

Emerging Themes and Approaches in Plant Virus Epidemiology

Mike Jeger,^{1,†} Fred Hamelin,² and Nik Cunniffe³

¹ Department of Life Sciences, Imperial College London, Silwood Park, U.K.

² IGEPP INRAE, University of Rennes, Rennes, France

³ Department of Plant Sciences, University of Cambridge, Cambridge, U.K.

Accepted for publication 12 January 2023.

Abstract

Plant diseases caused by viruses share many common features with those caused by other pathogen taxa in terms of the host–pathogen interaction, but there are also distinctive features in epidemiology, most apparent where transmission is by vectors. Consequently, the host–virus–vector–environment interaction presents a continuing challenge in attempts to understand and predict the course of plant virus epidemics. Theoretical concepts, based on the underlying biology, can be expressed in mathematical models and tested through quantitative assessments of epidemics in the field; this remains a goal in understanding why plant virus epidemics occur and how they can be controlled. To this end, this review identifies recent emerging themes and approaches to fill in knowledge gaps in plant virus epidemiology. We review quantitative work on the impact of climatic fluctuations and change on plants, viruses, and vectors under different scenarios where impacts on the individual components of the plant–virus–vector interaction may vary disproportionately; there is a continuing, sometimes discordant, debate on host resistance and tolerance as plant defense mechanisms, including aspects of farmer behavior and attitudes toward disease management that may affect deployment in crops; disentangling host–virus–vector–environment interactions, as these contribute to temporal and spatial disease progress in field populations; computational techniques for estimating epidemiological parameters from field observations; and the use of optimal control analysis to assess disease control options. We end by proposing new challenges and questions in plant virus epidemiology.

Keywords: climate change, disease management, estimation optimization, virus–vector interaction

Epidemiology is the study of the rates of temporal and spatial change of disease in populations and the determining factors underlying change. Of necessity, epidemiology is a quantitative science. For plant viruses, transmission is a key determining factor of disease dynamics and, in most cases, depends on the interactions of viruses, host plants, and vectors, subject to the biotic and abiotic environment (Jeger 2020). The complexity of these interactions makes field-based studies difficult to interpret without supporting experimental studies, either laboratory or microcosm-based, that provide information on the parameters involved in transmission. Problems then arise in scaling up information to the field. The expectation has been that mathematical models based on the known or assumed biology can make a bridge between the specific information provided by laboratory or microcosm studies and field observations on disease dynamics, whether to provide a greater understanding, to test hypotheses, to make predictions on future change, or to improve disease management through deployment of host resistance and tolerance, phytosanitation, and vector control (Jeger et al. 2004).

†Corresponding author: M. Jeger; m.jeger@imperial.ac.uk

The author(s) declare no conflict of interest.

In practice, there are few examples of such bridges being made and models used, largely because of the broader biotic and abiotic environment of plant and vector populations, including the impact of climatic fluctuations and the spatial component of both within- and between-spread factors, which add further layers of ecological complexity. Any approach to model plant virus epidemics needs to recognize when assumptions previously made are no longer tenable (Jones 2014a) and when an epidemiological approach must be subsumed into an overall systems approach based on modeling constraints for a particular crop (Chavez et al. 2022). There is a need to consider wild plants as a major biotic factor in the epidemiology of viruses in crops. Much activity may occur in wild plant populations but has rarely been modeled (Djidjou-Demasse et al. 2017; Fabre et al. 2012, 2015). How to address these challenges is an emerging theme in plant virus epidemiology.

Thematic areas for which gaps in current modeling efforts in plant virus epidemiology were identified by Jeger et al. (2017) are shown in Box 1. Although directed mainly at modeling, these areas are relevant for all aspects of quantitative epidemiological research and disease management. These areas of identified gaps are reexamined in this review, in which we provide an update on recent work and discuss emerging themes as both challenges and opportunities in plant virus epidemiology and disease management. We review recent work on climatic influences on plant virus diseases, where

predictions can be made on the impact of climate change, different strategies for disease control (including plant responses to virus infection and disease development), and the different approaches that can be taken in disentangling the virus–vector–host interaction. These approaches will be illustrated by the extent to which spatial and landscape aspects can be included in epidemiological analysis, the assessment of the consequences of virus manipulation of hosts and vectors in the field, and the widespread occurrence of co-infections in plants. We also note where new applications of statistical and computational techniques have been made in quantitative epidemiology and finish by proposing new challenges, questions, and opportunities for research.

Climate Change and Fluctuations

More than half of current human infectious diseases, including those caused by viruses and vector-borne pathogens, have been aggravated by climate change (Mora et al. 2022). Largely detrimental effects have been noted on the emergence, transmission, and consequences on viruses of animals and plants (Dash et al. 2021). For plant viruses, elevated CO₂, increasing temperature, changes in water availability, and extreme events will have effects on viruses through changes in plant hosts and vectors (Trebicki 2020). Specific mechanisms for these effects include temperature-sensitive interactions between viruses and host plants, such as the effects of warming on plasmodesmata and systemic cell-to-cell movement of viruses (Amari et al. 2021).

Impacts of climate change on disease in wild plant populations and communities are also expected (Jeger 2022a). There is a need to consider the crop ecosystem, including managed, wild,

and invasive plants more generally. Interactions between wild hosts, crop plants, and climate should be studied dynamically—with time (Burdon and Zhan 2020). In some cases, such as '*Candidatus Phytoplasma solani*' affecting grapevine ('bois noir') and solanaceous crops ('stolbur'), these cultivated crops suffer major damage and loss with infection but are essentially incidental hosts, being dead ends for the phytoplasma. Bindweed (*Convolvulus arvensis*) and stinging nettle (*Urtica dioica*) are wild hosts for the pathogen and reproductive hosts for the planthopper vector, *Hyalesthes obsoletus* (Cixiidae) and possibly other invasive vectors.

A variety of papers have dealt with the effects of climate change on virus diseases but without explicitly considering a vector. Sardanyés et al. (2022) modeled temperature effects on pepino mosaic virus strains, which are mostly seed, mechanically, or water transmitted, although there is some evidence for bumble bees, whiteflies, and *Olpidium* as vectors (Blystad et al. 2015). Virus replication rates were modeled as functions of temperature and incorporated into a logistic model for a single strain or a Lotka-Volterra model for competition between strains. The time trajectories for virus load within a single plant in both single and mixed infections are shown in Figure 1. This appears to be the first quantitative study on temperature effects on within-cell virus dynamics where there is mixed infection. Similarly, Gutiérrez-Sánchez et al. (2023) linked modeling with experimental data to look at likely climate change effects on seed transmission and viability and future infection risk. Environmental conditions predicted under climate change determine infection risk by modulating plant virus vertical transmission and viability of infected seeds.

Effects of climate on population dynamics of insect pests and virus vectors have been noted in extensive multiyear studies in rice and potato (Gutiérrez Illán et al. 2020; Yamamura et al. 2006) with both seasonal and between-year variations. In cases where there is predominantly vector transmission, the effects of temperature on transmission need to be modeled. Gamarra et al. (2020) developed a temperature-driven model for potato yellow vein virus transmission by the whitefly *Trialeurodes vaporariorum*, incorporating both a phenology component for the vector and a nonlinear

Box 1

Thematic areas for gaps in modeling effort in plant virus epidemiology (Jeger et al. 2017)

Theme 1. Identifying the consequences of large-scale climatic fluctuations, including global warming, for plant virus epidemics and shifts in virus and vector distributions.

Theme 2. Basing control of plant virus epidemics on locale-specific conditions, including crop, landscape, and farmer heterogeneity, and interactions and, by so doing, contributing to improved methods of disease control.

Theme 3. Disentangling the interactions between viruses, vectors, host plants, and the biotic and abiotic environment presents major challenges for experimental and epidemiological studies, where, typically, pairwise interactions are the norm. Some advances have been made by modelers in meeting these challenges, but more can realistically be achieved by the following:

- Integrating vector population dynamics and ecology into epidemiological models in a more realistic way, specifically, by recognizing that virus transmission and transmission type may affect vector life history parameters and flight, landing, and feeding behavior; and
- Developing evolutionary models for viruses, vectors, and the virus–vector interaction based on fitness tradeoffs and other population genetic approaches. Can viruses manipulate vectors, natural enemies, and host plants to enhance their fitness? How best to characterize virus–virus interactions within plants as synergistic, neutral, or antagonistic?

Theme 4. Advances in statistical and computational techniques should facilitate greater interrogation of observational data, estimation of epidemiological parameters, and evaluation of their relative importance in determining epidemic outcomes.

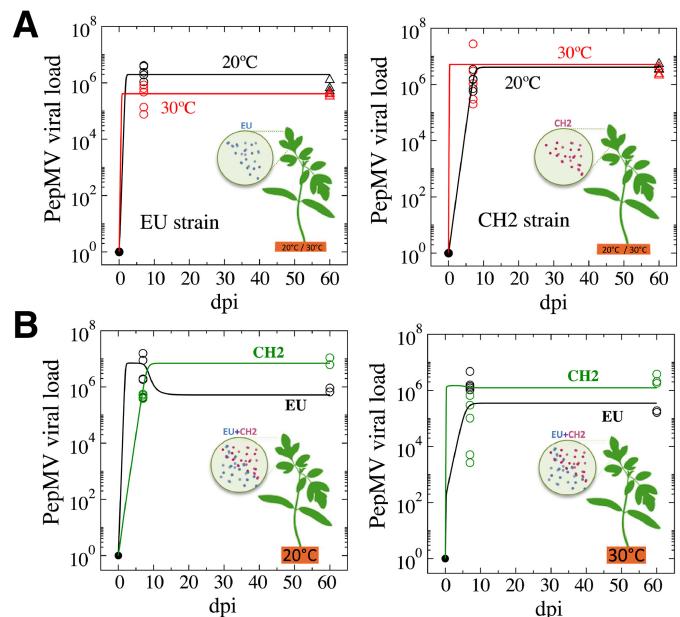


FIGURE 1

Viral load (days postinoculation [dpi]) of two strains of pepino mosaic virus (PepMV) in experiments at two temperatures (Reproduced, by permission, from Sardanyés et al. 2022). **A**, Single infections. **B**, Mixed infections.

dichotomous response for transmission efficiency based on laboratory experiments at constant and fluctuating temperatures. Maps were generated using risk indices derived from the model, evaluated against the current distribution of the virus, and used to predict areas of high risk where the virus had yet to be reported. Following subsequent surveillance, a first report of the virus was made in western Panama, predicted to be a high-risk area. Simulated maps to 2050 showed a predicted lowering of virus incidence in tropical regions but an increase in temperate regions, a shift in distribution due to projected climate change under a Representative Concentration Pathway (RCP 6.0) scenario with the Community Climate System Model (CCSM).

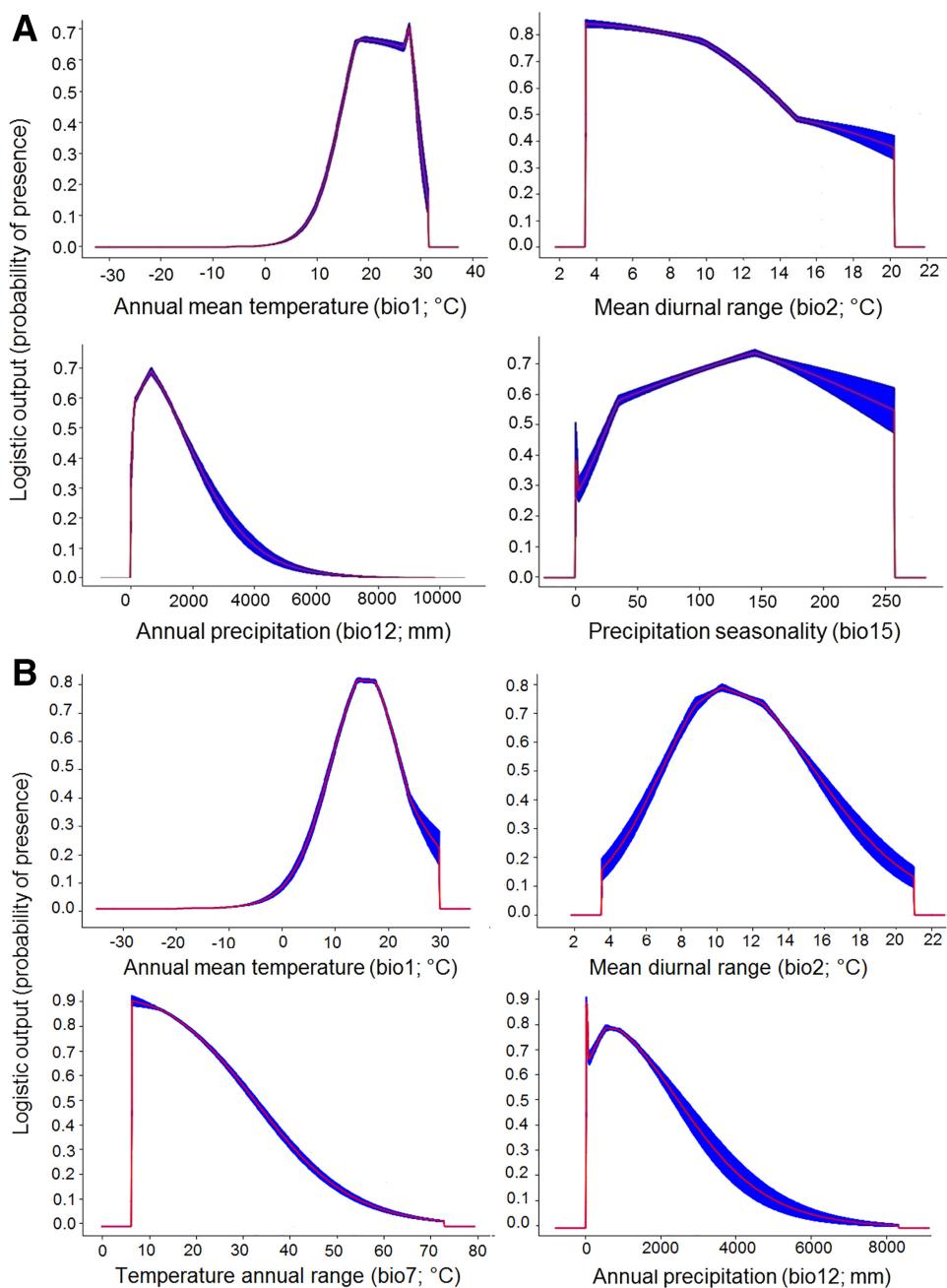
With plant viruses, there is the need to consider the integrated effects of climate change on host, pathogen, and vector, as done for tomato leaf curl disease, *Solanum lycopersicum*, and *Bemisia tabaci* (Ramos et al. 2018, 2019). Three of the four best predictor

variables (annual mean temperature, annual precipitation, and mean diurnal temperature range) were common for host and vector, but only the first two were closely aligned (Fig. 2). Also, the effects of climate change on associated biota, such as natural enemies as found in studies of elevated CO₂ and biological control of aphid and whitefly vectors, need to be integrated (Sun et al. 2011). Other examples based on climatic niche correlative models for the much studied and globally important vector *B. tabaci* are summarized in Table 1.

