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Mathematical model on the transmission dynamics of varroosis in honeybee colony with treatment and biocontrol agent

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Abstract: Honeybee colony is invariably invaded by vectors which negatively affect their survival and reproduction. The compartmental model approach was adopted and partitioned the honeybee population into three (3), the population of vectors into two (2), and a single compartment for the population of biocontrol agent respectively. The model is aimed at expending treatment and biocontrol agent as a combined control strategy for curbing *Varroosis* in honeybee colony. Disease-free and infestation-free steady state was obtained and its global stability was established. Also, the basic reproduction number R_0 of the model was computed. Furthermore, the numerical simulation indicated that *Varroa-mite* infestation in honeybee colony has a greater negative impact; if control measure is not taken, honeybee colony extinction is certain. Hence, with the treatment using Thymol powder as a control strategy; the numerical results indicated a sharp decline in the population of honeybees infested by *Varroa-mite*. In the same vein, a biocontrol mechanism was employed by introducing 1,500 biocontrol agents into the population of *Varroa-mite* in a honeybee colony. This effort swiftly triggered the mode of extinction of the *Varroa-mite* population within 5-6 months. As such, the findings indicated that treatment and biocontrol strategies are the most efficient methods of curbing Varroosis in honeybee colony. Thus, it is recommended that a higher initial value of biocontrol agents should be employed prudently to achieve the control of *Varroosis* via biological and treatment as a combined control strategy.

Keywords: Biocontrol; Treatment; Varroosis; Stability; Steady State.

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1 Introduction

Honeybee (*Apis melifera or Apis cerana*) is a social insect that modern agriculture is increasingly reliant on, to provide pollination services for several key horticultural crops. The importance of honeybees in sustaining ecosystems, regional, national, and global food supplies, and various agricultural industries cannot be underestimated ([22]). Today, the majority of food crops consumed by humans rely on bees' pollination (increases in abundance yields and quality) ([15, 20, 35]). Pollination is crucial to food production and the economy; food coming from pollinated plants accounts for 35% of an American's diet, with $15 billion annually in the United States, and exceeds $200 billion globally ([25, 18]). The substantial contribution of honeybees

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could not be over-emphasized in producing honey, beeswax, and other products which are used for vast purposes.

The honeybee population has been facing increasingly vast and complex challenges ranging from diseases, predators, parasitic *Varroa-mite* (*Varroa-destructor*), viruses, brood diseases, pesticides, inadequate nutrition, climate and seasonal changes, and the stresses of moving colonies for crop pollination. These numerous life-threatening factors of honeybee colony were also stressed by [7, 9, 28, 26, 8, 27].

Varroa-mite is an ectoparasite that attacks both *Apis melifera and Apis cerana. Varroa-mite* (a vector of viruses) and its associated viruses remain unarguably the leading cause of honeybee colony mortality worldwide [31]. It infests and transmits pathogens (Viruses) via vertically or horizontally within and between colonies. As stressed by [3, 6] *Varroa-mite* instills detrimental health hazards on the adult honeybee life by feeding on the bees' hemolymph and piercing its intersegment membrane while reproducing and surviving on brood cells. Hence, *Varroa-mites* suppress honeybee immunity which subsequently results in death. Viral infections may get injected into the bee's body during this feeding process. When a virus-carrying mite feeds on an uninfected bee, it might release the virus into the bee's hemolymph. Similarly, when a virus-free mite feeds on an already infected bee, it can acquire the virus. There have been around 20 known honeybee viruses, of which 12 are transmitted by *Varroa-mites* [14]. These viruses differ in their transmission routes, virulence, and impact on the host.

Various control strategies have been explored and exploited to gradually curb the life-threatening menace in apiculture. In that light, [1,11] stressed that these several controls include: Plant extracts and essential oils; biological methods (*entomopathogenic fungi* & *Varroa-mite* predator); oxalic and formic acid; mechanical and heating method; acaricides; and resistance of honeybee subspecies to *Varroa-mites.*

Substantial numbers of mathematical models were developed and studied on the dynamics of *Varroa-mite* infestation and vectored disease transmission into the honeybee population. [8] studied honeybee colony collapse and viral prevalence change associated with *Varroa-mites*. [5] developed and studied an epidemiological model of viral infection in a colony bee infested by *Varroa-mite*. [22] examined honeybee-mite interactions in the presence of migration effects on their population dynamics. [30] studied and analyzed a mathematical model of honeybee, *Varroa-mite,* and Acute bee paralysis virus interactions with seasonal. In addition, [9] studied the influence of brood death on honeybee population dynamics and the potential impact of insecticides. In addition, [9] developed an eco-epidemiological model interaction between the honeybee population and *Varroa-mite* population. The model was able to present the interplay between the two populations in which *Varroa-mite* spread disease on honeybees which distorted the ecosystem. The study introduced the recovery class and investigated the effect of social inhibition and disinfestation on a hive honeybee species from infection and infestation in the ecosystem. In a nutshell, [33, 11] are among other studies on honeybees, *Varroa-mites,* and viral interactions.

In specific, [11] developed and studied a mathematical model for a honeybee colony infested by virus-carrying *Varroa-mites*. However, the model didn't consider brood subpopulation, *Varroa-mite* population, treatment, and control strategies. Hence, this study intends to remedy the obvious potholes vividly identified in the model due to [11].

2 Material and Methods

2.1 Model formulation

The total population $N(t)$, subtotal populations includes: $N_s(t)$, $N_m(t)$ and $N_i(t)$ at time t, is divided into twelfth (12) mutually exclusive compartments, viz: Susceptible brood $B_s(t)$, Brood infested by virus-free *Varroa-mite* $B_m(t)$, Brood infested by *Varroa-mite* carrying virus $B_i(t)$, Susceptible hive bees $H_s(t)$, hive bees infested by virus-free *Varroa-mite* $H_m(t)$, hive bees infested by *Varroa-mite* carrying virus $H_i(t)$, Susceptible forager bees $F_s(t)$, Forager bees infested by virus-free *Varroa-mite* $F_m(t)$, Forager bees infested by *Varroa-mite* carrying virus Population of virus-free *Varroa-mite* $F_i(t)$, Population of *Varroa-mite* carrying $V_f(t)$, $V_v(t)$ and Population of biocontrol agent $A_B(t)$; for all compartments at time t.

Thus, $N(t) = N_s + N_m + N_i$ where: $N_s = B_s + H_s + F_s$, $N_m = B_m + H_m + F_m$ and $N_i = B_i + H_i + F_i$

It is assumed that infested and infected honeybee has (N_m and N_i) a shorter life span than healthy bees N_s. Also, assuming that *Varroa-mites* have higher interaction with broods and hives than forager and that the rate of disinfestation in honeybees depends on their state of health, hence, $\alpha_1 > \alpha_2$. It is assumed that the biocontrol agent feeds on both virus-free and virus-carrying *Varro-mite*, the population growth for the biocontrol agent is assumed to be logistic, the recruitment rate of brood population is assumed to be constant, the population growth for *Varroa-mite* is assumed to be logistic and the carrying capacity for the mite changes with host (honeybee) population size and the natural death rate for all the populations is assumed to be constant. The infection-induced death rate for all the populations is assumed to be constant. Also, it is only a horizontal transmission mode is assumed and *Varroa-mite* carrying viruses are constantly recruited into the colony. The schematic diagram of the model in Fig.1 describes the transition between compartments.

