

# Complete mitochondrial genome of *Rhaphidophora duxiu* (Orthoptera: Rhaphidophoridae: Rhaphidophorinae)

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**ABSTRACT** We present the complete mitochondrial genome of *Rhaphidophora duxiu* from China. The mitogenome of *R. duxiu* is circular, AT-rich (75.3%), and 15,898 bp in length. It comprises 13 protein-coding genes, 2 ribosomal RNA genes, and 22 transfer RNA genes. It is identical in gene content to *Rhaphidophora quadrispina*.

**KEYWORDS** mitogenome, China, Rhaphidophorinae

The raphidophorid subfamily Rhaphidophorinae, is a completely wingless taxon in Orthoptera, distributed from South Asia to Australia (1). In China, the subfamily is poorly understood. *Rhaphidophora duxiu* was first reported from Guangxi, China (2). It is a polyphagous species and often appears at night. To contribute to the phylogenomics of Rhaphidophorinae, the complete mitochondrial genome of *R. duxiu* from Guangxi was assembled and annotated.

The specimen of *R. duxiu* analyzed here was collected from Cenwanglaoshan, Tianlin, Guangxi, China (24.4897 N 106.4019 E). The voucher specimen was stored in absolute ethyl alcohol at  $-4^{\circ}\text{C}$  in the College of Life Sciences, Guangxi Normal University (GXNU). Total genomic DNA was extracted from the muscle tissues of the hind leg using the TIANamp Genomic DNA Kit (TIANGEN) following the instructions and sent to Beijing Berry Genomics Co., Ltd. for high-throughput sequencing. The 150-base-pair paired-end library was constructed with the MGIEasy Kit (MGI) as well as sequenced on an Illumina NovaSeq 6000 (Illumina Inc.). The raw data were processed with fastp v.0.20.0 (3), by trimming adapters and primers, filtering reads with phred quality  $<Q5$  and filtering reads with N base number  $>3$ . The sequencing generated 23,054,251 reads that were filtered. The number of reads listed is after QC. The entire mitochondrial genome sequence was assembled by NOVOPlasty 4.3.5 (4) using type mito, genome range 14,000–18,000, kmer 39, max memory 16, extended log 0, and *Rhaphidophora quadrispina* (NC067624) as reference sequence. A single *R. duxiu* mitochondrial contig with 191 $\times$  coverage was identified by Quast 5.2.0 using the default settings (5). The mitochondrial genome start position was adjusted to correspond with *Rhaphidophora quadrispina*. The annotation was performed on the MITOS webserver (6). Gene start and stop positions were confirmed by comparison to 33 complete mitochondrial genomes of Rhaphidophoroidea in GenBank and using standard, universally accepted initiation and termination codons as defined in the invertebrate mitochondrial genetic code (7, 8). Nucleotide identities were calculated by BLAST 2.15.0+ search using the default settings (9).

The complete circular mitochondrial genome of *R. duxiu* is 15,898 bp in length and has an AT bias of 75.3% (GenBank accession number PP953500). The GC content is 24.7%. The complete mitogenome contains 37 genes including 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, and a control region (D-loop) (Fig. 1). Except ND1 started with TTG, the other protein-coding genes initiate with ATN (Table 1). The TAA termination codon is found in all genes except ND1 (TAG), ATP8, and ND4 (T,

