

Mathematical Model of Effect of Yellow Virus on Tomato Plants Through *Bemisia tabaci* Insects Using *Verticillium lecanii* Fungus

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Abstract- The Yellow virus is a virus that causes tomato plants to die. The insect vector *Bemisia tabaci* spreads this virus. The goal of this study is to identify the shape of a mathematical model of the influence of yellow virus on tomato plants via the insect *Bemisia tabaci* and the fungus *Verticillium lecanii*, as well as to interpret the results of the mathematical model analysis. This is referred to as basic research. This study employs a descriptive method in which theories are analyzed in relation to the topics to be discussed, and these theories are based on a literature review. Stability analysis is carried out using Routh-Hurwitz criteria. It indicates that the disease-free equilibrium point is asymptotically stable when $\Lambda_t = \mu_t N$ and the endemic equilibrium point is asymptotically stable for $d_1 > e_1$, $d_2 > e_2$ and $a_1 > \frac{a_1^2 + a_3^2 a_0}{a_3 a_2}$. The model simulation shows that if the efficacy of *Verticillium lecanii* is high, the population of infected tomato plants, as well as the population of *Bemisia tabaci*, will go extinct.

1. Introduction

Tomatoes, which are members of the *Solanaceae* family, are the second most important fruit and vegetable crop after potatoes. Tomatoes are grown as fresh fruit and processed into processed items. Vitamins, carotenoids, and phenolic compounds are among the health-promoting substances found in tomatoes. Tomatoes have become a model for the study of the growth of fleshy fruits, in addition to being economically and nutritionally important. Tomatoes are a fruit with obvious metabolic changes during fruit development (Quinet et al., 2019).

According to 2020 horticultural statistics, the use of tomatoes plants is increasing year after year. The increased consumption of tomatoes necessitates an

increase in tomato plant output, yet there are various obstacles that cause tomato plant production to be less than optimal. The yellow virus that affects tomato plants is one of the causes of poor tomato plant productivity. The yellow virus is a pathogenic virus that is difficult to control since it lives as an obligatory parasite in plant cells, therefore eradicating the virus requires killing the host's cells or tissues (MAHENDRA et al., 2017).

The first Yellow Virus was discovered in Israel in the late 1930s, and tomato farming in the Middle East has been seriously impacted since the 1960s. The yellow virus is carried naturally by the whitefly *Bemisia tabaci*. The *Bemisia tabaci* has a diverse host range. Initially, the yellow virus only infects weed species before spreading to kill nearby cultivated plants, one of which is tomato plants (Moriones & Navas-Castillo, 2000). In 1989, the yellow virus was discovered destroying mangroves in Indonesia. The yellow virus was discovered to have affected chili plants in 2001. The yellow virus attack was so pervasive in 2004 that 984,6 ha were infected, resulting in financial losses of Rp.7.31 billion and a yield losses of 20-100% (Gunaeni et al., 2008).

The entomopathogenic fungus *Verticillium lecanii* can inhibit the spread of this yellow virus. *Verticillium lecanii*, an entomopathogenic fungus, is an excellent fungus for eradicating *Bemisia tabaci* insects. The fungus *Verticillium lecanii* has the advantage of preventing the hatching of vector insect eggs. This fungus can also infect all stages of *Bemisia tabaci*, including nymphs and imago (detritivores), as well as natural enemies, including parasitoids and predators (Prayogo, 2014). This problem can be described mathematically to describe the real-world characteristics of the problem and also as a tool for policy planning and control.

2. Methods

The research is referred to as basic research by descriptive research methods. This study was carried out using a literature review, which entailed gathering books and references. The theories developed will be used to solve existing problems and draw conclusions.

The following steps have been conducted to explain the model analysis:

1. Identifying the problem to be modeled.
2. Collecting and reviewing relevant theories about the problem.
3. Determine the variables, parameters, and assumptions that will be used in the formation of the model.
4. Forming a model of variables, parameters, and assumptions that have been determined.
5. Analyzing the mathematical model that has been formed.
6. Interpreting the results of the analysis
7. Draw a conclusion.

