



**ENBE 2025**

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**XXI International Meeting of the  
Portuguese Association for Evolutionary  
Biology**

**BOOK OF ABSTRACTS**

**18<sup>th</sup>-19<sup>th</sup> December 2025**

**Bragança**



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**XXI International Meeting of the Portuguese  
Association for Evolutionary Biology**

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Edited by

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## POSTER 25| LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE

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**Keywords:** *Apis mellifera*; pesticide exposure; genomic–environment association (GEA); environmental adaptation

### Abstract

Widespread pesticide use associated with intensive agriculture has been proven to impact the Western honey bee (*Apis mellifera*). However, despite evidence of declines in survival, development, foraging efficiency, and overall colony health, the genomic underpinning of this abiotic stressor is largely unknown. This study involved 102 whole-genome sequences from honey bee colonies from across Europe, sampled under the Better-B project, to search for genetic correlations to pesticide exposure using Genomic-Environment Association (GEA) analyses. The environmental exposure data were collected within the framework of the INSIGNIA-EU project, which used APIStrips (in-hive pesticide-adsorbing strips) to quantify pesticide residues brought into the hive by foraging in many of the sampled colonies. The APISTRIP data were complemented by modelled exposure grids from PEST-CHEMGRIDS and agriculture zones from the CORINE Land Cover. Employing three complementary GEA approaches—SAMBADA (spatial analysis tool), LFMM (latent factor mixed models), and RDA (Redundancy Analysis)—we identified SNPs in the bee’s genome significantly correlated with agricultural pressure and pesticide use. Notably, several genes with known roles in detoxification and stress response, including venom carboxylesterase6 and CYP336A1, were highlighted. These variants point to molecular pathways targeted by agrochemical toxicity, offering insights into the consequences of pesticide use. Such findings may, in the future and upon further validation, help refine risk assessment frameworks, support the development of resilience-oriented breeding programs, and promote sustainable apicultural practices.

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