Insights into Viral Interactions between Bees and Mites in Northern Thailand

Phaksorn Lawsubtawee[1,2] , **Eui-Joon Kil**[3*] , **Terd Disayathanoowat**[1,2*]

1. Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand
2. Research Center of Deep Technology in Beekeeping and Bee Products for Sustainable Development Goals (SMART BEE SDGs), Chiang Mai University, Chiang Mai 50200, Thailand
3. Department of Plant Medicals, Gyeongkuk National University, Andong, South Korea

Email address : phaksorn_lawsub@cmu.ac.th

INTRODUCTION



Decline of Honey Bees

Colony losses in Thailand reflect global trends associated with Colony Collapse Disorder (CCD).



The Mite-Virus Connection

Parasites such as *Varroa destructor* act as vectors, increasing viral transmission and disease prevalence.



Impact on Agriculture

Weakened colonies reduce seed yields and negatively affect the sustainability of plant communities.

PCR (Traditional)

PCR can only detect previously characterized viruses.

PCR has relatively low throughput.

PCR requires prior knowledge of target nucleotide sequences.

Virome Analysis (NGS)

Virome analysis can detect novel and divergent viral species.

Virome analysis enables high-throughput and comprehensive detection of viruses.

Does not require prior knowledge of target nucleotide sequences.

OBJECTIVES

- This study aims to investigate viral diversity in honey bees and mites in northern Thailand, analyze viral co-infection patterns and virus distribution, and examine virus–bee–mite interactions.

MATERIALS AND METHODS

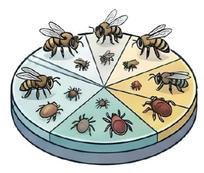
Phase 1: Discovery & Screening

Sample Collection

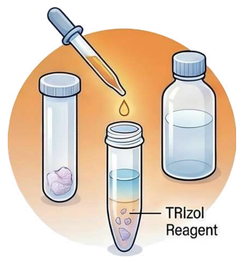
5 Honey bee (*Apis spp.*) species

2 Stingless bee species

2 Ectoparasitic mite species



RNA Extraction



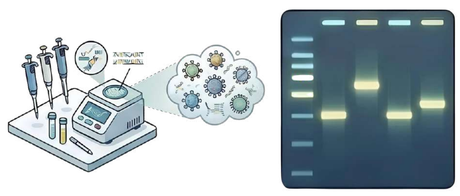
RNA extraction using TRIzol reagent

Virome Analysis



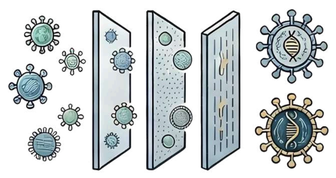
Phase 2: Validation & Identification

RT-PCR



Specific primers were designed from virome data.

