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Modelling the Transmission Dynamics of Banana Xanthomonas Wilt Disease with Contaminated Soil

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Abstract. Banana Xanthomonas Wilt disease (BXW) is a bacterial disease which highly threaten banana production in east and central Africa. It is caused by a bacteria known as *Xanthomonas campestris pv. musacearum (Xcm).* Mathematical modelling gives an insight on how to best understand the transmission dynamics and control of the disease. The existing mathematical models have not included contaminated soil in the dynamics of BXW. In this study we formulated a model which includes contaminated soil, calculated the basic reproduction number and carried out sensitivity analysis of some model parameters. We further conducted numerical simulation to validate the results. The simulations show that the infection rate by contaminated farming tools (β_i and β_e), the infection rate by contaminated soil (ω_2), vertical disease transmission rate (θ), and the shedding rate of Xcm bacteria in the soil (ϕ) are positively sensitive to the basic reproduction number. While, the most negative sensitive parameters are the clearance rate of Xcm bacteria from the soil (μ_h), removal of infected plants from the farm (r), harvesting (α_p), and banana plants disease induced death rate (d).The result also shows that contaminated soil contributes to the transmission and persistence of BXW disease. Therefore, we recommend that, along with the existing control measures scientist and technologist should carry out studies to find a way to reduce or avoid vertical disease transmission and increase the Xcm clearance rate in the soil. Furthermore, technology for early detection of infected plants should be brought down to the local farmers at affordable costs. This will help stakeholders to detect and remove the infected plants from the farm in time and hence reduce the number of secondary infections.

Keywords: Contaminated Soil; BXW; Mathematical Modelling; Banana Production; basic re-production number; sensitivity analysis

AMS Mathematics Subject Classification (2010): 97R20

1. Introduction

Bananas are among the most important food crops in the world after maize, cassava and sweet potatoes. Farmers use Banana fruits as food and for commercial purposes to support their livelihoods. Also, to a lesser extent, bananas are used to make fibre, wine and beer. In 2016 the world produced 113,280,302 tonnes (113,280kt) of bananas where 21,019,246 tonnes (21,019kt) were produced in Africa [1]. Despite the importance of this plant, the Banana Xanthomonas Wilt (BXW) disease is still a threat to banana production in Africa. The BXW disease can cause up to 100% loss of banana produce if not timely controlled. Even though the social and economic impact of BXW is not well quantified, it highly affects the food security status, livelihood of banana growing households and national economies at large [2]. BXW is caused by the bacterium known as *Xanthomonas campestris pv. musacearum (Xcm)*. It is transmitted through contaminated farming tools, insect vectors, soil, Infection from mother plant to its suckers, planting and transportation of latently (Asymptomatic) infected banana plants [3–5] . A symptomatic infected plant is identified by the yellowing and wilting of its leaves, premature ripening of the fruits and yellow ooze observed when pseudo stem is cut [6], [7]. The commonly used method to control the disease is through timely removing of the male bud using a forked stick, sterilization of the farming tools, debudding and rouging.

To best control the disease there is a need to understand its transmission dynamics. Mathematical modelling plays an important role in the study of the dynamics, predicting, assessing, and suggesting the best control measures to potential disease outbreaks. Researchers such as[7]–[11] have developed mathematical models to study the dynamics of BXW disease. These mathematical models did not take into account the role of contaminated soil in the dynamics of BXW disease. Nevertheless, the findings by [3, 12, 13] clearly shows that, contaminated soil plays a role in BXW transmission and persistence. [14] showed that there is a positive correlation between rain and BXW disease transmission. The rain increases the soil moisture and hence favorsthe survival of Xcm bacteria in the soil. Furthermore, through the flow of rain water, Xcm bacteria can be transported from one place to another. Therefore, in order to best understand the dynamics of BXW disease, there is a need to develop a mathematical model which takes consideration the role of contaminated soil. In this paper we developed a deterministic mathematical model which considers BXW transmission through contaminated soil, insects, farming tools and vertical transmission.

This paper is organized as follows. In Section 2, parameters and variables are described, assumptions satisfied by the parameters and variables are made, and model is formulated. In section 3, we calculated the basic reproduction number (R_0), checked the stability of the disease free equilibrium point, carried out sensitivity analysis and did simulations. Finally section 4 includes the conclusion and recommendations.

2. Material and methods

2.1. Model formulation

The model formulated in this study involves banana plant population, insect vector population and contaminated soil. Depending on the infection status, the banana plant population is subdivided into three compartments namely: Susceptible plant (S_p); asymptomatic infected plants (E_p); and Symptomatic infected plants (I_p). Susceptible are healthy banana plants which can be infected by BXW when come into contact with

the Xcm bacterium. It is assumed that susceptible banana plants have an equal chance of being infected when come into contact with Xcm bacterium. Susceptible banana plants acquire BXW disease through vertical transmission, contaminated farming tools, soil contaminated with Xcm bacteria, or insect vector [3, 4, 5].

The vectors such as birds, bats and other flying insects such as bees are the carrying agent of the Xcm bacteria from an infected banana plant to the susceptible plant. Birds transmit the Xcm bacteria after feeding on ripe banana bunches of an infected banana plant to the male buds of a susceptible plant [5]. Bats can transmit the disease through feeding on nectar or ripe banana fruits of an infected banana plant to the healthy banana plant [5]. Other vectors such as bees transmit the disease to a susceptible banana plant when contaminated with Xcm bacteria from a male bud of an infected plant [15]. In this paper, the vector population is subdivided into susceptible vectors (S_v) and contaminated vectors (I_v). An environment contaminated with Xcm bacteria is denoted by A_h .

