MITOCHONDRIAL DNA PART B: RESOURCES
2026, VOL. 11, NO. 12, 1431–1435
https://doi.org/10.1080/23802359.2026.2743228

Taylor & Francis
by informa

MITOGENOME REPORT

OPEN ACCESS Check for updates

The complete mitochondrial genome of *Batocera calanus* parry, 1844 (Coleoptera: Cerambycidae)

Jinning Du[a,b], Wenlong Jiao[a,b], Sihan Wang[a,b], Sikai Ke[a,b], Ruiheng Lin[a,b] and Feiping Zhang[a,b]

[a]College of Forestry, Fujian Agriculture and Forestry University, Fuzhou City, China; [b]Key Laboratory of Integrated Pest Management in Ecological Forests, Fujian Agriculture and Forestry University, Fuzhou City, China

ABSTRACT

The complete mitochondrial genome of *Batocera calanus* (Parry, 1844) was characterized using Illumina HiSeq 2500 sequencing, assembled with MitoZ and metaSPAdes, and annotated using the MITOS. The genome is 15,648 bp long, with a GC content of 24.06%, and contains 13 protein-coding genes, 22 tRNAs genes, and two rRNAs genes. Maximum Likelihood analysis, with *Callosobruchus maculatus* (Chrysomelidae) as the outgroup, indicated that *B. calanus* is closely related to *B. lineolata* , *B. horsfieldii* and *B. numitor*. These data provide additional molecular resources for species identification and phylogenetic studies within the genus *Batocera*.

ARTICLE HISTORY
Received 22 April 2025
Accepted 28 September 2026

KEYWORDS
Mitochondrial genome; *Batocera calanus*; Cerambycidae; molecular phylogeny

1. Introduction

Batocera calanus (Parry, 1844) (Coleoptera: Cerambycidae) is widely distributed across tropical and subtropical Asia, including China, India, and Malaysia (Arias and Torralba-Burrial 2020). As a member of the genus *Batocera* Dejean, 1835, this species has garnered attention because of its ecological impact and potential as an invasive species. A significant number of beetle species (Coleoptera) have been unintentionally introduced into Europe (Beenen and Roques 2010; Cocquempot and Lindelöw 2010; Denux and Zagatti 2010; Sauvard et al. 2010). Recent decades have seen increasing interceptions of alien Cerambycidae species at European ports, highlighting the need for robust molecular tools to monitor their spread (Sauvard et al. 2010; Eyre et al. 2018).

While congeneric species such as *B. horsfieldii* (Hope, 1839) have been studied (Wei et al. 2024), with research indicating that their basic biology is similar to other members of the Lamiinae subfamily (Fan et al. 2023), research on *B. calanus* remains limited. Mitochondrial genomes are invaluable for resolving phylogenetic relationships and evolutionary processes due to their maternal inheritance, high mutation rates, and conserved gene content (Zhang et al. 2021). This study presents the first complete mitochondrial genome of *B. calanus*, laying a foundation for comparative genomics and molecular taxonomy within Cerambycidae.

2. Materials and methods

2.1. Sample collection, DNA extraction and sequencing

Adult *B. calanus* specimens were collected in Dulongjiang, Gongshan County, Yunnan (27°53′47″N, 98°21′20″E) in July 2020 by Wenlong Jiao. The voucher specimen (no. TN-202501) was photographed and stored at the Key Laboratory of Integrated Pest Management in Ecological Forests, Fujian Agriculture and Forestry University (contact person: Feiyi Xin; email: xin feiyi2004@126.com) (Figure 1). We saved the remaining DNA in the above laboratory using an individual identifier (DNA-GS-202503).

2.2. Genome sequencing, assembly and annotation

In this study, genomic DNA was extracted from the legs of adult specimens using the Tissue Sample Genomic DNA Extraction Kit RC1003 (Concertbio, Xiamen, China).



Figure 1. Adult specimen of *Batocera calanus* collected in Yunnan province, China. The species reference image was captured by Wenlong jiao, and the sample number is No. TN-202501.

CONTACT Feiping Zhang fpzhang1@163.com College of Forestry, Fujian Agriculture and Forestry University, Fuzhou City, China.

© 2026 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. The terms on which this article has been published allow the posting of the Accepted Manuscript in a repository by the author(s) or with their consent.

