



Complete mitogenome data from a summer population specimen of the urticating pine defoliator

Thaumetopoea pityocampa (Lepidoptera, Notodontidae, Thaumetopoeinae, Thaumetopoea)

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Data Article

Complete mitogenome data from a summer population specimen of the urticating pine defoliator *Thaumetopoea pityocampa* (Lepidoptera, Notodontidae, Thaumetopoeinae, *Thaumetopoea*)

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Dataset link: [BioSample of the TpitSP mitogenome \(Original data\)](#)Dataset link: [BioProject comprising the TpitSP mitogenome \(Original data\)](#)Dataset link: [Genbank entry of the TpitSP mitogenome \(Original data\)](#)**Keywords:**

Annotation

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ABSTRACT

We present a *de novo* mitogenome assembly obtained from specimens sampled in the so-called summer population (SP) of *Thaumetopoea pityocampa* (Denis and Schiffermüller, 1775) in Portugal. Contrary to the typical larval development occurring in winter in this species, the larvae of this unique population develop during summer. The sequencing data used were obtained from genomic libraries originally generated to assemble the nuclear genome of *T. pityocampa* [1]. We also provide a complete annotation and a phylogenetic representation which positions the Portuguese summer population of *T. pityocampa* and an Italian typical individual of the same species among the Notodontidae family and more distant Noctuoidea species. This data represents a valuable new resource for an expanding and urticating insect pest.

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Specifications Table

| | |
|--------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Subject | Omics: Genomics |
| Specific subject area | Lepidoptera, Notodontidae, Mitogenomics |
| Type of data | <ul style="list-style-type: none"> • FASTA: mitochondrial genome assembly • TABLE: gene annotations, base composition, Lepidoptera species used for phylogenetic analysis • FIGURE: mitogenomic circular map, AT-rich region sequence, phylogenetic tree |
| How the data were acquired | Two whole-genome Illumina shotgun libraries were sequenced on an Illumina HiSeq2000 platform using the paired-end protocol (2×100 base pairs (bp)). |
| Data format | Analysed: <i>de novo</i> assembled and annotated mitogenome |
| Description of data collection | MITObim v1.9 assembled genomic libraries generated from male individuals. Genomic regions were annotated with MITOS v2 and represented as circular mitogenome map with OGDRAW. Multiple sequence alignments were generated with MAFFT v7.471 and subsequently concatenated to build phylogenetic trees with PHYLML v3.0 and MrBayes v3.2.7a. Trees were visualized with FigTree v1.4.4. |
| Data source location | <p>Institution: INRAE</p> <p>City/Town/Region: Mata Nacional de Leiria</p> <p>Country: Portugal</p> <p>Latitude and longitude (and GPS coordinates, if possible) for collected samples/data: 39°47'N, 8°58'W</p> |
| Data accessibility | <p>Repository name: NCBI BioProject</p> <p>Data identification number: PRJNA344465</p> <p>Direct URL to data: http://www.ncbi.nlm.nih.gov/bioproject/344465</p> <p>Repository name: NCBI BioSample</p> <p>Data identification number: SAMN24475646</p> <p>Direct URL to data: https://www.ncbi.nlm.nih.gov/biosample/24475646</p> <p>Repository name: NCBI Genbank</p> <p>Data identification number: OM478592</p> <p>Direct URL to data: https://www.ncbi.nlm.nih.gov/nuccore/OM478592</p> |

Value of the Data

- This data represents the mitogenome of a phenologically shifted specimen of *Thaumetopoea pityocampa* collected in Portugal.
- The present data can be used for phylogenetic studies of Lepidoptera especially for getting deeper insights in diversification dynamics of Notodontidae species.
- The resource will be helpful to study the evolution of the *Thaumetopoea* genus and the *T. pityocampa* / *T. wilkinsoni* species complex.

