Better-B policy briefs

On the overlooked genetic factor in pesticide risk assessment with honey bees: mutations in target sites that confer resilience to chemicals

The Better-B Consortium November 2026 Recommendation n°6

The Better-B project is a four-year Horizon Europe project funded by the European Commission that began in June 2023. The project aims to improve honey bee resilience by restoring balance within the colony and between the colony and its environment. The consortium comprises 16 partners and two associated partners coming from 14 countries. This document is part of a series translating our results into clear recommendations for a diverse target audience. Depending on whether a recommendation is practice-oriented or policy-supporting, it is classified as a "Practical Recommendation" or a "Policy Brief," respectively.

Summary

Genetic variation may influence how honey bees respond to insecticides, yet it remains largely overlooked in pesticide risk assessment. By analysing honey bee genomes from 54 countries, our study identified 154 non-rare mutations in seven major insecticide target sites and identified ten mutations that may alter sensitivity to insecticides. These findings highlight differences among honey bee populations and reveal potential trade-offs between insecticide resistance and normal receptor function. We recommend incorporating diverse genetic backgrounds into pesticide risk assessment, promoting genetic diversity, and investigating the broader genetic mechanisms underlying insecticide sensitivity. The high-throughput TaqMan assay developed in this study provides a practical tool for screening European honey bee populations, helping inform more representative risk assessments and targeted pesticide management strategies.

The problem

Insecticides are used to combat agricultural pests such as aphids, caterpillars, planthoppers, and locusts, or to limit the spread of disease-carrying mosquitoes. However, these insecticides affect not only their target species but also non-target species, such as pollinators, which inadvertently encounter them while foraging or inside the hive. Insecticides and other pesticides have lethal and sub-lethal effects that impact all aspects of honey bee physiology, including development, learning behaviour, fertility, immunity, and thermoregulation. Consequently, insecticide use is considered one of the contributing factors to pollinator decline. Despite extensive research into the toxic effects of insecticides on honey bees, the genetic basis of variation in insecticide sensitivity remains poorly understood.

The evidence

A genomic study on honey bee genomes from 54 countries and more than 20 populations revealed 154 non-rare mutations in the seven most important insecticide target sites. The functional effect of selected variants was evaluated through integrated genomic, structural, and experimental approaches, primarily electrophysiology and computational protein structural modelling, this work identified ten mutations in four insecticide target sites that may alter receptor sensitivity to their respective insecticides. Five of these mutations were found in Europe.

Policy recommendations

1. Inclusion of honey bees from different genetic backgrounds in pesticide risk assessment

Our study revealed differences in insecticide target-site mutations both among and within honey bee populations. Such variation may influence sensitivity to specific insecticides and, consequently, contribute to differences in susceptibility among populations. We therefore recommend including honey bees from diverse genetic backgrounds in future pesticide risk assessments to better account for population-level variation in insecticide sensitivity. Particular attention should be given to *Apis mellifera iberiensis*, which exhibited the most distinct profile of target-site mutations among the European populations examined.

Furthermore, regional genetic variation should be considered when granting emergency authorisations for pesticide use, as the potential impacts on honey bee populations may differ depending on the genetic characteristics of local populations. Incorporating this variation into risk assessment and regulatory decision-making would support more representative evaluations of pesticide risks and help ensure that potentially vulnerable populations receive adequate protection.

2. Promotion of genetic diversity in European honey bees

Our study revealed that European honey bee populations exhibit lower diversity in insecticide target-site mutations than populations sampled in South America and Africa. This finding underscores the importance of accounting for geographic variation when evaluating pesticide sensitivity and developing strategies for pollinator conservation. Promoting and preserving genetic diversity in European honey bee populations may help maintain their capacity to adapt to environmental stressors, including pesticide exposure, thereby improving their long-term resilience.

3. Awareness for potential genetic impact of pesticide use

In our study, we observed that the majority of mutations identified as potentially affecting insecticide sensitivity may also alter the normal functioning of the target receptor. This finding highlights the importance of considering the physiological trade-offs associated with insecticide resistance. Mutations that reduce insecticide sensitivity may also impair essential receptor functions, potentially affecting individual fitness and, ultimately, population viability.

Consequently, pesticide risk assessment and management should consider not only the direct toxic effects of insecticides but also their potential to exert selection pressure on genetic variation in non-target organisms. Sustained insecticide exposure may favour the spread of resistance-associated mutations, even when these mutations carry fitness costs under natural conditions.

4. Expand research on genetic differences in insecticide sensitivity

In our study, we focused on genetic differences in insecticide target sites. However, target-site mutations represent only one of several mechanisms that can influence susceptibility to insecticides. Other mechanisms, including metabolic resistance, reduced insecticide penetration, and sequestration, may also contribute to differences in sensitivity among individuals and populations.