Other host–virus–vector systems considered include pineapple wilt viruses/mealybug vectors and IPCC projections (Wei et al. 2020); sugarcane mosaic virus in maize/aphid vectors with socio-economic classifications and climate change models (Li et al. 2022); maize viruses, leaf and planthopper vectors, and time-lagged incidences in relation to environmental fluctuations (Reynaud et al. 2009); cucumber mosaic virus, aphid vectors, and water deficits

FIGURE 2

Response curves for probability of presence in relation to the best environmental predictor variables (Reproduced, by permission, from Ramos et al. 2018). Blue-shaded areas represent the coefficient of variation in response. **A**, *Bemisia tabaci*. **B**, *Solanum lycopersicum*.



under abiotic stress (Bergès et al. 2021); and population development rates for potato pathogens and pests, including potato viruses and aphids used as proxies (van der Waals et al. 2013). Along with the monitoring of vector populations, surveillance of plant virus disease has been found to be important for identifying climate change signals, including remote sensing for tomato yellow leaf curl disease (Oh et al. 2019) and maize streak disease (Chivasa et al. 2020).

Disease Management

Disease management, including the control of virus diseases and virus vectors, can rarely be considered isolated from other plant pest and agronomic practices. This can be illustrated in studies on seed health in vegetatively propagated crops (Buddenhagen et al. 2022; Thomas-Sharma et al. 2017), modeling aphid control in intercropping systems (Allen-Perkins and Estrada 2019), possible conflicts between management strategies based on insecticide resistance models and epidemiological models (Sisterson 2022), and management decisions on whether to rehabilitate or renovate perennial crops due to virus disease, aging, and other performance factors (Somarriba et al. 2021).

Field practices

The effectiveness of virus disease control depends on variation in farming practices and the environment. Within- and between-field processes that potentially affect maize lethal necrosis (MLN) disease dynamics, together with management practices that can be used to control the causal viruses, maize chlorotic mottle virus (MCMV), and sugarcane mosaic virus (SCMV), were modeled by Hilker et al. (2017) (see also De Groote et al. 2021). Long-term (cross-season) dynamics of MCMV and SCMV, as well as MLN prevalence, were modeled for different management strategies and epidemiological scenarios. A baseline parameterization was compared with scenarios where cointfected seed caused increased vertical transmission

and where there was exogenous infection. In general, crop rotation practiced in large farms was an effective means of controlling MLN, but eradication was not possible with exogenous infection. The potential of vector control (aphids for SCMV and assumed to be thrips species, but unproven, for MCMV) and rogueing of infected plants was evaluated using a mathematical model for coinfection (Chapwanya et al. 2021). Rogueing was proposed as a viable alternative to crop rotation for smallholder farms, but without considering the behavior and attitudes of the grower.

Grower behavior

The likelihood of an individual grower adopting rogueing, or any other disease management strategy, depends on the prevalence of the disease. Tradeoffs in perceived costs versus benefits in deciding on control options have been included in models of human disease for some time (Chang et al. 2020; Funk et al. 2010). The simplest class of models allows awareness of disease to spread concurrently with the pathogen, leading to heterogeneous risks of infection (Kiss et al. 2009), a situation analogous to grower awareness of the spread of a plant disease. More complex models allow for behavioral changes by individuals. The most notable examples for human diseases have focused on take-up of prophylactic vaccination (Bauch and Earn 2004), social distancing (Del Valle et al. 2013), and face masks (Karlsson and Rowlett 2020).

Fewer modeling studies of this type have focused on plant diseases, although some models do represent control behavior, which depends on an individual grower's assessment of the likely profitability of each action (Milne et al. 2016). The single example specifically targeting a plant virus epidemic (McQuaid et al. 2017a) uses a relatively complex, spatially explicit simulation model of cassava brown streak (McQuaid et al. 2017b) as an underpinning model. Arguably, this complexity obscures how the different components interrelate. The key feedback is that decisions made by any

TABLE 1
Bemisia papers

Authors	Crop/virus	Geographical relevance	Comments
Aregbesola et al. 2020. J. Pest Sci. 93:1225-1241.	Cassava viruses/cassava colonizing groups—East and Southern Africa (SSA-ESA)	Tanzania	Life history (oviposition, fecundity, survival, developmental time) was studied in relation to temperature in controlled environments and field experiments. A phenology model was developed that could be used for pest risk mapping under climate change.
Bradshaw et al. 2019. PLoS One 14:e0221057.	Multiple crops and viruses/biotypes MEAM1 and MED	Northwest Europe	A set of 49 indices was developed based on current climate to compare the U.K. (no outdoor populations recorded) with France (established populations). Climate projections (2 to 4°C warmer) suggest establishment in U.K. outdoor crops in summer months, with a clear south-north gradient for these indices.
Kriticos et al. 2020. Scientific Rep. 10:22049.	Cassava viruses/ sub-Saharan Africa (SSA) groups	East Africa	Historical changes in climate suitability for SSA subgroups were analyzed using the CLIMEX niche model corroborated with a 13-year time series of <i>B. tabaci</i> abundance. Modeled climatic suitability improved significantly over the almost 40 years of experienced cassava virus pandemics in East Africa.
Ramos et al. 2018. PLoS One 13:e0198925.	<i>Solanum lycopersicum</i> viruses/MEAM1 and MED groups	Global	Levels of risk to open field tomato production were assessed using species distribution and global climate models. Projections to 2050 showed an extension in area of 180% in high-risk areas but a reduction of 67 and 27% in medium and low-risk areas, respectively. Projections to 2070 showed an extension of 164% (high risk) and reductions of 49 and 64% (medium and low risk).
Ramos et al. 2019. Agric. Syst. 173:524-535.	Tomato yellow leaf curl virus (TYLCV)/MEAM1 and MED groups	Global	Distribution of TYLCV in areas suitable for open field tomato production and <i>B. tabaci</i> . Under climate change projections for 2050 and 2070, large regions are predicted to be at risk from TYLCV in areas suitable for both open field tomato production and <i>B. tabaci</i> . Where there are predicted optimal conditions for tomato and suitable conditions for <i>B. tabaci</i> , there will be a medium risk of TYLCV establishment.

one grower affect disease prevalence and, in turn, future decisions made by other growers.

A recent study by Murray-Watson et al. (2022) attempted to resolve these coupled tradeoffs in a deliberately simplified way by integrating aspects of game theory into a simple model of a clean seed system, again using cassava diseases as a motivation. The long-term proportion of growers deploying clean seed depends on the epidemiological and logistical parameters affecting its effectiveness and cost. However, the predictions of the model also depend on how the behavioral component of the model is formulated in terms of whether growers are assumed to behave according to rational or strategic-adaptive expectations, as well as how precisely growers estimate the current level of risk posed by disease.

Basic epidemiological theory tells us that successful disease management within a population of growers relies on a sufficiently large fraction adopting control (Jeger 2000). When insecticide sprays are used to control vectored diseases by reducing vector population densities, there can also be issues with spatiotemporal synchrony in management because control is most likely to be successful if done “area-wide” (Bassanezi et al. 2013). Milne et al. (2020) extended modeling behavior to account for this type of cooperative control scheme, focusing on the bacterial disease huanglongbing, a major threat to commercial citrus production. They used models of “opinion dynamics” (Moussaïd 2013) to understand the impact of social forces on growers’ decisions. Bate et al. (2021) took a somewhat similar approach, using coalition theory (Mesterton-Gibbons et al. 2011) to model voluntary participation in a regional biosecurity scheme. These types of ideas around how the choices made by individual growers can directly account for the behavior of others have not yet been applied to virus disease epidemics.

Resistance and tolerance

Resistance has long been considered the major means of controlling plant virus epidemics, with much recent work proposing the use of tolerance as an alternative or complementary disease management strategy. “Tolerance as a disease management strategy has been claimed to be as widespread as host resistance although problems remain in the strict definition of tolerance and how it can be assessed” (Jeger 2020). Tolerance has been defined as limited symptom development or reduction in plant vigor or yield despite normal virus accumulation as in a susceptible cultivar, or, alternatively, as a limited reduction in plant fitness (fecundity, reproduction period), whereas there is limited virus accumulation and symptom development for a resistant variety but a possible penalty in terms of reduced vigor and yield. A comprehensive review reconciling these viewpoints, but also pointing out the ambiguities and some of contradictions that remain, has been conducted (Pagán and García-Arenal 2020).

There has been limited modeling of tolerance for plant viruses (Cronin et al. 2014; Lázaro et al. 2017; Moore et al. 2011; Sisterson and Stenger 2018; van den Bosch et al. 2006; Zeilinger and Daugherty 2013). van den Bosch et al. (2006) proposed an epidemiological model to compare different forms of plant defense mechanisms, including tolerance, at the field and within-plant levels, and how deployment in cultivars affected virus evolution using an adaptive dynamics approach. The model structure proposed was motivated by African cassava mosaic virus disease and coupled a between-plant vector transmission component and a within-plant virus multiplication component. It was found that titer-reducing and symptom-reducing defense mechanisms impose selection on the virus, leading to an increase in within-plant virus multiplication. If symptom reduction is seen as an expression of tolerance, then the model predicts selection for an increased virus titer. However, the crop considered here was cassava, and comparison of defense mechanisms for cassava mosaic disease and hence symptom reduction, sometimes termed mortality tolerance, was considered rather than a reduction in fitness, measured as plant fecundity.

Recent experimental work has placed more emphasis on fecundity or reproductive stage stress tolerance to a range of biotic and abiotic stressors, for example, tolerance in *Arabidopsis thaliana* challenged with either cucumber mosaic virus (CMV) or turnip mosaic virus (Montes and Pagán 2019). Tolerance of CMV was associated with resource allocation from growth to reproduction; for turnip mosaic virus, it was associated with the time to and length of the reproductive period. A tradeoff in tolerance between the two viruses was found, carrying potential implications for disease management in crops. The emphasis on reproductive stage tolerance offers many opportunities to link the effects of biotic and abiotic stressors on plant genetics, physiology, and disease ecology (Jeger 2022b). This will require a whole life history approach. For example, with annual plants and indeterminate flowering, seed germination and seedling emergence occur on shorter time scales than vegetative plant growth. Flowering may occur at any time during the growth period, which also corresponds to the pollination period. At the end of the growth and pollination period, seeds drop, and eventually the plant dies, and only seeds that survive the overwintering period start a new cycle if there is no seedbank. The challenge is then to disentangle the interactions of reproductive stage tolerance with plant virus epidemiology.

As described for controls that are more effective when growers cooperate, the use of resistance or tolerance as a strategy for controlling plant virus disease carries implications beyond the choices made by individual farmers and extends to whole farming communities. This was modeled by Murray-Watson and Cunniffe (2022a) using tomato yellow leaf curl virus as a case study. Disease has relatively little effect on the yields of those growers who use tolerant crop varieties, but—by increasing the prevalence of disease in the system—can significantly affect the yields of those who do not deploy tolerance. In this sense, therefore, deployment of tolerant varieties can be viewed as “selfish.” In contrast, resistant crop varieties benefit not only those who grow them but also those who do not because the overall levels of disease are reduced. The distinct effects of resistance and tolerance lead to divergent consequences when modeling grower behavior. Resistant varieties can be associated with other growers “free riding,” that is, gaining the benefit in terms of reduced disease due to control enacted by other growers, without themselves incurring the costs of the resistant variety. Murray-Watson and Cunniffe (2022b) extended the set of strategies adopted by growers to allow for planting an unimproved, a resistant, or a tolerant crop. Additionally, growers’ use of resistant or tolerant varieties could be subsidized by a “social planner” to determine whether and how socially optimal outcomes could be promoted. Subsidizing a tolerant crop incurs a recurrent cost to the planner because when use of a tolerant crop becomes established, continued use of this crop becomes necessary via a feedback mechanism. Subsidizing a resistant crop, however, provides widespread benefits by reducing the prevalence of disease across the community of growers, including those that do not control. A reduction in the level of subsidy required for resistant crop occurs because only a subset of growers need to use it for the benefits to be felt across the community of growers, with other growers “free riding” on the control efforts of others.

Disentangling the Virus–Vector–Host–Environment Interaction

The disease triangle concept has been extended to vector-borne diseases by many authors, such as Islam et al. (2020). However, the disease triangle concept and its extension to include a vector is essentially static. The more fluid concept of the “ecological trinity” was proposed earlier in the 1930s (Jeger 2008, 2020) by the American entomologist Walter Carter. He developed the concept of the ecological trinity of viruses, hosts, and vectors within a partic-

ular environment based on interactions of viruses and vectors with crops, weeds, and other wild or volunteer hosts as influenced by the environment and cropping practices. Epidemics then result from disturbance to previously stable situations in which neither host nor virus had gained permanent ascendancy.

Transmission

Embedded in any concept of the virus–vector–host interaction is the importance of transmission and how the retention and movement of plant viruses leads to classification of transmission mode (Whitfield et al. 2015). The classification can be made in terms of stylet retention (also described as nonpersistent transmission), foregut retention (semipersistent transmission), and circulative movement (including both persistent-circulative and persistent-propagative transmission). With some systems, there is also the possibility of transovarial, transstadial, and venereal movement of viruses in the vector population.

To represent these transmission possibilities, a SEIR (Susceptible, Exposed, Infectious, Removed) model for a plant virus epidemic was proposed, linked with a vector population model in which compartments of nonviruliferous, viruliferous but noninoculative, and inoculative vectors were defined, including migration terms (Jeger et al. 1998; Madden et al. 2000). For plant diseases, “susceptible” equates to the disease-free state (healthy) and “exposed” equates to the latent state (infected but not yet infectious). Virus acquisition occurs when nonviruliferous vectors probe/feed on infectious plants; virus inoculation occurs when viruliferous vectors probe/feed on healthy plants. In this modeling framework, parameter values, where known, relevant to transmission mode, can be used.