3. Results and Discussion

(a) Mathematics Model

Creating a mathematical model begins with determining the problem to be solved. This step identifies the critical aspects, such as assumptions, variables, and parameters.

The following variables were used to create the mathematical model:

- S : The number of tomato plants that are susceptible to the yellow virus.
 I : The number of tomato plants that infected with the yellow virus.
 S_{BT} : The number of vectors that is susceptible to the yellow virus.
 I_{BT} : The number vector that is susceptible to the yellow virus infection.

While parameters of the mathematical model are:

- λ_t : The number of tillers or replanting of tomato plants.
 λ_b : The number of births of the insect *Bemisia tabaci*.
 δ_t : The effectiveness of the use of the fungus *Verticillium lecanii*.
 μ_t : The natural death rate of tomato plants.
 μ_b : The mortality rate of *Bemisia tabaci* insects.
 θ_b : The mortality rate of the insect *Bemisia tabaci* caused by the fungus *Verticillium lecanii*.
 α : The infection rate of tomato plants.

β : The infection rate of the insect *Bemisia tabaci*.

Assumptions in the formation of a mathematical model of the effect of the yellow virus on tomato plants through the insect *Bemisia tabaci* using the fungus *Verticillium lecanii*:

1. Newly planted tomato plants are included in the Susceptible compartment.
2. *Bemisia tabaci* insects that have not been infected are included in the susceptible compartment.
3. Susceptible tomato plants will become infected if there is contact with infected *Bemisia tabaci*.
4. Infected *Bemisia tabaci* insects will carry the yellow virus for the rest of their lives.
5. The level of infection of tomato plants is incidental (occurs at any time).
6. Tomato plants that have been infected with the yellow virus cannot recover.
7. All populations of tomato plants were sprayed with *Verticillium lecanii*.

The Variables, parameters, and assumptions of a mathematical model diagram of the effect of the yellow virus on tomato plants through the insect *Bemisia tabaci* using the fungus *Verticillium lecanii* are described below:

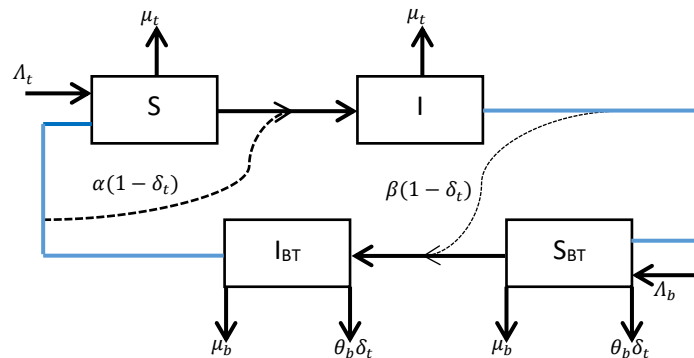


Figure 1. Diagram of a Mathematical Model of the Effect of the Yellow Virus on Tomato Plants through *Bemisia tabaci* Insects Using the *Verticillium lecanii* Fungus

Based on Figure 1, we get the mathematical model for yellow virus on tomato plants through the insect *Bemisia tabaci* using the fungus *Verticillium lecanii* as the following system:

$$\frac{dS}{dt} = \Lambda_t - \alpha(1 - \delta_t)SI_{BT} - \mu_t S \quad (1)$$

$$\frac{dI}{dt} = \alpha(1 - \delta_t)SI_{BT} - \mu_t I \quad (2)$$

$$\frac{dS_{BT}}{dt} = \Lambda_b - \beta(1 - \delta_t)IS_{BT} - \theta_b \delta_t S_{BT} N_t - \mu_b S_{BT} \quad (3)$$

$$\frac{dI_{BT}}{dt} = \beta(1 - \delta_t)IS_{BT} - \theta_b \delta_t I_{BT} N_t - \mu_b I_{BT} \quad (4)$$

Where, $(S(0) = S_0, I(0) = I_0, S_{BT}(0) = S_{BT_0}, I_{BT}(0) = I_{BT_0})$.