The model considers constant recruitment of banana plants by emerging of new healthy lateral shoots from the banana plants and replanting of healthy suckers at the rate of b_p . Through farming activities such as weeding, pruning, removing access suckers, harvesting and male bud removal, a farming tool can be contaminated with Xcm bacteria from symptomatic infected banana plants or asymptomatic infected banana plants and transmit the disease at the rate β_i or β_e respectively. We further assume that susceptible banana plant can be infected by the Xcm bacteria found in the soil at a rate of ω_2 . The average daily contact rate of an infected vector to a susceptible banana plant is given by a and the probability that the contact results to infection is given by ω_1 .

Matured banana plants are harvested at the rate of α_p . E_p proceed to I_p at the rate of q after showing BXW disease symptoms. An infected banana plant can be removed from the farm at the rate of r right after showing symptoms or die due to infection at a rate of d . It is assumed that the banana plant can be vertically an infected from infected banana plant at a rate q. We further assumed that the rate of vertical transmission is less than the sum of disease induced death rate and removal of infected banana plants ($\theta \le d + r$).

A susceptible vector population has a constant recruitment rate b_v , and it is assumed that both susceptible and contaminated vectors die naturally at the rate μ_v . ω_3 is the probability that a susceptible vector gets contaminated with Xcm bacteria upon coming into contact with a symptomatic infected banana plant. It is assumed that the vector becomes infective right after being contaminated with the Xcm bacteria. According to [5], contaminated vectors retain Xcm bacteria viable for 3-5 days from the day of inoculation. This implies that, after 5 days contaminated vectors become susceptible again at a rate η where $\eta < \mu_v$.

The shedding rate of Xcm bacteria from the infected banana plant in the soil is given by ϕ. The Xcm bacteria in the farm soil are cleared naturally at the rate μ_h due to lack of saprophytic or resting stage in soil [16].

The model is best described by the compartmental diagram in Figure 1, where $\lambda_1 = a\omega_3 \frac{I_p}{N_p}$ and $\lambda_2 = (a\omega_1 \frac{I_v}{N_p} + \beta_e \frac{S_p E_p}{N_p} + \beta_i \frac{S_p I_p}{N_p} + \omega_2 \frac{A_h}{N_p(K + A_h)})$.

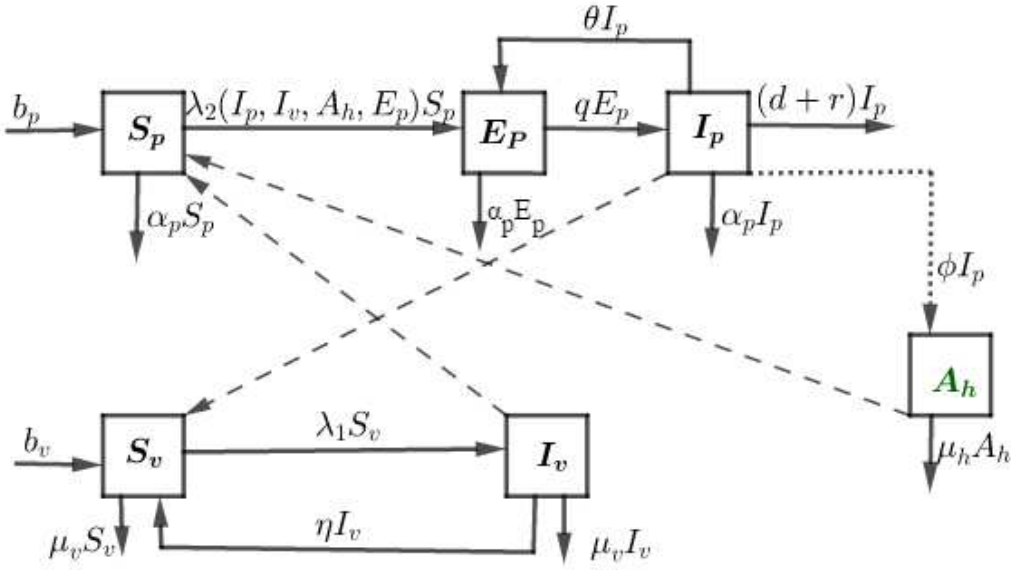


Figure 1: Basic Compartmental diagram for the transmission dynamics of BXW disease.

From the compartmental diagram, sold lines represent a transition from one infection stage to recruitment, harvesting, natural death rate of vectors and clearance of Xcm bacteria from the soil. The dash lines represent normal interactions between different compartments and shedding of Xcm bacteria onto the environment is represented by dotted lines.