2.1.1 State variables and parameters

The state variables and parameters of the modified model are presented in Table 1 and Table 2 respectively below:

Table 1: State Variables

Symbol	**Descriptions**
$B_s(t)$	Susceptible brood at a time t
$B_m(t)$	Brood infested by virus-free *Varroa-mite* at a time t
$B_i(t)$	Brood infested by *Varroa-mite* carrying virus at a time t
$H_s(t)$	Susceptible hive bees at a time t
$H_m(t)$	hive bees infested by virus-free *Varroa-mite* at a time t
$H_i(t)$	hive bees infested by *Varroa-mite* carrying virus at a time t
$F_s(t)$	Susceptible forager bees at a time t
$F_m(t)$	Forager bees infested by virus-free *Varroa-mite* at a time t
$F_i(t)$	Forager bees infested by *Varroa-mite* carrying virus at a time t
$V_f(t)$	Population of virus-free *Varroa-mite* at a time t
$V_v(t)$	The population of *Varroa-mite* carrying virus at a time t
$A_B(t)$	Population of biocontrol agent at a time t
N_s	Total subpopulation of healthy honeybees
N_m	Total subpopulation of infested honeybees by virus-free *Varroa-mite*
N_i	Total subpopulation of infected honeybee by *Varroa-mite* carrying virus
N	Total population of honeybee

Table 2: Parameters

Symbol	Descriptions
β_1	Transmission rate of infestation by virus-free *Varroa-mite*
β_2	Transmission rate of infestation by virus-carrying *Varroa-mite*
α_1	Disinfestation rate for honeybees infested by virus-free *Varroa-mite*
α_2	Disinfestation rate for honeybees infested by virus-carrying *Varroa-mite*
d	Natural death rate for all the populations of honeybees
δ	Infection induced death rate for all the populations of honeybees
ϕ	Eclosion rate of brood to hive bee
σ_1	Reversion rate of hive bee to forager bee
σ_2	Reversion rate of forager bee to hive bee
τ	Intrinsic growth rate of biocontrol agent
γ	Intrinsic growth rate of *Varroa-mite*
k	Environmental carrying capacity for biocontrol agent
Q	Environmental carrying capacity for *Varroa-mite*
η_1	Rate at which virus-free *Varroa-mite* acquires virus
η_2	Rate at which virus-carrying *Varroa-mite* loss it to the host healthy bees
η_3	Constant recruitment rate of *Varroa-mite* carrying virus into the colony
C_1	Conversation coefficient of virus-free *Varroa-mite* to bio-agent
C_2	Conversation coefficient of virus-carrying *Varroa-mite* to bio-agent
μ_v	Natural death rate for the populations of *Varroa-mite*
μ	Natural death rate for the population of biocontrol agent
π	Treatment using Thymol powder

A	Recruitment rate of healthy bees in the colony

2.1.2 Schematic diagram

The schematic diagram for the model is presented in Figure 1 below:

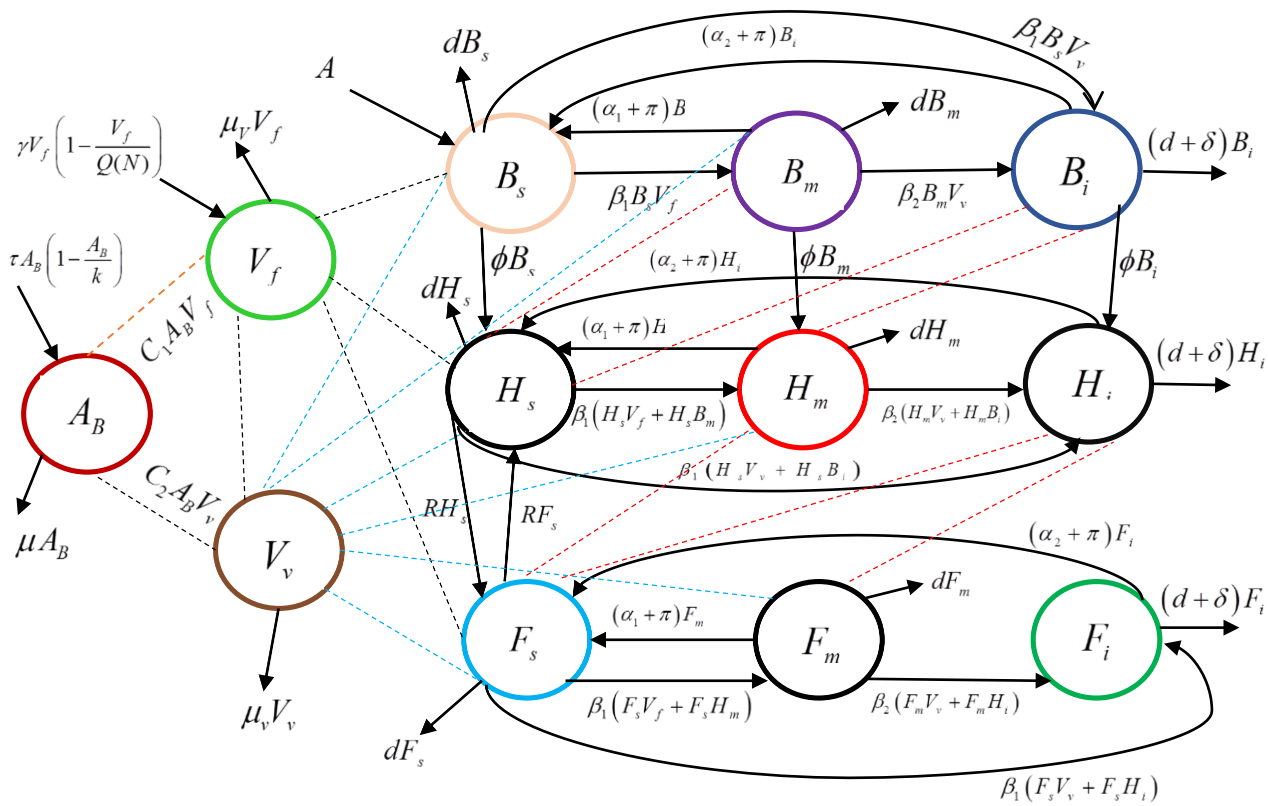

Figure 1: Schematic diagram

2.2 Model equations

$$\frac{dB_s}{dt} = A + (\alpha_1+\pi)B_m + (\alpha_2+\pi)B_i - \beta_1 B_s (V_f + V_v) - (\phi + d)B_s \quad (1)$$