(b) Mathematical Model Analysis

1. The Equilibrium Point of the Mathematical Model of the Spread of the Yellow Virus

a. The Disease-Free Equilibrium Point E_0

When the population is stable, the equilibrium point represents a disease-free equilibrium point, which means there is no yellow virus in the population. The equilibrium point can be determined as follows:

$$E_0 = \left(\frac{\Lambda_t}{\mu_t}, 0, \frac{\Lambda_b}{\theta_b \delta_t N_t + \mu_b}, 0 \right)$$

b. The Endemic Equilibrium point (E_1)

The equilibrium point (E_1) is the endemic equilibrium point. We get the endemic equilibrium point

$$E_1 = (S^*, I^*, S_{BT}^*, I_{BT}^*) \text{ follows:}$$

$$S^* = \frac{\Lambda_t \beta \theta_b \delta_t N_t (1 - \delta_t) + A_t \beta (1 - \delta_t) \mu_b + \theta_b \delta_t N_t \mu_t (\theta_b \delta_t N_t + 2\mu_b) + \mu_b^2 \mu_t}{\mu_t \theta_b \delta_t N_t \beta (1 - \delta_t) + \mu_t \mu_b \beta (1 - \delta_t) + \Lambda_b \alpha \beta (1 - \delta_t)^2}$$

$$I^* = \frac{\Lambda_t \Lambda_b \alpha \beta (1 - \delta_t)^2 - \mu_t^2 \theta_b \delta_t N_t (\theta_b \delta_t N_t + 2\mu_b) + \mu_b^2 \mu_t^2}{(\mu_t \theta_b \delta_t N_t \beta (1 - \delta_t) + \mu_t \mu_b \beta (1 - \delta_t) + \Lambda_b \alpha \beta (1 - \delta_t)^2) \mu_t}$$

$$S_{BT}^* = \frac{(\mu_t \theta_b \delta_t N_t \beta (1 - \delta_t) + \mu_t \mu_b \beta (1 - \delta_t) + \Lambda_b \alpha \beta (1 - \delta_t)^2) \mu_t}{(1 - \delta_t)^2 (\mu_t \theta_b \delta_t N_t + \mu_t \mu_b + \Lambda_t \beta (1 - \delta_t)) \alpha \beta}$$

$$I_{BT}^* = \frac{\Lambda_t \Lambda_b \alpha \beta (1 - \delta_t)^2 - \mu_t^2 \theta_b \delta_t N_t (\theta_b \delta_t N_t + 2\mu_b) - \mu_b^2 \mu_t^2}{(1 - \delta_t) (\Lambda_t \beta (1 - \delta_t) (\theta_b \delta_t N_t + \mu_b) + \theta_b \delta_t N_t \mu_t (\theta_b \delta_t N_t + 2\mu_b) + \mu_b^2 \mu_t) \alpha}$$

2. Stability of The Mathematical Model

Stability analysis of the equilibrium point is found by determining the eigenvalues of the Jacobian matrix in equations (1), (2), (3), and (4). While the Jacobian matrix is obtained as follows:

$$\text{Let } C = \alpha(1 - \delta_t)I_{BT} + \mu_t$$

$$D = \beta(1 - \delta_t)I + \theta_b \delta_t N_t + \mu_b$$

We get the Jacobian Matrix

$$J = \begin{bmatrix} -C & 0 & 0 & -\alpha(1 - \delta_t)S \\ \alpha(1 - \delta_t)I_{BT} & -\mu_t & 0 & \alpha(1 - \delta_t)S \\ 0 & -\beta(1 - \delta_t)S_{BT} & -D & 0 \\ 0 & \beta(1 - \delta_t)S_{BT} & \beta(1 - \delta_t)I & -(\theta_b \delta_t N_t + \mu_b) \end{bmatrix}$$

Since there are two equilibrium points, the stability analysis is carried out on the two equilibrium points. For the free-disease, the equilibrium point will be asymptotically stable if all the eigenvalues of the Jacobi matrix that are evaluated at the disease-free equilibrium point are negative. The Jacobian matrix of the equilibrium point E_0 is as follows:

$$J(E_0) = \begin{bmatrix} -\mu_t & 0 & 0 & -\frac{\Lambda_t \alpha (1 - \delta_t)}{\mu_t} \\ 0 & -\mu_t & 0 & \frac{\Lambda_t \alpha (1 - \delta_t)}{\mu_t} \\ 0 & -\frac{\beta(1 - \delta_t) \Lambda_b}{\theta_b \delta_t N_t + \mu_b} & -(\theta_b \delta_t N_t + \mu_b) & 0 \\ 0 & \frac{\beta(1 - \delta_t) \Lambda_b}{\theta_b \delta_t N_t + \mu_b} & 0 & -(\theta_b \delta_t N_t + \mu_b) \end{bmatrix}$$

