MODELING THE TRANSMISSION DYNAMICS OF BANANA BUNCH TOP DISEASE IN BANANA PLANTS

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Abstract Banana Bunch Top Disease (BBTD) is a severe viral infection that poses a significant threat to banana production in tropical regions. Caused by the Banana Bunchy Top Virus (BBTV) and transmitted primarily by the banana aphid (*Pentalonia nigronervosa*), BBTD results in stunted growth and poor fruit production, leading to substantial economic losses. This paper presents a mathematical model to analyze the transmission dynamics of BBTD in banana plants and evaluate various control strategies using the Next Generation Matrix approach to compute the basic reproduction number R_0. The study reveals that effective control of aphid populations, timely removal of infected plants, and the use of virus-free planting material significantly reduce the spread of BBTV and improve plant health. Increasing the removal rate γ and managing the transmission rate β are crucial strategies for controlling the disease, while elevated aphid infection rates λ and progression rates σ exacerbate its spread. Numerical simulations highlight the effectiveness of targeted interventions, including the application of pesticides and the introduction of resistant banana varieties. The study recommends that, in addition to current control measures, more focus should be placed on comprehensive monitoring programs, early detection of symptoms, and community education on BBTD management strategies. Enhanced efforts in these areas are crucial to reducing the incidence of BBTD and improving the resilience of banana crops.

Key words: Banana Bunch Top Disease, Transmission Dynamics, Banana Plants, Mathematical Modeling, Disease Management.

AMS Mathematics Subject Classification: 34A45, 49K40, 93A30.

1 Introduction

Banana *(Musa spp.)*, a crucial staple crop, stands as a cornerstone of agricultural systems globally. Originating from the Indo-Malaysian region, bananas have transcended geographic boundaries, becoming a backbone in the world's agricultural landscape [2]. Spanning all continents, bananas are cultivated across both temperate and tropical zones [3]. They stand as an agricultural linchpin, serving as a primary food source and economic foundation for millions of individuals across the African continent [4]. Its annual cultivation, spanning approximately 5 million hectares, predominantly involves small-scale farmers who rely on bananas for sustenance and income generation [5]. Banana production is a major contributor to Tanzania's economy [6]. It is one of the most important crops that bolsters the country's agribusiness subsector which is projected to grow by 10 percent by 2030 [8]. Bananas have long been a staple in people's diets at the household level and have become ingrained in their culture due to their versatile uses in cooking and wine production [9]. All banana varieties are cultivated throughout the year. However, banana production is constrained by various diseases,

including Banana Bunch Top Disease (BBTD). BBTD is considered the most harmful viral infection impacting bananas on a global scale [13]. BBTD is an invasive virus disease that seriously threatens banana and plantain production in Africa and Asia [10]. Recent outbreaks in Tanzania and Uganda have highlighted banana bunchy top disease (BBTD) as a major threat to banana crops in East Africa. In Tanzania, BBTD was first identified in the Kigoma region in 2020, posing a significant threat to banana cultivation [7, 11]. The disease is widespread in susceptible cultivars across eleven major banana-growing regions: Arusha, Dar es Salaam, Dodoma, Geita, Katavi, Kigoma, Kilimanjaro, Mbeya, Morogoro, Mwanza, and Pwani [12]. BBTD is caused by the banana bunchy top virus (BBTV, genus Babuvirus) [7]. The virus spreads through two primary methods: locally via the banana aphid (Pentalonia nigronervosa) and through the vegetative propagation of infected planting materials [14]. Long-distance distribution occurs through the movement of infected suckers, corms, and tissue-cultured plantlets [16]. BBTD is not soil-borne and is unlikely to be transmitted through cutting tools [14, 15]. Aphids can carry the virus for several weeks and may travel significant distances, especially when carried by the wind. Additionally, plants can be infected even if they do not display symptoms [13]. The virus leads to severe production loss, with affected plants failing to produce fruit and total production potentially ceasing within two years, resulting in 80% to 100% loss [17]. Key symptoms include stunted growth, narrow and erect leaves with dark green streaks, and the distinctive 'bunchy' top appearance. Infected plants typically do not produce fruit and eventually die.

Figure 1: A sample of a banana plant infected with Banana Bunch Top Disease.

Effective control of Banana Bunch Top Disease can only be accomplished by destroying infected plants [18]. This relies on the swift identification and removal of affected stools [19]. Strict quarantine measures are enforced to prevent the spread of contaminated planting materials [20, 21]. Additionally, controlling the disease involves using virus-free planting materials and implementing thorough eradication programs [22, 23]. Routine monitoring of crops and immediate removal of symptomatic plants are essential [24]. Employing tissue-cultured, pest-free planting materials is recommended. Mathematical modeling is a valuable tool in controlling Banana Bunch Top Disease as it helps in understanding and managing the disease's spread and impact. Several mathematical models have been developed by researchers to understand the transmission dynamics of various plant diseases and to propose

effective control strategies [25], [27], [26], [28], [29]. Grajales-Amorocho et al. [30] conducted a study that analyzes the propagation of Moko disease in plantains using a system dynamics model. The study indicated that promptly removing infected plants is crucial for decreasing the prevalence of the disease. Manickam et al. [31] proposed a mathematical model using fractional-order Caputo derivatives to study Banana Xanthomonas Wilt Disease. The study highlights that adjusting the fractional order values can significantly influence the model's behavior, offering a more nuanced understanding of the disease's progression and potential control strategies. Agouanet et al. [32] explored Banana Black Sigatoka disease using a mathematical model that incorporates delay and seasonal variations. Their study offers insights into how these factors affect the disease's dynamics. The findings of the study emphasize the importance of considering both types of spore production in managing the disease with only one control measure. Nakakawa et al. [33] examined the dynamics of Banana Xanthomonas wilt in mixed cultivars within a periodic environment. Their study sheds light on how cultivar mixtures influence disease progression. The study find that cultivars with high susceptibility significantly contribute to the spread of BXW, and effective control measures need to be implemented, especially during the rainy season, to achieve eradication of the disease. Fotso et al. [35] explored the impact of climatic factors on the population dynamics of Radopholus similis, a pest affecting banana and plantain. The research shows that biological control methods are superior to chemical ones. It also suggests that February is the most effective time for implementing these controls. Despite extensive research on various plant diseases and their management through mathematical models, there is a noticeable gap in applying these models specifically to BBTD. The paper is organized as follows: Section 2 covers the BBTD model formulation. Section 3 details the qualitative analysis of the BBTD model. Section 4 presents the results of numerical simulation, including algorithms and stability. In Section 5, sensitivity analysis of model is discussed. Section 6 shows graphical simulations of BBTD dynamics. Section 7 concludes with findings, implications, and future research recommendations.

