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MATHEMATICAL ANALYSIS AND NUMERICAL SIMULATION OF SPATIAL-TEMPORAL MODEL FOR RICE TUNGRO DISEASE SPREAD

WAHYU SURYANINGRAT[*,†], NURSANTI ANGGRIANI, ASEP K. SUPRIATNA

Department of Mathematics, Faculty of Mathematics and Natural Science, Universitas Padjadjaran, Bandung 45363, Indonesia

Abstract: Agricultural sector plays an important part in the issue of food security. Increasing agricultural productivity is a sustainable strategy in agricultural development and food security. Plant diseases can significantly reduce the quality and quantity of agricultural production. Plant disease control is needed to maintain the quality and quantity, including the spread of rice disease. Mathematical modeling can be used to study plant epidemiology. In modeling plant epidemiology, several aspects need to be considered. This study aims to develop and analyze a mathematical model of the spread of plant diseases by considering the presence of disease-carrying vectors, biological agents, and spatial environmental aspects. The purpose of this study is to investigate the behavior of disease spread in plants and the influence of the spatial-temporal model that was built. We analyze conditions for the existence of the solution of the model and the equilibrium point. Numerical simulations are performed to show dynamical solution of model and confirm the results of the analysis.

Keywords: dynamic system; mathematical modeling; plant epidemiology; spatial-temporal.

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[*] Corresponding author
E-mail address: wahyu16001@mail.unpad.ac.id
[†] Master of Mathematics Study Program
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1. INTRODUCTION

One of the important issues in the problem of global development is food security. Food security can be defined as “the condition in which all people, at all times, have physical and economic access to sufficient, safe and nutritious food to meet their dietary needs and food preferences for an active and healthy life” [1]. Efforts to maintain food security are listed in point 2 of the Sustainable Development Goals (SDGs) agreed by countries in the world, including Indonesia [2]. Furthermore, the global agenda for eliminating hunger, achieving good food and nutrition security, and promoting sustainable agriculture is explained.

The growing human population and the increasing demand for food are putting greater pressure on the agricultural sector and natural resources [3]. Some of the world's population does not fully have the ease of getting the food they need. Based on the FAO report, in 2019 there were still 820 million people who were malnourished [4]. In addition, in 2050 it is predicted that with 9.7 billion people in the world, the demand for food needs will increase by 70% more than what is needed today [1].

The agricultural sector plays an important part in the issue of food security. Increasing agricultural productivity is a sustainable strategy in agricultural development and food security. However, there are several factors that cause a decrease in the quantity and quality of agricultural production, especially in food crop commodities. Some of the main factors that influence it are the vulnerability of plants to disease, the presence of pests, weather, and global climate change [5].

A plant disease mathematical model was developed to provide a detailed description of how to describe, analyze and predict plant disease epidemics for the goal of developing and testing control strategies and tactics for crop protection [6]. Several important issues in modeling disease in humans and animals are found in plant epidemiology. However, there are aspects of plant epidemiology that are unique and present a challenge in modeling plant diseases [7].

Compartmental models have been developed to study plant epidemiology using a mathematical approach. Rida et al. (2016) proposed a mathematical model of vector-borne plant diseases with memory on the host and vectors with fractional integral forms [8]. Anggriani et al. (2018)

developed a plant epidemiological model involving fungicides with curative treatment [9].

Other research on the spread of plant diseases was carried out by developing a mathematical model by considering the policy of applying insecticides. Anggriani et al. (2017) developed a host-vector mathematical model for the problem of spreading tungro disease in rice [10]. In addition, Blas & David (2018) re-developed a model for the spread of tungro disease with two different types of infection and investigated roguing policies in rice [11]. Amelia et al. (2019) developed an optimal control model for the spread of jaundice in chili plants to determine the optimal policy for the system [12]. Suryaningrat et al. (2020) developed a host-vector model by taking into account the presence of biological agents and analyzing the optimal policy of insecticide application [13].

In an effort to consider environmental aspects into the model, several researchers developed a spatial-temporal model for human and plant epidemiology problems with the partial differential equation system approach. Zhu et al (2016) developed a model of the spread of chikungunya disease caused by the Aedes mosquito with the mobility of mosquitoes and humans [14]. Magal et al. (2020) developed a model for the spread of influenza by considering the diversity of spatial conditions in Puerto Rico [15]. Fitzgibbon et al. (2017) developed a host-vector model for the problem of the spread of Zika's disease in Rio De Janeiro using a partial differential equation approach [16].