When $|\lambda I - J(E_0)| = 0$, we get the characteristic equation as

$$\frac{1}{\mu_t (\theta_b \delta_t N_t + \mu_b)} ((\lambda + \mu_t)(\lambda + \theta_b \delta_t N_t + \mu_b)(a\lambda^2 + b\lambda + c)) = 0, \text{ with}$$

$$a = \mu_t \theta_b \delta_t N_t + \mu_t \mu_b,$$

$$b = \theta_b^2 \delta_t^2 N_t^2 \mu_t + 2\mu_t \mu_b \theta_b \delta_t N_t + \mu_b^2 \mu_t + \mu_t^2 \theta_b \delta_t N_t + \mu_t^2 \mu_b$$

$$c = \theta_b^2 \delta_t^2 N_t^2 \mu_t^2 + 2\theta_b \delta_t N_t \mu_t^2 \mu_b - \Lambda_t \Lambda_b \alpha \beta + 2\Lambda_t \Lambda_b \alpha \beta \delta_t - \Lambda_t \Lambda_b \alpha \beta \delta_t^2$$

Thus, for the free-disease equilibrium, stability occurs when $\Lambda_t = \mu_t N$ and $0 < \mu_t \leq 1$.

While the endemic equilibrium point represents the disease's persistence in the population.

$$\text{Let } F = \alpha(1 - \delta_t)I_{BT}^* + \mu_t$$

$$G = \beta(1 - \delta_t)I^* + \theta_b \delta_t N_t + \mu_b$$

The Jacobian matrix of the equilibrium point E_1 is:

$$J(E_1) = \begin{bmatrix} -F & 0 & 0 & -\alpha(1 - \delta_t)S^* \\ \alpha(1 - \delta_t)I_{BT}^* & -\mu_t & 0 & \alpha(1 - \delta_t)S^* \\ 0 & -\beta(1 - \delta_t)S_{BT}^* & -G & 0 \\ 0 & \beta(1 - \delta_t)S_{BT}^* & \beta(1 - \delta_t)I^* & -(\theta_b \delta_t N_t + \mu_b) \end{bmatrix}$$

We let

$$\begin{aligned}c_1 &= \alpha(1 - \delta_t)I_{BT}^* + \mu_t \\c_2 &= \alpha(1 - \delta_t)S^* \\c_3 &= \alpha(1 - \delta_t)I_{BT}^* \\c_4 &= \beta(1 - \delta_t)S_{BT}^* \\c_5 &= \beta(1 - \delta_t)I^* + \theta_b \delta_t N_t + \mu_b \\c_6 &= \beta(1 - \delta_t)I^* \\c_7 &= \theta_b \delta_t N_t + \mu_b\end{aligned}$$

Then

$$J(E_1) = \begin{bmatrix} -c_1 & 0 & 0 & -c_2 \\ c_3 & -\mu_t & 0 & c_2 \\ 0 & -c_4 & -c_5 & 0 \\ 0 & c_4 & c_6 & -c_7 \end{bmatrix}$$

The characteristic equation is obtained by setting $|\lambda I - J(E_1)| = 0$

$$\lambda^4 + (\mu_1 + c_1 + c_5 + c_7)\lambda^3 + (\mu_1 c_1 + \mu_1 c_5 + \mu_1 c_7 + c_1 c_7 + c_1 c_5 + c_5 c_7 - c_2 c_4)\lambda^2 + (\mu_1 c_1 c_7 + \mu_1 c_1 c_5 + \mu_1 c_5 c_7 + c_1 c_5 c_7 + c_2 c_3 c_4 + c_2 c_4 c_6 - c_1 c_2 c_4 - c_2 c_4 c_5)\lambda + \mu_1 c_1 c_5 c_7 + c_1 c_2 c_4 c_6 + c_2 c_3 c_4 c_5 - c_1 c_2 c_4 c_5 - c_2 c_3 c_4 c_6 = 0$$