2   BBTD Model Formulation

In this section, a compartment model is constructed to capture the transmission dynamics of Banana Bunch Top Disease (BBTD) among banana plants and the role of banana aphids in spreading the disease. The banana plant population (N_p) is divided into four compartments: Susceptible plants (S_p), which are at risk of infection; Exposed plants (E_p), which have been exposed to the Banana Bunchy Top Virus (BBTV) but are not yet symptomatic; Infected plants (I_p), which are currently infected and capable of transmitting the virus; and Removed plants (R_p), which have been removed from the population due to disease management. Thus, $N_p = S_p + E_p + I_p + R_p$. The dynamics entails that, susceptible plants S_p are introduced at a rate given by new seedlings denoted by Λ and become exposed E_p at a rate β through contact with infected plants I_p, with a natural death rate μ_p affecting all plant compartments. Exposed plants progress to the infected state I_p at a rate σ, and infected plants are removed from the system at a rate γ. The vector population (N_v) consists of Susceptible *aphids* (V_s) and Infected *aphids* (V_i). The dynamics of aphids are described by differential equations where V_s increase through a birth rate and decrease through natural death and infection at a rate λ when feeding on infected plants, leading to the transition of V_s to V_i. The model integrates these components to understand how BBTV spreads and to evaluate potential control measures.

Table 1: Model parameters and their description

Parameter	Description	Value	Source
Λ	New seedlings introduction rate	0.01667	[36]
β	Transmission rate from infected plants to susceptible plants	0.05	Estimated
μ_p	Natural death rate of plants	0.01	Estimated
σ	Progression rate from exposed to infected plants	0.03	Estimated
γ	Removal rate of infected plants	0.5	[31]
η	Natural birth rate of aphids	0.02	[36]
λ	Infection rate of aphids feeding on infected plants	0.04	Estimated
μ_v	Natural death rate of aphids	0.02	[36]

2.1 Compartmental Flow Diagram of Banana Bunch Top Disease Transmission Dynamics

A compartmental flow diagram illustrates the stages of disease transmission and the states of infection within a population of banana plants. Figure 1 depicts the relationships between
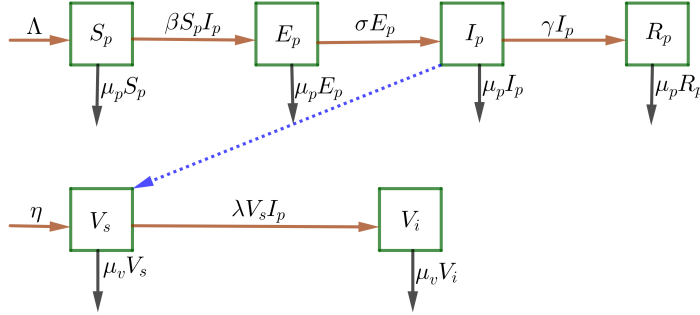

Figure 2: A schematic diagram for transmission dynamics of BBTD. The sold line indicates the rate of transfer into and out of the populations. The dotted lines indicates the usual interactions among populations.

Susceptible plants, Exposed plants, Infected plants, and Removed plants, along with the dynamics involving the banana aphid vector population. The following system of differential equations describe the dynamics:

$$
\begin{aligned}
\frac{dS_p}{dt} &= \Lambda - \beta S_p I_p - \mu_p S_p, & \frac{dR_p}{dt} &= \gamma I_p - \mu_p R_p, \\
\frac{dE_p}{dt} &= \beta S_p I_p - \sigma E_p - \mu_p E_p, & \frac{dV_s}{dt} &= \eta - \lambda V_s I_p - \mu_v V_s, \\
\frac{dI_p}{dt} &= \sigma E_p - \gamma I_p - \mu_p I_p, & \frac{dV_i}{dt} &= \lambda V_s I_p - \mu_v V_i.
\end{aligned}
\tag{1}
$$

3 Qualitative Analysis of the Model

3.1 Non-negativity of Solution

To ensure the ecological and epidemiological relevance of the model and to establish its mathematical robustness, it is crucial to demonstrate that all variables in the system, beginning with positive initial values, will remain non-negative as time progresses ($t \geq 0$).

Theorem. *For the model (1), the region* $\Omega_+ = \{(S_p, E_p, I_p, R_p, V_s, V_i), S_p \geq 0, E_p \geq 0, I_p \geq 0, R_p \geq 0, V_s \geq 0, V_i \geq 0\}$ *is a positive invariant.*

Proof. From the model system (1), we have:

$$\left.\frac{dS_p}{dt}\right|_{S_p=0} = \Lambda > 0, \qquad \left.\frac{dE_p}{dt}\right|_{E_p=0} = \beta S_p I_p > 0, \qquad \left.\frac{dI_p}{dt}\right|_{I_p=0} = \sigma E_p \geq 0,$$

$$\left.\frac{dR_p}{dt}\right|_{R_p=0} = \gamma I_p \geq 0, \qquad \left.\frac{dV_s}{dt}\right|_{V_s=0} = \eta > 0, \qquad \left.\frac{dV_i}{dt}\right|_{V_i=0} = \lambda V_s I_p \geq 0. \tag{2}$$

Therefore, the solutions remain within the region Ω_+ for all time. $\qquad\square$

3.2 Invariant region

In this subsection, we investigate whether model variables have biological interpretation and a unique bounded solution that exists for all the time. From the model system (1), we have:

Theorem. *For the model* (1), *the region* $\Omega_+ = \{(S_p, E_p, I_p, R_p, V_s, V_i) \in \mathbb{R}^6 \mid S_p \geq 0, E_p \geq 0, I_p \geq 0, R_p \geq 0, V_s \geq 0, V_i \geq 0\}$ *is a positive invariant.*

