

Chinese scientists decrypt the genetic code of the native bumblebee

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Recently, under the leadership of the Institute of Bee Research of the Chinese Academy of Agricultural Sciences and in cooperation with many domestic and foreign scientific research institutions, the high-quality reference genome sequences of 16 species of domestic bumblebees in China have been drawn for the first time. Based on the sequences, comparative genomics studies have been conducted and the molecular mechanism of bumblebee genome evolution has been revealed. The identification of genes related to the ecological adaptability and behavior characteristics of bumblebees in China. Related research results were published online in "Molecular Biology and Evolution".

According to the researcher Sun Cheng, bumblebees are important pollinators and play a huge role in the pollination of crops grown in greenhouses. They are excellent pollinators of many plants, especially Solanaceae crops. Making use of bumblebees to pollinate crops grown in greenhouses can not only increase yield but also improve fruit quality. At present, the bumblebees identified worldwide include 15 subgenus and about 250 species in total. China is the country with the richest bumblebee species resources in the world, and 125 species have been identified. However, in China, currently, the bumblebees for pollination used by the crops in greenhouses are highly dependent on imported bumblebees, and these introduced bumblebees have risks of biological invasion. Therefore, cultivating native pollinating bumblebee species is of great significance for promoting the green and sustainable development of agriculture in China and maintaining the national ecological environment.

The research team found through the sequencing of the whole genome of these 16 species of bumblebees in China and the comparative genomics study of the whole bumblebee genus, the chromosomal structure of these bumblebees is very stable, and some more chromosomal structural changes only occurred in parasitic bumblebees. Transposons are the main factor to determine the size of the bumblebee genome, and there is evidence shown that transposons are involved in the formation of bumblebee gene coding regions and regulatory regions. The internal structure of bumblebee genes is relatively stable but the boundaries of genes are variable. This is because stop codons of bumblebees cannot effectively terminate protein translation in many cases; the genetic tree of bumblebees should be based on independent genetic trees; the genetic variations related to traits such as bumblebee feeding preference, adaptation to high altitude, insecticide resistance, and external morphology were identified. The research further analyzed the genome sequence of the native bumblebee in China and identified the genetic basis of excellent traits, which can provide a theoretical basis for the breeding of native pollinating bumblebee species in China.

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