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MITOGENOME ANNOUNCEMENT

Characterization of the complete mitochondrial genome of *Pentatoma semiannulata* (Hemiptera: Pentatomidae)

Juan Wang[a]*, Yutong Ji[a]*, Hu Li[b], Fan Song[b], Lisheng Zhang[a] and Mengqing Wang[a]

[a]Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, China; [b]Department of Entomology, MOA Key Lab of Pest Monitoring and Green Management, College of Plant Protection, China Agricultural University, Beijing, China

ABSTRACT

The *Pentatoma semiannulata* is an important fruit pest in Chinese agricultural system. In current study, the complete mitochondrial genome of *P. semiannulata* is determined. This mitogenome is 15,515 bp in size and comprises of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and a control region. Gene order is identical to that of the putative ancestral arrangement of insects. All protein-coding genes initiate with ATN, except for *ATP8*, *COX1* and *NAD1* use GTG or TTG as the start codon, and terminate with TAA with the exception for *COX2* which uses a single T residue as the stop codon. All tRNAs, ranging from 62 to 72 bp, have the clover-leaf structure except for $tRNA^{Ser(AGN)}$. The monophyly of Pentatomidae is highly supported by the phylogenetic tree and *P. semiannulata* is very close to other herbivorous species of the remaining Pentatomidae species.

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Mitochondrial genome; Heteroptera; Pentatominae; *Pentatoma semiannulata*

Pentatomidae is one of the most diverse groups in Heteroptera, occurring world widely (Rider et al. 2018). *Pentatoma semiannulata* belongs to the subfamily Pentatominae in Pentatomidae, has gotten farmers' much attention by its harm to pear and birch. In this study, the complete mitochondrial genome of *P. semiannulata* was sequenced and described. Adult specimens were collected from Ningshan County (28°26′2″N, 108°26′52″E) of Shaanxi Province in China in 2018. Samples have been deposited at the Entomological Museum of China Agricultural University (No. HEM-1732).

The total genomic DNA was extracted from the whole body of the specimen using the QIAamp DNA Blood Mini Kit (Qiagen, Germany) and stored at −20 °C until needed. The mitogenome was sequenced in BeiRuiHeKang biotechnology company used NGS. An Illumina TruSeq library was prepared and sequenced using the Illumina Novaseq PE150 platform with 150 bp paired-end reads. Raw reads, low quality and short reads were trimmed and removed (Schmieder and Edwards 2011; Bolger et al. 2014). High quality reads were then used to produce a denovo assembly using IDBA-UD (Peng et al. 2012) with minimum and maximum k values of 40 and 160 bp, respectively. The accuracy of the assembly was verified by mapping clean reads onto the obtained mt contig (mismatches = 2%, maximum gap size = 3 bp and minimum overlap = 100 bp).

The complete mitogenome of *P. semiannulata* is 15,515 bp in size (GenBank accession number: MT985377) including 37 typical insect mitochondrial genes (13 protein-coding genes, 22 transfer RNA genes, and two ribosomal RNA genes) and a control region. Gene order is identical to that of the putative ancestral arrangement of insects (Cameron 2014; Xu et al. 2019). The nucleotide composition of the mitogenome is biased toward A and T, with 77.1% of A + T content (A = 42.2%, T = 34.9%, C = 12.8%, G = 10.1%). The AT-skew is positive (0.09) whereas GC-skew is negative (−0.12). Ten protein-coding genes initiate with ATN codons (three with ATA, four with ATG, two with ATT, and one with ATC), whereas *ATP8* starts with GTG and TTG is used by *COX1* and *NAD1* as the start codon. The stop codon TAA or TAG is distributed to twelve protein-coding genes (eleven with TAA, and one with TAG). However, the *COX2* uses a single T residue as an incomplete stop codon which is common in other true bug mitogenomes (Wang et al. 2017; Zhao et al. 2017; Zhang et al. 2019; Wu et al. 2020a).

There are 22 tRNA genes, ranging from 62 to 72 bp in length, and all of them can be folded into typical clover-leaf secondary structure except for $tRNA^{Ser(AGN)}$, the dihydrouridine (DHU) arm of which forms a loop, as is common phenomenon in most insects (Jiang et al. 2016; Xu et al. 2019; Wu et al. 2020a, 2020b). The length of *lrRNA* and *srRNA* is 1,273 bp and 829 bp, respectively. The A + T content of *lrRNA* and *srRNA* are 79.7% and 76.7%. The control region is located between *srRNA* and $tRNA^{Ile}$, which is 782 bp in length with an A + T content of 74.2%.