Proof. Let the total banana plant population be defined as:

$$N_p(t) = S_p(t) + E_p(t) + I_p(t) + R_p(t).$$

From the model equations, we compute the derivative of N_p:

$$\frac{dN_p}{dt} = \frac{dS_p}{dt} + \frac{dE_p}{dt} + \frac{dI_p}{dt} + \frac{dR_p}{dt}. \tag{3}$$

Substituting from equations (1), we get:

$$\frac{dN_p}{dt} = (\Lambda - \beta S_p I_p - \mu_p S_p) + (\beta S_p I_p - \sigma E_p - \mu_p E_p) + (\sigma E_p - \gamma I_p - \mu_p I_p) + (\gamma I_p - \mu_p R_p).$$

Simplifying, we obtain:

$$\frac{dN_p}{dt} = \Lambda - \mu_p N_p.$$

From this differential equation, we derive the inequality:

$$\frac{dN_p}{dt} \leq \Lambda - \mu_p N_p. \tag{4}$$

Integrating (6) from 0 to t:

$$\int_0^t \frac{dN_p}{\Lambda - \mu_p N_p} \leq \int_0^t dt \quad \Rightarrow \quad \left. -\frac{1}{\mu_p} \ln(\Lambda - \mu_p N_p) \right|_0^t \leq t.$$

Exponentiating both sides gives:

$$\frac{\Lambda - \mu_p N_p(t)}{\Lambda - \mu_p N_p(0)} \geq e^{-\mu_p t}.$$

Rearranging for $N_p(t)$:

$$N_p(t) \leq \frac{\Lambda}{\mu_p} - \left(\frac{\Lambda - \mu_p N_p(0)}{\mu_p}\right) e^{-\mu_p t}.$$

Therefore, the feasible region for the banana plant population, ensuring that the total population $N_p(t)$ does not exceed $\frac{\Lambda}{\mu_p}$, is:

$$\Gamma = \{(S_p(t), E_p(t), I_p(t), R_p(t)) \in \mathbb{R}^4 \mid N_p(t) \leq \frac{\Lambda}{\mu_p}\}.$$

Similarly, let the total aphid population be defined as:

$$N_v(t) = V_s(t) + V_i(t).$$

From the model equations, we compute the derivative of N_v:

$$\frac{dN_v}{dt} = \frac{dV_s}{dt} + \frac{dV_i}{dt}. \tag{5}$$

Substituting from equations (1), we get:

$$\frac{dN_v}{dt} = (\eta - \lambda V_s I_p - \mu_v V_s) + (\lambda V_s I_p - \mu_v V_i).$$

Simplifying, we obtain:

$$\frac{dN_v}{dt} = \eta - \mu_v N_v.$$

From this differential equation, we derive the inequality:

$$\frac{dN_v}{dt} \leq \eta - \mu_v N_v. \tag{6}$$

Integrating (6) from 0 to t:

$$\int_0^t \frac{dN_v}{\eta - \mu_v N_v} \leq \int_0^t dt \quad \Rightarrow \quad -\frac{1}{\mu_v} \ln(\eta - \mu_v N_v)\Big|_0^t \leq t.$$

Exponentiating both sides gives:

$$\frac{\eta - \mu_v N_v(t)}{\eta - \mu_v N_v(0)} \geq e^{-\mu_v t}.$$

Rearranging for $N_v(t)$:

$$N_v(t) \leq \frac{\eta}{\mu_v} - \left(\frac{\eta - \mu_v N_v(0)}{\mu_v}\right) e^{-\mu_v t}.$$

Therefore, the feasible region for the aphid population, ensuring that the total population $N_v(t)$ does not exceed $\frac{\eta}{\mu_v}$, is:

$$\Gamma_v = \{(V_s(t), V_i(t)) \in \mathbb{R}^2 \mid N_v(t) \leq \frac{\eta}{\mu_v}\}.$$

Thus, combining both feasible regions, the total feasible region for the model (1), ensuring that the populations remain bounded, is:

$$\Omega = \{(S_p(t), E_p(t), I_p(t), R_p(t), V_s(t), V_i(t)) \in \mathbb{R}^6 \mid N_p(t) \leq \frac{\Lambda}{\mu_p}, N_v(t) \leq \frac{\eta}{\mu_v}\}.$$

$\square$

3.3   BBTD-Free Equilibrium Point (DFE)

The BBTD-free equilibrium point E^0, is found by setting the equations of model system (1) to zero:

$$E^0 = \left(S_p^0, E_p^0, I_p^0, R_p^0, V_s^0, V_i^0\right) = \left(\frac{\Lambda}{\mu_p}, 0, 0, 0, \frac{\eta}{\mu_v}, 0\right) \tag{7}$$

3.4   Basic Reproduction Number

The basic reproduction number, referred to as R_0, represents the average count of secondary infections potentially arising when a single infected individual is introduced into a susceptible population [34]. By considering the disease compartments, R_0 can be computed as follows:

$$\dot{X}_i = F_i(x) - V_i(x) \tag{8}$$

Computing the Matrices $\mathcal{F}_i$ and $\mathcal{V}_i$:

$$\dot{X}_i = \begin{bmatrix} \beta S_p I_p \\ 0 \\ \lambda V_s I_p \\ 0 \end{bmatrix} - \begin{bmatrix} \sigma E_p + \mu_p E_p \\ -\sigma E_p + \gamma I_p + \mu_p I_p \\ -\lambda V_s I_p + \mu_v V_s \\ \lambda V_s I_p - \mu_v V_i \end{bmatrix} \tag{9}$$

For the compartments E_p, I_p and V_i:

$$\mathcal{F}_i = \begin{bmatrix} \beta S_p I_p \\ 0 \\ \lambda V_s I_p \\ 0 \end{bmatrix}, \qquad \mathcal{V}_i = \begin{bmatrix} \sigma E_p + \mu_p E_p \\ -\sigma E_p + \gamma I_p + \mu_p I_p \\ -\lambda V_s I_p + \mu_v V_s \\ \lambda V_s I_p - \mu_v V_i \end{bmatrix}$$

