

## The complete mitochondrial genome of the assassin bug *Sycanus croceovittatus* (Hemiptera: Reduviidae)

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### ABSTRACT

The complete mitochondrial genome (mitogenome) of the assassin bug, *Sycanus croceovittatus*, was sequenced and analyzed in the present study. This mitogenome spans 15,644 bp in size with a high A + T content (71.7%), containing 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and a putative control region. All protein-coding genes are initiated by ATN codons except *ND1* use GTG as start codons and terminated with TAG or TAA, except *COX3* use a single T— residue as the stop codon. All tRNAs have the typical clover-leaf like structures except for *tRNA<sup>Ser(AGN)</sup>*. A phylogenetic analysis of *S. croceovittatus* and 33 other assassin bugs is also presented using 13 protein-coding genes and 2 rRNA genes. The result supports the monophyly of Harpactorinae and the sister relationship between *S. croceovittatus* and *Agriosphodrus dohrni*.

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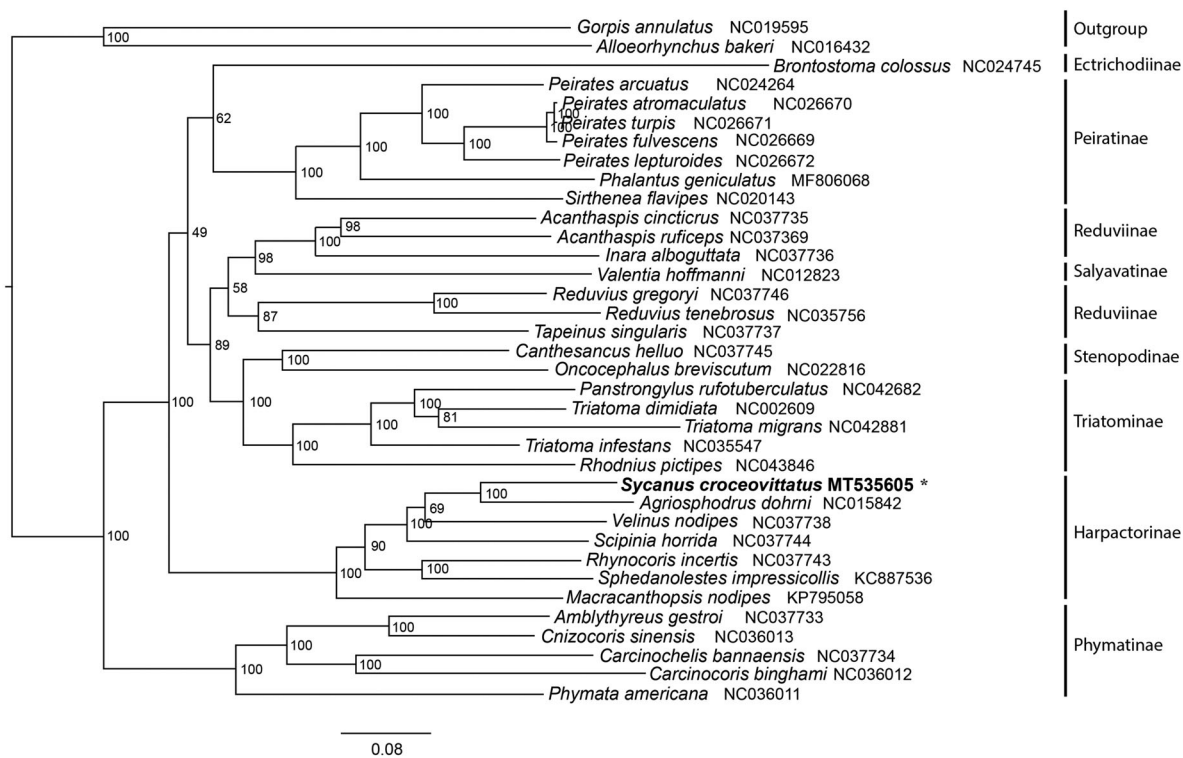
The assassin bugs Reduviidae is the second largest family in Heteroptera, including ~7000 species ranked in almost 1000 genera and 25 subfamilies (Weirauch et al. 2014). In Reduviidae, the Harpactorinae is the largest subfamily distributed around the world mainly in tropical and subtropical regions. Here, we sequenced and described the complete mitochondrial genome (mitogenome) of *Sycanus croceovittatus* from subfamily Harpactorinae. Total genomic DNA was extracted from the samples collected from Xishuangbanna, Yunnan, China (21°56'N 101°15'E). Voucher specimen and the genomic DNA were stored at the Entomological Museum of China Agricultural University (No. HEM-019). The complete mitogenome was obtained by the next-generation sequencing method with Illumina Hiseq 2500 and the sequence has been submitted to the GenBank (Accession number: MT535605).