$$\frac{dB_m}{dt} = \beta_1 B_s V_f - \beta_2 B_m V_v - (\alpha_1 + \pi + \phi + d)B_m \quad (2)$$

$$\frac{dB_i}{dt} = (\beta_1 B_s + \beta_2 B_m)V_v - (\alpha_2 + \pi + \phi + d + \delta)B_i \quad (3)$$

$$\frac{dH_s}{dt} = -\beta_1 H_s\left(V_f + B_m + V_v + B_i\right) + \phi B_s + \left(\alpha_1 + \pi\right)H_m + \left(\alpha_2 + \pi\right)H_i + R(H_s, F_s)F_s - R(H_s, F_s)H_s - dH_s \quad (4)$$

$$\frac{dH_m}{dt} = \beta_1 H_s\left(V_f + B_m\right) - \beta_2 H_m\left(V_v + B_i\right) + \phi B_m - \left(\alpha_1 + \pi + d\right)H_m \quad (5)$$

$$\frac{dH_i}{dt} = \beta_1 H_s\left(V_v + B_i\right) + \beta_2 H_m\left(V_v + B_i\right) + \phi B_i - \left(\alpha_2 + \pi + d + \delta\right)H_i \quad (6)$$

$$\frac{dF_s}{dt} = R(H_s, F_s)H_s - R(H_s, F_s)F_s - \beta_1 F_s\left(V_f + H_m + V_v + H_i\right) + \left(\alpha_1 + \pi\right)F_m + \left(\alpha_2 + \pi\right)F_i - dF_s \quad (7)$$

$$\frac{dF_m}{dt} = \beta_1 F_s\left(V_f + H_m\right) - \beta_2 F_m\left(V_v + H_i\right) - \left(\alpha_1 + \pi + d\right)F_m$$

(8)

$$\frac{dF_i}{dt} = \beta_1 F_s\left(V_v + H_i\right) + \beta_2 F_m\left(V_v + H_i\right) - \left(\alpha_2 + \pi + d + \delta\right)F_i \quad (9)$$

$$\frac{dV_f}{dt} = \gamma V_f\left(1 - \frac{V_f}{Q(N)}\right) - \left(C_1 A_B + \mu_v\right)V_f \quad (10)$$

$$\frac{dV_v}{dt} = \eta_1\left(N_v - V_v\right)\frac{N_i}{N_s + N_m + N_i} - \eta_2 V_v\frac{N_s}{N_s + N_m + N_i} + \eta_3 - \left(C_2 A_B + \mu_v\right)V_v \quad (11)$$

$$\frac{dA_B}{dt} = \tau A_B\left(1 - \frac{A_B}{k}\right) + \left(C_1 V_f + C_2 V_v\right)A_B - \mu A_B \quad (12)$$

$N = N_s + N_m + N_i$ Where $N_s = B_s + H_s + F_s$, $N_m = B_m + H_m + F_m$, $N_i = B_i + H_i + F_i$, $N_v = V_f + V_v$, $N_v - V_v = V_f$ (13)

With initial conditions

$B_s(0) \geq 0$, $B_m(0) \geq 0$, $B_i(0) \geq 0$, $H_s(0) \geq 0$, $H_m(0) \geq 0$, $H_i(0) \geq 0$, $F_s(0) \geq 0$, $F_m(0) \geq 0$, $F_i(0) \geq 0$, $V_f(0) \geq 0$, $V_v(0) \geq 0$, $A_B(0) \geq 0$

All variables and parameters are considered non-negative.

3 Model Analysis

Transforming model equations of (1) to (12) has an advantage of reducing the number of model equations and thus; the study defined the following:

$$\left.\begin{aligned} \dot{S}(t) &= \dot{B}_s(t) + \dot{H}_s(t) + \dot{F}_s(t) \\ \dot{M}(t) &= \dot{B}_m(t) + \dot{H}_m(t) + \dot{F}_m(t) \\ \dot{I}(t) &= \dot{B}_i(t) + \dot{H}_i(t) + \dot{F}_i(t) \end{aligned}\right\}$$

(14) Now applying equation (14) on equations (1) to (12) gives the following equations:

$$\dot{S}(t) = A - \beta_1 S\left(V_f + V_v + M + I\right) + \left(\alpha_1 + \pi\right)M + \left(\alpha_2 + \pi\right)I - dS \quad (15)$$

$$\dot{M}(t) = \beta_1 S\left(V_f + M\right) - \beta_2 M\left(V_v + I\right) - \left(\alpha_1 + \pi + d\right)M$$

(16)

$$\dot{I}(t) = \beta_1 S\left(V_v + I\right) + \beta_2 M\left(V_v + I\right) - \left(\alpha_2 + \pi + d + \delta\right)I$$

(17)

$$\dot{V}_f(t)=\gamma V_f\left(1-\frac{V_f}{Q(N)}\right)-\left(C_1A_B+\mu_v\right)V_f \quad (18)$$

$$\dot{V}_v(t)=\eta_1V_f\frac{N_i}{N}-\eta_2V_v\frac{N_s}{N}+\eta_3-\left(C_2A_B+\mu_v\right)V_v \quad (19)$$

$$\dot{A}_B(t)=\tau A_B\left(1-\frac{A_B}{k}\right)+\left(C_1V_f+C_2V_v\right)A_B-\mu A_B \quad (20)$$

With initial conditions $S(0)\geq 0$, $M(0)\geq 0$, $I(0)\geq 0$, $V_f(0)\geq 0$, $V_v(0)\geq 0$ and $A_B(0)\geq 0$

3.1 Basic properties of the model

3.1.1. Positivity and boundedness of the model

Theorem 1*:* Let the initial data for the model (15)-(20) be $S(0)\geq 0$, $M(0)\geq 0$, $I(0)\geq 0$, $V_f(0)\geq 0$, $V_v(0)\geq 0$, $A_B(0)\geq 0$. Then the solutions $\left(S,M,I,V_f,V_v,A_B\right)$ of the model equations (15)-(20) with positive initial data will remain positive for all time $t>0$.

Proof: Let $t_1=Sup\left\{t>0:S\geq 0,M\geq 0,I\geq 0,V_f\geq 0,V_v\geq 0,A_B\geq 0\in\left[0,t\right]\right\}$, thus $t>0$. Then, it follows from the equations of the model equations (15)-(20), give the followings:
From equation (15) considering only negative terms in S, it gives:

$$\frac{dS}{dt}\geq-\beta_1S\left(V_f+V_v+M+I\right)-dS\geq-\left[\beta_1\left(V_f+V_v+M+I\right)+d\right]S$$

Using separation of variables method, it gives:

$$\frac{dS}{S}\geq-\left[\beta_1\left(V_f+V_v+M+I\right)+d\right]dt$$

Integrating both sides and taking anti-log, it gives:

$$InS\geq-\int_0^{t_1}\beta_1\left(V_f(y)+V_v(y)+M(y)+I(y)\right)dy-\int d\,dt$$

So that, $S(t)\geq e^{-\int_0^{t_1}\beta_1\left(V_f(y)+V_v(y)+M(y)+I(y)\right)dy-dt}$

At $t_1=0$ and with initial condition $S(0)$

Then,

$$S(t)\geq S(0)e^{-\int_0^{t_1}\beta_1\left(V_f(y)+V_v(y)+M(y)+I(y)\right)dy-dt}>0\text{, since }\beta_1\left(V_f(y)+V_v(y)+M(y)+I(y)\right)>0\text{ and }d>0 \quad (21)$$

Using similar argument, it can be shown that the state variables are all positive for all $t>0$. Hence, the solution of model (15)-(20) remains positive for all $t>0$.