From the compartmental diagram we formulate a system of differential equations as follows:

$$\frac{dS_p}{dt} = b_p - a\omega_1 \frac{S_p I_v}{N_p} - \beta_e \frac{S_p E_p}{N_p} - \beta_i \frac{S_p I_p}{N_p} - \omega_2 \frac{S_p A_h}{N_p(K + A_h)} - \alpha_p S_p \quad (1)$$

$$\frac{dE_p}{dt} = a\omega_1 \frac{S_p I_v}{N_p} + \beta_e \frac{S_p E_p}{N_p} + \beta_i \frac{S_p I_p}{N_p} + \omega_2 \frac{S_p A_h}{N_p(K + A_h)} + \theta I_p - \alpha_p E_p - qE_p \quad (2)$$

$$\frac{dI_p}{dt} = qE_p - \alpha_p I_p - dI_p - rI_p \quad (3)$$

$$\frac{dA_h}{dt} = \phi I_p - \mu_h A_h \tag{4}$$

$$\frac{dS_v}{dt} = b_v + \eta I_v - a\omega_3 \frac{S_v I_p}{N_p} - \mu_v S_v \tag{5}$$

$$\frac{dI_v}{dt} = a\omega_3 \frac{S_v I_p}{N_p} - \eta I_v - \mu_v I_v \tag{6}$$

The equations of the total population of banana plants and total population of vectors are given by:

$$\frac{dN_p}{dt} = b_p - \alpha_p N_p + \theta I_p - (d+r) I_p \tag{7}$$

$$\frac{dN_v}{dt} = b_v - \mu_v N_v \tag{8}$$

2.2. Basic properties of the model

In this section we are going to check whether the model system is epidemiologically and mathematically well posed. This is done by checking the invariant region of the model and positivity of the model solution to make sure that there is no negative solution to the model variables. From equation (7) we have

$$\frac{dN_p}{dt} \leq b_p - \alpha_p N_p \tag{9}$$

$$N_p(t) \leq \frac{b_p}{\alpha_p} + (N_p(0) - \frac{b_p}{\alpha_p}) e^{-\alpha_p t} \tag{10}$$

From equation(10), two cases are emerging. Case 1: When $N_p(0) \leq \frac{b_p}{\alpha_p}$ as $t \to \infty$ the total number of banana plants $N_p(t)$ increases to $\frac{b_p}{\alpha_p}$. This implies that

$$N_p(0) \leq N_p(t) \leq \frac{b_p}{\alpha_p}, \forall_{t \geq 0} \tag{11}$$

Case 2: When $N_p(0) \geq \frac{b_p}{\alpha_p}$, $N_p(t)$ decreases to $\frac{b_p}{\alpha_p}$ as $t \to \infty$. This implies that

$$N_p(t) \leq \frac{b_p}{\alpha_p} \leq N_p(0), \forall_{t \geq 0} \tag{12}$$

Generally, $D_1 = \{S_p(t), E_p(t), I_p(t) \in \mathbb{R}_+^3 : N_p(0) \leq N_p(t) \leq \frac{b_p}{\alpha_p}, \forall_{t \geq 0}\}$. Again, from equation (8) we have

$$\frac{dN_v}{dt} \leq b_v - \mu_v N_v \tag{13}$$

Solving this, results into

$$N_v(t) \leq \frac{b_v}{\mu_p} + (N_v(0) - \frac{b_v}{\mu_v})e^{-\mu_v t}. \quad (14)$$

From equation (14) it follows that, when $N_v(0) \geq \frac{b_v}{\mu_v}$, as $t \to \infty$, the total number of vectors $N_v(t)$ reduces to $\frac{b_v}{\mu_v}$. This means that

$$N_v(t) \leq \frac{b_v}{\mu_v} \leq N_v(0), \forall_{t\geq 0}. \quad (15)$$

Again, when $N_p(0) \leq \frac{b_p}{\alpha_p}$, as $t \to \infty$ the number of vectors $N_v(t)$ approaches to $\frac{b_v}{\mu_v}$. This means that

$$N_v(0) \leq N_v(t) \leq \frac{b_v}{\mu_v}, \forall_{t\geq 0} \quad (16)$$

Therefore,

$$D_2 = \{S_v(t), I_v(t) \in \mathbb{R}^2_+ : N_v(0) \leq N_v(t) \leq \frac{b_v}{\mu_v}, \forall_{t\geq 0}\} \quad (17)$$

Furthermore, it is proved that

$$D_3 = \{A_h(t) \in \mathbb{R}^1_+, \forall_{t\geq 0}\} \quad (18)$$

Considering the non-negative initial solutions of the model $S_p(0) > 0, E_p(0) \geq 0, I_p(0) \geq 0, A_h(0) \geq 0, S_v(0) \geq 0, I_v(0) \geq 0$, the model system (1) - (6)is positive invariant and attracting in the region

$$D = \{D_1 \times D_2 \times D_3 : D \in \mathbb{R}^6_+, \forall_{t\geq 0}\} \quad (19)$$

Therefore, the model solutions remain positive and bounded in the region D, $\forall_{t\geq 0}$

3. Results and discussion

3.1. Disease free equilibrium point

A disease free equilibrium (DFE) is the point at which there is no infection in the population. Thus, the populations comprise of only susceptible banana plants and vectors and no Xcm bacteria in the soil. Let, $X_{dfe} = (S_p^0, E_p^0, I_p^0, S_v^0, I_v^0, A_h^0)$ be the disease free equilibrium point of the system (1) - (6). Setting the rate of change of each model variable in the system in (1) - (6) to zero and solving the system results into DFE in (20)

$$X_{dfe} = (S_p^0, E_p^0, I_p^0, S_v^0, I_v^0, A_h^0) = (\frac{b_p}{\alpha_p}, 0, 0, \frac{b_v}{\mu_v}, 0, 0) \quad (20)$$

