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PP-064 [Bee Health]

RNA metagenomics-based surveillance of diverse honey bee (*Apis mellifera*) pathogens revealing the seasonal pathogen dynamics in Taiwan

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Abstract

The honey bee (*Apis mellifera*) plays a crucial role in maintaining biodiversity within ecosystems. There has been a rising interest in beekeeping in Taiwan. However, the beekeeping industry still faces many challenges, especially various pests and diseases. In this study, RNA metagenomics was employed to investigate the composition of pathogens in honey bees collected from northern, central, southern, and eastern Taiwan in January, March, July, and November in 2024. This study aiming to elucidate the relationships between pathogen dynamics, seasonality, and geographic distribution. Our results showed that the fungal pathogen *Vairimorpha ceranae* was predominant throughout Taiwan in 2024, with *Vairimorpha apis* coexisting, except in northern Taiwan in January. Furthermore, *Serratia marcescens* and *Hafnia alvei* were prevalent bacterial pathogens in honey bees across Taiwan. For the honey bee viruses, Deformed wing virus, Black queen cell virus, Lake Sinai virus, and Sacbrood virus were the core honey bee viruses detected in all samples. This study represents the comprehensive honey bee pathogen surveillance and provides valuable insights into the temporal and spatial dynamics of honey bee pathogens in Taiwan. This information can improve disease management strategies to support bee health and the beekeeping industry.

Research gap

We are under threat from various pathogens, which affect colony health and survival.

Despite the importance of honey bee health, little is known about the spatial distribution and seasonal variation of pathogens in Taiwan.

Materials & Methods

1 Sample collection

- Northern region
- Central region
- Southern region
- Eastern region

Honey bee samples were collected from four regions of Taiwan in January, March, July, and November 2024.

2 RNA extraction

3 Next-generation sequencing

4 Metagenomic analysis

Trimmomatic
Bowtie 2
Trinity
RSEM
Diamond

Results

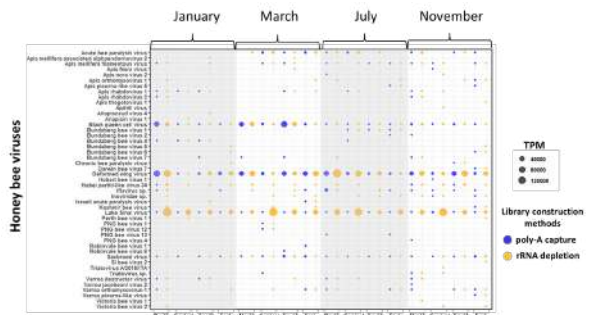

Figure 1. Transcripts per million reads (TPM) of viruses associated with *Apis mellifera* were quantified for each sample using two library construction methods: poly-A capture and rRNA depletion.

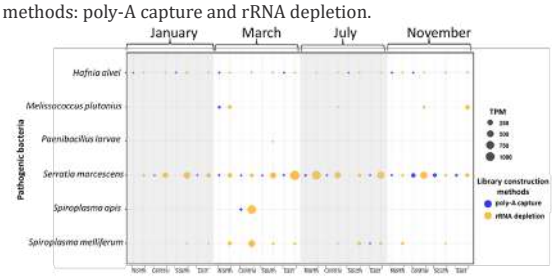

Figure 2. Transcripts per million reads (TPM) of pathogenic bacteria in *Apis mellifera* were quantified for each sample using two library construction methods: poly-A capture and rRNA depletion.

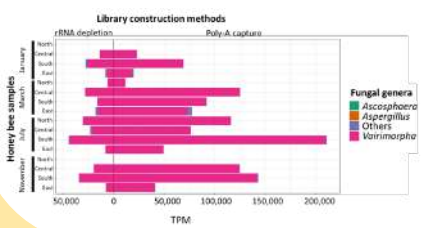

Figure 3. Transcripts per million reads (TPM) of fungi in *Apis mellifera* were quantified for each sample using two library construction methods: poly-A capture and rRNA depletion.

Conclusions and future works

- Sacbrood virus (SBV), Black queen cell virus (BQCV), Deformed wing virus (DWV), and Lake Sinai virus (LSV) represented the core viruses in the Taiwanese honey bee population.
- *Vairimorpha ceranae* was the predominant fungal pathogen, while *Vairimorpha apis* was also detected.
- *Serratia marcescens* and *Hafnia alvei* were prevalent bacterial pathogens in honey bees across Taiwan.
- Future work involves tracking the transmission routes of pathogens, elucidating pathogen interactions, and developing effective control strategies for honey bee diseases to enhance colony health and support the beekeeping industry.

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The honey bee (Apis mellifera) plays a crucial role in maintaining biodiversity within ecosystems. There has been a rising interest in beekeeping in Taiwan. However, the beekeeping industry still faces many challenges, especially various pests and diseases. In this study, RNA metagenomics was employed to investigate the composition of pathogens in honey bees collected from northern, central, southern, and eastern Taiwan in January, March, July, and November in 2024. This study aiming to elucidate the relationships between pathogen dynamics, seasonality, and geographic distribution. From the results, the fungal pathogens, Vairimorpha ceranae was predominant throughout Taiwan in 2024 with Vairimorpha apis coexisted, except northern Taiwan in January. Ascosphaera apis was only identified in July in southern Taiwan. Furthermore, the highest diversity of bacterial pathogens (Melissococcus plutonius, Spiroplasma apis, and Spiroplasma melliferum) was found in March. For the honey bee viruses, Deformed wing virus, Black queen cell virus, Lake Sinai virus, and Sacbrood virus were the core honey bee viruses detected in all samples. The highest diversity of honey bee viruses was observed in honey bees collected from central and eastern Taiwan. Among different seasons, a greater diversity of honey bee viruses was identified in samples collected in November. This study represents the comprehensive honey bee pathogen surveillance and provides valuable insights into the temporal and spatial dynamics of honey bee pathogens in Taiwan. This information can improve disease management strategies to support bee health and the beekeeping industry.