1. Data Description

The *T. pityocampa* Summer Population (“TpitSP”) mitogenome presented here had an A+T content of 77.8% and a size of 15,729 bp. All 38 genetic regions reported for arthropod mitogenomes [2], were identified (Supplementary GFF annotation file): 13 protein-coding genes, 22 tRNA and 2 rRNA (12S rRNA and 16S rRNA) genes, and one AT-rich control region. Genes were ordered identically to the Italian *T. pityocampa* [3] and other Notodontidae [4] mitogenomes. Start and stop codons of the protein-coding genes corresponded also to those observed in other Noc-tuoidea. In total, 22 intergenic spacer regions (see Table 1: positive intergenic nucleotide values) with an average size of 20 bp and a total length of 437 bp were identified. These regions ranged from 1 to 96 bp. The longest intergenic spacer was located between the ND4 and ND4L genes. Furthermore, three gene pairs showed overlaps (see Table 1: negative intergenic nucleotide values) of 1 to 8 bp. All annotation details are given in Table 1. In Fig. 1 the TpitSP mitogenome genetic regions are depicted as a circular map. Table 2 further shows type base compositions, AT and GC skews for each annotation type. The typical clover-leaf secondary structures can be

Table 1Gene features of the SP *T. pityocampa* mitogenome.

| Gene (anticodon) | Start | 0 | Strand | Size | Intergenic nucleotides | Start/stop codon |
|------------------|--------|--------|--------|-------|------------------------|------------------|
| trnM(cat) | 1 | 68 | + | 68 | 0 | |
| trnl(gat) | 69 | 135 | + | 67 | 2 | |
| trnQ(ttg) | 138 | 206 | - | 69 | 63 | |
| ND2 | 270 | 1,283 | + | 1,014 | 2 | ATT/TAA |
| trnW(tca) | 1,286 | 1,351 | + | 66 | -8 | |
| trnC(gca) | 1,344 | 1,408 | - | 65 | 10 | |
| trnY(gta) | 1,419 | 1,484 | - | 66 | 4 | |
| COX1 | 1,489 | 3,021 | + | 1,533 | 2 | CGA/TAA |
| trnL(taa) | 3,024 | 3,093 | + | 70 | 2 | |
| COX2 | 3,096 | 3,774 | + | 679 | 0 | ATG/ATT |
| trnK(ctt) | 3,775 | 3,845 | + | 71 | 10 | |
| trnD(gtc) | 3,856 | 3,931 | + | 76 | 0 | |
| ATP8 | 3,932 | 4,102 | + | 171 | -7 | ATT/TAA |
| ATP6 | 4,096 | 4,776 | + | 681 | 28 | ATG/TAA |
| COX3 | 4,805 | 5,593 | + | 789 | 7 | ATG/TAA |
| trnG(tcc) | 5,601 | 5,675 | + | 75 | 0 | |
| ND3 | 5,676 | 6,029 | + | 354 | 64 | ATT/TAA |
| trnA(tgc) | 6,094 | 6,162 | + | 69 | 1 | |
| trnR(tcg) | 6,164 | 6,230 | + | 67 | 13 | |
| trnN(gtt) | 6,244 | 6,312 | + | 69 | 24 | |
| trnS1(gct) | 6,337 | 6,402 | + | 66 | 62 | |
| trnE(ttc) | 6,465 | 6,534 | + | 70 | 6 | |
| trnF(gaa) | 6,541 | 6,612 | - | 72 | 3 | |
| ND5 | 6,616 | 8,364 | - | 1,749 | 0 | ATT/TAA |
| trnH(gtg) | 8,365 | 8,430 | - | 66 | 0 | |
| ND4 | 8,431 | 9,769 | - | 1,339 | 96 | ATG/TTT |
| ND4L | 9,866 | 10,156 | - | 291 | 5 | ATG/TAA |
| trnI'(tgt) | 10,162 | 10,225 | + | 64 | 0 | |
| trnP(tgg) | 10,226 | 10,290 | - | 65 | 8 | |
| ND6 | 10,299 | 10,829 | + | 531 | -1 | ATG/TAA |
| CYT B | 10,829 | 11,983 | + | 1,155 | 3 | ATG/TAA |
| trnS2(tga) | 11,987 | 12,053 | + | 67 | 22 | |
| ND1 | 12,076 | 13,011 | - | 936 | 0 | GTG/TAA |
| trnL1(tag) | 13,012 | 13,082 | - | 71 | 0 | |
| 16S rRNA | 13,083 | 14,463 | - | 1,381 | 0 | |
| trnV(tac) | 14,464 | 14,531 | - | 68 | 0 | |
| 12S rRNA | 14,532 | 15,309 | - | 778 | 0 | |
| AT-rich region | 15,310 | 15,729 | + | 420 | 0 | |

The gene names, the coordinates, the orientation, the size, the gene overlaps/intergenic spacers (column 6) and the start/stop codons of the SP mitogenome are listed.