It can be written as $a_4 \lambda^4 + a_3 \lambda^3 + a_2 \lambda^2 + a_1 \lambda + a_0 = 0$, with

$$\begin{aligned}a_4 &= 1 \\a_3 &= \mu_1 + c_1 + c_5 + c_7 \\a_2 &= \mu_1 c_1 + \mu_1 c_5 + \mu_1 c_7 + c_1 c_7 + c_1 c_5 + c_5 c_7 - c_2 c_4 \\a_1 &= \mu_1 c_1 c_7 + \mu_1 c_1 c_5 + \mu_1 c_5 c_7 + c_1 c_5 c_7 + c_2 c_3 c_4 + c_2 c_4 c_6 - c_1 c_2 c_4 - c_2 c_4 c_5 \\a_0 &= \mu_1 c_1 c_5 c_7 + c_1 c_2 c_4 c_6 + c_2 c_3 c_4 c_5 - c_1 c_2 c_4 c_5 - c_2 c_3 c_4 c_6\end{aligned}$$

By using the Routh-Hurwitz Criteria we got the conclusion

Theorem 1:

If $d_1 > e_1$, $d_2 > e_2$, and $a_1 > \frac{a_1^2 + a_3^2 a_0}{a_3 a_2}$ then the endemic equilibrium point is asymptotically stable.

Proof.

By using the Routh-Hurwitz criteria, we must meet the following criteria to make the endemic equilibrium point asymptotically stable:

$$a_4 > 0, a_3 > 0, a_1 > 0, a_1 a_2 a_3 > a_3^2 + a_1^2 a_4$$

Then the characteristic equation $a_4 \lambda^4 + a_3 \lambda^3 + a_2 \lambda^2 + a_1 \lambda + a_0 = 0$ can be obtained as follows:

i) $a_4 > 0$

$$\text{With } a_4 = \mu_1 + c_1 + c_5 + c_7$$

Since all parameters are positive then $a_4 > 0$

ii) $a_1 > 0$

$$\text{With } a_1 = \mu_1 c_1 c_7 + \mu_1 c_1 c_5 + \mu_1 c_5 c_7 + c_1 c_5 c_7 + c_2 c_3 c_4 + c_2 c_4 c_6 - c_1 c_2 c_4 - c_2 c_4 c_5$$

Suppose:

$$d_1 = \mu_1 c_1 c_7 + \mu_1 c_1 c_5 + \mu_1 c_5 c_7 + c_1 c_5 c_7 + c_2 c_3 c_4 + c_2 c_4 c_6$$

$$e_1 = c_1 c_2 c_4 + c_2 c_4 c_5$$

$$\text{then } a_1 > 0 \Leftrightarrow d_1 > e_1$$

iii) $a_0 > 0$

$$\text{With } a_0 = \mu_1 c_1 c_5 c_7 + c_1 c_2 c_4 c_6 + c_2 c_3 c_4 c_5 - c_1 c_2 c_4 c_5 - c_2 c_3 c_4 c_6$$

Suppose:

$$d_2 = \mu_1 c_1 c_5 c_7 + c_1 c_2 c_4 c_6 + c_2 c_3 c_4 c_5$$

$$e_2 = c_1 c_2 c_4 c_5 + c_2 c_3 c_4 c_6$$

$$\text{So } a_0 > 0 \Leftrightarrow d_2 > e_2$$

iv) $a_3 a_2 a_1 > a_1^2 + a_3^2 a_0$

$$\text{With } a_1 > \frac{a_1^2 + a_3^2 a_0}{a_3 a_2}$$

Since $d_1 > e_1$, $d_2 > e_2$, and $a_1 > \frac{a_1^2 + a_3^2 a_0}{a_3 a_2}$ are satisfied, the endemic equilibrium point is asymptotically stable.