The quality and concentration of the extracted DNA were assessed using a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). During library preparation, paired-end sequencing was performed using the Illumina HiSeq 2500 platform (Illumina, San Diego, CA, USA) with a read length of 2 × 150 bp (Yin et al. 2016). After quality filtering, 1,228,768 clean reads were retained from the initial dataset of 74,224,994 raw reads. The mitochondrial genome assembly was conducted using MitoZ v2.4 (Meng et al. 2019) and metaSPAdes (Nurk et al. 2017). Subsequently, gene annotation was carried out using the MITOS webserver (Bernt et al. 2013). To improve the precision of the annotations, we referenced the mitochondrial genome sequence of *Batocera lineolata* (Cerambycidae; GenBank accession number: NC_022671.1), which is phylogenetically more closely related to the target species. Finally, the mitochondrial genome map was visualized using Geneious Prime (v 2023.2) (Kearse et al. 2012).

2.3. Phylogenetic analysis

Systematic evolutionary analyses were conducted utilizing concatenated nucleotide sequences from 13 protein-coding genes (PCGs) and two ribosomal RNAs (rRNAs) obtained from eight species of Cerambycidae and one outgroup belonging to Chrysomelidae (Zhang et al. 2021; Wu et al. 2023). The sequences of each PCG and rRNA were independently aligned using MUSCLE (Edgar 2022) and subsequently integrated into a unified dataset. The MEGA11 (Tamura et al. 2021) software was used to generate phylogenetic trees through the maximum likelihood method and to select the best-fit nucleotide substitution models. The phylogenetic relationships inferred from these protein-coding genes are in agreement with traditional morphological classification, suggesting that mitochondrial genomes are useful markers for studying the evolutionary history of Lamiinae.