Computing the Jacobian matrices for $\mathcal{F}_i$ and $\mathcal{V}_i$ at the BBTD-free equilbrium point gives:

$$F = \frac{\partial \mathcal{F}_i}{\partial(E_p, I_p, V_i)} = \begin{bmatrix} 0 & \beta\frac{\Lambda}{\mu_p} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & \lambda\frac{\eta}{\mu_v} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \quad V = \frac{\partial \mathcal{V}_i}{\partial(E_p, I_p, V_i)} = \begin{bmatrix} \sigma+\mu_p & 0 & 0 & 0 \\ -\sigma & \gamma+\mu_p & 0 & 0 \\ 0 & 0 & \mu_v & 0 \\ 0 & 0 & -\lambda\frac{\eta}{\mu_v} & \mu_v \end{bmatrix}$$

The inverse of V is:

$$V^{-1} = \begin{bmatrix} \frac{1}{\sigma+\mu_p} & 0 & 0 & 0 \\ \frac{\sigma}{(\sigma+\mu_p)(\gamma+\mu_p)} & \frac{1}{\gamma+\mu_p} & 0 & 0 \\ 0 & 0 & \frac{1}{\mu_v} & 0 \\ 0 & 0 & \frac{\lambda\frac{\eta}{\mu_v}}{\mu_v^2} & \frac{1}{\mu_v} \end{bmatrix}$$

Thus, FV^{-1} gives:

$$FV^{-1} = \begin{bmatrix} 0 & \beta\frac{\Lambda}{\mu_p}\frac{\sigma}{(\sigma+\mu_p)(\gamma+\mu_p)} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & \lambda\frac{\eta}{\mu_v}\frac{1}{\mu_v} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

The basic reproduction number R_0 is the spectral radius of FV^{-1} which gives:

$$R_0 = \beta\frac{\Lambda}{\mu_p}\left(\frac{\sigma}{(\sigma+\mu_p)(\gamma+\mu_p)}\right) + \lambda\frac{\eta}{\mu_v^2}$$

This simplifies to:

$$R_0 = \frac{\beta \Lambda}{\mu_p(\gamma + \mu_p)} \left(\frac{\sigma}{\sigma + \mu_p} \right) + \frac{\lambda \eta}{\mu_v^2}$$

Thus, The basic reproduction number R_0 is given by:

$$R_0 = \frac{\beta \Lambda}{\mu_p(\gamma + \mu_p)} \left(\frac{\sigma}{\sigma + \mu_p} \right) + \frac{\lambda \eta}{\mu_v^2}$$

3.5 Local Stability of BBTD-Free Equilbrium

Theorem. *The BBTD-free equilbrium point for the model system (1) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.*

Proof. To prove the local stability of the equilibrium point free of BBTD, we demonstrate that the eigenvalues of the Jacobian matrix of the model system (1) at the BBTD-free equilibrium point are all negative. The Jacobian matrix for the model system (1) is given by:

$$J(E_0) = \begin{bmatrix} -\mu_p & 0 & -\beta\frac{\Lambda}{\mu_p} & 0 & 0 & 0 \\ 0 & -(\sigma + \mu_p) & \beta\frac{\Lambda}{\mu_p} & 0 & 0 & 0 \\ 0 & \sigma & -(\gamma + \mu_p) & 0 & 0 & 0 \\ 0 & 0 & \gamma & -\mu_p & 0 & 0 \\ 0 & 0 & -\lambda\frac{\eta}{\mu_v} & 0 & -\mu_v & 0 \\ 0 & 0 & \lambda\frac{\eta}{\mu_v} & 0 & 0 & -\mu_v \end{bmatrix}$$

We observe that the Jacobian matrix $J(E_0)$ at the BBTD-free equilibrium has the eigenvalues $\lambda_1 = -\mu_p$, $\lambda_2 = -(\sigma + \mu_p)$, $\lambda_3 = -(\gamma + \mu_p)$, $\lambda_4 = -\mu_p$, $\lambda_5 = -\mu_v$, and $\lambda_6 = -\mu_v$ as its eigenvalues. Since all eigenvalues are negative. Hence, the BBTD-free equilibrium point is locally asymptotically stable.   □

3.6 Global Stability of BBTD-Free Equilbrium Points

To analyze the global stability of the disease-free equilibrium of the model system, we employ the Castillo-Chavez approach [1]. Using this approach, the model system (1) can be expressed as:

$$\frac{dX_n}{dt} = B_1(X_n - X_{E_0}) + B_{12}X_i,$$

$$\frac{dX_i}{dt} = B_2 X_i$$

where, X_n represents the non-transmitting state variables, X_i represents the transmitting state variables and X_{E_0} denotes X_n at the disease-free equilibrium point.

The matrices B_1 and B_{12} are obtained by differentiating the non-transmitting equations of the model system to non-transmitting and transmitting state variables, respectively. If the real parts of the eigenvalues of B_1 are negative and B_2 is a Metzler matrix (i.e., its off-diagonal components are non-negative), then the disease-free equilibrium point is globally asymptotically stable. Thus, based on the model system (1):

$$B_1 = \begin{bmatrix} -\mu_p & 0 & 0 \\ 0 & -\mu_v & 0 \\ 0 & 0 & -\mu_p \end{bmatrix}, \quad B_{12} = \begin{bmatrix} -\beta I_p & 0 & 0 \\ 0 & -\lambda V_s & 0 \\ 0 & 0 & 0 \end{bmatrix}, \quad B_2 = \begin{bmatrix} -\sigma - \mu_p & \sigma & 0 \\ \beta S_p & -\gamma - \mu_p & \lambda V_s \\ 0 & 0 & -\mu_v \end{bmatrix}$$

It can be seen that, the eigenvalues are both negative. Likewise, it can be noted that, the matrix B_2 qualifies as a Metzler matrix because its off-diagonal elements are non-negative. Therefore, the system

$$\frac{dX_n}{dt} = B_1(X_n - X_{E_0}) + B_{12}X_i$$

at the BBTD-free equilbrium point, is globally asymptotically stable.