Basic reproduction number

From this basic model, the basic reproduction number can be derived, the average number of new infections arising from the introduction of one infected unit into an otherwise healthy population during the unit's period of infectiousness. In the case of vector-borne diseases, there are two cycles, one in the vector and one in the plant, with the basic reproduction number represented in squared form as R_0^2 ; if >1 , an epidemic will develop (van den Bosch et al. 2008). Given the complexity of host–virus–vector models, the next-generation method is often used to derive R_0^2 using classical mathematical methods (van den Bosch and Jeger 2017). The basic reproduction number is now a standard epidemiological concept and tool for assessing disease management actions.

Spatial dynamics of vectored plant virus diseases

Selecting an appropriate model framework to track spatial aspects of plant virus disease epidemics remains a key challenge (Cunniffe et al. 2015) because various classes of epidemiological model are available that can account for spatial effects (Cunniffe and Gilligan 2020). Early work for spread at relatively small scales, such as within individual fields or orchards, often involved detailed simulations (Ferriss and Berger 1993). These simulations tracked the movements made by, and the infective status of, individual vectors. This class of model is still used (Ferris et al. 2020; Kho et al. 2020) and sits within the broader class of individual-based models (DeAngelis and Grimm 2014). However, even for plant virus diseases, individual-based models often concentrate only on the disease status of the plant host (Atallah et al. 2015; Gibson and Austin 1996; Varghese et al. 2020). This is particularly the case for diseases of fruit trees, for which the number of individual hosts within a given production setting, such as a block, grove, or orchard, is not too large. This type of compartmental individual-based modeling approach focusing on the disease status of individual plants is routinely used for diseases that are not vectored (Adrakey et al. 2017; Cunniffe et al. 2014, 2015; Hyatt-Twynnam et al. 2017; Neri et al. 2014), as well as for vector-borne bacterial diseases, such as

citrus greening (Craig et al. 2018; Parnell et al. 2015; Parry et al. 2014). The influence of vectors on transmission is subsumed into a dispersal kernel, a statistical representation of how the rate at which an infected host causes infection of susceptible hosts falls off with distance (Fabre et al. 2021).

When larger scale predictions are required, a simple approach is to use essentially the same idea, with the disease status of an entire field or farm tracked as a simple binary variable. Disease transmission can then occur between entities via either a dispersal kernel (Murray-Watson et al. 2022) or an explicit network parameterized to represent certain types of movement, for example, movements of planting material or seed (Andersen et al. 2019). When more finely resolved information on the level of disease within each field or farm is required, transmission can still be captured via a dispersal kernel, but with the dynamics of disease within each “node” also modeled. This can be done relatively simplistically, via an increase in within-node prevalence at a predetermined rate (Holt and Chancellor 1997) or by allowing the dynamics within each node to follow an internal compartmental model (McQuaid et al. 2017b; Moslonka-Lefebvre et al. 2012). The approach can also be adopted at very large scales (Gilligan et al. 2007). Often, the host distribution is then further approximated by discretization to a lattice of a certain size (Godding et al. 2022), an approach that has proved useful in modeling landscape-scale spread of various plant diseases (Cunniffe et al. 2016).

Conditional vector preference

There has been much recent work over the last two decades on vector preference: How the landing and feeding behavior of virus vectors depends on the disease status of both the host (healthy or infected) and the vector (viruliferous or nonviruliferous) and whether the virus can manipulate the plant and vector to its own advantage (Eigenbrode et al. 2018; Mauck and Chesnais 2020; Zhao et al. 2022). In some cases, there may be an environmental influence on vector preference such as water stress (Del Cid et al. 2018).

Following on from previous vector preference models (Roosien et al. 2013; Shaw et al. 2017; Shoemaker et al. 2019), Cunniffe et al. (2021) developed a model that explored the epidemiological and ecological consequences of virus manipulation of host and vector in plant virus transmission, while echoing the original models (Jeger et al. 1998; Madden et al. 2000) by allowing distinct features of different transmission types to be represented. The assumptions made in developing the model are listed in Box 2. The epidemiological model was structured in compartments. Parameters were defined for the flying, settling, and feeding behaviors of vectors and combined in the model with the plant–virus–vector interaction (Table 1 of Cunniffe et al. 2021). A distinction was made between the preference parameters for viruliferous and nonviruliferous vectors, at least for persistently transmitted viruses, and these are shown in Table 2.

A basic reproductive number was derived from the model equations, which shows the importance of the bias of a nonviruliferous vector for an infected plant and the number of healthy plants visited by a vector once a virus has been acquired. This basic reproduction number has a direct heuristic interpretation of the successive terms in the following expression:

$$\begin{aligned} &\text{Average number of vectors per plant in absence of virus} \times \\ &\text{average infectious period (time units) of a single infected plant} \times \\ &\text{average number of plants visited by a vector (per unit time)} \times \text{probability of virus acquisition by a single vector during a single visit} \times \\ &\text{average period (time units) a vector remains viruliferous} \times \text{average} \\ &\text{number of plants visited per vector (per unit time)} \times \text{probability} \\ &\text{of inoculation by a single viruliferous vector.} \end{aligned}$$

Models were parameterized to ensure a default value of $R_0 = 2$ for both nonpersistent and persistent transmission so that the dynamics

of healthy and infected hosts and nonviruliferous and viruliferous vectors could be directly compared and used as a baseline (Fig. 3A to C for nonpersistent transmission and Fig. 3D to E for persistent transmission). For certain sets of parameters, the model has multiple stable biologically plausible equilibria, where which of two locally stable equilibria in disease incidence is attained depends on the initial conditions. Even without conditional vector preference, the outcome can depend on the initial disease incidence (Fig. 3A). When vector population dynamics are introduced, there is a rich dynamical behavior with, again, bistability and stable or unstable outcomes in disease incidence as birth rate changes whenever infected hosts are more able to support vector reproduction (Fig. 3F and G).

Importantly, the consequences of vector preference and manipulation in terms of crop loss and economic returns have been modeled using data for three viruses: pea enation mosaic virus, bean leaf roll virus, and potato leaf roll virus (Eigenbrode and Gomulkiewicz 2022). In each case, the effect on performance of a single insecticide spray was greater with than without vector manipulation. For the psyllid vector of huanglongbing, additional returns for multiple sprays diminished more with than without vector manipulation.

Evolution of conditional vector preference

Conditional vector preferences occur when viruliferous and nonviruliferous vectors show contrasting preferences for infected versus uninfected hosts. The question is whether evolution shaped these preferences in a way to promote vector performance and/or virus spread (Mauck et al. 2018). The evolution of conditional vector preferences has been addressed by Gandon (2018), making reference to barley yellow dwarf virus, tomato yellow leaf curl virus, and potato leaf roll virus, but with most relevance for animal systems. More specifically, the author explored a relatively simple epidemiological model akin to Roosien et al. (2013), itself a simple adaptation of the classical Ross model of 1911 for vector-borne diseases. Vector fecundity depends on whether it feeds on infected or uninfected hosts. Extreme preferences for uninfected or infected hosts may drive the vector to extinction; hence, the vector should avoid rare and low-quality hosts. If preferences are controlled by the vector (as opposed to the virus), and if infected hosts are of relatively low quality, evolution may select for increasing preferences against infected hosts, leading to ultimate extinction of both the vector and the virus. Other evolutionary outcomes are possible as well, depending on whether the vector, the virus or both control preferences. For instance, intermediate preferences may evolve if there is a trade-off between the virus's ability to drive viruliferous vectors toward uninfected hosts and its ability to make infected hosts attractive to

vectors. The main thrust of Gandon (2018) was to model vector preference and parasite manipulation in animal systems but could be adapted for plant viruses.

Epidemiology of coinfecting plant viruses

Coinfection of plant hosts by two or more viruses is common in agricultural crops and natural plant communities. It has long been recognized that some diseases are associated with multiple pathogens, including viruses and mollicutes, such as the corn stunt disease, but models for this disease previously concentrated only on one pathogen component (Vandermeer and Power 1990). Standard methods of analysis are not sufficient to investigate interactions within and among plants across different viruses or virus strains, which adds further levels of complexity. Coinfection has been shown to interact with vector preferences in cases where two viruses have the same or different vectors (Table 3). However, the results reported are difficult to generalize due to differences in vector taxonomies, behaviors, reproductive systems, and transmission modes.

As already described, maize lethal necrosis is a disease arising from coinfection with MCMV and a potyvirus such as SCMV (De Groot et al. 2021; Hilker et al. 2017). Analysis of field surveys of MLN and the individual viruses, MCMV and SCMV, in a range of surveys suggests the prevalence of MLN is given by the product of MCMV and SCMV prevalence (Mahuku et al. 2015) (Fig. 4), indicating independent transmission of the two viruses. This result may reflect the differences in vectors and transmission type between the coinfecting viruses.

Independence and interaction between coinfecting viruses

In wild rather than crop populations where natural mortality and regrowth occur, the probability of coinfection by noninteracting pathogens was shown to be greater than the product of their individual incidences (Hamelin et al. 2019) (Fig. 5A) unless host natural mortality can be neglected. This deviation from independence raises questions on the validity of statistical tests performed to detect interactions between pathogens responsible for long-lasting diseases.

Box 2

Assumptions made in the vector preference model of Cunniffe et al. (2021)

1. Vectors are attracted by plant cues (visual or olfactory) to land on infected plants.
2. Whether vectors settle and feed for an extended period, or only probe and then depart, depends on the plant's infection status.
3. The strength of vector preference can differ for viruliferous and nonviruliferous vectors; that is, preference is conditional on vector status, as well as plant infection status.
4. The proportion of probes that leads to vectors settling for an extended feed affects the number of plants visited by vectors per unit of time and thus the overall transmission rate.
5. Whether vectors probe or feed has different effects on transmission for non-persistent versus persistent viruses.
6. The fecundity of the vector can be affected by the plants it feeds on, with vectors that predominantly feed on infected plants potentially having either a higher or lower birth rate.
7. The loss rate of the vector, from additional mortality or movement away from the plant population, may be affected by the number of plants visited per extended feed.
8. The flight duration of a vector may depend on whether it is viruliferous or nonviruliferous.

TABLE 2

Four parameters are labeled according to whether the vector is nonviruliferous (–) or viruliferous (+)

ν_-	Bias of nonviruliferous vector to land on infected plants
ν_+	Bias of viruliferous vector to land on infected plants
ω_-	Probability that a nonviruliferous vector settles to feed on a susceptible plant
ω_+	Probability that viruliferous vector settles to feed on a susceptible plant
ϵ_-	Bias of nonviruliferous vector to settle to feed on an infected plant
ϵ_+	Bias of a viruliferous vector to settle to feed on an infected plant
ϕ_-	The average number of plants visited by a nonviruliferous vector per unit of time (derived)
ϕ_+	The average number of plants visited by a viruliferous vector per unit of time (derived)

Hamelin et al. (2019) provided a novel method to test for interactions among pathogens. The method was tested with data on strains of anther smut, human papillomavirus, tick-transmitted bacteria, and *Plasmodium*. For plant viruses, the authors reanalyzed the data set for barley and cereal yellow dwarf viruses from Seabloom et al. (2013) and found, with this method controlling for host mortality, that the five virus species co-occurred more often than expected by chance (Fig. 5B).

Vector transmission and coinfecting plant viruses

A variety of studies have investigated the dynamics of coinfection but track only the disease status of infected and coinfected plants. Much less attention has been paid to the role of vector transmission in coinfection, that is, acquisition and inoculation and their synergistic and antagonistic interactions. A vector-explicit model for coinfection was proposed for one vector species and one plant species with potential coinfection by two viruses (Allen et al. 2019). This model included both vector and host plant components. The basic reproduction number provides conditions for successful invasion of a single virus. The main question asked in this study is what determines invasion of a coinfecting plant virus? A new invasion threshold was proposed that provides conditions for successful invasion of a second virus.

Two special cases were considered. In the first case, one virus depends on an autonomous virus for successful transmission, with

only one of the viruses invading in the absence of the other. The equilibrium prevalence for the vector and host and the corresponding invasion reproduction numbers were derived as functions of acquisition of the established virus and inoculation of both the established and invading virus by the vector. In the second case, both viruses are unable to invade alone but can both establish themselves when initial prevalence is high. This case leads to interesting dynamics in which the outcome depends on the initial prevalence of each virus and can lead to bistability (Fig. 6), with a disease-free equilibrium and a coinfecting equilibrium as a function of the initial frequencies of the two viruses.

Recently, McLaughlin et al. (2022) reported experiments on transmission, infection, and replication of tomato yellow leaf curl virus and tomato mottle virus in tomato: Data on acquisition and co-inoculation by *B. tabaci* were found to be fundamental in disentangling the vector–virus–host interaction and the spread of single and coinfections.