The basic reproduction number is a measurement that is used to determine whether or not a population is endemic. To calculate the basic reproduction number, we use the next generation matrix, where F is the transition matrix and V is the transmission matrix.

$$F = \begin{bmatrix} 0 & \frac{\Lambda_t \alpha (1 - \delta_t)}{\mu_t} \\ \frac{\Lambda_b \beta (1 - \delta_t)}{\theta_b \delta_t N_t + \mu_b} & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \mu_t & 0 \\ 0 & \theta_b \delta_t N_t + \mu_b \end{bmatrix}$$

The basic reproduction number (R_0) is the largest spectral radius or eigenvalue of the matrix (FV^{-1}), thus it determines as:

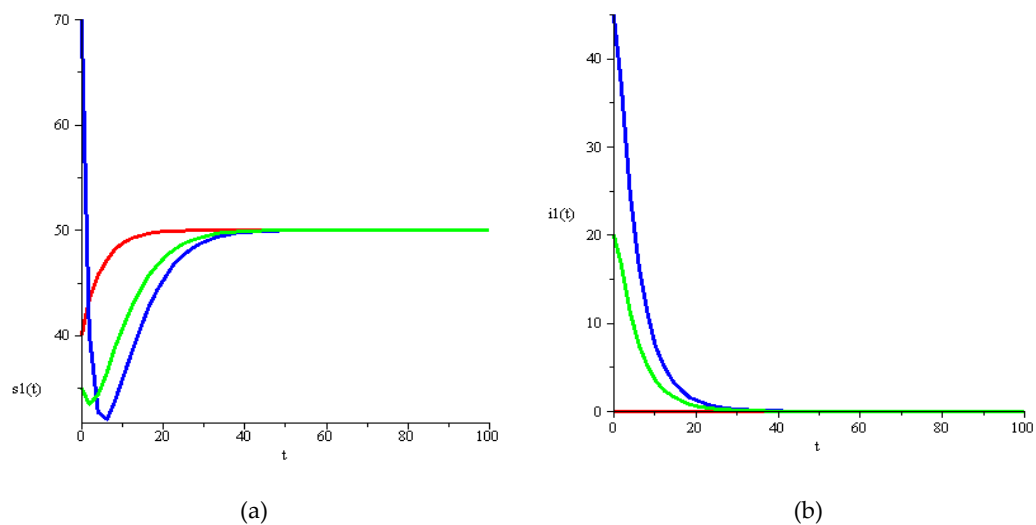
$$R_0 = \frac{(1 - \delta_t)}{\mu_t (\theta_b \delta_t N_t + \mu_b)} \sqrt{\Lambda_t \Lambda_b \alpha \beta}$$

To simulate the model, we use Maple Software to show the trajectory near the steady states. The parameters used to simulate the model are:

Table 1. The Model's Parameter Values Near Free Disease Equilibrium

Parameter	Value
N_t	50
Λ_t	10
Λ_b	8
δ_t	0,8
μ_t	0,2
μ_b	0,07
θ_b	0,05
α	0,03
β	0,2

From the parameter values in Table 1, R_0 will be calculated so that the basic reproduction number is obtained $R_0 = 0,3346958083$. Since $R_0 < 1$, the free-disease equilibrium is asymptotically stable. The parameter values in Table 1 then are substituted in the disease-free equilibrium E_0 such that $E_0 = (50, 0, 3.8647, 0)$. The trajectory is given in Figure 2:



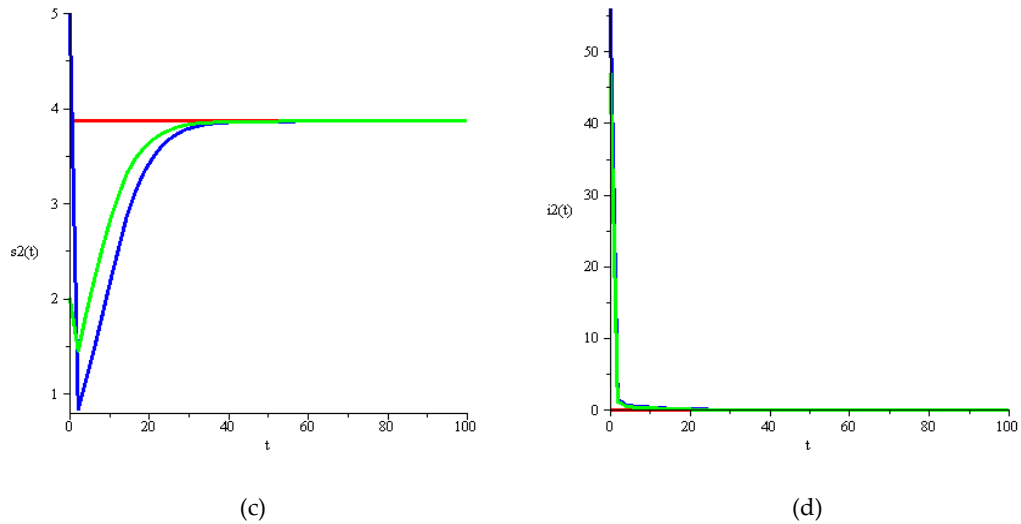


Figure 2. Trajectory around the Disease-Free Equilibrium Point (a) Graph $S(t)$, (b) Graph $I(t)$, (c) Graph $S_{BT}(t)$, and (d) Graph $I_{BT}(t)$

Based on Figure 2, with a disease-free equilibrium point $S(0) = 50; I(0) = 0; S_{BT}(0) = 3.8647; I_{BT}(0) = 0$ which is approximated by two initial values i.e.:

$$\begin{aligned} S(0) &= 70; I(0) = 45; S_{BT}(0) = 5; I_{BT}(0) = 56 \\ S(0) &= 35; I(0) = 20; S_{BT}(0) = 2; I_{BT}(0) = 47 \end{aligned}$$

This indicates that E_0 is asymptotically stable and the value of $R_0 < 1$, which means that within a certain time the spread of the yellow virus will disappear.

While the simulation for the endemic equilibrium point uses the following parameter values:

Table 2. The Model's Parameter Values Near Endemic Equilibrium

Parameter	Value
N_t	50
Λ_t	10
Λ_b	8
δ_t	0,3
μ_t	0,2
μ_b	0,07
θ_b	0,05
α	0,03
β	0,2

From the parameter values in Table 2, R_0 is calculated as $R_0 = 2.957159915$. Since $R_0 > 1$, then the equilibrium is asymptotically stable. The endemic equilibrium is $E_1 = (27.59208, 22.40792, 2.02168, 7.73442)$. The following figure shows the trajectory near the steady states:

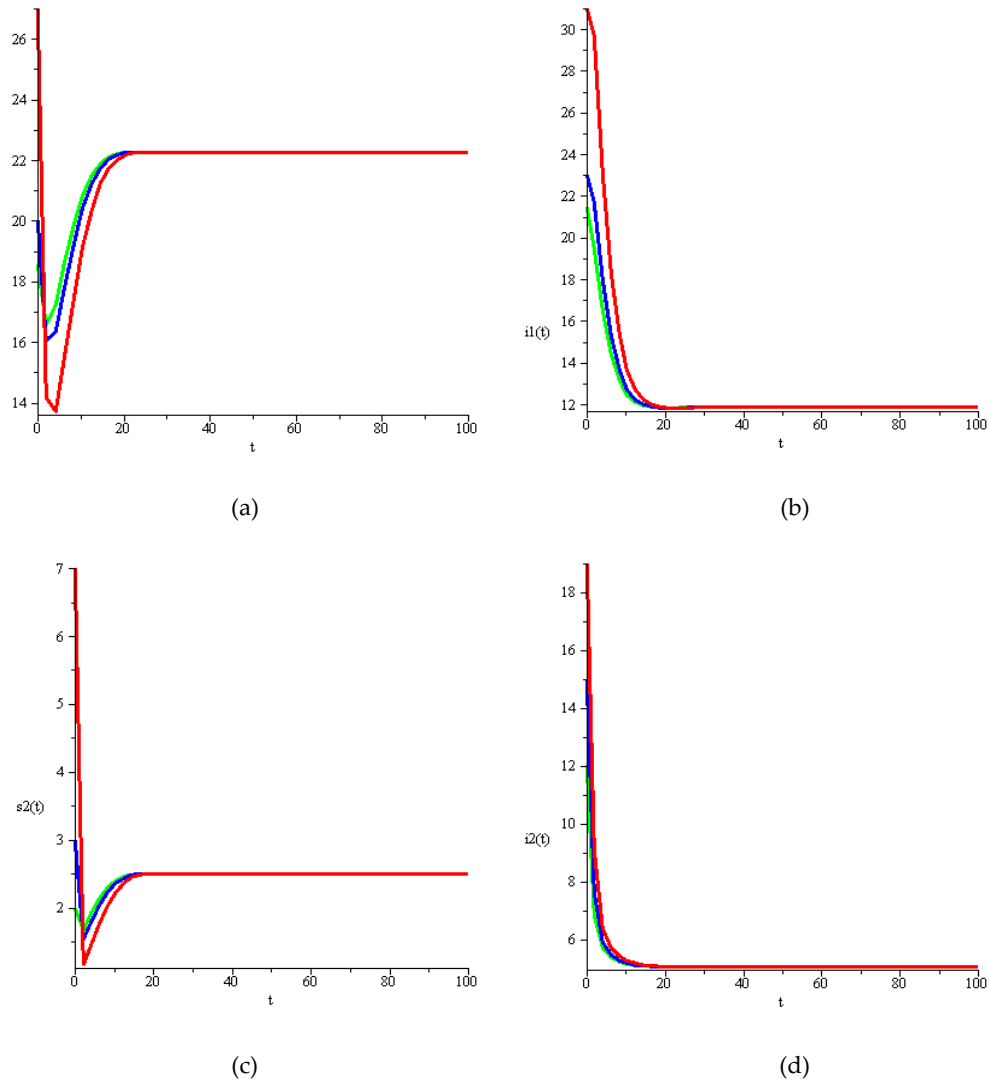


Figure 3. Trajectory Near the Yellow Virus Endemic Equilibrium Point (a) Graph $S(t)$, (b) Graph $I(t)$, (c) Graph $S_{BT}(t)$, and (d) Graph $I_{BT}(t)$

Based on Figure 3, with a endemic equilibrium point $S(0) = 50; I(0) = 0; S_{BT}(0) = 3.8647; I_{BT}(0)$ which is approximated by two initial values i.e.:

$$\begin{aligned} S(0) &= 20; I(0) = 23; S_{BT}(0) = 3; I_{BT}(0) = 15 \\ S(0) &= 27; I(0) = 31; S_{BT}(0) = 7; I_{BT}(0) = 19 \end{aligned}$$

The numerical simulation shows E_1 is asymptotically stable and $R_0 > 1$, which means that the yellow virus will spread for a long time.

(c) Interpretation

Based on the stability analysis, the disease-free equilibrium point is asymptotically stable if $\Lambda_t = \mu_t N$ which means the yellow virus can disappear within a certain time. Meanwhile, the endemic equilibrium point will be asymptotically stable if $d_1 > e_1$, $d_2 > e_2$, and $a_1 > \frac{a_1^2 + a_3^2 a_0}{a_3 a_2}$ which means that the yellow virus will spread for a long time.

The simulation results given indicated that if the parameter value of the effectiveness of the use of the fungus *Verticillium lecanii* is large, the population of infected tomato plants will decrease to extinction as well as the insect population of *Bemisia tabaci*. And conversely, if the parameter value of the effectiveness of using *Verticillium lecanii* is small, the yellow virus will spread for a long time.

4. Conclusion

The mathematical model of the spread of the yellow virus in tomato plants is stated in the system of differential equations. There are two equilibrium points, namely the disease-free equilibrium point and the endemic equilibrium point. The stability analysis for disease-free equilibrium point is asymptotically stable if $\Lambda_t = \mu_t N$ and for the endemic equilibrium point it is asymptotically stable if $d_1 > e_1$, $d_2 > e_2$, and $a_1 > \frac{a_1^2 + a_3^2 a_0}{a_3 a_2}$. The numerical simulation model shows that if the effectiveness of the fungus *Verticillium lecanii* is large, the infected tomato plant population will decrease to extinction as well as the *Bemisia tabaci* insect population.

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