
Diversity and evolution of Sinaivirus and related viruses in honeybees and wild hymenoptera

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Abstract

By providing pollination services, bees are among the most important insects, both ecologically and economically. In this study, we used next generation sequencing technologies to discover and study new insect viruses, potentially harmful for bees. The initial sampling included 30 wild ants (6 species from genus *Messor*) and 13 wild bees (3 species from genus *Halictus*). Individual transcriptomes were sequenced using Illumina technology. A bioinformatic pipeline was developed and allowed transcriptome assembly, protein homology detection with known viruses. Five viral genomes closely related to *Lake Sinaï Virus* (*Sinaivirus*, new genus proposed to ICTV) were discovered in wild ants and bees. After sequence alignments with other known viruses, Maximum Likelihood phylogenies showed that virus found in ants were closely-related to the honeybees infecting LSV-1 and 2. In contrast, viruses found in wild bees were not included in the *Sinaivirus* clade and may correspond to a new viral genus. This species was termed *Halictus scabiosae Associated Virus*. To build a more exhaustive phylogeny of Sinaiviruses, we made a second sampling targeting French and Italian honeybees. Total RNA extraction, RT-PCR of the ORF1/RDRP region and Sanger sequencing were used to detect new *Sinaivirus* sequences. The phylogeny was built from the 42 known *Sinaivirus* sequences, along with 19 new sequences obtained from this study. This analysis revealed the great diversity of the *Sinaivirus* genus, and allowed us to build a robust phylogenetic framework for testing hypothesis of virus transfers between honeybees and wild hymenoptera.

Keywords: Bee Viruses, Viral Discovery

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