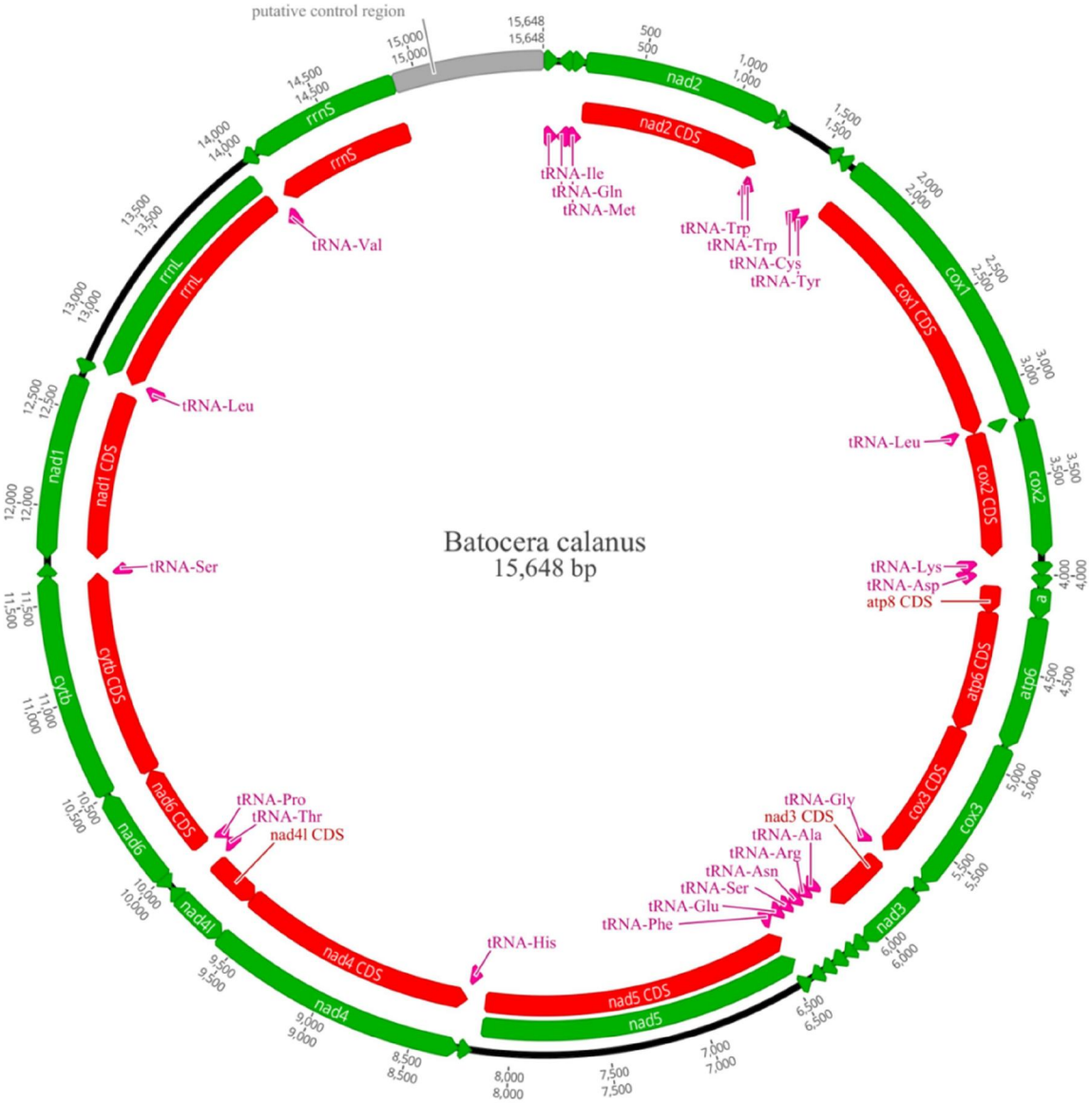

Figure 2. Circular map of the *B. calanus* mitochondrial genome, with the outer ring showing genes on the majority strand (J-strand), the inner ring on the minority strand (N-strand), arrows indicating transcription direction, and the putative control region marked.

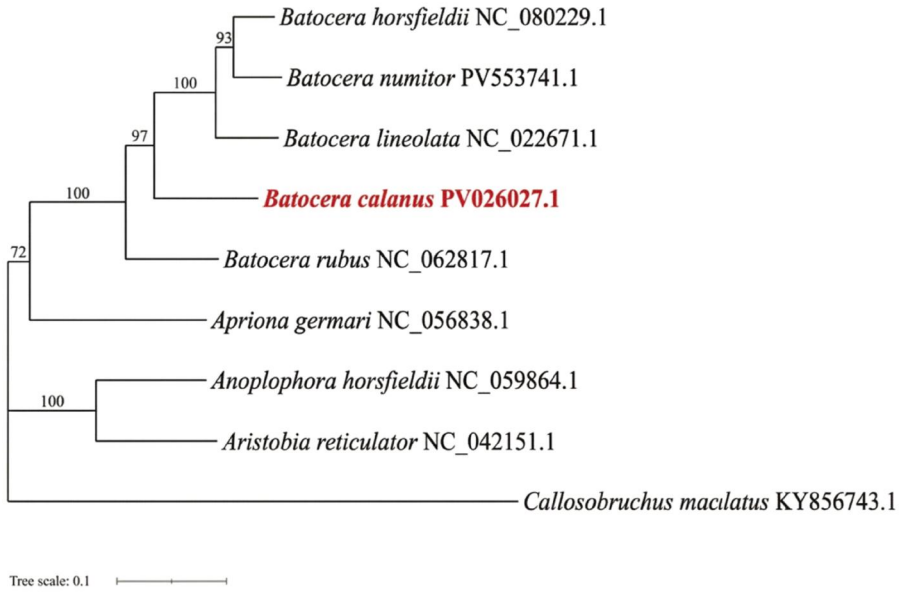

Figure 3. A maximum-likelihood phylogenetic tree was constructed for eight cerambycidae species and one chrysomelidae species, based on the concatenated nucleotide sequences of 13 protein-coding genes (PCGs) and two ribosomal RNAs (rRNAs). Bootstrap support values are indicated adjacent to the branches. Mitochondrial genome sequences for the various species were retrieved from the GenBank database (with accession numbers noted in the figure). The highlighted species represent the newly sequenced mitochondrial genomes in this study (*B. calanus*, accession number PV026027.1), which represents the newly sequenced mitogenome in this study. The following sequences were used: *B. horsfieldii* NC_080229.1 (Wu et al. 2023), *B. numitor* PV553741.1, *B. lineolata* NC_022671.1 (Wang et al. 2012), *B. rubus* NC_062817.1 (Deng et al. 2023), *apriona germari* NC_056838.1 (Zhang et al. 2021), *anoplophora horsfieldii* NC_059864.1 (Zhang et al. 2023), *aristobia reticulator* NC_042151.1 (Behere et al. 2019), *callosobruchus maculatus* KY856743.1 (Sayadi et al. 2017).