3.2. Basic reproduction number R_0

A basic reproduction number (R_0), is an average number of new infection caused by one infective individual in a population where all its members are susceptible. It helps to understand the ability of the disease to invade the population [17]. In this

paper we apply the next generation method as described by [17, 18]. From the system of equations(1) - (6), consider the infected sub-system

$$\frac{dE_p}{dt} = a\omega_1 \frac{S_p I_v}{N_p} + \beta_e \frac{S_p E_p}{N_p} + \beta_i \frac{S_p I_p}{N_p} + \omega_2 \frac{S_p A_h}{N_p (K + A_h)} + \theta I_p - \alpha_p E_p - qE_p \quad (21)$$

$$\frac{dI_v}{dt} = a\omega_3 \frac{S_v I_p}{N_p} - \eta I_v - \mu_v I_v \quad (22)$$

$$\frac{dI_p}{dt} = qE_p - \alpha_p I_p - dI_p - rI_p \quad (23)$$

$$\frac{dA_h}{dt} = \phi I_p - \mu_h A_h \quad (24)$$

Let $x = (E_p, I_v, I_p, A_h)$ and $y = (S_p, S_v)$, where x and y are infected and susceptible compartments of the model, respectively. Separating the infected subsystem (21) - (24) into two parts, results into (25) and (26), where $\mathcal{F}(x, y)$ is the transmission part which portray the generation of new infections and $\mathcal{V}(x, y)$ is the transition part which involves change of states.

$$\mathcal{F}(x, y) = \begin{pmatrix} a\omega_1 \frac{S_p I_v}{N_p} + \beta_e \frac{S_p E_p}{N_p} + \beta_i \frac{S_p I_p}{N_p} + \omega_2 \frac{S_p A_h}{N_p (K + A_h)} + \theta I_p \\ a\omega_3 \frac{S_v I_p}{N_p} \\ 0 \\ 0 \end{pmatrix} \quad (25)$$

$$\mathcal{V}(x, y) = \begin{pmatrix} -\alpha_p E_p - qE_p \\ -\eta I_p - \mu_v I_v \\ qE_p - \alpha_p I_p - dI_p - rI_p \\ \phi I_p - \mu_h A_h \end{pmatrix} \quad (26)$$

Let $F = \frac{\partial \mathcal{F}(x, y)}{\partial x_i}$ and $V = \frac{\partial \mathcal{V}(x, y)}{\partial x_i}$ where $x_i = (E_p, I_v, I_p, A_h)$ for $i = 1, 2, 3, 4$ At the DFE every member of the population is susceptible, thus $S_p^0 = N_p(0)$. Differentiating and evaluating at X_{dfe} results into

$$F = \begin{pmatrix} \beta_e & a\omega_1 & \beta_i + \theta & \frac{\omega_2}{K} \\ 0 & 0 & \frac{a\omega_3 \alpha_p b_v}{\mu_v b_p} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \quad (27)$$

$$V=\begin{pmatrix}(\alpha_p+q) & 0 & 0 & 0\\ 0 & (\eta+\mu_v) & 0 & 0\\ -q & 0 & (\alpha_p+d+r) & 0\\ 0 & 0 & -\phi & \mu_h\end{pmatrix} \tag{28}$$

$$V^{-1}=\begin{pmatrix}\frac{1}{(\alpha_p+q)} & 0 & 0 & 0\\ 0 & \frac{1}{(\eta+\mu_v)} & 0 & 0\\ \frac{q}{(\alpha_p+q)(\alpha_p+d+r)} & 0 & \frac{1}{(\alpha_p+d+r)} & 0\\ \frac{q\phi}{(\alpha_p+q)(\alpha_p+d+r)\mu_h} & 0 & \frac{\phi}{(\alpha_p+d+r)\mu_h} & \frac{1}{\mu_h}\end{pmatrix} \tag{29}$$

Then it follows that

$$FV^{-1}=\begin{pmatrix}T_R & \frac{a\omega_1}{\eta+\mu_v} & T_C & \frac{\omega_2}{k\mu_h}\\ \frac{a\omega_3\alpha_p b_v q}{\mu_v b_p(\alpha_p+q)(\alpha_p+d+r)} & 0 & \frac{a\omega_3\alpha_p b_v}{\mu_v b_p(\alpha_p+d+r)} & 0\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0\end{pmatrix} \tag{30}$$

Now, let the matrix $Q=FV^{-1}$, the basic reproduction number R_0 of the model is a dominant eigenvalue of the matrix Q. Therefore,

$$R_0=\frac{1}{2}T_R+\frac{1}{2}\sqrt{(T_R)^2+4\frac{a^2\omega_1\omega_3\alpha b_v q}{(\eta+\mu_v)\mu_v b_p(\alpha+q)(\alpha+d+r)}} \tag{31}$$

where

$$T_R=\frac{\beta_e}{\alpha_p+q}+\frac{(\beta_i+\theta)q}{(\alpha_p+q)(\alpha_p+d+r)}+\frac{\omega_2\phi q}{k(\alpha_p+d+r)(\alpha_p+q)\mu_h} \tag{32}$$

And

$$T_C=\frac{\beta_i+\theta}{\alpha_p+d+r}+\frac{\omega_2\phi}{k(\alpha_p+d+r)\mu_h}$$

From(31), $\frac{1}{\alpha_p+q}$ is the average time that a banana plant stays in an asymptomatic infected stage before proceeding to the symptomatic infected stage. In this duration β_e

new infection are generated. $\frac{q}{\alpha_p + q}$ is the probability that an asymptomatic infected banana plant proceeds to an infected compartment. $\frac{1}{\alpha_p + d + r}$ is the duration by which an infected banana plant stays in an infected group during its lifetime. $\beta_i + \theta$ is the expected number of new infections to the banana plant produced by a symptomatic infected banana plant before being harvested, removed from the farm or dying due to BXW disease infection. $\frac{\omega_2 \phi}{k\mu_h}$ are the expected new infections caused by the contaminated soil.

