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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome sequence of the hawkmoth, *Dahira obliquifascia* (Lepidoptera: Sphingidae) and phylogenetic analysis

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ABSTRACT

In this study, we sequenced and analyzed the complete mitogenome *Dahira obliquifascia* to compare mitogenomic structures and reconstruct phylogenetic relationships. The complete mitogenome sequence of *D. obliquifascia* is circular, 15,939 bp in size and encodes 13 protein-coding genes (PCGs), 2 ribosomal RNA genes (rRNA), 22 transfer RNA genes (tRNA) and a control region (CR). Nucleotide composition is highly biased toward A + T nucleotides (80.3%). All 13 protein-coding genes (PCGs) initiate with the standard start codon of ATN and terminate with the typical stop codon TAA/TAG. Phylogenetic analyses were performed using 13 protein coding genes (PCGs) showed that *D. obliquifascia* is closely related to *Theretra oldenlandiae*.

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Sphingidae; mitochondrial genome; phylogenetic

Dahira obliquifascia Hampson, 1910 (Lepidoptera: Sphingidae) is a kind of hawkmoth which is widely distributed in Southeast Asia. The mitogenome sequence of *D. obliquifascia* so far remains unknown. Therefore, we sequenced the complete mitochondrial DNA genome of *D. obliquifascia* to provide more comprehensive data for this species and reconstructed the phylogenetic relationship of Sphingidae.

Dahira obliquifascia was collected from the Menghai County, Yunnan Province, China (100°03′24″, 21°41′53″), April 17 of 2021, specimens and DNA were deposited in the Entomological Museum, College of Life Sciences, Anhui Normal University (https://www.ahnu.edu.cn/, YX, Huang, huangyx@ahnu.edu.cn) under the accession no. YN20210418. All animal-related experiments were performed according to the protocols approved by the Institutional Animal Care and Use Committee of Anhui Normal University (Grant number AHNU-ET2021032). A whole genome shotgun (WGS) strategy was used after the exacted total DNA was quantified. Illumina Novaseq S6000 platform was employed for sequencing with a strategy of 150 paired-ends (PE) (Andrews 2020). The raw paired reads were quality-trimmed and assembled into the complete circular mitogenome in Novoplasty 2.7.2.

The mitogenome sequence data of *D. obliquifascia* is available in the GenBank (https://www.ncbi.nlm.nih.gov/) under the accession number MZ343807. The mitogenome of *D. obliquifascia* is 15,939 bp in size and includes 13 PCGs, 22 tRNAs, 2 rRNAs and a control region (Cameron 2014). The composition of *D. obliquifascia* is similar to many insect mitogenomes reported previously. *D. obliquifascia* mitochondrial genomes had a total length of 15,939, which were typical double-chain circular molecular structures. The average nucleotide composition of overall base composition of the mitogenome was A: 41.3%, T: 39%, C: 12.4% and G: 7.3%. The nucleotide composition of all the mitogenomes had a high A + T content, with an average of 80.3%, showing a strong A/T bias. In *D. obliquifascia*, 24 genes (15 tRNAs and nine PCGs) were encoded by the majority-strand (J-strand) and 13 genes (4 PCGs, 2 rRNAs and 7 tRNAs) were encoded by the minority- strand (N-strand). Among the 13 PCGs in the *D. obliquifascia* mitogenome, 9 PCGs (*nad2, nad3, nad6, cox1, cox2, cox3, atp6, atp8,cytb*) are encoded by the J strand, while the other 4 PCGs are encoded on the N strand. All 13 PCGs start with ATN and stop with traditional TAA or TAG codons, which is similar to most other insect mitogenomes (Crozier and Crozier 1993; Korkmaz et al. 2015).

Tweenty six Sphingidae species were selected to reconstructed the phylogeny of Sphingidae. Each protein coding genes were aligned by MAFFT (Katoh et al. 2005). W-IQ-Tree web server was used to reconstruct the phylogeny under the ML (maximum-likelihood) method (Trifinopoulos et al. 2016). The result was clearly exhibited that all the subfamilies of Sphingidae were monophyly, which was in accordance with previous study (Wang et al. 2021). Smerinthinae was the most derived group in Sphingidae, and the most closely related with Sphinginae (Figure 1). Macroglossinae was recovered as sister to the clade formed by Smerinthinae and

