

Epidemiology and Management of Plant Viruses Under a Changing Climate

Michael J. Jeger,^{1,†}  Alberto Fereres,² Carolyn E. Malmstrom,³ Kerry E. Mauck,⁴ and William M. Wintermantel^{5,†} 

¹ Imperial College London, Division of Biology, Wye Campus, High Street, Wye, Ashford TN25 5AH, United Kingdom of Great Britain and Northern Ireland

² Institute of Agricultural Sciences, ICA, CSIC, Madrid, Spain

³ Michigan State University, Plant Biology, 612 Wilson Road, East Lansing, MI 48824, U.S.A.

⁴ University of California, Riverside, Entomology, 163 Entomology Bldg., Riverside, CA 92521, U.S.A.

⁵ U.S. Department of Agriculture-Agricultural Research Service, Salinas, CA 93905, U.S.A.

Accepted for publication 19 August 2023.

Abstract

Plant viruses are an ever-present threat to agricultural production and provide a wide array of symptoms resulting in economic losses throughout the world. Diseases can be transmitted by insect vectors, as well as through pollen, seed, and other means. With the increased globalization of agriculture, the introduction of new viruses from exotic locations and their establishment in new production regions and even new crops is a growing concern. Advancing knowledge of the epidemiology of plant viruses

including development of new diagnostic methods, virus surveillance, and modeling, virus ecology and evolution, virus interactions with insect vectors, and other factors are important toward reducing the spread of plant viruses and managing virus diseases.

Keywords: climate, diagnostic, modeling, plant virus epidemiology, plant virus–vector interactions, surveillance, virus ecology, virus evolution

This special issue of *Phytopathology* is focused on plant virus epidemiology and includes papers originating from presentations made at the 15th International Symposium on Plant Virus Epidemiology held in Madrid, Spain from June 5 to 8, 2022. The symposium was organized by the International Committee on Plant Virus Epidemiology (ICPVE) of the International Society of Plant Pathology (ISPP) and the Spanish National Research Council (CSIC) in Madrid, Spain, and hosted by CSIC in Madrid. The symposium was global in scope, attended by 152 participants from 24 countries, and included seven keynote speeches, 61 oral and 77 poster presentations, offering a rich diversity of perspectives on plant virus epidemiological research from throughout the world.

The mission of the ICPVE is to promote research and worldwide exchange of information on the epidemiology and management of plant virus diseases. The first International Symposium on Plant Virus Epidemiology (ISPVE) was held in Oxford, U.K. in 1981, and symposia have been held at 2 to 4 year intervals since at locations throughout the world, including the following: Corowa, Australia 1983; Orlando, U.S.A. 1986; Montpellier, France 1989; Bari, Italy 1992; Jerusalem, Israel 1995; Almeria, Spain 1999; Aschersleben, Germany 2002; Lima, Peru 2005; Hyderabad, India 2007; Ithaca, U.S.A. 2020; Arusha, Tanzania 2013; Avignon, France 2016; Seoul, Korea 2019; and Madrid, Spain 2022. The next ISPVE is scheduled to be held in Sao Paulo, Brazil in 2025 (<https://www.isppweb.org/icpve/>). The 14 ISPVE Symposia have resulted in the publication of two books, seven special Issues in *Virus Research*, and this special issue in *Phytopathology*.

Papers contributed to this Special Issue include research from six continents and cover a range of topics influencing plant virus epidemiology as presented in the sessions of the symposium, including

the latest information on general epidemiology, diagnostics, virus surveillance and modeling, virus ecology and evolution, virus interactions with insect vectors, vector-borne diseases transmitted by non-viral microorganisms, disease management, and the impact of climate change on plant viruses, their transmission, and prevalence.

Two papers focus on general plant virus epidemiology. A study by Jeger et al. (2023) highlights current challenges in this area, including the complexity of interactions, scaling of experimental approaches, and the application of models. Research by Rabadán et al. (2023) examined aphid-transmitted viruses affecting cucurbit crops over a 10-year period in Spain, and found frequent co-infections between a polerovirus, cucurbit aphid borne yellows virus, and a poty virus. These co-infections are likely to influence disease outcomes and suggest that agricultural practices may influence polerovirus evolution.

Research on virus diagnostics, surveillance, and modeling by Kreuze et al. (2023) used high-throughput sequencing (HTS)-based surveillance approaches to better understand the impact of plant viruses on crops, and how modeling approaches can be used to support surveillance and preparation for virus emergence in the face of climate change. A related paper by Alvarez-Quinto et al. (2023) used some of these methods to evaluate the occurrence of a newly described torradovirus and its potential relationship with a disease of Andean potatoes. Readers are also encouraged to visit *Phytopathology*'s sister journal, *PhytoFrontiers*, for a related study by Fowkes et al. (2023) that describes the advantages and limitations of using HTS in pea virus surveillance, and demonstrated the value of HTS through the identification of unexpected viruses in the United Kingdom.