3.3. Local stability of the DFE point

Theorem 3.1. If X_{dfe} is a DFE of the model given by(1)–(6), then X_{dfe} is locally asymptotically stable if $R_0 < 1$, and unstable if $R_0 > 1$

Proof: The proof of Theorem 3.1 is similar that of Theorem 2.1 of [17]

3.4. Global stability of the DFE point

Global stability of the disease-free equilibrium point means that the solutions of the system are attracted to the DFE point over indefinite time.

Theorem 3.2. If X_{dfe} is a DFE of the model given by (1) - (6), then X_{dfe} is locally asymptotically stable if $R_0 < 1$, and unstable if $R_0 > 1$.

Proof: Lyapunov function constructed using matrix theoretic method based on the Perron eigenvector is applied to prove the Global Stability of the DFE X_{dfe} as done in [20, 21]. Now, let $x = (E_p, I_v, I_p, A_h)$ and $y = (S_p, S_v)$. From a subsystem(21) - (24), the function $f(x, y)$ and x' can be written as in (33)and (34)respectively.

$$f(x, y) = (F - V)x - \mathcal{F}(x, y) + \mathcal{V}(x, y) \tag{33}$$

and

$$x' = (F - V)x - f(x, y) \tag{34}$$

Solving for $f(x, y)$ results to (35)

$$f(x, y) = \begin{pmatrix} \frac{\beta_e (S_p^* - S_p) E_p}{N_p} + \frac{a\omega_1 (S_p^* - S_p) I_p}{N_p} + \frac{\beta_i (S_p^* - S_p) I_p}{N_p} + \frac{\omega_2 (S_p^* - S_p) A_h}{N_p} \\ \frac{a\omega_3 (S_p^* - S_p) I_p}{\mu_v N_p} \\ 0 \\ 0 \end{pmatrix} \tag{35}$$

Referring to Theorem 2.1 of [21]. Since from (27) $F \geq 0$, in (29) $V^{-1} \geq 0$ and from (35) $f(x,y) \geq 0$ then (36) is a Lyapunov function of the model (21)-(24) where ϑ^T is the left eigenvector of the matrix $V^{-1}F$ Corresponding to its spectral radius R_0.

$$Q = \vartheta^T V^{-1} x \tag{36}$$

Reducing the matrix $V^{-1}F$ to its row echelon form, the left eigenvector is $\vartheta^T = (1,0,0,0)$.

$$Q = \frac{E_p}{\alpha_p + q} \tag{37}$$

Since $\vartheta^T > 0$ and the matrix $V^{-1}F$ is irreducible and non negative, then Theorem 2.2 of [21] can be applied. Differentiating (36) results to (38)

$$Q' = \vartheta^T V^{-1} x' \tag{38}$$

Substituting (34) into (38) gives (39)

$$Q' = \vartheta^T V^{-1}((F-V)x - f(x,y)) \tag{39}$$
$$= \vartheta^T V^{-1}(F-V)x - \vartheta^T V^{-1} f(x,y) \tag{40}$$
$$= (R_0 - 1)\vartheta^T x - \vartheta^T V^{-1} f(x,y) \tag{41}$$

Substituting the required equations in (41) yields (42).

$$Q' = (R_0 - 1)E_p - \frac{1}{\alpha_p + q}\left(\frac{\beta_e(S_p^0 - S_p)E_p}{N_p} + \frac{a\omega_1(S_p^0 - S_p)I_p}{N_p} + \frac{\beta_i(S_p^0 - S_p)I_p}{N_p} + \frac{\omega_2(S_p^0 - S_p)A_h}{N_p}\right) \tag{42}$$

From (42) it can be observed that $Q' \leq 0$ if $R_0 \leq 1$. But if $R_0 = 1$, $Q' = 0 \Leftrightarrow S_p^0 = S_p$ or $E_p = I_p = I_v = A_h = 0$. Thus, by Theorem 2.2 of [20], X_{dfe} is Global Asymptotically Stable in D when $R_0 \leq 1$ and unstable when $R_0 > 1$.

3.5. Parameter values

The parameter values are obtained from related literature and some are assumed in the interval (0,1). The values for the parameters d, α_p, r, μ_v and b_v, are adopted from [10]. $\beta_i, \omega_1, \omega_3$ and a are from [11]. b_p from [8] and θ from [15]. Table 1 shows the parameter value per day.

Table 1: Values of the model parameters

Parameter	Value/Range	Parameter	Value/Range	Parameter	Value/Range
d	0.0167	ω_2	0:4	b_v	0.02
ϕ	0.89	β_i	0.1429	ω_1	0:2
α_p	0.0056	K	1000	μ_v	0.02
θ	0.0286	μ_h	0.01	ω_3	0.2
r	0.0105	q	0.3	η	0.0286
b_p	0.01667	a	0.2	β_e	0.3

3.6. Sensitivity analysis

Sensitivity analysis is the process of determining the influence of each model parameter in the basic reproduction number (R_0). This guides the selection of the disease control measures, where the most sensitive parameters are highly considered. This study applied the Normalized forward sensitivity index to determine the sensitivity of the model parameters as in[21]. If the R_0 is differentiable with respect to its parameter u, then the sensitivity index of u is given by(43).

$$\Upsilon_u^{R_0} = \frac{\partial R_0}{\partial u} \times \frac{u}{R_0} \tag{43}$$

Since the R_0 in (31)is differentiable to all its parameters, now we apply (43)to calculate the sensitivity indices of the model parameters using the values in table 2. This results to sensitivity indices as indicated in Figure 2.

