

Complete mitochondrial genome of the gelechioid *Stathmopoda auriferella* (Lepidoptera: Stathmopodidae)

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ABSTRACT

Although Gelechioidea is the second most species-rich group of Lepidoptera, comprising ~18,000 species, mitochondrial genomes (mitogenomes) have been sequenced from only eight species. In this study, we determined the complete mitogenomic sequence of the gelechioid *Stathmopoda auriferella* (Lepidoptera: Stathmopodidae) for a future phylogenetic study of Lepidoptera. The 15,456-bp-long *S. auriferella* genome was the largest among sequenced gelechioids. The cytochrome c oxidase subunit I (*COI*) gene had a CGA start codon as most other lepidopteran species do, including the eight gelechioid species for which datasets are available. An A + T-rich region (375 bp in length) harbored blocks of conserved sequences, which are typically found in lepidopteran insects. Bayesian inference (BI) phylogeny using 13 protein-coding genes (PCGs) indicated that *S. auriferella* belongs to the Stathmopodidae family and is grouped together with the within-familial species *Hieromantis kurokoi* with a strong nodal support (Bayesian posterior probabilities = 0.95).

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The lepidopteran superfamily Gelechioidea is distributed worldwide, comprising of 18,489 species in 1428 genera. It is the second most species-rich group of Lepidoptera (van Nieukerken et al. 2011) that is important to attaining a better understanding of higher-level phylogeny (Kaila et al. 2011; van Nieukerken et al. 2011). Nevertheless, prior to this study, only eight mitochondrial genomes (mitogenomes) have been sequenced (Timmermans et al. 2014; Park et al. 2016a, b; Zhao et al. 2016). Greater focus on additional species from a diverse taxonomic group is essential to conduct comprehensive mitogenome-based phylogenetic studies on Lepidoptera (including Gelechioidea).



In this study, we sequenced the mitogenome of the gelechioid *Stathmopoda auriferella* (Lepidoptera: Stathmopodidae) (Park et al. 1994; Yu & Park 1994). One adult was captured at Gyeongsangnam-do Province, South Korea (34°45'14" N, 127°58'57" E) and one hind leg was used for DNA extraction. Leftover DNA and specimen were deposited at Chonnam National University, Gwangju, Korea, under the accession number CNU 6207. Three long overlapping fragments (LFs; *COI-ND4*, *ND5-IrrRNA* and *IrrRNA-COI*) were amplified from genomic DNA and 26 short overlapping fragments were subsequently amplified using the LFs as templates. The primers used in this study were all lepidopteran-specific primers that were previously designed (Kim et al. 2012).

The complete mitogenome of *S. auriferella* (GenBank accession number KX138529) (15,456 bp in length) was larger than those of other sequenced gelechioids that typically range from

15,131 bp (*Perimede* sp.) to 15,408 bp (*Oegoconia novimundi*) (Timmermans et al. 2014; Park et al. 2016a, b; Zhao et al. 2016). The gene arrangement of *S. auriferella* was identical to that of other ditrysian Lepidoptera, including gelechioids. Instead of the ancestral *trnI-trnQ-trnM* order found in most insects (Boore 1999), the gene arrangement of *S. auriferella* had the order *trnM-trnI-trnQ* (where the underlined indicates gene inversion) between the A + T-rich region and *ND2* (Timmermans et al. 2014; Zhao et al. 2016; Park et al. 2016a, b).

Twelve of the 13 PCGs started with ATN codons (data not shown); however, the *COI* gene began with CGA (arginine). Eleven of the 13 PCGs had a complete stop codon; however, *COII* and *ND4* had T as the stop codon (data not shown). The 375-bp A + T-rich region displayed several lepidopteran-specific features, such as the ATAGA motif and adjacent poly-T stretch (21 bp), microsatellite-A/T repeats (one, four and another 17 TA repeats, respectively), and a poly-A stretch (intermittently interrupted by T; data not shown).