3.1.2 Invariant region

Theorem 2: The closed set $\Psi = \left\{ \left(S, M, I, V_f, V_v, A_B \right) \in \Re_+^6 : N \leq \frac{A}{d}, N_v \leq \frac{\eta_3}{C + \mu_v}, A_B \leq k \right\}$ is positively invariant and attracting with respect to the model (15)-(20)

Proof: Given the system of equation (15)-(20), sum the first three equations which is the total population of honeybees, it gives:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dM}{dt} + \frac{dI}{dt} \qquad (22)$$

Simplifying equation (22) gives:

$$\frac{dN}{dt} \leq A - Nd \qquad (23)$$

Solving the linear equation in (23) and by comparison theorem of Kribs-Zaleta (1999), it gives:

$$N(t) = N_0 e^{-dt} + \frac{A}{d}\left(1 - e^{-dt}\right) \qquad (24)$$

Where N_0 is an arbitrary constant, taking the limit of equation (24) as $t \to \infty$ it gives:

$$N(t) \leq \frac{A}{d} \qquad (25)$$

Therefore, the total population of honeybee $N(t)$ is bounded above by $\frac{A}{d}$ as $t \to \infty$. Furthermore, $N(t) \leq \frac{A}{d}$ if $N(0) \leq \frac{A}{d}$. Also, if $N(0) > \frac{A}{d}$ then, $\frac{dN}{dt} < 0$.

Using similar argument, it can be shown for the *Varroa-mite* and biocontrol population.

Thus, every solution of the dynamical system (15)-(20) with initial in $\Re_+^6$, tends toward the region Ψ as $t \to \infty$. Hence, the region Ψ is positively invariant and as well, attracts all possible solution trajectories.

3.2 Stability Analysis of the Model

3.2.1 Disease-free and infestation-free steady state of the model

In this steady state, there is absolutely absence of *Varroa-mite* which invariably implies the absence of both infestation and virus, then:

$$M = I = V_f = V_v = A_B = 0 \qquad (26)$$

Substituting equation (26) into the system (15)-(20), it gives:

$$A - dS = 0 \qquad (27)$$

Make S subject of the formula, it gives:

$$S = \frac{A}{d} \qquad (28)$$

Therefore, we obtain the disease-free and infestation-free steady state of the model given as

$$E_1^*\left(S^*, 0, 0, 0, 0, 0\right) = E_1^*\left(\frac{A}{d}, 0, 0, 0, 0, 0\right) \qquad (29)$$

3.2.2 Basic reproduction number of the model

To compute basic reproduction number R_0, next generation method developed by ([34]) was adopted. The matrix F of the new infection terms and the matrix V of the transmission terms associated with the model (15)-(20) are given in (30) and (31) respectively below:

$$F=\begin{bmatrix}F_1\\F_2\\F_3\\F_4\end{bmatrix}=\begin{bmatrix}\beta_1 S\left(V_f+M\right)\\ \beta_1 S\left(V_v+I\right)+\beta_2 M\left(V_v+I\right)\\ 0\\ \eta_1\frac{N_i}{N}V_f\end{bmatrix} \tag{30}$$

$$V=\begin{bmatrix}V_1\\V_2\\V_3\\V_4\end{bmatrix}=\begin{bmatrix}-\left[-\beta_2 M\left(V_v+I\right)-\left(\alpha_1+\pi+d\right)M\right]\\ -\left[\beta_2 M\left(V_v+I\right)-\left(\alpha_2+\pi+d+\delta\right)I\right]\\ -\left(-\mu_v V_f\right)\\ -\left(-\eta_2 V_v\frac{N_s}{N}-\mu_v V_v\right)\end{bmatrix}=\begin{bmatrix}\beta_2 M\left(V_v+I\right)+\left(\alpha_1+\pi+d\right)M\\ -\beta_2 M\left(V_v+I\right)+\left(\alpha_2+\pi+d+\delta\right)I\\ \mu_v V_f\\ \eta_2 V_v\frac{N_s}{N}+\mu_v V_v\end{bmatrix} \tag{31}$$

Manipulating equations (30) and (31) respectively at disease-free and infestation-free steady state in line with the next generation method, it gives:

$$\left|FV^{-1}-\lambda I\right|=\begin{vmatrix}\frac{A\beta_1}{d\left(\alpha_1+\pi+d\right)}-\lambda & 0 & \frac{A\beta_1}{d\mu} & 0\\ 0 & \frac{A\beta_1}{d\left(\alpha_2+\pi+d+\delta\right)}-\lambda & 0 & \frac{AN\beta_1}{dN\mu+\eta_2 N_s}\\ 0 & 0 & 0-\lambda & 0\\ 0 & 0 & \frac{1}{N\mu}\eta_1 N_i & 0-\lambda\end{vmatrix}=0 \tag{32}$$

The roots of equation (32) are given as follows:

$\lambda_1=\lambda_2=0$, $\lambda_3=\dfrac{A\beta_1}{d\left(\alpha_1+\pi+d\right)}$ and $\lambda_4=\dfrac{A\beta_1}{d\left(\alpha_2+\pi+d+\delta\right)}$

The reproduction numbers are $R_{01}=\dfrac{A\beta_1}{d\left(\alpha_1+\pi+d\right)}$ and $R_{02}=\dfrac{A\beta_1}{d\left(\alpha_2+\pi+d+\delta\right)}$. Hence, the reproduction number $R_0=Max\left(R_{01},R_{02}\right)$

The study obtained two reproduction numbers by introducing a single infested honeybee population in which neither virus-free *Varroa-mite* nor virus-carrying *Varroa-mite* are present in E_1^*. If we introduce a honeybee population infested by virus-free *Varroa-mite* into the disease-free and infestation-free steady state E_1^*. Hence, the study obtained the reproduction number

$$R_{01}=\frac{A\beta_1}{d\left(\alpha_1+\pi+d\right)} \tag{33}$$

Also, by introducing a honeybee population infested by virus- carrying *Varroa-mite* into the same steady state E_1^*, it also obtained another reproduction number from same E_1^*

$$R_{02} = \frac{A\beta_1}{d\left(\alpha_2 + \pi + d + \delta\right)} \tag{34}$$

Lemma 1: The disease-free and infestation-free of the model (15)-(20), given by (29), is Locally Asymptotically Stable (LAS) in Ψ, whenever $R_{01} < 1$, and unstable if $R_{01} > 1$.