Another key topic covered in the special issue includes papers on virus ecology and evolution. Research by Zamfir et al. (2023) reports use of deep sequencing to compare virus infection dynamics among four habitat types. They demonstrated that environmental heterogeneity can lead to non-random plant–virus associations, and that associations between communities of plants that serve as virus reservoirs and the prevalence of host infection were largely independent of virus adaptation to a host plant. Another study by Rivarez et al. (2023) also described unexpected virus–host associations. They evaluated sequence divergence among populations of

[†]Corresponding authors: W. M. Wintermantel; bill.wintermantel@usda.gov, and M. J. Jeger; m.jeger@imperial.ac.uk

The author(s) declare no conflict of interest.

This article is in the public domain and not copyrightable. It may be freely reprinted with customary crediting of the source. The American Phytopathological Society, 2023.

a recently described ilarvirus collected from locations around the world from both plant and non-plant sources, including endophytic fungi.

The impact of virus–vector interactions on plant virus epidemiology was examined in two studies. One by Krieger et al. (2023) discussed the importance of plants being attractive to aphids for virus spread to occur. The authors document how viruses may affect plant traits in ways that facilitate their transmission through examination of polerovirus–aphid interactions using studies involving transcriptomic, metabolomic, genetic, and behavioral approaches. A study by McLaughlin et al. (2022) published elsewhere, but addressing this theme, investigated how the acquisition of each of two begomoviruses by *Bemisia tabaci* MEAM1 in tomato influenced the probability of virus acquisition, virus accumulation in vectors, and probability of virus transmission and virus accumulation in infected host plants. This demonstrated a complex interplay during virus interactions with vectors and plants.

Three papers addressed factors influencing the epidemiology of non-viral pathogens transmitted by insect vectors. Levy et al. (2023) studied mechanisms used by ‘*Candidatus Liberibacter solanacearum*’ to manipulate host plant and potato psyllid vector immunity by examining effector proteins. Additionally, Bodino et al. (2023) studied the transmission of *Xylella fastidiosa*, causal agent of olive quick decline syndrome in olive by its spittlebug vector. This work provides important details on vector population dynamics and dispersal, including the impact of factors such as insect abundance, survival, and seasonality of host plants. A related study on *Xylella* by Giménez-Romero et al. (2023) developed global risk predictions for Pierce’s disease in grapevines. Overall, a global expansion of epidemic-risk zones is projected for 2050, although climate variability and vector distributions need to be taken into account when developing risk maps.

Two papers focus on disease management, including the application of new technologies such as the use of genomics and other ‘omics approaches for improving management of viral diseases. In a review, Kasi Viswanath et al. (2023) highlight use of topical dsRNA applications for inducing RNA interference, CRISPR-based genome editing for virus resistance, and new uses for high throughput sequencing and bioinformatics resources. Riahi et al. (2023) examined methods behind the performance of antixenosis and antibiosis-based resistance in tomato, which is derived from the wild relative, *Solanum pimpinellifolium*, and functions through glandular trichomes. This resistance was successful for control of sweetpotato whitefly (*B. tabaci*) and greenhouse whiteflies (*Trialeurodes vaporariorum*) and limited spread of the persistently transmitted begomovirus, tomato yellow leaf curl virus and the semi-persistently transmitted crinivirus, tomato chlorosis virus. The authors found that the walking behavior of a predator, *Nesidiocoris tenuis*, on tomato leaves triggers the jasmonic acid pathway and subsequent production of type IV glandular trichomes and acylsucrose production. This upregulation of trichome-based defenses protects plants from whiteflies and whitefly-transmitted viruses.

Finally, two papers specifically addressed the theme of this issue and the symposium in Madrid, which was focused on the influence of climate change on plant virus epidemiology. A study by Puthanveed et al. (2023) found that milder autumns may increase the risk of turnip yellows virus infection of rapeseed crops, and that the virus, although normally associated with *Brassica* species, was found coinfecting sugar beet along with beet mild yellowing virus and beet chlorosis virus. This is one of the first detections of turnip yellows virus in sugar beet and may represent a spill-over from oilseed rape. Gutiérrez-Sánchez et al. (2023) used a modeling approach to study the effects of climate change on plant virus vertical transmission and prevalence, finding that elevated CO₂ concentration, light intensity, and temperature influenced cucumber mosaic virus and turnip mosaic virus seed transmission and seed survival

in *Arabidopsis thaliana*. Simulations indicated that climate change conditions impacted virus prevalence only when both seed transmission and survival were simultaneously enhanced, with important consequences for virus epidemiology.

We hope that this special issue provides a valuable and informative overview of emerging topics, challenges, and novel strategies for research and advancement of the science of plant virus epidemiology. We are grateful for the support and assistance provided by Nian Wang, Editor-in-Chief of *Phytopathology*, and the APS staff, as well as the many anonymous reviewers who contributed to this effort.

