitism on colony dynamics, focusing on worker longevity reduction [16]. The BEEHAVE model, developed by Becher et al. (2014), incorporates Varroa mites, viruses, landscape changes, and pesticide exposure on colony growth and survival. It generates cohorts of individuals aged from egg to adult, identifying critical factors for overwintering success, including weather conditions and fall supplemental feeding. The model also simulates the sublethal effects of pesticides, including impaired forager orientation, floral handling time, brood care, and increased forager mortality [17].

In this study, we proposed an agent-based model that will aid in exploring, quantitatively, the mode of spread of DWV variants A and B. In order to intervene in virus transmission, the model includes intervention techniques such as mite resistance breeding, hive cleaning, and miticide use.

2 Methodology

2.1 Modeling the environment

We use Agent-Based Modeling, where the interactions of an autonomous agent (in this case, Varroa mites) with a spatially explicitly modeled environment can be formalized using defined memory and decision heuristics, to validate adaptive hypotheses in disease transmission and parasite infestation (Chittka, 2006). Specifically, we used NetLogo (Wilensky, 1999), a simple programmable agent-based modeling system for simulating natural and social phenomena, to model the environment of Varroa mites and the bee agents. We modeled the interaction that developed over time between the agents and environmental changes, such as illuminant variations.

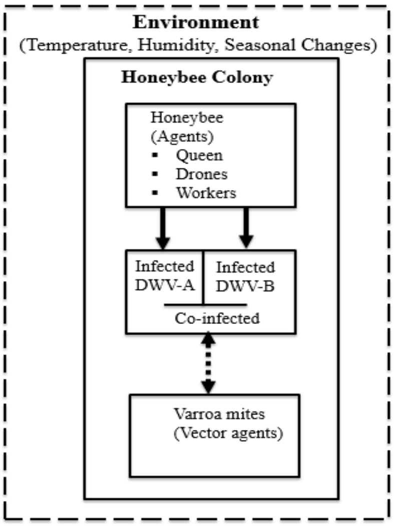


Fig. 1. The schematic diagram describes the interaction between honeybees, Varroa mites, and their environment.

In case of the environment, external factors such as temperature and humidity could affect the transmission rates of DWV. Also, interventions by the beekeepers, for example, treatments or good hive management practices, can affect the transmission dynamics of the DWV-A. Within the colony, the role of primary agents members of the colony (workers, drones, queen) can facilitate or delay the transmission. Furthermore, the transition between various states (healthy, infected, coinfected, dead) plays a role in the dynamics of the members. Varroa Mites act as vectors for DWV, transmitting the virus from infected bees to healthy bees. *Note that, dashed arrows indicate interactions, while solid arrows show transitions.*

2.2 Modeling the Colony

The model considers interaction between susceptible honeybees and infected mites and virus-free mites and infected honeybees. The model considers the following assumptions as follows:

1. As in [10] we assume that effective egg survival into adults results from broodcare through division of labor.
2. In accordance with [3] we presume that neither of the illness variations has affected the queen bee. This presumption is thought to be essential in order for us to presume that the queen's rate of egg production is unaffected by viruses or mites.
3. The assumption that the rate of mite parasitism is proportionate to the amount of mite-honeybee encounters accounts for the severity of mite infestation.
4. There is a strong correlation between the mite's lifespan and the honeybee's lifespan. Our model incorporates this by considering the population of honeybees, including both adult and brood bees, as a function of carrying capacity.
5. The two stages of female mite life phoretic and reproductive within brood cells are taken into account in the model formulation.
6. In consistent with [10] we presume that both adult and brood bees orally consume the virus pathogens.