3. Results

The complete mitochondrial genome of *B. calanus* (PV026027.1) is 15,648 bp long with a GC content of 24.06% (A: 39.3%, T: 36.7%, C: 14.8%, and G: 9.2%). This genome encodes 13 PCGs, 22 tRNAs, and 2 rRNAs. Gene arrangement follows the ancestral insect mitochondrial pattern, with 15 genes located on the majority strand (J-strand) and 22 on the minority strand (N-strand). The 13 PCGs are: *cox1-3*, *nad1-6*, *nad4L*, *atp8*, *atp6*, and *cytb*. Most PCGs are initiated by typical ATN start codons. Nine PCGs (*atp8*, *atp6*, *cox3*, *nad1*, *nad2*, *nad4*, *nad4L*, *nad5*, and *nad6*) terminate with the TAA codon, while two (*nad3* and *cytb*) end with TAG. Notably, *cox1* and *cox2* terminate with an incomplete T residue. The small ribosomal RNA (*rrnS*) and large ribosomal RNA (*rrnL*) genes are 777 bp and 1,296 bp in length, respectively. Moreover, the phylogenetic tree showed that *B. calanus* clustered with other Cerambycidae species and was closely related to *B. lineolata* (Chevrolat, 1852), *B. horsfieldii* (Hope, 1839), and *B. numitor* (Newman, 1842) (Figure 2).

4. Discussion and conclusions

In the present study, we report the first complete mitochondrial genome sequence of *Batocera calanus* (15,648 bp). Compared with previous studies that relied on fragmented markers such as *cox1*, the complete mitogenome provides a more accurate representation of the species' genetic makeup. The genome size and high A + T content (75.94%) are consistent with the documented range for coleopteran mitogenomes (Wang et al. 2019). As expected, the gene content is conserved and comprises 13 PCGs (*cox1-3*, nad1-6, nad4L, atp8, atp6, and cytb), 22 tRNAs, and two rRNAs, with most PCGs initiated by typical ATN start codons. Notably, *cox1* and *cox2* terminate with an incomplete T stop codon, a common feature of metazoan mitogenomes in which the complete TAA stop codon is restored by post-transcriptional polyadenylation (Ojala et al. 1981). These features together confirm that the *B. calanus* mitogenome retains the canonical organization of insect mitochondrial genomes.

Based on comparisons with other members of the tribe Batocerini (Kim et al. 2013; Wang et al. 2019; Wu et al. 2023), the newly sequenced *B. calanus* mitogenome shows remarkable structural conservation, with no gene rearrangements detected, representing the typical ancestral insect architecture (Zhang et al. 2021). The genome size of *B. calanus* (15,648 bp) falls within the range documented for congeneric species, i.e. 16,158 bp in *B. rubus* (Deng et al. 2023), and the GC content (24.06%) is comparable to that of *B. rubus* (23.9%). The sizes of the rRNA genes (*rrnS*: 777 bp; *rrnL*: 1,296 bp) are also consistent with those of other Cerambycidae, and the start/stop codon usage of the PCGs shows no deviation from the patterns reported in these species. Collectively, these comparisons support the overall stability of the mitogenome architecture within the genus *Batocera*.

Furthermore, the maximum likelihood phylogenetic tree robustly placed *B. calanus* within the genus *Batocera* with high bootstrap support, and the newly sequenced species was recovered as closely related to *B. lineolata*, *B. horsfieldii* and *B. numitor* (Figure 3). This clear topological structure confirms that *B. calanus* forms a monophyletic group with its congeneric species, congruent with traditional morphological classifications, and highlights the value of using entire mitogenomes to resolve complex evolutionary histories within Cerambycidae (Zhang et al. 2021). Nevertheless, because only eight Cerambycidae species from a limited number of genera

were sampled, the intergeneric relationships recovered here should be interpreted with caution.

