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The complete mitogenome of *Halictus* (*Seladonia*) *aerarius* (Hymenoptera: Halictidae) and phylogenetic analysis

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ABSTRACT

The Halictidae, where the *Seladonia aeraria* belongs, was an important model organism for studying the evolution of insect social behavior. We first sequenced the complete mitochondrial genome (mitogenome) of *Seladonia aeraria*. The mitogenome was 15, 410 bp in length, including 13 protein-coding genes (PCGs), 2 rRNA genes, 22 tRNA genes, and a hypothetical control region. In order to reveal the phylogenetic position of *Seladonia aeraria* form mitogenomic level, we performed phylogenetic analysis of 13 PCGs from 15 species. The results revealed that the genus-level relationship of Halictidae was *Seladonia* + *Lasioglossum* and *Seladonia aeraria* was more closely related to *Seladonia tumulorum* than *Lasioglossum sp. SJW_2017*. The complete mitogenome of *S. aeraria* will provide a basis for further study evolution and phylogenetic analysis of Halictidae.

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Seladonia aeraria; Hymenoptera; mitogenome; phylogeny

Seladonia aeraria (Smith, 1873) was identified as the genus *Halictus* of the family Halictidae based on traditional taxonomy. Halictidae is the world's second largest bee group among Anthophila, and has been found on all continents except Antarctica (Murao et al. 2017). Halictid bees (Halictidae) are model organisms for studying the evolution of social behavior in insects (Danforth et al. 1999). However, due to the lack of molecular data of Halictidae, researchers cannot further understand the evolution and phylogenetic analysis of insect social behavior from the molecular level. In this study, we sequenced the complete mitogenome of *S. aeraria* and enriched the basic data of Halictidae. At the same time, *S. aeraria* was compared with the mitogenomes of other Apoidea, which clarified the phylogenetic position of *S. aeraria* from the molecular level. Our results provide a basis for further study evolution and phylogenetic analysis of Halictidae.

Adult female specimen of *S. aeraria* was collected by the sweeping net method from Shaoyang City, Hunan Province, China (26°21′ N and 110°19′ E, Aug, 2018) and deposited at College of Life Sciences, Chongqing Normal University (https://smkx.cqnu.edu.cn/, 20170054@cqnu.edu.cn) under

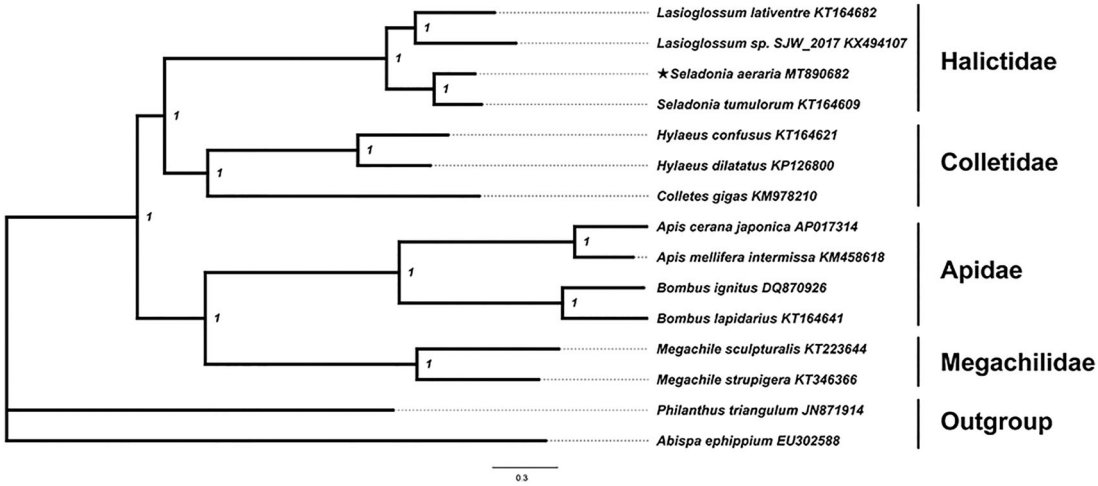

Figure 1. Phylogenetic relationships of *Seladonia aeraria* based on the mitogenome of the 13 PCGs. The right of the species name is the GenBank accession number, which is on the NCBI website [https://www.ncbi.nlm.nih.gov/].

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the voucher number ZK-2019-HA-1. Total genomic DNA of one adult was extracted with the Tissue DNA Kit (Omega Biotek, Norcross, GA, USA). The mitochondrial DNA was fragmented to an average size of 450 bp using the Covaris M220 system (Covaris, Woburn, MA, USA) and used for the library preparation. The library was constructed using the Illumina TruSeq™ Nano DNA Sample Prep Kit (Illumina, San Diego, CA, USA) and sequenced on the platform of Illumina Hiseq 4000 (Illumina, San Diego, CA, USA). The complete nucleic acid sequence was assembled by MITObim v1.7 (Hahn et al. 2013) based on the reference sequence of *Seladonia tumulorum* (Linnaeus, 1758) (Tang et al. 2015) (GenBank acc. no. KT164609). Mitochondrial sequences were annotated using the MITOS web server (Bernt et al. 2013) and by manual proof-reading.

The complete mitogenome of *S. aeraria* is 15, 410 bp in length with 18.1% GC content. It contained 13 PCGs, 22 tRNA, two rRNAs and a hypothetical control region (CR), which was consistent with the general composition of invertebrate mitogenome (Li et al. 2020). The start codons of all PCGs are ATA for *nad2*; ATC for *atp8*; ATG for *atp6*, *cox3*, *cytb*, *nad4*, *nad6* and ATT for *cox1*, *cox2*, *nad1, nad3, nad4L*, *nad5*. *nad4L* and *cytb* ended in TAG as termination codons and other 11 PCGs ended in TAA. The total length of 22 tRNA genes was 1, 444 bp. All tRNAs could form typical cloverleaf structure except *trnS1*. The two rRNA genes contained 16S rRNA (1361 bp) and 12S rRNA (785 bp), which were separated by *trnV*, this phenomenon was common in the mitogenome of Hymenoptera (Lu et al. 2020). The length of CR was 337 bp, of which GC content was 8.0%. Furthermore, the mitogenome had two intergenic regions and nine overlapping regions.

We downloaded 13 mitogenomes of Anthophila and two outgroup species in the nearest family-level, *Abispa ephippium* (Fabricius, 1775) (Hymenoptera: Vespidae) and *Philanthus triangulum* (Fabricius, 1775) (Hymenoptera: Crabronidae) from the NCBI website (Figure 1), and the phylogenetic inference using the 13 protein coding genes was done through PhyloSuite v1.2.2 (Zhang et al. 2019). FigTree v1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/) to visualize the phylogenetic tree. The results indicate that Halictidae, Colletidae, Apidae and Megachilidae families were a monophyletic group with high support (Figure 1). The phylogenetic relationship of Anthophila was (Apidae + Megachilidae) (long-tongued bees) and (Halictidae + Colletidae) (short-tongued bees), which was consistent with previous phylogenetic studies about Anthophila (Lu et al. 2021). *S. aeraria* and *S. tumulorum* formed a group (genus *Seladonia*), which was close to *Lasioglossum sp. SJW_2017* (genus *Lasioglossum*). The genus-level relationship of Halictidae was *Seladonia* + *Lasioglossum* and the monophyly of each genus is highly supported in this study. The complete mitogenome of *S. aeraria* will provide a basis for further study evolution and phylogenetic analysis of Halictidae.

Disclosure statement

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

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MT890682. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA698285, SRR13590458, and SAMN17711357, respectively.

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