The set up of the model depicted in Fig. 2 is designed to investigate the impact of the transmission dynamics of the two variants and the possibility of their co-infection in the presence of some control strategies. The model considers three (3) populations, viz., brood bees, B; adult bees, H; and mites (P-parasitic mites and R-reproductive mites). The brood bees are set to acquire infection following parasitism by infected reproductive mites, while the adult bees acquire infection from parasitic mites. Both brood and adult bees could acquire a second infection despite being infected with one variant (DWV-A or DWV-B). Literature has shown that, mites are the transmitters of the variants of DWV and thus, we allow the mites to acquire either of the variants. However, we assume that a mite carry only one infection at a time. To simulate the model, we set up an uncontaminated hive with 25,000 brood bees (out of which 5000 are drone broods, 20,000 are walker drones) 20,000 healthy adult honeybees, 10 virus-free carrying mites. We then introduced 5 infected honeybees and 1 virus-carrying mite. The virus was set to occur as the infected mite parasite on the healthy bee. We assume that throughout the simulation time, the queen bee will not be infected by either of the virus variants. The assumption is integrated to allow us assume that the queen bee's egg-laying rate will not be affected by either the mites or the virus.

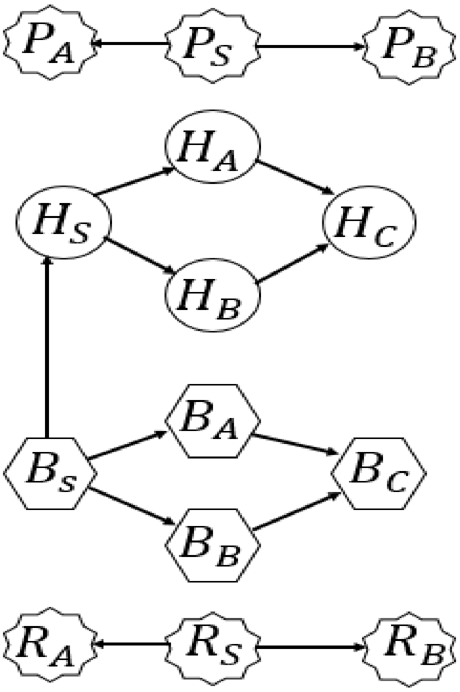


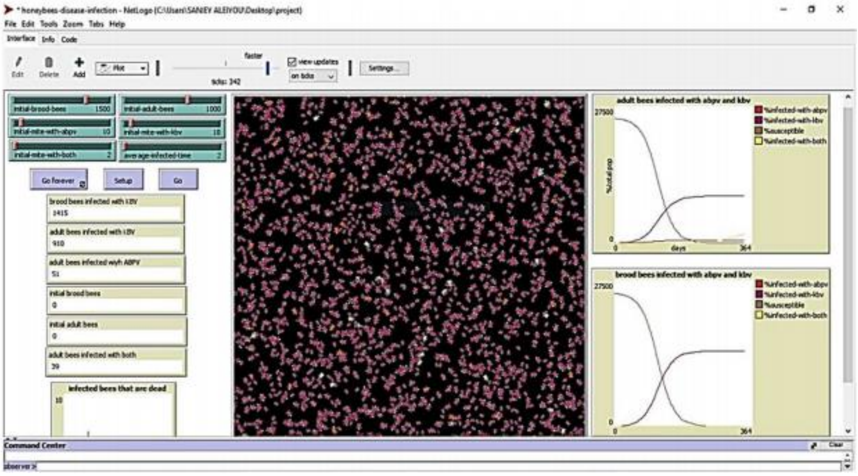
Fig. 2: The flow diagram describing the interaction between honey bees and mites.

The indeces *A*, *B* and *C* denote variants A, B and coinfection, respectively. The compartments *H*, *B*, *P* and *R* denote adult bees, brood bees, parasitic mite and reproductive mites, respectively. The arrows show progression from one class to the other.

2.3 NetLogo

NetLogo is a programmable modeling environment designed for social and natural phenomena simulation. Since its inception in 1999 by Uri Wilensky, the Center for Connected Learning and Computer-Based Modeling has been actively updating it (Wilensky, 1999–2019). NetLogo has been an excellent tool for beginners because of its simplicity. Thousands or even hundreds of thousands of autonomous "agents" can be programmed by modelers. This allows for the investigation of the relationship between an individual's microbehavior and the macro-level patterns resulting from their interaction. However, it has some challenges or limitations, such as performance, scalability, and flexibility. These limitations may make it less suitable for large-scale, complex, or highly detailed simulations. The next multiagent modeling language in the StarLogo and StarLogoT family is NetLogo.

