APIMONDIA SCANDINAVIA 2025
SWEDEN | DENMARK | NORWAY

PP-435 [Bee Biology]

Field realistic stressors alter the bee gut microbiome

Marcela A Díaz, Carmelo Fruciano, Cristina Botías, Darren P O'Connell, Katie-Jane Marshall, Falk Hildebrand, Nicholas JB Brereton, Dave Goulson, William OH Hughes, Julia C Jones

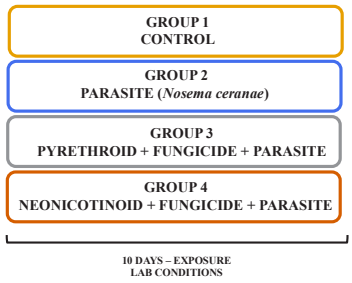
Introduction

Pollinator populations are declining worldwide. Bumblebees are some of the most important wild pollinators in natural and agricultural habitats and are no exception to these declines. Such declines are reportedly due to a combination of factors including exposure to pesticides and pathogens. These factors likely alter the bee gut microbial community. However, the interactions, potential sensitivity, and role of key gut bacterial taxa in combating these factors, remain largely undetermined. Insight can be gained by investigating the interaction between bumblebee gut microbial communities and field-realistic combinations of pesticides and a pathogen.

Methods

Forty *Bombus terrestris* colonies were exposed to different field-realistic combinations of stressors (pesticides and a pathogen) under controlled laboratory conditions. Groups of 10 colonies were assigned to four different treatments, and exposed to the treatments for 10 days. The gut bacterial communities of the bees were subsequently determined using amplicon sequencing (16S rRNA).

Bumblebee colonies ✕ 40



Results and Discussion

- We find that there are no significant differences in gut bacterial community diversity, including alpha and beta diversity, in bees exposed to field-realistic combinations of stressors (Shannon diversity, Kruskal-Wallis, $\chi^2 = 0.250$, df=3, p=0.969; PERMANOVA: p=0.395 using Bray-Curtis dissimilarity) (Fig. 2). This suggests that the overall gut microbial community remains stable when bees are exposed to pesticide and parasite combinations.

- Using the DESeq2-based procedure, no significant differences in relative abundance of the core gut bacterial taxa were detected in pairwise comparisons between any of the treatment groups.

- However, interestingly, we find that some non-core gut bacterial taxa differ in relative abundance between controls and bees exposed to the different stressor combinations (Fig. 3).

- One key example is the gut bacterial taxa *Burkholderiaceae.* This taxa was significantly reduced in relative abundance in the treatment groups exposed to a neonicotinoid, fungicide and parasite; and a pyrethroid, fungicide and parasite, compared to controls. This suggests that *Burkholderiaceae* taxa may be contributing to bumblebee adaptation to pesticides and pathogens, and are therefore important targets for future functional analyses.

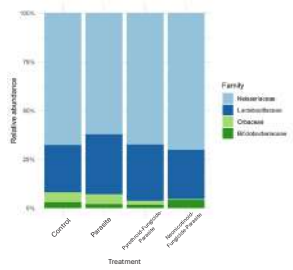


Figure 1. Taxonomic composition (relative abundance) of bumblebee gut microbial communities when exposed to different field-realistic stressors.

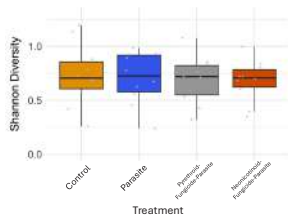


Figure 2. Shannon's diversity index of OTU frequencies. Lines represent the median index value, boxes mark the interquartile range. No significant difference was found in diversity between treatments.

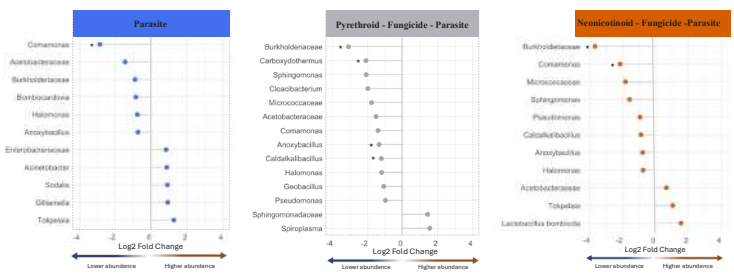


Figure 3. Log2 Fold Change in relative abundance of gut microbial taxa in bees exposed to different field-realistic stressors. The Fold Change shown is between the control group and each of the treatment groups (parasite; pyrethroid-fungicide-parasite; and neonicotinoid-fungicide-parasite). Significant differences are indicated by*.

Conclusion

Together our results suggest that exposure to field-realistic pesticide-pathogen combinations in bumblebee colonies does not impact the core gut microbial taxa, however there is an impact on some non-core taxa, including declines in relative abundance of *Burkholderiaceae*. These often overlooked taxa may play important roles in bumblebee host health and resilience to human-induced stressors.

PP-435 [Bee Biology]
Field-realistic stressors alter the bumblebee gut microbiome

Marcela Alexandra Díaz Rivadeneira[1], Carmelo Fruciano[2], Cristina Botías[3], Darren O'Connell[1], Katie Jane Marshall[1], Falk Hildebrand[4], Nicholas JamesBeresford Brereton[1], Dave Goulson[5], William Hughes[5], Julia C Jones[1]
[1]School of Biology and Environmental Science, University College Dublin, Dublin, Ireland
[2]Institute for Marine Biological Resources and Biotechnology (CNR-IRBIM), National Research Council, Messina, Italy; National Biodiversity Future Center, Palermo, Italy
[3]Department of Life Sciences, University of Alcalá, Alcalá de Henares, Spain
[4]Gut Microbes and Health, Quadram Institute Bioscience, Norwich, Norfolk, UK; Digital Biology, Earlham Institute, Norwich, Norfolk, UK
[5]School of Life Sciences, Department of Evolution, Behaviour & Environment, University of Sussex, Falmer, Brighton, East Sussex, UK

Like many pollinators, some bumblebee species are declining, threatening bee health and colony survival, which in turn has an impact on environmental health and food security. In bumblebees, the specialised gut microbial community, ubiquitous across Bombus species, is thought to contribute to host digestion, metabolism, and pathogen defence, influencing how bees respond to stressors. Stressors such as pesticides and pathogens are thought to alter the bee gut microbial community composed by core and non-core taxa; however, the interactions and potential sensitivity of these important taxa and their functions remain undetermined. Here, the interactions of Bombus terrestris gut microbial community with field-realistic combinations of pesticides, including the neonicotinoid insecticide thiamethoxam, the pyrethroid insecticide cypermethrin, and the fungicide tebuconazole, and the gut pathogen Nosema ceranaeare investigated. The gut microbial community of 40 B. terrestris colonies exposed to different stressor combinations were assessed using the molecular technology known as amplicon sequencing. Non-core taxa of the Bombus gut microbiome, particularly within the Burkholderiaceae family, showed significant differences in relative abundances in bees exposed to the field-realistic combination of pathogen, fungicide and pesticide stressors when compared to controls. In contrast, core gut bacterial taxa showed no significant difference in relative abundance between treatments. These findings highlight the bacterial family Burkholderiaceae as a key target for future functional analyses of microbial responses to pesticide degradation. Understanding the complex interaction between environmental stressors and the bumblebee gut microbiome is an important priority for developing strategies to protect and restore beneficial gut microbial communities supporting resilience of bees and other pollinators to environmental challenges.