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.

*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 *Schlechtendalia chinensis* in Hubei, China (Wufeng Co., 30°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 subfamily 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\(^{Glu}\)* 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
**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.

**Funding**

This work was supported by the National High Technology Research and Development ‘863’ Program [2014AAA021802]; the National Natural Science Foundation of China, [31170359]; the Hundred-talent Project in Shanxi Province; the Scholarly Studies Program of the Smithsonian Institution, and the Laboratory of Analytical Biology, the Small Grants Program and the Global Genome Initiative of the National Museum of Natural History, Smithsonian Institution.

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