

MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of *Calliptamus abbreviatus* Ikovnnikov (Orthoptera: acridoidea)

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ABSTRACT

Calliptamus abbreviatus Ikovnnikov (Orthoptera: Acridoidea) is one of the important pests in the grasslands in northern China. The complete mitochondrial genome of this insect was sequenced. This genome is 16,615 bp long, with an AT content of 73.3%, containing 37 typical animal mitochondrial genes and an AT-rich region. All 13 PCGs share the start codon ATN, and the usual termination codons (TAA) are found from 13 protein-coding genes. All of the 22 typical animal tRNA genes were found in *C. abbreviatus* mt-genome, and most of the tRNAs could be folded into the classic cloverleaf secondary structure except for tRNA-Ser (AGN), which lacks the dihydrouracil (DHU) stem. The sizes of the large and small ribosomal RNA genes are 1555 and 799 bp long, respectively. The AT content of the AT-rich region is 87.0%. Phylogenetic analysis supports that the coleopteran insects from the same family cluster in the same group.

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Calliptamus abbreviatus (Ikovnnikov) (Orthoptera: Acridoidea) is one of the most dominant important grasshopper species in the grasslands in northern China. In this paper, we report on the complete mitogenome sequence of *C. abbreviatus* and describe the complete mitochondrial genome sequence of *C. abbreviatus* and analyze their structure.

The adult specimen of *C. abbreviatus* was collected from Duolun, Inner Mongolia, China, on July 2015 and stored at -80°C in Institute of Grassland Research of CAAS, Hohhot, China (no accession number). Eighteen pairs of PCR primers were used to amplify the overlapping segments of its entire mitogenome. Purification products were later sequenced by Sangon Biological Engineering Technique & Service, Co. Ltd (www.sangon.com). Nucleotide composition and codon usage were analyzed with MEGA 5.0 (MEGA Inc, Englewood, NJ) (Tamura et al. 2011). Sequence files were assembled into contigs in DNAMAN (Lynnon Biosoft Inc, San Ramon, CA). Transfer RNA analysis was conducted using tRNAscan-SE version 1.21 (University of California, Santa Cruz, CA) (Lowe & Eddy 1997). Only a few of tRNA genes that could not be detected by tRNAscan-SE were identified by RNAstructure version 5.3 (University of Rochester Medical Center, Rochester, NY). The AT-rich region and ribosomal RNA genes were determined by sequence comparison with published grasshopper mitochondrial sequences (Ma et al. 2009). Strand asymmetry was calculated using the formulas: $\text{AT skew} = [A - T]/[A + T]$ and $\text{GC skew} = [G - C]/[G + C]$ (Perna & Kocher 1995).

The mitogenome is a circular molecule of 16,615 bp long and had been deposited in GenBank with an accession num-

ber of KX289321. The sequence analysis reveals that the typical gene content found in arthropod mitogenomes consist of 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes and the AT-rich region. Gene overlaps in the mitogenome of *C. abbreviatus* in a total 43 bp in 8 locations with 1–8 bp length. The longest overlap occurs between trnW and trnC, and between trnY and COI. The mitogenome has 21 intergenic spacers in a total of 107 bp, with length varying from 1 to 21 bp. The longest intergenic spacer occurs between trnS and ND1. The AT content of all 13 PCGs is 72.7% in *C. abbreviatus* mitogenome. The nucleotide skew statistics of PCGs show that the J-strand PCGs (AT-skew = 0.01, GC-skew = -0.16) were much less AT and GC-skewed than the N-strand PCGs (AT-skew = -0.38 , GC-skew = 0.23). All 13 PCGs share the start codon ATN which include ATG (ND2, COII, ATP6, COIII, ND4, ND4L, ND6 and CytB), ATT (ND3 and ND5), ATA (ND1) and ATC (COI and ATP8). The mitochondrial PCGs take TAA (ND2, ATP6, COIII, ND4, ND4L, ND6, CytB, COII, ND3, COI and ATP8) and TAG (ND5 and ND1) as termination codons. All 22 tRNA genes were found in *A. rhodopa* mitogenome, ranging from 65 to 71 bp. Most of the tRNAs could be folded into the classic cloverleaf secondary structure except for tRNA-Ser (ANG), which lack the dihydrouracil (D) stem. The lengths and AT content of two rRNA were determined to be 1555 and 799 bp, and 76.4% and 72.3%, respectively. The 441 bp-long AT-rich region was located between rrnS and tRNAIle genes with 87.0% AT content.

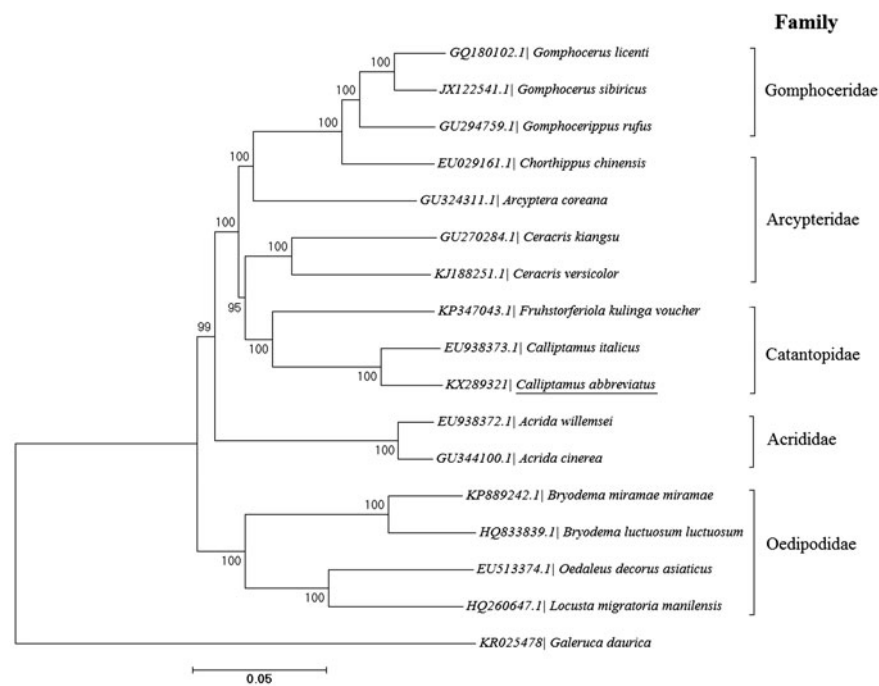


Figure 1. Neighbour-joining estimation of the phylogenetic relationship among species from Orthoptera. Tree based on 13 complete protein coding gene sequence from complete mitochondrial genome sequences. *Galeruca daurica* (Coleoptera: Chrysomelidae) was used to root the tree.

Phylogenetic analysis (Figure 1) supports that the Acridoidea insects from the same family cluster in the same group, and Oedipodidae are basal to the other families in the Acridoidea.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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