Interaction between vectors

In some cases, coinfection may occur when the coinfecting viruses have different vector species. In these cases, there may be interactions between vectors due to differing life history characteristics and transmission mode and efficiencies. In the case of competition between two vectors, a Lotka–Volterra model was used in deriving a basic reproduction number for a single virus (van

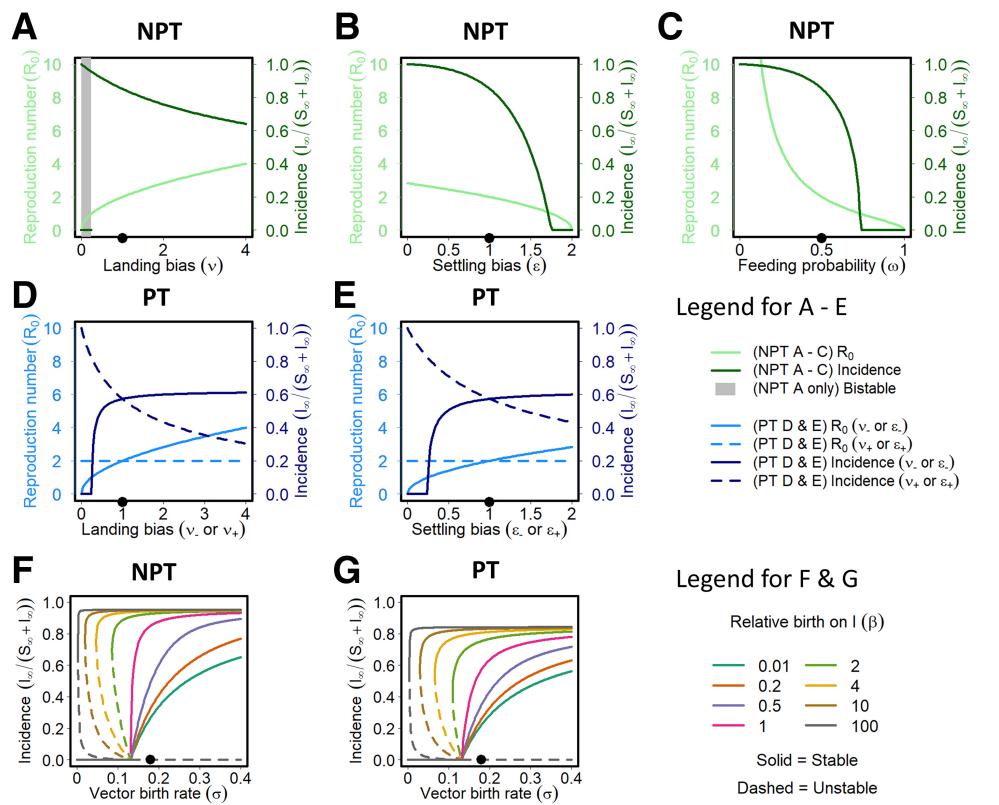


FIGURE 3

Selected results from the vector preference model (Reproduced, by permission, from Cunniffe et al. 2021). **A to C**, Effects of vector preference parameters controlling landing bias (v), settling bias (ϵ), and the probability of feeding (ω) on the basic reproduction number (R_0) and the terminal disease incidence ($I_\infty / (S_\infty + I_\infty)$) when the model is parameterized for nonpersistent transmission (NPT). The baseline parameterization, for which $R_0 = 2$, is marked with a black dot. The model exhibits bistability for a small range of values of the landing bias parameter (marked in gray in panel A). **D and E**, The results of the model when parameterized for persistent transmission (PT), when conditional vector preference is possible. Here, the responses of viruliferous and nonviruliferous vectors are distinguished (for example, v_+ is the landing bias shown by viruliferous vectors, whereas v_- is the corresponding response for nonviruliferous vectors). **F and G**, The responses of the final incidence to vector birth rate (σ) for both classes of transmission as the relative birth rate on infected plants (β) varies (the different colored lines). Whenever vectors can reproduce more rapidly on infected plants ($\beta > 1$), this induces bistability (dotted lines) for both classes of transmission. In these cases, disease can spread even when $R_0 < 1$, so long as there is sufficient infection initially present in the system, because infected plants lead to larger vector population densities, promoting spread of disease.

den Bosch and Jeger 2017) but not for the case where they each transmit a different virus. Often, particularly important for non-persistently transmitted viruses are interactions between transient and resident aphids (Zaffaroni et al. 2021). Transient aphids probe several plants per day and thus are important vectors of viruses both within and between fields, whereas resident aphids complete their life cycle on a single plant host and thus tend to lead to plant host damage via herbivory rather than by their vectoring activity. Many agronomic practices, most notably spraying with pesticides, have more pronounced effects on resident aphid populations. Under mild assumptions about how transient aphids can be dissuaded from probing plants that are already heavily infested with resident aphids, this in turn means that pesticide application can potentially have the counterintuitive effect of increasing the amount of disease.

Advances in Statistical and Computational Techniques

Optimal control theory

Two areas seem to be highly relevant in plant virus epidemiology. The first relates to the optimization of disease management

practices. Such techniques have been used to evaluate the choices farmers make when selecting planting material for the next season's cassava crop (Bokil et al. 2019). In a similar vein, Hamelin et al. (2021) used dynamic optimal control theory to evaluate the use of clean seed, motivated in part by work on MLN referred to at several points in this review. More specifically, the authors showed that depending on epidemiological and economical parameters, controlling plant viruses with clean seeds may or may not be economically viable, and when viable, may or may not lead to disease eradication. Subsidizing clean seeds may help in switching from unviable to viable control but cannot lead to disease eradication. The only way to achieve disease eradication in this case is additionally to use control methods that decrease horizontal transmission of the pathogen.

A key limitation of optimal control theory is that the underpinning mathematics rapidly becomes rather complex, making its use intractable for more detailed models. However, Bussell et al. (2019) recently proposed a methodology to allow optimal control theory to be applied to models that attempt to capture significant biological detail. Essentially, the machinery of optimal control theory is applied to a simplified "approximate" model, carefully calibrated to adequately reflect the results of the "full" model of interest over

TABLE 3
Vector preference with co-infecting viruses

Authors	Host plant	Viruses	Vector(s)	Comments
Srinivasan and Alvarez 2007	<i>Solanum tuberosum</i>	Potato virus Y Potato leafroll virus	<i>Myzus persicae</i> <i>Macrosiphum euphorbiae</i>	Alatae and apterae preferentially settled on coinfected rather than singly infected or noninfected plants.
Gautam et al. 2020a	<i>Cucurbita pepo</i>	Cucurbit leaf crumple virus Cucurbit yellow stunting disorder virus Tomato yellow leaf curl virus	<i>Bemisia tabaci</i> MEAM1	A wide and complex range of effects on settling preferences, acquisition, inoculation, and vector virus load between singly- and coinfecting plants were noted, but no effects on vector fitness.
Gautam et al. 2020b	<i>Capsicum annuum</i>	Cucumber mosaic virus Tomato spotted wilt orthopoxvirus	<i>Myzus persicae</i> <i>Frankliniella fusca</i>	Vector preferences were not greatly different between coinfecting and singly infected plants. Overall, coinfection in pepper plants did not enhance vector(s) fitness, although in singly infected plants, vector fitness was enhanced.
Lightle and Lee 2014	<i>Rubus idaeus</i>	Raspberry leaf mottle virus (RLMV) Raspberry latent virus (RbLV)	<i>Amphorophora agathonica</i>	Aphid fecundity only increases on coinfecting plants. After 24 h, aphids preferred to settle on RLMV-infected over healthy plants, but on healthy over RbLV plants. There were no differences in settling between healthy and coinfecting plants.
Peñaflor et al. 2016	<i>Glycine max</i>	Soybean mosaic virus (SMV) Bean pod mottle virus	<i>Aphis glycines</i> <i>Epilachna varivestis</i>	Single infection by either virus increased palatability for <i>E. varivestis</i> , but coinfecting plants were no more palatable than healthy plants. SMV infection increased aphid feeding preference (nonconducive for nonpersistent transmission), but this effect was reduced with coinfection.
Salvaudon et al. 2013	<i>Cucurbita pepo</i>	Watermelon mosaic virus (WMV) Zucchini yellow mosaic virus (ZYMV)	<i>Aphis gossypii</i>	ZYMV replicated at similar rates in single and coinfecting plants, whereas WMV replication was reduced in the presence of ZYMV. ZYMV enhanced aphid recruitment to infected plants, whereas WMV did not, although it was readily transmitted from coinfecting plants.
Ban et al. 2021	<i>Nicotiana tabacum</i>	Tomato yellow leaf curl virus Tomato yellow leaf curl China virus	<i>Bemisia tabaci</i> MEAM1	Plants infected by the two viruses showed amplified symptoms, but vector performance and preferences were not affected compared with singly infected plants.
Zhao and Rosa 2020	<i>Emilia sonchifolia</i>	Tomato spotted wilt orthopoxvirus (TSWV) Impatiens necrotic spot orthopoxvirus (INSV)	<i>Frankliniella occidentalis</i>	Thrips prefer to oviposit on TSWV and INSV coinfecting plants compared with singly infected or healthy plants, providing the opportunity for acquisition by nymphs. However, inoculation generally favored one of the two viruses rather than co-inoculation of both.

a range of parameterizations. Optimal strategies identified in the approximate model can then be “lifted” back to the full model, informing disease control in the situation of particular interest. Although this approach has to date not yet been applied to virus disease epidemics, but to an oomycete pathogen (Bussell and Cunniffe 2020, 2022), the technique promises much for vectored virus disease in terms of going beyond the simplified models consid-

ered by, for example, Hamelin et al. (2021), and accounting for the various ways in which virus disease epidemics are distinctive.

Estimation of epidemiological parameters

The second area refers to advances in computational techniques that allow for estimation of epidemiological parameters from field data. Such techniques in principle allow for a link between estimates made in the laboratory or microcosm experiments and estimates made in the field. Certain parameters required by mathematical models, for example, the delay between first infection of a plant host and the emergence of symptoms, can be estimated from the results of designed experiments involving individual plants. Experiments can also be used to obtain relatively detailed information concerning the preferences of vector species, as well as their vital dynamics (Tungadi et al. 2017, 2020; Wamonde et al. 2020). These parameters are particularly important in models that focus predominantly on the behavior of individual vectors (Donnelly et al. 2019). However, parameters controlling the rate of spread of disease often must be inferred by fitting the output of an epidemiological model to data. Often, the key uncertainty is around the dispersal kernel, which tends to be only very loosely characterized for many pathogens (Fabre et al. 2021). For virus diseases, it reflects the probability of vector-borne transmission linking pairs of plants at a certain distance.

Often, this is done in an explicitly Bayesian framework, which allows prior knowledge to constrain model fitting. However, this requires a likelihood function to be written for the model of interest, which in turn tends to require information on epidemiological transitions that are not recorded and in many cases never could be, such as the time at which a plant was first infected. Although some methods based on approximations to the likelihood function which do not require this type of information have been developed (Pleydell et al. 2018), the calculations rapidly become complex. A more general method, introduced into plant disease epidemiology by Gibson and Austin (1996); and Gibson (1997a, b) relies on “data augmentation,” which, in this context, means treating unknown/unknowable parameters as additional parameters to be estimated by using Markov chain Monte Carlo (MCMC) techniques to draw samples from the relevant posterior distribution. These methods work particularly well for field data consisting of successive snapshots from different

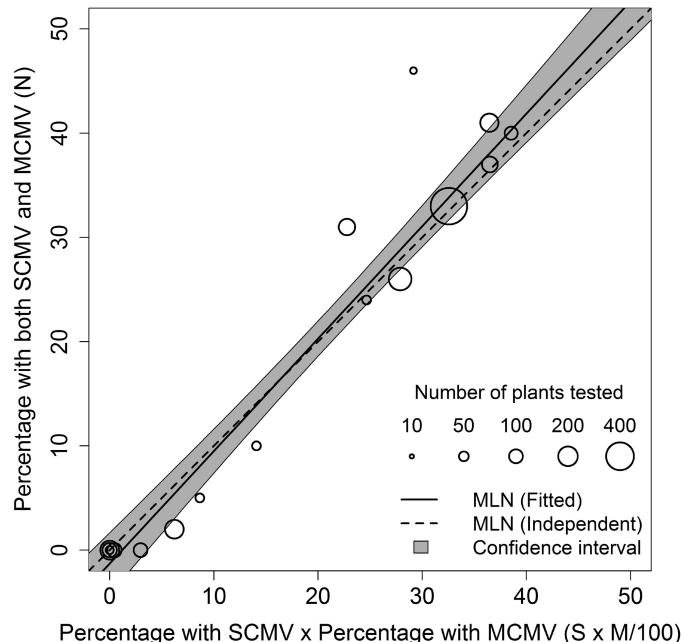


FIGURE 4

Field survey data on maize chlorotic mottle virus (MCMV) and sugarcane mosaic virus (SCMV) in maize lethal necrosis (MLN) reported by Mahuku et al. (2015). The best-fitting linear response ($N = -1.28 + 1.08SM$) is shown with a solid black line, where MLN is represented by N , MCMV by M , and SCMV by S . The dotted line corresponding to the assumption of independence ($N = SM$) is contained within the 95% confidence interval (Reproduced, by permission, from Hilker et al. 2017).

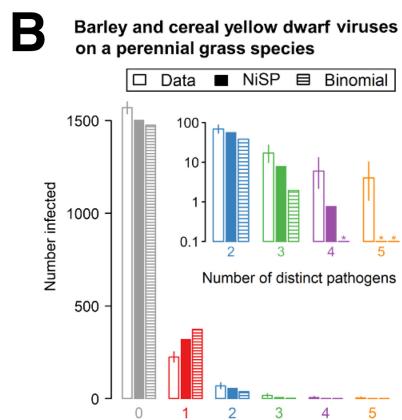
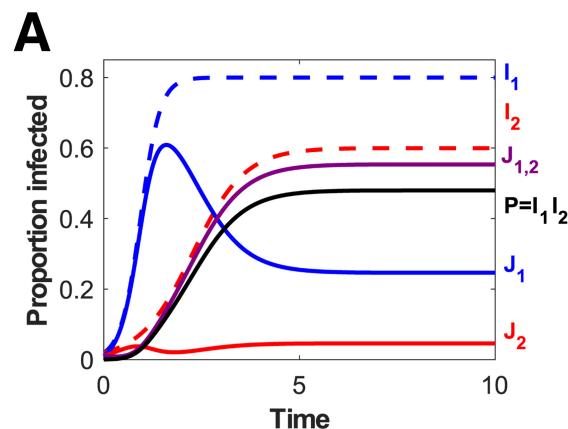


FIGURE 5

A, Dynamics of a coinfection model (Reproduced, by permission, from Hamelin et al. 2019 and supporting information) in which pathogens have no interactions. J_1 and J_2 are the proportion of hosts infected with a single pathogen 1 or 2; $J_{1,2}$ is the proportion of coinfected hosts; and $I_1 = J_1 + J_{1,2}$ and $I_2 = J_2 + J_{1,2}$ are the net incidences of pathogen 1 or pathogen 2, respectively. The proportion of coinfections, $J_{1,2}$, is not equal to the product of the pathogens’ net incidences, $P = I_1 + I_2$. This deviation from statistical independence is due to host mortality and therefore mostly concerns pathogens causing long-lasting infections. **B**, The Binomial model assumes that noninteracting pathogens are statistically independent, whereas the Non-interacting Similar Pathogens (NiSP) model does not make this assumption, which is especially strong in plant viruses making long-lasting infections in their hosts. Although the NiSP model is a better fit to the data than the Binomial model, there is evidence of a lack of goodness of fit, and so, our test indicates that these pathogens interact (or are epidemiologically different). Data from Seabloom et al. (2013).

surveys (Neri et al. 2014; Parry et al. 2014). The example shown in Figure 7 is from Cunniffe et al. (2014) and shows pairwise posterior distributions as sampled via MCMC for key parameters in an individual-based model of Bahia bark scaling fitted to data from a small experimental plot.