A positive index implies the direct proportionality of the basic reproduction number with the corresponding parameter. A negative index means that the parameter is inversely proportional to the basic reproduction number. Increasing the R_0 implies increase in the BXW disease endemicity while decreasing R_0 to less than one lowers the endemicity of the BXW disease. From Figure 2, the parameters $\omega_2, \phi, \theta, \beta_i$ and β_e have positive indices, which sends the message that increasing (or decreasing) any of these parameters keeping other parameters constant, results into the increase (or decrease) of the basic reproduction number (R_0). For instance, $\beta_i = 0.6024153$ means that increasing (or decreasing) the value of the parameter β_i increases (or decreases) the R_0 by 6.024153%. Thus, decreasing the rate of infection by farming tools, vertical transmission, rate of shedding Xcm bacteria in the soil and reducing the rate of infection through contaminated soil reduces the value of the R_0 and hence helps to contain the disease. Conversely, the parameters with negative indices are r, d, α_p, q, K and μ_h which means that, increasing (or decreasing) any of these parameters results to decrease (or increase) of the R_0. In order to best control the disease these parameters with negative indices should be increased so as to reduce the value of the R_0.

According to [4] Xcm bacterium is systemic in nature, it can invade the whole plant from the point of infection to its lateral shoots if the diseased plant is not properly removed on time. Now, leaving the diseased plant to die in the farm gives a chance of

the Xcm bacteria to spread wider and hence spread of the disease. Therefore, the parameter d should be carefully considered during the selection of control measures. Other parameters whose indices are more close to zero are considered to be less sensitive to the R_0, hence they can be tolerated.

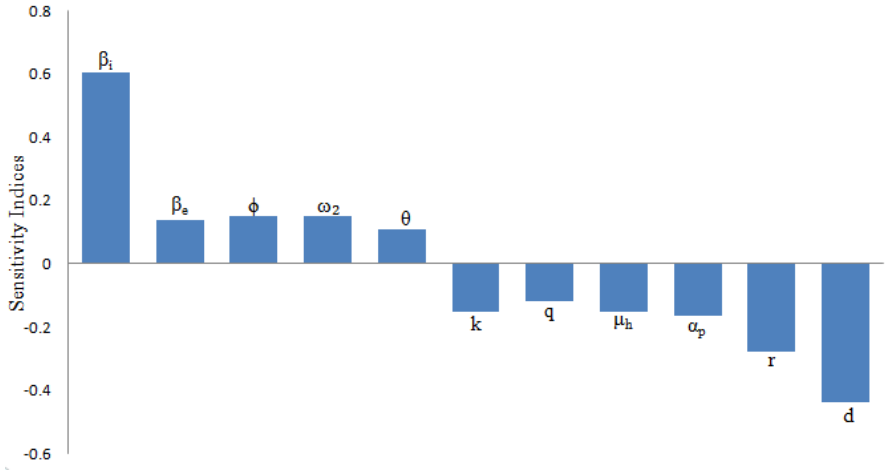
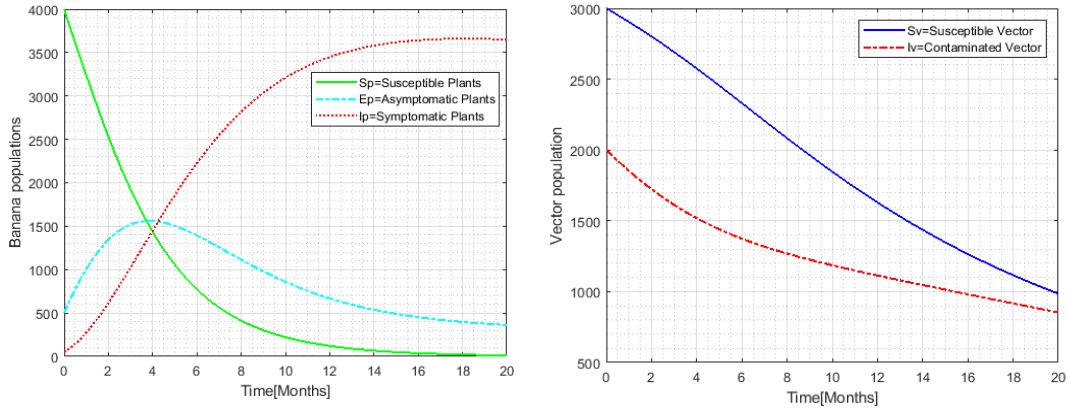


Figure 2: Sensitivity Indices for the model parameters

3.7. Numerical simulations

In this section we simulate the basic model to study the dynamics of BXW disease when control measures are not included. Although these results seem to be the expected behaviour, however this study has established the optimal rate that will reduce the new infections to the lowest possible level. From Figure3, it is observed that the number of susceptible plants decreases exponentially due to infection by BXW disease. The number of asymptomatic banana plants increases during the first four months of infection. After four months the number of asymptomatic plants starts to decrease while the number of symptomatic plants continues to increase. This is because most of the banana cultivars start showing symptoms after 3 months and hence reduce the number of a symptomatic plants.



