Complete mitochondrial genome of the gelechioid *Hieromantis kurokoi* (Lepidoptera: Stathmopodidae)

Jeong Sun Park,a Su Yeon Jeonga, Sung Soo Kimb and Iksoo Kim a

aDepartment of Applied Biology, College of Agriculture & Life Sciences, Chonnam National University, Gwangju, Republic of Korea; bResearch Institute for East Asian Environment and Biology, Seoul, Republic of Korea

### ABSTRACT

Although the Gelechioidea is the second most species-rich group of Lepidoptera, comparatively few mitochondrial genomes (mitogenomes) have been sequenced in this superfamily. Here, we determined the complete mitogenomic sequence of the gelechioid *Hieromantis kurokoi* (Lepidoptera: Stathmopodidae) as the basis for a future study of the phylogeny of butterflies and moths (clade Ditrysia). The *H. kurokoi* genome was 15,208 bp with a typical set of genes (13 protein-coding genes [PCGs], two rRNA genes and 22 tRNA genes) and one major non-coding A + T-rich region. The cytochrome c oxidase subunit 1 (COI) gene had a CGA start codon, which is the start codon for this gene in the majority of lepidopteran species, whereas other PCGs began with an ATN codon. A 360-bp-long A + T-rich region harbored the blocks of conserved sequences that are typically found in lepidopteran insects. Phylogenetic analysis using the 13 PCGs and Bayesian inference (BI) and maximum-likelihood (ML) methods indicated that *H. kurokoi* belonged to the family Stathmopodidae and grouped together with the within-familial species *Atrijuglans hetaohei* with the highest nodal support (BI, 1.0; ML, 100%).

The superfamily Gelechioidea is the second most species-rich group of Lepidoptera and is important for the understanding of the higher phylogeny of the Ditrysia clade (Kaila et al. 2011; van Nieukerken et al. 2011). Nevertheless, prior to this study, only seven mitochondrial genomes (mitogenomes), representing six of the 19 families, have been sequenced (Park et al. 2016; Timmermans et al. 2014; Zhao et al. 2016). Thus, more species from a diverse taxonomic group will be essential for mitogenome-based phylogenetic studies.

In this study, we sequenced the mitogenome of the gelechioid *Hieromantis kurokoi* (Lepidoptera: Stathmopodidae) (Sohn 2007). One adult was captured at Joongge-ri in Jeollabuk-do Province, South Korea (35°39′14.9″ N, 126°32′14.9″ E). A voucher specimen was deposited in Chonnam National University, Gwangju, Korea. Total DNA was used as the template to amplify three long overlapping fragments (COI-ND4, NDS-IrRNA and IrRNA-COI). Subsequently, 26 short overlapping fragments were amplified using the long fragments as templates. All primer used were Lepidoptera-specific primers designed previously (Kim et al. 2012).

The complete mitogenome of *H. kurokoi* (GenBank accession number KU605775) was 15,208 bp and consisted of two rRNAs, 22 tRNAs, 13 protein-coding genes (PCGs) and one major non-coding region (referred to as the A + T-rich region). The gene arrangement of *H. kurokoi* is identical to that of other ditrysian Lepidoptera, including gelechioids, that have the order *Atrijuglans hetaohei* with the highest nodal support (BI, 1.0; ML, 100%).

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CONTACT Iksoo Kim ikkim81@chonnam.ac.kr Department of Applied Biology, College of Agriculture & Life Sciences, Chonnam National University, Gwangju 500-757, Republic of Korea

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group with the sole member of Autostichidae, *Oegoconia novimundi* and *P. suzukiella* formed a group with the sole member of Gelechiidae, *Pectinophora gossypiella*, although these groups were very weakly supported by the ML method. These results may indicate that it is too early to determine within-superfamilial inferences for Gelechioidea with the currently available mitogenome data.

**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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**Figure 1.** Phylogenetic tree for apoditrysian and ditrysian superfamilies, including Gelechioidea in 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 percentages by Bayesian inference method (first value) and bootstrap percentages of 1,000 pseudoreplicates by maximum-likelihood method (second value). 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: *Urodus 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); *Endrosis sarcitrella*, KJ508037 (Timmermans et al. 2014); *Promalactis suzukiella*, KM875542 (Park et al. 2014); *Oegoconia novimundi*, KJ508036 (Timmermans et al. 2014); *Atrijuglans hetaohei*, KTS81634 (Unpublished); *Pectinophora gossypiella*, KM225798 (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).