The complete mitochondrial genome of Hemathlophorus brevigenatus Wei, 2005 (Hymenoptera: Tenthredinidae) with phylogenetic analysis

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ABSTRACT

The mitochondrial genome of Hemathlophorus brevigenatus Wei, 2005 collected from Huanggang Mountain of China is described using the NGS approach. The length of the sequence is 15,452 bp containing 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and one control region. The overall A + T content is 79.5%. tRNA rearrangements occur in the MQI cluster. Phylogenetic analysis of H. brevigenatus resolved it in a clade with Allantus togatus in Allantinae which provides new evidence for the phylogeny of Tenthredinidae.
terminal codon T—. Compared with the ancestral insect (Drosophila) mitochondrial genome (Boore 1999), the control region- trnI (+)- trnQ (-)- tmM (+) is rearranged to tmM (-)- trnQ (+)- control region- trnI (+) in H. brevigenatus. There are five gene overlapping regions that appeared among trnI-nad2 (1 bp), trnW-trnC (1 bp), atp6 - atp8 (7 bp), atp6 - cox3 (1 bp), and nad6-cob (1 bp). The mitogenome has nine intergenic spacers with a total length of 173 bp in 18 locations varying in size from 1 to 39 bp with the longest located between trnF and nad5.

Phylogenetic analysis of H. brevigenatus fully resolved it in a clade with Allantus togatus (MW464859) and Allantoides lucifer (K1713152) classified in the Allantinae as suggested by Wei and Nie (1998) and Taeger et al. (2010). Its placement was remote from the Siobla of Tenthredininae and clearly denied Lacourt’s system (Lacourt 1996). The phylogenetic relationships of Tenthredininae are inferred as (Athalia + ((Conaspida + Selandriinae) ((Hoplocampinae + Nematinae) (Tenthredininae + Allantinae) + (Fenusinae + Blennocampinae) + Caliroinae)))) (Figure 1). All related files are publicly available in figshare (https://figshare.com/account/home#/projects/114354).

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No potential conflict of interest was reported by the authors. The authors alone are responsible for the content and writing of the article.

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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 number MW632125. The associated BioProject, SRA, and BioSample numbers are PRJNA714776, SRR14233978, and SAMN18397095 respectively.

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