

***Conserved highly heterogeneous
genomic landscapes of diversity
in honey bees***

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Honey bees, especially the Western honey bee (*A. mellifera*), are the main pollinators for agricultural landscapes worldwide. Estimating and safeguarding their genetic diversity is of crucial importance to tackle environmental challenges and ensure global food security.

Here, we investigated the variation along the genome, the genomic landscape, of the levels of genetic diversity and Tajima's D across populations from four *Apis* species.

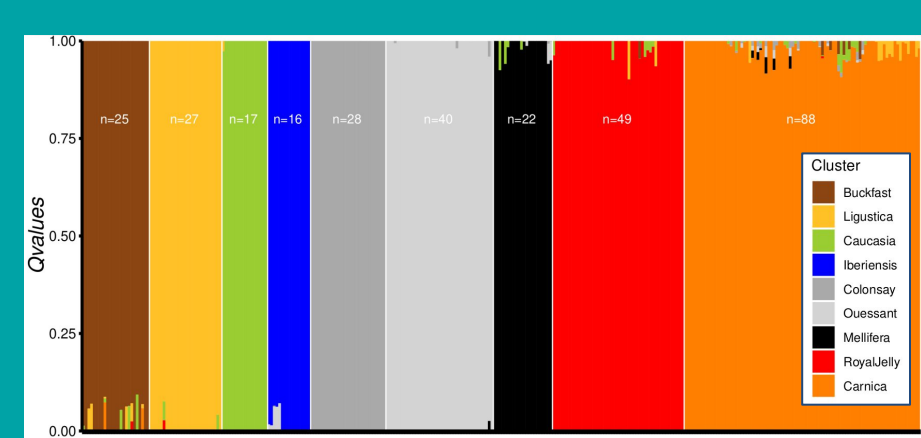


Figure 1



Apis mellifera
(Ligustica)

