Complete mitochondrial genome of Spodoptera littoralis (Lepidoptera: Noctuidae) from Egypt

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\textbf{ABSTRACT}

The polyphagous cotton leafworm (Spodoptera littoralis) is one of the most destructive herbivorous insects worldwide. The present study reports the complete mitochondrial genome of S. littoralis collected from Egypt. The circular-mapping mitogenome was 15,408 bp in length with an overall A + T content of 81.1\%, encoding a common set of 37 genes, including 13 protein-coding genes (PCGs), 22 tRNA genes, and two rRNA genes. Most PCGs were found to use conventional ATN as the start codon and TAN as the stop codon. The phylogenetic tree based on the nucleic acid sequences of 13 shared PCGs of 29 Noctuidae species revealed that S. littoralis and Spodoptera litura are sister species. The data in this study will be helpful to understand geographical genetic variations, phylogenetic relationships, and species identification of S. littoralis.

In this study, the genomic DNA of S. littoralis was extracted from a male moth of an inbred strain established from eggs collected near Alexandria (31°07′52.6″N 29°56′02.5″E) in Egypt in 2011. The voucher specimen's genomic DNA was assigned with a unique code (AGIS-SL-EG-2011) and deposited at the Agricultural Genomics Institute, Chinese Academy of Agricultural Sciences, Shenzhen, China. Total genomic DNA was extracted using the Qiagen Genomic DNA kit (Cat. no.13323, Qiagen). DNA quality and concentration were determined using NanoDrop One UV-Vis spectrophotometer (Thermo Fisher Scientific). A total of 0.5 μg of genomic DNA was used to construct a 350-bp insert library, which was then sequenced using the Illumina NovaSeq 6000 platform with 150-bp paired-end reads. The mitogenome was assembled using the software NOVOPlasty v2.5.6 (Dierckxsens et al. 2017). Gene annotation was performed and circularity was checked using the web-based MITOS2 (http://mitos2.bio-inf.uni-leipzig.de/index.py) (Bernt et al. 2013).

The complete mitogenome of S. littoralis (GenBank accession number MT816470) is 15,408 bp in length and contains 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (rRNAs), and one non-coding A + T-rich region (putative control region). In the genome, the content of A + T is 81.1\% (A 41.0\%; T 40.0\%), which represents a typical high A + T content among insect mitogenomes (Yang et al. 2019a). However, the A + T content varied among genes as follows: control region (96.0\%), rRNAs (84.4\% – 85.0\%), PCGs (72.4\% – 92.0\%), and tRNAs (70.4\% – 91.2\%).
The negligible AT-skew (0.012) and negative GC-skew (-0.198) in the mitogenome of *S. littoralis* were found to be similar to those of other Lepidoptera insects (Cameron and Whiting 2008). The total length of the 13 PCGs was determined to be 11,150 bp. All PCGs use conventional ATN as the start codon, with one exception being CGA for *cox1*. These special structures of the start codon are a common feature of lepidopteran mitogenomes (Wu et al. 2016). Ten genes are terminated with a complete stop codon (TAA), one gene (*nad3*) has a complete stop codon (TAG), and two genes (*cox2* and *nad4*) end with an incomplete stop codon (T). Further, 22 tRNA genes ranged in size from 65 to 71 bp. All tRNAs harbor typical predicted secondary cloverleaf structures, except for *trnN* and *trnY*.

To validate the phylogenetic position of *S. littoralis*, we downloaded mitogenomes of 29 Noctuidae species and one outgroup species *Cydia pomonella* (Tortricidae) published in GenBank. Multiple nucleic acid sequence alignments of 13 PCGs were conducted using MAFFT v7.455 (Katoh and Standley 2013). The phylogenetic tree was constructed based on the maximum likelihood method using RAxML-NG v0.9.0 (Kozlov et al. 2019) with the best-fit model (GTR + F + R4) estimated by IQ-TREE v1.6.10 with parameter ‘-m MF’ (Nguyen et al. 2015). The bootstrap replicates were 1000 and the tree was visualized with FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/). The phylogenetic analysis showed that the *Spodoptera* genus was monophyletic, and *S. littoralis* and *S. litura* were sister species. In summary, the current mitogenome sequence will be useful for the phylogenetic analysis of this species (Figure 1). Furthermore, the mitochondrial DNA molecules within a cell are subject to evolutionary processes such as selection and drift. The high evolutionary rate of mitochondrial DNA makes it played an integral role in further revealing population structure and demographic history (Tikochinski et al. 2020; Johri et al. 2019; Hurst and Jiggins, 2005). *S. littoralis* is native to Africa and Israel (Yones et al. 2012), thus, the mitochondrial genome from Egypt provides the basis for further study of population genetics.

**Disclosure statement**

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

This work was supported by the Special Funds for the Industrial Development of the Dapeng New District, Shenzhen City, under Grant number KY20180216.

Data availability statement

Mitogenome data supporting this study are openly available in GenBank at https://www.ncbi.nlm.nih.gov/nuccore/MT816470. Associated BioProject, BioSample, and SRA accession numbers are PRJNA678763, SAMN16812461, and SRR13083392, respectively.

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