Phylogenetic tree was constructed by maximum-likelihood (ML) analysis and generated by IQ-TREE 2.0.6 (Bui et al. 2020), based on the dataset of the 13 protein-coding genes and two rRNA genes from 12 species of different families and two

CONTACT Mengqing Wang mengqingsw@163.com Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, China
*These authors have contributed equally to this work.

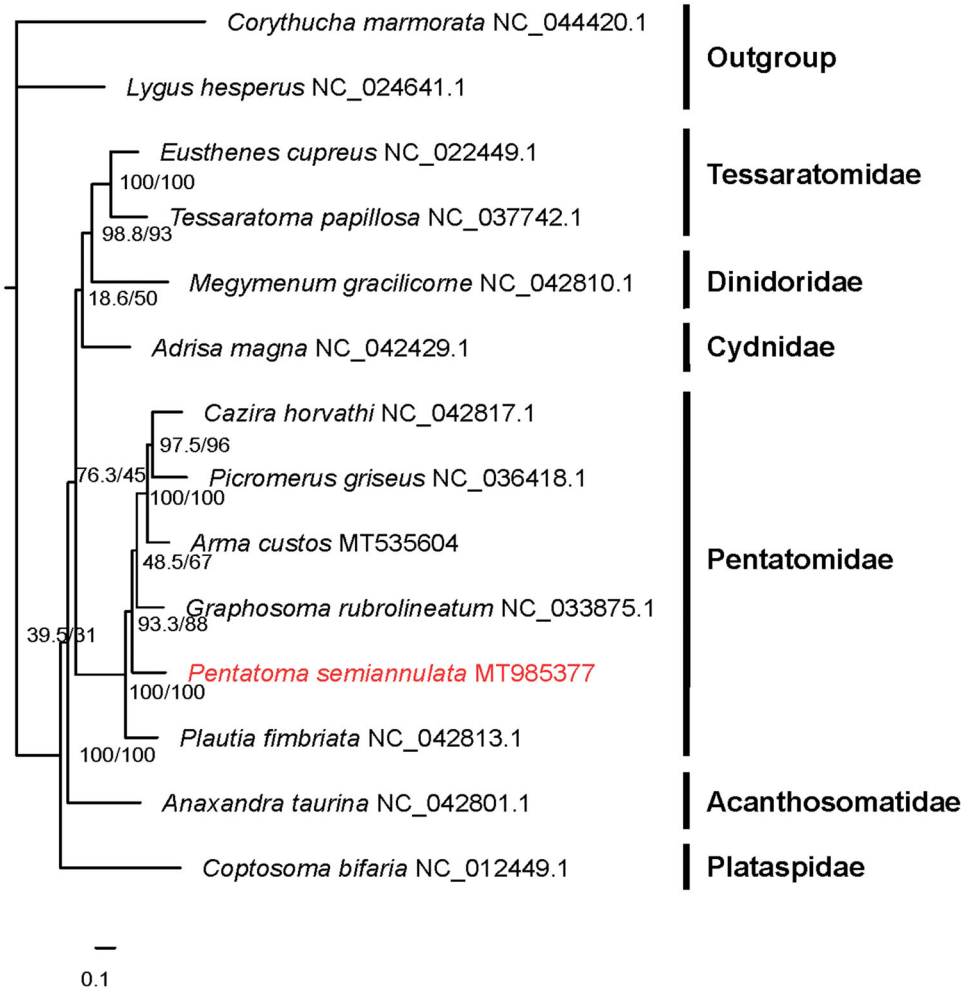

Figure 1. Phylogeny of *Pentatoma semiannulata* and other 11 Pentatomoidea species which was inferred from ML analysis of the 13 protein-coding genes and two rRNAs genes. Numbers above each node separated by '/' indicated support values of SH-aLRT (left) and ultrafast bootstrap (right) respectively. The newly sequenced mitochondrial genome was highlighted in red.

outgroups (Figure 1). Each family showed a monophyletic cluster. The monophyly of the Pentatomidae was highly supported in this phylogenetic analysis, and predatory species were evolved from herbivorous species in the family Pentatomidae. The complete mitogenome of *P. semiannulata* could provide the molecular genetic markers for the further phylogenetic analysis in Pentatomidae.

Disclosure statement

All authors have read and approved the final manuscript. The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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Data availability statement

The data that support the findings of this study are openly available in [NCBI] at [https://www.ncbi.nlm.nih.gov/], reference number [MT985377].

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