

Development of Compartmental Mathematical Model of Disease Transmission of Basal Stem Rot in Oil Palm Plantation

Halina Hanim Mustafa, Nor Azah Samat, Zulkifley Mohamed, Faizah Abu Kassim

Abstract: The mathematical modelling is one of the major research areas for mathematician and biologist in understanding the dynamics of transmissible infections. There might also be a mathematical model used to research the dynamics of plant disease and estimate the number of cases of outbreaks. In this research, we developed the compartmental mathematical model of the dynamical spread of transmission of plant disease with reference to basal stem rot (BSR) disease in oil palm plantation. The dynamics of the BSR disease were studied by a prone-contagious-sustained (PCS) compartmental mathematical model involving ordinary differential equations for three classes of hosts; prone, contagious and sustained. The equilibrium points and epidemic threshold conditions were analytically determined and numerical simulations were analyzed to support analytical results. From the numerical results, the solutions converge to each equilibrium state and PCS model simulation indicated that BSR disease has not become endemic. In particular, the threshold parameters that summarize the dynamics of the system will help to choose strategies for crop protection.

Keywords: Compartmental mathematical model, basal stem rot disease, prone-contagious-sustained, disease transmission and threshold parameters

I. INTRODUCTION

Mathematical models are an essential instrument for studying the propagation of infectious diseases. This instrument can be utilized in identifying the most influential features in the spread of the disease, predicting disease progression and propose prevention and control strategies. The development of mathematical models provides a useful role in analyzing problems arising in various fields including health, chemistry, and biology.

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Mathematical models are also used in life science and medicine [12]. Moreover, mathematical models have been widely used in economics, physics, chemistry, biology and engineering fields [13].

Many dynamical social phenomena were modelled by using mathematical epidemiology model [14] spread of political parties [15], [16] and others. Mathematical modelling is also an important tool for assessing the problems faced in the agricultural sector and also examining the diseases that impact the country's agricultural produce. Nowadays, the usage of mathematical models to research agricultural diseases that may influence crop yields is increasing rapidly.

Numerous studies in agriculture apply mathematical theory, such as the Susceptible-Infected-Recovered (SIR) model, as a mechanism to view and study the dynamics of plant disease spread. According to [17], the use of models to understand epidemics has grown from the 1960s to an important approach for understanding plant diseases. Many researchers have numerically and analytically analyzed infectious plant disease models such as soil-borne disease [18], [19], vector-borne disease [20], plant virus disease [21] and many more.

II. PURPOSE OF THE STUDY

This study will focus on developing a flexible compartmental mathematical model to understand the transmission of BSR disease caused by *Ganoderma boninense* fungus in oil palm plantation in Malaysia. The basic reproduction number of BSR disease will be determined and discussed. This study aims to analyze the features and predict the spread of BSR disease to help control disease transmission. The compartmental mathematical model is needed as it works based on the changing from susceptible into infected populations.

III. METHODOLOGY

A. The Compartmental Mathematical Model

The basic compartmental mathematical model for BSR disease transmission within a closed population is introduced. It will be a modification of the initial general compartmental framework of SIR model formulated by [22], [23] for epidemics of plant disease. However, this compartmental framework is named as PCS instead of SIR.



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The dynamics of BSR disease are analyzed using a PCS compartmental mathematical model comprising ordinary differential equations of three classes of palm host; prone palm hosts P(t), contagious palm hosts C(t) and sustained palm hosts S(t), where S(t) = P(t) + C(t) + S(t). Total palm hosts, S(t) = P(t) + C(t) + S(t) are assumed constant. The PCS compartmental transmission model is displayed in Fig. 1.

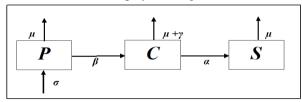


Fig. 1. PCS Compartmental Transmission Model

Fig. 1 describes the transition of the palm host from P to C to S. The arrow heading into the interior of the compartment indicates a positive term. On the other hand, the reverse sign is a negative term in the differential equation. It means that when a palm host becomes infected, it becomes immediately contagious and is able to infect other palm hosts. However, the contagious palm host may recover from BSR disease and sustained. In the compartmental model, all parameters (σ , μ , β , α and γ) are non-negative constants considered for the following definitions: denotes σ the host recruitment/replanting rate, μ corresponds to the rate of natural mortality, β is the rate of replication of the disease, α denotes the rate of survival of the infected host and γ is the risk of death induced by the disease.

