

## DECODING THE CYP3 LANDSCAPE IN *APIS MELLIFERA*: Allelic Diversity, Detoxification, and Beyond

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### 1 Introduction & Aim

Honey bees (*Apis mellifera*) rely on cytochrome P450 (CYP) enzymes to detoxify pesticides. CYP clan 3 genes are assumed to function in xenobiotic metabolism, but this classification lacks population genomic validation. We characterized natural allelic diversity across CYP3 genes to test whether evolutionary signatures support uniform detoxification roles or reveal functional heterogeneity within this clan.

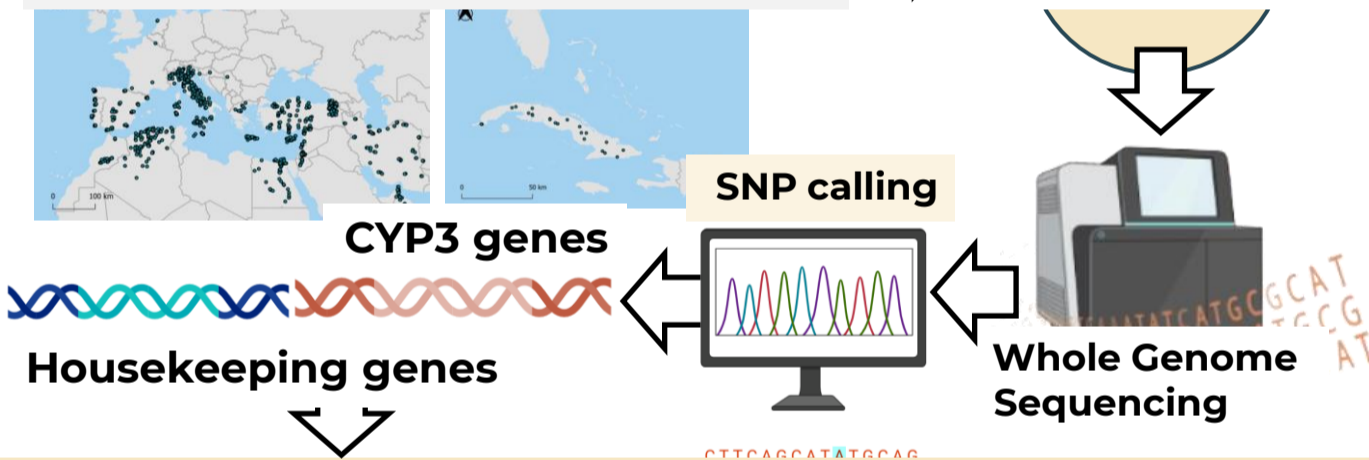
**Housekeeping genes show expected low diversity:** low haplotype diversity, low non-synonymous mutations per amino acid (nsyn/a.a), and nsyn/syn < 1 (Figures 1 & 2).

**CYP3 genes display heterogeneous patterns:** some resemble housekeeping genes, while xenobiotic metabolizers genes exhibit high haplotype diversity and elevated nsyn/a.a ratios (Figures 1 & 2).