3.7 Endemic Equilbrium Points

These points represents a situation where the disease persists in the banana plantation at a constant level. This means that despite the ongoing presence of the disease, the number of infected plants and other variables stabilize over time. The endemic equilibrium points are given by the following expressions:

$$S^* = \frac{\Lambda(\sigma+\mu_p)^2(\gamma+\mu_p)}{\beta^2\sigma^2+\mu_p(\sigma+\mu_p)^2(\gamma+\mu_p)}, \qquad E^* = \frac{\beta S^*\sigma}{(\sigma+\mu_p)(\gamma+\mu_p)}, \qquad I^* = \frac{\beta S^*\sigma^2}{(\sigma+\mu_p)^2(\gamma+\mu_p)},$$

$$R^* = \frac{\gamma I^*}{\mu_p}, \qquad V_s^* = \frac{\eta}{\lambda I^* + \mu_v}, \qquad V_i^* = \frac{\lambda V_s^* I^*}{\mu_v}.$$

3.8 Global Stability of Endemic Equilibrium Points

Theorem. *The BBTD-endemic equilibrium point of the model system (1) is globally asymptotically stable on Ω if $R_0 > 1$.*

Proof.

$$L = P_1\left(S_p - S_p^* - S_p^*\ln\frac{S_p}{S_p^*}\right) + P_2\left(E_p - E_p^* - E_p^*\ln\frac{E_p}{E_p^*}\right) + P_3\left(I_p - I_p^* - I_p^*\ln\frac{I_p}{I_p^*}\right)$$

$$+ P_4\left(R_p - R_p^* - R_p^*\ln\frac{R_p}{R_p^*}\right) + P_5\left(V_s - V_s^* - V_s^*\ln\frac{V_s}{V_s^*}\right) + P_6\left(V_i - V_i^* - V_i^*\ln\frac{V_i}{V_i^*}\right).$$

where P_i are positive constants, and $S_p^*, E_p^*, I_p^*, R_p^*, V_s^*, V_i^*$ are equilibrium values. The Lyapunov function L is zero at the equilibrium $E^* = (S_p^*, E_p^*, I_p^*, R_p^*, V_s^*, V_i^*)$ and positive for all other values. Then:

$$\frac{dL}{dt} = P_1\left(1 - \frac{S_p^*}{S_p}\right)\frac{dS_p}{dt} + P_2\left(1 - \frac{E_p^*}{E_p}\right)\frac{dE_p}{dt} + P_3\left(1 - \frac{I_p^*}{I_p}\right)\frac{dI_p}{dt}$$

$$+ P_4\left(1 - \frac{R_p^*}{R_p}\right)\frac{dR_p}{dt} + P_5\left(1 - \frac{V_s^*}{V_s}\right)\frac{dV_s}{dt} + P_6\left(1 - \frac{V_i^*}{V_i}\right)\frac{dV_i}{dt}. \qquad (10)$$

Substituting the derivatives from (1) into (10), we get:

$$\frac{dL}{dt} = P_1\left(1 - \frac{S_p^*}{S_p}\right)(\Lambda - \beta S_p I_p - \mu_p S_p) + P_2\left(1 - \frac{E_p^*}{E_p}\right)(\beta S_p I_p - \sigma E_p - \mu_p E_p)$$

$$+ P_3\left(1 - \frac{I_p^*}{I_p}\right)(\sigma E_p - \gamma I_p - \mu_p I_p) + P_4\left(1 - \frac{R_p^*}{R_p}\right)(\gamma I_p - \mu_p R_p) \qquad (11)$$

$$+ P_5\left(1 - \frac{V_s^*}{V_s}\right)(\eta - \lambda V_s I_p - \mu_v V_s) + P_6\left(1 - \frac{V_i^*}{V_i}\right)(\lambda V_s I_p - \mu_v V_i).$$

$$\frac{dL}{dt} = -P_1\beta S_p I_p \left(\frac{S_p^*}{S_p} - 1\right) - P_2\sigma E_p \left(\frac{E_p^*}{E_p} - 1\right) - P_3\gamma I_p \left(\frac{I_p^*}{I_p} - 1\right)$$
$$- P_4\mu_p R_p \left(\frac{R_p^*}{R_p} - 1\right) - P_5\lambda V_s I_p \left(\frac{V_s^*}{V_s} - 1\right) - P_6\mu_v V_i \left(\frac{V_i^*}{V_i} - 1\right). \tag{12}$$

The terms in (12) are all non-positive. Hence, $\frac{dL}{dt} \leq 0$. Using LaSalle's extension to Lyapunov's method, the limit set of each solution is contained in the largest invariant set where $S_p = S_p^*$, $E_p = E_p^*$, $I_p = I_p^*$, $R_p = R_p^*$, $V_s = V_s^*$, and $V_i = V_i^*$. This implies that the endemic equilibrium point E^* is globally asymptotically stable when $R_0 > 1$. $\qquad\square$

4 Sensitivity analysis

To identify the parameters that most significantly impact the basic reproduction number, a sensitivity analysis is conducted. This analysis pinpoints the parameter with the greatest influence on the basic reproduction number, guiding where control efforts should be focused to reduce disease transmission. The sensitivity index of R_0 is determined using the normalized forward sensitivity index, expressed as

$$\Delta_{R_0}^Y = \frac{\partial R_0}{\partial Y} \times \frac{Y}{R_0}$$

where Y represents a parameter affecting R_0. For instance, the sensitivity index for the parameter η is calculated as

$$\Delta_{R_0}^\eta = \frac{\partial R_0}{\partial \eta} \times \frac{\eta}{R_0} = +0.9422523990.$$

Table 2: Sensitivity Indices

Parameter	Index
Λ	+0.05774760108
β	+0.05774760108
σ	+0.01443690027
λ	+0.9422523990
η	+0.9422523990
μ_p	-0.07331680726
μ_v	-1.884504798
γ	-0.05661529514

Similar methods are used to calculate indices for other parameters, with the findings summarized in Table 2 and illustrated in Figure 3.

