The complete mitochondrial genome of invasive insect *Leptinotarsa decemlineata* Say 1824 (Coleoptera: Chrysomelidae)

Tian-Mei Dai, Hu Tian, Xu Liu, Gui-Fen Zhang and Yu-Sheng Wang

*Hunan Provincial Key Laboratory for Control of Forest Diseases and Pests, College of Forestry, Central South University of Forestry and Technology, Changsha, China; bCaofeidian Customs District P. R. China, Tangshan, China; cState Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, China; dHunan Provincial Key Laboratory for Biology and Control of Plant Diseases and Insect Pests and College of Plant Protection, Hunan Agricultural University, Changsha, China

The Colorado potato beetle, *Leptinotarsa decemlineata* Say 1824 (Coleoptera: Chrysomelidae), is one of the most destructive insect pests of potato (Cingel et al. 2016). Native to North America, it has now spread to and invaded countries worldwide (Hare 1990; Alyokhin 2009). The larvae and adults feed on foliage and tubers, causing severe damage to the plants (Alyokhin 2009). In 2017, adult specimens of *L. decemlineata* were collected from No.3 Donghuan Road, Gongliu County, Ili Kazak Autonomous Prefecture, Xinjiang Uygur Autonomous Region, China (82.3226°E, 43.4721°N). Voucher specimens were preserved in 99.7% ethanol and deposited in the Insect Collection at the College of Plant Protection, Hunan Agricultural University (please contact Yu-Sheng Wang, email: yushengwang01@163.com) under the voucher number cpb2017083101. The genomic DNA was extracted from a single specimen using the DNeasy Tissue kit (Qiagen, Germany). The mitogenome was sequenced using the Illumina Hiseq X platform (Macrogen Inc., South Korea) and assembled by SPAdes v3.11.1 (Bankevich et al. 2012). MitoZ (Meng et al. 2019) software was used to annotate the mitogenome with reference to other Chrysomelinae species (MF563962, MK049855, MF198406).

The complete mitogenome of *L. decemlineata* (GenBank accession number MZ189364) is a 16,741 bp long circular molecule, comprised 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), 2 ribosomal RNA genes (*rrnL* and *rrnS*), and one control region. Nine PCGs and 14 tRNAs were encoded on the H-strand, whereas the others were located on the L-strand. The nucleotide composition of the *L. decemlineata* mitogenome is significantly biased (39.4% A, 37.5% T, 14.1% G, and 8.9% C), with an overall A + T content of 76.9%. Meanwhile, the mitogenome presented a positive AT-skew and GC-skew (0.025 and 0.226, respectively). The gene arrangement is identical with the ancestral gene order of insects (Boore 1999) and Chrysomelinae species (Gómez-Rodriguez et al. 2015), but some Chrysomelinae species have translocations of *rrnL* and *rrnS* (Nie et al. 2020). All 13 PCGs initiate with typical ATN codons: three (COX1, ND5, and ND6) with ATA, and one (ATP8) with ATT, four (ATP6, COX3, ND1, and ND4) with ATG, five (*COX2, CYTB, ND2, ND3, and ND4L*) with ATC. ATP6, ATP8, COX1, COX2, CYTB, ND2, ND3, ND4L, and ND6 ended by TAA as the stop codon. ND1 and ND5 ended by TAG as the stop codon. Only ND4 and COX3 use the incomplete codon TA as their stop codon. The *rrnL* gene is 1,337 bp long with an A + T content of 82.1%, and the *rrnS* gene is 811 bp long with an A + T content of 80.3%, as is found in most insect mitogenomes. The control region, located between the *rrnS* and *tRNl* genes, is 2,109 bp long with a remarkably high A + T content (80.5%). All 22 tRNAs range from 62 bp (*trnL2*) to 77 bp (*trnl*), comprising a total length of 1,435 bp. Gene overlaps are found at 21 gene junctions and account for a total length of 177 bp, ranging from 1 to 38 bp long. The longest 38 bp overlap was located between *rrnL* and *trnl*. A total of 86 bp intergenic spacer regions are present in nine positions, ranging from 1 to 21 bp long. The largest spacer sequence of 21 bp resided between *trnl2* and COX2.
Phylogenetic analysis was performed with the concatenated nucleotide sequences of 13 PCGs genes from 30 Chrysomelidae species and *Spiniphilus spinicornis* (Vesperidae, as the outgroup). The 13 PCGs were partitioned using PartitionFinder2 (Lanfear et al. 2017). The phylogeny of Chrysomelidae was reconstructed using IQ-TREE (Nguyen et al. 2015) with the Maximum likelihood method. The ML phylogenetic tree supported that *L. decemlineata* clustered with three other Chrysomelinae species, and produced a Chrysomelidae phylogeny (Figure 1) which was consistent with previous analyses (Nie et al. 2020).

**Ethical approval**

This study has been granted an exemption by the ethics committee of Hunan Agricultural University. Specific permission is not needed, because no relevant animals were involved.

**Author contributions**

TMD and YSW conceived and designed the study. All authors (TMD, HT, XL, GFZ, and YSW) analyzed and interpreted the results. TMD and YSW drafted the manuscript. All authors critically revised it for intellectual content and approved the final version to be published. All authors agree to be accountable for all aspects of the work.

**Disclosure statement**

No potential conflict of interest was reported by the authors.
Gómez-Rodríguez C, Crampton-Platt A, Timmermans MJTN, Baselga A, Vogler AP. 2015. Validating the power of mitochondrial metagenomics for community ecology and phylogenetics of complex assemblages. Methods Ecol Evol. 6(8):883–894.

Hare JD. 1990. Ecology and management of the Colorado potato beetle. Annu Rev Entomol. 35(1):81–100.

Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B. 2017. PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. Mol Biol Evol. 34(3):772–773.

Meng GL, Li YY, Yang CT, Liu SL. 2019. MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Res. 47(11):e63.

Nguyen LT, Schmidt HA, Haeseler AV, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Nie RE, Andújar C, Gómez-Rodríguez C, Bai M, Xue HJ, Tang M, Yang CT, Tang P, Yang XK, Vogler AP. 2020. The phylogeny of leaf beetles (Chrysomelidae) inferred from mitochondrial genomes. Syst Entomol. 45(1):188–204.