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The basic reproduction number of vector-borne plant virus epidemics

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Highlights:

- The basic reproduction number R_0 for vector-borne plant virus diseases is defined
- The Next Generation Matrix approach to calculating R_0 is illustrated using examples
- Parameters of plant host and vector population dynamics are introduced in the R_0 expression through their steady-state values in the disease-free system
- Competition between vectors when acting as herbivores affects the R_0 expression
- Further developments and uses of R_0 methodology in epidemiological studies are outlined

Abstract

The basic reproduction number R_0 is a key parameter in plant disease epidemiology, which largely determines whether or not an epidemic will occur in a plant population. The next generation matrix approach to deriving and calculating the basic reproduction number of a plant virus epidemic is described. The approach is illustrated through a series of examples of increasing complexity, ranging from the simplest case of one vector transmitting one virus to a single host, to the case of multiple vectors, to combined horizontal (vector) and vertical (seed) transmission, and where vector control using insecticides is practised. The importance of parameters representing host and vector population dynamics and their interaction in the absence of disease is stressed, and the constraints these place on the calculation of the basic reproduction number. Finally, mention is made of further elaborations to the approach that could prove useful in plant virus epidemiology.

1. Introduction

The basic reproduction number is defined as the total number of infections arising from one newly infected individual introduced into a healthy population. On the population level the basic reproduction ratio is the ratio between subsequent generations. Originally developed with an emphasis on infectious diseases of humans and animals, the generality of the approach is recognised as equally applicable for plant diseases. In that context, specification of R_0 gives a calculation tool that enables the estimation of the number of secondary infections that will occur in a healthy and susceptible plant population following the introduction of the pathogen, in the case considered here a virus. For disease to persist and for an epidemic to develop the value of R_0 must be greater than one. Hence R_0 is also the

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