3.2.3 Global stability of disease-free and infestation-free steady state of the model

([10]) method is used to investigate the global asymptotic stability of the disease-free and infestation-free steady state. It is noteworthy that model (15)-(20) undergoes backward bifurcation when it's corresponding reproduction number $R_{01} < 1$. This occurs due to imperfect efficacy of treatment ($\pi \neq 1$). However, when treatment is 100% effective (i.e $\pi = 1$), then, global asymptotic stability of disease-free and infection-free steady state of the model (15)-(20) is sufficiently traceable.

In this section, the study highlights two conditions that if met, guarantee the global asymptotic stability of the disease-free and infestation-free steady state. First, the system of equation (15)-(20) must be written in the form:

$$\left.\begin{aligned} \frac{dX}{dt} &= H\left(X, Z\right) \\ \frac{dZ}{dt} &= G\left(X, Z\right), G\left(X, Z\right) = 0 \end{aligned}\right\} \tag{35}$$

Where $X \in \Re^m$ denotes (its components) the number of uninfected individuals and $Z \in \Re^n$ denotes (its components) the number of infected individuals.

The conditions $\left(H_1\right)$ and $\left(H_2\right)$ below must be met to guarantee global asymptotic stability.

$\left(H_1\right)$: $\frac{dX}{dt} = H\left(X, 0\right)$, X^* is Globally Asymptotically Stable (G.A.S)

$\left(H_2\right)$: $G\left(X, Z\right) = PZ - \hat{G}(X, Z), \hat{G}(X, Z) \geq 0$, for $\left(X, Z\right) \in \Psi$

Where $P = D_1 G\left(X^*, 0\right)$ is an M-matrix (the off-diagonal elements of P are nonnegative) and Ψ is the region where the model makes biological sense. If the system of equation (15)-(20) is modified with special case $\pi = 1$; then, it satisfies the two conditions $\left(H_1\right)$ and $\left(H_2\right)$ when theorem 3 holds.

Theorem 3: The fixed point $E_1^* = \left(X_1^*, 0\right)$ is a globally asymptotic stable (G.A.S) of disease-free and infestation-free steady state of the system (15)-(20) provided that $R_{01} < 1$ is Locally Asymptotically Stable (L.A.S) and that $\left(H_1\right)$ and $\left(H_2\right)$ are satisfied.

Proof:

Let $X = \left(S, A_B\right)$, $Z = \left(M, I, V_f, V_v\right)$, $X \in \Re^2$, $Z \in \Re^4$, $E_1^* = \left(X^*, 0\right)$ and $X^* = \left(\frac{A}{d}, 0\right)$

Thus, the uninfected compartments from the system of equation (15)-(20), it gives:

$$H(X,Z)=\begin{bmatrix} A-\beta_1 S\left(V_f+V_v+M+I\right)+\left(\alpha_1+1\right)M+\left(\alpha_2+1\right)I-dS \\ rA_B\left(1-\frac{A_B}{k}\right)+\left(C_1V_f+C_2V_v\right)A_B-\mu A_B \end{bmatrix} \tag{36}$$

Evaluating (36) at the disease-free and infestation-free steady state, it gives:

$$H(X,0)=\begin{bmatrix} A-dS \\ 0 \end{bmatrix} \tag{37}$$

Taking the first entry in (37), it gives:

$$\frac{dS}{dt}=A-dS \tag{38}$$

Solving the linear equation in (38), it gives:

$$S(t)=S_0e^{-dt}+\frac{A}{d}\left(1-e^{-dt}\right) \tag{39}$$

Where N_0 is an arbitrary constant, taking the limit of equation (39) as $t\rightarrow\infty$ it gives

$$S(t)\rightarrow\frac{A}{d} \tag{40}$$

Taking the infected compartment of the system (15)-(20) with treatment $\pi=1$, it gives:

$$G(X,Z)=\begin{bmatrix} \beta_1 S\left(V_f+M\right)-\beta_2 M\left(V_v+I\right)-\left(\alpha_1+1+d\right)M \\ \beta_1 S\left(V_v+I\right)+\beta_2 M\left(V_v+I\right)-\left(\alpha_2+1+d+\delta\right)I \\ \gamma V_f\left(1-\frac{V_f}{Q(N)}\right)-\left(C_1A_B+\mu_v\right)V_f \\ \eta_1 V_f\frac{N_i}{N}-\eta_2 V_v\frac{N_s}{N}-\left(C_2A_B+\mu_v\right)V_v \end{bmatrix} \tag{41}$$

Taking the partial derivatives of the state variables in an infected compartments and evaluating equation (41) at disease-free and infestation-free steady state, it gives:

$$P=\begin{bmatrix} \beta_1 S-\left(\alpha_1+1+d\right) & 0 & -\beta_1 S & 0 \\ 0 & \beta_1 S-\left(\alpha_2+1+d+\delta\right) & 0 & \beta_1 S \\ 0 & 0 & \gamma-\mu_v & 0 \\ 0 & 0 & \eta_1\frac{N_i}{N} & -\eta_2\frac{N_s}{N}-\mu_v \end{bmatrix} \tag{42}$$

Multiply (42) by $Z=\left(M,I,V_f,V_v\right)^T$, it gives:

$$PZ=\begin{bmatrix}\left(\beta_1 S-\left(\alpha_1+1+d\right)\right)M-\beta_1 SV_f\\ \left(\beta_1 S-\left(\alpha_2+1+d+\delta\right)\right)I+\beta_1 SV_v\\ \left(\gamma-\mu_v\right)V_f\\ \left(\eta_1\dfrac{N_i}{N}\right)V_f-\left(\eta_2\dfrac{N_s}{N}+\mu_v\right)V_v\end{bmatrix} \tag{43}$$

Thus, subtracting (41) from (43), it gives:

$$G(X,Z)=PZ-\hat{G}(X,Z)=\begin{bmatrix}\beta_2 M\left(1-S+V_v+I\right)\\ \beta_2 I\left(1-S+M\right)\\ C_1 A_B V_f\\ C_2 A_B V_v\end{bmatrix} \tag{44}$$

Thus, rewriting (44) gives:

$$\hat{G}(X,Z)=\begin{bmatrix}\hat{G}_1(X,Z)\\ \hat{G}_2(X,Z)\\ \hat{G}_3(X,Z)\\ \hat{G}_4(X,Z)\end{bmatrix}=\begin{bmatrix}\beta_2 M\left(1-S+V_v+I\right)\\ \beta_2 I\left(1-S+M\right)\\ C_1 A_B V_f\\ C_2 A_B V_v\end{bmatrix}$$

Since C_1 and C_1 are between zero and one $\left\{0\le C_1,C_2\le 1\right\}$ and $0\le S+V_v+I\le S+M$; then, $\hat{G}(X,Z)\ge 0$. Hence, the global stability of $X^*=\left(\dfrac{A}{d},0\right)$ of the system (15)-(20) satisfying the two conditions guaranteed that E_1^* is Globally Asymptotically Stable (G.A.S).

