

Editorial: Mixed Infections of Plant Viruses in Nature and the Impact on Agriculture

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Editorial on Research Topic

Mixed Infections of Plant Viruses in Nature and the Impact on Agriculture

Plants are grown under adverse conditions of multiple plant viruses in the field, and inevitably, mixed infections are common. Several important virus diseases of plants are the outcomes of interactions between different viral agents. An example is maize lethal necrosis, a devastating disease caused by the synergistic combination of corn chlorotic mottle virus and potato Y virus (Wangai et al., 2012; Redinbaugh and Stewart, 2018). Although significant advances have been made toward understanding the biology of individual viruses, in most cases, the diverse outcomes resulting from within-host interactions between viruses in mixed infections are poorly understood.

In nature, mixed infections with two or more plant viruses are frequent in plants, interacting in multiple and intricate ways. The objectives of this Research Topic were to provide a platform for researchers interested in plant viruses to share their recent results related to the various aspects of mixed infections: synergistic, antagonistic and neutral interactions, virus-plant host/vector interactions, ecology and control strategies. A total of 4 research articles have been contributed by 29 authors to the topic with more than 4,600 views to date.

High-throughput sequencing (HTS) technologies have become indispensable tools to characterize plant virus diversity, being very powerful to characterize mixed infections as virtually all viruses present in a plant sample might be identified without prior sequence knowledge (Adams et al., 2009; Al Rwahnih et al., 2009; Donaire et al., 2009; Kreuze et al., 2009; Villamor et al., 2019). In this Research Topic, Miljanić et al. used HTS to identify the viruses and viroids in preclonal candidates of grapevine (*Vitis vinifera* L.) varieties from a Slovenian wine-growing region. A complete description of coinfection in each plant was well documented. Interestingly, they showed that no grapevine was found to be virus- and viroid-free, and no grapevine was found to be infected with only one virus or viroid, while the highest number of viral entities in a plant was eight, indicating that mixed infections of viruses and viroids is the rule. These results will improve the early diagnostics of preclonal candidates of grapevine varieties, which is especially important to control virus diseases in grapevines at their early growing stage.

In nature, most of the plant viruses are transmitted horizontally by insect vectors, and deciphering virus-vector interactions are an emerging research subject in plant virology (Whitfield et al., 2015; Dietzgen et al., 2016). Two research articles published in this Research Topic deal with vector transmissions which are affected by mixed infections of different viruses. Chen et al.

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experimentally analyzed the interactions between the four causal agents of the tobacco bushy top disease (TBTD) in symptom induction and aphid transmission by successful construction of infectious clones. They showed clear evidence that only coinoculation of these four causal agents to tobacco plants could cause typical TBTD symptoms. Moreover, they showed that the successful transmission of tobacco bushy top virus (TBTV, an umbravirus), TBTV satellite RNA, and tobacco vein distorting virus (TVDV) satellite RNA by Myzus persicae depended on the presence of TVDV (a polerovirus), while the presence of TBTV satellite RNA increased the aphid transmission efficiency of TBTV and TVDV, indicating a mutual interaction between different viruses and their associated satellites. Jia et al. studied another interesting field within the scope of this Research Topic. In addition to the synergistic effect of rice stripe mosaic virus (RSMV), a newly discovered plant cytorhabdovirus, and rice gall dwarf virus (RGDV) on viral replication potential and pathogenicity in rice plants, these authors also found that RGDV significantly promoted the propagation of RSMV when co-infecting the vector, Recilia dorsalis. Accordingly, coinfection significantly promoted the acquisition and transmission efficiencies of RSMV by R. dorsalis, Showing that the synergy between plant viruses also takes place in the transmitting vectors.

A mixed virus infection that results in more severe symptoms is usually referred to synergistic interactions (Syller, 2012). Tatineni et al. analyzed the results of infection in wheat with up to four viruses in different combinations. The outcome of the infections was evaluated by observations of symptoms as well as measurement of the amount of viral RNA and coat protein. Interestingly, for some virus combinations, stronger

REFERENCES

- Adams, I. P., Glover, R. H., Monger, W. A., Mumford, R., Jackeviciene, E., Navalinskiene, M., et al. (2009). Next-generation sequencing and metagenomic analysis: a universal diagnostic tool in plant virology. *Mol. Plant Pathol.* 10, 537–545. doi: 10.1111/j.1364-3703.2009. 00545.x
- Al Rwahnih, M., Daubert, S., Golino, D., and Rowhani, A. (2009). Deep sequencing analysis of RNAs from a grapevine showing Syrah decline symptoms reveals a multiple virus infection that includes a novel virus. *Virology.* 387, 395–401. doi: 10.1016/j.virol.2009.02.028
- Dietzgen, R. G., Mann, K. S., and Johnson, K. N. (2016). Plant virus-insect vector interactions: current and potential future research directions. *Viruses*. 8. doi: 10.3390/v8110303
- Donaire, L., Wang, Y., Gonzalez-Ibeas, D., Mayer, K. F., Aranda, M. A., and Llave, C. (2009). Deep-sequencing of plant viral small RNAs reveals effective and widespread targeting of viral genomes. *Virology*. 392, 203–214. doi: 10.1016/j.virol.2009.07.005
- Kreuze, J. F., Perez, A., Untiveros, M., Quispe, D., Fuentes, S., Barker, I., et al. (2009). Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: a generic method for diagnosis, discovery and sequencing of viruses. *Virology*. 388, 1–7. doi: 10.1016/j.virol.2009.03.024
- Redinbaugh, M. G., and Stewart, L. R. (2018). Maize lethal necrosis: an emerging, synergistic viral disease. *Annu. Rev. Virol.* 5, 301–322. doi: 10.1146/annurev-virology-092917-043413
- Syller, J. (2012). Facilitative and antagonistic interactions between plant viruses in mixed infections. *Mol. Plant Pathol.* 13, 204–216. doi: 10.1111/j.1364-3703.2011.00734.x

virus symptoms were not accompanied by increasing virus titers. This study shows that there are complex antagonistic and synergistic interactions between viruses in field-grown crops. Overall, the papers in this Research Topic reveal different perspectives of current research on mixed infections of plant viruses in nature, from staple crop studies to investigations into the important cash crops and then into the intricate synergistic effects on the tripartite interactions between viruses, plants, and vectors. Illuminating the mechanisms of these mixed infections is crucial for understanding viral pathogenesis and evolution and, consequently, developing efficient and stable control strategies in the field.

AUTHOR CONTRIBUTIONS

YX and YL wrote the first draft of the editorial. MG revised the draft and added additional sections. All authors contributed to the article and approved the submitted version.

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- Villamor, D. E. V., Ho, T., Al Rwahnih, M., Martin, R. R., and Tzanetakis, I. E. (2019). High throughput sequencing for plant virus detection and discovery. *Phytopathology*. 109, 716–725. doi: 10.1094/PHYTO-07-18-0257-RVW
- Wangai, A. W., Redinbaugh, M. G., Kinyua, Z. M., Miano, D. W., Leley, P. K., Kasina, M., et al. (2012). First Report of Maize chlorotic mottle virus and maize lethal necrosis in Kenya. *Plant Dis.* 96, 1582. doi: 10.1094/PDIS-06-12-0576-PDN
- Whitfield, A. E., Falk, B. W., and Rotenberg, D. (2015). Insect vectormediated transmission of plant viruses. *Virology*. 479–480, 278–289. doi:10.1016/j.virol.2015.03.026

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