Algerian honey bees : a case study of the impact of breeding management on genetic structure

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Background

- The genetic diversity of honey bees (*A. mellifera sp.*) results from the trade of queens by beekeepers (sometimes on long distance) and mating with local males (possibly feral/wild). This combination yields variable patterns of biogeographical distribution.

- Little is known about genomics of Algerian bees. We recently suggested that the 2 known subspecies (*A. m. intermissa* and *A. m. sahariensis*) do not play a primary role in the genetic structure of the population, the variation pattern being rather geographic (Fig. 1c).

  ❯ **Here, we investigate the causes of that structure, in particular using ancestral recombination graphs**

Material

- Sampling of male Algerian honey bees from 2 subspecies (N = 102 after filters; 16 *A. m. sahariensis* and 86 *A. m. intermissa*), in 49 geo-localized sites
- Small (~230 Mb) and haploid genome, with high variant density: 1.38M biallelic SNPs retained after stringent filtering (including LD pruning)
- For *Relate* purposes: selection of 38 samples equally distributed between clusters and determination of ancestral allele by comparison to *A. Cerana* (1.54M SNPs retained)

Geo. vs. genetic distances

PC-based genetic distances correlate well with geographic distances (*r* = 45%): however, the trend is mostly driven by the Western cluster (*r* = 72%, **Fig. 2a**), suggesting long-range exchange of genetic material in the Eastern cluster.
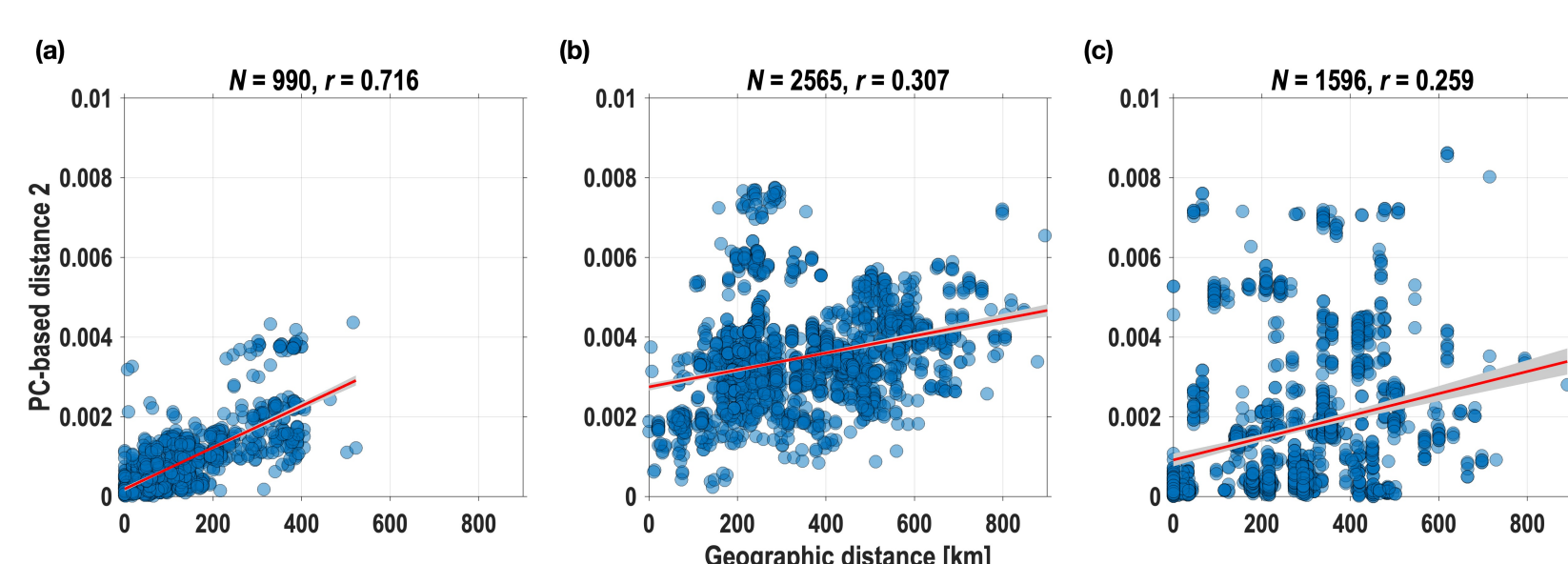
Fig. 2. Geographic vs. genetic distances, in the main clusters (a: Western, c: Eastern) and between clusters (b).