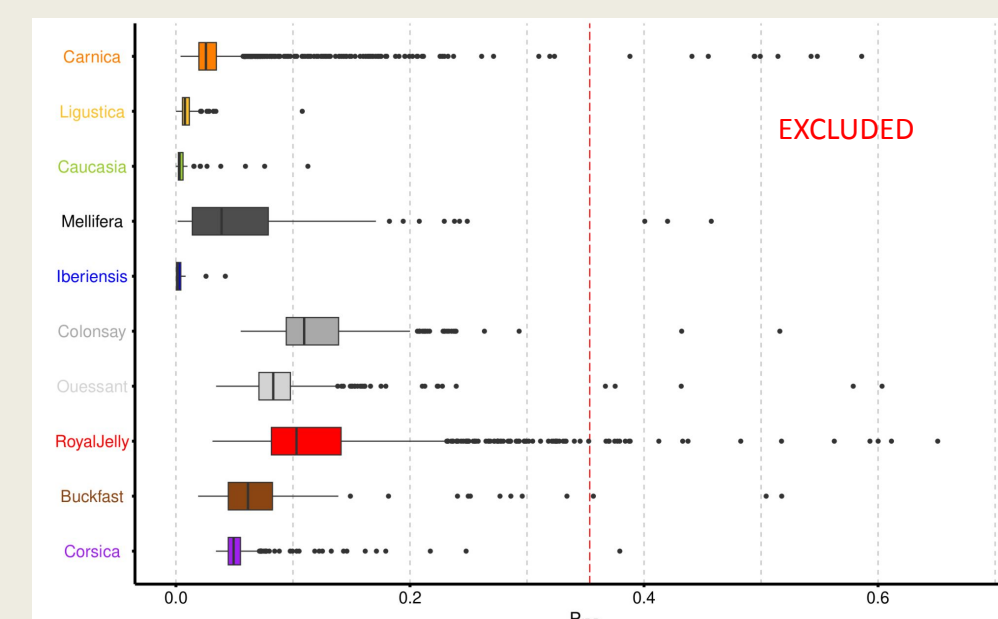


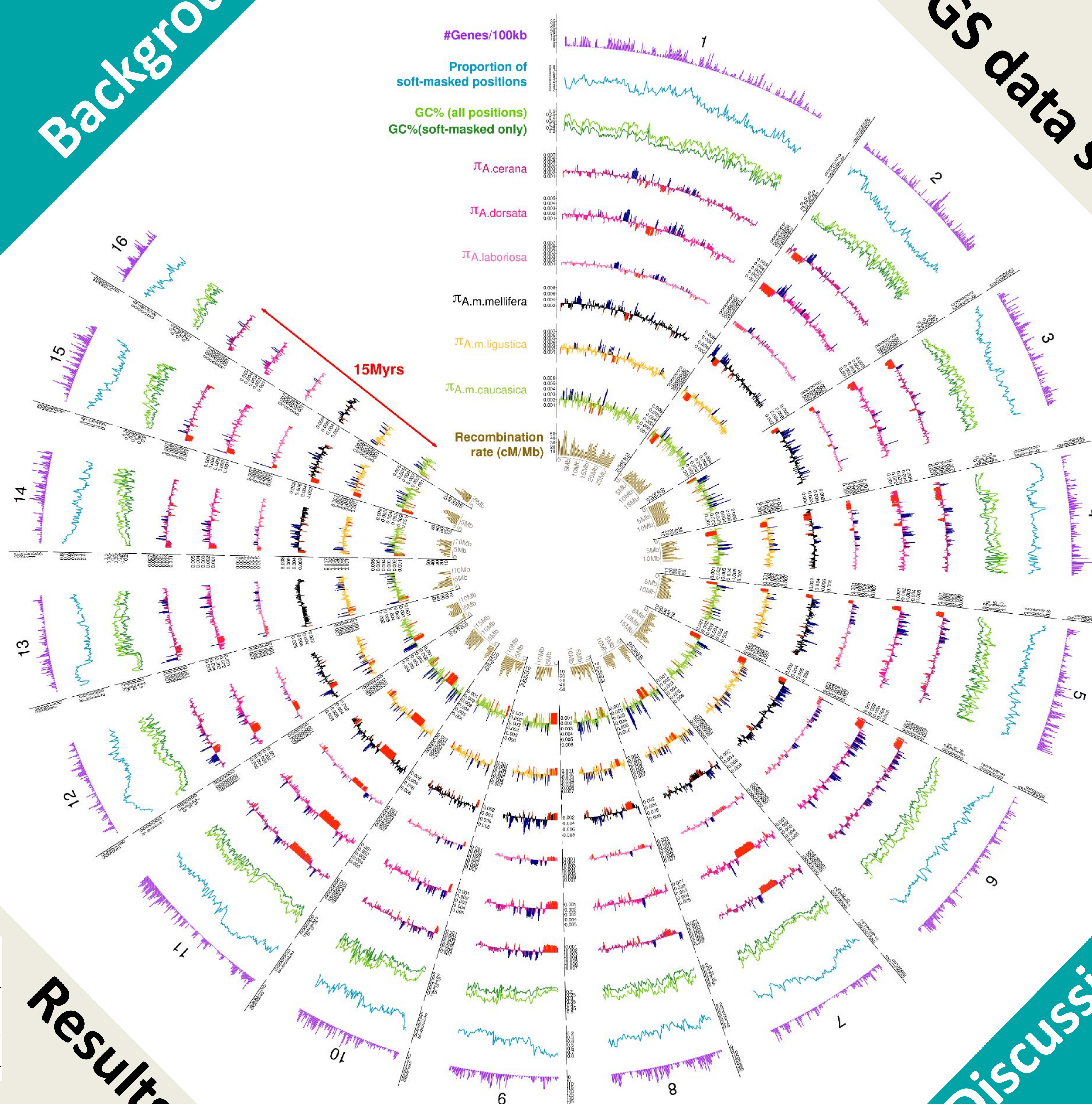
Figure 2

We reanalyzed publicly available data from >300 *Apis* genomes, most of which from *A. mellifera*, but also from *A. cerana*, *A. dorsata* and *A. laboriosa*, to investigate levels of the genetic diversity of the different species and subspecies. We excluded hybrids (Fig. 1) as well as family-related individuals (Fig. 2)

WGS data:

<i>A. laboriosa</i>	Cao 2023
<i>A. dorsata</i>	
<i>A. cerana</i>	Chen 2018
<i>A. mellifera</i>	Wragg 2022