From Table 2, it is clear that parameters such as Λ, β, λ, σ and η have positive indices. This means that increasing these parameters, while keeping others unchanged, will elevate the basic reproduction number, thus raising the risk of a disease outbreak. In contrast, parameters like μ_p, μ_v, and γ have negative indices. This signifies that raising these parameters, with others held constant, will lower the basic reproduction number, thereby reducing the disease burden. Enhancing control-related parameters (μ_p, μ_v, γ) results in a decrease in the basic reproduction number (R_0). This finding indicates that effectively applying these control measures in an endemic area will help mitigate the spread of the disease.
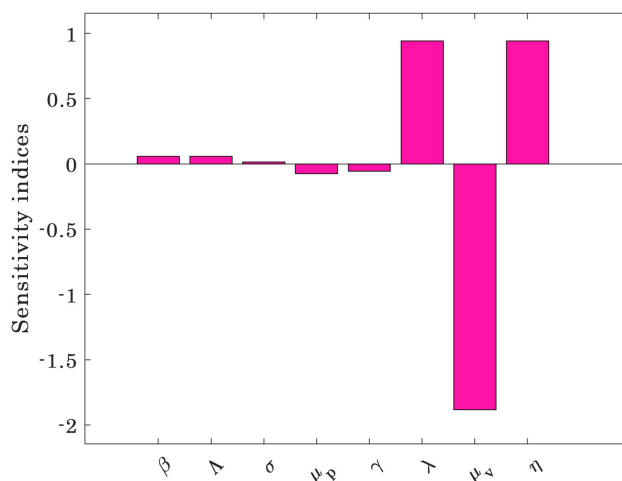
Figure 3: Sensitivity analysis of the basic reproduction number R_0 to model parameters.

5 Numerical Simulation and Discussion

In this section, we perform numerical simulations to explore the dynamics of the proposed model over a time interval. The goal is to visualize and analyze the behavior of the model using graphical representations. We initialize the simulation with the following conditions: $S_p(0) = 4{,}000$, $E_p(0) = 500$, $I_p(0) = 200$, $R_p(0) = 10$, $V_s(0) = 3{,}500$ and $V_i(0) = 500$. These initial values are chosen to represent a plausible starting point for the simulation, providing a basis for understanding how the system evolves over time. The results of the simulations are presented graphically to illustrate the dynamics of the compartments and to gain insights into the behavior of the disease model under various conditions.

5.1 BBTD prevalence trend over time in the population

This involves tracking and analyzing changes in the proportion of banana plants infected with Banana Bunch Top Disease (BBTD) over a defined period. Figure 2 and Figure 3 illustrates the trend in the prevalence of Banana Bunch Top Disease (BBTD) within the population of banana plants over the specified time period.

As shown in Figure 4, the number of infected plants tends to decrease over time, while the number of removed plants tends to increase. This trend indicates that removal or treatment practices are successful in controlling the spread of the disease and reducing the number of infected plants. Similarly, the number of infected aphids decreases as the number of infected plants declines over time. Since aphids are known vectors of BBTD, a reduction in their infection rate suggests that controlling the primary source of infection (i.e., the infected plants) also helps to lower the disease burden in the aphid population.

5.2 BBTD prevalence trend with and without intervention

This examines how the proportion of banana plants affected by Banana Bunch Top Disease (BBTD) changes after implementing control measures or interventions. By tracking the prevalence of BBTD before and after the intervention, it is possible to assess the impact and effectiveness of these measures over time. Figure 4 shows the BBTD trend over time with and
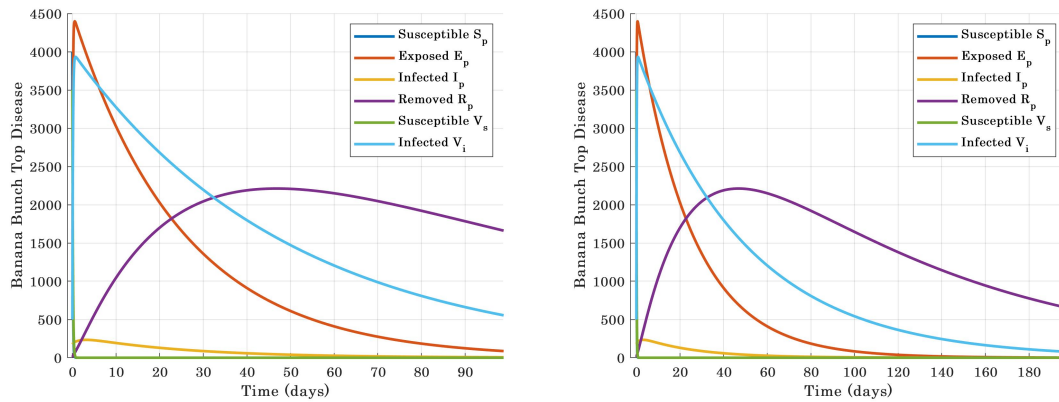
(a) Evolution of BBTD model over the time (b) Evolution of BBTD model over the time
$t \in [0, 100]$. $t \in [0, 200]$.

Figure 4: Time evolution of BBTD model.

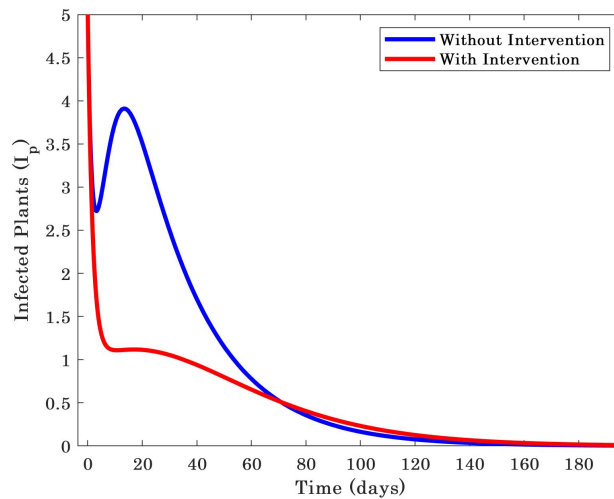without intervention. As shown in Figure 5, applying interventions such as removing infected

Figure 5: Evolution of Banana bunch top disease with and without intervention.

plants, applying pesticides to control aphid vectors, or introducing resistant banana varieties typically lead to a decline in BBTD prevalence, indicating a reduction in the disease's spread and impact. In contrast, without such measures, the disease trend remains high, reflecting an increase in the spread and impact of BBTD. These findings underscore the importance of ongoing monitoring, effective pest control, and farmer education to manage and mitigate the disease.