The development of a spatial-temporal model has also been carried out in plant epidemiology, one of which is by Martin et al. (2020) who developed a mathematical model in the form of a system of partial differential equations to explain pathogenic infections in plants [17]. The modeling considers *Xylella fastidiosa* bacteria for a large number of plants that transmit from infected plants to susceptible plants.

Based on the description above, this research proposed the spatio-temporal model formulation and analysis for the spread of tungro disease in rice plants by taking into account the presence of biological agents. Dynamical systems analysis is used to study the dynamic behavior of the model. In confirming the results of the analysis, a numerical simulation is performed.

2. MODEL FORMULATION

The mathematical model for the problem of the spread of tungro disease in rice was built by developing a mathematical model researched by Anggriani et al. (2017), Suryaningrat et al. (2020) and Martin et al. (2020). In this research, the model is constructed by applying the following assumptions:

1. The observed population types consisted of plants, disease-carrying vectors and predators (P).
2. The plant population is divided into two groups: susceptible plants (S_h) infected plants (I_h).
3. The vector population is divided into two groups: vulnerable vectors (S_v) & infected vectors (I_v).
4. Newly grown plant and vector populations are vulnerable populations, where they have not been infected with Tungro disease.
5. Tungro disease transmission can occur because the vector carries the virus from infected plants.
6. Plants and vectors that are infected do not recover.
7. It is assumed that the spatial position of the environment is limited to 1-dimensional space $\Omega \subset \mathbb{R}$.
8. Vectors and predators are assumed to move randomly in the observed environment Ω.

Based on the assumptions and descriptions in the previous section, a flow diagram is formed as shown in Figure 1.

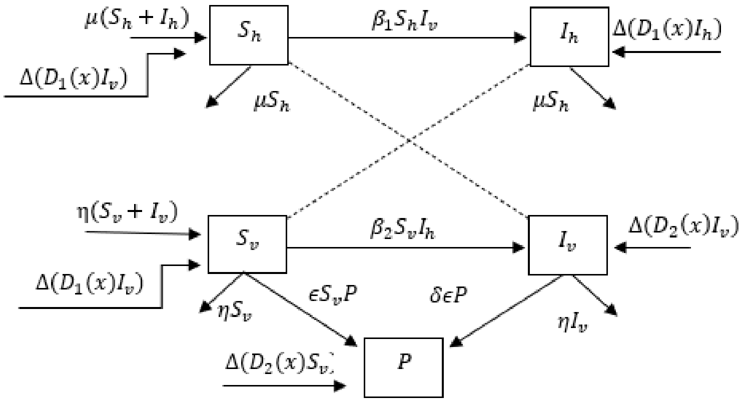


Figure 1. The rice tungro disease transmission flow with diffusion

All the parameters contained in the model are described in Table 1.

Table 1. Parameters Description.

Parameters/Variables	**Description**	**Unit**
t	Time	Day
μ	Natural birth rate of plants	1/day
η	Natural birth rate of vector	1/day
β_1	The rate of transmission from vector to plants	1/individual × day
β_2	The rate of transmision from plants to vector	1/ individual × day
ε	Predation rate	1/ individual × day
$D(x)$	Difussion coefficient	Individual ^2 / day

Thus, the mathematical model of the spread of tungro disease in rice plants with biological agents is shown in equation (1) - (5).

(1) $$\frac{\partial S_h}{\partial t} = \Delta\left(D_1(x) S_h(x,t)\right) + \mu\left(S_h(x,t) + I_h(x,t)\right) - \beta_1 S_h(x,t) I_v(x,t) - \mu\, S_h(x,t)$$

(2) $$\frac{\partial I_h}{\partial t} = \Delta\left(D_1(x) I_h(x,t)\right) + \beta_1 S_h(x,t) I_v(x,t) - \mu\, I_h(x,t)$$

(3) $$\frac{\partial S_v}{\partial t} = \Delta\left(D_2(x) S_v(x,t)\right) + \eta\left(S_v + I_v\right) - \beta_2 S_v(x,t) I_h(x,t) - \varepsilon\, S_v(x,t) P(x,t) - \eta S_v(x,t)$$

(4) $$\frac{\partial I_v}{\partial t} = \Delta\left(D_2(x) I_v(x,t)\right) + \beta_2 S_v(x,t) I_h(x,t) - \varepsilon\, I_v(x,t) P(x,t) - \eta I_v(x,t)$$