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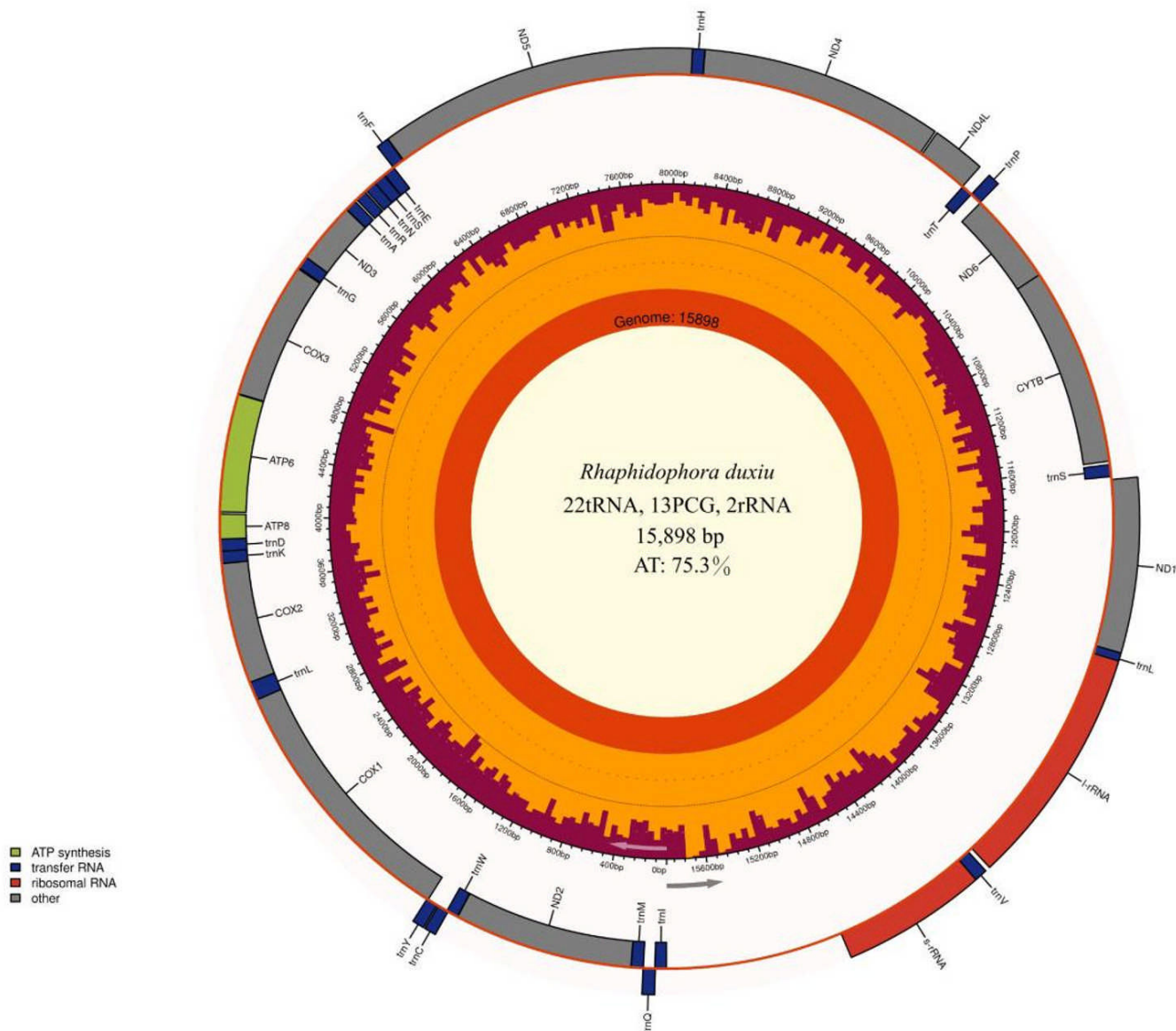
The authors declare no conflict of interest.

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**FIG 1** The complete mitochondrial genome map of *Rhaphidophora duxiu*. The genome was annotated using MITOS webserver and mapped with Chloroplot 0.2.4 (12). The innermost ring displays the GC content and direction of transcription, as indicated by the two arrows. The final ring shows the genes. Genes transcribed clockwise are on the inside, while counterclockwise transcriptions are on the outside. The color coding corresponds to genes of different groups as listed in the key in the bottom left.

stop codon is completed by the addition of 3' A residues to the mRNA, as is common in animal mitochondrial genomes [10, 11]). The entire mitochondrial genome sequence of *R. duxiu* is 85.86% similar to the genome of *R. quadrispina* from China.