4 Discussion of Results

4.1 The numerical values used for the experiments

The numerical values for the experiment of the model are given in table 3

Table 3**:** Parameters

Symbol	**Description**	**Value**	**References**
β_1	Infestation rate by virus-free *Varroa-mite*	0.1984	([29])
β_2	Infestation rate by virus-carrying *Varroa-mite*	0.05	Assumed
α_1	Disinfestation rate for honeybees infested by virus-free *Varroa-mite*	0.6	Assumed
α_2	Disinfestation rate for honeybees infested by virus-carrying *Varroa-mite*	0.4	Assumed
d	Natural death rate for all the populations of honeybees	0.2	([20])

δ	Infection induced death rate for all the populations of honeybees	0.3	Assumed
τ	Intrinsic growth rate of biocontrol agent	0.6	Assumed
γ	Intrinsic growth rate of *Varroa-mite*	0.0165	([20])
k	Environmental carrying capacity for biocontrol agent		
Q	Environmental carrying capacity for *Varroa-mite*	0.5	([29])
η_1	Rate at which virus-free *Varroa-mite* acquires virus	0.1593	([32])
η_2	Rate at which virus-carrying *Varroa-mite* loss it to the host healthy bees	0.04959	([32])
η_3	Constant recruitment rate of *Varroa-mite* carrying virus into the colony	300	Assumed
C_1	Conversation coefficient of virus-free *Varroa-mite* to biocontrol agent	1.5	([13])
C_2	Conversation coefficient of virus-carrying *Varroa-mite* to biocontrol agent	1.5	([13])
μ_v	Natural death rate for the populations of *Varroa-mite*	0.002	([22])
μ	Natural death rate for the populations of biocontrol agent	0.005	Assumed
π	Treatment using thymol powder	0.1-1.35	([30])
A	Recruitment rate of healthy bees in the colony	60,000	Assumed
N	Total population of Honeybee	80,000	Assumed

Experiment 1: Impact of Initial Value of Infestation of Virus-Free *Varroa-mite* on Healthy Honeybee Population

In this experiment, the study examined the impact of infestation of virus-free *Varroa-mite* on healthy honeybee population with different initial values. So, parameter values in table 3 is used alongside the estimated initial conditions given as: for healthy honeybee population in $S(0) = 20,000$ while for the virus-free *Varroa-mite* is varied as follows: $V_f(0) = 500$, $V_f(0) = 700$, $V_f(0) = 1,000$ and $V_f(0) = 2,000$. The numerical results are given below:

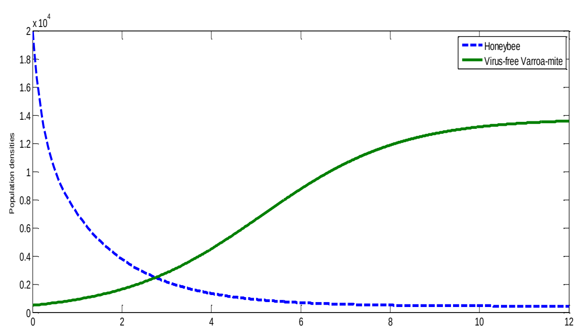

Figure 1: Impact of 500 virus-free *Varroa-mite* on the healthy (susceptible) honeybee population

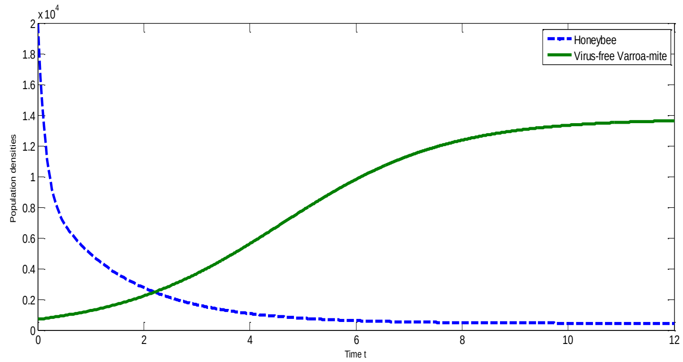

Figure 2: Impact of 700 virus-free *Varroa-mite* on the healthy (susceptible) honeybee population

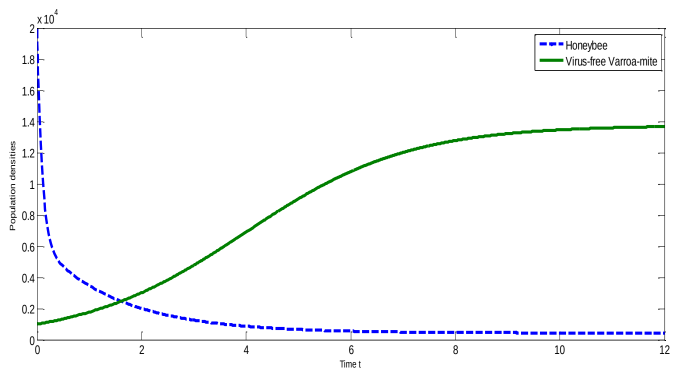

Figure 3: Impact of 1,000 virus-free *Varroa-mite* on the healthy (susceptible) honeybee population

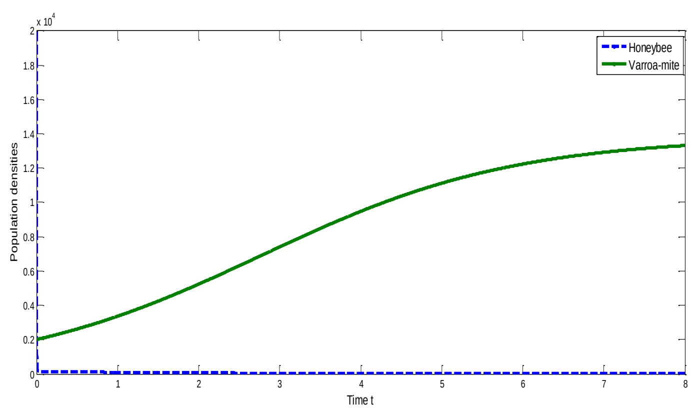

Figure 4: Impact of 2,000 virus-free *Varroa-mite* on the healthy (susceptible) honeybee population

It follows from the experiment that the initial population size of virus-free *Varroa-mite* plays an important role in sustaining or wiping off a healthy honeybee colony. The introduction of virus-free *Varroa-mite*s into a healthy honeybee colony was shown to have direct effects on the colony growth and can generate extinction mode on the dynamics of the colony population of honeybee as indicated from figure 1 through 4. Hence, with these numerical results, extinction of the honeybee colony is certain with *Varroa-mite* infestation as further claimed by ([23]). Furthermore, ([24, 16, 12]) confirmed that, without treatment, a colony of honeybee infested with *Varroa-mite* dies within one to three years.

