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ABSTRACT BOOK

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PP-054 [Bee Health]

The diversity of insecticide target site mutations in *Apis mellifera*

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Insecticides are widely used to combat agricultural pest species, such as aphids, caterpillars, planthoppers and locusts, or to limit the spread of disease-carrying mosquitos. However, these insecticides do not only affect their target species but also non-target species such as pollinators which inadvertently encounter them while foraging. Over one hundred different pesticides and pesticide derivatives have been found in honey bee hives. Insecticides are one of the factors behind the decline of pollinator populations.

Pest species, such as aphids and Lepidoptera, have developed widespread resistance to a large number of compounds. However, research on insecticide resistance in honey bees is rather limited and focuses on only one type of resistance: metabolic resistance. Therefore, we aim to expand the available data on insecticide resistance in honey bees by studying another type of insecticide resistance: target site resistance. In this study, we screened 4897 publicly available *Apis mellifera* genomes for mutations in 17 insecticide target site genes covering all commonly used insecticides. These genomes originated from 54 countries and cover more than 20 subspecies and honey bee breeds. A total of 5269 synonymous and 4465 non-synonymous mutations were identified. These mutations show differing geographical and functional patterns of diversity.

While the majority of mutations were classified as rare mutations or could not be linked directly to insecticide resistance, several potential insecticide resistance mutations have been identified. Furthermore, mutations potentially associated with previously reported local adaptation to high altitude and *Varroa destructor* are described. This study serves as a basis for further research on insecticide resistance and local adaptation in pollinators.

PP-057 [Bee Health]

Exploring the role of opportunistic pathogens in honeybee health: the case of *Serratia marcescens* synergy with *Nosema ceranae*

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Honeybee's population losses show periodic fluctuations in intensity at global level, with their decline often driven by specific pathogens, such as the gut microsporidia *Nosema ceranae* and a multitude of viruses. However, many of these pathogens alone rarely bring honeybee colonies to death. Indeed, negative synergies with other pathogens or environmental factors often occur and get the colonies to collapse. The study of honeybees' pathogen synergies at the colony level is a little explored aspect and has focused especially on the pathogens-pesticides negative effects. However, other biological synergies, especially with pathogen and non-core opportunistic gut bacteria such as *Serratia marcescens*, is rarely explored and may explain important drawbacks in colony losses and may help beekeepers with a more accurate diseases management. To achieve this goal, our research wants to explore the development dynamics of *S. marcescens* within the co-infection of *N. ceranae*, determining the incidence of *S. marcescens* on the survival rate of honeybees and proposing possible solution (e.g. beneficial bacteria uptake and medicaments) on controlling these pathogens. Briefly, different *Serratia* strains were isolated from weak honeybees and inoculated into new-born, healthy honeybees' in co-infection with *N. ceranae*. Infected honeybees were reared in cages, and the impact of the multiple infections on their survival was observed in controlled lab conditions. Quantitative PCR was used to quantify *Serratia* and *N. ceranae* in the honeybee gut and hemocoel. Moreover, by feeding specific additives based on beneficial bacteria such as Lactobacillaceae or antimicrobial agents such as fumagillin, a possible co-infection control strategy was tested. Our results, showed that all tested *Serratia* strains were found capable to cross the gut epithelium and proliferate in the hemocoel and the co-infection with *N. ceranae* facilitated the surge of *Serratia* population within the gut, leading honeybees to a rapid death. Beneficial microbes from flowers, particularly *Apilactobacillus kunkeei*, effectively reduced *Serratia* load, suggesting it as a potential organic microbial resource management, easily applicable in commercial apiaries. These findings underscore the complexity of microbial interactions in the honeybee, recalling the need for wider research in determining multifactorial interactions between pathogens and environmental bacteria within the honeybee's gut.

