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Complete nucleotide sequence and organization of the mitochondrial genome of *Sirthenea flavipes* (Hemiptera: Reduviidae: Peiratinae) and comparison with other assassin bugs

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Abstract

The complete sequence of the mitochondrial (mt) genome of the assassin bug, *Sirthenea flavipes* (Stål), was determined. The circular genome is 15, 961 bp long and contains a standard gene complement, i.e., the large and small ribosomal RNA (rRNA) subunits, 22 transfer RNA (tRNA) genes, 13 protein-coding genes (PCGs), and the 1, 295 bp control region. The nucleotide composition of *S. flavipes* mt genome is 71.8% AT-rich, reflected in the predominance of AT-rich codons in PCGs. Compared with the other three reduviid species available in complete mt genomes, the genome architecture as well as the nucleotide composition, codon usage, and amino acid composition reflected high similarity. All PCGs use standard initiation codons (ATN); however, *ND4L* and *ND1* started with GTG. Canonical TAA and TAG termination codons are found in nine PCGs, the remaining four (*COIII*, *ND3*, *ND5*, and *ND1*) have incomplete termination codons. All tRNAs have the typical clover-leaf structure, except the dihydrouridine (DHU) arm of $tRNA^{Ser\ (AGN)}$ forms a simple loop as seen in many other metazoans. Secondary structure models of the ribosomal RNA genes of *S. flavipes* are presented and are similar to those proposed for other insects. The structure of *rrnL* is more conservative than that of *rrnS* among sequenced assassin bugs. The monophyly of Reduviidae is highly supported by Bayesian inferences, and the Peiratinae presents a sister position to the Triatominae+ (Salyavatinae + Harpactorinae).

Key words: Mitochondrial genome, *Sirthenea flavipes*, RNA secondary structure

Introduction

Mitochondria are involved in most of the chemical reactions in cellular respiration. They are the center of the cell power. The mitochondria are proposed to have originated from eubacteria ancestors undergoing endosymbiosis (Kita & Takamiya 2002). During the last ten years, insect mt genomes have been extensively sequenced and studied as a result of the improvements of genomic technologies and the interest in mt genome organization and evolution (Boore 2006).

As most metazoans, the hexapod mt genome is a double-stranded circular molecule of 14-19 kb in size (Lewis *et al.* 1995; Beckenbach & Joy 2009). The typical mt genome has a remarkably conserved set of 37 genes: 13 PCGs, two rRNA genes, and 22 tRNA genes (Wolstenholme 1992; Boore 1999). Additionally, it contains at least one sequence of variable length known in insect mt genome as the control region, which contains initiation sites for transcription and replication (Clayton 1992). Mt genome size variation is usually because of a variation in the number of intergene locations, the most common size variation occurring in the control region. Previous studies show that the control region varies from 70 bp in *Ruspolia* (Orthoptera) to 4, 599 bp in *Drosophila* (Diptera) (Garesse 1998; Zhou *et al.* 2007). However, these differences in genome length have yet to be broadly used as effective phylogenetic markers. Gene content of insect mt genome is well conserved, but some exceptions have also been reported. For example, the screw-worm *Chrysomya chloropyga*, has an extra $tRNA^{Ile}$ (Junqueira *et al.* 2004) and several species of Hemiptera contain variable numbers of tRNA genes (Shao & Barker 2003; Thao *et al*. 2004)

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