Kinship estimation

We used *hmmIBD* to estimate Identical-By-Descent (IBD) segments and kinship between all pairs of samples of each main cluster. Samples sharing IBD kinship > 10% are considered to form a close-related family. Most of the identified pairs (31/33) are found in the Eastern cluster, sometimes at large distances (orange lines in **Fig. 1c**).

Genetic structure

We assessed the genetic structure with PCA, *Admixture* and *FineStructure*: PC1 correlates with longitude (*r* = 72%), *Admixture* and *FineStructure* consistently classify samples between Western and Eastern clusters (concordance = 96%).
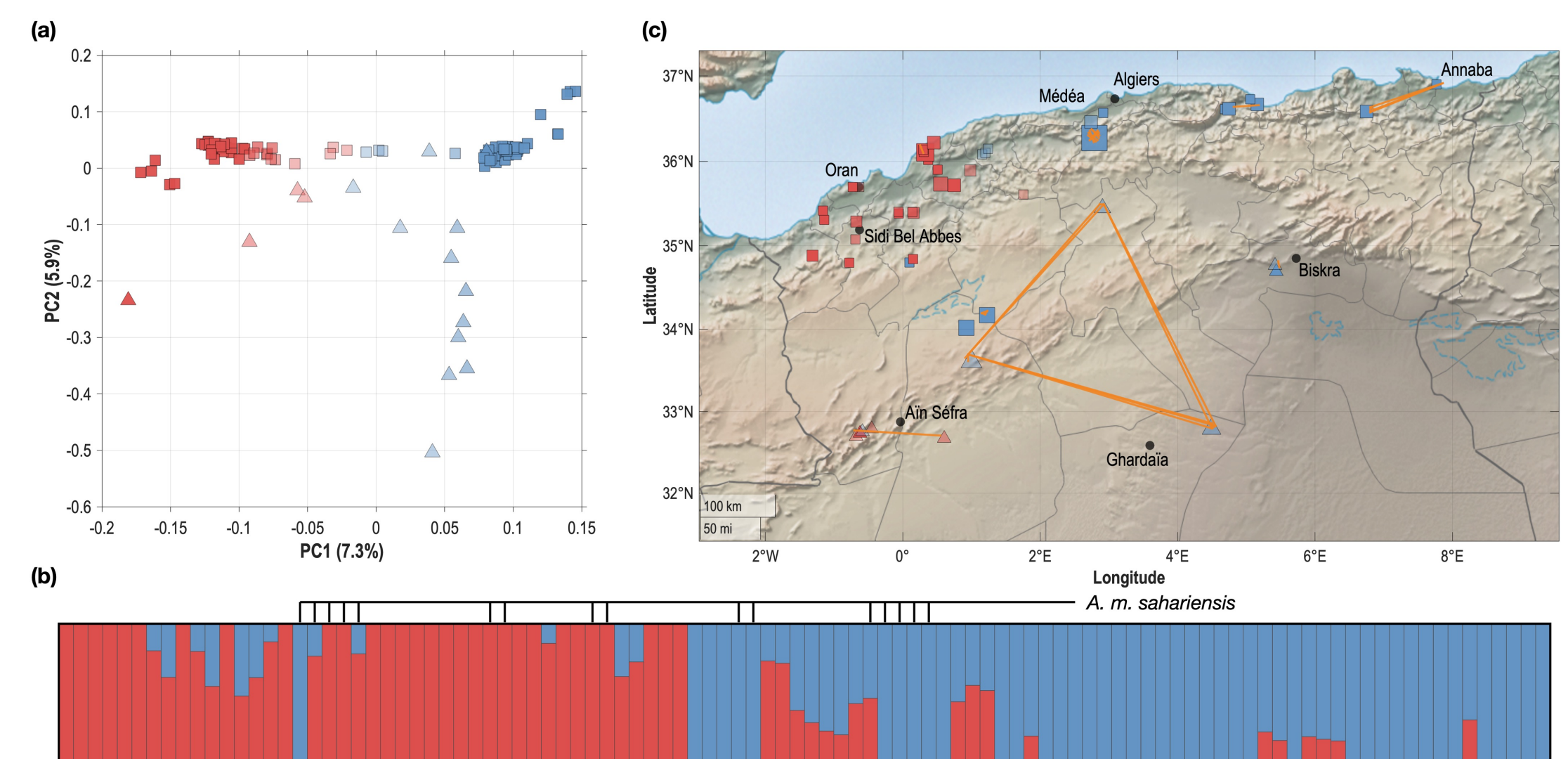
Fig. 1. PCA and Admixture analyses and geographic distribution of samples. Individuals (in **a**) and sampling sites (in **c**) are coloured in accordance to their main component (shown in **b**) and mark shapes denote the subspecies (□ for *A. m. intermissa*, △ for *A. m. sahariensis*). Admixture plot (**b**) is ordered by longitude. The marker size in (**c**) reflects the number of samples per site.

