

# Exploring the influence of abiotic factors on the community structure and antimicrobial resistance spread in the insect gut microbiome

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## Introduction

- Insects establish symbiotic relationships with **bacteria**, which constitute their **gut microbiome**<sup>1</sup>.
- The gut microbiome of insects has a wide range of **beneficial** roles, contributing to host development, nutrition and physiology<sup>2</sup>.
- Insect gut microbiome can be **influenced by different factors**, such as the developmental stage of the insect, the degree of sociality, the dietary regime, and the environmental conditions<sup>2</sup>.



- Some factors can lead to **dysbiosis**: **pesticides** can cause perturbations in the gut microbiome of **pollinators** such as **honeybees**<sup>3</sup>, with major consequences on **crop productivity**.
- Pesticides** exposure can also promote the **spread of bacterial antimicrobial resistance**, through the movement of **antibiotic resistance genes (ARGs)** by **horizontal gene transfer (HGT)**<sup>4</sup>.

## Aim of the project

- Assess the **impact** of various abiotic factors on the **structure** of the **gut microbiome of insects**.
- Study the effect of abiotic factors on **ARGs spread** via **HGT** within the **insect gut microbiome**.

### Model insects:

- Drosophila melanogaster*
- Apis mellifera* and other pollinating insects

### Abiotic factors:

- Diet composition
- Pesticides

## Workplan of the project

**1. Evaluation of the abundance and taxonomic composition of insect gut bacterial community**

to assess if the abiotic factors caused a shift in the structure of the insect gut microbiome

**2. Investigation of the presence of antibiotic resistance genes**

to obtain the resistome profile of the insects

**3. HGT evaluation through conjugation experiments**

to evaluate the spread of ARGs within the insect gut microbiome

## Expected outcomes

- Deeper understanding of how the **gut microbiome** of **beneficial insects** responds to different abiotic factors.
- Assessment of the **extent of conjugation events** within the insect gut microbial community.

## References

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