

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.

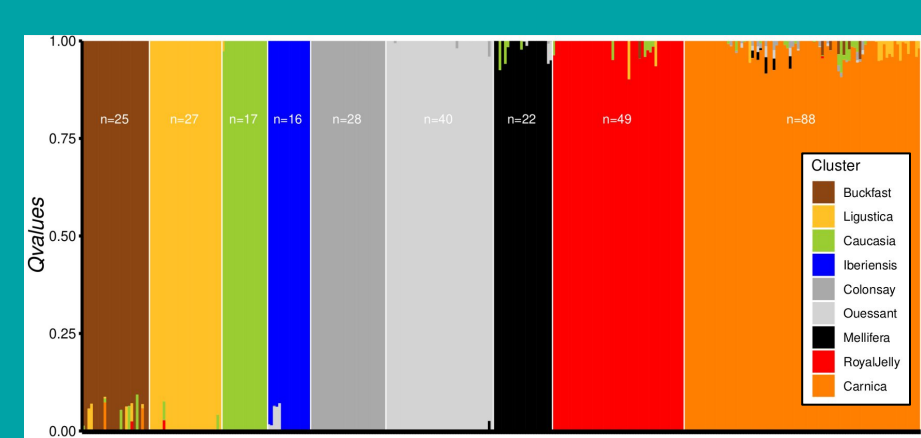


Figure 1



Apis mellifera
(Ligustica)

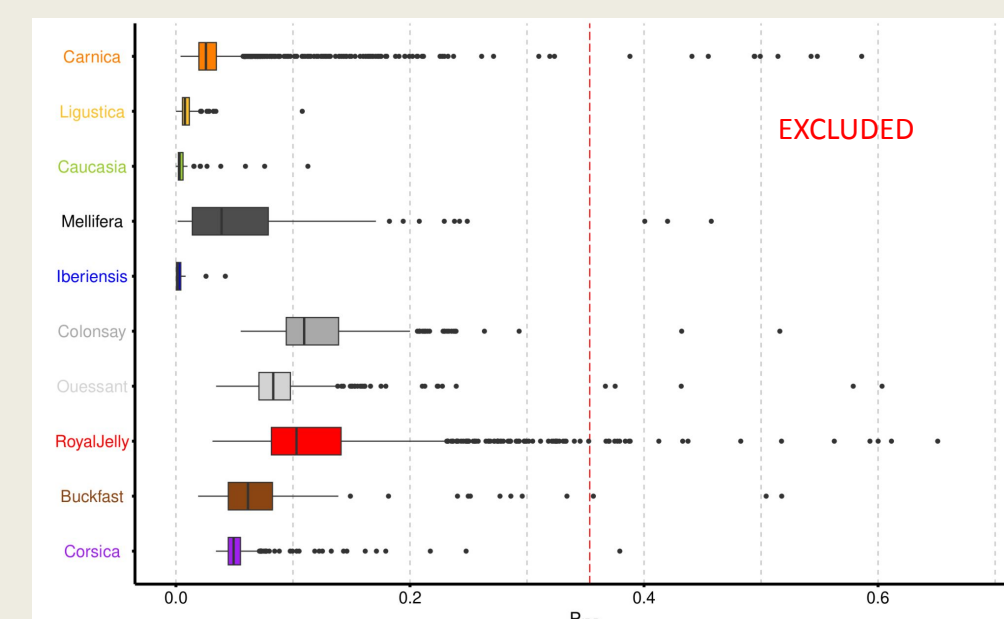


Figure 2

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)

Background

WGS data set

WGS data:

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



Apis dorsata

Apis cerana

Apis laboriosa

Results

Discussion

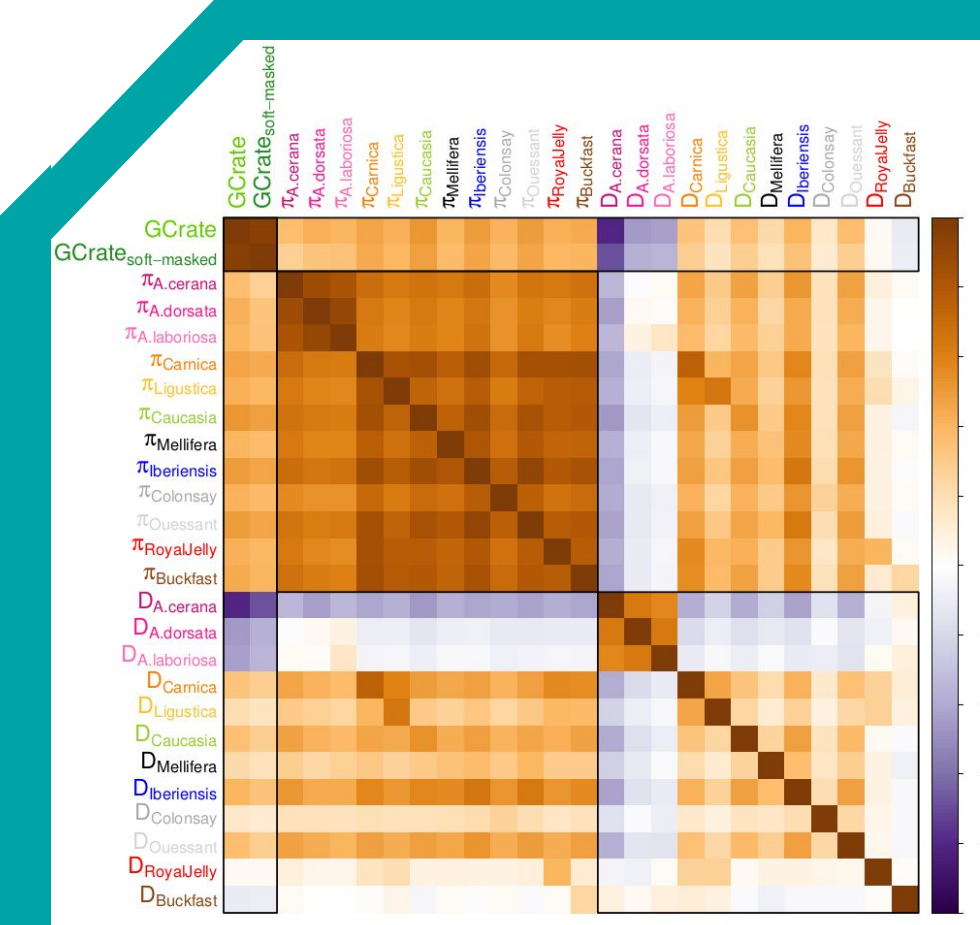


Figure 4

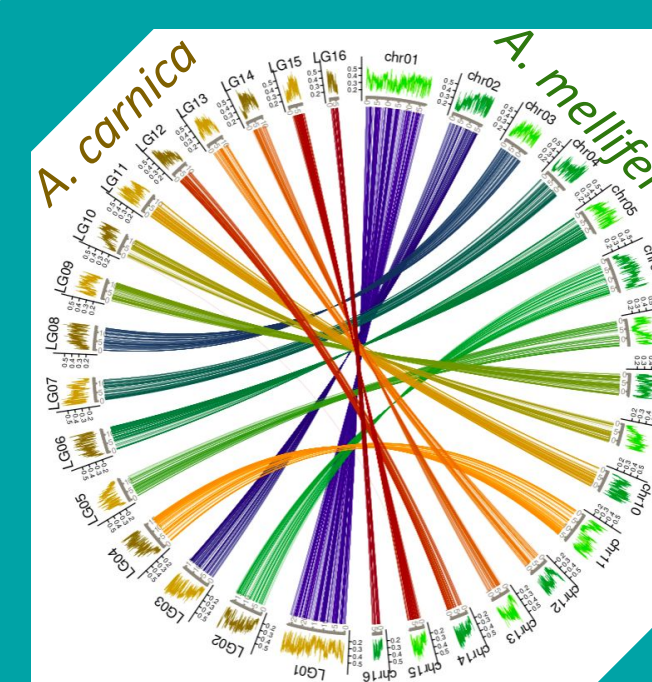


Figure 5

In honey bees, the landscapes of nucleotide diversity are highly heterogeneous along the genome, due to high synteny 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 3

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:

- Cao, L. *et al.* Population Structure, Demographic History, and Adaptation of Giant Honeybees in China Revealed by Population Genomic Data. *Genome Biol Evol* 15, (2023).
 Chen, C. *et al.* Population Genomics Provide Insights into the Evolution and Adaptation of the Eastern Honey Bee (*Apis cerana*). *Molecular Biology and Evolution* 35, 2260–2271 (2018).
 Leroy, T. *et al.* A bird's white-eye view on avian sex chromosome evolution. *Peer Community Journal* 1, e63 (2021).
 Wragg, D. *et al.* Complex population structure and haplotype patterns in the Western European honey bee from sequencing a large panel of haploid drones. *Molecular Ecology Resources* 22, 3068–3086 (2022).

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To know more or continue to follow the project:

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