Table 2Base composition and skewness indices for each gene region of the SP *T. pityocampa* mitogenome.

| Type | Size [bp] | A% | G% | T% | C% | A+T% | ATskewness | GCskewness |
|----------------------|-----------|------|------|------|------|------|------------|------------|
| Entire mitogenome | 15,729 | 40.6 | 7.6 | 37.3 | 14.6 | 77.8 | 0.042 | -0.318 |
| Protein-coding genes | 11,222 | 32.6 | 12.1 | 43.0 | 12.4 | 75.5 | -0.138 | -0.009 |
| tRNA | 1,507 | 41.4 | 11.3 | 39.3 | 7.9 | 80.8 | 0.025 | 0.179 |
| rRNA | 2,159 | 39.2 | 13.1 | 43.1 | 4.6 | 82.3 | -0.048 | 0.482 |
| AT-rich region | 420 | 43.6 | 2.9 | 50.0 | 3.6 | 93.6 | -0.069 | -0.111 |

observed for all tRNA except trnS1 in which the dihydrouridine (DHU) arm was replaced by an unstable loop (Supplementary Fig. 1). Fig. 2 shows characteristics of the AT-rich region. At last, Fig. 3 and Supplementary Fig. 2 show phylogenies built on the mitogenomes of SP, 30 other Noctuoidea and two Geometridae species representing the outgroup (Table 3).

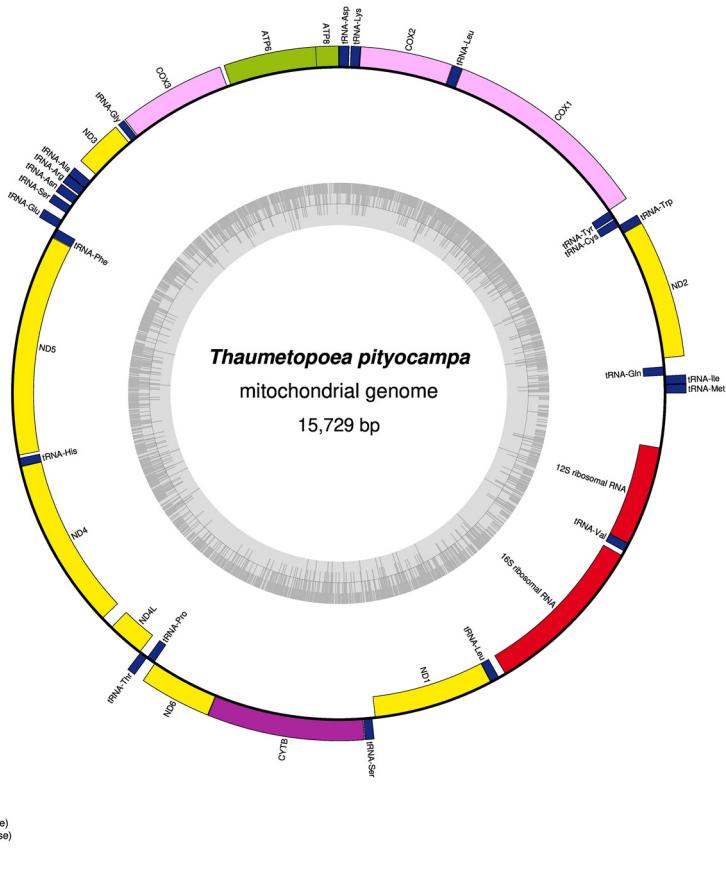


Fig. 1. Map of the *T. pityocampa* SP mitogenome generated with OGDRAW. Annotated genes are highlighted.