Experiment 2: Impact of Initial Value of Infestation of Virus-Carrying *Varroa-mite* on Healthy Honeybee Population

In this experiment, the impact of initial value size of virus-carrying *Varroa-mite* on healthy honeybee population was studied. Parameter values used in table 3 alongside with the varied initial condition of virus-carrying *Varroa-mite* population is given as: $V_v(0)=100$, $V_v(0)=250$, $V_v(0)=500$ and $V_v(0)=700$ while initial population of honeybee is given as $S(0)=20000$. Therefore, the numerical results are given below:

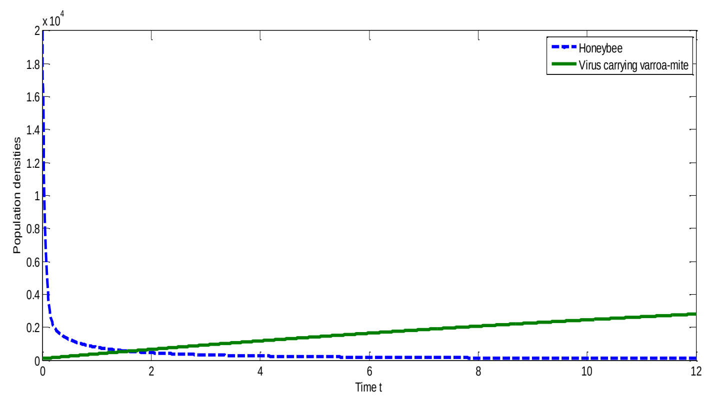

Figure 5: Impact of 500 virus-carrying *Varroa-mite* on the healthy (susceptible) honeybee population

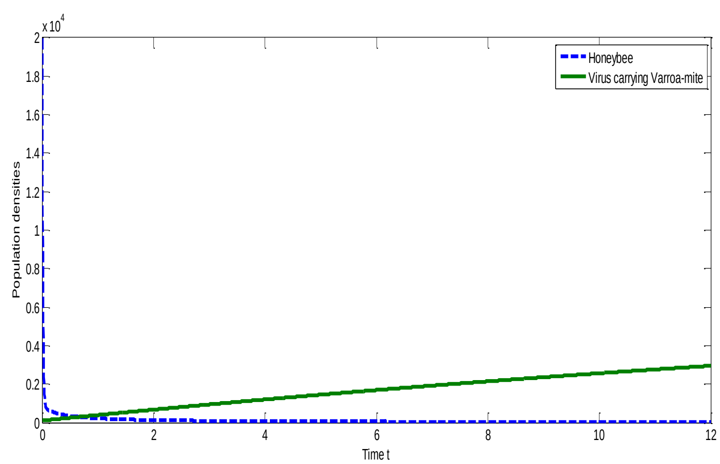

Figure 6: Impact of 700 virus-carrying *Varroa-mite* on the healthy (susceptible) honeybee population

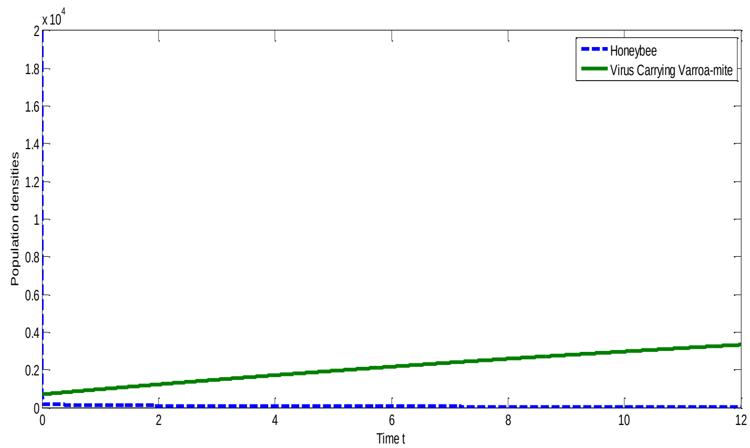

Figure 7: Impact of 1,000 virus-carrying *Varroa-mite* on the healthy (susceptible) honeybee population

The experiment hitherto studied had clearly explain the substantial role of the initial population size of virus-carrying *Varroa-mite* infesting healthy honeybee colony. This infestation encapsulates *Varroa-mite* plus virus invasion which has much higher impact than that of virus-free *Varroa-mite*. The experiment is clearly indicating that, a larger initial value of virus-carrying *Varroa-mite* has the ability to drive honeybee colonies to collapse within shortest possible time (4 months) as further verified by ([19]). Hence, such result highlights the impact of initial value of virus-carrying *Varroa-mite* as in figure 5 through 7.

Experiment 3: Impact of Treatment Using Thymol Powder on Honeybee Infested by *Varroa-mite*

In this experiment, impact of treatment using thymol powder on honeybee infested *Varroa-mite* is studied by considering different values of treatment rate: $\pi = 0$ $\pi = 0.2$, $\pi = 0.4$, $\pi = 0.6$ $\pi = 0.8$ and $\pi = 0.9$. The parameter values in Table 3 were used for this experiment with an initial condition $M(0) = 1000$. Hence, the numerical results are as follows:

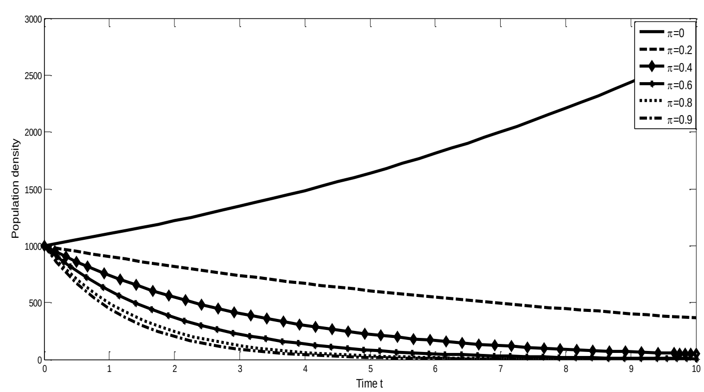

Figure 8: Impact of different treatment rate on honeybee population infested by *Varroa-mite*

From figure 8, it is clearly shown that honeybee infested by *Varroa-mite* is treated by applying thymol powder. Thus, as treatment rate increases the population of honeybee infested by *Varroa-mite* declines steadily.

Though, the honeybee population infested by *Varroa-mite* declines sharply at $\pi = 0.9$. This result confirmed that treatment is feasible when honeybee is infested by *Varroa-mite*.