Based on the visualization in Fig. 1, the basic disease transmission model for BSR disease is given by the subsequent deterministic system of non-linear differential equations:

$$\frac{dP}{dt} = \sigma - \beta PC - \mu P \tag{1}$$

$$\frac{dC}{dt} = \beta PC - (\mu + \gamma)C - \alpha C \tag{2}$$

$$\frac{dS}{dt} = \alpha C - \mu S \tag{3}$$

The assumptions used in developing the PCS model are listed in Table 1.

Table 1: PCS Model Assumptions

Criteria	Assumptions	
Pathogen	The palm host infected by Ganoderma boninense fungus	
Transmission type	BSR disease outbreak caused by soil-borne disease transmission	
Soil	All palm hosts are planted in a soil which is prone to BSR disease	
Age	Involves all ages of infected oil palm trees	
Other factors	BSR disease factors caused by other pathogens and environmental conditions are not considered	
Population	This model was considered in a closed plant population	
Treatment	All palm hosts are assumed to have been treated	
Sustained hosts	Not fully recovered or immune to BSR disease	

B The Analysis of the Compartmental Mathematical Model

The standard dynamical method is used to analyze the model. Equilibrium of system (Eq. 1-3) can be solved by letting each of the equations equal to zero, so that the possible equilibrium of the system in Eq. 1-3 are $E_0(1,0,0)$ and

$$E_{1}\left(\frac{\mu+\gamma+\alpha}{\beta}, -\frac{\mu^{2}+\mu\gamma+\mu\alpha-\sigma\beta}{\beta(\mu+\gamma+\alpha)}, -\frac{\alpha(\mu^{2}+\mu\gamma+\mu\alpha-\sigma\beta)}{\beta(\mu+\gamma+\alpha)\mu}\right) \text{ Eq}$$

uilibrium points E_0 and E_1 are the disease-free equilibrium

point and the endemic equilibrium point, respectively. The equilibrium point of disease-free is a steady-state solution, where the population has no disease in the population, while the equilibrium point of endemic is a steady-state solution where the disease exists in the population. The linear stabilization of the disease can be achieved by utilizing the next generation matrix process [24] on the system in Eq. 1-3. The matrix **A** and **B** for the new terms of infection and the remaining terms of transition respectively can be written as:

$$\mathbf{A} = \left[\beta P \right] \tag{4}$$

$$\mathbf{B} = \left[\mu + \gamma + \alpha\right] \tag{5}$$

The equilibrium of disease-free is $E_0(1,0,0)$, thus the basic reproduction number is written as $R_0 = \rho(AB^{-1})$, where ρ is the spectral radius can be written as

$$R_0 = \frac{\beta}{\mu + \gamma + \alpha} \tag{6}$$

Next, the dynamics of these equilibrium point will be discussed. The purpose of doing this analysis is to determine whether the equilibrium point of disease-free and the equilibrium point of endemic are stable.

At E_0 , when $R_0 < 1$, the equilibrium of disease-free of the system (Eq. 1-3) is locally asymptotically stable. In order to accomplish this step, the above differential equations is linearized to a Jacobian matrix to stabilize the equilibrium point of disease-free. At this equilibrium E_0 , the Jacobian matrix can be written as

$$\mathbf{J}(E_0) = \begin{bmatrix} -\mu & -\beta \\ 0 & \beta - \mu - \gamma - \alpha \end{bmatrix}$$

with $\det(\mathbf{J}(E_0)) = \mu(-\beta + \mu + \gamma + \alpha)$ and $\operatorname{trace}(\mathbf{J}(E_0)) = -2\mu + \beta - \mu - \gamma - \alpha$. If $R_0 < 1$, the value of $\det(\mathbf{J}(E_0)) > 0$ and $\operatorname{trace}(\mathbf{J}(E_0)) < 0$ are obtained. Therefore, the equilibrium point of disease-free, E_0 is locally asymptotically stable for $R_0 < 1$ and the equilibrium of endemic does not exists. This shows that the disease is being phased out of the population. On the other hand, the equilibrium point of disease-free is unstable if $R_0 > 1$.