First coalescence times

We inferred the ARG using *Relate* over 38 samples. Over all local trees, we identified sub-trees gathering samples from only one cluster (example in **Fig. 3**), then computed the average age of their terminal leaves (i.e. first coalescence time - **Fig. 4**). These times are ~1.3× larger in the Western cluster compared to the Eastern cluster.
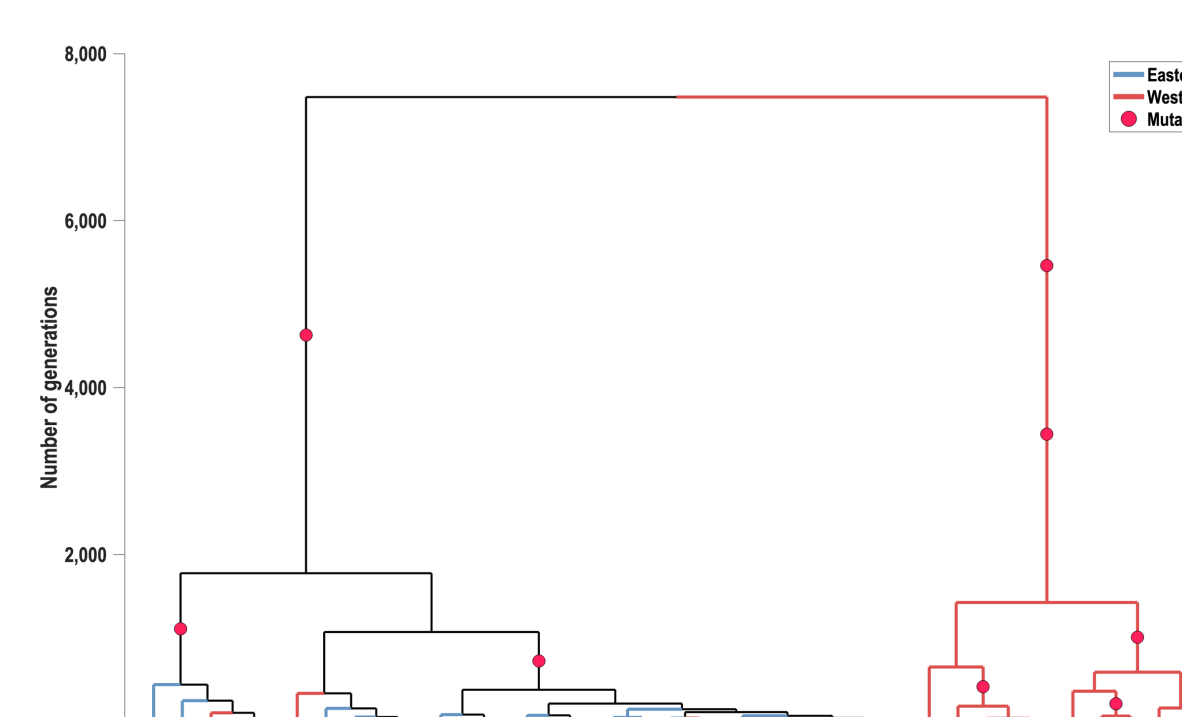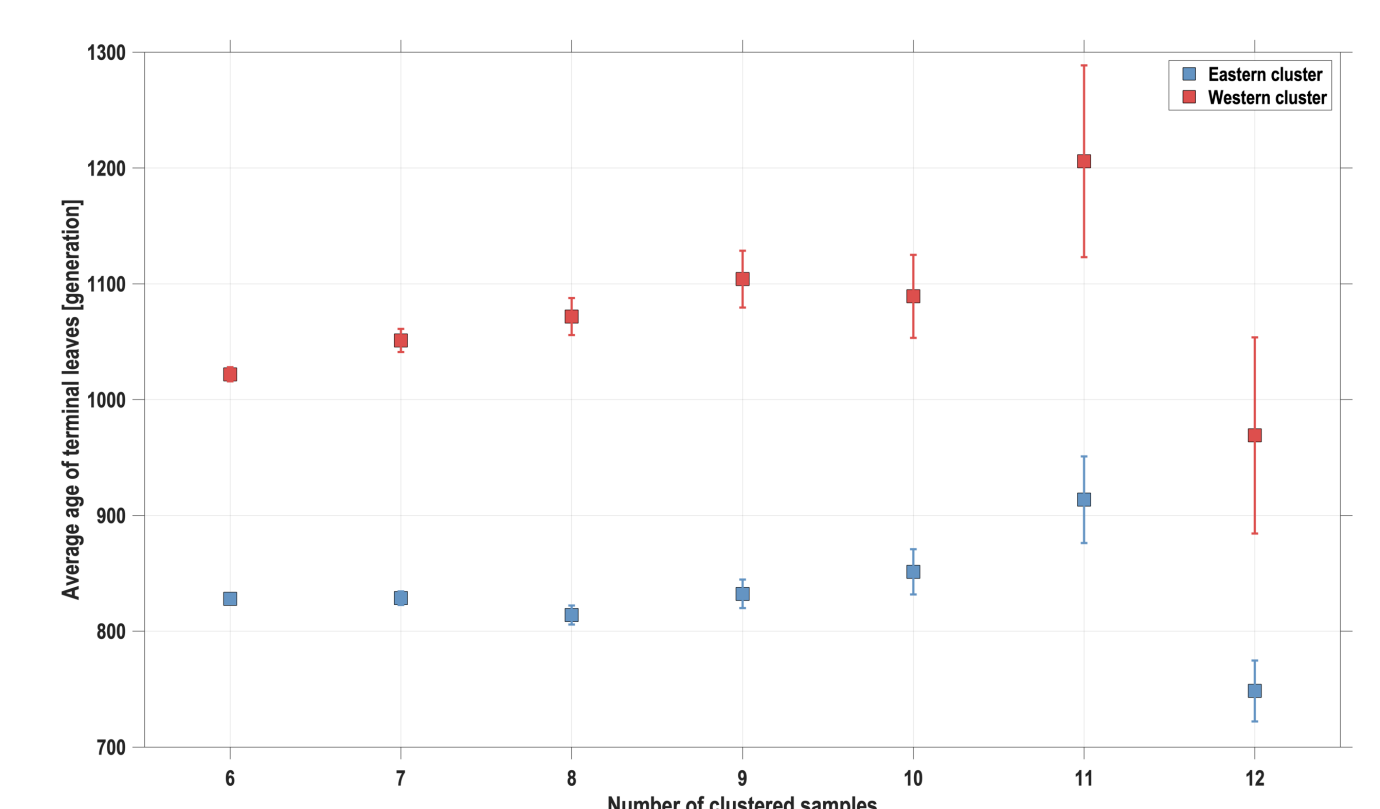
Fig. 3. Example of local tree, with a sub–tree of 11 Western samples.

Fig. 4. Average age of terminal leaves, per sub-tree size and per cluster. Vertical bars show standard errors.

Conclusions

- Our results are consistent with differential breeding practices reported from the field: population evolving rather in free-range mating (or local trade) in the West *versus* long-distance (presumably commercial) exchanges in the East.

- The Algerian bees nicely illustrate a species ranging from natural to domesticated behaviour.

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