

The complete mitochondrial genome of *Schoutedenia ralumensis* Rübсаamen, 1905 (Hemiptera: Aphididae: Greenideinae)

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ABSTRACT

We sequenced the complete mitochondrial genome of *Schoutedenia ralumensis*. The mitogenome is 16,051 bp long with an A + T content of 84.5%, including 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, a control region, and an aphid-specific repeat region located between *trnE* and *trnF*. All protein-coding genes are initiated by ATN and terminated with TAA or TAG except for *cox1* and *nad5*. All transfer RNAs display the typical clover-leaf secondary structure except for *trnS* (*AGN*). The unique repeat region is 974 bp long, in which a 305-bp repeat unit repeats 3.19 times. The phylogenetic tree supports a sister relationship of *S. ralumensis* and *Greenidea psidii*.

ARTICLE HISTORY

Received 7 May 2020
Accepted 9 May 2020

KEYWORDS

Aphids; mitogenome; repeat region; phylogeny

Schoutedenia ralumensis Rübсаamen, 1905 is an aphid species widely distributed in southeastern Asia, India, Africa and Australia. It feeds on the plants of Euphorbiaceae, with a monoecious and partially holocyclic life cycle (Blackman and Eastop 2020). In this study, using Illumina sequencing, we characterize the complete mitochondrial genome of *S. ralumensis*, the first representative from the aphid tribe Schoutedeniini (Aphididae: Greenideinae). The aphid samples were collected on *Breynia fruticosa* from Mt. Wuzhi, Hainan, China (18.9045°N, 109.6820°E) and deposited in the National Zoological Museum of China, Institute of Zoology, Chinese Academy of Sciences, Beijing, China (NZMC no. 24309).

The *S. ralumensis* mitogenome is 16,051 bp long (GenBank accession number MT381994), which comprises 13 protein-coding genes, 22 transfer RNA genes (tRNAs), 2 ribosomal RNA genes (rRNAs), a control region, and a repeat region located between *trnE* and *trnF*. All 37 genes are arranged in the same order as the inferred ancestral arrangement of insects (Clary and Wolstenholme 1985). The overall nucleotide composition is 38.9% T, 9.8% C, 45.6% A and 5.7% G, with an A + T content of 84.5%. All protein-coding genes use the typical ATN start codons and TAA or TAG stop codons except for *cox1* and *nad5*, which end with a single T. The tRNA genes range from 62 to 73 bp in length. All tRNAs exhibit a typical clover-leaf secondary structure except for *trnS* (*AGN*), which losses the dihydrouridine (DHU) arm. The *rrnL* and *rrnS* genes are 1267 and 767 bp in length, with an A + T content of 86.2% and 84.9%, respectively.

The control region located between *rrnS* and *trnI* is 542 bp long with an A + T content of 84.2%. The unique repeat region between *trnE* and *trnF*, which has been found in previously reported mitogenomes of Greenideinae species (i.e. *Greenidea psidii* van der Goot and *Greenidea ficicola* Takahashi) (Chen et al. 2019; Liu et al. 2020), is also present in the mitogenome of *S. ralumensis*. It is 974 bp in length with an A + T content of 85.5%. A 305-bp repeat unit repeats 3.19 times in this region.

Based on the whole mitochondrial genome sequences of *S. ralumensis* and 23 other aphid species, we constructed a maximum-likelihood phylogenetic tree of aphids using RAXML v8.2.10 (Stamatakis 2014). The Greenideinae was recovered as a monophyletic clade with strong support and *S. ralumensis* was firmly placed as a sister to *G. psidii* (Figure 1). The subfamilies Hormaphidinae, Calaphidinae and Aphidinae were all monophyletic, whereas the Eriosomatinae was polyphyletic.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

This work was supported by the National Natural Science Foundation of China [No. 31772492], the Strategic Priority Research Program of the Chinese Academy of Sciences [No. XDA19050303], the Youth Innovation Promotion Association of the Chinese Academy of Sciences [No.

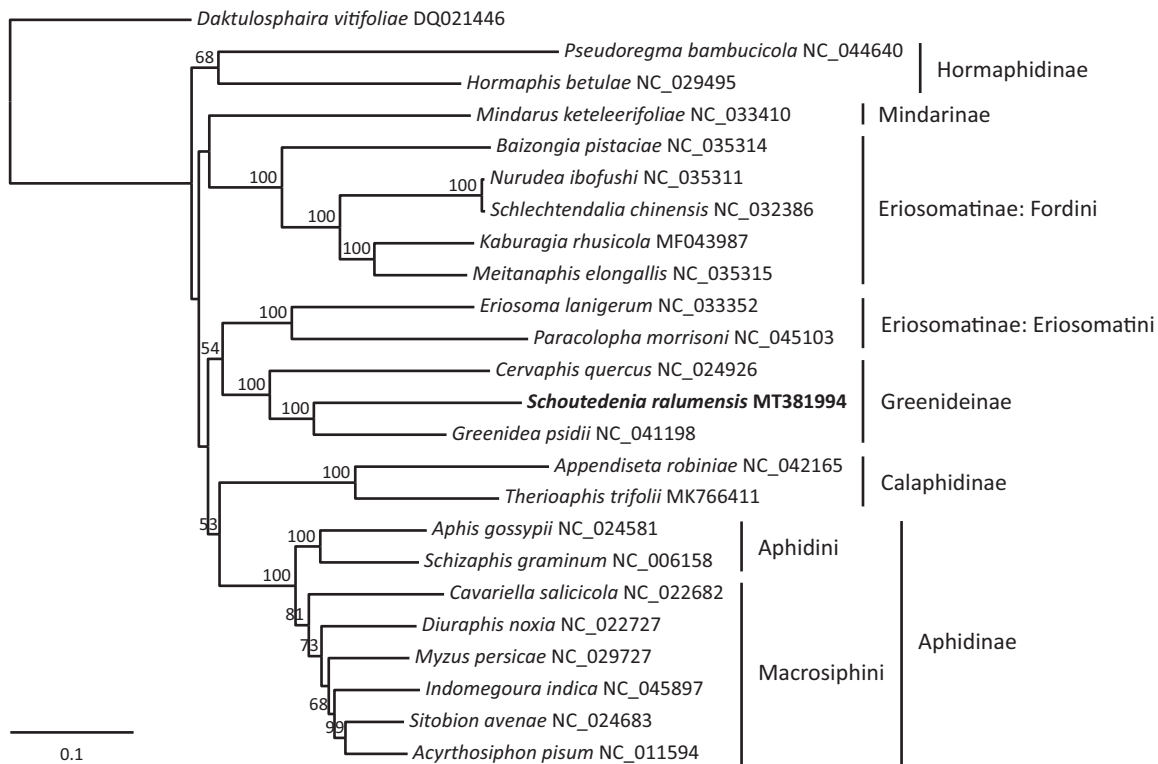


Figure 1. The maximum-likelihood tree inferred from the whole mitochondrial genomes of *Schoutedenia ralumensis* and 23 other aphids. Bootstrap values (>50%) are shown above the branches.

2020087], and the Second Tibetan Plateau Scientific Expedition and Research (STEP) program [No. 2019QZKK0501].

Data availability statement

The data that support the findings of this study are openly available in Dryad at <https://doi.org/10.5061/dryad.dv41ns1vg>.

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