Complete mitochondrial genome of *Ostrinia kasmirica* (Lepidoptera: Crambidae)

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**ABSTRACT**

The complete mitochondrial genome of *Ostrinia kasmirica* (Moore, 1888) was sequenced in this study. The circular mitogenome is 15,214 bp in length, containing 37 typical encoded genes and a non-coding control region. The gene organization and nucleotide composition are similar to those of most other sequenced *Ostrinia* species. All protein-coding genes (PCGs) initiate with ATN and terminate with TAN, except *cox1* starts with CGA and *cox1*, *cox2*, *nad5* terminate with an incomplete codon T. The control region of 308 bp contains three conserved features including the motif ‘TTAGA’ preceded a poly-T stretch, a microsatellite-like (TA)\(_n\) element, and a poly-A stretch upstream of *trnM*. Phylogenetic analysis based on mitogenome sequences revealed that the *O. kasmirica* (the second species group) was more closely related to the third species group of the genus and the first species group was not at the basal position of this genus as that Mutuura and Munroe indicated.

The genus *Ostrinia* Hübner, 1825 (Crambidae: Pyraustinae) includes 23 species, with a few well-known destructive pests that caused huge economic losses (Mutuura and Munroe 1970). Mutuura and Munroe (1970) recognized three species groups of the genus based on the morphology of male genitalia. The first species group (Group I) only contains a single species *Ostrinia penalis* (Grote, 1876) with unarmed sacculus and one-lobed uncus which is regarded as the ‘primitive’ species of this genus. The second species group (Group II) includes nine species with simple or weakly bifid uncus in the male genitalia. The third species group (Group III) comprises 10 species such as *Ostrinia fumacalis* (Guenée, 1854) and *Ostrinia nubilalis* (Hübner, 1796) . The remaining species including *Ostrinia maysalis* Leraut, 2012, *Ostrinia ovalipennis* Ohno, 2003, and *Ostrinia avarialis* Amsel, 1970 not classified into the above three species groups.

The *Ostrinia kasmirica* (Moore, 1888) is commonly found in the northeast India, southeastern Russia, and Siberia (Mutuura and Munroe 1970). It was first recorded by Li and Tang in 1981 in China (Li and Tang 1985). The larva of this species mainly feeds on the thistle *Cnicus wallichii*. Mutuura and Munroe (1970) purported that the *O. kasmirica*, having bell-shaped and weakly bifid uncus, is most likely to be closely related with *Ostrinia latipennis* (Warren, 1892) and *Ostrinia palustralis* (Hübner, 1796) based on the male genitalia within the second species group. However, the *O. kasmirica* is similar to *O. nubilalis* and *Ostrinia scapulalis* (Walker, 1859) in appearance (Bidzilya and Budadshkin 2017), implying that *O. kasmirica* is closely related to the members of the third species group. Due to the lack of the molecular data of *O. kasmirica* its phylogenetic position is still unclear. To address this question, we sequenced the complete mitogenome sequence of *O. kasmirica* and inferred the phylogenetic relationships of this genus based on this mitogenome and other six published mitogenome sequences of the genus *Ostrinia*.

The adult specimens of *O. kasmirica* were collected by light trap in July 2018 from Jalai Nur District (49°31’N, 117°43’E), Hulunbuir Prefecture, Inner Mongolia Autonomous Region, China. Specimens were preserved in a freezer in pure ethanol at −20 °C. The voucher sample was deposited at the Entomological Museum (Voucher number ZLN3), Northwest A&F University, Yangling, Shaanxi, China. Genomic DNA was extracted from thoracic muscle. Illumina HiSeq platform (Illumina, San Diego, CA) was used for sequencing and generated \(2 \times 150\) bp paired-end reads. Mitochondrial gene annotation was performed by MitoZ version 2.4 (Meng et al. 2019) under all module which includes four steps: raw data pretreatment, *de novo* assembly with SOAPdenovo-Trans, mitogenome sequence identification, and mitogenome annotation. Before data analyses, the annotated mitogenome was rechecked with previously published mitogenomes of *Ostrinia* species.

The complete mitogenome of *O. kasmirica* (GenBank accession number. MT978075) is circular molecular structure of 15,214 bp in length, containing 37 typical genes (13 PCGs, ...
22 transfer RNAs and 2 ribosomal RNAs) and a non-coding control region. The gene arrangement and content are identical to most of the mitogenomes in Lepidoptera. Nucleotide compositions of 41.8% A, 39.2% T, 11.3% C, and 7.7% G indicated that the O. kasmirica mitogenome is biased toward higher A + T content. All PCGs terminate with TAN, whereas most of the mitogenomes in Lepidoptera. Nucleotide compositions of 41.8% A, 39.2% T, 11.3% C, and 7.7% G indicated that the O. kasmirica mitogenome is biased toward higher A + T content. All PCGs terminate with TAN, whereas most of the mitogenomes in Lepidoptera. Nucleotide compositions of 41.8% A, 39.2% T, 11.3% C, and 7.7% G indicated that the O. kasmirica mitogenome is biased toward higher A + T content. All PCGs terminate with TAN.

**Disclosure statement**
No potential conflict of interest was reported by the authors.

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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, reference number MT978075.
The associated BioProject accession number, SRA data, and BioSample accession number are PRJNA716609, SRR14044899, and SAMN18439942 respectively.

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