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Systemic Spread and Propagation of a Plant-Pathogenic Virus in European Honeybees, *Apis mellifera*

Ji Lian Li^a, R. Scott Cornman^b, Jay D. Evans^b, Jeffery S. Pettis^b, Yan Zhao^c, Charles Murphy^d, Wen Jun Peng^a, Jie Wu^a, Michele Hamilton^b, Humberto F. Boncristiani Jr.^e, Liang Zhou^f, John Hammond^g, Yan Ping Chen^b

Author Affiliations

Address correspondence to Yan Ping Chen, Judy.Chen@ars.usda.gov.

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ABSTRACT

Emerging and reemerging diseases that result from pathogen host shifts are a threat to the health of humans and their domesticates. RNA viruses have extremely high mutation rates and thus represent a significant source of these infectious diseases. In the present study, we showed that a plant-pathogenic RNA virus, tobacco ringspot virus (TRSV), could replicate and produce virions in honeybees, *Apis mellifera*, resulting in infections that were found throughout the entire body. Additionally, we showed that TRSV-infected individuals were continually present in some monitored colonies. While intracellular life cycle, species-level genetic variation, and pathogenesis of the virus in honeybee hosts remain to be determined, the increasing prevalence of TRSV in conjunction with other bee viruses from spring toward winter in infected colonies was associated with gradual decline of host populations and winter colony collapse, suggesting the negative impact of the virus on colony survival. Furthermore, we showed that TRSV was also found in ectoparasitic *Varroa* mites that feed on bee hemolymph, but in those instances the virus was restricted to the gastric cecum of *Varroa* mites, suggesting that *Varroa* mites may facilitate the spread of TRSV in bees but do not experience systemic invasion. Finally, our phylogenetic analysis revealed that TRSV isolates from bees, bee pollen, and *Varroa* mites clustered together, forming a monophyletic clade. The tree topology indicated that the TRSVs from arthropod hosts shared a common ancestor with those from plant hosts and subsequently evolved as a distinct lineage after transkingdom host alteration. This study represents a unique example of viruses with host ranges spanning both the plant and animal kingdoms.

IMPORTANCE Pathogen host shifts represent a major source of new infectious diseases. Here we provide evidence that a pollen-borne plant virus, tobacco ringspot virus (TRSV), also replicates in honeybees and that the virus systemically invades and replicates in different body parts. In addition, the virus was detected inside the body of parasitic *Varroa* mites, which consume bee hemolymph, suggesting that *Varroa* mites may play a role in facilitating the spread of the virus in bee colonies. This study represents the first evidence that honeybees exposed to virus-contaminated pollen could also be infected and raises awareness of potential risks of new viral disease emergence due to host shift events. About 5% of known plant viruses are pollen transmitted, and these are potential sources of future host-jumping viruses. The findings from this study showcase the need for increased surveillance for potential host-jumping events as an integrated part of insect pollinator management programs.

FOOTNOTES

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