

EDITORIAL

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# Perspicacious insights into plant-virus-vector interactions applying omics

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## Abstract

Transmission of plant viruses by insect vectors is facilitated by unequivocal tri-partite interactions among host plants, viruses, and associated vectors. The advent of next-generation sequencing including whole genome sequencing, RNA/small RNA sequencing, proteomics, and metabolomics aided in elucidating the molecular mechanisms involved in virus transmission by insect vectors and infection in host plants.

**Keywords** RNA-seq, Aphids, Thrips, Whiteflies, Planthoppers, Leafhoppers, Viral entry and transmission

The outbreaks of plant viral diseases are likely to increase under changing environmental conditions. Over 30 billion dollars annual crop losses caused by viral diseases threaten global food security. The majority of these plant viral diseases are transmitted by insect vectors. Aphids, leafhoppers, planthoppers, thrips, and whiteflies are important vectors, responsible for transmitting over 90% of the known plant viruses. The order Hemiptera holds the highest occurrence of insect vectors. The actual occurrence of insect vectors might be much higher and the potential of the insect diversity in transmitting innumerable viruses is yet to be explored.

Virus infection leads to changes in plant phenotypical and biochemical traits such as leaf color or morphology, which affect the yield and quality of the produce. It also modifies the composition of volatile organic compounds

and metabolites which compromises the plant's defense towards the vectors, resulting in improving vector's performance and thus a more efficient spread of the former. Changes in feeding behavior, host preference, survival, fitness, and reproductive potential of insect vectors post-virus exposure are well-studied [1]. However, the molecular mechanisms interplaying the tri-partite relation of virus-host-vector only recently started to attract the attention of academic communities. The interfaces of the molecular mechanisms vary among the host-virus-vector combinations. The established molecular interactions between insect vectors and plant viruses [2] and between plant viruses with their receptors in both hosts and vectors [3] are discussed in recent reviews. The advent of modern "omics" technologies, including genomics, transcriptomics, proteomics, and metabolomics, has enabled more in-depth analyses of these interactions. A detailed account of transcriptomic approaches employed to elucidate host-virus interactions is provided in a review by Zanardo et al. (2019) [4]. Whole genome and mitochondrial genome sequences of nearly all major insect vectors of plant viruses are available in the public domain enabling a more complete study of the coevolution of plant viruses and vectors.

Leafhoppers and planthoppers are known to transmit several plant viruses in semi-persistent, persistent, or

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persistent-propagative manners. Members of *Badnavirus*, *Fijivirus*, *Marafivirus*, *Mastrevirus*, *Nucleorhabdovirus*, *Phytoreovirus*, *Tenuivirus*, and *Waikavirus* multiply within the insect vectors. RNA sequence analysis of *Dalbulus maidis* in response to *Maize rayado fino virus* infection revealed conserved biochemical pathways associated with innate immunity. Responses of several differentially expressed genes are conserved among *Sogatella furcifera* in response to *Southern rice black-streaked dwarf virus*, *Graminella nigrifrons* to *Maize fine streak virus* infection, and *Peregrinus maidis* to *Maize mosaic virus* infection [5]. Differential gene expression analysis of *Laodelphax striatellus* (small brown planthopper) in response to *Rice stripe virus* (RSV) infection showed that genes for vitellogenin receptor (VgR), ubiquitin-protein ligase (E3), and ecdysone response (E74A) are involved in virus transmission [6]. Virus-derived siRNAs regulate the expression profile of mRNA and small RNA in RSV-infected rice and SBPH. Rice genes involved in kinase activity and carbohydrate and protein binding are potential targets of virus-derived siRNAs (vsiRNAs). Among 265 down-regulated genes in RSV-infected plant hopper, 126 are potential targets of vsiRNAs [7].

RNA-seq and proteomics of aphids reveal key genes and proteins associated with feeding, development, cuticle formation, and salivary proteins are differentially expressed upon potyvirus infection [8]. RNA-seq was also helpful in understanding the virus-vector interactions between thrips and orthotospoviruses [9]. Metabolome analysis is likewise important in understanding the plant-virus-vector tri-partite interactions however, it is not widely explored in its full potential. Omics give an idea of the molecular events in the infection process that could be linked with the phenotypes by metabolite profiling. In other words, the genome, transcriptome, and proteome ultimately manifest their effects as metabolites. For example, *Cucurbit chlorotic yellow virus* hijacks plant metabolites to compromise the plant's defense and attract the vectors [10]. However, discriminating between the metabolites of plants and the pathogens is challenging and is largely unexplored.

The progressive omics data have led to the identification of several genes and proteins involved in the tri-partite relationships among plants, viruses, and vectors. However, limited genes and proteins have been functionally characterized for their roles in virus acquisition, transmission, and replication in the hosts. This collection contains novel findings making use of omics to explain molecular mechanisms involved in virus interactions with its hosts and vectors. It updates the current knowledge of tri-partite interactions among virus, vector, and host and provides novel targets for sustainable management. Additionally, the studies on the characterization of receptors involved in these interactions, mechanisms of

viral entry in plants and their vectors, and elucidation of genes, proteins, and metabolites involved in viral infection at the different stages of infection are welcomed. Findings on the role of small RNAs in viral entry and transmission are encouraged. The collection aims to accumulate omics resources and advancements in functional biology studies to comprehend existing knowledge on plant-virus-vector interactions. The goal of the collection is to develop a clear illustration of molecular pathways involved in the tri-partite interactions and help in managing the plant-virus-vector complex to ensure food security for an increasing global population.

#### Abbreviations

RNA	Ribonucleic acid
mRNA	Messenger RNA
siRNAs	Small interfering RNAs
RNA-seq	RNA sequencing
SBPH	Small brown planthopper
RSV	Rice stripe virus

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SJ, RD, and AG wrote and edited the editorial. All the authors have read and approved the submission.

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