

Complete mitochondrial genome of *Pterodecta felderi* (Lepidoptera: Callidulidae)

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ABSTRACT

We report the mitochondrial genome (mitogenome) of *Pterodecta felderi* (Callidulidae: Lepidoptera), which is the first mitogenome sequences in the family Callidulidae, a monotypic family in the superfamily Calliduloidea. The 15,340-bp long complete mitogenome consists of a typical set of genes (13 protein-coding genes [PCGs], 2 rRNA genes, and 22 tRNA genes) and 1 major non-coding A + T-rich region, which are arranged in a way that is frequently observed in Lepidoptera. Of the 13 PCGs, 12 *P. felderi* start with ATN, except for COI, which starts with CGA. The *P. felderi* mitogenome consists of 210-bp long intergenic-spacer sequences and 27-bp long overlaps. Phylogenetic analysis of superfamilial relationships in the lepidopteran clade Obtectomera with concatenated sequences of the 13 PCGs and 2 rRNA genes using the Bayesian inference method showed that Calliduloidea, which is only represented by *P. felderi*, was placed as the most basal lineage about Macroheterocera (Lasiocampoidea, Bombycoidea, Mimallonoidea, Noctuoidea, and Drepanoidea), Papilionoidea, and Pyraloidea.

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Pterodecta felderi Bremer, 1864 belongs to the monotypic family Callidulidae in the lepidopteran superfamily Calliduloidea. The species is distributed in Korea, southeastern Siberia, China, Taiwan, and Japan, and is found casually in mountainous regions of Korea (Shin 2001). Adults fly during the daytime in the spring and summer, and, at first glance, the shape and color appear to be similar to that of *Libythea lepita*, which belongs to the subfamily Libytheinae (snout butterflies) of the lepidopteran family Nymphalidae (Shin 2001). Up to now, no mitochondrial genome (mitogenome) of Callidulidae has been reported; despite the family is one of the essential taxa for phylogenetic reconstruction in Lepidoptera. Thus, in this study, we sequenced the complete mitogenome of the *P. felderi* that would be helpful for subsequent lepidopteran phylogeny by adding previously unavailable lepidopteran family.

Two legs of *P. felderi* adult were obtained from the tissue stocks preserved in Genetic Resources Bank of the National Institute of Biological Resources (NIBR), Ministry of Environment (MOE) of the Republic of Korea (NIBRGR0000073718). The collection information is as follows: Hwaya Mountain, Seorak-myeon, Gapyeong-gun, Gyeonggi-do Province, South Korea (37°41'22.4" N, 127°24'26.6" E). DNA was extracted using the Wizard Genomic DNA Purification Kit, in accordance with the manufacturer's instructions (Promega, Madison, WI), and the remaining DNA was stored at Chonnam National University, Gwangju, Korea, under the accession number CNU12053. Using Lepidoptera-specific primers (Kim et al. 2012), three overlapping long

fragments (LFs; COI to ND4, ND5 to IrRNA, and IrRNA to COI) were amplified. These LFs were then used as templates for the amplification of 26 short fragments using Lepidoptera-specific primers (Kim et al. 2012). Sequencing was performed for both strands by Sanger's method.

Phylogenetic analysis using the nucleotide sequences of 13 protein-coding genes (PCGs) and two rRNA genes (12,514 bp) was performed for 10 species of Obtectomera including *P. felderi*, along with one species from Gelechioidea that was used as an outgroup (*Mesophleps albilinella*). Bayesian inference (BI) method implemented in CIPRES Portal version 3.1 (Miller et al. 2010) was conducted using MrBayes version 3.2.2 (Ronquist et al. 2012). An optimal substitution model (GTR + G, GTR + I + G, TVM + I + G) was determined using PartitionFinder 2 and Greedy algorithm (Lanfear et al. 2012, 2014, 2016).

The *P. felderi* mitogenome is 15,340 bp in length, with typical sets of genes (2 rRNA genes, 22 tRNA genes, and 13 PCGs) and a 400-bp long major non-coding A + T-rich region (GenBank accession number MT370823). The gene arrangement of *P. felderi* is identical to that of most lepidopteran species, and consists of the order tRNA^{Met}-tRNA^{Ile}-tRNA^{Gln} between the A + T-rich region and ND2 (Kim et al. 2010). This arrangement is different from that found in the ancient lepidopteran superfamilies like Hepialoidea (Timmermans et al. 2014) and Nepticuloidea (Cao et al. 2012) and from that of the ancestral arrangement found in the majority of insects (Boore 1999). The overall A/T nucleotide composition of the *P. felderi* mitogenome was as follows: 79.33% in the whole

