VECTOR-BORNE PLANT DISEASES: IMPACT OF VECTOR PREFERENCES ON THE SPATIAL SPREADING OF INFECTIOUS DISEASES.

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Crop vector-borne diseases, similar to human vector-borne diseases, are significant global concerns. However, they are generally under-explored from a mathematical perspective, despite exhibiting a variety of unique biological characteristics that could lead to more complex models and mathematical challenges. For example, see [6, 7, 8].

In many models of vector-borne diseases, it is assumed that vector-host interactions are random. However, this assumption does not always hold true. In reality, vectors may be more attracted to infected hosts than to uninfected ones, depending on whether the host carries the pathogen. In [1], we demonstrate that these differential preferences of vectors can influence the dynamics of the disease and its spatial spread.

We examine a system of partial differential equations with vector diffusion, which leads to a monotone dynamical system [2]. For the diffusion-free model, we demonstrate that conditional vector preferences can induce bistability between the disease-free equilibrium and an endemic equilibrium. A backward bifurcation may also occur, enabling the disease to persist even when its basic reproductive number is less than one. Bistability can arise only if both infected and uninfected vectors exhibit a preference for uninfected hosts.

For the diffusion model, we show that bistable traveling waves can exist [3, 4], with both positive and negative spreading speeds, allowing the disease to either invade or retreat spatially. In the case of a monostable traveling wave, we find that the disease's spreading speed [5] depends not only on the preference of uninfected vectors for infected hosts, but also on the preference of infected vectors for uninfected hosts under certain conditions (when the spreading speed is not linearly determined).

We illustrate these theoretical results with several simulations and discuss the implications of our findings for control strategies.

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