The complete mitochondrial genome of *Monolepta hieroglyphica* (Motschulsky) (Coleoptera: Chrysomelidae)

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**ABSTRACT**

*Monolepta hieroglyphica* (Motschulsky) (Coleoptera: Chrysomelidae) is an important agricultural insect pest. In this study, the complete mitochondrial genome of *M. hieroglyphica* (GenBank accession number MW732714) was sequenced using Illumina HiSeq X Ten. The mitogenome was 16,213 bp long and comprised 13 protein-coding genes (PCGs), two ribosomal RNA genes (rRNAs), 22 transfer RNA genes (tRNAs) and a putative control region (CR). The nucleotide composition of the *M. hieroglyphica* mitochondrial genome was significantly biased (A, G, C and T accounted for 41.04%, 8.01%, 11.76% and 39.18%, respectively) with 80.23% A + T content. Two tRNAs were located between tRNA-Leu and the CR, separated by tRNA-Val. The CR, located between 12 s rRNA and tRNA-Ile, was 1,661 bp long. The length of the 22 tRNAs ranged from 61 to 71 bp. Phylogenetic analyses of 29 Chrysomelidae-Galerucinae species based on 13 mitochondrial protein-coding genes reconstructed using Bayesian 3.2.0 showed that the *M. hieroglyphica* mitogenome was clustered with the existing three different species of the *Monolepta* genus mitogenomes in a monophyletic manner. The *M. hieroglyphica* mitogenome provides an important data resource for further studies and contributes to our understanding of the phylogeny of this group.

*Monolepta hieroglyphica* (Motschulsky) belongs to the Galerucinae of Chrysomelidae of Coleoptera (Yu et al. 1996). It is mainly distributed in more than a dozen countries and regions in East Asia and Southeast Asia and is widely distributed in China. It is a high-temperature, drought-type pest and is characterized by its large occurrence area, long damage period, fast reproduction and migratory flight, miscellaneous feeding habits, and a wide range of hosts (Chen et al. 2007). In recent years, the damage to soybean, corn, rice, some vegetables and other crops caused by *M. hieroglyphica* has increased significantly, and its area of occurrence continues to expand (Zhang et al. 2014). There has been considerable research on its prevention and treatment (Tian et al. 2014). In this study, the mitochondrial genome of *M. hieroglyphica* was sequenced and analyzed, and phylogenetic trees were established. The findings are of great significance in providing insights for early warning and management of this pest.

The *M. hieroglyphica* sample was collected from Yinchuan, Ningxia, China (38°54’30”N, 106°32’2”E) in July 2020 and deposited in the insect herbarium of the School of Agriculture, Ningxia University (SAXU; voucher number SBCFYYJ202007-01). The complete mitochondrial genome of *M. hieroglyphica* (GenBank accession number MW732714) was sequenced using Illumina HiSeq X Ten. Genes were assembled by MITOBim v1.9 (Hahn et al. 2013). Ribosomal RNA (rRNA) and transfer RNA (tRNA) annotations were confirmed and corrected by MITOS online (Bernt et al. 2013). This mitogenome was a circular DNA molecule, 16,213 bp in length and contained the typical set of 37 genes, including 13 protein-coding genes (PCGs: ATP6, ATP8, COI-III, ND1-6, ND4L and CYTB), two rRNA genes (12S rRNA and 16S rRNA), 22 tRNA genes (12S rRNA and 16S rRNA), 22 tRNAs and a putative CR. The nucleotide composition of the *M. hieroglyphica* mitochondrial genome was 41.04% A, 39.18% T, 11.76% C and 8.01% G; therefore, A + T content was 80.23%. Fourteen genes were located on the H-strand and the others were transcribed on the L-strand. The start codon ATT was shared with COX1, COX2, ND2, ND3, ND5 and ND6; the start codon ATG was shared with COX3, ATP6, ND4, ND4L and CYTB; ATP8 started with codon ATC; and ND1 started with codon TTG. The conservative stop codon TAA was shared with COX1, COX3, ATP6, ATP8, ND2, ND4L and ND6; the stop codon TAG was shared with ND1, ND3 and CYTB; and COX1, ND4 and ND5 terminated with T−. 16 s rRNA and 12 s rRNA were located between tRNA-Leu and the putative CR, separated by tRNA-Val. The 16S rRNA was 1,249 bp in length and the 12S rRNA was 744 bp. The mitogenome had a total of 51 bp intergenic spacer sequences and 46 bp overlap sequences, which comprised 8 and 14 regions ranging from 1 to 20 bp and 1 to 8 bp, respectively.

Another twenty-nine Chrysomelidae-Galerucinae species and three outgroups (*Caryopemon giganteus*, *Acanthoscelides obsoletus* and *Caryopemon abbreviatus*) were selected as mitogenomes of the outgroup. The complete mitochondrial genomes of the three outgroups were downloaded from GenBank (Table 1).

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obectus and Bruchidius uberatus) were selected to reconstruct the phylogenetic tree. This was reconstructed using Bayesian 3.2.0 (Ronquist et al. 2012) based on 13 mitochondrial PCGs. The best-fit nucleotide substitution model was selected as ‘GTR + G+I’ using the Akaike Information Criterion (AIC) in jModelTest 0.1.1 (Posada 2008). The phylogenetic analysis showed that the M. hieroglyphica mitogenome was clearly clustered with the mitogenomes of the existing three different species of the Monolepta genus in a monophyletic manner. It was genetically closest to Galeruca sp. and Apophylia sp. (Figure 1).

In conclusion, the M. hieroglyphica mitogenome sequence will provide a useful data resource for further studies of M. hieroglyphica and contributes to understanding of the phylogenetic relationships of the Galerucinae clade.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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Data availability statement
Mitochondrial genome sequence can be accessed via accession number MW732714 in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/. The associated BioProject, SRA, and BioSample numbers are PRJNA713524, SRR13959601 and SAMN18253528, respectively.

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