(5) $$\frac{\partial P}{\partial t} = \Delta\left(D_1(x) P(x,t)\right) + \varepsilon\left(S_v(x,t) + I_v(x,t)\right) P(x,t)$$

$$\forall t \geq 0, x \in \Omega \subset \mathbb{R},$$

with the initial conditions and the limitation of Neuman conditions, where there are no populations out of their habitat, as follows

(6) $$\begin{cases} S_h(x,0) = S_h^0(x) \geq 0 \\ I_h(x,0) = I_h^0(x) \geq 0 \\ S_v(x,0) = S_v^0(x) \geq 0 \\ I_v(x,0) = I_v^0(x) \geq 0 \\ P(x,0) = P^0(x) \geq 0 \end{cases}$$

$$\partial_n S_h(x,t) = \partial_n I_h(x,t) = \partial_n S_v(x,t) = \partial_n I_v(x,t) = \partial_n P(x,t) = 0.$$

All parameters used in models (1) - (5) are non-negative and the model will be analyzed in its feasible area. Let $S_h\left(x,t\right)+I_h(x,t)=N(x)$, where N is a spatially dependent function. $S_h\left(x,0\right), I_h(x,0), S_v(x,0), I(x,0), \text{and } P(x,0)$ are continuous, non-negative functions in Ω.

3. MATHEMATICAL ANALYSIS

To ensure that models (1) - (5) are well defined and have epidemiological significance, it is necessary to check the existence and solution positivity of the model.

Theorem 1. If the initial value of the system follows equations (7) and (8), then the solution $S_h\left(x,\text{t}\right), I_h(x,\text{t}), S_v(x,\text{t}), I(x,\text{t}), \text{and } P(x,\text{t})$ of models (1) - (5) exist and unique. Furthermore, there are positive constants M and $\max_{x\in\Omega}\left\{\gamma\left(x\right)/\beta\left(x\right)\right\}$ such that $0<S_h\left(x,t\right), I_h\left(x,t\right)\le M$ for $x\in\Omega, t\in\left(0,\infty\right)$.

The disease-free equilibrium point is obtained when each population growth rate in the system (1) - (5) is zero or in other words zero growth rate, which is an equilibrium condition in which the population of rice and vectors does not grow or decreases to near zero. So that it is obtained four equilibrium point as shown in Table 2.

Table 2. Equilibrium Point of Model

Equilibrium	$T=\left(S_h,I_h,S_v,I_v,P\right)$
Non-endemic predator not exists	$T_1=\left(N\left(x\right),0,\dfrac{C^*}{D_1\left(x\right)\lvert\Omega\rvert_\mu},0,0\right)$
Non-endemic predator exists	$T_2=\left(N\left(x\right),0,0,\dfrac{C^*}{D_1\left(x\right)\lvert\Omega\rvert_\mu}\right)$
Endemic predator not exists	$T_3=\left(\dfrac{\eta}{\beta_2\left(x\right)},\dfrac{\beta_1\left(x\right)\eta C*}{D_1\left(x\right)\lvert\Omega\rvert_\mu\beta_2\left(x\right)\mu},\dfrac{C*}{D_1\left(x\right)\lvert\Omega\rvert_\mu},\dfrac{C*}{D_1\left(x\right)\lvert\Omega\rvert_\mu},0\right)$
Endemic predator exists	$T_1=\left(S_h,I_h,S_v,I_v,P\right)$

4. NUMERICAL SIMULATION

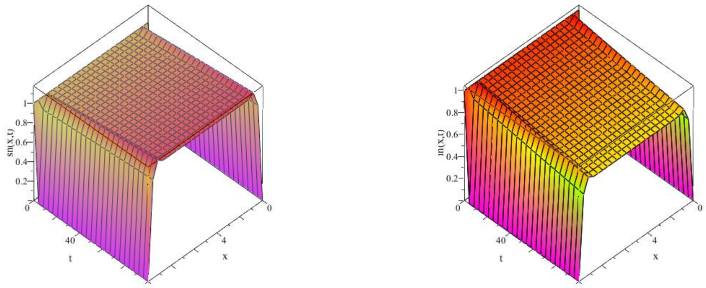
Numerical simulation is used to find out the solution to the population dynamics of each compartment on Model (1)-(5). The numerical method we used is Runge-kutta order 4 with Maple 15 software. We defined three scenarios with some parameter changes and initial values as shown in the Tabel III.

In these three simulations we show the difference between the values for the transmission rate parameters and the initial values for each compartment, to show their effect on the dynamics of the number and spatial distribution of each compartment. The first scenario specifies a constant transmission rate and initial value for each location x. The second scenario shows a simulation when the transmission rate is spatially heterogeneous, where a location-dependent function is used. While in the third scenario it is assumed that the transmission rate and initial value for each compartment also depend on the location.