Phylogenetic analysis using nucleotide sequences of 13 PCGs was conducted with nine species of gelechioids from six families, including *S. auriferella* and one species each from Urodoidea, Tortricoidea, Tineoidea, and Gracillarioidea, which are phylogenetically close to Gelechioidea (Figure 1). The Bayesian inference (BI) method was performed using the GTR + GAMMA + I model in the CIPRES Portal v. 3.1 (Miller et al. 2010). *S. auriferella* of the Stathmopodidae family was grouped together with the within-familial species *H. kurokoi* with a high nodal support and Bayesian posterior probabilities

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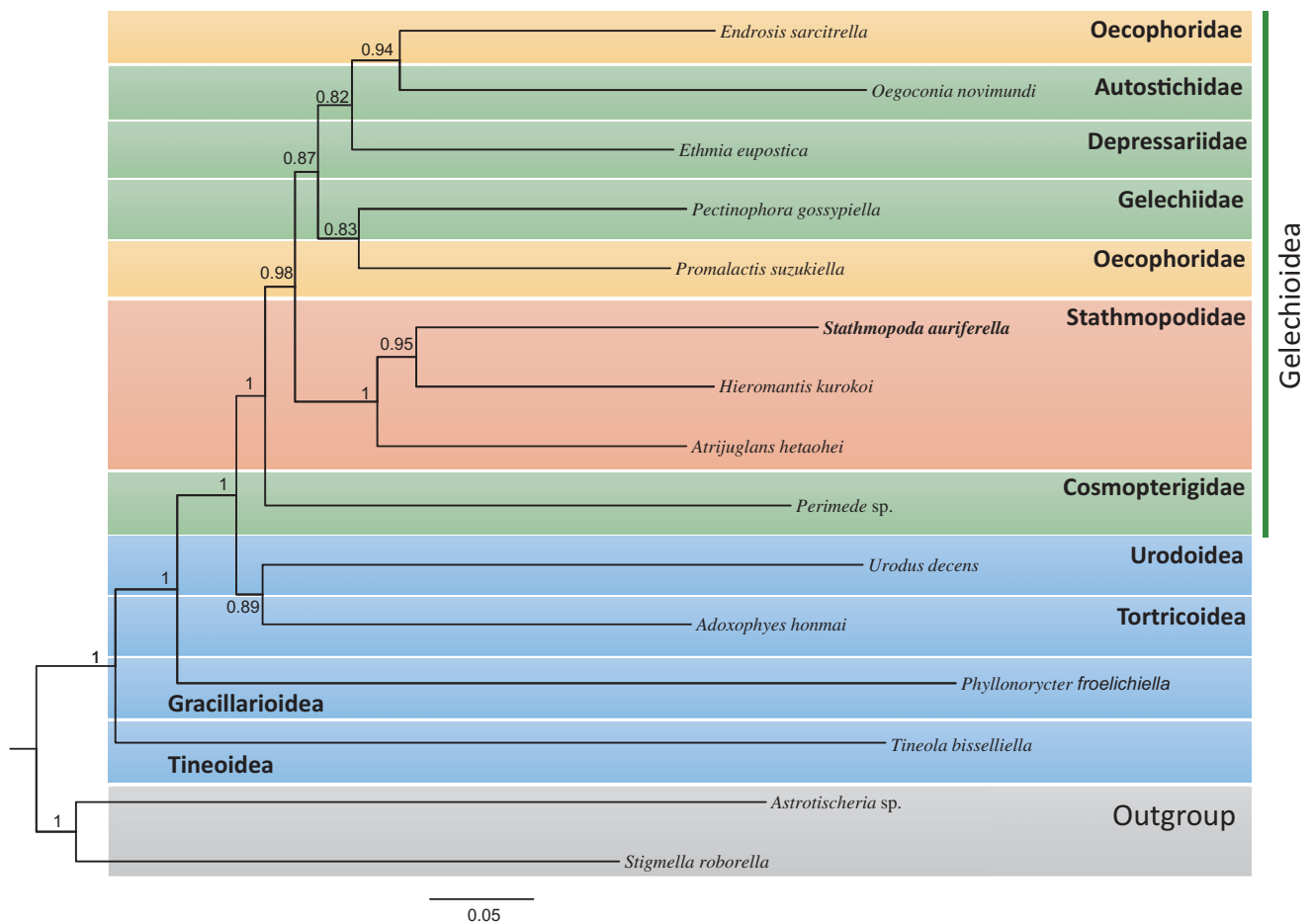