12S rRNA-15,310-

TATTTATTACAAAATTCAAGAATAGATTTTTTTTTTT
TATATTAAATTATTAATGTAATTAAATATTAATTTATTAAAT
TATAGTATTATAAAAATTTAATATAAATTATTAAATATTAAAT
ATTTCTTTATTCTTTTCTAAATATTGTATTAAATACAA
ACTTGGAATTAAAATTATAATTCAAATATTTACATTTAA
TTATAAATATATTATTTCTAAATTAATGTATTAT
TAAATTGAATAATAATTAAATTATTTAAATAATATAAATATA
AAATAAAATTAAATATTTAATATATATATATATATGTATA
TTTATATGTATACATGTATATAATTAAATTTCTAAACCATT
TTATAATTAAATATAAATATAAAATATC
-15 729-trpM

-15, 729-CLIM

Fig. 2. Characteristics of the Al-rich region of the *L. pityocampa* SP mitogenome. The region consists of an ATACA (red) motif followed by a 17 bp poly-T stretch (brown).

The AI-rich region consists of an AIAGA (red) motif followed by a 17 bp poly-I stretch (brown). Furthermore, the control region contains ten ATTTA motifs (blue) and an (AT)9 microsatellite stretch (purple). The region ends with a polyT/polyA region (green).

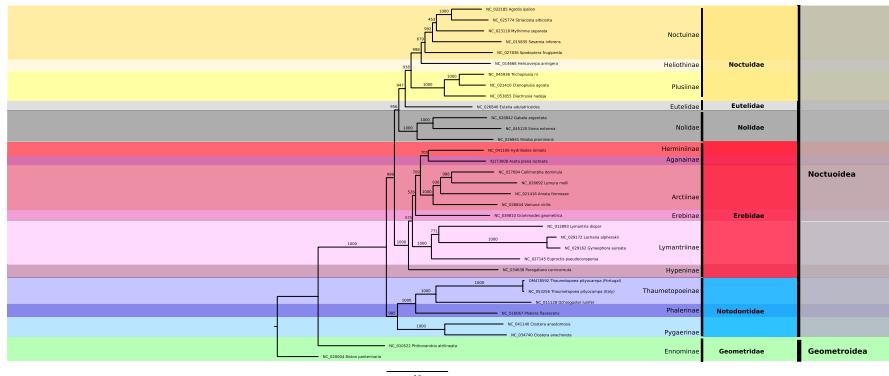


Fig. 3. Phylogenetic tree built on concatenated alignments of the nucleotide sequences of the 13 protein-coding and both rRNA genes applying a Maximum Likelihood approach with PHYML. For both *T. pityocampa* populations the countries are given.

Table 3

Lepidoptera mitogenomes used to build the phylogenetic trees. For both *T. pityocampa* populations the countries are given.