Literature Cited

- Alvarez-Quinto, R., Amao, M., Muller, G., Fuentes, S., Grinstead, S., Fuentes-Bueno, I., Roenhorst, A., Westenberg, M., Botermans, M., Kreuze, J., and Molloy, D. 2023. Evidence that an unnamed isometric virus associated with potato rugose disease in Peru is a new species of genus *Torradovirus*. *Phytopathology* 113:1716-1728.
- Bodino, N., Cavalieri, V., Dongiovanni, C., Saponari, M., and Bosco, D. 2023. Bioecological traits of spittlebugs and their implications for the epidemiology and control of the *Xylella fastidiosa* epidemic in Apulia (Southern Italy). *Phytopathology* 113:1647-1660.
- Fowkes, A., Duffy, S., McGreig, S., Vazquez, I., Alraiss, K., Barrett, B., Conyers, C., Webster, G., Ward, R., Chisnall, K., Mynett, M., Adams, I., Macarthur, R., Howard, B., and Fox, A. 2023. Comparison of sequencing methods for obtaining a whole genome of pea necrotic yellow dwarf virus from UK peas. *PhytoFrontiers*. <https://doi.org/10.1094/PHYTOFR-01-23-0003-R>
- Giménez-Romero, A., Moralejo, E., and Matías, M. A. 2023. A compartmental model for *Xylella fastidiosa* diseases with explicit vector seasonal dynamics. *Phytopathology* 113:1686-1696.
- 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.
- Jeger, M., Hamelin, F., and Cuniffe, N. 2023. Emerging themes and approaches in plant virus epidemiology. *Phytopathology* 113:1630-1646.
- Kasi Viswanath, K., Hamid, A., Ateka, E., and Pappu, H. R. 2023. CRISPR/Cas, multicomplex, and RNA interference in virus disease management. *Phytopathology* 113:1661-1676.
- Kreuze, J. F., Cuellar, W. J., Kumar, P. L., Boddupalli, P., and Omondi, A. B. 2023. New technologies provide innovative opportunities to enhance understanding of major virus diseases threatening global food security. *Phytopathology* 113:1622-1629.
- Krieger, C., Halter, D., Baltenweck, R., Cognat, V., Boissinot, S., Maia-Grondard, A., Erdinger, M., Bogaert, F., Pichon, E., Huguency, P., Brault, V., and Ziegler-Graff, V. 2023. An aphid-transmitted virus reduces the host plant response to its vector to promote its transmission. *Phytopathology* 113:1745-1760.
- Levy, J. G., Oh, J., Mendoza, A., Prida, A., Lao, L., Starkey, J., Yuan, P., Kan, C.-C., and Tamborindeguy, C. 2023. A ‘*Candidatus Liberibacter solanacearum*’ haplotype B-specific family of candidate bacterial effectors. *Phytopathology* 113:1708-1715.
- McLaughlin, A. A., Hanley-Bowdoin, L., Kennedy, G. G., and Jacobsen, A. L. 2022. Vector acquisition and co-inoculation of two plant viruses influences transmission, infection, and replication in new hosts. *Sci. Rep.* 12: 20355.
- Puthanveed, V., Singh, K., Poimenopoulou, E., Pettersson, J., Siddique, A. B., and Kvarnheden, A. 2023. Milder autumns may increase risk for infection of crops with turnip yellows virus. *Phytopathology* 113:1788-1798.
- Rabadán, M. P., Juárez, M., and Gómez, P. 2023. Long-term monitoring of aphid-transmitted viruses in melon and zucchini crops: Genetic diversity and population structure of cucurbit aphid-borne yellows virus and watermelon mosaic virus. *Phytopathology* 113:1761-1772.
- Riahi, C., Urbaneja, A., Fernández-Muñoz, R., Fortes, I. M., Moriones, E., and Pérez-Hedo, M. 2023. Induction of glandular trichomes to control *Bemisia tabaci* in tomato crops: Modulation by the natural enemy *Nesidiocoris tenuis*. *Phytopathology* 113:1677-1685.
- Rivarez, S. M. P., Faure, C., Svanella-Dumas, L., Pecman, A., Tušek-Žnidarić, M., Schönegger, D., De Jonghe, K., Blouin, A., Rasmussen, D., Massart, S., Ravnikaar, M., Kutnjak, D., Marais, A., and Candresse, T. 2023. Diversity and pathobiology of an ilarvirus unexpectedly detected in diverse plants and global sequencing data. *Phytopathology* 113:1729-1744.
- Zamfir, A. D., Babalola, B. M., Fraile, A., McLeish, M. J., and García-Arenal, F. 2023. Tobamoviruses show broad host ranges and little genetic diversity among four habitat types of a heterogeneous ecosystem. *Phytopathology* 113:1697-1707.