There is extensive literature on the principles and use of MCMC techniques in plant disease epidemiology, including viruses and other vector-borne diseases, for example, spatiotemporal dynamics of plum pox disease (Pleydell et al. 2018); temporal dynamics and emergence of *Xylella fastidiosa* (Soubeyrand et al. 2018); disease mapping of citrus huanglongbing (Luo et al. 2012); and diagnosis/detection of tomato viruses and bacteria (Hernández and López 2020; Mohanty et al. 2016).

However, there are limits on the size of the system that can be adequately represented in this way. Data augmentation becomes

infeasible for models with large numbers of individuals and/or complex transitions between states. However, most models—including very complex models—can be simulated relatively easily. This is the motivation for approximate Bayesian computation (ABC), which uses statistics drawn from simulation results as a proxy for the likelihood function (Jabot et al. 2013; Toni et al. 2009). By using the fraction of simulation results that are sufficiently close to the data as an estimator of the likelihood for any given set of parameters, estimation can be done without ever writing down any mathematics. The challenge, however, is to identify the “correct” summary of experimental results to use in the comparison between model results and data. An example for plant virus disease is shown in Figure 8; it shows two snapshots of the disease status in a citrus grove infected by citrus tristeza virus (reproduced from Marcus et al. 1984). As shown by Minter and Retkute (2019), an ABC algorithm using a spatial statistic based on the minimum distance between newly infected trees in the 1982 snapshot and infected trees in the 1981 snapshot can be used to drive model fitting.

There is also extensive literature on ABC techniques, widely used in ecological and evolutionary studies (Beaumont 2010) and in epidemiological studies, for example, within-field dynamics of banana bunchy top disease (Varghese et al. 2020); colonization history of the fungal pathogen causing South American leaf blight (Barres et al. 2012); and pollen dispersal (Soubeyrand et al. 2013).

Challenges and Opportunities

Quantitative epidemiological analysis, including mathematical models, has given insights into how a changing environment, the host–virus–vector association, and vector life history, behavior, and population dynamics interact at the systems level in plant virus epidemiology. A broader perspective and synthesis are needed to account for the ecological context and the evolutionary implications of these interactions. How do new evolved strains emerge (Antia et al. 2003), and what are the consequences for host ranges, crop losses, and natural wild populations?

Epidemiological analysis

Much progress has been made on integrating vector life history parameters with epidemiological parameters, although the difficulties in scaling up from laboratory/microcosm experiments to field observations remains a challenge. The complex spatial dynamics of virus disease means that the “mean-field” assumption of randomness in host–vector association is untenable, especially when vector preference is conditional on the vector–virus association. At the field level, “one-off” observations on the size of vector populations and the association with virus incidence have been made, but rates of change in each variable need to be assessed to better describe time delays, vector and epidemic dynamics, and options for disease management.

Innovative field-based research and further modeling are required to determine the epidemiological significance of the different forms of vector preference. Further research is required on further aspects of vector behavior, for example, on the energetic costs associated with number of vector flights per individual feed with respect to virus transmission and vector preference and on competitive and other interactive effects in relation to coinfection, vector preference, and transmission.

Does a link between vector preference, transmission type, and natural enemies lead to increased virus fitness? Tritrophic plant–virus–vector–parasitoid relationships potentially add a further level of signaling mechanisms (Jeger et al. 2012) in which the vector shows preference for either healthy or infected host plants, the host plant uses a “cry-for-help” signal to attract parasitoids, the parasitoid induces an “alarm signal” initiating vector movement, and, once the virus has been acquired, the vector switches to a preference for healthy plants. The first element in increasing virus fitness

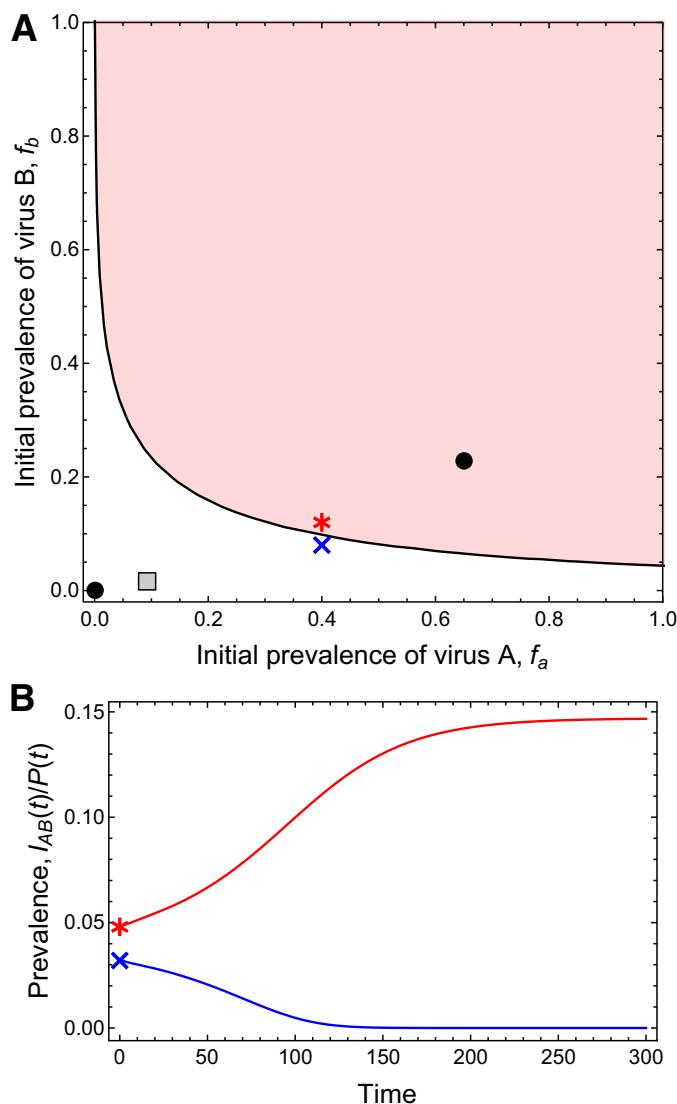


FIGURE 6

Dynamics of coinfection with two viruses (Reproduced, by permission, from Allen et al. 2019). In this special case, neither virus can invade in the absence of the other. **A**, Prevalence of coinfection with virus A and virus B as a function of the initial frequencies of the two viruses. The black dots represent the endemic coinfection equilibrium in the shaded area and the disease-free equilibrium in the white area. **B**, In time plots of coinfection, the blue cross and red asterisk indicate initial conditions in different basins of attraction and show convergence either to the disease-free state or to the coinfection equilibrium.

through transmission is then conditional vector preference, with nonviruliferous vectors preferring infected plants and viruliferous vectors preferring healthy plants. Parasitoids may then be attracted by the “cry-for-help” signal from infected plants infested with an

insect vector. The alarm signal among vectors may encourage the movement of vectors from infected plants. If viruliferous vectors then show a preference for healthy plants, a virtuous circle has been completed, thereby increasing virus fitness. A further element that

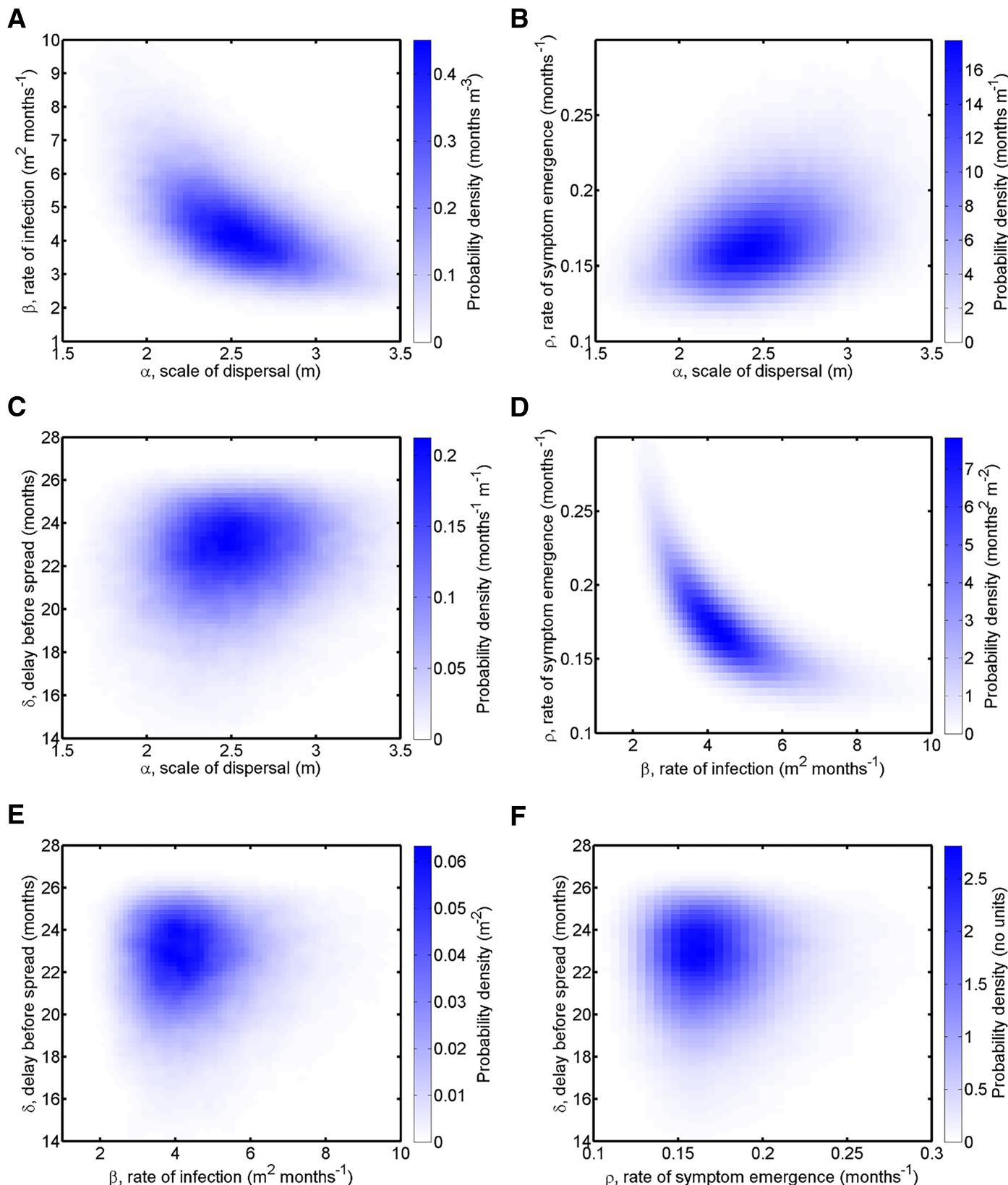


FIGURE 7

A to F: Estimation of epidemiological parameters (pairwise distributions) from experimental data of Bahia bark scaling of citrus using a stochastic model and Monte Carlo Markov chain (MCMC) techniques (Reproduced, by permission, from Cunniffe et al. 2014).

needs to be accounted for is that natural enemies, as well as affecting vector population dynamics and behavior, may affect vector developmental rates. This was modeled by Keissar et al. (2020) who counterintuitively showed that slowing down development rate increased disease prevalence due to an apparent competition between infected and uninfected vectors.

Ecological context

There have been many recent reviews on plant virus ecology (Aranda and Freitas-Astúa 2017; Jones 2014b; Lefevre et al. 2019; Shates et al. 2019). Often, most concern has been with molecular virology, diversity, evolution, and disease in (semi-)natural plant populations, and studies do not always make clear the link with epidemiology, where the interchange between crops and wild plants mediated by vectors contributes to a complex ecology that merits further study (Jeger 2022a).

Multiple infections, plant fitness effects and life history traits, transmission, and movement ecology of vectors in heterogeneous environments are major drivers of plant-virus-vector systems and require a higher level of analysis than provided by molecular virological studies if forecasting models of disease risk are to become a reality (McLeish et al. 2020). These authors consider that the next major step in plant virus epidemiology will come from the synthesis of high-throughput sequencing systems ecology and remote sensing. Such a synthesis is wide and ambitious, but the interrogation of intensive data sets is receiving much attention in genomic studies, field observations, and environmental monitoring and, as the authors suggest, may prove to be a major development in plant disease epidemiology.

Research in disease ecology has stressed the interactions between host composition and structure, diversity, and infection risk (Seabloom et al. 2013). In studies on barley and cereal yellow dwarf viruses in grassland communities, researchers have found that niche differentiation arising from nutrient treatment was an important factor in virus species distribution and assemblages. The spatial structure of virus species in these grassland communities, especially pairs, was found to be aggregated, resulting from shared vectors and their distribution (Kendig et al. 2017). The prevalence and diversity of potyvirus species was studied in natural riparian forests in Spain (Rodríguez-Nevado et al. 2020). A novel generalist virus was found, accounting for the highest proportion of infected plants, and was best predicted by host abundance and species richness. These ecological factors, together with virus prevalence, largely determined selection and genetic diversity in the virus population.

A mathematical model was proposed describing the joint effect of a mycorrhizal mutualist and a viral pathogen (Rúa and Umbanhowar 2015) one of the few models exploring cross-taxon and cross-functional group interactions. Where there was low plant productivity due to limited resource availability, the pathogen de-

pended on the mutualist for persistence; when plant productivity was high, under some circumstances, the mutualist could go extinct. Cyclical virus dynamics were only found with the presence of the mutualist but were not consistently associated with high viral pathogenicity.

Environmental conditions may affect the ecology of insect vectors if they affect host preferences. High temperature tolerance of insects affects population dynamics under extreme temperature events, and this would include aphid vectors of plant viruses. The cowpea aphid *Aphis craccivora* showed an ecological niche switch from cotton to soybean under high temperatures, showing that heat tolerance was host associated (Zhaozhi et al. 2017). The aphid is known as a vector of soybean viruses and has been reported as transmitting cotton leaf roll viruses, although the main vector is predominantly *A. gossypii*. The consequences of such host switching have been little explored in plant virus epidemiology.