| Super-family | Family | Subfamily | Species | Genbank no. |
|--------------|--------------|-----------------|-------------------------------------------|-------------|
| Geometroidea | Geometridae | Ennominae | <i>Biston panterinaria</i> | NC_020004 |
| Geometroidea | Geometridae | Ennominae | <i>Phthonandria atrilineata</i> | NC_010522 |
| Noctuoidea | Erebidae | Aganainae | <i>Asota plana lacteata</i> | KJ173908 |
| Noctuoidea | Erebidae | Arctiinae | <i>Amata formosae</i> | NC_021416 |
| Noctuoidea | Erebidae | Arctiinae | <i>Callimorpha dominula</i> | NC_027094 |
| Noctuoidea | Erebidae | Arctiinae | <i>Lemyra melli</i> | NC_026692 |
| Noctuoidea | Erebidae | Arctiinae | <i>Vamuna virilis</i> | NC_026844 |
| Noctuoidea | Erebidae | Erebinae | <i>Grammodes geometrica</i> | NC_039810 |
| Noctuoidea | Erebidae | Herminiae | <i>Hydrillodes lentalis</i> | NC_041106 |
| Noctuoidea | Erebidae | Hypeninae | <i>Paragabara curvicornuta</i> | NC_034638 |
| Noctuoidea | Erebidae | Lymantriinae | <i>Euproctis pseudoconspersa</i> | NC_027145 |
| Noctuoidea | Erebidae | Lymantriinae | <i>Gynaephora aureata</i> | NC_029162 |
| Noctuoidea | Erebidae | Lymantriinae | <i>Lachana alpherakii</i> | NC_029172 |
| Noctuoidea | Erebidae | Lymantriinae | <i>Lymantria dispar</i> | NC_012893 |
| Noctuoidea | Euteliidae | Euteliinae | <i>Eutelia adulatrixoides</i> | NC_026840 |
| Noctuoidea | Noctuidae | Heliothinae | <i>Helicoverpa armigera</i> | NC_014668 |
| Noctuoidea | Noctuidae | Noctuinae | <i>Agrotis ipsilon</i> | NC_022185 |
| Noctuoidea | Noctuidae | Noctuinae | <i>Mythimna separata</i> | NC_023118 |
| Noctuoidea | Noctuidae | Noctuinae | <i>Sesamia inferens</i> | NC_015835 |
| Noctuoidea | Noctuidae | Noctuinae | <i>Spodoptera frugiperda</i> | NC_027836 |
| Noctuoidea | Noctuidae | Noctuinae | <i>Striacosta albicosta</i> | NC_025774 |
| Noctuoidea | Noctuidae | Plusiinae | <i>Ctenoplusia agnata</i> | NC_021410 |
| Noctuoidea | Noctuidae | Plusiinae | <i>Diachrysia nadeja</i> | NC_053855 |
| Noctuoidea | Noctuidae | Plusiinae | <i>Trichoplusia ni</i> | NC_045936 |
| Noctuoidea | Nolidae | Chloephorinae | <i>Gabala argentata</i> | NC_026842 |
| Noctuoidea | Nolidae | Chloephorinae | <i>Sinna extrema</i> | NC_045120 |
| Noctuoidea | Nolidae | Risobinae | <i>Risoba prominens</i> | NC_026841 |
| Noctuoidea | Notodontidae | Phalerinae | <i>Phalera flavescens</i> | NC_016067 |
| Noctuoidea | Notodontidae | Pygaerinae | <i>Closteria anachoreta</i> | NC_034740 |
| Noctuoidea | Notodontidae | Pygaerinae | <i>Closteria anastomosis</i> | NC_041140 |
| Noctuoidea | Notodontidae | Thaumetopoeinae | <i>Ochrogaster lunifer</i> | NC_011128 |
| Noctuoidea | Notodontidae | Thaumetopoeinae | <i>Thaumetopoea pityocampa (Italy)</i> | NC_053256 |
| Noctuoidea | Notodontidae | Thaumetopoeinae | <i>Thaumetopoea pityocampa (Portugal)</i> | OM478592 |

2. Experimental Design, Materials and Methods

2.1. DNA sequence libraries

To generate the present SP mitogenome assembly we used two shotgun whole-genome paired-end sequence libraries originally built to produce the reference nuclear genome of *T. pityocampa* SP [1]. Each of these libraries was built from one SP male which was sampled between 2010 and 2012 from the Mata Nacional de Leiria in Portugal (39°47'N, 8°58'W). The libraries had insert sizes of 300 bp and 600 bp, respectively, and were sequenced on an Illumina HiSeq2000 platform at the Edinburgh Genomics sequencing facility in Scotland, UK.

The raw whole-genome shot-gun sequence reads were trimmed and cleaned with Trimmomatic v0.22 [5] (specific parameters were: window size of 20 bp, minimum PHRED quality of 20, minimum length of 70 bp), and subsequently assembled by Eurofins MWG Operon using their own bioinformatics pipeline (CONVEY, <http://www.conveycomputer.com>), implementing multiple Velvet assemblies.

