The mitochondrial genome of the assassin bug *Sclomina erinacea* (Hemiptera: Reduviidae)

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**ABSTRACT**

The complete mitochondrial genome (mitogenome) of the assassin bug, *Sclomina erinacea* Stål, was determined in the present study. The sequenced mitogenome is a typical circular DNA molecule which is 15,828 bp in length, containing 13 protein-coding genes, two rRNA genes, 22 tRNA genes and a putative control region. All protein-coding genes are initiated by ATN codons and terminated by TAA or TAG codons except COII, COIII and ND4 which use a single T residue as the stop codon. All tRNAs have the cloverleaf structure with the exception of tRNA^{Ser(GCU)} and the length of them range from 62 to 70 bp. The control region is 818 bp long with an A + T content of 67.1%. The phylogenetic analysis supports the monophyly of Harpactorinae and *Sclomina erinacea* is the closest relative to *Macracanthopsis nodipes*.

The assassin bug Harpactorinae (Hemiptera: Reduviidae) is the largest subfamily of Reduviidae distributed around the world mainly in tropical and subtropical regions. The Harpactorinae currently contains about 180 species in China, occurring in the southern region of China. *Sclomina erinacea*, which belongs to the subfamily Harpactorinae, is a widely distributed predatory natural enemy insect in China and can prey on a variety of agricultural pests (Zhao and Liu 2015). In this study, the complete mitogenome of *Sclomina erinacea* is sequenced and annotated for the first time. The samples were collected in Meiling, Jiangxi, China (28°48′39.00″N 115°41′52.1″E). Voucher specimen was deposited at the Entomological Museum of China Agricultural University (No. VCim-00168) and the sequence has been submitted to GenBank (Accession number: MK696614).

The mitogenome is a single circular DNA molecule of 15,828 bp in size that encode 37 genes (13 protein-coding genes, 22 tRNA genes, and two rRNA genes) and a control region. Gene order is identical to the putative ancestral gene arrangement of insect (Cameron 2014; Song et al. 2016a; Li et al. 2017; Liu et al. 2019). Except control region, this mitogenome has 3 inter-genic regions > 90 bp. A 126 bp noncoding region could be found between trna^Cys^ and trna^Tyr^ and a 94 bp noncoding region exist between CytB and trna^Ser^ (UCN). Another 218 bp noncoding region is located between trna^Ser^ (UCN) and ND1, which has also been found in other assassin bugs (Sun et al. 2019). There are totally 51 bp overlapped nucleotides between neighboring genes in 12 locations, ranging from 1 to 14 bp in size.

The nucleotide composition of the whole mitogenome shows highly A + T biased. The A + T content is 71.6% with positive AT-skew (0.14) and negative GC-skew (~0.17). All protein-coding genes initiate with ATN codons and terminated by TAA or TAG codons except COII, COIII and ND4 which use a single T residue as the stop codon. All tRNAs have the cloverleaf structure with the exception of tRNA^{Ser(GCU)} and the length of them range from 62 to 70 bp. The control region is 818 bp long with an A + T content of 67.1%. The phylogenetic analysis supports the monophyly of Harpactorinae and *Sclomina erinacea* is the closest relative to *Macracanthopsis nodipes*.
Disclosure statement
No potential conflict of interest was reported by the authors.

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