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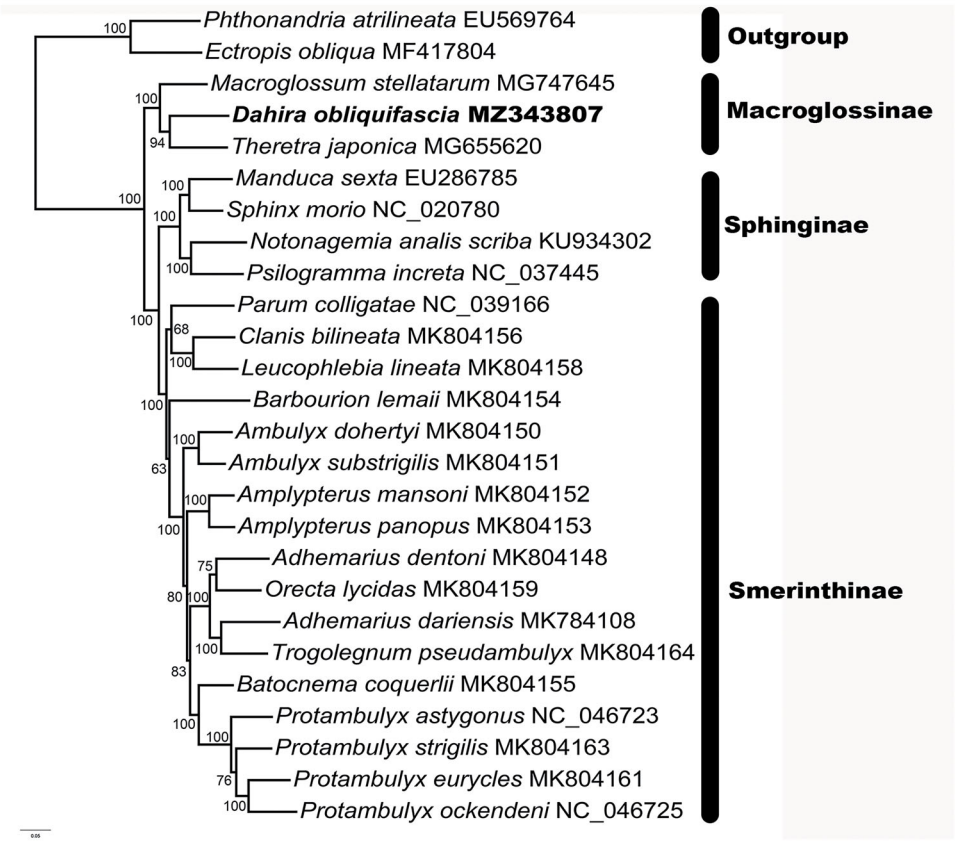

Figure 1. Phylogenetic relationships within Sphingidae based on 13 protein-coding genes were performed using ML methods.

Sphinginae. In Macroglossinae, *Macroglossum stellatarum* was first diverged. *D. obliquifascia* is closely related to *Theretra oldenlandiae*.

Credit authorship statement

Li-Qing Qi: methodology, writing – original draft. **Hong Zhang**: methodology. **Xu Wang**: conceptualization, funding acquisition. **Yi-Xin Huang**: conceptualization, funding acquisition. All authors agree to be accountable for all aspects of the work.

Disclosure statement

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

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Data availability statement

The data that support the findings of this study are openly available in GenBank at https://www.ncbi.nlm.nih.gov/genbank/, reference number MZ343807. The associated BioProject, Bio-Sample numbers, and SRA are PRJNA735332, SAMN19579703, and SRR14741682, respectively.

References

Andrews S. 2020. FastQC: a quality control tool for high throughput sequence data. http://www.bioinformatics.babraham.ac.uk/projects/fastqc [accessed 2020 Jul 10].

Cameron SL. 2014. Insect mitochondrial genomics: implications for evolution and phylogeny. Annu Rev Entomol. 59:95–117.

Crozier RH, Crozier YC. 1993. The mitochondrial genome of the honeybee *Apis mellifera*: complete sequence and genome organization. Genetics. 133(1):97–117.

Katoh K, Kuma KI, Toh H, Miyata T. 2005. MAFFT version 5: improvement in accuracy of multiple sequence alignment. Nucleic Acids Res. 33(2): 511–518.

Korkmaz EM, Doğan Ö, Budak M, Başıbüyük HH. 2015. Two nearly complete mitogenomes of wheat stem borers, *Cephus pygmeus* (L.) and *Cephus sareptanus* Dovnar-Zapolskij (Hymenoptera: Cephidae): An unusual elongation of *rrnS* gene. Gene. 558(2): 254–264.

Trifinopoulos J, Nguyen L-T, Von Haeseler A, Minh BQ. 2016. W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Res. 44(W1):W232–W235. doi:10.1093/nar/gkw256.

Wang X, Zhang H, Kitching I, Xu ZB, Huang YX. 2021. First mitogenome of subfamily Langiinae (Lepidoptera: Sphingidae) with its phylogenetic implications. Gene. 789:145667.