



The complete mitochondrial genome of the flat bug *Aradacanthia heissi* (Hemiptera: Aradidae)

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Abstract

The 15528 bp long complete mitochondrial genome (mt-genome) of a flat bug, *Aradacanthia heissi* Bai, Zhang & Cai, was determined. The entire genome contains typical 37 genes with an A+T content of 74.7%. The gene arrangement differs from that of *Drosophila yakuba* Burla which is considered the representative ground pattern for insect mt-genomes, as the results of inversion of *tRNA^{Ile}* - *tRNA^{Gln}* and *tRNA^{Cys}* - *tRNA^{Trp}*. All protein-coding genes (PCGs) use standard initiation codons (methionine and isoleucine), except *COI* which starts with TTG. Three of the 13 PCGs harbor the incomplete termination codon. Meanwhile, opposite CG-skew tendency occurs on the nucleotide composition and codon usage and this tendency is also reflected on the J-strand and N-strand of PCGs. All tRNAs can fold into classic clover-leaf structure, whereas the dihydrouridine (DHU) arm of *tRNA^{Ser(AGN)}* forms a simple loop. Secondary structure models of the ribosomal RNA genes of *A. heissi* are predicted and similar to those proposed for other insects. The control region is located between *srRNA* and *tRNA^{Gln}* with 81.5% A+T content, which was the most A+T-rich region of the mt-genome and four 68 bp tandem repeat units were found in this region. Phylogenetic analyses of available species of Pentatomomorpha showed Aradoidea and the Trichophora are sister groups that bolstered the mainstream hypothesis, and provide the evidence for the feasibility of mt-genome data to resolve relationships at the subfamily level in Aradidae.

Key words: Mitochondrial genome, *Aradacanthia heissi*, RNA secondary structure, Gene arrangement, Phylogenetic analyses

Introduction

In metazoans, mitochondrial genome (mt-genome) is a double-stranded, circular molecule, ranging in size from 13 to 36 kb and usually composed of 13 protein-coding genes (PCGs), two ribosomal RNA, and 22 transfer (tRNA) genes (Wolstenholme 1992; Boore 1999). Additionally, a major non-coding region is known as the A+T-rich region or the control region (CR), which is typically considered as initiation of transcription and replication (Wolstenholme 1992). In recent years, mitochondrial genomes are increasingly applied to comparative and evolutionary genomics, molecular evolution, phylogenetics, and population genetics (Wilson *et al.* 2000; Salvato *et al.* 2008), because of their relatively simple structures and their mutation rates which are higher than in nuclear DNA (Avisé *et al.* 1987; Simon *et al.* 1994). Mt-genome has become an extensively used molecular marker for the reconstruction of phylogenetic relationships at different insect taxonomic levels. Gene rearrangement events that may serve as useful models for evolutionary studies have been frequently discussed in insects, such as frequent rearrangements of tRNA clusters within Hymenoptera and Lepidoptera (Boore & Brown 1998; Downton *et al.* 2002; Cameron & Whiting 2008; Kurabayashi *et al.* 2008; Wei *et al.* 2010).

A better understanding of the mt-genome evolution allows potential pitfalls in data analysis to be recognized and avoided (Simon *et al.* 2006). However, because of unbalanced studies in mt-genomes, the available data of insect mt-genome is scarce compared to vertebrate taxa (Salvato *et al.* 2008).