

Complete mitochondrial genome of *Zeuzera multistrigata* Moore, 1881 (Lepidoptera: Cossidae)

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ABSTRACT

We sequenced the complete mitochondrial genome (mitogenome) of *Zeuzera multistrigata* Moore, 1881 (Lepidoptera: Cossidae), which is an economically damaging pest to a diverse range of *Casuarina* trees. The 15,260-bp-long mitogenome of this species consists of a typical set of genes, with an arrangement typical of ditrysian Lepidoptera. Of the 13 protein-coding genes (PCGs), 12 have a typical ATN start codon, whereas the *COI* gene begins with CGA. Ten of the 13 PCGs end with TAA, whereas *COI*, *COII*, and *ND5* ended with an incomplete termination codon, T. Phylogenetic analysis using 13 PCGs of available superfamilies in Apoditrysia indicated that *Z. multistrigata*, belonging to the superfamily Cossoidea, formed a sister group with the confamilial species *Eogystia hippophaecolus*; however, the nodal support for this group was low (46%). As more mitogenomes from ancient groups of Lepidoptera become available, further robust phylogenetic analysis and inference will be possible.

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Zeuzera multistrigata, a moth belonging to the Cossidae family, is found in several Asian countries including Korea (Shin 2001). Adults, which have a wingspan of 40–60 mm, are found from July to August every two years (Shin 2001). The larvae are borers of a diverse range of *Casuarina* trees (Shin 2001).

In this study, the complete mitochondrial genome (mitogenome) of *Z. multistrigata* was sequenced to determine the mitogenomic characteristics of this species and its phylogenetic position within the Lepidoptera. An adult *Z. multistrigata* was captured at Mongtan-myeon, in Jeollanamdo Province, South Korea, in 7 August 2012 (34°55′00″N, 126°27′18″E). This voucher specimen was deposited in Chonnam National University, Gwangju, Korea, under the accession no. CNU5711. Using the total DNA from this specimen as a template, three long-overlapping fragments (*COI-ND4* for LF1, *ND5-IrRNA* for LF2, and *IrRNA-COI* for LF3) were amplified using three sets of Lepidoptera-specific primers adapted from Kim et al. (2014). These LFs were used as templates for 26 short fragments.

The *Z. multistrigata* mitogenome is 15,260 bp in length and includes typical sets of genes and a major non-coding 374-bp A + T-rich region (GenBank accession no. MF491642). The mitogenome size is slightly smaller than that of the available confamilial species *Eogystia hippophaecolus* (Gong et al. 2014), but is well within the range found in apoditryasian Lepidoptera (Timmermans et al. 2014; Liu et al. 2016, 2017). The gene arrangement of the *Z. multistrigata* mitogenome is identical to that of the ditrysian Lepidoptera that have the

order *trnM-trnI-trnQ* in the A + T-rich region and *ND2* junction (Kim et al. 2014). The AT content among genes and regions varies considerably in the *Z. multistrigata* mitogenome (from 93.9% in the A + T-rich region to 84.7% in rRNAs). Twelve *Z. multistrigata* PCGs start with a typical ATN codon, whereas *COI* starts with the atypical sequence CGA, as found in the majority of lepidopteran species (Kim et al. 2014; Park et al. 2016).

We downloaded available mitogenome sequences of 10 apoditryasian species (seven superfamilies) from GenBank along with that of one species of Tineoidea in Ditrysia for use as an outgroup, and 13 PCGs were utilized for phylogenetic analysis. The Maximum-likelihood (ML) method was performed using the GTR + GAMMA + I model and using RAXML-HPC2 in XSEDE ver. 8.0.24 (Stamatakis 2014), which is implemented in the CIPRES Portal ver. 3.1 (Miller et al. 2010). *Zeuzera multistrigata*, belonging to the superfamily Cossoidea, formed a sister group with the confamilial species *E. hippophaecolus*, and these two species of Cossoidea formed a sister group to Urodoidea (Figure 1). With exception of the sister relationships between two species of Zygaenoidea (100%) and between two species of Tortricidae (100%), the nodal supports for most groups, including the sister relationships between the two species of Cossoidea (46%) and between Cossoidea and Urodoidea (17%), were low. In most cases, these results contribute little to the recent progress made in lepidopteran phylogeny (e.g. Bazinet et al. 2013). One possible reason for such results could be the lack of taxonomic diversity. Thus, more mitogenomes from ancient lepidopteran

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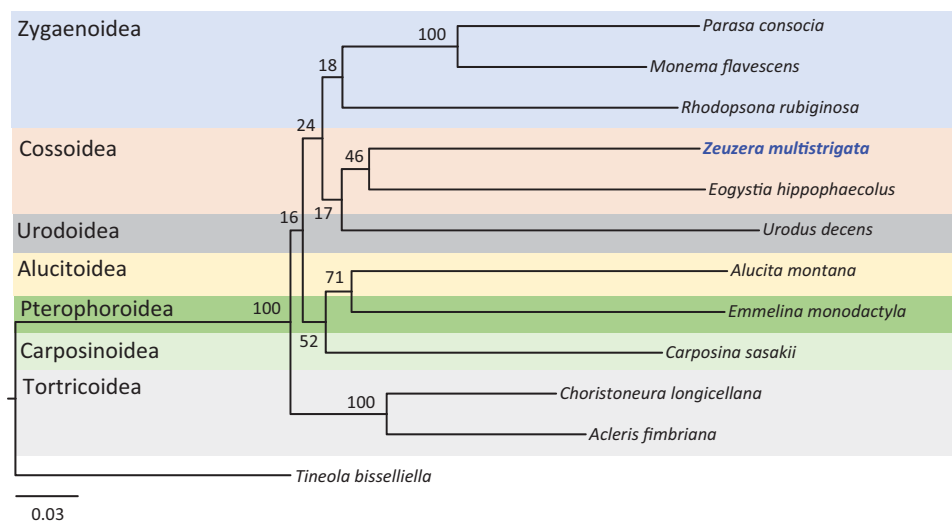


Figure 1. Phylogeny of Apoditrysia, including *Z. multistrigata* belonging to Cossoidea, derived using the Maximum-likelihood (ML) method based on 13 concatenated PCGs. The numbers at each node specify bootstrap percentages of 1000 pseudoreplicates. The scale bar indicates the number of substitutions per site. *Tineola bisselliella* belonging to the superfamily Tineoidea in Ditrysia was utilized as an outgroup. GenBank accession numbers are as follows: *Eogystia hippophaecolus*, KC831443; *Monema flavescens*, KU946971; *Parasa consocia*, KX108765; *Rhodopsona rubiginosa*, KM244668; *Choristoneura longicellana*, HQ452340; *Acleris fimbriana*, HQ662522; *Urodus decens*, KJ508062; *Emmelina monodactyla*, KJ508063; *Alucita montana*, KJ508059; *Carposina sasakii*, HQ840719; and *Tineola bisselliella*, KJ508045.

groups could be essential for further robust phylogenetic analysis and inference.

Disclosure statement

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

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