Evolutionary history of honeybees revealed by genomics

The honeybee (*Apis mellifera*) is of crucial importance for humanity. One third of our food is dependent on the pollination of fruits, nuts and vegetables by bees and other insects. Honeybees face threats from disease, climate change, and management practices. To combat these threats it is important to understand the evolutionary history of honeybees and how they are adapted to different environments across the world.

High-throughput genomics was used to address these questions by researchers at Uppsala University, Sweden, and have identified high levels of genetic diversity in honeybees. In contrast to other domestic species, management of honeybees seems to have increased levels of genetic variation by mixing bees from different parts of the world. The findings also indicate that high levels of inbreeding are not a major cause of global colony losses.

Another unexpected result was that honeybees seem to be derived from an ancient lineage of cavity-nesting bees that arrived from Asia around 300,000 years ago and rapidly spread across Europe and Africa. This stands in contrast to previous research that suggests that honeybees originate from Africa. The evolutionary tree constructed from genome sequences does not support an origin in Africa, this gives us new insight into how honeybees spread and became adapted to habitats across the world. Climatic changes also strongly impacted honeybee populations historically. The researchers also identified specific mutations in genes important in adaptation to factors such as climate and pathogens, including those involved in morphology, behaviour and innate immunity.

The study provides new insights into evolution and genetic adaptation, and establishes a framework for investigating the biological mechanisms behind disease resistance and adaptation to climate, knowledge that could be vital for protecting honeybees in a rapidly changing world.

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