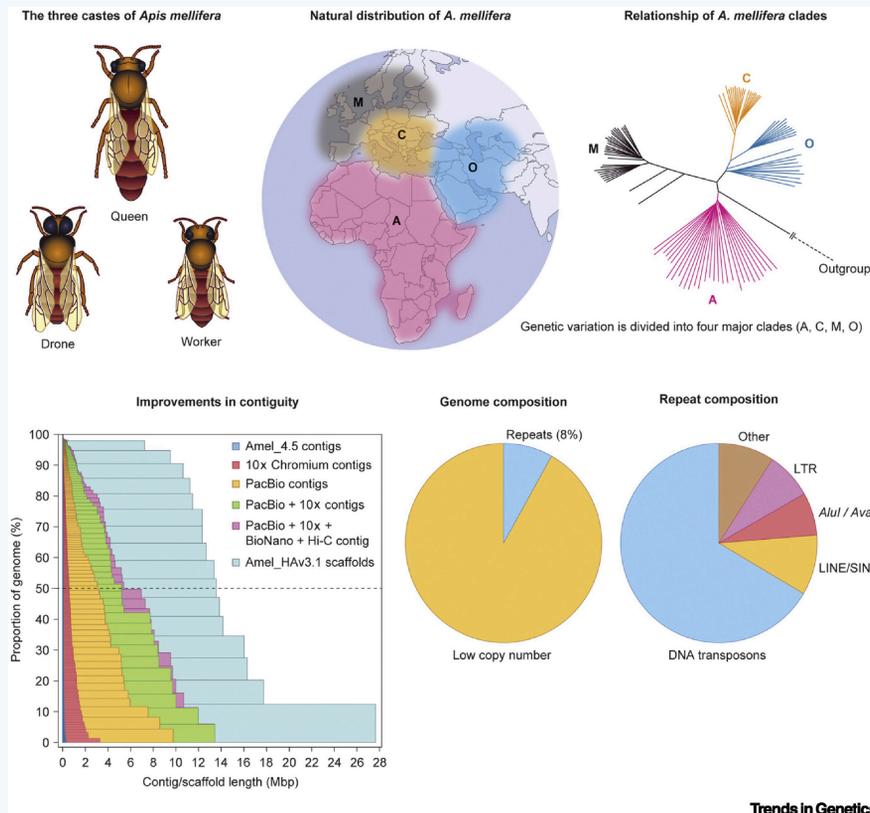


# Apis mellifera

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**GENOME FACTS:**

The genome of *A. mellifera* (~240 Mb) is AT rich and has low repeat content. It also has unexpectedly high CpG content, with the exception of protein-coding sequences.

The rate of meiotic recombination in *A. mellifera* is among the highest observed in any animal (17–26 cM/Mb, or ~20× higher than in humans). Elevated recombination rates appear to be characteristic of social insects.

Honeybees are among the 20% of animal species that have a haplodiploid sex determination system (males are haploid and develop from unfertilised eggs and females are diploid). Honeybees lack sex chromosomes and sex is determined by a single locus.

**SPECIES FACTS:**

Honeybee colonies contain three distinct castes. Each colony contains sterile worker bees, a single reproductive female queen bee, and males called drones, whose sole task is to mate with queens.

Worker bees perform a variety of tasks during their lives. Younger bees remain in the hive, performing tasks such as cleaning, caretaking, guarding, and building honeycomb. Older bees leave the hive and forage for nectar, pollen, and water.

Bees share information about the location of food and water sources with their nestmates by performing a characteristic dance.

*A. mellifera* has a widespread native distribution, which spans Europe, Africa, and the Middle East. Genetic variation within this range can be apportioned into four or five major clades.

The Western honeybee *Apis mellifera* is a species of enormous importance to farming and ecology and occupies a unique place in human culture due to production of honey and other hive products. The honeybee is also an important model organism for studying the genetics of behaviour and cognition, the regulation and maintenance of complex societies, and how species with complex societies evolved. A new genome assembly (Amel\_HAV3.1) was produced using a hybrid approach combining long-read sequencing (PacBio), linked-read sequencing (10x Chromium), optical mapping (BioNano), chromatin conformation capture (Hi-C), and a genetic linkage map. This resulted in a >100-fold improvement in contiguity compared with the previous assembly and each of the 16 chromosomes is now represented by a single scaffold. The new genome will be instrumental in uncovering the molecular mechanisms of disease resistance in honeybees and will allow us to probe the connection between complex phenotypes and genetics in much greater detail.



**TAXONOMY AND CLASSIFICATION**

- KINGDOM:** Animalia
- PHYLUM:** Arthropoda
- CLASS:** Insecta
- ORDER:** Hymenoptera
- FAMILY:** Apidae
- GENUS:** *Apis*

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# Trends in Genetics | Genome of the Month

## Fun facts about the genome

Honeybees in mountains in Africa harbour two megabase-scale chromosomal inversions that appear to govern adaptation to high altitudes. Analysis of structural variants such as inversions is facilitated by the new genome assembly.

## Literature

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