

Complete mitochondrial genome of *Apis cerana* (Hymenoptera: Apidae) from two geographical regions: insights into structure and genetic differentiation

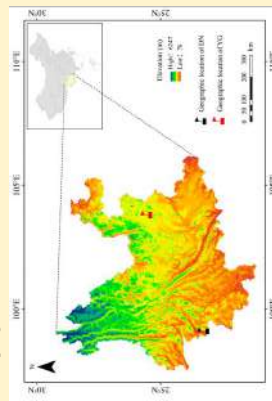
Yuhui Chen, Runlang Su, Rui Zhu, Guiling Ding, Zhanbao Guo, Lin Du, **Jiaxing Huang**
State Key Laboratory of Resource Insects, Institute of Apicultural Research, Chinese Academy of Agricultural Sciences

Introduction

- Honeybee *Apis cerana* as an important pollinator in China.
- Apis cerana* evolved rapidly under diverse ecological environments.
- Apis cerana*-Dianman (DN) and *A. cerana*-Yun-Gui (YG) are two distinguish geographic populations.
- Genetic diversity is fundamental to the conservation and utilization of the local honeybee.
- Mitochondrial DNA is inherited maternally in bees, the mtDNA of a single bee can represent the entire colony.
- The difference of mtDNA genome was used to compare the differentiation of these two geographical populations.

Methods

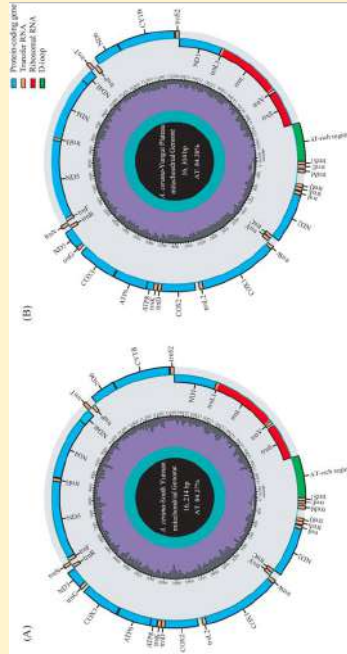
- Sampling site information on DN and YG.



- Sequencing, genome assembly, annotation and phylogenetic analyses.

Mitogenome organization and base composition

- The length of the complete mtDNA for DN was 16214 bp, with an A+T content of 84.27%, while that for YG was 16304 bp, with an A+T content of 84.38%.
- 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and an AT-rich region.



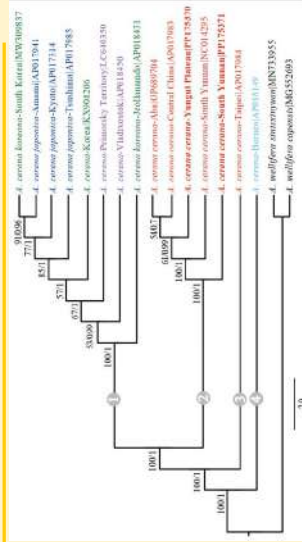
Protein-coding genes

- The total length of the 13 PCGs in both DN and YG was 11,048 bp, accounting for 68.14% and 67.76%, respectively, of the entire mitochondrial genome.
- Except for the A+T content of COXI and COX2 in DN and YG, the A+T content of the other PCGs was greater than 80%, indicating an AT preference.
- The RSCU values for the 13 PCGs were greater than 1, except for those of the two amino acids Met and Trp, which were encoded by only one codon.
- Codons with an A at the third position were the most frequent.

Transfer RNAs and Ribosomal RNAs

- The typical set of 22 tRNAs was scattered throughout each circular, double-stranded DNA molecule, ranging from 60 bp for trnS1 to 78 bp for trnP.
- The total tRNA lengths in DN and YG were 1486 bp and 1487 bp.
- The tRNA A+T% was 87.28% for DN and 87.35% for YG.
- Both large ribosomal RNA and small ribosomal RNA were located on the N chain, and the lengths of the 16S rRNAs and 23S rRNAs were 1322 bp and 773 bp.

Phylogenetic analysis



Conclusion

- Apis cerana* with different geographic distributions exhibit genetic diversity at the mitochondrial genome level.
- A large fragment was found to be inserted or deleted in the A-T-rich region, shedding light on the genetic differentiation of *A. cerana* in different ecological environments.

Complete Mitochondrial Genome of *Apis cerana* (Hymenoptera: Apidae) from Two Geographical Regions: Insights into Structure and Genetic Differentiation

Chen Yuhui¹, Su Runlang², Zhu Rui¹, Ding Guiling¹, Guo Zhanbao¹, Du Lin³, Huang Jiaying¹

¹State Key Laboratory of Resource Insects, Key Laboratory for Insect-Pollinator Biology of the Ministry of Agriculture and Rural Affairs, Institute of Apicultural Research, Chinese Academy of Agricultural Sciences, Beijing 100093, China;

²College of Animal Science and Technology, Yunnan Agricultural University, Kunming 650201, China

³Guizhou Livestock and Poultry Genetic Resources Management Station, Guiyang 550000, China;

The honeybee *Apis cerana* is an important pollinator that is distributed across most regions in China. Mitochondrial DNA (mtDNA) is inherited maternally in bees; therefore, the mtDNA characteristics of a single bee can represent those of the entire colony. Comparing the mitochondrial genomes of *A. cerana* from different geographic regions via third-generation sequencing technology could provide insights into species differentiation and enable the identification of stable molecular markers to distinguish among geographically distinct populations. Here, we determined the complete mitochondrial genomes of the *Apis cerana*-Diannan and *Apis cerana*-Yun-Gui Plateau populations by using PacBio HiFi sequencing technology. The *A. cerana*-Diannan and *A. cerana*-Yun-Gui Plateau mitochondrial genome lengths were 16,214 and 16,304 bp, respectively. Both *A. cerana* mitochondrial genomes contained 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), 2 ribosomal RNAs (rRNAs) and an AT-rich region. The relative synonymous codon usage (RSCU) values for 13 PCGs were greater than 1. The length of the AT-rich region of *A. cerana* in different regions was different. Phylogenetic analyses revealed that these two geographically distinct *A. cerana* populations belong to the same phylogenetic branch, but the genetic distance between DN and YG is further than that between YG and *A. cerana*-Aba and *A. cerana*-Central China. Overall, *A. cerana* with different geographic distributions exhibit genetic diversity at the mitochondrial genome level. A large fragment was found to be inserted or deleted in the AT-rich region, shedding light on the genetic differentiation of *A. cerana* in different ecological environments.