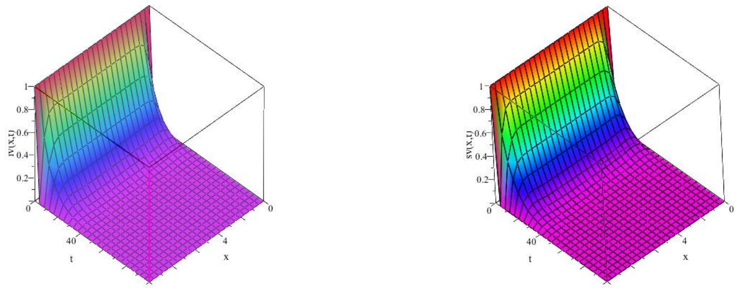
Table 3. Parameters Value

Parameters	**Scenario**		
	1	**2**	**3**
μ	0.0015	0.0015	0.0015
η	0.0125	0.0125	0.0125
$\beta_1(x)$	1.5 × 10-1	1.5 × 10-4	$\left(1-\frac{x}{10}\right)\left(1-\exp\left(\frac{-20x}{10}\right)\right)$
$\beta_2(x)$	2.5 × 10-4	2.5 × 10-4	$\frac{2}{3}\beta_2(x)$
ε	5 × 10-4	5 × 10-4	5 × 10-4
$D_1(x)$	0.1	0.1	0.1
$D_2(x)$	0.2	0.2	0.2

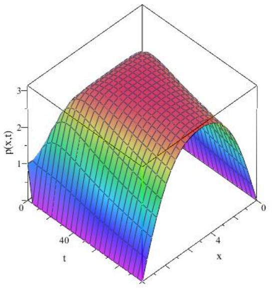
4.1. Scenario 1



(2a) Susceptible Plant $S_h(x,\mathrm{t})$ (2b) Infected Plant $I_h(x,\mathrm{t})$



(2c) Susceptible Vector $S_v(x,\mathrm{t})$ (2b) Infected Vector $I_v(x,\mathrm{t})$

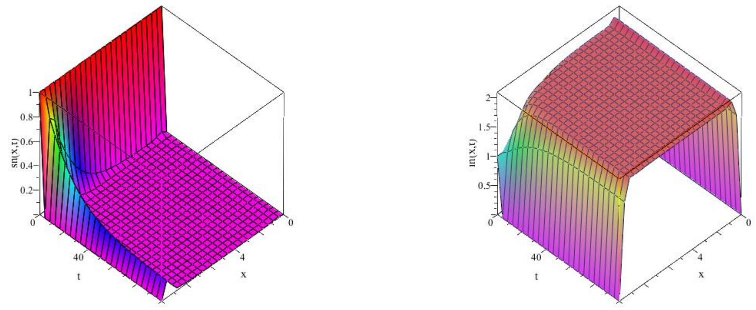


(2d) Predator $P(x,\mathrm{t})$

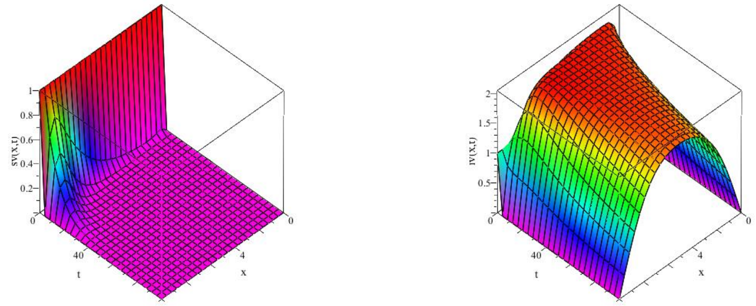
Figure 2. First scenario spatial-temporal plot for population

The simulation in the first scenario is carried out by setting all parameter values and the initial value of each compartment constant regardless of location x. Figure 2 shows the population dynamics plot of each compartment in first scenario. After passing 40 days, the susceptible vector (S_v) and infected vector (I_v) compartments for each location x are getting closer to zero. The susceptible plant population (S_h) increases slowly over time, followed by a decrease in the infected plant population (I_h). The predatory population (P) persists and approaches a fixed distribution for every x.