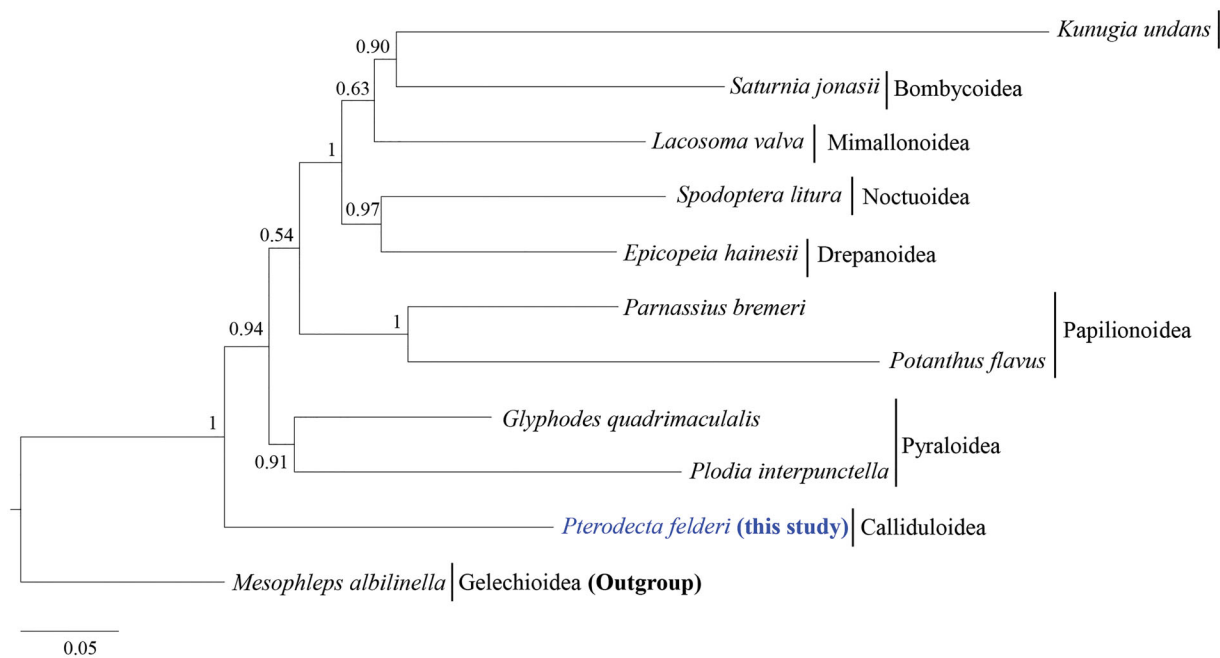


Figure 1. Phylogenetic tree of Obtectomera. Bayesian inference (BI) method was used for phylogenetic analysis based on the concatenated 13 PCGs and 2 rRNA genes (12,514 bp) using three partition schemes. The numbers at node indicate the Bayesian posterior probabilities (BPPs) determined by the BI method. The scale bar indicates the number of substitutions per site. *Mesophleps albilinella* belonging to Gelechioidea (KU366707; Park et al. 2016) was utilized as the outgroup. GenBank accession numbers are as follows: *Pterodecta felderi*, MT370823 (This study); *Spodoptera litura*, JQ647918 (Wan et al. 2013); *Saturnia jonasii*, MF346379 (Kim et al. 2018); *Kunugia undans*, KX822016 (Kim et al. 2017); *Glyphodes quadrimaculalis*, KF234079 (Park et al. 2015); *Plodia interpunctella*, KP729178 (Liu et al. 2016); *Parnassius bremeri*, FJ871125 (Kim et al. 2009); *Potanthus flavus*, KJ629167 (Kim et al. 2014); *Lacosoma valva*, KJ508050 (Timmermans et al. 2014); and *Epicopeia hainesii*, MK033610 (Yang et al. 2019).

genome, 77.51% in PCGs, 84.61% in srRNA, 83.72% in lrRNA, 80.98 in tRNAs, and 95.50% in the A + T-rich region. Of the 13 PCGs, 12 *P. felderi* start with ATN, except for COI, which starts with the alternative CGA codon, as observed in other lepidopteran insects (Kim et al. 2012).

The phylogenetic tree showed that Calliduloidea is located as the most basal group about Macroheterocera (Lasiocampoidea, Bombycoidea, Mimallonoidea, Noctuoidea, and Drepanoidea), Papilionoidea, and Pyraloidea (Figure 1). Similar results have been obtained in studies by Cho et al. (2011), Mutanen et al. (2010), Regier et al. (2013), Heikkilä et al. (2015), and Breinholt et al. (2018); however, taxon diversity in this study is far limiting. Before this study, no complete mitogenome sequences of Callidulidae were available. Thus, more complete mitogenome sequences of the family would be required for further analysis of the relationships of the family and superfamily with other taxonomic groups.

Disclosure statement

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

Data availability statement

Mitogenome data supporting this study are openly available in GenBank at: <https://www.ncbi.nlm.nih.gov/nuccore/MT370823>. The data that support the findings of this study are openly available in Mendeley Data at <http://dx.doi.org/10.17632/mdfnrcv2.1>

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