The complete mitochondrial genome of a slug moth, _Narosa nigrisigna_ (Lepidoptera: Limacodidae)

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**ABSTRACT**

The slug moth, _Narosa nigrisigna_ Wileman (Lepidoptera: Limacodidae), is a major tea pest in China. We have sequenced the complete mitochondrial genome of _N. nigrisigna_. The entire genome is 15,292 bp in length (GenBank accession No. MH675969) with consisting of 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, and a 377 bp A + T-rich region. The gene order is consistent with other sequenced mt genome of moths and butterflies in Ditrysia. The A + T-rich region contains a motif ‘ATAGA’ and a 16 bp poly-T stretch. Phylogenetic analysis was performed using 13 protein-coding genes with 17 moths showed that _N. nigrisigna_ is more closely related to other slug moths in family Limacodidae.

The complete mitochondrial genome of _N. nigrisigna_ is shown to be a typical closed-circular and double-stranded DNA molecule in size of 15,292 bp (GenBank accession MH675969). It is low level among all reported Lepidoptera species and the smallest mt genome among all sequenced Limacodidae species: _Monema flavescens_ (15,396 bp) (Liu et al. 2016), _Cnidocampa flavescens_ (15,406 bp) (Peng et al. 2017) and _Parasa consocia_ (15,296 bp) (Liu et al. 2017). The overall nucleotide composition of the major strand of the slug moth mt genome as follows: A = 38.97% (5,960), C = 11.12% (1,700), G = 7.67% (1,173), and T = 42.24% (6,459), with a total A + T content of 81.21%, that is heavily biased toward A and T nucleotides. AT- and GC-skew of the whole J-strand of _N. nigrisigna_ is −0.040 and −0.183, respectively.

The mt genome encodes all 37 genes usually found in animal mt genomes, including 13 protein-coding genes (PCG), two ribosomal RNAs and 22 transfer RNAs. The gene arrangement in the mitochondrial genome of _N. nigrisigna_ is conserved as other butterflies and moths mt genome in Ditrysia. In the mt genome of _N. nigrisigna_, a total of 21 bp overlaps have been found at seven gene junctions of the genome (atp8 and atp6 share 7 nucleotides; atp6 and cox3 share a nucleotide; trnR and trnN share 3 nucleotides; trnS, and trnE share 1 nucleotides; nad4 and nad4L share 4 nucleotides; trnL and trnQ share 3 nucleotides; and nad2 and trnW share 2 nucleotides). The mt genome is loose and has a total of 151 bp intergenic sequence without the putative A + T-rich region. The intergenic sequences are at 15 locations ranging from 1 to 50 bp, the longest one locates between trnQ and nad2. The A + T-rich region of _N. nigrisigna_ mt genome is 377 bp long and located between the mts and trnM genes. The A + T content of this region is 96.82%, the highest level of each region in this mt genome. This region includes the motif ‘ATAGA’ and a 16 bp poly-T stretch.

All 22 tRNA genes usually found in the mt genomes of insects are present in _N. nigrisigna_. 14 tRNA genes are encoded by J-strand and the others encoded by the N-strand. The nucleotide length of tRNA genes is ranging from 63 bp (trnR) to 71 bp (trnK and trnA), and A + T content is ranging from 70.42% (trnK) to 92.75% (trnE). 21 tRNA genes have the conventional 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 _N. nigrisigna_ mt genome: the _rrnL_ gene locates between _tml_ and _trnV_ genes, and the _rrnS_ gene between the _trnV_ gene and the A + T-rich region. The length of _rrnL_ and _rrnS_ genes was 1,357 bp and 777 bp, and their A + T content was 85.56% and 86.49%, respectively. The total length of all 13 protein-coding genes is 11,172 bp, which is accounting for 73.06% of the whole genome sequence. The A + T content of the 13 genes ranges from 71.98% (cox1) to 88.89% (atp8). Twelve of the 13 PCGs start with ATN codons (ATG for atp6, cox2, cox3,
cob, nad1, and nad4L; ATT for atp8, and nad2-3; ATA for nad4-6, and cox1 used CGA as start codon which has the same situation exists in most Lepidoptera species (Chen et al. 2015). Three PCGs (cox1-2 and nad4) have incomplete terminal codons consisting of single T nucleotide, and the other PCGs stop with TAA. The incomplete stop codon T is common and usually be demonstrated by the tRNA punctuation model, also could generate functional stop codons in polycistrionic transcriptional division and polyadenylation mechanisms could (Ojala et al. 1981; Boore 2001; Stewart and Beckenbach 2009).

We analyzed nucleotides sequences of 13 PCGs with maximum likelihood (ML) method to understand the phylogenetic relationship of N. nigrisigna with other moths. The mt genome sequence of Drosophila melanogaster (GenBank accession no. DMU37541) was used as an outgroup. N. nigrisigna, C. flavescens, M. flavescens, and P. consocia belong to the family Limacodidae and they are clustered into a branch with 99% bootstrap value. Meanwhile, the two families Limacodidae and Zygaenidae (Rhodopsona rubiginosa) belong to the superfamily Zygaenoidea and they are clustered into a same branch in the phylogenetic tree (Figure 1).

**Disclosure statement**

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