

Characterization of the complete mitochondrial genome of *Eysarcoris aeneus* (Heteroptera: Pentatomidae), with its phylogenetic analysis

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ABSTRACT

In this study, the complete 16,065 bp mitochondrial genome of *Eysarcoris aeneus* was determined from China using next-generation sequencing technology. It consists of 13 protein-coding genes, 22 tRNAs, 2 ribosomal RNAs, and a control region. Among them, 23 genes were located on J-strand, and the other genes (*nad5*, *nad4*, *nad4L*, *nad1*, *trnQ*, *trnC*, *trnY*, *trnF*, *trnH*, *trnP*, *trnL1*, *trnV*, *12S rRNA*, and *16S rRNA*) were located on the N-strand. The phylogenetic tree was constructed using MrBayes method based on the 13 protein-coding genes (PCGs) showed the present species clustered within the Pentatomidae. The complete mitogenome data would be useful for further study of Pentatomoidea and Pentatomomorpha.

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The genus *Eysarcoris* Hahn, 1834 (Heteroptera: Pentatomidae) is an agricultural pest. Both the mature and immature stages of insects injure rice plants by chewing leaf and root tissues, or sucking fluid sap from stems and grains. The injury from feeding leads to damage showing symptoms of skeletonized and defoliated leaves, dead hearts, whiteheads, or stunted and wilted plants (Lee et al. 2009; Nasiruddin and Roy 2012). However, most researches were focused on the morphology, and no mitogenome data was available. Here, we sequenced the complete mitochondrial genome of *Eysarcoris aeneus* for the first time.

The specimens of *E. aeneus* were collected from Pangquangou National Nature Reserve (N 37°51', E 111°28'), Shanxi Province, and the voucher specimens were deposited in the Entomology Institute of Shanxi Agricultural University, Shanxi, China. These sequences were annotated in comparison with previously reported mitogenome sequence of *Eurydema gebleri* (Genbank accession number: NC027489), using Geneious 8.1.4 (Kearse et al. 2012). Additionally, we used the mitochondrial genome annotation (MITOS) server (Bernt et al. 2013) and tRNAscan-SE server (Lowe and Chan 2016) for annotation. The Bayesian Inference (BI) tree was constructed to investigate the molecular taxonomic position of *E. aeneus* using the nucleotide sequences of 13 protein-coding genes (PCGs). The optimal partitioning schemes and corresponding nucleotide substitution models for each dataset were determined using PartitionFinder v1.1.1 (Lanfear et al. 2012).

The complete mitogenome of *E. aeneus* is 16,065 bp in length (Genbank accession number: MK841489), and has 13 PCGs, 22 tRNAs (transfer RNA genes), 2 rRNAs (ribosomal RNA genes), and a control region. The gene arrangement and structure of the genes are similar to those of other pentatomid species (Zhao et al. 2018). The overall base composition of the genome is 43.08% A, 12.84% C, 9.81% G, and 34.27% T, exhibiting an obvious A + T bias (77.354%). The AT-skew (0.114) for the whole mitogenome is slightly positive while GC-skew (−0.134) is negative, indicating a higher occurrence of As than Ts and Cs than Gs. The four PCGs (*cox1*, *atp8*, *nad6*, and *nad1*) get off by the typical TTG start codon, and other nine PCGs use ATG as the initiation codon. The 12 PCGs use TAA as the stop codon, except *cox2*, which ends with T. The lengths of tRNAs range from 63 to 73 bp and all tRNAs have the typical cloverleaf structure except for *trnS1*, which lacks a dihydrouridine (DHU) arm. The lengths of two rRNAs were 809 bp (12S rRNA) and 1279 bp (16S rRNA).

In the BI tree of concatenated nucleotide sequences from 13 PCGs, *E. aeneus* was clustered together with other species within Pentatomoidea with a high bootstrap value and is close to *Carbula sinica* (Figure 1), which is in accordance with the traditional morphological classification. The mitogenome of *E. aeneus* will be useful for inferring the phylogenetic relationships among the members of Pentatomidae within the Pentatomoidea and Pentatomomorpha.