A more comprehensive understanding of the genetic basis of these resistance mechanisms would improve pesticide risk assessment by enabling a more accurate evaluation of population-specific vulnerabilities and supporting the development of more effective strategies to protect honey bee populations from pesticide exposure.

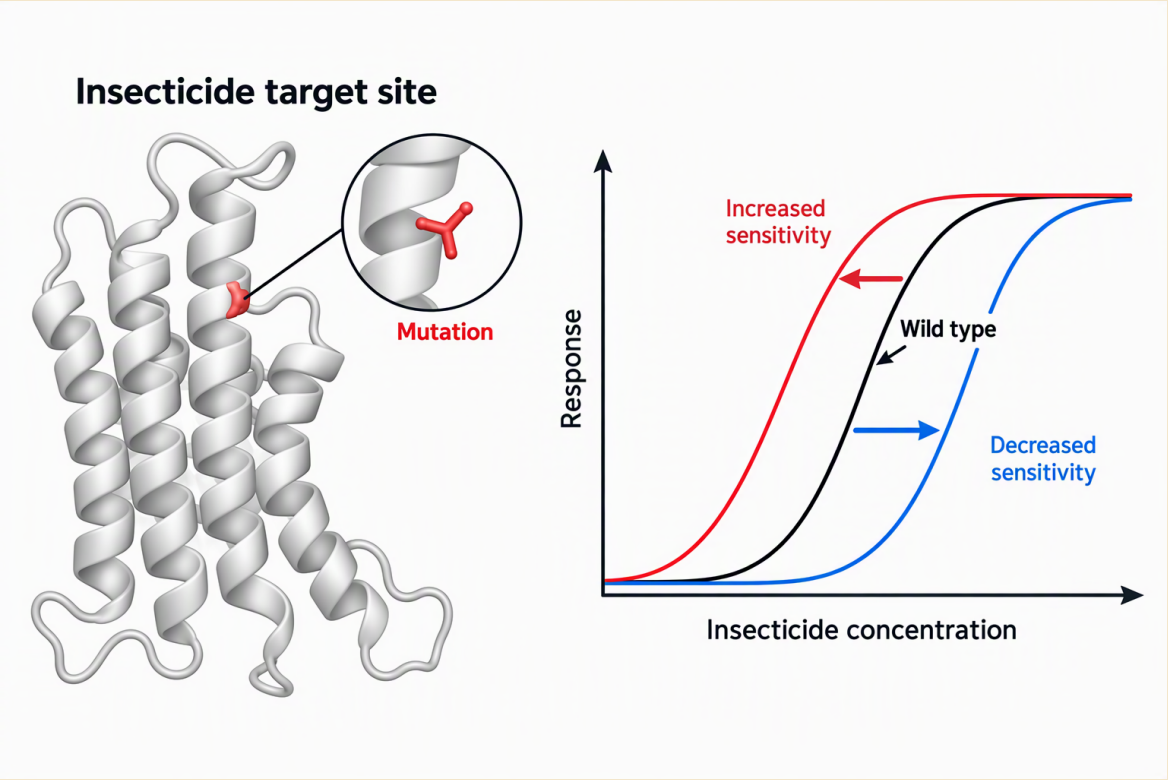


Figure 1: Insecticide target-site mutations can change how effectively an insecticide acts on its target in the insect. These mutations can make it easier or more difficult for the insecticide to bind and produce its effect. The dose–response curves illustrate how these changes influence insecticide sensitivity: a shift to the left (red) means that less insecticide is needed to achieve an effect, while a shift to the right (blue) means that more insecticide is required compared with the normal target (wild type, black).

Path to implementation:

We have developed a high-throughput TaqMan assay that enables the screening of European honey bee populations for genetic variants in key insecticide target sites, including the GABA receptor variant A406T, the acetylcholinesterase 2 variant E245D, and the octopamine receptor beta 2 variants V348I, T411V, and CTL. This tool provides a practical approach for monitoring the distribution and frequency of these variants across European honey bee populations. In the longer term, this approach could support the development of more representative risk assessment protocols and inform evidence-based, region-specific pesticide management strategies to better protect honey bee populations.

Further reading:

Verbinnen G., De Smet L., Henriques D., Tytgat J., Pinto M.A., de Graaf D.C. (2026) The diversity of insecticide target site mutations in *Apis mellifera*. *BMC Genomics* **27 (1):** 446. doi: 10.1186/s12864-026-12770-3

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This work was supported by the Better-B project, which has received funding from the European Union, the Swiss State Secretariat for Education, Research and Innovation (SERI) and UK Research and Innovation (UKRI) under the UK government's Horizon Europe funding guarantee (grant number 10068544).

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