5.3   Effects of varying parameter values on BBTD spread

This section examines the effects of varying key parameters on the dynamics of Banana Bunch Top Disease (BBTD). Figures reveal how changes in specific parameters influence disease spread and aphid populations. As it can be noted in Figure 6 increasing the removal

rate parameter γ in Figure 6a reduces the number of infected plants (I_p), indicating improved disease control. On the other hand, when the rate at which aphids become infected by feeding on infected plants (λ) in Figure 6b and Figure 6c is higher, it leads to more susceptible aphids (V_s) and a greater number of infected aphids (V_i). This illustrates how crucial transmission dynamics are in the spread of the disease. Additionally, variations in transmission rates (β) in Figure 6d and progression rates (σ) in Figure 6e significantly affect the number of exposed plants (E_p) and infected plants (I_p) respectively. Higher values of β and σ contribute to a greater spread of the disease by increasing both the number of plants exposed to and infected by the pathogen. Effective management of these parameters is essential for controlling BBTD and minimizing its impact on banana crops.

5.4 Effects of Parameter Combinations on Basic Reproduction Number R_0

This section evaluates how various parameters influence the basic reproduction number R_0, which is crucial for understanding disease spread. Figure 7 presents the results from numerical simulations exploring the combined effects of these parameters on R_0. Figure 7a illustrates the impact of varying transmission rates (β) and removal rates (γ) on R_0. As depicted, increasing γ reduces the number of infected plants (I_p), suggesting that higher removal rates improve disease control. Figure 7b shows the effect of varying transmission rates (β) and aphid infection rates (λ) on R_0. Higher values of λ lead to more susceptible aphids (V_s) and a greater number of infected aphids (V_i), underscoring the critical role of transmission dynamics. Figure 7c highlights how changes in transmission rates (β) and progression rates (σ) affect R_0. Increased β and σ result in more exposed plants (E_p) and infected plants (I_p), indicating that higher transmission and progression rates contribute to a greater spread of the disease. Figure 7d examines the combined effects of aphid death rates (η) and infection rates (λ) on R_0. Variations in these parameters show how changes in aphid mortality and infection rates impact disease spread. Figure 7e depicts the influence of plant death rates (μ_p) and aphid death rates (μ_v) on R_0.
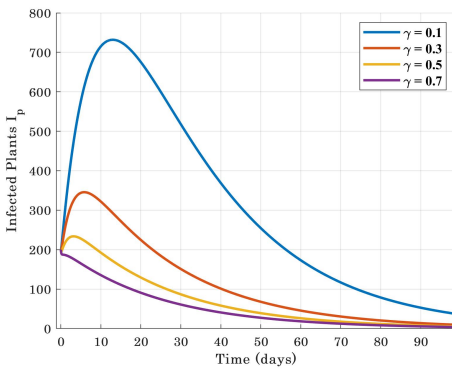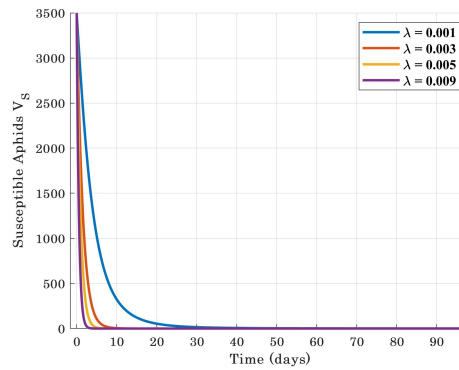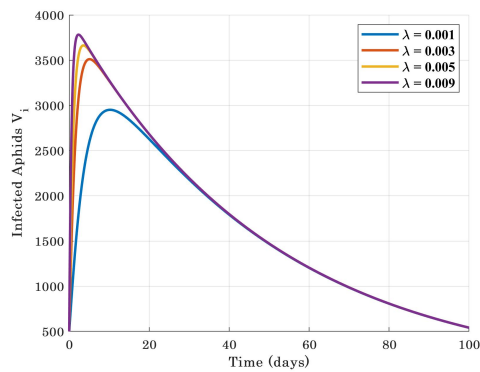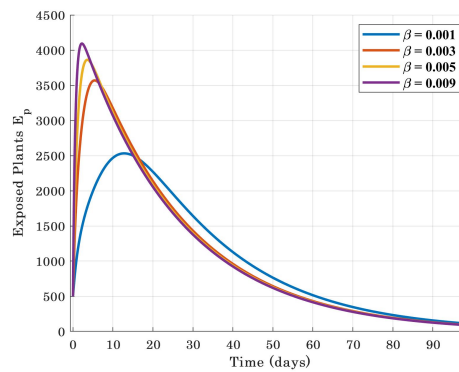
(a) Effects of varying γ on I_p.

(b) Effects of varying λ on V_s.

(c) Effects of varying λ on V_i.

(d) Effects of varying β on E_p.
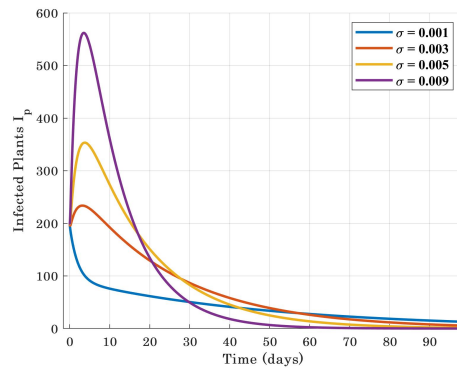
(e) Effects of varying σ on I_p.

Figure 6: Effects of varying parameters on different aspects of the model: (a) γ on I_p, (b) λ on V_s, (c) λ on V_i, (d) β on E_p, (e) σ on I_p.

