**MITOGENOME ANNOUNCEMENT**

**Complete mitochondrial genome of nipa palm hispid beetle Octodonta nipae Maulik (Coleoptera: Chrysomelidae: Cassidinae)**

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**ABSTRACT**

Octodonta nipae (Maulik 1921) is a dangerous forestry quarantine pest, which mainly harms palms. In the present study, we determined complete mitogenome of O. nipae. This mitogenome was 15,397 bp in length (GenBank Accession no. MW802252), which contained 2 ribosomal RNA genes, 13 protein-coding genes (PCGs) and one non-coding AT-rich region with the length of 883 bp. All of the 22 tRNA genes displayed a typical clover-leaf structure, with the exception of tRNA Phe, tRNA Leu, tRNA Asn, tRNA Pro and tRNA Thr. Twelve PCGs were initiated by ATN codons, and NAD1 started with TTT. Ten PCGs used the typical stop codons ‘TA’ and ‘TA’, while three PCGs (COX2, COX3, NAD4) used the incomplete stop codons ‘TA’ or ‘T’. Phylogenetic tree demonstrated that O. nipae belongs to the family Chrysomelidae and closer to the superfamily Cassidinae.

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Octodonta nipae (Maulik 1921); mitochondrial genome; phylogenetic relationship; phylogenetic analysis
vide essential and important DNA molecular data for further phylogenetic and evolutionary analysis of Chrysomeloidea.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/) under the accession No. MW802252. The associated BioProject, BioSample and SRA numbers are PRJNA723914, SAMN18837207 and SRR14306651, respectively.

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