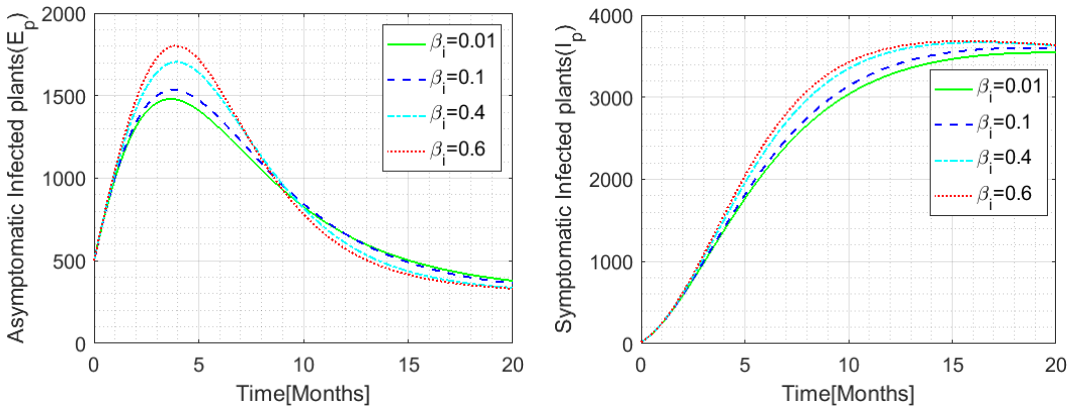
(a) Banana population (b) Vector population

Figure 3: Population dynamics

It can also be observed that without control measures, after 18 months all the banana plants will be infected with or without symptoms, which implies that there will be no susceptible plants. Figure 3 shows that the number of both susceptible and contaminated vectors in the farm decreases with time as the number of banana plants decrease. This may be attributed by low recruitment rate vs. high mortality rate.

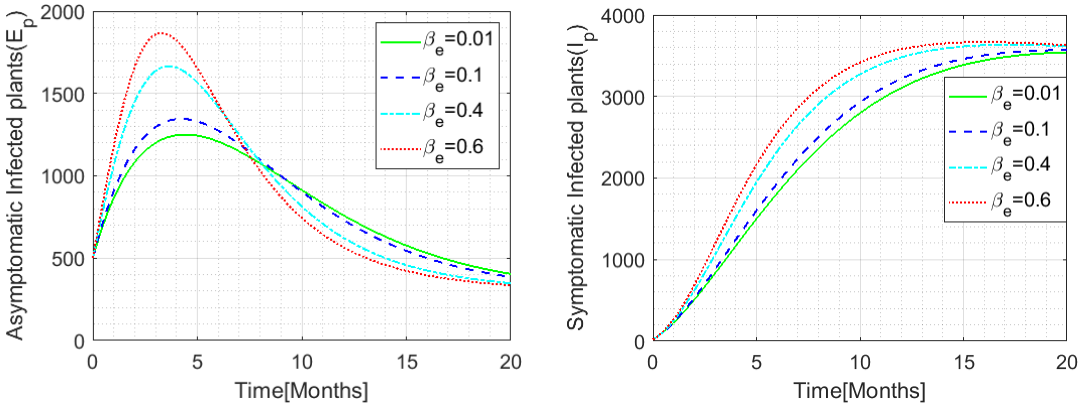
Sensitive parameters

Figure 4 shows that as the rate of infection through farming tools contaminated with Xcm bacteria from symptomatic infected banana plants (β_i) increases dramatically increases the number of asymptomatic and symptomatic infected banana plants. This eventually results to the increase in number of symptomatic infected plants. Figure 5 shows that increasing the rate of infection through farming tools contaminated with Xcm bacteria by an asymptomatic infected banana plant (β_e) increases the number of secondary infections.



(a) Effect on E_p (b) Effect on I_p

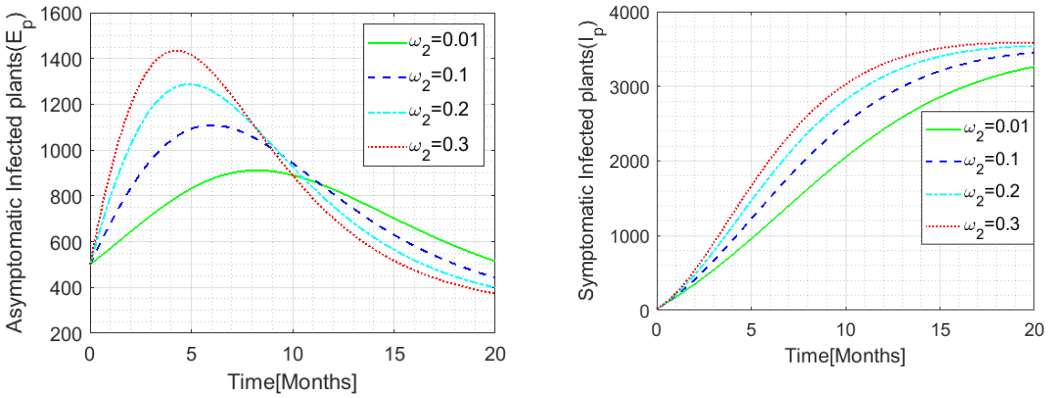
Figure 4: Variations in the rate of infection through farming tools contaminated from symptomatic infected banana plants



(a) Effect on E_p (b) Effect on I_p

Figure 5: Variations in the rate of infection through farming tools contaminated from asymptomatic infected banana plants

This implies that when performing farming activities, farmers may transmit the BXW disease unknowingly through asymptomatic infected banana plants thinking that they are health plants. In Figure6 it can be observed that increasing the rate of infection through contaminated soil (ω_2) increases the number of asymptomatic and symptomatic infected banana plants.