### 2 Methods

Sampling of 1,467 drones of *A. mellifera* from 25 countries

DNA extraction: bee thorax



Annotation of variants, allele frequency and haplotype analysis

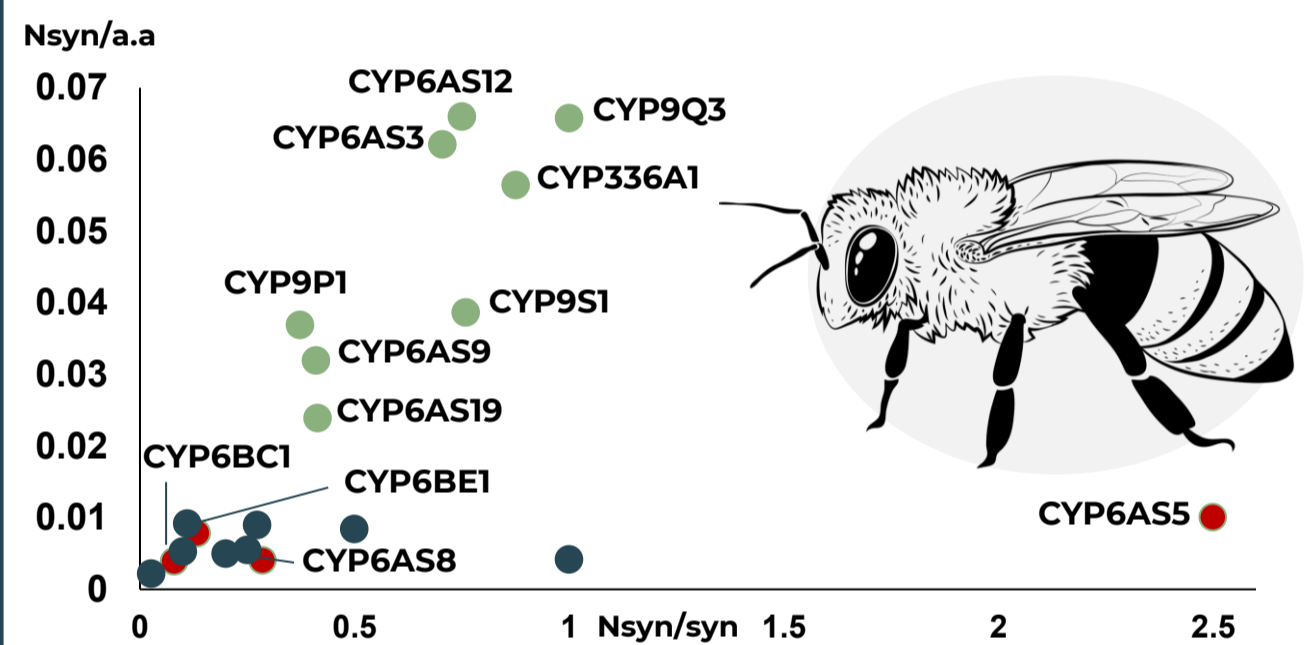


Figure 2. Nsyn/syn ratio vs Nsyn/a.a. High-diversity genes (Hd > 0.85, green dots) and low-diversity genes (Hd < 0.2, red dots) are highlighted. Blue dots are housekeeping genes.

### 3 Results

We identified 5,213 variants across analyzed genes, with >50% in CYP3. CYP3 genes harbor 3.4× more non-synonymous variants than housekeeping genes

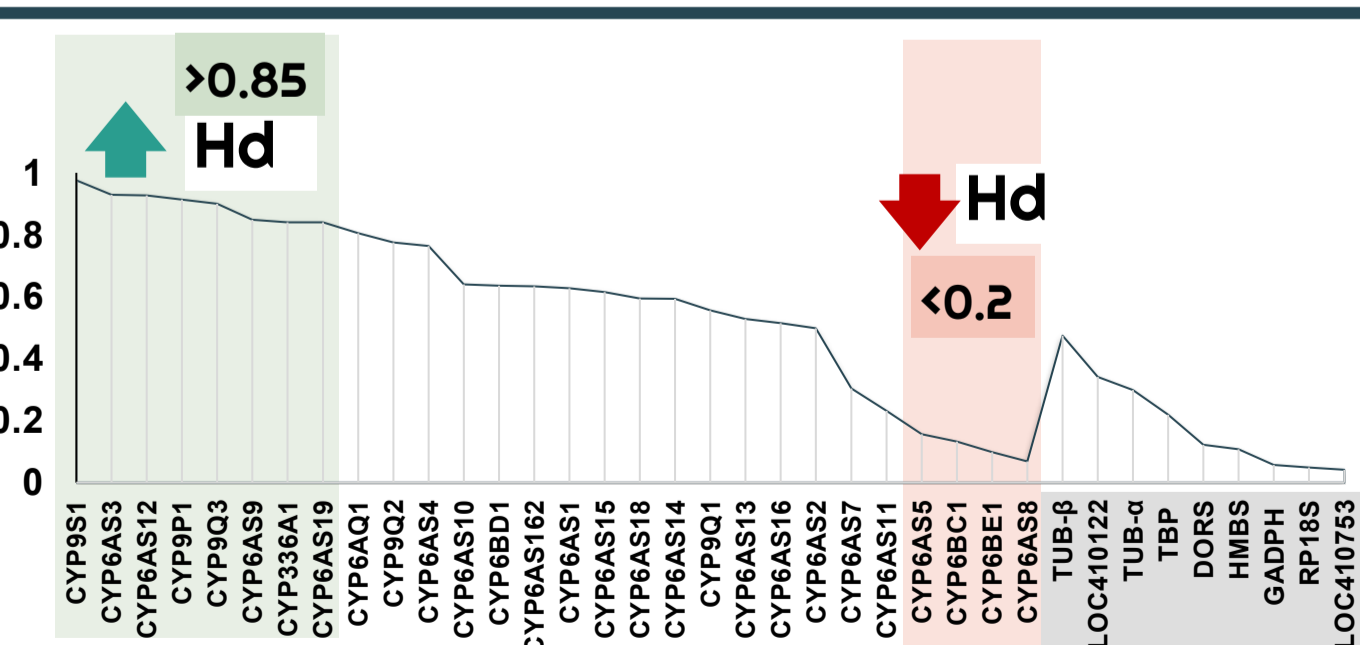


Figure 1. Haplotype diversity (Hd) of CYP3 gene vs Housekeeping genes (grey). CYP3 genes with high and low Hd are highlighted.

### 4 Conclusion & References

**CYP3 genes exhibit functional duality:**

some most likely evolve rapidly under pesticide selection (e.g., CYP9Q3, CYP6AS12), while others remain constrained like housekeeping genes (e.g., CYP6AS8), revealing conserved physiological roles. This heterogeneity challenges traditional classification paradigms that assume uniform xenobiotic metabolism across this clan.



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