

Organized by:

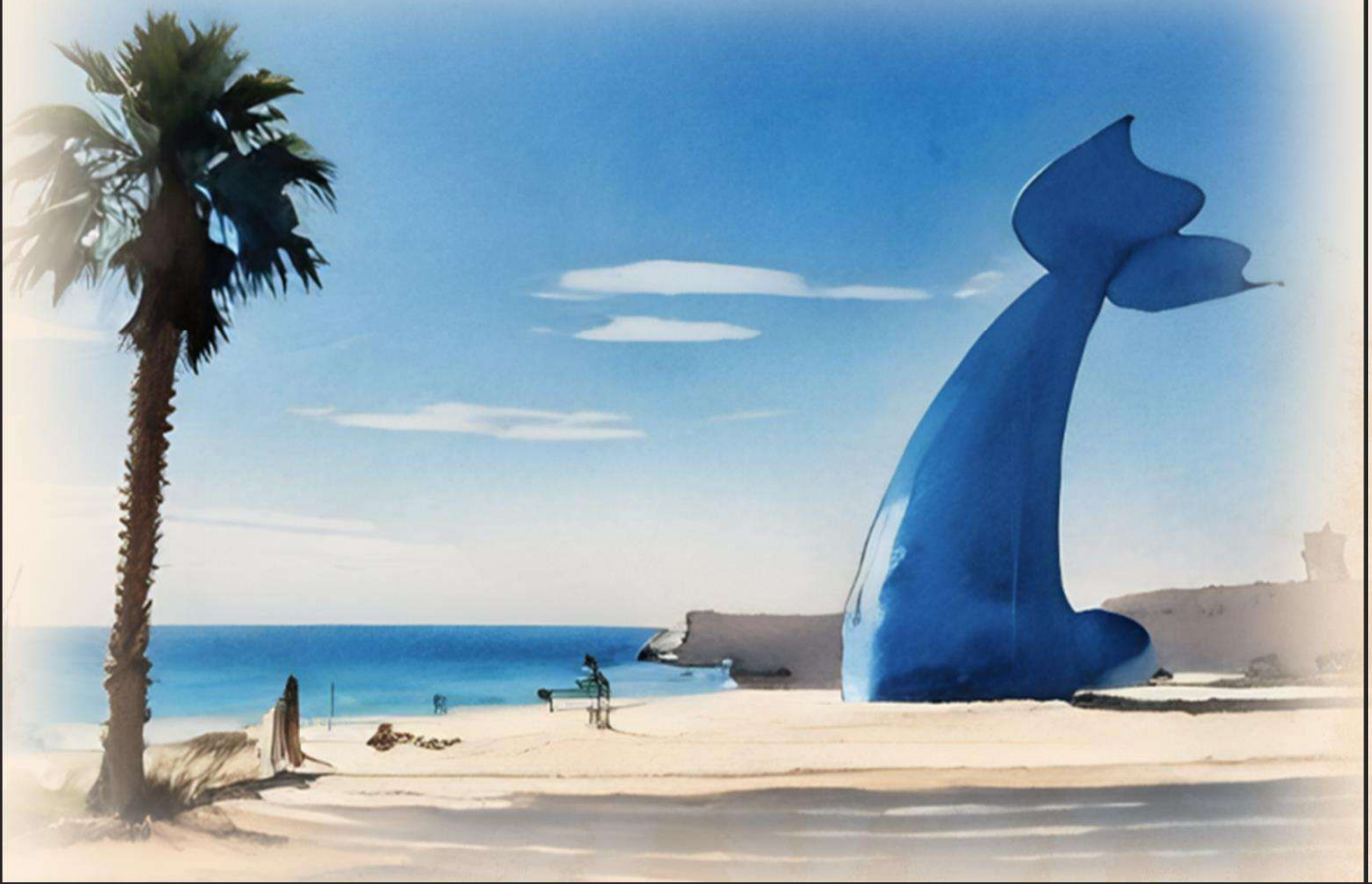


itqb nova

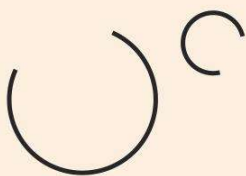
**Instituto de Tecnologia
Química e Biológica**
Universidade NOVA de Lisboa

SPG Conference

International Conference of the **Portuguese Society of Genetics**



5-6 June 2025, Oeiras



Genetic Diversity of Detoxification Genes in 18 Honey Bee Subspecies

Fernanda Li¹, Daniela Barbosa¹, Sana Bashir^{1,2}, Leandro Moreira de Sá¹, Carlos Ariel Yadró Garcia¹, José Rufino^{2,3}, Annelise Rosa-Fontana¹, Gilles Verbinnen⁴, Dirk C. de Graaf⁴, Lina de Smet⁴, Demetris Taliadoros⁵, Matthew Webster⁵, Maria Alice Pinto¹, Dora Henriques¹

¹CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300- 253 Bragança, Portugal

²Pontifícia Universidade Católica de Minas Gerais, 30140-108, Belo Horizonte MG, Brasil

³SusTEC - Laboratório Associado para a Sustentabilidade e Tecnologia em Regiões de Montanha, Instituto Politécnico de Bragança, Bragança, Portugal

³Research Centre in Digitalization and Intelligent Robotics (CeDRI), Instituto Politécnico de Bragança, Campus de Santa Apolónia, Portugal

⁴Laboratory of Molecular Entomology and Bee Pathology (L MEB), Department of Biochemistry and Microbiology, Faculty of Sciences, Ghent University, Ghent, Belgium

⁵Department of Medical Biochemistry and Microbiology, Science for Life Laboratory, Uppsala University, 75237 Uppsala, Sweden

E-mail: fernandali@ipb.pt

The honey bees (*Apis mellifera*) is a key pollinator that is exposed to a wide array of xenobiotics, both natural (plant allelochemicals) and synthetic (pesticides), while foraging or through contaminated food within the hive. These compounds have both lethal and sub-lethal effects, impairing foraging activity and negatively affecting bee development and colony health. Similar to other insects, honey bees rely on detoxification pathways to metabolise xenobiotics into less toxic or more readily excretable forms. This process is a key mechanism underlying insecticide resistance and is influenced by genetic variation. Therefore, investigating polymorphisms in detoxification-related genes is a promising approach to predict species-specific responses to pesticide exposure.

Five major gene families are involved in xenobiotic detoxification: cytochrome P450 monooxygenases (CYPs), carboxyl/cholinesterases (CCEs), glutathione S-transferases (GSTs), ATP-binding cassette transporters (ABCs), and uridine 5'-diphospho-glucuronosyltransferases (UGTs). In this study, we examined the genomic detoxification inventory of over 1,600 individuals representing 18 *A. mellifera* subspecies representing the four main evolutionary lineages. For each lineage and subspecies, single-nucleotide polymorphism (SNP) loci were identified within these genes, allele frequency and FST (fixation index) were calculated. Additionally, all variants were annotated to assess their potential impact on protein function. Findings from this study have the potential to inform breeding and conservation strategies by identifying populations more vulnerable to chemical stressors, ultimately supporting honey bee health in changing environments.