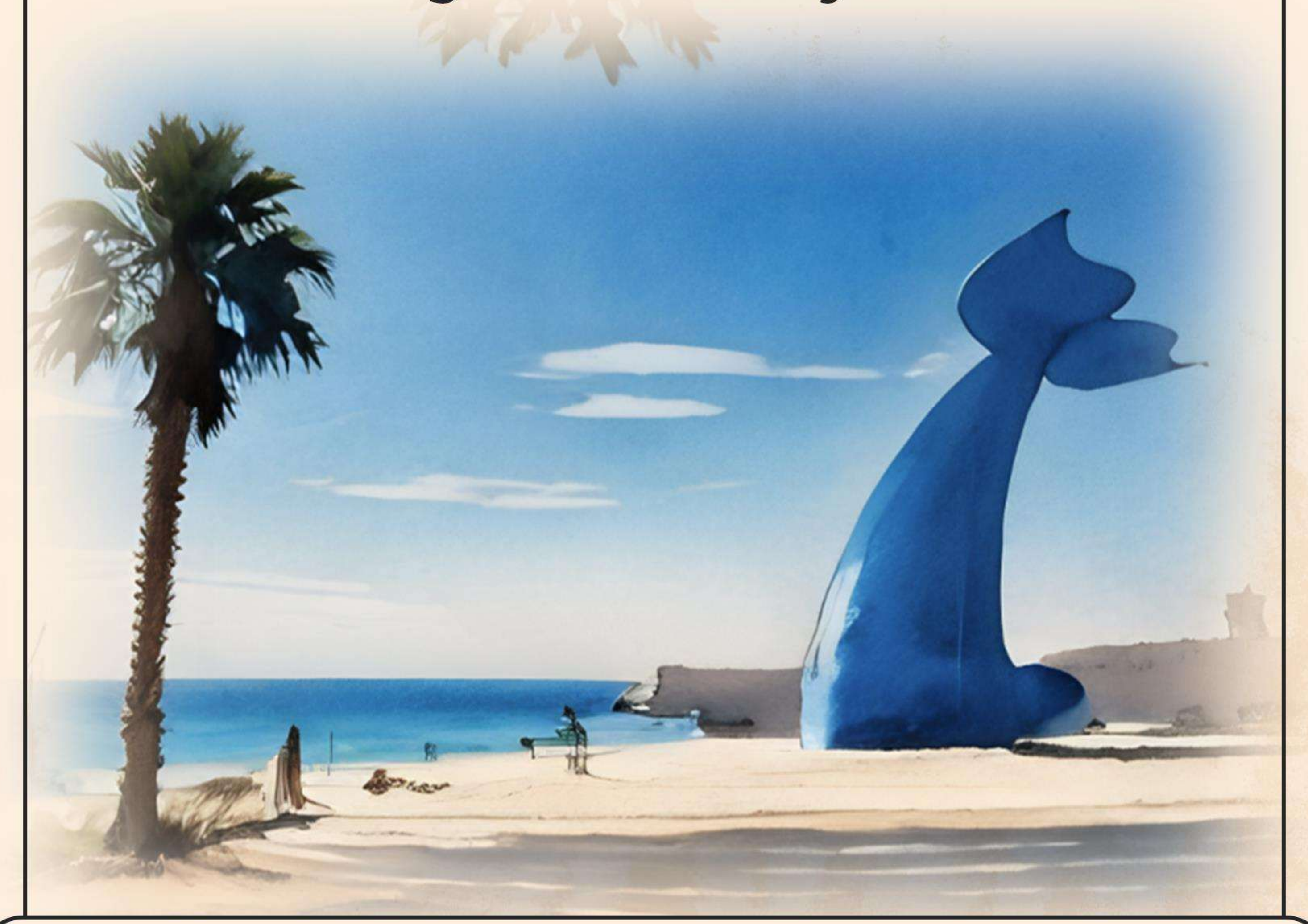
Organized by:

Instituto de Tecnologia Química e Biológica
Universidade NOVA de Lisboa

SPG Conference

International Conference of the Portuguese Society of Genetics



5-6 June 2025, Oeiras

Evaluating the consequences of plant protection products in the Western honey bee (*Apis mellifera*) genome

Daniela Barbosa[1,2], Fernanda Li[1], Sana Bashir[1], Carlos Ariel Yadró Garcia[1], Demetris Taliadoros[3], Matthew Webster[3], José Rufino[4,5], Ivo Roessink[6], Bas Buddendorf[6], Jozef van der Steen[7], Maria Murcia[8], Amadeo Rodríguez Fernández-Alba[8], Maria Alice Pinto[1], Dora Henriques[1]

[1] CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300- 253 Bragança, Portugal
[2]Pontificia Universiade de Minas Gerais , 30140-108, Belo Horizonte MG, Brasil
[3]Department of Medical Biochemistry and Microbiology, Science for Life Laboratory, Uppsala University, 75237 Uppsala, Sweden
[4]Laboratório Associado para a Sustentabilidade e Tecnologia em Regiões de Montanha (SusTEC), Instituto Politécnico de Bragança, Bragança, Portugal
[5]Research Centre in Digitalization and Intelligent Robotics (CeDRI), Instituto Politécnico de Bragança,Campus de Santa Apolónia, Portugal
[6]Wageningen Environmental Research (WENR), Droevendaalsesteeg 3, NL-6708 PB Wageningen, The Netherlands
[7]Alveus AB Consultancy, Kerkstraat 96, NL-5061 EL Oisterwijk, The Netherlands
[8]Chemistry and Physics Department, University of Almeria, Agrifood Campus of International Excellence (ceiA3), 04120 Almería, Spain

E-mail: daniela.s.lima2003@gmail.com

The Western honey bee (*Apis mellifera*)is a key model organism for evaluating risks from Plant Protection Products (PPPs). Despite well-documented impacts of PPPs on honey bees survival and behaviour, their molecular consequences remain underexplored. Herein, over 472 whole genomes from samples collected across Europe in the framework of the project Better-B were used to investigate the genetic basis of PPP exposure through Genomic-Environment Association (GEA) analysis. By integrating genomic data from honey bee colonies with processed PPP exposure data collected in the framework of the project INSIGNIA-EU and from the PEST-CHEMGRIDS database as well as from environmental datasets from CORINE land cover, this study used SAMBADA (a spatial analysis tool) and Redundancy Analysis (RDA) scripts to identify candidate genes potentially linked to pesticide stress.

This research addresses a knowledge gap, offering a pathway to mitigate PPP-related molecular effects and support sustainable beekeeping, and can inform breeding programs to bolster honey bee resilience. Ultimately, this work advances our understanding of PPP impacts at the molecular level, fostering resilience in a key pollinator essential for global food security.