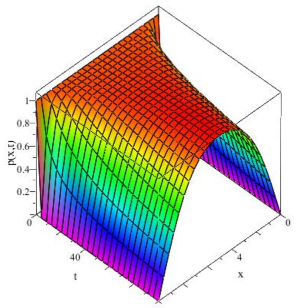
4.2. Scenario 2



(3a) Susceptible Plant $S_h(x, \mathrm{t})$ (3b) Infected Plant $I_h(x, \mathrm{t})$



(3c) Susceptible Vector $S_v(x, \mathrm{t})$ (3b) Infected Vector $I_v(x, \mathrm{t})$

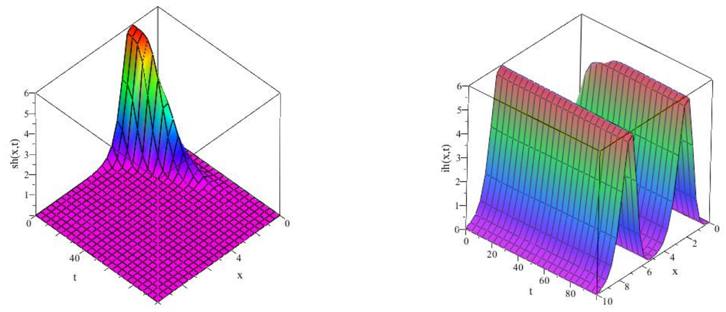


(3d) Predator $P(x, \mathrm{t})$

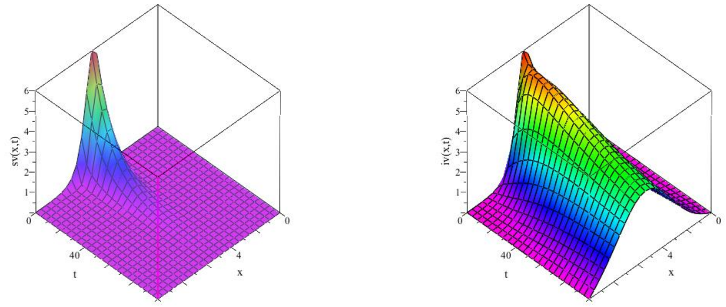
Figure 3. Second scenario spatial-temporal plot for population

Figure 3 shows the population dynamics plot of each compartment in second scenario. In this second scenario we applied the disease transmission rates β_1 and β_1 depending on location x. We set initial condition for each compartemen have equal to one for every location x. The numerical simulation shows that the population of susceptible plants (S_h) and susceptible vectors (S_v) decreases significantly and approaches zero over time. This shows the continuous transmission of disease in the system. Meanwhile, infected plant populations (I_h), infected vectors (I_v), and predators (P) still exist and approach a fixed spatial distribution.

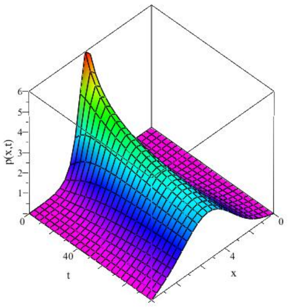
4.3. Scenario 3



(4a) Susceptible Plant $S_h(x,\mathrm{t})$ (4b) Infected Plant $I_h(x,\mathrm{t})$



(4c) Susceptible Vector $S_v(x,\mathrm{t})$ (4b) Infected Vector $I_v(x,\mathrm{t})$



(4d) Predator $P(x,\mathrm{t})$

Figure 4. Third scenario spatial-temporal plot for population

Figure 4 shows the population dynamics plot of each compartment in third scenario. The simulation in the third scenario determines the disease transmission rate depending on location x, as applied to scenario two, and the initial value for each compartment which depends also on location x. The numerical simulation shows that the susceptible plant population $\left(S_h\right)$ and the susceptible vector $\left(S_v\right)$ decrease and will be depleted for each location x over time. Meanwhile, infected plant populations $\left(I_h\right)$, infected vectors $\left(I_v\right)$, and predators $\left(P\right)$ exist and approach a relatively fixed distribution.

5. CONCLUSIONS

Based on the results and discussion in previous section, it can be constructed a mathematical model of the spread of tungro disease in rice plants using biological agents, involving spatial-temporal aspects with a partial differential equation system approach. The spatial-temporal model of tungro disease spread can be shown to have a bouned and positive solution. Numerically, the endemic equilibrium points in the tungro disease spread model with the spatial-temporal aspect exists and is stable. In the third scenario heterogeneous spatial conditions can be included in the model so that it can approach a more realistic situation.

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CONFLICT OF INTEREST

The author(s) declare that there is no conflict of interest.

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