Experiment 4: Impact of Initial Number of Biocontrol Agent (*Pseudoscorpion*) on *Varroa-mite*

In this experiment, the study examined the substantial impact of introducing a biocontrol agent (*Pseudoscorpion*) on the population of *Varroa-mite*. Obviously, the central focus of the experiment is to determine at what initial value of the biocontrol agent would be able to drive the population of *Varroa-mite* to extinction. This is achieved by varying the initial value of the biocontrol agent estimated as follows: $A_B(0) = 50$, $A_B(0) = 500$, $A_B(0) = 1,000$ and $A_B(0) = 1,500$. The population of *Varroa-mite* is estimated to have initial condition as: $V_f(0) = 2,500$ and $V_v(0) = 1,000$. The numerical results are given as below:

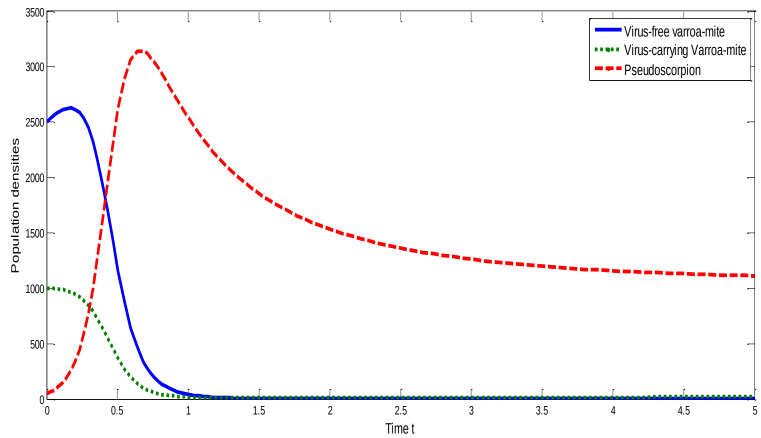

Figure 9: Impact of 50 *Pseudoscorpion* on both virus-free and virus-carrying *Varroa-mites*

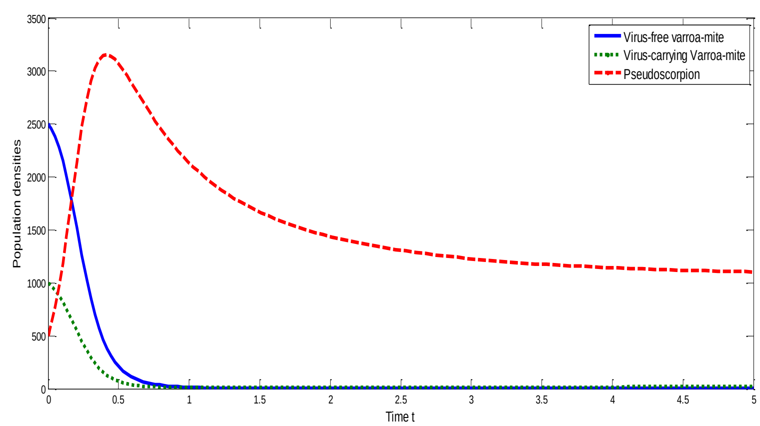

Figure 10: Impact of 500 *Pseudoscorpion* on both virus-free and virus-carrying *Varroa-mites*

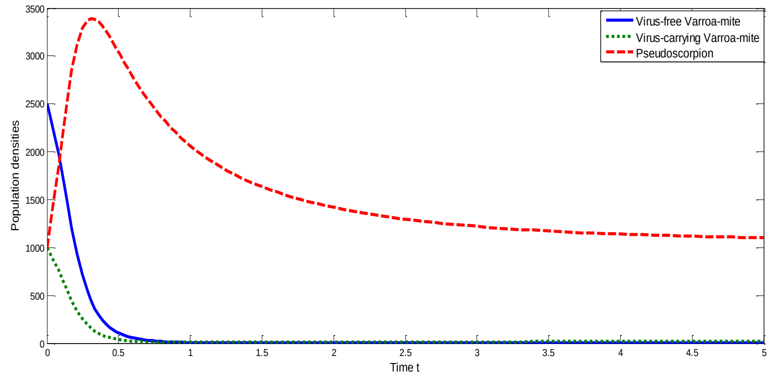

Figure 11: Impact of 1,000 *Pseudoscorpion* on both virus-free and virus-carrying *Varroa-mites*

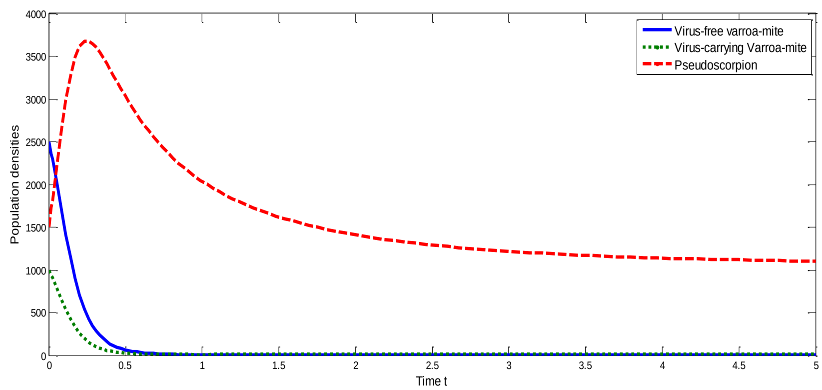

Figure 12: Impact of 1,500 *Pseudoscorpion* on both virus-free and virus-carrying *Varroa-mites*

The experiment results presented in figure 9 through figure 12 when *Pseudoscorpion* was introduced at varied initial values on *Varroa-mite* population purposely to pull stop to the infestation in the honeybee colony. It was clearly shown from figure 12 that, larger initial value (1,500) of *Pseudoscorpion* is capable of swiftly getting rid of *Varroa-mite* population within 5-6 months. Thus, this result indicated an efficiency in biological control of *Varroosis* in honeybee colony.

5 Conclusion

A mathematical model of *Varroosis* in honeybee colony was developed and analysed. The study established the existence of disease-free and infestation-free steady state, reproduction number and global stability analysis of the disease-free and infestation-free steady state of the model. The study aimed to pull stops to the spread of *Varroosis* in honeybee colony. It therefore, device an avenue of *Varroosis* control via treatment and biocontrol strategies. The numerical results have shown the impact of treatment using Thymol powder on honeybee infested by *Varroa-mite*. The result indicated significantly sharp decline of honeybee infested by *Varroa-mite* at $\pi = 0.9$. Similarly, numerical results revealed a little impact of introducing a lower initial population of biocontrol agent (*Pseudoscorpion*) on the *Varroa-mite* population. However, with larger initial population of *Pseudoscorpion* being introduced to *Varroa-mite* population much impact within a small time was observed. Using both treatment and biocontrol strategies are effective, but biocontrol is more effective and efficient with regards to time taken to eliminate *Varroa-mite*. Thus, the study findings suggest that, biocontrol when implemented, is the most effective and efficient in curbing the menace of *Varroosis*.

The study centrally focused on *Varroosis* impact on a single honeybee colony rather than intercolony transmission which naturally portrays the complexity of real-life phenomena. Also, honeybee and *Varroa-mite* interaction in discrete model which has truly quantitative predictive tool with desired accuracy has not been captured in this study.

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