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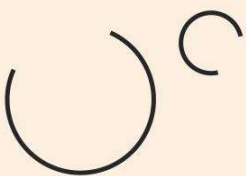
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# Bioinformatics pipeline to evaluate patterns of diversity in detoxification genes in the Western honey bee (*Apis mellifera*)

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The Western honey bee, *Apis mellifera*, displays significant genetic diversity in detoxification genes, which is pivotal for environmental adaptation and resilience. Herein, we developed a bioinformatics pipeline to investigate patterns of diversity in these genes, focusing on single nucleotide polymorphisms (SNPs) across *A. mellifera* populations, with variant annotation performed using both snpEff and the Variant Effect Predictor (VEP). Our pipeline integrates GATK, VCFtools, PLINK, bcftools, snpEff, and VEP to process genomic data systematically. Regions of interest were defined in a BED file for variant filtering. Using GATK, SNPs were extracted from a VCF file and conversion to PLINK format for population genetics analyses. Variants were filtered by minor allele frequency (MAF) and population differentiation (FST index) to identify SNPs with considerable. Variants were annotated with snpEff and VEP to predict functional impacts, enabling a comparative analysis of their annotation consistency and depth.

Custom scripts were developed to map SNPs to detoxification genes, quantify SNP density, and integrated gene descriptions and lineage data. The resulting data were visualized using a combination of and generate different graphs using ggplot2 and chromoMap for chromosomal maps. Quality control steps were applied through the pipeline ensuring data reliability. Our findings reveal distinct SNP patterns in detoxification genes, highlighting candidate SNPs associated with *A. mellifera* subspecies-specific adaptations. The comparison of snpEff and VEP annotations provides insights into their strengths and limitations, which can help optimize software selection for genomic studies. This pipeline offers a reproducible framework for studying genetic diversity in *A. mellifera* that is adaptable to other species, advancing conservation and evolutionary genomics.