Increasing either mortality rate generally lowers R_0, as higher death rates reduce the number of susceptible hosts. Figure 7f focuses on the impact of progression rates (σ) and removal rates (γ) on R_0. Higher values of both parameters are associated with an increase in R_0, highlighting the importance of both progression and removal rates in disease dynamics. Effective management of these parameters is essential for controlling the spread of the disease and minimizing its impact on banana crops.
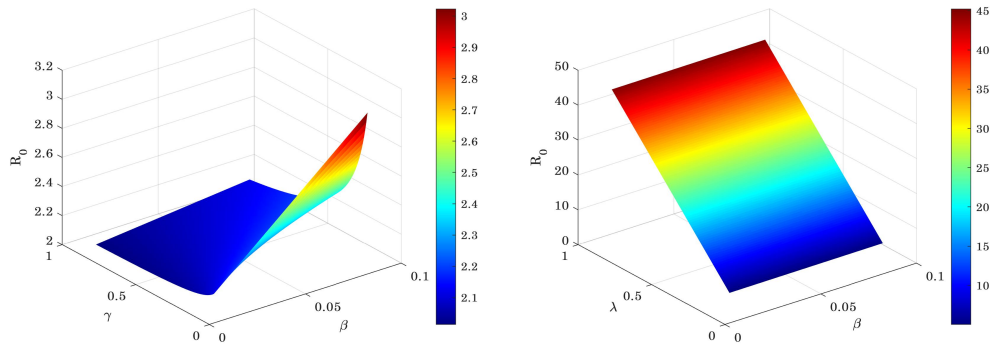
(a) Impact of combined effect of β and γ on R_0.

(b) Impact of combined effect of β and λ on R_0.
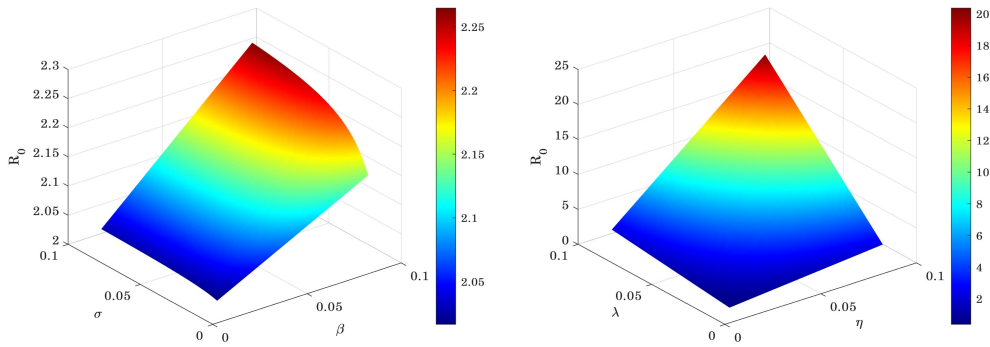
(c) Impact of combined effect of β and σ on R_0.

(d) Impact of combined effect of η and λ on R_0.
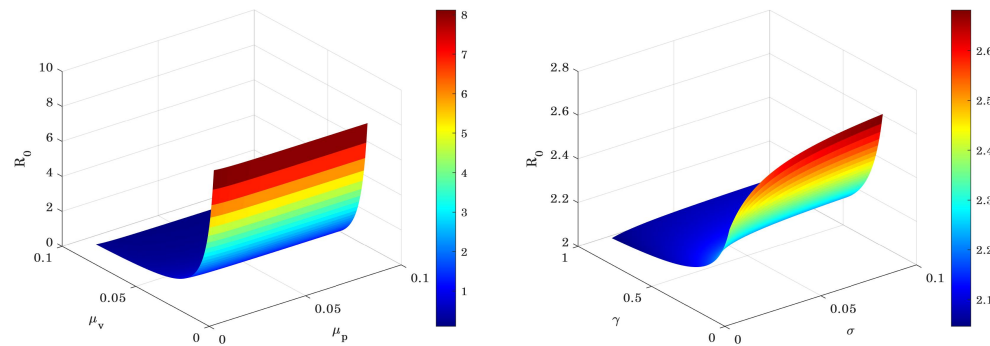
(e) Impact of combined effect of μ_p and μ_v on R_0.

(f) Impact of combined effect of σ and γ on R_0.

Figure 7: Effects of varying parameters on R_0: (a) β and γ, (b) β and λ, (c) β and σ, (d) η and λ, (e) μ_p and μ_v, (f) σ and γ.

6   Conclusion

This study focuses on creating and analyzing a mathematical model to capture the transmission dynamics and control strategies for Banana Bunchy Top Disease (BBTD) in banana crops. Utilizing the Next Generation Matrix approach to compute the basic reproduction

number R_0 has been crucial in defining the conditions for equilibrium point stability and existence. The study reveals that the spread of BBTD is significantly affected by various parameters. Specifically, increasing the removal rate γ and effectively managing the transmission rate β are essential strategies for reducing the number of infected plants and controlling the disease. Conversely, elevated aphid infection rates λ and progression rates σ exacerbate the spread of the disease, highlighting the critical need to manage these parameters to mitigate the impact of BBTD. From the findings, to effectively manage BBTD, several policy changes and recommendations should be implemented at regional or national levels. Guidelines for banana farmers should include routine monitoring and removal of infected plants, the use of resistant varieties, and training in integrated pest management practices. Agricultural extension services should focus on capacity building, providing training and resources to farmers, and supporting disease management. Government interventions are essential, such as establishing regulations for mandatory reporting and monitoring of BBTD, increasing funding for research and development of resistant varieties, and launching public awareness campaigns to educate the community. Coordinated regional task forces and a comprehensive national policy framework should also be developed to ensure uniform control measures and facilitate effective disease management across different regions. These policies and interventions will enhance disease control, promote sustainable agricultural practices, and improve the livelihoods of banana farmers. Despite these findings, the study is limited by its assumption of homogeneity in banana plant populations and does not account for seasonal variations or potential differences in plant susceptibility. Additionally, the model could be enhanced by considering more detailed data on aphid behavior and environmental factors influencing disease dynamics. Future research should focus on incorporating these aspects by analyzing the effects of seasonal changes and heterogeneity in plant populations. Extending the model to include detailed pest management strategies and assessing the cost-effectiveness of various control measures would provide a more comprehensive understanding of BBTD management. Moreover, integrating data on asymptomatic infection rates and exploring more dynamic environmental interactions would enhance the robustness of the model.

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