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# Complete mitochondrial genome of the *Rhus* gall aphid *Schlechtendalia chinensis* (Hemiptera: Aphididae: Eriosomatinae)

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**ABSTRACT**

We sequenced the first complete mitochondrial genome for the aphid subfamily, Eriosomatinae, from a *Rhus* gall aphid, *Schlechtendalia chinensis*. The mitogenome of *S. chinensis* is 16,047 bp in length with a high A + T content of 84.2% and consists of 13 protein-coding genes, 24 tRNA genes including two extra $tRNA^{Phe}$, two rRNA genes, a repeat region, and a control region. All protein-coding genes have a typical ATN initiation codon and TAA termination codon except *COI* and *ND4,* which terminate with a single T. All 24 tRNAs have the expected clover-leaf secondary structure and range in size from 62 to 73 bp. The lengths of *rrnL* and *rrnS* genes are 1274 and 772 bp, respectively. The repeat region is 335 bp and is uncommon among known aphid sequences for starting with a $tRNA^{Phe}$. The control region is 705 bp in length and is located between *rrnS* and $tRNA^{Ile}$. We present a phylogeny of mitogenomes showing that *S. chinensis* is sister to Aphidinae.

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*Rhus* gall aphids belong to the subtribe Melaphidina (Aphididae: Eriosomatinae: Fordini) and exhibit alternating sexual and parthenogenetic generations using two distantly related host plants (Remaudière & Remaudière 1997). The primary hosts of the *Rhus* gall aphids are trees of *Rhus* subgenus *Rhus*, and the secondary hosts are mosses. On *Rhus*, the aphids induce the formation of galls, which are valuable as a commercial product (Eastop & Hille Ris Lambers 1976; Zhang et al. 1999; Ren et al. 2013).

In this study, we assembled the complete mitochondrial genome of *Schlechtendalia chinensis* (Bell), which is a representative *Rhus* gall aphid in Melaphidina. We sampled parthenogenetic *S. chinensis* individuals from a gall, which we collected on *Rhus chinensis* in Hubei, China (Wufeng Co., 30°9′30.80″ N, 110°45′ 17.58″ E, altitude 1000 m). We preserved some individuals as a voucher at the School of Life Science, Shanxi University, Taiyuan, China (Voucher no. A1798).

We obtained the mitogenome sequence of *Schlechtendalia chinensis* primarily using primer walking, which comprises standard PCR with short and long primers. We supplemented the primer walking data with contigs from genome skimming generated on the Illumina NextSeq 500 platform (Zimmer & Wen 2015). Our study is the first to report a complete mitogenome of an aphid from subfam. Eriosomatinae and complements ten previously published mitogenomes from other subfamilies (GenBank Accession Nos. were shown in Figure 1).

The complete mitogenome of *Schlechtendalia chinensis* (GenBank Accession No. KX852297) is circular with a length of 16,047 bp. It contains 13 protein-coding genes (PCGs), 24 transfer RNA (tRNA) genes, two ribosomal RNA genes (*rrnL* and *rrnS*), a repeat region, and a control region. All protein-coding genes have typical initiation and termination codons of ATN and TAA, respectively, except *COI* and *ND4*, which terminate with a single T. The single T is an incomplete stop codon, which are frequent in the mitogenomes of insects (Wang et al. 2014). All of the tRNAs exhibit a classic clover-leaf secondary structure, which we predicted with tRNAscan-SE v1.21 and/or RNA structure (Lowe & Eddy 1997; Bellaousov et al. 2013). The mitogenome of *S. chinensis* has a high A + T content of 84.2% (A: 45.1%; T: 39.1%; C: 10.2%; G: 5.6%), which is similar to other aphids (range: 82.8–84.7%; $n = 10$).

In general, the gene content in the *Schlechtendalia chinensis* mitogenome is typical of aphids. However, *S. chinensis* has two extra $tRNA^{Phe}$ for a total of three, each with identical sequences and exhibits a position exchange between one $tRNA^{Gln}$ and $tRNA^{Met}$. The mitogenome of *S. chinensis* also differs from other aphids in the composition of its repeat region by possessing two tandem repeats (335 bp long total), starting with a $tRNA^{Phe}$.

We used the mitogenome of *Schlechtendalia chinensis* to resolve its phylogenetic position as sister to subfamily Aphidinae (Figure 1). We expect that the mitogenome of

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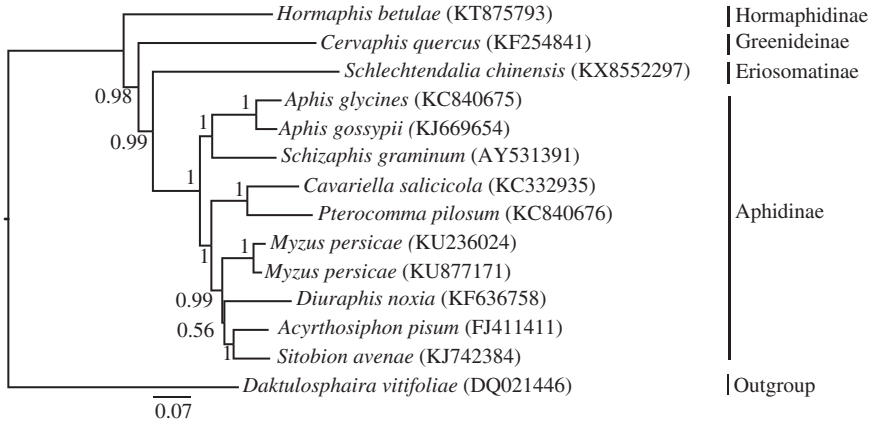


**Figure 1.** Maximum clade credibility tree resulting from a Bayesian phylogenetic analyses was performed in MrBayes v.3.2.5 (Ronquist et al. 2012) for the 13 combined protein-coding genes of mitochondrial genome sequence with gene partitions. We applied GTR + G model parameters to each partition with the gamma distribution of rates approximated by ten categories. We performed two independent, simultaneous runs of the Markov Chain Monte Carlo for 10,000,000 generations starting from different random trees. We applied three hot chains and one cold chain for each run, and sampled the hot chain every 1000 generations. The tree shows posterior probabilities of clades to the left of nodes and Genbank accession numbers and subfamily affiliation to the right of terminals.

*S. chinensis* may be an important resource for resolving phylogenetic relationships within *Rhus* gall aphids and Aphididae as well as understanding the mitochondrial genome evolution in aphids.

## Disclosure statement

The authors have no conflicts of interest to report. The authors alone are responsible for the content and writing of this article.

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