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The complete mitochondrial genome of the plant bug *Nesidiocoris tenuis* (Reuter) (Hemiptera: Miridae: Bryocorinae: Dicyphini)

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Abstract

Nesidiocoris tenuis (Reuter) is a zoophytophagous mirid which is considered both as a significant natural enemy and an important pest of crops. The complete mitochondrial genome (mitogenome) of *N. tenuis* was determined using long PCR and a primer walking sequencing strategy. The genome is 17,544 bp in length and contains 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA genes (*lrRNA* and *srRNA*), and a duplicate control region. The gene order of this newly sequenced genome is identical with the ground plan of insects. The nucleotide composition is biased toward adenine and thymine with a high AT content (75.0%). The most frequent codons are ATA, TTA, TTT, and ATT. All the PCGs initiate with the standard start codon ATN. All tRNAs have the classic cloverleaf structures, with the exception of *tRNA^{Ser(UCG)}*, which lacks the dihydrouridine (DHU) arm. Secondary structures of the two ribosomal RNAs were shown referring to previous models. Variable numbers of tandem repeats were detected in the control region. The phylogenetic analyses shows that *N. tenuis* is the sister group to *Lygus lineolaris* (Palisot de Beauvois).

Key words: *Nesidiocoris tenuis*, mitogenome, gene organization and order, phylogeny

Introduction

Nesidiocoris tenuis is a mirid of Mediterranean origin whose status as a beneficial and/or pest species has been controversial for a long time (Hughes *et al.* 2009; Perdikis *et al.* 2009; Arno *et al.* 2010). It is not only a predatory bug of whiteflies, leafminers, thrips, and spider mites (Torreno 1994; Torreno & Magallona 1994; Carnero *et al.* 2000; Urbaneja *et al.* 2005; Perdikis *et al.* 2009), but also an important pest of tobacco and other crops (El-Dessouki *et al.* 1976; Prasad *et al.* 1979; Patel 1980).

Mitogenomes are chosen as common molecular markers because of their abundance in animal tissues, small genome size, faster rate of evolution, low rate or absence of sequence recombination, and their evolutionary conserved gene products (Lin & Danforth 2004; Simon *et al.* 2006; Gissi *et al.* 2008). Mitochondrial DNA forms a small double-stranded circular molecule and its length varies from 13 kb to 36 kb. It encodes 13 protein-coding genes (PCGs), 22 tRNA genes, and two ribosomal RNA genes (rRNAs) (Wolstenholme 1992a; Boore 1999). In addition, each mitochondrial DNA contains a major non-coding region with high A+T content that plays a role in initiation of transcription and replication (Wolstenholme 1992a). High rate of nucleotide substitutions, insertions/deletions, and a variable number of tandem repeats, contribute to the length of the control region, being highly variable among different insects (Fauron & Wolstenholme 1980; Inohira *et al.* 1997).

Overall, mitochondrial DNA plays an important role in metabolism, apoptosis, disease, and aging and comparative genomics (Boore 1999); although there is some criticism on using mitochondrial DNA for phylogenetics, especially at the deeper levels (Rubinoff & Holland 2005; Cameron *et al.* 2007).