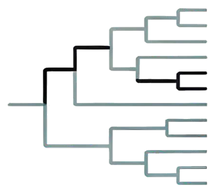
Identification



Identification criteria

- % sequence identity

Phylogenetic analysis

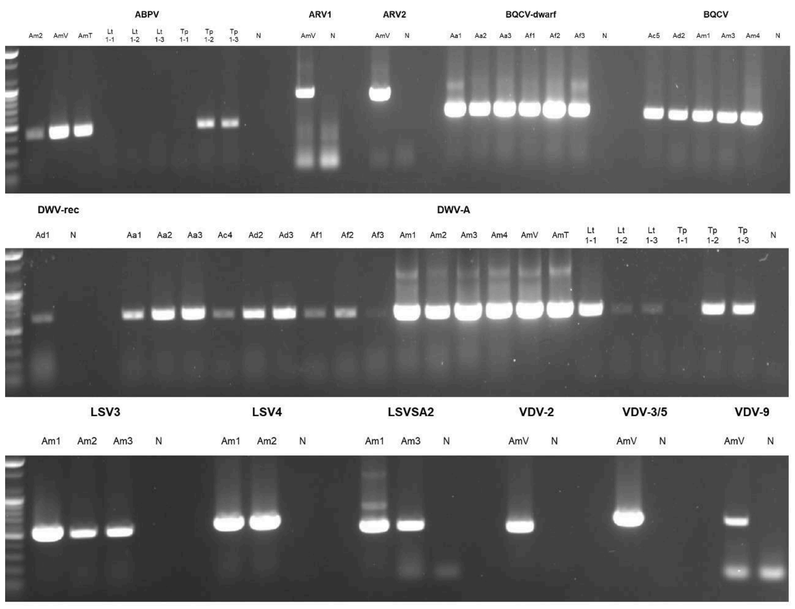


1,000 bootstrap replicates

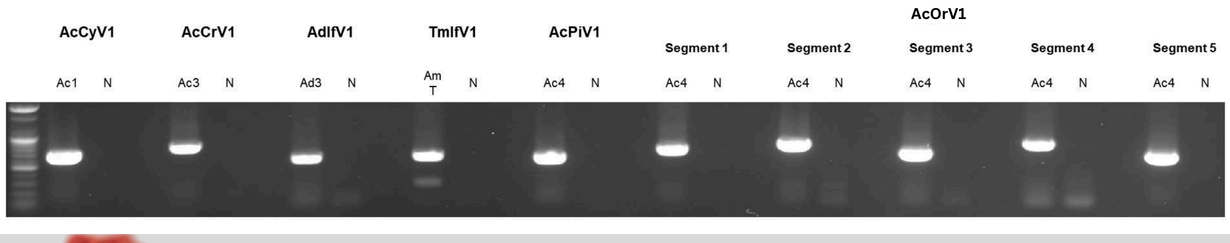
RESULTS

Virus detection by RT-PCR.

(A) Common viruses detected



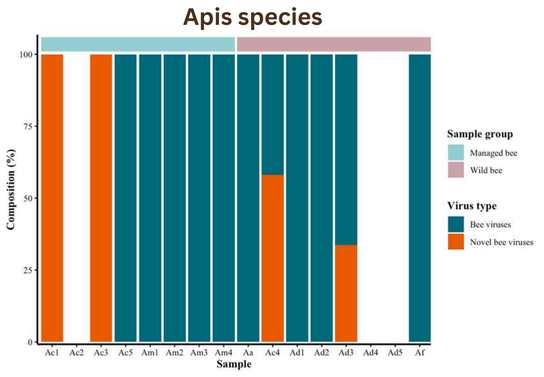
(B) Novel viruses detected



Phylogenetic relationships of the novel virus

- Maximum-likelihood phylogenetic trees were constructed using IQ-TREE 2 with the GTR+G+I model.
- Node support assessed with 1,000 ultrafast bootstrap replicates.

Novel viruses phylogenetic trees



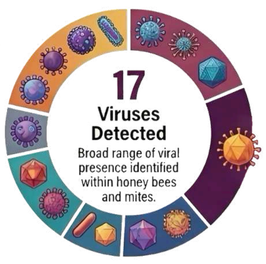
- **Co-infection was less frequent** in managed Apis colonies than in wild populations.
- **Managed colonies** are maintained in more **controlled environments**, potentially limiting exposure to **environmental viral sources** (Guzman-Novoa, 2024).
- Wild bees encounter **more diverse ecological interactions**, which may increase opportunities for **viral transmission and co-infection** (Guzman-Novoa, 2024).

- **No co-infection** between common and novel viruses was observed in **Stingless bees.**
- This suggests that **common bee viruses** are unlikely to be **endemic to** stingless bees.
- Their presence may reflect **incidental environmental exposure**, possibly through shared **floral resources with Apis**, facilitating **cross-species viral transmission** (Graystock et al., 2015).

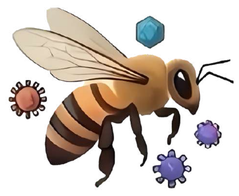
CONCLUSIONS

Viral Diversity

6 novel viruses were detected, accounting for 35.29%



Co-Infection Rates

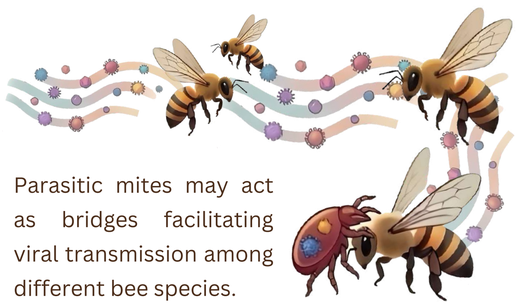


Managed Colonies
Lower co-infection rates



Stringless Bees
Showed no co-infection

Virus-Bee-Mite Interaction



Parasitic mites may act as bridges facilitating viral transmission among different bee species.

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Graystock, P., Goulson, D., & Hughes, W. (2015). Parasites in bloom: Flowers aid dispersal and transmission of pollinator parasites within and between bee species. Proceedings of the Royal Society B: Biological Sciences, 282. https://doi.org/10.1098/rspb.2015.1371

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