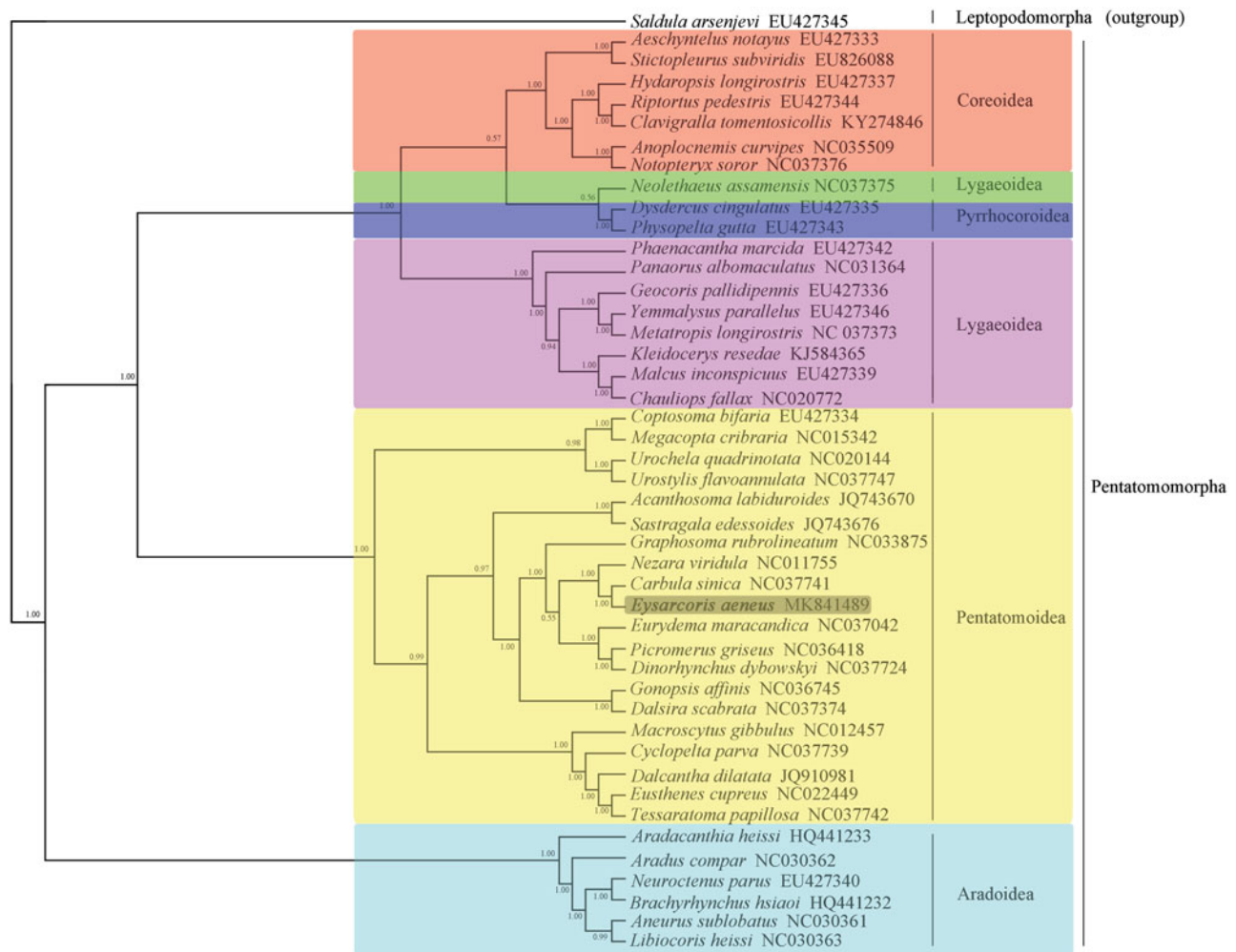


Figure 1. Phylogenetic relationship of *E. aeneus* within Pentatomomorpha inferred from 13 PCGs. Numbers on branches are Bayesian posterior probabilities.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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