TABLE 1 Annotation and gene organization of the *Rhaphidophora duxiu*

| Gene     | Type | Minimum nucleotide position | Maximum nucleotide position | Length | Start codon    | Stop codon | Direction |
|----------|------|-----------------------------|-----------------------------|--------|----------------|------------|-----------|
| tRNA-Ile | tRNA | 1                           | 67                          | 67     | — <sup>a</sup> | —          | Forward   |
| tRNA-Gln | tRNA | 64                          | 133                         | 70     | —              | —          | Reverse   |
| tRNA-Met | tRNA | 132                         | 202                         | 71     | —              | —          | Forward   |
| ND2      | CDS  | 203                         | 1,231                       | 1,029  | ATG            | TAA        | Forward   |
| tRNA-Trp | tRNA | 1,233                       | 1,301                       | 69     | —              | —          | Forward   |
| tRNA-Cys | tRNA | 1,293                       | 1,357                       | 65     | —              | —          | Reverse   |
| tRNA-Tyr | tRNA | 1,366                       | 1,432                       | 67     | —              | —          | Reverse   |
| COX1     | CDS  | 1,425                       | 2,966                       | 1,542  | ATT            | TAA        | Forward   |
| tRNA-Leu | tRNA | 2,976                       | 3,042                       | 67     | —              | —          | Forward   |
| COX2     | CDS  | 3,043                       | 3,735                       | 693    | ATT            | TAA        | Forward   |
| tRNA-Lys | tRNA | 3,736                       | 3,806                       | 71     | —              | —          | Forward   |
| tRNA-Asp | tRNA | 3,805                       | 3,873                       | 69     | —              | —          | Forward   |
| ATP8     | CDS  | 3,874                       | 4,017                       | 144    | ATA            | T          | Forward   |
| ATP6     | CDS  | 4,029                       | 4,703                       | 675    | ATA            | TAA        | Forward   |
| COX3     | CDS  | 4,707                       | 5,495                       | 789    | ATG            | TAA        | Forward   |
| tRNA-Gly | tRNA | 5,502                       | 5,573                       | 72     | —              | —          | Forward   |
| ND3      | CDS  | 5,574                       | 5,927                       | 354    | ATT            | TAA        | Forward   |
| tRNA-Arg | tRNA | 5,930                       | 5,995                       | 66     | —              | —          | Forward   |
| tRNA-Ala | tRNA | 6,008                       | 6,072                       | 65     | —              | —          | Forward   |
| tRNA-Asn | tRNA | 6,083                       | 6,149                       | 67     | —              | —          | Forward   |
| tRNA-Ser | tRNA | 6,149                       | 6,216                       | 68     | —              | —          | Forward   |
| tRNA-Glu | tRNA | 6,219                       | 6,286                       | 68     | —              | —          | Forward   |
| tRNA-Phe | tRNA | 6,284                       | 6,352                       | 69     | —              | —          | Reverse   |
| ND5      | CDS  | 6,355                       | 8,088                       | 1,734  | ATT            | TAA        | Reverse   |
| tRNA-His | tRNA | 8,088                       | 8,155                       | 68     | —              | —          | Reverse   |
| ND4      | CDS  | 8,156                       | 9,476                       | 1,321  | ATA            | T          | Reverse   |
| ND4L     | CDS  | 9,488                       | 9,781                       | 294    | ATG            | TAA        | Reverse   |
| tRNA-Thr | tRNA | 9,783                       | 9,848                       | 66     | —              | —          | Forward   |
| tRNA-Pro | tRNA | 9,848                       | 9,915                       | 68     | —              | —          | Reverse   |
| ND6      | CDS  | 9,918                       | 10,445                      | 528    | ATA            | TAA        | Forward   |
| CYTB     | CDS  | 10,445                      | 11,581                      | 1,137  | ATG            | TAA        | Forward   |
| tRNA-Ser | tRNA | 11,600                      | 11,669                      | 70     | —              | —          | Forward   |
| ND1      | CDS  | 11,686                      | 12,636                      | 951    | TTG            | TAG        | Reverse   |
| tRNA-Leu | tRNA | 12,636                      | 12,704                      | 69     | —              | —          | Reverse   |
| 16S rRNA | rRNA | 12,681                      | 13,997                      | 1,317  | —              | —          | Reverse   |
| tRNA-Val | tRNA | 14,024                      | 14,095                      | 72     | —              | —          | Reverse   |
| 12S rRNA | rRNA | 14,095                      | 14,884                      | 790    | —              | —          | Reverse   |

<sup>a</sup>—, not applicable.

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## DATA AVAILABILITY

The complete mitochondrial genome sequence of *Rhaphidophora duxiu* is available in GenBank under accession number [PP953500](https://doi.org/10.11646/zootaxa.4683.1.6). The associated BioProject, SRA, and BioSample numbers are [PRJNA1148785](https://doi.org/10.11646/zootaxa.4683.1.6), [SRS22390203](https://doi.org/10.11646/zootaxa.4683.1.6), and [SAMN43221142](https://doi.org/10.11646/zootaxa.4683.1.6), respectively. The mitochondrial genome referenced in the text is *Rhaphidophora quadrispina*. GenBank accession number [NC067624](https://doi.org/10.11646/zootaxa.4683.1.6).

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