Beyond its phylogenetic utility, the mitogenome of *B. calanus* constitutes a valuable resource for the molecular identification and DNA barcoding of *Batocera* species, several of which are important wood-boring pests of timber and fruit trees and are increasingly intercepted as alien species at ports of entry (Eyre et al. 2018; Arias and Torralba-Burrial 2020). The complete genome sequence also provides a reference for developing species-specific markers and for population genetic analyses of *B. calanus* across its wide distribution range in Asia, which may facilitate future studies on the invasion biology and pest management of this species.

In conclusion, the genomic information provided here not only supplements the existing database of the tribe Batocerini but also plays a crucial role in taxonomic analyses and wood-boring pest management, which is vital for improving productivity in timber and fruit tree cultivation. To conclusively resolve the broader taxonomic status within Batocerini, future studies should incorporate expanded taxon sampling and employ phylogenomic approaches to further enrich the genetic database of longhorn beetles.

Ethical approval

This study does not involve ethical considerations. As insects are invertebrates, their use in experiments does not present any ethical issues. Specimens were collected following the protocols established by the authors' institution (Key Laboratory of Integrated Pest Management in Ecological Forests, Fujian Agriculture and Forestry University) and national standards.

Author contributions

CRediT: **Jinning Du**: Formal analysis, Investigation, Writing – original draft, Writing – review & editing; **Wenlong Jiao**: Investigation, Methodology; **Sihan Wang**: Formal analysis; **Sikai Ke**: Formal analysis; **Ruiheng Lin**: Formal analysis, Writing – review & editing; **Feiping Zhang**: Conceptualization, Project administration. All authors approved the final manuscript and agree to be accountable for all aspects of the work.

Disclosure statement

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

Funding

This work was supported by the Forestry Key Program of Science and Technology in Fujian Province [grant number 2021FKJ03].

Data availability statement

The following information was supplied regarding the availability of DNA sequences: the new mitogenomes were deposited in GenBank of NCBI (https://www.ncbi.nlm.nih.gov/) and the accession number is PV026027.1. The associated BioProject, SRA, and BioSample numbers were PRJNA1217106, SRR32174722, and SAMN46479201, respectively.

References

Arias A, Torralba-Burrial A. 2020. First detection of the exotic longhorn beetle *Batocera parryi* (Hope) (Coleoptera: cerambycidae) in Europe. Coleopterists Bull. 74(2):327–330. https://doi.org/10.1649/0010-065X-74.2.327

Beenen R, Roques A. 2010. Leaf and seed beetles (Coleoptera, Chrysomelidae). Chapter 8.3. BR. 4(1):267–292. https://doi.org/10.3897/biorisk.4.52

Behere GT, Tay WT, Firake DM, Kunz D, Burange PS, Ramamurthy VV. 2019. Characterization of draft mitochondrial genome of guava trunk borer, Aristobia reticulator (Fabricius, 1781) (Coleoptera: cerambycidae: lamiinae) from India. Mitochondrial DNA Part B. 4(1):1592–1593. https://doi.org/10.1080/23802359.2019.1602004

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2):313–319. https://doi.org/10.1016/j.ympev.2012.08.023

Cocquempot C, Lindelöw Å. 2010. Longhorn beetles (Coleoptera, Cerambycidae). Chapter 8.1. BR. 4(1):193–218. https://doi.org/10.3897/biorisk.4.56

Deng R, Zhou B, Lin Y, Sun Y, Lin X, Wu S. 2023. The complete mitochondrial genome of *Batocera rubus* Linnaeus, 1785 (Coleoptera: cerambycidae). Mitochondrial DNA B Resour. 8(10):1045–1048. https://doi.org/10.1080/23802359.2023.2262692

Denux O, Zagatti P. 2010. Coleoptera families other than Cerambycidae, Curculionidae sensu lato, Chrysomelidae sensu lato and Coccinelidae. Chapter 8.5. BR. 4(1):315–406. https://doi.org/10.3897/biorisk.4.61

Edgar RC. 2022. Muscle5: high-accuracy alignment ensembles enable unbiased assessments of sequence homology and phylogeny. Nat Commun. 13(1):6968. https://doi.org/10.1038/s41467-022-34630-w

Eyre D, Macarthur R, Haack RA, Lu W, Krehan H. 2018. Variation in inspection efficacy by member states of wood packaging material entering the European Union. J Econ Entomol. 111(2):707–715. https://doi.org/10.1093/jee/tox357