2.2. Mitogenome assembly and feature analyses

The SP mitogenome was generated in two subsequent steps. First, as described in [1] the nuclear genome assembly contained one scaffold of 15,717 bp which was identified as partial mitochondrial based on *blastn* searches against the NCBI nucleotide database. In a second step, MITObim v1.9 [6] was applied to extend and refine this mitogenome backbone using the cleaned (-clean) Illumina paired-end (-pair) reads with a k-mer size of 41 bp (-kbait 41), a maximum of 5 mismatches per mapped read (-mismatch 5) and a minimum average contig coverage of 500 reads per base (-min_cov 500). Furthermore, the PPM mitogenome was globally aligned with MAFFT v7.471 [7] (executable mafft-ginsi, using a maximum of 1,000 refinement iterations (-maxiterate 1000)) to five other Notontidae mitogenomes of the following species: *Thaumetopoea pityocampa* (Italian population, Genbank no. NC_053256), *Ochrogaster lunifer* (Genbank no. NC_011128), *Clostera anastomosis* (Genbank no. NC_041140), *Clostera anachoreta* (Genbank no. NC_034740), *Phalera flavescens* (Genbank no. NC_016067). This allowed to identify overlapping repeat regions at both sequence termini which were then identified as assembly artefacts and thus manually removed (linear vs circular structure). This resulted in a mitogenome size of 15,729 bp. Annotation of the genetic regions was conducted by the MITOS web server v2 [8], using as reference set 'RefSeq 89 Metazoa' and the genetic code '5' for invertebrates. Furthermore, the MITOS gene annotations were manually curated by aligning the predicted genes via web service of NCBI blastn [9] (with default parameters, version of January 2022) to gene annotations of other Notodontidae mitogenomes (same as described above). The web tool OGDRAW v1.3.1 [10] was run to create the circular map of the SP *T. pityocampa* mitogenome with its annotations. We applied the *wordcount* program of the EMBOSS toolkit v6.6.0.0 [11] to calculate the base content of each genetic region type. The genomic compositional asymmetry of the SP mitogenome of each specific annotation type region was described by the AT/GC skewness indices which were calculated as follows with each base count being represented by the corresponding base letter: AT skew = [A-T] / [A + T] and GC skew = [G-C] / [G + C].

2.3. Phylogenetic analyses

For phylogenetic trees were built on 33 Lepidoptera mitogenomes – including 30 Noctuoidea species (Table 3). Two representatives of the Geometroidea were used as outgroup to root the trees following the conclusions of Wahlberg et al. [12]. We obtained the nucleotidic sequences of the 13 PCGs and 2 rRNA genes from the NCBI 'nucleotide' database (<https://www.ncbi.nlm.nih.gov/nuccore>, July 2021). The superfamily Noctuoidea was chosen for taxon sampling, encompassing five species belonging to the Notodontidae (including *T. pityocampa*). Regarding *T. pityocampa*, we included the mitogenomes of the Portuguese TpitSP (provided here) and an Italian typical population [3].

The nucleotide sequences of all species were grouped into 15 gene-specific sequence sets, corresponding to 13 PCG and 2 rRNA genes. Global sequence alignment on each gene set using the Needleman-Wunsch algorithm was conducted with the program MAFFT v7.471 (executable mafft-ginsi for PCGs and mafft-qinsi for rRNA sequences), applying a maximum of 1,000 refinement iterations (-maxiterate 1000). Finally, in-house Perl and Python scripts were run to concatenate for each species all gene-specific alignments following the same gene order.

A local installation of MrBayes v3.2.7a [13] and the PHYML web server v3.0 [14] were run to calculate phylogenetic tree structures. For each gene a distinct partition was configured in the MrBayes analysis with the following parameters each: GTR substitution model (nst = 6) with gamma-distributed rate variation (rates = invgamma) across sites and a proportion of invariable sites (GTR + I + #). As substitution model the standard nucleotide model (nucmodel = 4by4) was chosen with priors being left to default settings. We configured MrBayes to use 100,000 samples (ngen = 1,000,000, samplefreq = 10) in order to generate phylogenetic trees. Additional settings were: printfreq = 100, diagnfreq = 1,000, nchains = 4, savebrlens = yes, starttree = random, start-

params = reset, outgroup bipan (corresponding to *Biston panterinaria*), sump burnin = 25,000, sumt burnin = 25,000. Regarding the PHYML analysis, the Smart Model Selection [15] parameter was chosen with the Akaike Information Criterion and the tree searching method BIONJ being set. Furthermore, 1,000 bootstraps were applied. Finally, the program FigTree v1.4.4 [16] was run to draw the phylogenetic tree.

CRediT Author Statement

Bernhard Gschloessl: Conceptualization, Methodology, Formal analysis, Validation, Writing – review & editing; **Carole Kerdelhué:** Project administration, Funding acquisition, Writing – review & editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data Availability

[BioSample of the TpitSP mitogenome \(Original data\)](#) (NCBI BioSample).

[BioProject comprising the TpitSP mitogenome \(Original data\)](#) (NCBI BioProject).

[Genbank entry of the TpitSP mitogenome \(Original data\)](#) (NCBI Genbank).

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Supplementary Materials

Supplementary material associated with this article can be found in the online version at doi:[10.1016/j.dib.2022.108376](https://doi.org/10.1016/j.dib.2022.108376).

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