Evolutionary implications

In the paper on the evolution of conditional vector preferences, Gandon (2018) assumed, for simplicity, that the manipulation of infected vectors is fully governed by the pathogen in the vector and that the pathogen in the infected host can affect only the behavior of uninfected vectors. However, a pathogen strain making hosts more attractive to vectors may attract vectors carrying a pathogen strain that would otherwise drive the vector to uninfected hosts. Research further exploring the evolution of vector preferences should account for such indirect interactions between pathogen strains.

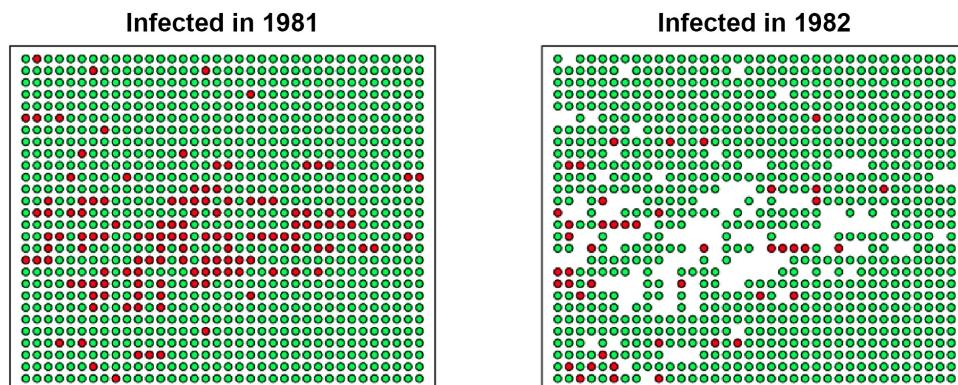
Future work should also address the evolution of conditional mutualism. Specifically, conditional mutualism occurs when infected plants have lower fecundity than uninfected plants under favorable conditions and higher fecundity than uninfected plants under unfavorable conditions such as water stress (Hily et al. 2016). Hamelin et al. (2017) explored the evolution of unconditional mutualism, a situation in which infected plants' fecundity is greater than uninfected plants' fecundity. The authors showed, among other results, that mutualism may evolve from and evolutionarily exclude parasitism under certain conditions. However, it would be interesting to extend this type of approach to conditional (environment-dependent) mutualism in plant viruses.

Further synthesis and questions

This review has attempted to identify emerging themes and approaches in plant virus epidemiology. Perhaps an overarching theme is how these themes are linked and how experimental, observational, and modeling studies can contribute to these linkages. For example, the deployment of tolerance as a disease management option or as a natural phenomenon in wild plant populations has received much attention recently (Jeger 2022b). Linking across the other themes in

FIGURE 8

Spread of citrus tristeza virus in an orchard (data reproduced, by permission, from Marcus et al. 1984, reanalyzed by Minter and Retkute 2019). Green circles represent healthy trees, and red circles represent infected trees.



this review, we can ask how virus epidemiology interacts with the various forms of tolerance in plants? Can direct damage from vector feeding be disentangled from that resulting from virus infection when there is plant tolerance to the vector as pest as well as to the virus? How are interactions of virus epidemiology with reproductive stage stress tolerance manifested where there are other biotic and abiotic stressors in both wild plants and crops? Do interactions of vector preference with tolerance impact reproductive fitness? Does deploying tolerant varieties affect vector population dynamics, and how does this in turn feed into disease dynamics? How is tolerance to single viruses affected when there is coinfection with multiple viruses? Perhaps most importantly, and applicable to all themes, how can mathematical models with the theoretical framework(s) outlined here be fitted to observations from the field and/or designed experiments to allow us to disentangle the significant complexity underpinning these—and other—interactions? Finally, the choices made by growers of necessity are based on making linkages across all aspects of disease epidemiology and management. Can the choices made by individual growers directly account for the behavior of others and be applied to virus disease epidemics in future studies?

Acknowledgments

We thank Linda Allen (Texas Tech University, Lubbock, U.S.A.), Vrushali Bokil (Department of Mathematics, Oregon State University, U.S.A.), Frank Hilker (Institute for Environmental Systems Research, Osnabrück, Germany), and other participants in working groups on multi-scale aspects of vector transmission of plant viruses at the NSF-sponsored National Institute for Mathematical and Biological Synthesis, University of Tennessee, U.S.A. We also acknowledge long-term collaborations by one or other of us with Frank van den Bosch, Larry Madden, Chris Gilligan, John Carr, and Ruairí Donnelly and the vision and continued inspiration provided by the epidemiological studies of the late Michael Thresh.

Literature Cited

- Adrakey, H. K., Streftaris, G., Cunniffe, N. J., Gottwald, T. R., Gilligan, C. A., and Gibson, G. J. 2017. Controlling spatio-temporal epidemics using latent processes in a Bayesian framework. *J. R. Soc. Interface*. 14: 20170386.
- Allen, L. J. S., Bokil, V. A., Cunniffe, N. J., Hamelin, F. M., Hilker, F. M., and Jeger, M. J. 2019. Modelling vector transmission and epidemiology of co-infecting plant viruses. *Viruses* 11:1153.
- Allen-Perkins, A., and Estrada, E. 2019. Mathematical modelling for sustainable aphid control in agriculture via intercropping. *Proc. R. Soc. A.* 475:20190136.
- Amari, K., Huang, C., and Heinlein, M. 2021. Potential impact of global warming on virus propagation in infected plants and agricultural productivity. *Front. Plant Sci.* 12:649768.
- Andersen, K. F., Buddenhagen, C. E., Rachkara, P., Gibson, R., Kalule, S., Phillips, D., and Garrett, K. A. 2019. Modeling epidemics in seed systems and landscapes to guide management strategies: The case of sweet potato in Northern Uganda. *Phytopathology* 109:1519-1532.
- Antia, R., Regoes, R. R., Koella, J. C., and Bergstrom, C. T. 2003. The role of evolution in the emergence of infectious diseases. *Nature* 426:658-661.
- Aranda, M. A., and Freitas-Astúa, J. 2017. Editorial, Virtual issue on viruses: Ecology and diversity of plant viruses, and epidemiology of plant virus-induced diseases. *Ann. Appl. Biol.* 171:1-4.
- Aregbesola, O. Z., Legg, J. P., Lund, O. S., Sigsgaard, L., Sporleder, M., Carhuapoma, P., and Rapisarda, C. 2020. Life history and temperature-dependence of cassava-colonising populations of *Bemisia tabaci*. *J. Pest Sci.* 93:1225-1241.
- Atallah, S. S., Gomez, M. I., Conrad, J. M., and Nyrop, J. P. 2015. A plant-level, spatial, bioeconomic model of plant disease diffusion and control: Grapevine leafroll disease. *Am. J. Agric. Econ.* 97:199-218.
- Ban, F., Zhong, Y., Pan, L., Mao, L., Wang, X., and Liu, Y. 2021. Coinfection by two begomoviruses aggravates plant symptoms but does not influence the performance and preference of vector *Bemisia tabaci* (Hemiptera: Aleyroididae). *J. Econ. Entomol.* 114:547-554.
- Barrès, B., Carlier, J., Seguin, M., Fenouillet, C., Cilas, C., and Ravigné, V. 2012. Understanding the recent colonization history of a plant pathogenic fungus using population genetic tools and approximate Bayesian computation. *Heredity* 109:269-279.
- Bassanezi, R. B., Montesino, L. H., Gimenes-Fernandes, N., Gottwald, T. R., Amorim, L., and Bergamin Filho, A. 2013. Efficacy of area-wide inoculum reduction and vector control on temporal progress of Huanglongbing in young sweet orange plantings. *Plant Dis.* 97:789-796.
- Bate, A. M., Jones, G., Kleczkowski, A., and Touza, J. 2021. Modelling the effectiveness of collaborative schemes for disease and pest outbreak prevention. *Ecol. Model.* 442:109411.
- Bauch, C. T., and Earn, D. J. D. 2004. Vaccination and the theory of games. *Proc. Natl. Acad. Sci.* 101:13391-13394.
- Beaumont, M. A. 2010. Approximate Bayesian computation in evolution and ecology. *Annu. Rev. Ecol. Evol.* 41:379-406.
- Bergès, S. E., Vile, D., Yvon, M., Masclef, D., Dauzat, M., and van Munster, M. 2021. Water deficit changes the relationship between epidemiological traits of cauliflower mosaic virus across diverse *Arabidopsis thaliana* accessions. *Sci. Rep.* 11:24103.
- Blystad, D.-R., van der Vlugt, R., Alfaro-Fernández, A., del Carmen Córdoba, M., Bese, G., Hristova, D., Pospieszczy, H., Mehle, N., Ravnikar, M., Tomassoli, L., Varveri, C., and Nielsen, S. L. 2015. Host range and symptomatology of pepino mosaic virus strains occurring in Europe. *Eur. J. Plant Pathol.* 143:43-56.
- Bokil, V. A., Allen, L. J. S., Jeger, M. J., and Lenhart, S. 2019. Optimal control of a vectored plant disease model for a crop with continuous replanting. *J. Biol. Dyn.* 13: 325-353.
- Bradshaw, C. D., Hemming, D., Baker, R., Everett, M., Eyre, D., and Korycinska, A. 2019. A novel approach for exploring climatic factors limiting current pest distributions: A case study of *Bemisia tabaci* in north-west Europe and assessment of future establishment in the United Kingdom under climate change. *PLoS One* 14:e0221057.
- Buddenhagen, C. E., Xing, Y., Andrade-Piedra, J. L., Forbes, G. A., Kromann, P., Navarrete, I., Thomas-Sharma, S., Choudhury, R. A., Andersen Onofre, K. F., Schulte-Geldermann, E., Etherton, B. A., Plex Sulá, A. I., and Garrett, K. A. 2022. Where to invest project efforts for greater benefit: A framework for management performance mapping with examples for potato seed health. *Phytopathology* 112:1431-1443.
- Burdon, J. J., and Zhan, J. 2020. Climate change and disease in plant communities. *PLoS Biol.* 18:e3000949.
- Bussell, E. H., and Cunniffe, N. J. 2020. Applying optimal control theory to a spatial simulation model of sudden oak death: Ongoing surveillance protects tanoak while conserving biodiversity. *J. R. Soc. Interface* 17:20190671.
- Bussell, E. H., and Cunniffe, N. J. 2022. Optimal strategies to protect a sub-population at risk due to an established epidemic. *J. R. Soc. Interface* 19:20210718.
- Bussell, E. H., Dangerfield, C. E., Gilligan, C. A., and Cunniffe, N. J. 2019. Applying optimal control theory to complex epidemiological models to inform real-world disease management. *Phil. Trans. R. Soc. B* 374:20180284.
- Chang, S. L., Piraveenan, M., Pattison, P., and Prokopenko, M. 2020. Game theoretic modelling of infectious disease dynamics and intervention methods: A review. *J. Biol. Dyn.* 14:57-89.
- Chapwanya, M., Matusse, A., and Dumont, Y. 2021. On synergistic co-infection in crop diseases. The case of the maize lethal necrosis disease. *Appl. Math. Modelling* 90:912-942.
- Chavez, V. A., Milne, A. E., van den Bosch, F., Pita, J., and McQuaid, C. F. 2022. Modelling cassava production and pest management under biotic and abiotic constraints. *Plant Mol. Biol.* 109:325-349.
- Chivasa, W., Mutanga, O., and Biradar, C. 2020. UAV-based multispectral phenotyping for disease resistance to accelerate crop improvement under changing climatic conditions. *Remote Sens.* 12:2445.
- Craig, A. P., Cunniffe, N. J., Parry, M., Laranjeira, F. F., and Gilligan, C. A. 2018. Grower and regulator conflict in management of the citrus disease Huanglongbing in Brazil: A modelling study. *J. Appl. Ecol.* 55: 1956-1965.
- Cronin, J. P., Rúa, M. A., and Mitchell, C. E. 2014. Why is living fast dangerous? Disentangling the roles of resistance and tolerance of disease. *Am. Nat.* 184:172-187.
- Cunniffe, N. J., Cobb, R. C., Meentemeyer, R. K., Rizzo, D. R., and Gilligan, C. A. 2016. Modeling when, where and how to manage a forest epidemic, motivated by sudden oak death in California. *Proc. Natl. Acad. Sci.* 113: 5640-5645.
- Cunniffe, N. J., and Gilligan, C. A. 2020. Using mathematical models to predict epidemics and to optimize disease detection and management. Chapter 12 in: *Emerging Plant Diseases and Global Food Security*. J. B. Risitano and A. R. Records, eds. American Phytopathological Society, St. Paul, MN.
- Cunniffe, N. J., Koskella, B., Metcalf, C. J., Parnell, S., Gottwald, T. R., and Gilligan, C. A. 2015. Thirteen challenges in modelling plant diseases. *Epidemics* 10:6-10.
- Cunniffe, N. J., Laranjeira, F. F., Neri, F. M., DeSimone, R. E., and Gilligan, C. A. 2014. Cost-effective control of plant disease when epidemiological

