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Host vector dynamics of pine wilt disease model with convex incidence rate

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ABSTRACT

The present studies provide qualitative aspects of pine wilt disease model while incorporating convex incidence rate. Studying the nature of the proposed model, it is shown that the basic reproductive number completely determine various dynamics of the model. The global asymptotic stability analysis is expounded at different equilibrium points. The model has shown that the disease disappear, when the threshold quantity falls below unity. Numerical results are presented graphically to illustrate theoretical discussions.

1. Introduction

Pine wilt disease (PWD), caused by the pinewood nematode is a devastating disease as it usually kills effected trees with in few weeks. The disease has already caused severe devastation of pine trees in Eastern Asiatic countries, with its sudden spread in Japan, China, South Korea and extending to western Europe. Around the world in the quarantine list of many countries pine wood nematode (PWN) is one of the major pests [16]. PWN is native to North America however it was first reported in 1905 in Japan and since then it is a major invasive nematode with widespread occurrence in China Korea, Mexico and Portugal. Its prolific spread renders severe threats to forest ecology, ecosystem functioning and forest industry. Basically pine wilt kills Scots pine, beside this many other pine species such as Jack, Austrian, Mogo and Red pines are occasionally destroyed by the pine wilt. In living trees, PWN disturb the xylem conduits and affects the cortical and xylem resin canals. Through the resin canal they can reach rapidly to all parts of the system and its branches. Initially both virulent and non-virulent forms of PWN produces localized embolism in xylum tissue [3]. Afterward the virulent PWN disturb the stem as well as leaf and suddenly decreases water availability till it destroy the trees [3]. When a susceptible tree is infected by pine wood nematode there is no treatment except standard techniques that are used for protection. The best technique is to separate non-native pine species from areas where the normal temperature exceeds 200^{o}C. In the area of non-native trees, sufficient supply of water in dry season is another technique for the protection. Similarly, to increase the rate of mortality of insects in timber through the specialized treatment, the damaged branches of the effected trees or even the dead trees can be removed.

Mathematical modeling is a handy tool to understand how a disease can spread and also it determines various factors that can play vital role in the spread of a disease. Such models require to unify the non-decreasing volume of data which is being generated on host pathogen interactions. Several theoretical surveys of population dynamics, evolution of infectious diseases of humans, animals and plants are connected with this problem. Different techniques can be used to analyze the spread of a disease. On pest-tress dynamics, several models have been developed. The authors in [11,12] explored some results for the transmission of PWD models. While incorporating nonlinear incidence rate K. S. Lee et al.

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investigated the global stability analysis of host vector pine wood disease model [13]. Recently Awan and his coauthors in [2] explored the stability analysis of pine wilt while incorporating the periodic use of insecticides. The authors showed that epidemic level of infected vectors do not depend upon the saturation while assuming the transmission through mating.

In mathematical epidemiology incidence is a measure which shows the probability of occurrence of a given medical condition in a population of a particular time interval. In mathematical epidemiology transmission of a disease depends upon the type of incidence rate. In medicine and public health, transmission is passing of a pathogen causing communicable disease from one infected host individual or group to a particular individual or group. In literature incidence rate is also known as force of infection and it plays important role in SIR, QSIR, SEIR, and other biological models. Generically this term is a mathematical function and it shows the mechanism of transmission of disease. In most cases it depends on the susceptible or potential as well as infective compartment of the population, say $g(S, I)$. Using the principle of mass action a simple form for the force of infection is described by bilinear incidence rate. If per capita contact rate is represented by α, then the disease will spread at rate $g(S, I) = \alpha SI$. Nevertheless, V. Capasso et al. and other researchers gave emphasis to assume non-linear incidence rate for particular diseases like cholera etc. [4–6]. Afterward some authors developed a new kind of nonlinear incidence rate [1]. Among the important incidence rates following is one of the function which describes the relationship of susceptible and infected individual in a new scenario [17].

$$g(S, I) = kIS(1 + \alpha I), \tag{1}$$

where the parameters k and α are positive constants. For a short time period it corresponds to an increase rate of infection which causes due to two exposures. The contact rate kIS results from single contact, while the term αkI^2S corresponds to a new infective which come into being due to the double exposure. One of the benefits of the force of infection is that it can be considered in SIR model which do not acquire permanent immunity. Therefore, a portion of the compartment R re-enter the susceptible class. Such type of models show various kinds of dynamics, which include detection of Hopf and Bogdanov bifurcation as well as saddle-node.