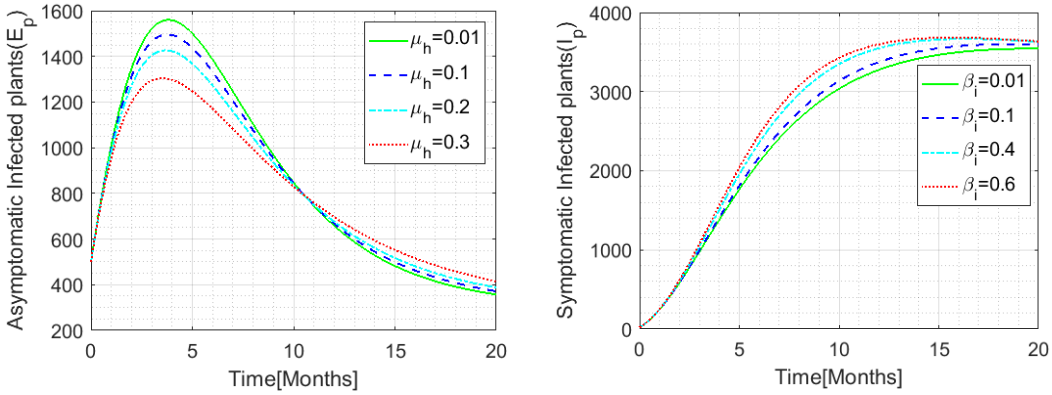


(a) Effect on E_p (b) Effect on I_p

Figure 6: Variations in the rate of infection through contaminated soil

With reference to Figure 7, the natural clearance rate of Xcm bacteria in the soil (μ_h) has an impact of on the dynamics of BXW disease. Increasing μ_h reduces the number of new infections generated through contaminated soil. Therefore increasing this parameter decreases the number of Xcm bacterium in the soil and hence reduces the number of secondary infection through contaminated soil. Furthermore, Figure 8 shows

that timely removal of infected symptomatic plants reduces the number of new infections generated by a symptomatic infected banana plant.



(a) Effect on E_p (b) mEffect on I_p

Figure 7: Variations in the natural mortality rate of Xcm bacteria in the soil

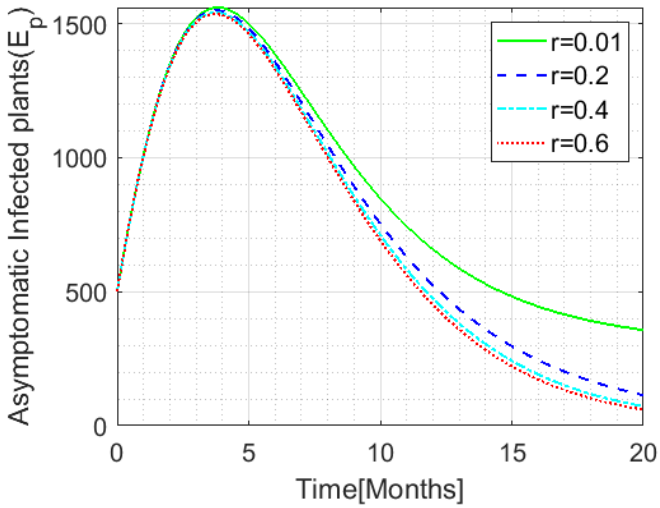


Figure 8: Variations in the rate of removing symptomatic infected plants from the farm

4. Conclusions

From the results, it is observed that the most sensitive parameters of the model are: the rate of infection through farming tools contaminated by Xcm bacteria from symptomatic infected plants (β_i), the rate of infection through farming tools contaminated by Xcm bacteria from asymptomatic infected plants (β_e), the rate of infection through contaminated soil (ω_2), rate of removing infected banana plant from the farm (r), Clearance rate of bacteria in the environment (μ_h), vertical transmission (θ), and

disease induced death rate of an infected banana plant (d). Results from the parameter ω_2 and μ_h show that contaminated soil contributes to BXW disease transmission and persistence. Thus ignoring this component of the model may lead to underestimation of BXW disease transmission.

Therefore, in order to best contain the disease, along with the current control measures we propose the following recommendations to scientists and technologist:

- To carry out studies that will find a way infection from infected mother plant to its suckers can be reduced or completely stopped.
- To carry out studies that will find a way to speed up the clearance rate of Xcm bacteria in the soil without disturbing the ecosystem so as to avoid soil inoculum which is the source of soil borne infections and persistence of the disease in farm.
- Furthermore, technology for early detection of infected plants should be brought down to the local farmers at affordable costs, this will help stakeholders to detect and remove the infected plants from the farm on time. Also farmers when performing farming activities such as harvesting, pruning, weeding and removing of the infected symptomatic banana plants should sterilize their farming tools before moving to another banana plant.

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