Figure 1. Phylogenetic tree for apoditrysian and ditrysian superfamilies, including Gelechioidea in the order Lepidoptera. Tree was constructed using nucleotide sequences of 13 protein-coding genes via the Bayesian inference method. The numbers at each node specify Bayesian posterior probabilities. The scale bar indicates the number of substitutions per site. One species each of Tischerioidea (*Astrotischeria* sp.) and Nepticuloidea (*Stigmella roborella*) were included as outgroups. GenBank accession numbers are as follows: *Uroodus decens*, KJ508062 (Timmermans et al. 2014); *Adoxophyes honmai*, DQ073916 (Lee et al. 2006); *Ethmia eupostica*, KJ508047 (Timmermans et al. 2014); *Perimede* sp., KJ508041 (Timmermans et al. 2014); *Endrosia sarcitrella*, KJ508037 (Timmermans et al. 2014); *Hieromantis kurokoi*, KU605775 (Park et al. 2016a); *Promalactis suzukiella*, KM875542 (Park et al. 2016b); *Oegoconia novimundi*, KJ508036 (Timmermans et al. 2014); *Atrijuglans hetaohei*, KT581634 (unpublished data); *Pectinophora gossypiella*, KM225795 (Zhao et al. 2016); *Tineola bisselliella*, KJ508045 (Timmermans et al. 2014); *Phyllonorycter froelichiella*, KJ508048 (Timmermans et al. 2014); *Astrotischeria* sp., KJ508056 (Timmermans et al. 2014); and *Stigmella roborella*, KJ508054 (Timmermans et al. 2014).

(BPP) of 0.95. Furthermore, these species formed the sister group to another within-familial species, *Atrijuglans hetaohei*, with the highest nodal support (BPP = 1.0), making Stathmopodidae a monophyletic group. However, Oecophoridae, the only family represented by two or more species (excluding Stathmopodidae) in this analysis did not form a monophyletic group (Figure 1). These results suggest that current mitogenome data remain limited in their ability to examine within-superfamilial and within-familial relationships of this diverse superfamily.

Disclosure statement

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

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References

- Boore JL. 1999. Animal mitochondrial genomes. *Nucleic Acids Res.* 27:1767–1780.
- Kaila L, Mutanen M, Nyman T. 2011. Phylogeny of the mega-diverse Gelechioidea (Lepidoptera): adaptations and determinants of success. *Mol Phylogenet Evol.* 61:801–809.
- Kim JS, Park JS, Kim MJ, Kang PD, Kim SG, Jin BR, Han YS, Kim I. 2012. Complete nucleotide sequence and organization of the mitochondrial genome of eri-silkworm, *Samia Cynthia ricini* (Lepidoptera: Saturniidae). *J Asia Pac Entomol.* 15:162–173.
- Lee ES, Shin KS, Kim MS, Park H, Cho S, Kim CB. 2006. The mitochondrial genome of the smaller tea tortrix *Adoxophyes honmai* (Lepidoptera: Tortricidae). *Gene.* 373:52–57.
- Miller MA, Pfeiffer W, Schwartz T. Creating the CIPRES science gateway for inference of large phylogenetic trees. *Proceedings of the Gateway Comput Environ Workshop (GCE)*, 2010; New Orleans, LA.
- Park JS, Jeong SY, Kim SU, Kim I. 2016a. Complete mitochondrial genome of the gelechioid *Hieromantis kurokoi* (Lepidoptera: Stathmopodidae). *Mitochondrial DNA Part B.* 1:312–313.
- Park JS, Kim SS, Kim KY, Kim I. 2016b. Complete mitochondrial genome of Suzuki's Promolactis moth *Promalactis suzukiella* (Lepidoptera: Oecophoridae). *Mitochondrial DNA A DNA MappSeq Anal.* 27:2093–2094.

- Park JD, Park IJ, Han KP. 1994. Investigation of insect pests and injury characteristics of *Stathmopoda auriferella* (Walker) on kiwi fruit tree. *Korean J Appl Entomol.* 33:148–152.
- Timmermans MJ, Lees DC, Simonsen TJ. 2014. Towards a mitogenomic phylogeny of Lepidoptera. *Mol Phylogenet Evol.* 79:169–178.
- van Nieukerken EJ, Kaila L, Kitching IJ, Kristensen NP, Lees DC, Minet J, Mitter C, Mutanen M, Regier JC, Simonsen TJ, et al. 2011. Order Lepidoptera Linnaeus, 1758. *Zootaxa.* 3148:212–221.
- Yu SS, Park KT. 1994. A preliminary list of Stathmopodidae, Batrachedridae, Blastodacnidae and Cosmopterigidae (Lepidoptera: Gelechiidae) of the Korean Peninsula. *Korean J Appl Entomol.* 33:194–200.
- Zhao J, Sun Y, Xiao L, Tan Y, Dai H, Bai L. 2016. Complete mitochondrial genome of the pink bollworm *Pectinophora gossypiella* (Lepidoptera: Gelechiidae). *Mitochondrial DNA Part A.* 27:1575–1576.