Fan JT, Zheng KW, Xie P, Dong YF, Gu YT, Wickham JD. 2023. Electrophysiological and behavioral responses of *Batocera horsfieldii* Hope to volatiles from *Pistacia chinensis* Bunge. Insects. 14(12):911. https://doi.org/10.3390/INSECTS14120911

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12):1647–1649. https://doi.org/10.1093/bioinformatics/bts199

Wang CY, Feng Y, Chen XM. 2012. Complete sequence and gene organization of the mitochondrial genome of *Batocera lineolata* Chevrolat (Coleoptera: Cerambycidae). Chin Sci Bull. 57(27):3578–3585. https://doi.org/10.1007/s11434-012-5271-3

Meng G, Li Y, Yang C, Liu S. 2019. MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Res. 47(11):e63. https://doi.org/10.1093/nar/gkz173

Nurk S, Meleshko D, Korobeynikov A, Pevzner PA. 2017. MetaSPAdes: a new versatile metagenomic assembler. Genome Res. 27(5):824–834. https://doi.org/10.1101/gr.213959.116

Ojala D, Montoya J, Attardi G. 1981. tRNA punctuation model of RNA processing in human mitochondria. Nature. 290(5806):470–474. https://doi.org/10.1038/290470a0

Sauvard D, Branco M, Lakatos F, Faccoli M, Kirkendall L. 2010. Weevils and bark beetles (Coleoptera, Curculionoidea). Chapter 8.2. BR. 4(1):219–266. https://doi.org/10.3897/biorisk.4.64

Sayadi A, Ghani IA, Tuda M. 2017. The complete mitochondrial genome of the cowpea weevil Callosobruchus maculatus (Coleoptera: chrysomelidae: bruchinae). Mitochondrial DNA Part B. 2(2):502–503. https://doi.org/10.1080/23802359.2017.1361352

Tamura K, Stecher G, Kumar S. 2021. MEGA 11: molecular Evolutionary Genetics Analysis Version 11. Mol Biol Evol. 38(7):3022–3027. https://doi.org/10.1093/molbev/msab120

Wang ZJ, Lu XM, Li CJ, Li ZH. 2019. Characteristics of the complete mitochondrial genome of *Batocera horsfieldii* (Coleoptera: cerambycidae)

and phylogenetic analysis. Gene. 684:147–156. https://doi.org/10.1016/j.gene.2018.10.052

Wei X, Xu D, Ali H, Qin P, Zhuo ZH. 2024. Molecular mechanisms uncovers differentially expressed genes in male and female adults of *Batocera horsfieldii* (Coleoptera: cerambycidae). Asia-Pac Entomol. 27(3):102296. https://doi.org/10.1016/j.aspen.2024.102296

Wu SQ, Zhuo ZH, Deng R, Lin YQ, Lin XY. 2023. Characterization of the complete mitochondrial genome of Batocera horsfieldii (Coleoptera: cerambycidae). Mitochondrial DNA Part B. 8(11):1227–1230. https://doi.org/10.1080/23802359.2023.2275463

Yin D, Ritchie ME, Jabbari JS, Beck T, Blewitt ME, Keniry A. 2016. High concordance between Illumina HiSeq2500 and NextSeq500 for reduced representation bisulfite sequencing (RRBS). Genom Data. 10:97–100. 10.1016/j.gdata.2016.10.002.27766205

Zhang BL, Zhang J, Zhang D, Feng Y, Qiu J, Ye XJ, Wang BX. 2023. Complete mitochondrial genome of the longicorn *Anoplophora horsfieldii* Hope (Coleoptera: cerambycidae). Mitochondrial DNA B Resour. 8(2):220–221. https://doi.org/10.1080/23802359.2021.1915717

Zhang J, Nie ZL, Zhang QZ, Yang MF. 2021. The complete mitochondrial genome of *Apriona germari* (Coleoptera: cerambycidae) and its phylogenetic implications. Mitochondrial DNA Part B. 6(11):3195–3197. https://doi.org/10.1080/23802359.2021.1983301

Zhang ZY, Guan JY, Cao YR, Dai XY, Storey KB, Yu DN, Zhang JY. 2021. Mitogenome analysis of four Lamiinae species (Coleoptera: cerambycidae) and gene expression responses by *Monochamus alternatus* when infected with the parasitic nematode, *Bursaphelenchus mucronatus*. Insects. 12(5):453. https://doi.org/10.3390/insects12050453