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Recently identified bee viruses and their impact on bee pollinators

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Bees are agriculturally and ecologically important plant pollinators. Recent high annual losses of honey bee colonies, and reduced populations of native and wild bees in some geographic locations, may impact the availability of affordable food crops and the diversity and abundance of native and wild plant species. Multiple factors including viral infections affect pollinator health. The majority of well-characterized bee viruses are picorna-like RNA viruses, which may be maintained as covert infections or cause symptomatic infections or death. Next generation sequencing technologies have been utilized to identify additional bee-infecting viruses including the Lake Sinai viruses and Rhabdoviruses. In addition, sequence data is instrumental for defining specific viral strains and characterizing associated pathogenicity, such as the recent characterization of Deformed wing virus master variants (DWV-A, DWV-B, and DWV-C) and their impact on bee health.

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in [31**]). Bee-infecting viruses are primarily positive sense single-stranded RNA viruses (+ssRNA) in the order *Picornavirales* [32,33]. Common bee viruses include: the *Dicistroviruses* (Israeli acute paralysis virus (IAPV), Kashmir bee virus (KBV), Acute bee paralysis virus (ABPV), and Black queen cell virus (BQCV)); the *Iflaviruses* (Deformed wing virus (DWV), Kakugo virus, Varroa destructor virus-1/DWV-B, Sacbrood virus (SBV), and Slow bee paralysis virus (SBPV)); and taxonomically unclassified viruses (Chronic bee paralysis virus (CBPV) and the Lake Sinai viruses (LSVs)) (reviewed in [32,33]). Recently identified +ssRNA viruses include Bee macula-like virus (BeeMLV) in the *Tymoviridae* family, *Apis mellifera* flavivirus and *Apis mellifera* nora virus 1 [34,35**]. The first bee-infecting negative sense single-stranded RNA viruses (–ssRNA) were also recently described, specifically *Apis mellifera* rhabdovirus-1 (ARV-1) and *Apis mellifera* rhabdovirus-2 (ARV-2) [35**], also known as Bee rhabdovirus (BRV) [36]. To date, only a single honey bee-infecting double-stranded DNA virus, *Apis mellifera* filamentous virus (AmFV), has been sequenced and characterized [37–39].

Bee virus discovery has been facilitated and accelerated by next generation sequencing technologies and it is likely that additional bee-associated viruses will be discovered. Virus identification and characterization are important first steps toward understanding the role of viruses in bee health. Typically, bee viruses are defined by the organism from which they were first identified (e.g., honey bee viruses), though many bee viruses have wide host ranges and are transmitted between genera [23,25,30,40,41*,42,43,44*,45–48] (reviewed in [31**]). Virus nomenclature varies; a virus may be named after the symptoms or diseases associated with infection, the host from which it was isolated, or for the geographic regions or features (e.g., mountains, rivers, and so on) near where the virus was first identified. Viruses are assigned to families based on the type and sequence of nucleic acid