

Abstract

European honey bee (*Apis mellifera*) is major pollinator for agriculture and vital for food production. Large number of viruses infecting *A. mellifera* have been discovered over the years, but it isn't yet known if they are pathogenic for their host. However, presence of non-viral pathogens like *Varroa destructor* can greatly increase their virulence and have fatal consequences for the colony. The aim of this study was to test and verify robustness of the method for virome detection on healthy honey bees from the Czech Republic. Last but not least we aimed to detect non-viral parasites and correlate their presence with detected viruses.

We have successfully identified large number of viral sequences from different viral families. Viral composition was found to be influenced mainly by colony from where the honey bees were collected. That was mainly given by a large amount of bacteriophages in the samples. However, analysis of individual viruses, known to infect honey bee, indicated that viral prevalence and viral loads of specific viruses is quite different among individual honey bees from the same colony. Interestingly we were able to find highly diverse Lake Sinai viruses. We were able to observe correlations either between individual viruses or viral other non-viral pathogens. Further analysis is needed to confirm and explore these correlations by methods which allows for quantitative analyses of detected pathogens.

Key words:

Honey bee, *Apis mellifera*, virome, Deformed wing virus, Lake Sinai virus, NGS, *Varroa destructor*, *Nosema ceranae*, Czech Republic