Characterization of the complete mitochondrial genome of *Arma custos* (Hemiptera: Pentatomidae)

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**ABSTRACT**

The *Arma custos* is an important natural enemy of agricultural and forest pests. The complete mitochondrial genome (mitogenome) of *A. custos* was determined in the present paper. This mitogenome is 15,629 bp in size and comprises of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and a control region. All protein-coding genes are initiate with ATN, except *ND2*, *COX1*, *ATP8* and *ND1* use TTA or TTG as the start codon, and terminate with TAA with the exception of *COX2* and *ND5* which use a single T residue as the stop codon. All tRNAs, ranging from 63 to 72 bp, have the cloverleaf structure except *tRNA^{Ser(AGN)}*. The monophyly of the subfamily Asopinae is highly supported by the phylogenetic tree and *A. custos* is recovered as sister to the remaining Asopinae species.

Pentatomidae is one of the most diverse groups in Heteroptera. This family currently contains more than 4,949 species distributed in 940 genera and ten subfamilies, occurring in the Neotropical region exclusively (Rider et al. 2018). In Pentatomidae, the subfamily Asopinae is a group of predators that present great potential for biological control (De Clercq 2000; Lupoli 2019). *Arma custos* has been used as predators because of its ability to effectively suppress a wide range of agricultural and forest pests (Zou et al. 2013; Zhao et al. 2018). In this study, the complete mitochondrial genome (mitogenome) of *A. custos* was sequenced and described. The sample was collected from Yongzhou, Hunan, China (26°21′16″N 111′11′39″E). Voucher specimen is stored at the Entomological Museum of China Agricultural University (No. HEM-047).

The complete mitogenome of *A. custos* is 15,629 bp long including 37 typical insect mitochondrial genes (13 protein-coding genes, 22 transfer RNA genes, and two ribosomal RNA genes) and a control region. No rearrangement occurs in this mitogenome and gene order is identical to the putative ancestral arrangement of insects (Cameron 2014; Xu et al. 2020). Except for the control region, 19 inter-genic regions, ranging from 1 to 27 bp, have been found in this mitogenome. There are totally 33 bp overlapped nucleotides between neighboring genes in 7 locations, ranging from 1 to 8 bp in size.

The A+T content of the mitogenome is 75.8% (A = 42.1%, T = 33.7%, C = 13.7%, G = 10.5%) which is significantly biased toward AT. The AT-skew is positive (0.11) whereas GC-skew is negative (−0.13). The nucleotide skew statistics for the minority strand (N strand) exhibited moderate T skew and G skew, and the majority strand (J strand) display a slight T skew and C skew. Nine protein-coding genes initiate with ATN codons (3 with ATA, 4 with ATG, and 2 with ATT), whereas *ND2* start with TTA and TTG is used by *COX2*, *ATP8* and *ND1* as the start codon, which were also reported common in other true bugs (Wang et al. 2017). The stop codon TAA was assigned to 11 protein-coding genes. The exceptions are the *COX2* and *ND5* use a single T residue as incomplete stop codon which is common in true bug mitogenomes (Zhao et al. 2017; Zhang et al. 2019).

There are 22 tRNA genes, ranging from 63 to 72 bp in length, in this mitogenome determined by the tRNAscan-SE (Lowe and Chan 2016) and ARWEB (Laslett and Canbäck 2008). The secondary structure of 21 tRNAs were typical clover-leaf structure except *tRNA^{Ser(AGN)}*, in which the dihydrouridine (DHU) arm formed a loop, as is common phenomenon in most insects (Jiang et al. 2016). The length of *IrRNA* and *srRNA* is 1,285 bp and 797 bp, respectively. The A+T content of *IrRNA* and *srRNA* are 79.1% and 77.4% which are higher than the whole genome. The control region is located between *srRNA* and *tRNA^{Met*}, which is 923 bp in length with an A+T content of 74.1%.

Phylogenetic tree was constructed by maximum-likelihood (ML) analysis and generated by IQ-TREE 1.6.5 (Trifinopoulos et al. 2016), based on the dataset of the 13 protein-coding genes and two rRNA genes from 11 species in Pentatomidae and two outgroups (Figure 1). Each subfamily showed a monophyletic cluster except the Podopinae, since *Graphosoma rubrolineatum* presented a sister position to Asopinae. This result indicate that the subfamily Podopinae...
may be a paraphyly group, which is congruent with previous hypotheses (Liu et al. 2019). The monophyly of the Asopinae is highly supported in this phylogenetic analysis and *A. custos* is recovered as sister to the remaining Asopinae species. The mitogenome information of *A. custos* could provide basic data for the future studies of the mitogenomic diversities and evolution of the true bugs.

**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 will be available in GenBank at https://www.ncbi.nlm.nih.gov/, Accession number MT535604.

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**Figure 1.** Phylogeny of *Arma custos* and other 12 Pentatomoidea species which was inferred from ML analysis of the 13 protein-coding genes and two rRNAs genes. Number above each node indicates the ML bootstrap support values. The newly sequenced mitochondrial genome is highlighted by the asterisk.
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