

# A worldwide survey of genome sequence variation provides insight into the evolutionary history of the honeybee *Apis mellifera*

Andreas Wallberg, Fan Han, Gustaf Wellhagen, Bjørn Dahle, Masakado Kawata, Nizar Haddad, Zilá Luz Paulino Simões, Mike H Allsopp, Irfan Kandemir, Pilar De la Rúa, Christian W Pirk & Matthew T Webster

[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

*Nature Genetics* **46**, 1081–1088 (2014) | doi:10.1038/ng.3077

Received 17 January 2014 | Accepted 01 August 2014 | Published online 24 August 2014



Citation



Reprints



Rights & permissions



Article metrics

## Abstract

[Abstract](#) · [Accession codes](#) · [References](#) · [Author information](#) · [Supplementary information](#)

The honeybee *Apis mellifera* has major ecological and economic importance. We analyze patterns of genetic variation at 8.3 million SNPs, identified by sequencing 140 honeybee genomes from a worldwide sample of 14 populations at a combined total depth of 634×. These data provide insight into the evolutionary history and genetic basis of local adaptation in this species. We find evidence that population sizes have fluctuated greatly, mirroring historical fluctuations in climate, although contemporary populations have high genetic diversity, indicating the absence of domestication bottlenecks. Levels of genetic variation are strongly shaped by natural selection and are highly correlated with patterns of gene expression and DNA methylation. We identify genomic signatures of local adaptation, which are enriched in genes expressed in workers and in immune system- and sperm motility-related genes that might underlie geographic variation in reproduction, dispersal and disease resistance. This study provides a framework for future investigations into responses to pathogens and climate change in honeybees.

**Subject terms:** [DNA sequencing](#) · [Population genetics](#)