- knowledge Is Incomplete: Modelling Bahia bark scaling of citrus. *PLoS Comput. Biol.* 10:e1003753.
- Cunniffe, N. J., Taylor, N. P., Hamelin, F. M., and Jeger, M. J. 2021. Epidemiological and ecological consequences of virus manipulation of host and vector in plant virus transmission. *PLoS Comput. Biol.* 17:1-41.
- Dash, S. P., Dipankar, P., Burange, P. S., Rouse, B. T., and Sarangi, P. P. 2021. Climate change: How it impacts the emergence, transmission, resistance and consequences of viral infections in animals and plants. *Crit. Rev. Microbiol.* 47:307-322.
- DeAngelis, D. L., and Grimm, V. 2014. Individual-based models in ecology after four decades. *F1000 Prime Reports* 6:39.
- De Groot, H., Munyua, B. G., Palmas, S., Suresh, L. M., Bruce, A. Y., and Kimenju, S. 2021. Using panel community surveys to track the impact of crop pests over time and space – The case of maize lethal necrosis (MLN) disease in Kenya from 2013 to 2018. *Plant Dis.* 105:1259-1271.
- Del Cid, C., Krugner, R., Zeilinger, A. R., Daugherty, M. P., and Almeida, R. P. P. 2018. Plant water stress and vector feeding preference mediate transmission efficiency of a plant pathogen. *Environ. Entomol.* 47: 1471-1478.
- Del Valle, S., Mniszewski, S., and Hyman, J. 2013. Modeling the impact of behavior changes on the spread of pandemic influenza. Chapter 4 in: *Modeling the Interplay Between Human Behavior and the Spread of Infectious Diseases*. P. Manfredi and A. D'Onofrio, eds. Springer, New York.
- Djidjou-Demasse, R., Moury, B., and Fabre, F. 2017. Mosaics often outperform pyramids: Insights from a model comparing strategies for the deployment of plant resistance genes against viruses in agricultural landscapes. *New Phytol.* 216:239-253.
- Donnelly, R., Cunniffe, N. J., Carr, J. P., and Gilligan, C. A. 2019. Pathogenic modification of plants enhances long-distance dispersal of non-persistently transmitted viruses to new hosts. *Ecology* 100:e02725.
- Eigenbrode, S. D., Bosque-Pérez, N., and Davis, T. S. 2018. Insect-borne plant pathogens and their vectors: Ecology, evolution, and complex interactions. *Annu. Rev. Entomol.* 63:169-191.
- Eigenbrode, S. D., and Gomulkiewicz, R. 2022. Manipulation of vector host preference by pathogens: Implications for virus spread and disease management. *J. Econ. Entomol.* 115:387-400.
- Fabre, F., Coville, J., and Cunniffe, N. J. 2021. Optimising reactive disease management using spatially explicit models at the landscape scale. Chapter 4 in: *Plant Diseases and Food Security in the 21st Century*. P. Scott, R. Strange, L. Korsten, and L. Gullino, eds. Springer, Cham.
- Fabre, F., Rousseau, E., Mailleret, L., and Moury, B. 2012. Durable strategies to deploy plant resistance in agricultural landscapes. *New Phytol.* 193: 1064-1075.
- Fabre, F., Rousseau, E., Mailleret, L., and Moury, B. 2015. Epidemiological and evolutionary management of plant resistance: Optimizing the deployment of cultivar mixtures in time and space in agricultural landscapes. *Evol. Appl.* 8:919-932.
- Ferrari, A. C., Stutt, R. O. J. H., Godding, D., and Gilligan, C. A. 2020. Computational models to improve surveillance for cassava brown streak disease and minimize yield loss. *PLOS Comput. Biol.* 16:e1007823.
- Ferriss, R. S., and Berger, P. H. 1993. A Stochastic simulation model of epidemics of arthropod-vectored plant viruses. *Phytopathology* 83:1269-1278.
- Funk, S., Salathé, M., and Jansen, V. A. 2010. Modelling the influence of human behaviour on the spread of infectious diseases: A review. *J. R. Soc. Interface* 7:1247-1256.
- Gamarra, H., Carhuapoma, P., Cumapa, L., González, G., Muñoz, J., Sporleder, M., and Kreuze, J. 2020. A temperature-driven model for potato yellow vein virus transmission efficiency by *Trialeurodes vaporariorum* (Hemiptera: Aleyrodidae). *Virus Res.* 289:198109.
- Gandon, S. 2018. Evolution and manipulation of vector host choice. *Am. Nat.* 192:23-34.
- Gautam, S., Gadhave, K. R., Buck, J. W., Dutta, B., Coolong, T., Adkins, S., and Srinivasan, R. 2020a. Virus–virus interactions in a plant host and in a hemipteran vector: Implications for vector fitness and virus epidemics. *Virus Res.* 286:198069.
- Gautam, S., Mugerwa, H., Sunderaj, S., Gadhave, K. R., Murphy, J. S., Dutta, B., and Srinivasan, R. 2020b. Specific and spillover effects on vectors following infection of two RNA viruses in pepper plants. *Insects* 11:602.
- Gibson, G. J. 1997a. Investigating mechanisms of spatiotemporal epidemic spread using stochastic models. *Phytopathology* 87:139-146.
- Gibson, G. J. 1997b. Markov chain Monte Carlo methods for fitting and testing spatiotemporal stochastic models in plant epidemiology. *J. R. Stat. C-AppL* 46:215-233.
- Gibson, G. J., and Austin, E. J. 1996. Fitting and testing spatio-temporal stochastic models with application in plant epidemiology. *Plant Pathol.* 45: 172-184.
- Gilligan, C. A., Truscott, J. E., and Stacey, A. J. 2007. Impact of scale on the effectiveness of disease control strategies for epidemics with cryptic infection in a dynamical landscape: An example for a crop disease. *J. R. Soc. Interface* 4:925-934.
- Godding, D., Stutt, R. O. J. H., Alicai, T., Abidrabo, P., Okao-Okuja, G., and Gilligan, C. A. 2022. Developing a predictive model for an emerging epidemic on cassava in sub-Saharan Africa. *bioRxiv* 491768.
- Gutiérrez Illán, J., Bloom, E. H., Wohleb, C. H., Wenninger, E. J., Rondon, S. I., Jensen, A. S., Snyder, W. E., and Crowder, D. W. 2020. Landscape structure and climate change drive population dynamics of an insect vector within intensively managed agroecosystems. *Ecol. Applic.* 30:e02109.
- Gutiérrez-Sánchez, A., Cobos, A., López-Herranz, M., Canto, T., and Pagán, I. 2023. Environmental conditions modulate plant virus vertical transmission and survival of infected seeds. *Phytopathology* 113:1773-1787.
- Hamelin, F. M., Allen, L. J. S., Bokil, V. A., Gross, L. J., Hilker, F. M., Jeger, M. J., Manore, C. A., Power, A. G., Rúa, M. A., and Cunniffe, N. J. 2019. Coinfections by noninteracting pathogens are not independent and require new tests of interaction. *PLoS Biol.* 17:e3000551.
- Hamelin, F. M., Bowen, B., Bernhard, B., and Bokil, V. A. 2021. Optimal control of plant disease epidemics with clean seed usage. *Bull. Math. Biol.* 83:46.
- Hamelin, F. M., Hilker, F. M., Sun, T. A., Jeger, M. J., Hajimorad, M. R., Allen, L. J. S., and Prendeville, H. R. 2017. The evolution of parasitic and mutualistic plant–virus symbioses through transmission–virulence trade-offs. *Virus Res.* 241:77-87.
- Hernández, S., and López, J. L. 2020. Uncertainty quantification for plant disease detection using Bayesian deep learning. *Appl. Soft Comp. J.* 96:106597.
- Hilker, F. M., Allen, L. J. S., Bokil, V. A., Briggs, C. J., Feng, Z., Garrett, K. A., Gross, L. J., Hamelin, F. M., Jeger, M. J., Manore, C. A., Power, A. G., Redinbaugh, M. G., Rúa, M. A., and Cunniffe, N. J. 2017. Modeling virus coinfection to inform management of maize lethal necrosis in Kenya. *Phytopathology* 107:1095-1108.
- Hily, J.-M., Poulicard, N., Mora, M.-Á., Pagán, I., and García-Arenal, F. 2016. Environment and host genotype determine the outcome of a plant–virus interaction: From antagonism to mutualism. *New Phytol.* 209: 812-822.
- Holt, J., and Chancellor, T. C. B. 1997. A model of plant virus disease epidemics in asynchronously-planted cropping systems. *Plant Pathology* 46: 490-501.
- Hyatt-Twynam, S. R., Parnell, S., Stutt, R. O. J. H., Gottwald, T. R., Gilligan, C. A., and Cunniffe, N. J. 2017. Risk-based management of invading plant disease. *New Phytol.* 214:1317-1329.
- Islam, W., Noman, A., Naveed, H., Alamri, S. A., Hashem, M., Huang, Z., and Chen, H. Y. H. 2020. Plant–insect vector–virus interactions under climate change. *Sci. Total Environ.* 701:135044.
- Jabot, F., Faure, T., and Dumoulin, N. 2013. Easy ABC: Performing efficient approximate Bayesian computation sampling schemes using R. *Methods Ecol. Evol.* 4:684-687.
- Jeger, M. 2008. Modeling transmission: Disentangling the ecological trinity of plant host, virus and vector. Pages S189-S189 in: 100th Annual Meeting of The American Phytopathological Society. American Phytopathological Society, St. Paul, MN.
- Jeger, M., Chen, Z., Cunningham, E., Martin, G., and Powell, G. 2012. Population biology and epidemiology of plant virus epidemics: From tripartite to tritrophic interactions. *Eur. J. Plant Pathol.* 133:3-23.
- Jeger, M. J. 2000. Theory and plant epidemiology. *Plant Dis.* 49:651-658.
- Jeger, M. J. 2020. The epidemiology of plant virus disease: Towards a new synthesis. *Plants* 9:1768.
- Jeger, M. J. 2022b. Tolerance to plant virus disease: Its genetic, physiological, and epidemiological significance. *Food and Energy Security online* 14 December 2022: e440.
- Jeger, M. J. 2022a. The impact of climate change on disease in wild plant populations and communities. *Plant Pathol.* 71:111-130.
- Jeger, M. J., Holt, J., van den Bosch, F., and Madden, L. V. 2004. Epidemiology of insect-transmitted plant viruses: Modelling disease dynamics and control interventions. *Physiol. Entomol.* 29:291-304.
- Jeger, M. J., Madden, L. V., and van den Bosch, F. 2017. Plant virus epidemiology: Applications and prospects for mathematical modelling and analysis to improve understanding and disease control. *Plant Dis.* 102:837-854.
- Jeger, M. J., van den Bosch, F., Madden, L. V., and Holt, J. 1998. A model for analysing plant–virus transmission characteristics and epidemic development. *IMA J. Math. Appl. Med. Biol.* 15:1-18.
- Jones, R. A. C. 2014a. Trends in plant virus epidemiology: Opportunities from new or improved technologies. *Virus Res.* 186:3-19.
- Jones, R. A. C. 2014b. Plant virus ecology and epidemiology: Historical perspectives, recent progress and future prospects. *Ann. Appl. Biol.* 164:320-347.
- Karlsson, C.-J., and Rowlett, J. 2020. Decisions and disease: A mechanism for the evolution of cooperation. *Sci. Rep.* 10:1-9.
- Keissar, O., Scharf, I., and Sadeh, A. 2020. Predator modulation of plant pathogen spread through induced changes in vector development rates. *Ecol. Entomol.* 45:213-222.