Next, the system around E_1 is shown locally asymptotically stable if $R_0>1$ under some sufficient conditions, otherwise unstable. At E_1 of the equilibrium point of endemic, the Jacobian matrix can be written as

$$\mathbf{J}(E_1) = \begin{bmatrix} \frac{\mu^2 + \mu\gamma + \mu\alpha - \sigma\beta}{\mu + \gamma + \alpha} - \mu & -\mu - \gamma - \alpha \\ \frac{\mu + \gamma + \alpha}{\mu + \gamma + \alpha} & 0 \end{bmatrix}$$

with $\det(\mathbf{J}(E_1)) = -\mu^2 - \mu\gamma - \mu\alpha + \sigma\beta$ and





trace
$$(\mathbf{J}(E_1)) = \frac{\mu^2 + \mu\gamma + \mu\alpha - \sigma\beta}{\mu + \gamma + \alpha}$$
 trace. If $R_0 > 1$,

 $\det(\mathbf{J}(E_1))$ is always a positive value and $\operatorname{trace}(\mathbf{J}(E_1))$ is always a negative one. Thus, it is concluded that the equilibrium point of endemic, E_1 is locally asymptotically stable for $R_0 > 1$. In this case, the disease has become endemic in the population. While, the equilibrium point of endemic, E_1 is not stable if $R_0 < 1$.

IV. FINDINGS AND DISCUSSIONS

The model's numerical analysis of Eq. 1-3 is presented to show the dynamical changes of each population with the transmission of BSR disease in oil palm plantations. According to [25], the understanding of dynamics of an infectious disease provides an insight into dynamical characteristics and as stated by [26] this will help in formulating appropriate and effective strategies to prevent the spread in a population. The parameters used in developing of the PCS model were shown in Table 2.

Table 2: Parameter Values of PCS Model

Param eter	Symbol	Parameter value
Recruitment of palm host	σ	9,119,812
Natural death rate	μ	0.04
BSR disease incidence rate	β	0.0371
BSR disease-induced mortality rate	γ	0.05433
Recovery rate of infected host	α	1.3333

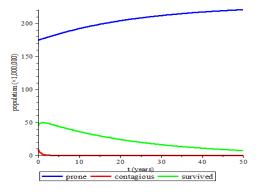


Fig. 2. The Dynamics of PCS Model for BSR Disease

The model was simulated using Maple15 software using the set of estimated parameter as tabulated in Table 2 and the numerical results are shown in Fig. 2. The result is presented graphically in the subsequent figure.

Fig. 2 illustrates the dynamics of BSR disease in oil palm plantations in Malaysia. In this figure, it can be seen that dynamically changes happen in every population. The solutions converge to the BSR disease free equilibrium state. From this figure, starting from the initial condition, the number of prone palm hosts increases while the number of contagious palm hosts decreases. The population P moves up and in the long term, this population will converge to the total population. Population P moves down dramatically and this

population will be disappeared very fast. Meantime, the population S moves up a little bit to about 50 million populations. Finally, population S is decreasing and in the long term this population converge to zero.

From the result, the basic reproduction number obtained is $R_0 = 0.026$, or $R_0 < 1$. This means that in the long run, the pathogen will not spread the disease to the other palm host and within a certain amount of time BSR disease will be phased out.

V. CONCLUSION

In this study, a differential system to model a soil-borne plant disease was proposed. The primary purpose is to investigate the dynamics of BSR disease in oil palm plantations. The analysis on the findings revealed that if the basic number of reproductions is less than 1, the equilibrium

point of disease-free, E_0 is locally asymptotically stable. It implies that the population will be free from disease for a given period of time. The results show that the basic reproductive number, R0 serves a crucial function in establishing the disease's survival or death. Efforts need to be done to ensure that oil palms cultivations are free from BSR disease. In conclusion, the model and presented results may be useful as a step in the decision-making process as well as improvement of the approaches to prevent and monitor BSR disease.