The screenshot is portrayed in Fig. 3.



ticks: 342

☑ view updates: on ticks

initial-brood-bees 1500

initial-adult-bees 1000

initial-mite-with-abpv 10

initial-mite-with-kbv 10

initial-mite-with-both 2

average-infected-time 2

brood bees infected with KBV: 1415

adult bees infected with KBV: 910

adult bees infected wyh ABPV: 51

initial brood bees: 0

initial adult bees: 0

adult bees infected with both: 39

Fig. 3: NetLogo simulation environment

3 Result and Discussion

In this section, we simulated the model described in Figure 1 using an agent based model software, NetLogo 6.0.2. We experimented with a colony set as in Section 2.2. Deep learning techniques are used to train the model designed and with the help of Machine learning algorithms, we make some forecast. The accuracy of the analysis results was assessed via a combination of both linear and nonlinear algorithms. The dataset used in the analysis is generated from Netlogo software.

The dataset is split into 10 groups, and we used 9 groups for training and 1 for testing. Validation is performed ten times through a random selection of groups for training and testing. Average Classification Accuracy (ACA) is calculated. The result of the 10-Fold Cross Validations is presented in Table:

Table 1: Classifier performance of 10-Fold Cross Validations on the dataset

Categories	**10-Fold Cross Validation**						
	Accuracy Rate (%) for Classification Methods						
	ACA	LR	LDA	KNN	CART	NB	SVM
DWV-A infected bees	0.6782	0.4712	0.6851	0.6978	0.8892	0.7767	0.5762
DWV-B infected bees	0.2522	0.2622	0.2966	0.4401	0.5763	0.4132	0.2322
Co- infected with DWV-A and DWV-B	0.4251	0.5321	0.5475	0.7677	0.8723	0.7675	0.4201

Using MATLAB, the dataset generated from the simulation environment is used for the following plot.

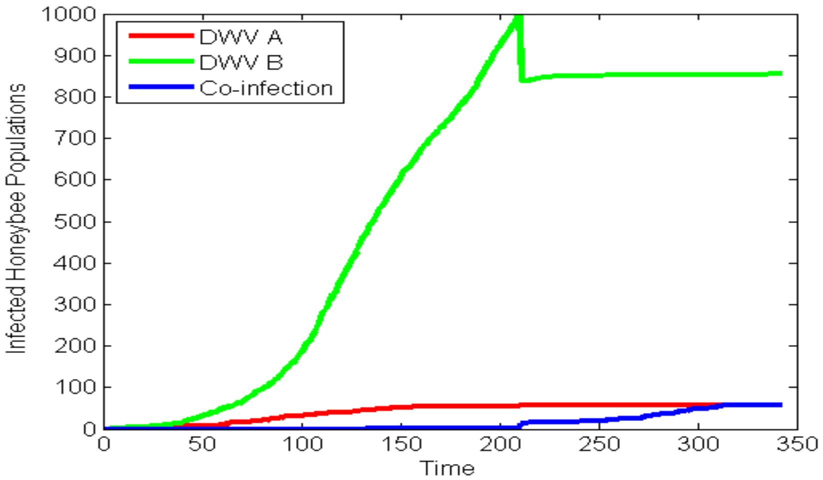


Fig. 4: Graph of estimated cases of DWV-A, B and co-infections.

It is evident from the graph Fig. 4 that, DWV-A cases maintain a steady but slow increase, indicating that this strain of the virus spreads more slowly through the population. In the case of DWV B, a rapid increase in the infected population is realized, suggesting a much higher transmission rate or a more aggressive infection dynamic. The plateau observed around the 200 days might indicate a temporary saturation point, followed by another increase due to new susceptible individuals or environmental changes. Cases of co-infection follow a steady increase similar to DWV A but at a slightly faster rate. This suggests that co-infection might have a compounded effect, but it is not as aggressive as DWV B alone.

This result implies that,, a rapid increase in the cases of DWV-B infections is of major concern for honeybee populations. This is because it can lead to a high number of infected bees within the shortest possible time. Consequently, this will have a serious effect on colony health and survival. DWV-A and co-infection have a less dramatic effect but still show a significant increase in populations, which can contribute to colony decline over a long time compared to DWV-B.

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