- Kendig, A. E., Borer, E. T., Mitchell, C. E., Power, A. G., and Seabloom, E. W. 2017. Characteristics and drivers of plant virus community spatial patterns in US west coast grasslands. *Oikos* 126:1281-1290.
- Kho, J.-W., Kim, K. H., and Lee, D.-H. 2020. Comparing the plant virus spread patterns of non-persistently transmitted virus and persistently transmitted virus using an individual-based model. *J. Asia-Pac. Entomol.* 23:371-379.
- Kiss, I., Cassell, J., Recker, M., and Simon, P. 2009. The impact of information transmission on epidemic outbreaks. *Math. Biosci.* 225:1-10.
- Kriticos, D. J., Darnell, R. E., Yonow, T., Ota, N., Sutherst, R. W., Parry, H. R., Mugerwa, H., Maruthi, M. N., Seal, S. E., Colvin, J., Macfadyen, S., Kalyebi, A., Hulthen, A., and De Barro, P. J. 2020. Improving climate suitability for *Bemisia tabaci* in East Africa is correlated with increased prevalence of whiteflies and cassava diseases. *Sci. Rep.* 10:22049.
- Lázaro, E., Armero, C., and Rubio, L. 2017. Bayesian survival analysis to model plant resistance and tolerance to virus diseases. International Conference on Bayesian Statistics in Action. R. Argiento, E. Lanzarone, I. Antoniano Villalobos, and A. Mattei, eds. Springer Proceedings in Mathematics & Statistics 194:173-181.
- Lefevre, P., Martin, D. P., Elena, S. F., Shepherd, D. N., Roumagnac, P., and Varsani, A. 2019. Evolution and ecology of plant viruses. *Nat. Rev. Microbiol.* 17:632-644.
- Li, D., Li, Z., Wang, X., Wang, L., Li, Y., and Liu, D. 2022. Increasing risks of aphids spreading viruses in maize fields on both sides of China's Heihe-Tengchong line under climate change. *Pest Manag. Sci.* 78:3061-3070.
- Lightle, D., and Lee, J. 2014. Raspberry viruses affect the behavior and performance of *Amphorophora agathonica* in single and mixed infections. *Entomol. Exp. Appl.* 151:57-64.
- Luo, W., Pietravalle, S., Parnell, S., van den Bosch, F., Gottwald, T. R., Irey, M. S., and Parker, S. R. 2012. An improved regulatory sampling method for mapping and representing plant disease from a limited number of samples. *Epidemics* 4:68-77.
- Madden, L. V., Jeger, M. J., and van den Bosch, F. 2000. A theoretical assessment of the effects of vector-virus transmission mechanism on plant virus disease epidemics. *Phytopathology* 90:576-594.
- Mahuku, G., Lockhart, B. E., Wanjala, B., Jones, M. W., Kimunye, J. N., Stewart, L. R., Cassone, B. J., Sevyan, S., Nyasani, J. O., Kusia, E., Kumar, P. L., Niblett, C. L., Kiggundu, A., Asea, G., Pappu, H. R., Wangai, A., Prasanna, B. M., and Redinbaugh, M. G. 2015. Maize lethal necrosis (MLN), an emerging threat to maize-based food security in sub-Saharan Africa. *Phytopathology* 105:956-965.
- Marcus, R., Fishman, S., Talpaz, H., Salomon, R., and Bar-Joseph, M. 1984. On the spatial distribution of citrus tristeza virus disease. *Phytoparasitica* 12:45-52.
- Mauck, K. E., and Chasnais, Q. 2020. A synthesis of virus-vector associations reveals important deficiencies on host and vector manipulation by plant viruses. *Virus Res.* 285:197957.
- Mauck, K. E., Chasnais, Q., and Shapiro, L. R. 2018. Evolutionary determinants of host and vector manipulation by plant viruses. *Adv. Virus Res.* 101: 189-250.
- McLaughlin, A. A., Hanley-Bowdoin, L., Kennedy, G. G., and Jacobson, A. L. 2022. Vector acquisition and co-inoculation of two plant viruses influences transmission, infection, and replication in new hosts. *Sci. Rep.* 12:20355.
- McLeish, M. J., Fraile, A., and García-Arenal, F. 2020. Trends and gaps in forecasting plant virus disease risk. *Ann. Appl. Biol.* 176:102-108.
- McQuaid, C. F., Gilligan, C. A., and van den Bosch, F. 2017a. Considering behaviour to ensure the success of a disease control strategy. *R. Soc. Open Sci.* 4:170721.
- McQuaid, C. F., van den Bosch, F., Szyniszewska, A., Alicai, T., Pariyo, A., Chikoti, P. C. and Gilligan, C. A. 2017b. Spatial dynamics and control of a crop pathogen with mixed-mode transmission. *PLoS Comput. Biol.* 13: 1-18.
- Mesterton-Gibbons, M., Gavrilets, S., Gravner, J., and Akcay, E. 2011. Models of coalition or alliance formation. *J. Theor. Biol.* 274:187-204.
- Milne, A. E., Bell, J. R., Hutchison, W. D., van den Bosch, F., Mitchell, P. D., Crowder, D., Parnell, S., and Whitmore, A. P. 2016. The effect of farmers' decisions on pest control with Bt crops: A billion dollar game of strategy. *PLoS Comput. Biol.* 11:1-18.
- Milne, A. E., Gottwald, T., Parnell, S. R., Chavez, A. V., and van den Bosch, F. 2020. What makes or breaks a campaign to stop an invading plant pathogen. *PLoS Comput. Biol.* 16:1-20.
- Minter, A., and Retkute, R. 2019. Approximate Bayesian computation for infectious disease modelling. *Epidemics* 29:100368.
- Mohanty, S., Hughes, D. P., and Salathé, M. 2016. Using deep learning for image-based plant disease detection. *Front. Plant Sci.* 7:1419.
- Montes, N., and Pagán, I. 2019. Light intensity modulates the efficiency of virus seed transmission through modifications of plant tolerance. *Plants* 8:304.
- Moore, S. M., Manore, C. A., Bokil, V. A., Borer, E. T., and Hosseini, P. R. 2011. Spatiotemporal model of barley and cereal yellow dwarf virus transmission dynamics with seasonality and plant competition. *Bull. Math. Biol.* 73: 2707-2730.
- Mora, C., McKenzie, T., Gaw, I. M., Dean, J. M., von Hammerstein, H., Knudson, T. A., Setter, R. O., Smith, C. Z., Webster, K. M., Patz, J. A., and Franklin, E. C. 2022. Over half of known human pathogenic diseases can be aggravated by climate change. *Nat. Clim. Change* 12:869-875.
- Moslonka-Lefebvre, M., Harwood, T., Jeger, M. J., and Pautasso, M. 2012. SIS along a continuum (SIS(c)) epidemiological modelling and control of diseases on directed trade networks. *Math. Biosci.* 236:44-52.
- Moussaïd, M. 2013. Opinion formation and the collective dynamics of risk perception. *PLoS One* 8:e84592.
- Murray-Watson, R. E., and Cunniffe, N. J. 2022a. How the epidemiology of disease resistant and tolerant varieties affects grower behaviour. *J. R. Soc. Interface* 19.
- Murray-Watson, R. E., and Cunniffe, N. J. 2022b. Expanding growers' choice of disease management options can promote suboptimal social outcomes. *bioRxiv* 506581.
- Murray-Watson, R. E., Hamelin, F. M., and Cunniffe, N. J. 2022. How growers make decisions impacts plant disease control. *PLoS Comput. Biol.* 18:e1010309.
- Neri, F. M., Cook, A. R., Gibson, G. J., Gottwald, T. R., Gilligan, C. A. 2014. Bayesian analysis for inference of an emerging epidemic: Citrus canker in urban landscapes. *PLoS Comput. Biol.* 10:e1003587.
- Oh, S., Ashapure, A., Marconi, T. G., Jung, J., and Landivar, J. 2019. UAS based tomato yellow leaf curl virus (TYLCV) disease detection system. *Proc. SPIE 1108, Autonomous Air and Ground Sensing Systems for Agricultural Optimization and Phenotyping IV*, 11080P.
- Pagán, I., and García-Arenal, F. 2020. Tolerance of plants to pathogens: A unifying view. *Annu. Rev. Phytopathol.* 58:77-96.
- Parnell, S., Gottwald, T. R., Cunniffe, N. J., Alonso-Chavez, V., and van den Bosch, F. 2015. Early-detection surveillance for an emerging plant pathogen. *Proc. R. Soc. B.* 282:20151478.
- Parry, M., Gibson, G. J., Parnell, S., Gottwald, T. R., Irey, M. S., Gast, T. C., and Gilligan, C. A. 2014. Bayesian inference for an emerging arboreal epidemic in the presence of control. *Proc. Natl. Acad. Sci.* 111:6258-6262.
- Peñaflor, M. F. G. V., Mauck, K. E., Alves, K. J., De Moraes, C. M., and Mescher, M. C. 2016. Effects of single and mixed infections of Bean pod mottle virus and soybean mosaic virus on host-plant chemistry and host-vector interactions. *Funct. Ecol.* 30:1648-1659.
- Pleydell, D. R. J., Soubeiran, S., Dallot, S., Labonne, G., Chadœuf, J., Jacquot, E., and Thébaud, G. 2018. Estimation of the dispersal distances of an aphid-borne virus in a patchy landscape. *PLoS Comput. Biol.* 14:e1006085.
- Ramos, R. S., Kumar, L., Shabarni, F., and Picanço, M. C. 2018. Mapping global risk levels of *Bemisia tabaci* in areas of suitability for open field tomato cultivation under current and future climates. *PLoS One* 13:e0198925.
- Ramos, R. S., Kumar, L., Shabarni, F., and Picanço, M. C. 2019. Risk of spread of tomato yellow leaf curl virus (TYLCV) in tomato crops under various climate change scenarios. *Agric. Syst.* 173:524-535.
- Reynaud, B., Delatte, H., Peterschmitt, M., and Fargette, D. 2009. Effects of temperature increase on the epidemiology of three vector-borne viruses. *Eur. J. Plant Pathol.* 123:269-280.
- Rodríguez-Nevado, C., Gavrilán, R. G., and Pagán, I. 2020. Host abundance and identity determine the epidemiology and evolution of a generalist plant virus in a wild ecosystem. *Phytopathology* 110:94-105.
- Roosien, B. K., Gomulkiewicz, R., Ingwell, L. L., Bosque-Pérez, N., Rajabaskar, D., and Eigenbrode, S. D. 2013. Conditional vector preference aids the spread of plant pathogens: Results from a model. *Environ. Entomol.* 42: 1299-1308.
- Rúa, M., and Umbanhowar, J. 2015. Resource availability determines stability for mutualist-pathogen-host interactions. *Theor. Ecol.* 8:133-148.
- Salvaudon, L., De Moraes, C. M., and Mescher, M. C. 2013. Outcome of co-infection by two potyviruses: Implications for the evolution of manipulative strategies. *Proc. R. Soc. B.* 280:20122959.
- Sardanyés, J., Alcaide, C., Gómez, P., and Elena, S. F. 2022. Modelling temperature-dependent dynamics of single and mixed infections in a plant virus. *Appl. Math. Modelling* 102:694-705.
- Seabloom, E. W., Borer, E. T., Lacroix, C., Mitchell, C. E., and Power, A. G. 2013. Richness and composition of niche-assembled viral pathogen communities. *PLoS One* 8:e55675.
- Shates, T. M., Sun, P., Malmstrom, C. M., Dominguez, C., and Mauck, K. E. 2019. Addressing research needs in the field of plant virus ecology by defining knowledge gaps and developing wild dicot study systems. *Front. Microbiol.* 9:3305.
- Shaw, A. K., Peace, A., Power, A. G., and Bosque-Pérez, N. A. 2017. Vector population growth and condition-dependent movement drive the spread of plant pathogens. *Ecology* 98:2145-2157.
- Shoemaker, L. G., Hayhurst, E., Weiss-Lehman, C. P., Strauss, A. T., Porath-Krause, A., Borer, E. T., Seabloom, E. W., and Shaw, A. K. 2019. Pathogens

- manipulate the preference of vectors, slowing disease spread in a multi-host system. *Ecol. Lett.* 22:1115-1125.
- Sisterson, M. 2022. Mitigating an epidemic of resistance with integrated disease management tactics: Conflicting management recommendations from insecticide resistance and epidemiological models. *Phytopathology* 112: 1753-1765.
- Sisterson, M. S., and Stenger, D. C. 2018. Modelling effects of vector acquisition threshold on disease progression in a perennial crop following deployment of a partially resistant variety. *Plant Pathol.* 67:1388-1400.
- Somarriba, E., Peguero, F., Cerda, R., Orozco-Aguilar, L., López-Sampson, A., Leandro-Muñoz, M. E., Jagoret, P., and Sinclair, F. L. 2021. Rehabilitation and renovation of cocoa (*Theobroma cacao* L.) agroforestry systems. A review. *Agron. Sustain. Dev.* 41:64.
- Soubeyrand, S., Carpentier, F., Guiton, F., and Klein, E. K. 2013. Approximate Bayesian computation with functional statistics. *Stat. Appl. Genet. Med.* 12:17-37.
- Soubeyrand, S., de Jerphanion, P., Martin, O., Saussac, M., Manceau, C., Hendrikx, P., and Lannou, C. 2018. Inferring pathogen dynamics from temporal count data: The emergence of *Xylella fastidiosa* in France is probably not recent. *New Phytol.* 219:824-836.
- Srinivasan, R., and Alvarez, J. M. 2007. Effects of mixed viral infections (potato virus Y—potato leafroll virus) on biology and preference of vectors *Myzus persicae* and *Macrosiphum euphorbiae* (Hemiptera: Aphididae). *J. Econ. Entomol.* 100:646-655.
- Sun, Y.-C., Fin, Y., Chen, F.-J., Wu, G., and Ge, F. 2011. How does atmospheric elevated CO₂ affect crop pests and their natural enemies? Case histories from China. *Insect Sci.* 18:393-400.
- Thomas-Sharma, S., Andrade-Piedra, J., Carvajal Yepes, M., Hernandez-Nopsa, J. F., Jeger, M. J., Jones, R. A. C., Kromann, P., Legg, J. P., Yuen, J., Forbes, G. A., and Garrett, K. A. 2017. A risk assessment framework for seed degeneration: Informing a seed health strategy for vegetatively propagated crops. *Phytopathology* 107:1123-1135.
- Toni, T., Welch, D., Strelkowa, N., Ipsen, A., and Stumpf, M. P. H. 2009. Approximate Bayesian computation scheme for parameter inference and model selection in dynamical systems. *J. R. Soc. Interface* 6:187-202.
- Trebicki, P. 2020. Climate change and plant virus epidemiology. *Virus Res.* 286:198059.
- Tungadi, T., Donnelly, R., Ling, Q., Iqbal, J., Murphy, A. M., Pate, A. E., Cunniffe, N. J., and Carr, J. P. 2020. Cucumber mosaic virus 2b proteins inhibit virus-induced aphid resistance in tobacco. *Mol. Plant Pathol.* 21:250-257.
- Tungadi, T., Groen, S. C., Murphy, A. M., Pate, A. E., Iqbal, J., Bruce, T. J. A., Cunniffe, N. J., and Carr, J. P. 2017. Cucumber mosaic virus and its 2b protein alter emission of host volatile organic compounds but not aphid vector settling in tobacco. *Virol. J.* 14:91-100.
- van den Bosch, F., Akudibilah, G., Seal, S., and Jeger, M. 2006. Host resistance and the evolutionary response of plant viruses. *J. Appl. Ecol.* 43:506-516.
- van den Bosch, F., and Jeger, M. J. 2017. The basic reproduction number of vector-borne plant virus epidemics. *Virus Res.* 241:196-202.
- van den Bosch, F., McRoberts, N., van den Berg, F., and Madden, L. V. 2008. The basic reproduction number of plant pathogens: Matrix approaches to complex dynamics. *Phytopathology* 98:239-249.
- Vandermeer, J., and Power, A. 1990. An epidemiological model of the corn stunt system in Central America. *Ecol. Modelling* 52:235-248.
- van der Waals, J. E., Krüger, K., Franke, A. C., Haverkort, A. J., and Steyn, J. M. 2013. Climate change and potato production in contrasting South African agro-ecosystems 3. Effects on relative developmental rates of selected pathogens and pests. *Potato Res.* 56:67-84.
- Varghese, A., Drovandi, C., Mira, A., and Mengersen, K. 2020. Estimating a novel stochastic model for within-field disease dynamics of banana bunchy top virus via approximate Bayesian computation. *PLoS Comput. Biol.* 16:e1009787.
- Wamonde, F. O., Tungadi, T. D., Murphy, A. M., Pate, A. E., Woodcock, C., Caulfield, J. C., Mutuku, J. M., Cunniffe, N. J., Bruce, T. J. A., Gilligan, C. A., Pickett, J. A., and Carr, J. P. 2020. Three aphid-transmitted viruses encourage vector migration from infected common bean (*Phaseolus vulgaris*) plants through a combination of volatile and surface cues. *Front. Plant Sci.* 11:1981.
- Wei, J., Peng, L., He, Z., Lu, Y., and Wang, F. 2020. Potential distribution of two pineapple pests under climate change. *Pest Manag. Sci.* 76:1652-1663.
- Whitfield, A. E., Falk, B. W., and Rotenberg, D. 2015. Insect vector-mediated transmission of plant viruses. *Virology* 479-480:278-289.
- Yamamura, K., Yokozawa, M., Nishimori, M., Ueda, Y., and Yokosuka, T. 2006. How to analyze long-term insect population dynamics under climate change: 50-year data of three insect pests in paddy fields. *Popul. Ecol.* 48:31-48.
- Zaffaroni, M., Rimbaud, L., Mailleret, L., Cunniffe, N. J., and Bevacqua, D. 2021. Modelling interference between vectors of non-persistently transmitted plant viruses to identify effective control strategies. *PLoS Comput. Biol.* 17:e1009727.
- Zeilinger, A. R., and Daugherty, M. P. 2013. Vector preference and host defense against infection interact to determine disease dynamics. *Oikos* 123:613-622.
- Zhao, K., Liu, S.-S., Wang, X.-W., Yang, J.-G., and Pan, L.-L. 2022. Manipulation of whitefly behavior by plant viruses. *Microorganisms* 10:2410.
- Zhao, K., and Rosa, C. 2020. Thrips as the transmission bottleneck for mixed infection of two Orthotospoviruses. *Plants* 9:509.
- Zhaozhi, L., Likai, F., Guizhen, G., Lin-Ling, G., Han, P., Sharma, S., and Zalucki, M. P. 2017. Differences in the high-temperature tolerance of *Aphis craccivora* (Hemiptera: Aphididae) on cotton and soybean: Implications for ecological niche switching among hosts. *Appl. Entomol. Zool.* 52:9-18.