



The *Bidens pilosa* phytogetic treatment reveals a negative impact on *Vairimorpha ceranae* through the suppression of V-Type ATPase expression in infected honey bees (*Apis mellifera*)

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Abstract

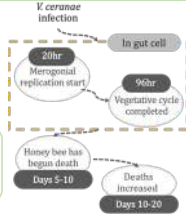
Microsporidia are obligate intracellular fungal parasites. *Vairimorpha ceranae* is a microsporidian pathogen that is primarily causes microsporidiosis in honey bees (*Apis mellifera*). Despite extensive research on *V. ceranae* pathogenesis, the effects of phytogetic extract treatments on its infection dynamics still unknown. In particular, the precise role of *Bidens pilosa* (BP) in modulating *V. ceranae* gene expression during infection has not been thoroughly investigated. Herein, the **transcriptome** data revealed that the BP treatment significantly suppresses *V. ceranae* gene expression during infection, particularly affecting metabolic pathways. Among these pathways, the **V-type ATPase pathway** has demonstrated that positively correlated with spore counts and infection load in this study. The highly expressed genes, which were identified in previous study, during *V. ceranae* infection were investigated under BP treatment. The expression levels of these genes were down-regulated at the early stage of infection, suggesting that BP treatment influences *V. ceranae* infection process. Besides, **RNA interference (RNAi)** targeting to the V-type ATPase gene of *V. ceranae* was performed and further demonstrated that knock-down of *V. ceranae* ATPase gene can improved honey bee survival rate and also reduced the *V. ceranae* infection. Both mature spore counts and genome copy numbers decreased by approximately two-fold at 15 d.p.i., by dsRNA of V-type ATPase-related gene treatment, highlighting the importance of V-type ATPase in the life cycle of *V. ceranae*. Given its ability to suppress *V. ceranae* gene expression at the early infection stage, BP treatment could potentially serve as a promising strategy for reduction of microsporidiosis.

Background

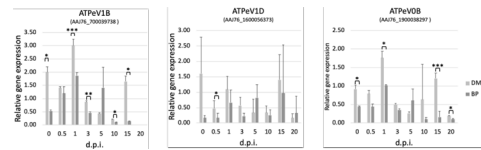
Vairimorpha ceranae infections of honey bees.



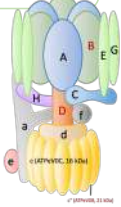
Bidens pilosa (BP) has showed the effect to against protistan pathogens. This study uses transcriptomics to explain how BP treatment changes the *V. ceranae* infection.



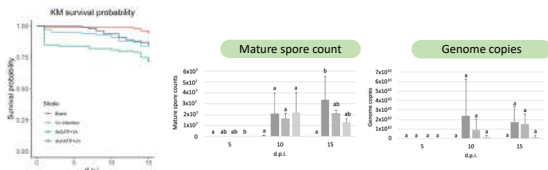
Relative gene expression during BP treatment



ATP5V showed the most significant and consistent decrease after BP treatment. It's also a key part of the V-ATPase complex, which is stable expression and more noticeable reduction.



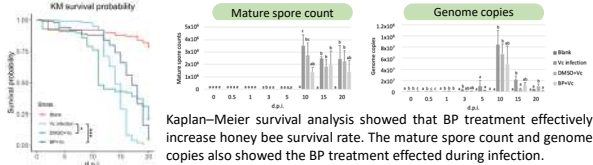
dsRNA treatment of *V. ceranae* infection



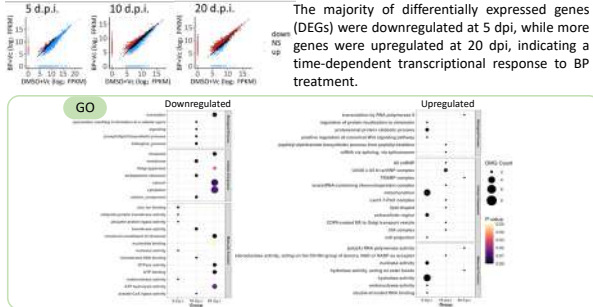
We designed a dsRNA targeting ATP5V, which we refer to as **dsVATP**. *V. ceranae* infection honey bee treated with dsVATP showed a higher survival rate and a significant reduction in *V. ceranae* spore and genome counts in the later stages of infection.

dsVATP treatment consistently lowered the expression of ATP5V in *V. ceranae*, with the most significant effect seen at 15 dpi, confirming that the treatment successfully altered the gene's expression.

BP treatment of *V. ceranae* infection



Transcriptome of BP treatment

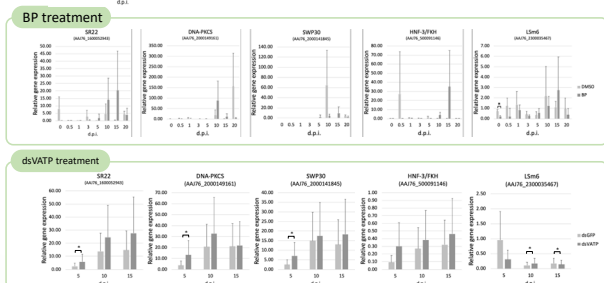


Gene Ontology (GO)

- GO annotation analysis highlighting the dynamic impact of BP treatment on gene functions during *V. ceranae* infection. Upregulated DEGs at 5, 10, and 20 dpi were annotated to 73, 285, and 1,226 GO terms, downregulated DEGs at the same time points were annotated to 152, 228, and 130 terms, respectively.

KEGG

- KEGG pathway analysis further clarified the functional roles of DEGs and revealed dynamic changes in biological pathways and key metabolic modules under BP treatment. Over all, "V-type ATPase, eukaryotes (M00160)" show the high match numbers of KEGG pathway, also is directly involve in host cell environment modulation, making it suitable target for validation.



Five DEGs under dsVATP treatment exhibited expression patterns similar to those observed in the BP treatment.

Conclusions

- BP treatment helped bees survive longer by slowing down the *V. ceranae* infection. It reduced the number of germs and delayed their growth.
- Transcriptome analysis showed that BP affects many pathways, especially V-type ATPase.
- By turning off the V-type ATPase gene with RNAi, we proved that this pathway is important for the germ's ability to grow and spread inside the bee.

Acknowledgments

This research was supported by 112-2313-B-005-023- from the National Science and Technology Council (NSTC). Thanks to all the IPG lab members.



Reference

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