The complete mitochondrial genome of a tea geometrid, *Ectropis obliqua* (Lepidoptera: Geometridae)

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**ABSTRACT**

The tea geometrid, *Ectropis obliqua* Prout (Lepidoptera: Geometridae), is a major leaf-feeding pest of tea plantation, and poses a considerable economic threat to tea industry. We have sequenced the complete mitochondrial genome of *E. obliqua*. The entire genome is 16,535 bp in length with an \(A + T\) content of 81.32% (GenBank accession No. KX827002). The tea geometrid mt genome encodes all 37 genes that are typically found in animal mt genomes, consists of 13 protein-coding genes (PCG), two ribosomal RNA genes, and 22 transfer RNA genes. The gene order is consistent with other sequenced mt genome of moths and butterflies in Ditrysia. The \(A + T\)-rich region is 1523 bp long and consisting of the motif ‘ATAGA’, a 19 bp poly-T stretch, and a tandem repeat sequence with seven 194 bp repeat units. Phylogenetic analysis was performed using 13 PCG with 16 moths showed that *E. obliqua* clusters with other Geometridae species.

The tea geometrid, *Ectropis obliqua* Prout (Lepidoptera: Geometridae), is a major leaf-feeding pest of tea plantation, and poses a considerable economic threat to tea industry. In this study, the samples of *E. obliqua* were collected from a tea plantation in Xinyang, Henan, China in 2014, and identified to species by morphology and sequence of cox1. Voucher specimens (#CQNKY-LE-01-01-01) were deposited at the Insect Collection, Tea Research Institute of Chongqing Academy of Agricultural Science, Chongqing, China.

The complete mitochondrial genome of *E. obliqua* is a typical closed-circular DNA molecule of 16,535 bp in length (GenBank accession No. KX827002). It is the biggest mt genome among all sequenced Geometridae species: *Phthionandria atrilineata* (15,499 bp) (Yang et al. 2009), *Biston panterinaria* (15,517 bp) (Yang et al. 2013), *Apocheima cineraria* (15,722 bp) (Liu et al. 2014), *Buzura suppressaria* (15,628 bp) (Chen et al. 2016), and *Jankowskia athlete* (15,534 bp) (Xu et al. 2016). The total nucleotide composition of the J-strand of the mt genome is as follows: \(A = 41.45\%\) (6,853), \(C = 11.07\%\) (1,830), \(G = 7.61\%\) (1,258), and \(T = 39.88\%\) (6594), with a total \(A + T\) content of 81.32%, that is heavily biased toward A and T nucleotides. AT- and GC-skew of the whole J-strand of *E. obliqua* is 0.019 and 0.185, respectively.

The mt genome of *E. obliqua* encodes all 37 genes usually found in animal mt genomes, including 13 protein-coding genes (PCG), two ribosomal RNA genes, and 22 transfer RNA genes. The gene arrangement in the mitochondrial genome of *E. obliqua* is identical to all other loopers. In the mt genome of *E. obliqua*, a total of 27 bp overlaps have been found at six gene junctions (atp8 and atp6 share seven nucleotides; trnN and trnS\(_1\) share two nucleotides; nad4 and nad4L share a nucleotide; cob and trnS\(_2\) share two nucleotides; nad1 and trnL\(_1\) share six nucleotides; trnI and trnQ share three nucleotides and trnW and trnC share eight nucleotides). The mt genome has a total of 197 bp intergenic sequence without the putative \(A + T\)-rich region. The intergenic sequences are at 14 locations ranging from 1 to 64 bp, the longest one locates between trnQ and nad2. The \(A + T\)-rich region of this genome is 1523 bp long and located between the rrnS and rrnM genes. The \(A + T\) content of this region is 93.17%, the highest level of each region is in this mt genome. This region consists of the motif ‘ATAGA’, a 19 bp poly-T stretch, and a tandem repeat sequence with seven 194 bp repeat units.

All 22 tRNA genes usually found in the mt genomes of insects have been identified in *E. obliqua*, 14 tRNA genes are encoded by the J-strand and the others encoded by the N-strand. The nucleotide length of tRNA genes is ranging from 65 bp (trnA, trnR, and trnT) to 72 bp (trnK), and \(A + T\) content is ranging from 73.61% (trnK) to 92.42% (trnE). Like other loopers, 21 tRNA genes have cloverleaf shaped secondary structure and trnS, gene lacks the dihydrouridine (DHU) arm. The two rRNA genes have been identified on the N-strand in the mt genome: the rrnL gene locates between trnL\(_1\) and trnV, and the rrnS gene between the trnV and the \(A + T\)-rich region. The length of rrnL and rrnS is 1375 bp and 787 bp, and their \(A + T\) content is 84.95% and 85.51%, respectively.
The total length of all 13 PCG is 11,203 bp, which is accounting for 68.51% of the whole genome sequence. The A + T content of the 13 genes ranges from 71.78% (cox1) to 89.29% (atp8). Twelve of the 13 PCGs start with ATN codons (ATG for atp6, cox2, cox3, cob, nad4, and nad4L; ATA for nad1, nad2, and nad6; ATT for nad3 and nad5; ATC for atp8) and cox1 uses CGA as start codon, this phenomenon exists in most Lepidoptera species. Four PCGs (cox1, cox2, nad4, and nad5) have incomplete terminal codons consisting of single T nucleotide, and the other PCGs stop with TAA. The incomplete stop codon T is commonly reported and could produce functional stop codons in polycistronic transcription cleavage and polyadenylation mechanisms (Boore 2001). We analysed the amino acid sequences of 13 PCGs with maximum likelihood (ML) method to learn the phylogenetic relationship of E. obliqua with other moths. In the tree, E. obliqua and other five geometrids were clustered into a branch (Figure 1). It infers that E. obliqua is closely related to species of Geometridae.

Disclosure statement

No potential conflict of interest was reported by the authors.

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