

Accepted Manuscript

Modeling plant virus propagation with seasonality

Mark Jackson, Benito M. Chen-Charpentier

PII: S0377-0427(18)30374-1
DOI: <https://doi.org/10.1016/j.cam.2018.06.022>
Reference: CAM 11752

To appear in: *Journal of Computational and Applied Mathematics*

Received date: 21 December 2017
Revised date: 11 May 2018

Please cite this article as: M. Jackson, B.M. Chen-Charpentier, Modeling plant virus propagation with seasonality, *Journal of Computational and Applied Mathematics* (2018), <https://doi.org/10.1016/j.cam.2018.06.022>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



Modeling Plant Virus Propagation with Seasonality

Mark Jackson¹, Benito M. Chen-Charpentier^{1,*}

^a*Department of Mathematics, University of Texas at Arlington, Arlington, TX 76019-0408.*

Abstract

Plants are essential to life. They are a source of food, medicine, clothing, and are important to a healthy environment. Unfortunately, plants can become infected with a disease. A viral infection is one way that a plant may become diseased. Often times, plants die from this infection. These viruses hurt the agriculture industry as billions of dollars are lost due to crop loss every year. An insect vector is typically the cause for the virus propagation. The vectors exhibit seasonal behavior as they are active in the warm months, but not as much so in the cooler months. To defend against the vectors, pesticides have been used. While the pesticides might be effective in controlling the vectors, they can have harmful side effects on the environment. An alternative solution is to introduce a predator, or just increase the number of a naturally present one, to prey on the insects. In this paper, we use a mathematical model of ordinary differential equation to model the dynamics of this biological process. We first present an autonomous system, then two nonautonomous systems, accounting for the periodic nature of the insects. To analyze the models, the basic reproductive number is used. We demonstrate a couple of approaches for determining this number: a time average approach and a linear operator approach. Afterwards, numerical simulations are used to demonstrate the results. Finally, comparisons are made between the models and the approaches.

Keywords: periodic coefficients, plant virus propagation, mathematical modeling

1. Introduction

Plants are a food source for man and many species. They also are sources of medicines, fibers for clothes, and are essential for a healthy environment. But plants are subject to diseases many of which are caused by viruses. These viruses often kill the plant. Specific examples can be seen in [5], [6], [11]. As a result, billions of dollars are lost every year because of virus related crop loss [10]. Most of the time, virus propagation is done by an insect vector. Insect vectors typically have a seasonal behavior. For example, aphids, a vector that transmits plant viruses, are more active in the growing season than other times of the year [7]. In general, vectors are very active in the warm months and not very active, almost dormant, in the cool or wet months. To combat the vectors, chemical insecticides are commonly used as a control. Unfortunately, these chemicals have toxic effects on humans, animals and the environment in general. An alternative is to introduce a predator, or just increase the number of a naturally present one, to prey on the insects. To understand the dynamics, we will use a mathematical model of differential equations.

Mathematical models have been used to model plant virus propagation [3], [4], [5], [9], [12]. However, these models do not take into consideration of the periodic nature of the vectors. In this paper, we extend the work in [4] to include this fact by introducing periodic coefficients to the model. We will consider a Holling Type 1 interaction. To analyze the model, the basic reproductive number R_0 is used. This is the number of secondary infections an infected individual generates. If $R_0 < 1$, the disease will die out as $t \rightarrow \infty$, but if $R_0 > 1$, an endemic will occur. For autonomous systems, the authors in [2] developed a method to determine basic reproductive number using the next generation approach. For nonautonomous systems, there have been several approaches to determining R_0 . The authors in [8], and [14] used a time average approach by replacing the periodic coefficients with their long time averages. This approach works in some specific cases, but can overestimate or underestimate R_0 in others. In [1], the authors defined

* Author for correspondence

Email addresses: mark.jackson@mavs.uta.edu (Mark Jackson), bmchen@uta.edu (Benito M. Chen-Charpentier)

Download English Version:

<https://daneshyari.com/en/article/8901697>

Download Persian Version:

<https://daneshyari.com/article/8901697>

[Daneshyari.com](https://daneshyari.com)