The complete mitogenome of *S. croceovittatus* is a single circular DNA molecule of 15,644 bp in length containing 13 protein-coding genes (PCGs), 22 transfer RNA (tRNAs), 2 ribosomal RNA (rRNAs), and a control region locating between *srRNA* and *tRNA<sup>lle</sup>*. The nucleotide composition of the whole mitogenome sequence is significantly biased towards A + T (71.7%) and exhibits positive AT-skew (0.10) and negative GC-skew (−0.16). Gene order is identical to the putative ancestral arrangement of insect (Boore 1999; Cameron 2014). In total, there are 52 bp overlapped nucleotides between neighboring genes in 13 locations, ranging from 1 to 14 bp in size.

The PCGs is 11,101 bp in length and nine PCGs are located on the majority strand (J strand) while the remaining genes are transcribed on the minority strand (N strand). All PCGs are initiated with ATN (two with ATA, two with ATC, two with ATT and six with ATG), except the *ND1* uses the GTG as the start codon, and this unconventional start codon was also found in other assassin bugs (Li et al. 2012; Zhao, Jiang, et al. 2019). The typical stop codon TAA and TAG are assigned to 12 PCGs, whereas a single T residue is used by *COX3* as stop codon which was repeatedly found in Reduviidae mitogenomes (Chen et al. 2018; Sun et al. 2019).

This mitogenome has the complete set of 22 tRNA genes, ranging from 61 to 71 bp. All tRNAs can be determined by the ARWEN (Laslett and Canbäck 2008) and folded into the typical clover-leaf structure except the *tRNA<sup>Ser(AGN)</sup>* with the dihydrouridine (DHU) arm formed a loop, which is commonly discovered in insect mitogenomes (Li et al. 2012; Song et al. 2019). Fourteen tRNAs are located on the J strand and the rest are encoded by the N strand. The length of *lrRNA* and *srRNA* is 1270 bp and 769 bp with A + T content of 75.4% and 72.7%, respectively. The largest noncoding region is the control region which is located between *srRNA* and *tRNA<sup>lle</sup>* with 932 bp in length. Except for the control region, there are 12 inter-genic regions ranging from 1 to 92 bp in size, of which the longest one is located between *tRNA<sup>Ser(UCN)</sup>* and *ND1*.

Maximum-likelihood (ML) tree was constructed by IQ-TREE 1.6.5 (Trifinopoulos et al. 2016) under the GTR + I + G model, using sequences of 13 protein-coding genes and 2 rRNA



**Figure 1.** Maximum-likelihood (ML) phylogenetic tree of 34 Reduviidae species inferred from analysis of the 13 protein-coding genes and 2 rRNAs genes (12,726 bp). Number above each node indicates the ML bootstrap support values. Alphanumeric terms indicate the GenBank accession numbers.

genes from 34 Reduviidae and 2 Nabidae species (Figure 1). The phylogenetic relationships among Reduviidae is (((Ectrichodiinae + Peiratinae) + ((Salyavatinae + Reduviinae) + (Stenopodinae + Triatominae))) + Harpactorinae) + Phymatinae). In the phylogenetic tree, each family forms a monophyletic cluster with high support except the subfamily Reduviinae. The subfamily Reduviinae was also suspected to be a paraphyletic group in previous studies (Zhao, Chen, et al. 2019). The sister relationship between *S. croceovittatus* and *Agriosphodrus dohrni* is recovered with the high bootstrap support value.

## Disclosure statement

No potential conflict of interest was reported by the author(s).

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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 MT535605.

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