



# Article

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## The mitochondrial genome of *Coridius chinensis* (Hemiptera: Dinidoridae)

LI LIU<sup>1</sup>, HU LI<sup>1</sup>, FAN SONG<sup>1</sup>, WEN SONG<sup>1</sup>, XUN DAI<sup>2</sup>, JIAN CHANG<sup>2</sup> & WANZHI CAI<sup>1,2</sup>

<sup>1</sup>Department of Entomology, China Agricultural University, Yuanmingyuan West Road, Beijing 100193, China

<sup>2</sup>Research Center of Hongta Group, Yuxi, Yunnan 653100, China

<sup>3</sup>Corresponding author. E-mail: caiwz@cau.edu.cn

### Abstract

The nearly complete mitochondrial genome of *Coridius chinensis* (Dallas) is reported in this study. The mitogenome is a double-stranded circular molecule of more than 14,648 bp in length with an A+T content of 75.1%. It encoded 37 genes as in other insect mtDNAs, including 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes and a control region (unsuccessful sequencing), and the gene order is the same as most other known heteropteran mitogenomes. All of the 22 transfer RNAs can be folded into the typical cloverleaf structure except *tRNA*<sup>Ser(AGN)</sup>, which can only form a simple loop at the site of dihydrouridine (DHU) arm as known in other metazoans. The secondary structures of the large and small ribosomal RNAs of *C. chinensis* are similar to other presented insects. The *rrnL* consisted of six structural domains and 40 helices, and the *rrnS* consisted of three structural domains and 26 helices. Nine PCGs are initiated with the standard initiation codons (ATN), while *ND6* and *ND1* use GTG, and *COI* and *ATP8* use TTG. All PCGs stopped with TAA/TAG termination codons except the *COII* terminated with a single T residue. Asymmetry in the nucleotide composition between J-strand and N-strand was observed in this mitogenome.

**Key words:** Mitochondrial genome, *Coridius chinensis*, RNA secondary structure

### Introduction

The mitochondrial genome (mitogenome) is a small double-stranded circular molecule in metazoans, which ranges in size from 13 to 36 kb and usually composed of 13 protein-coding genes (PCGs), two ribosomal RNA (rRNA) genes, and 22 transfer (tRNA) genes (Wolstenholme 1992; Boore 1999). In addition, 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). The mitogenome is widely used to provide information on comparative and evolutionary genomics, on molecular evolution and patterns of gene flow, on phylogenetics and population genetics (Wilson *et al.* 2000; Salvato *et al.* 2008), as their structures are simple and mutation rates are higher than nuclear DNA (Avisé *et al.* 1987; Simon *et al.* 1994).

Dinidoridae is a relatively small family of Heteroptera with approximately 100 species and 16 genera. Some species are crop pests, others may be as experimental animals in the laboratory, and at least one is used as a condiment (Rolston *et al.* 1996). In recent years, many mitochondrial and nuclear DNA sequences of some Dinidoridae species, including the 12S rDNA and 16S rDNA subunits, cytochrome oxidase I (COI) sequences, 18S rDNA and 28S rDNA subunits, and *Hox* gene, have been sequenced and used for phylogenetic inference (Li *et al.* 2005, 2006a, 2006b; Xie *et al.* 2005; Grazia *et al.* 2008; Lis *et al.* 2011, 2012; Tian *et al.* 2011).

Because no complete mitogenome of Dinidoridae species has been reported yet, we decided to determine the first one in this family. *Coridius chinensis* is a crop pest; however, it has also been used as a traditional Chinese medicine, which can regulate breath and relieve pain (Yao 2006). In this study, we report the mitogenome of *C. chinensis* and provide analyses of the nucleotide composition, tRNA and rRNA secondary structure, codon usage, and compositional biases.