WGS data set



Apis cerana

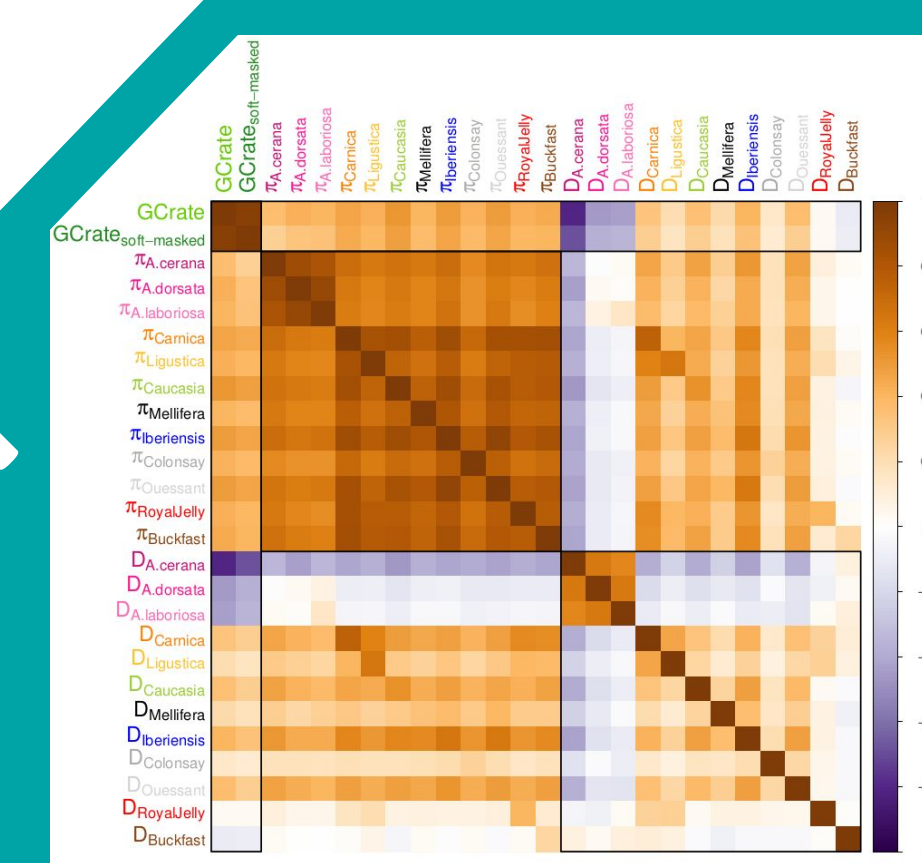


Figure 4

Discussion

In honey bees, the landscapes of nucleotide diversity are highly heterogeneous along the genome, due to high syntenic and recombination landscape (Figs. 4 & 5). The genomic landscapes of nucleotide diversity are remarkably well-conserved among the four species (main & Fig. 4), despite over 15 million years of divergence.

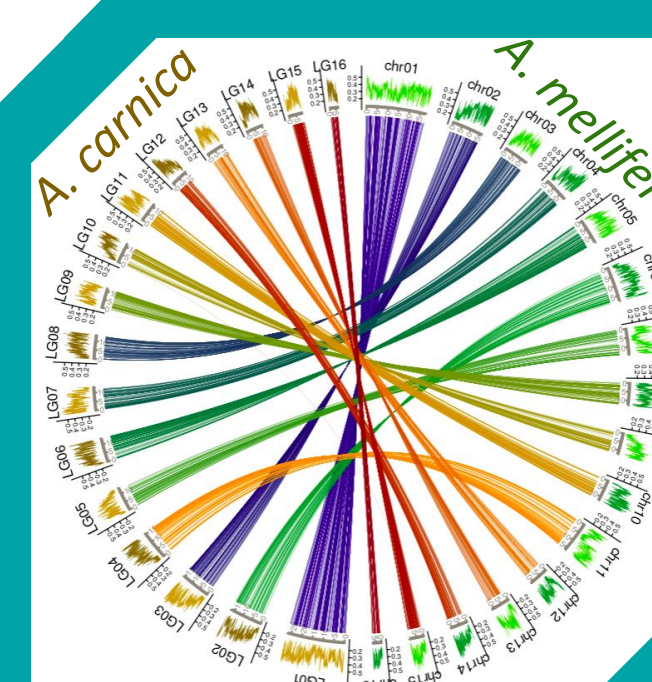


Figure 5



Apis laboriosa

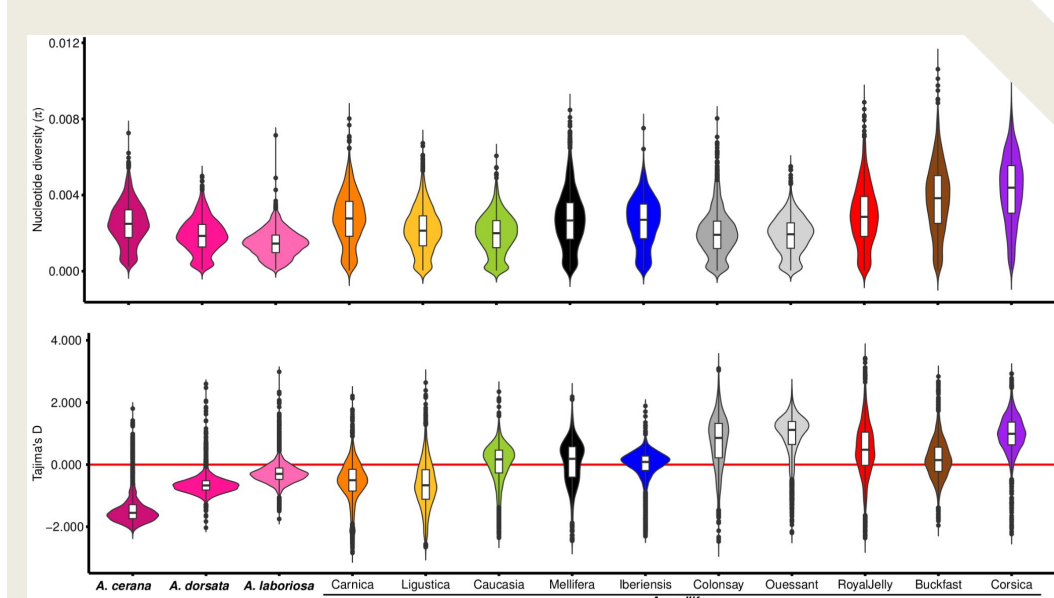


Figure 3

Results

We computed nucleotide diversity (π) and Tajima's D using 100-kb sliding windows spanning the genome, after hard-masking regions with extreme coverage, following Leroy *et al.* 2021. Diversity is variable depending on the backgrounds (Fig. 3), with higher π in the Buckfast breeding line and lower in the black bees from the Ouessant and Colonsay conservatories, questioning the effectiveness of the conservation efforts.

References:

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