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OP-093 [Bee Biology]
Genetic variation of detoxification genes: from genes to proteins

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Honey bees (Apis mellifera) are exposed to natural and synthetic xenobiotics, requiring genetic adaptations for survival. Several gene families have been implicated in insect pesticide resistance, including cytochrome P450s, glutathione-S-transferases (GSTs), esterases, and uridine diphosphate (UDP)-glycosyltransferases. This study investigates genetic variation in these detoxification gene families and predicts the structural and functional effects of non-synonymous SNPs (single nucleotide polymorphisms) on protein structure and function. We analyzed SNPs mapped to these detoxification genes extracted from over 1,500 whole genomes representing 15 subspecies and the four main honey bee lineages: M, C, A, and O. Functional annotation and variant effects were predicted using SnpEff. Allele frequencies and each SNP's fixation index (FST) were calculated per population and evolutionary lineage. Bioinformatics and molecular modeling techniques were employed to evaluate non-synonymous SNPs' structural and functional consequences. Protein structures were generated from FASTA files using AlphaFold3, converted from mmCIF to PDB format, and visualized in PyMOL. Functional site predictions were performed using Proteins Plus, and molecular dynamics simulations were conducted in YASARA to assess stability and conformational changes in proteins. Our results indicate many non-synonymous SNPs in some subspecies, such as A. m. jemenitica and A. m. intermissa. The genes with the highest number of non-synonymous mutations belong to the CYP family, particularly Probable cytochrome P450 6a14 and CYP9Q1. Conversely, genes such as Cytochrome P450 6k1 and Methyl farnesoate epoxidase exhibit no non-synonymous SNPs. By understanding intraspecific genetic variation, we move closer to reliably predicting how honey bee populations will respond to pesticide exposure.

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