

# The Honey Bee Virus Has Been Discovered in Mosquitos

The **black queen cell virus** is a major issue for beekeepers. It infects developing queen honey bee larvae, causing other pupal cells to become black and eventually killing the larval queen. The virus has the potential to wipe out entire honey bee colonies and has no known deterrent other than preventing its spread.

When **Canadian researchers** were seeking for viruses and other germs conveyed by mosquitoes in 2020, the last thing they expected to find was a virus known to infect honey bees (***Apis mellifera***). But they did.

According to the findings published in the Journal of Insect Science in April, black queen cell virus (BQCV) has been detected in North American mosquitos for the first time. Researchers also sequenced the virus's genome for the first time.

**Cole Baril, Christophe LeMoine, Ph.D., and Bryan Cassone, Ph.D.,** of Brandon University in Manitoba, Canada, identified BQCV in a mosquito (*Aedes vexans*) using a genetic sequencing technology known as massively parallel next-generation sequencing. The researchers suspect that the virus was acquired indirectly by mosquitoes grazing at the same nectar sources as honey bees.

BQCV has been recognized as one of the most frequent honey bee viruses since its discovery in 1955. It is also one of the most poorly understood bee viruses. The black queen cell virus infects both queens and adult bees, however adults rarely show signs of illness. It belongs to the picornavirus order and has an RNA genome of around 8,550 nucleotides. It is not quite clear how it is spread from host to host. It is disseminated by the microsporidia *Nosema apis* and the Varroa mite, however it can also be transferred by adult honey bee foraging missions.

The researchers were doing a genomes examination of several mosquitoes in the Canadian prairie regions. They discovered several new viruses and microbial flora throughout their hunt and were startled to uncover BQCV.

Using microscopic light traps, the Brandon researchers collected mosquitos in 2019 and 2020. *Aedes vexans* mosquitos were found and their RNA was extracted. In 2019, 1,783 pooled mosquitos were sequenced; in 2020, 2,208 were sequenced. Using the National Centre for Biotech Information (NCBI) database, the sequencing data was matched against BQCV sequences.

The researchers also wanted to understand the evolutionary links within BQCVs, so they compared the novel Canadian strain to viral genomes already in the NCBI database. One of the sequencing sequences matched a Swedish BQCV isolate. There were no genomic matches to Varroa mites or Nosema apis, therefore ruling out the possibility of transmission through those organisms. However, three sequences were mapped to plants, trees, and shrubs and matched to plant chloroplasts, indicating a foraging route of viral transmission.

Although mosquitoes must consume blood in order to lay eggs, flower nectar is also an important source of nutrition. Sugar deficiency has been linked to decreased female survival and reproduction capacity. However, there is no evidence that BQCV can replicate in mosquitoes, implying that mosquitoes are a dead end for the viruses. However, more research is needed to determine whether mosquitoes can transmit the virus to honey bees.

"To the best of our knowledge, this is the first report of BQCV being detected in mosquitoes or any other dipteran," the authors write. "Interspecies transmission of BQCV has been hypothesized to be due to direct (parasitism, predation, and scavenging) and/or indirect (foraging at the same nectar source) interactions between honey bees and these arthropods.

**According to Cassone**, much remains unclear. "The virus has been found in North America; however, it has never been found in mosquitoes, and the genome sequence has never been characterized," he explains. "It's surprising to me that so little research has been done on this virus, given its potentially devastating effects on apiculture."

The study is also one of the first to characterize the insect and viral genomes using newly developed next-generation sequencing (NGS) techniques. "Although it requires considerable integration of bioinformatics, many limitations of traditional approaches for pathogen identification (PCR methods and serological testing) can be overcome using NGS," the researchers said, adding a disclaimer common to sequencing. In addition to higher resolution and sensitivity, NGS does not necessitate prior knowledge of the nucleic acid being sequenced or specific antibodies.

Research Published by: **Canadian researchers**