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## The complete mitochondrial genome of a tessaratomid bug, *Eusthenes cupreus* (Hemiptera: Heteroptera: Pentatomomorpha: Tessaratomidae)

WEN SONG<sup>1</sup>, HU LI<sup>1</sup>, FAN SONG<sup>1</sup>, LI LIU<sup>1</sup>, PEI WANG<sup>1</sup>, HUAIZHU XUN<sup>1</sup>, XUN DAI<sup>2</sup>,  
JIAN CHANG<sup>2</sup> & WANZHI CAI<sup>1,3</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](mailto:caiwz@cau.edu.cn)

### Abstract

The 16,299 bp long mitochondrial genome (mitogenome) of a tessaratomid bug, *Eusthenes cupreus* (Westwood), is reported and analyzed. The mitogenome represents the first sequenced complete mitogenome of the heteropteran family Tessaratomidae. The mitogenome of *E. cupreus* is a typical circular DNA molecule with a total AT content of 74.1%, and contains 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes, and a control region. The gene arrangement is identical with the most common type in insects. Most PCGs start with the typical ATN codon, except that the initiation codon for *COI* is TTG. All tRNAs possess the typical clover-leaf structure, except *tRNA<sup>Ser(AGN)</sup>*, in which the dihydrouridine (DHU) arm forms a simple loop. Six domains with 45 helices and three domains with 27 helices are predicted in the secondary structures of *rrnL* and *rrnS*, respectively. The control region is located between *rrnS* and *tRNA<sup>Ile</sup>*, including some short microsatellite repeat sequences. In addition, three different repetitive sequences are found in the control region and the *tRNA<sup>Ile</sup>-tRNA<sup>Gln</sup>-tRNA<sup>Met</sup>-ND2* gene cluster. One of the unusual features of this mitogenome is the presence of one *tRNA<sup>Gln</sup>*-like sequence in the control region. This extra *tRNA<sup>Gln</sup>*-like sequence is 73 bp long, and the anticodon arm is identical to that of the regular *tRNA<sup>Gln</sup>*.

**Key words:** Mitochondrial genome, *Eusthenes cupreus*, RNA secondary structure, *tRNA<sup>Gln</sup>*-like sequence

### Introduction

The mitogenome of insects is a typically double-stranded, circular molecule, and commonly includes 13 PCGs, 22 tRNA genes, 2 rRNA genes (*rrnL* and *rrnS*), and one non-coding region known as the control region which plays a role in initiation of transcription and replication (Wolstenholme 1992; Boore 1999). The mitogenome is becoming increasingly important for the study of population genetics and molecular evolution and has been widely regarded as the molecular marker for the phylogenetic analysis in metazoans because of its relatively simple genetic structure, high rate of evolution, low or absence of sequence recombination, and evolutionary conserved gene products (Lin *et al.* 2004; Gissi *et al.* 2008). In addition, the comparative study of mitogenome sequences can give us a better understanding of the genome structure, gene arrangement, and the evolution of arthropod lineages (Boore 1999; Shao *et al.* 2001; Hwang *et al.* 2001; Nardi *et al.* 2003).

Tessaratomidae is a family of true bugs with approximately 240 species and 55 genera (Rolston *et al.* 1994; Rider 2006). All tessaratomids are large to extremely large (often over 20 mm, some longer than 40 mm), robustly ovate or elongate, and phytophagous. They generally feed upon plants belonging to the plant orders Rosales and Sapindales, and spend most of their lives in tree leaves and stems. Many species are of economic importance as agricultural pests, such as the litchi stink bug, *Tessaratomia papillosa* (Westwood), which are destructive pests of litchi trees in China (Cassis & Gordon 2002, <http://en.wikipedia.org/wiki/Tessaratomidae> - cite\_ref-cassisgross\_7-0#cite\_ref-cassisgross\_7-0). A few species are also consumed as human food in some countries, such as the edible stink bug *Encosternum delegorguei* Spinola, which is a well known food in Zimbabwe and among the Venda people of South Africa (Dzerefos *et al.* 2002).