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REFERENCES

- H.J. Chang, "Estimation of basic reproduction number of the Middle East respiratory syndrome coronavirus (MERS-CoV) during the outbreak in South Korea." Biomedical Engineering, 2017; 16(1), 79.
- O. Zakary, M. Rachik and I. Elmouki, "On the impact of awareness programs in HIV/AIDS prevention: an SIR model with optimal control." International Journal of Computer Applications, 2016; 133(9), 1-6.
- H. Nishiura, "Correcting the actual reproduction number: a simple method to estimate R0 from early epidemic growth data." International Journal of Environmental Research and Public Health, 2010; 7(1), 291–302.
- L.E. Aik, L.C. Kiang, T.W. Hong and M.S. Abu, "The SIR model of Zika virus disease outbreak in Brazil at year 2015." AIP Conference Proceedings, 2017; 1847.
- N.A. Samat and A.C. Awang, "The discrete time- space SIR-SI age-structured model for leptospirosis." International Journal of Engineering & Technology, 2018; 5(x), 1-4.
- M.A. Khan, S.F. Saddiq, S. Islam, I. Khan and S. Shafie, "Dynamic behavior of leptospirosis disease with saturated incidence rate." International Journal of Applied and Computational Mathematics, 2016; 2(4), 435-452.
- A. Enagi and M. Ibrahim, "A mathematical model of effect of bacillus calmette-guerin vaccine and isoniazid preventive therapy in controling the spread of tuberculosis in Nigeria." Journal of Modern Mathematics and Statistics, 2011; 5(1), 25-29.
- I.A. Adetunde, "On the control and eradication strategies of mathematical models of the tuberculosis in a community." Environmental Research Journal, 2008; 2(4), 155-158.



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- J. Lamwong and P. Pongsumpun, "Mathematical model of avian influenza when there is the traveling of tourists from the risk countries. International Journal of Soft Computing, 2016; 11(3), 120-126.
- S. Mushayabasa, "A simple epidemiological model for typhoid with saturated incidence rate and treatment effect." International Journal of Mathematical, Computational, Physical, Electrical and Computer Engineering, 2012; 6(6), 688-695.
- S. Mushayabasa, "Impact of vaccines on controlling typhoid fever in Kassena-Nankana district of upper east region of Ghana: Insights from a Mathematical Model." Journal of Modern Mathematics and Statistics, 2011; 5(2), 54-59.
- H. Takeuchi, O. Georgiev, M. Fetchko, M. Kappeler, W. Schaffner and D. Egli, "In vivo construction of transgenes in drosophila." Genetics, 2007; 175(4): 2019-2028.
- 13. S. Strogatz, "Exploring complex networks." Nature, 2001; 410, 268-276.
- K. Kawachi, "Deterministic models for rumor transmission." Nonlinear Analysis: Real World Applications, 2008; 9(5), 1989-2028.
- A.K. Misra, "A simple mathematical model for the spread of two political parties." Nonlinear Analysis: Modelling and Control, 2012; 17(3), 343–354.
- B. Yong and N.A. Samat, "Effect of (social) media on the political figure fever model: Jokowi-fever model." AIP Conference Proceedings, 2016; 050021.
- A. Van Maanen and X.M. Xu, "Modelling plant disease epidemics." European Journal of Plant Pathology, 2003; 109(7), 669-682.
- M. Su, and H. Zhang, "Optimal strategies for biological ontrol of soil-borne plant pathogens the basic model." International Journal of Nonlinear Science, 2014; 18(3), 210-216.
- D.J. Bailey and C.A. Gilligan, "Modeling and analysis of disease-induced host growth in the epidemiology of take-all." Phytopathology, 2004; 94(5), 535-540.
- R. Shi, H. Zhao and S. Tang, "Global dynamic analysis of a vector-borne plant disease model." Advances in Difference Equations, 2014; 2014(1), 59.
- Y. Luo, S. Gao, S., D. Xie and Y. Dai, "A discrete plant disease model with roguing and replanting." Advances in Difference Equations, 2015; 2015(1), 12.
- C.A. Gilligan, "Sustainable agriculture and plant diseases: An epidemiological perspective." Philosophical Transactions of the Royal Society B: Biological Sciences, 2008; 363(1492), 741-759.
- 23. C.A. Gilligan, "An epidemiological framework for disease management." Advances in Botanical Research, 2002; 38, 1-64.
- P. Driessche, Van Den and J. Watmough, "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission." Mathematical Biosciences, 2002; 180, 29-48.
- 25. A.G. Selvam and D.J. Praveen, "Qualitative analysis of a discrete SIR epidemic model." International Journal of Computational Engineering Research, 2015; 5(3), 35-39.
- P.R. Sekhara and M.N. Kumar, "A dynamic model for infectious diseases: the role of vaccination and treatment." Chaos, Solitons and Fractals, 2015; 75, 34-

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