In the present manuscript we propose host vector model for pine wilt disease with convex incident rate and will discuss the qualitative aspects of the model. Significance of convex incidence rate is that when the infected population I grows, the possibility of a single infected individual to transfer the disease further to other potential individuals increases. This kind of effect is usually associated with some form of community effect or cooperation. Moreover, local and global stabilities are expounded at disease present equilibrium point, using the techniques described in [7,14]. At the end of paper numerical simulations are provided to support the main results of the manuscript.

2. Formulation of mathematical model

This part of the paper is concern with formulation of the mathematical model governing the proposed phenomena. It represents the transmission of disease induced by vectors. The threshold quantity will be used to explore the dynamics of the model. It is observed that during the maturation feeding of infected vectors the transmission of nematodes occur in pine trees bark beetles. When pine sawyers come out from infected pine trees it possess pinewood nematode Bursephelendus. In some situation the beetles catch infection directly during mating. We suppose the following hypothesis on various compartments of the populations in the environment.

2.1. Compartments in pine trees population:

The population of trees is divided into three subclasses, susceptible host, exposed and infected trees. The description is given as;

Susceptible pine trees S_H: It denotes those individuals in pine trees that have capability to catch infection viz nematode and can exude oleoresin. It plays a role of physical barrier to beetle oviposition and beetles cannot oviposit on them.

Exposed pine trees E_H: Those infected pine trees that possess the potential for oleoresin exudation.

Infected pine trees I_H: Those pine trees such that beetles can oviposit on them.

2.2. Compartments in bark beetles population:

Since there is no concept of exposed and recovered population in Bark beetles therefore the whole population is divided into two subclasses. (i) The susceptible adults $S_t(V)$, beetles which do not have pine wild nematode. (ii) The infected beetles I_V, which posses pine wild nematode.

2.3. Description of the model

If M_H and M_V represent the total population of pine trees and beetles respectively, then in light of the divisions of both populations we can express it mathematically as, $M_H = S_H + E_H + I_H$ and $M_V = S_V + I_V$. The rate at which new induction enter in trees and beetles are denoted by a_H and b_V respectively. While the death rate for trees is represented by μ_1 and μ_2 for beetles. The term $\alpha I_V S_H$ shows the single contact that leads to infection while the new infective come into being from double exposures at the rate $m\alpha I_V^2 S_H$. The possibility of natural death rate of pine wild and of beetles are incorporated in the model. The parameter γ is used to represent the rate at which grown up beetles carry the pine wild nematode when they come out from dead trees. The levels at which the infections saturate in trees and beetles are denoted by m and n respectively.

Now describing all the above mentioned parameters, the compact mathematical form obtained from the aforesaid biological model get the following form:

$$\begin{aligned}
\frac{dS_H}{dt} &= a_H - \alpha S_H I_V (1 + mI_V) - \mu_1 S_H,\\
\frac{dE_H}{dt} &= \alpha S_H I_V (1 + mI_V) - (\beta + \mu_1) E_H,\\
\frac{dI_H}{dt} &= \beta E_H - \mu_1 I_H,\\
\frac{dS_V}{dt} &= b_V - \gamma I_H S_V (1 + nI_H) - \mu_2 S_V,\\
\frac{dI_V}{dt} &= \gamma I_H S_v (1 + nI_H) - \mu_2 I_V,
\end{aligned} \tag{2}$$

and the initial conditions for the model are given as

$$S_H(0) \geq 0, E_H \geq 0, I_H(0) \geq 0, I_V(0) \geq 0, S_V(0) \geq 0. \tag{3}$$

Studying the nature of compartments and their dependency upon each other, we can reduce the system (2) to the following form, while removing S_H and S_V receptively.

$$\begin{aligned}
\frac{dE_H}{dt} &= \alpha \phi I_V (1 + mI_V)\left(\frac{a_H}{\mu_1} - I_H - E_H\right) - (\beta + \mu_1) E_H,\\
\frac{dI_H}{dt} &= \beta E_H - \mu_1 I_H,\\
\frac{dI_V}{dt} &= \gamma I_H (1 + nI_H)\left(\frac{b_V}{\mu_2} - I_V\right) - \mu_2 I_V.
\end{aligned} \tag{4}$$