



**Complete mitogenome data from a summer population
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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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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	• 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 PHYML v3.0 and MrBayes v3.2.7a. Trees were visualized with FigTree v1.4.4.
Data source location	Institution: INRAE City/Town/Region: Mata Nacional de Leiria Country: Portugal Latitude and longitude (and GPS coordinates, if possible) for collected samples/data: 39°47'N, 8°58'W
Data accessibility	Repository name: NCBI BioProject Data identification number: PRJNA344465 Direct URL to data: http://www.ncbi.nlm.nih.gov/bioproject/344465 Repository name: NCBI BioSample Data identification number: SAMN24475646 Direct URL to data: https://www.ncbi.nlm.nih.gov/biosample/24475646 Repository name: NCBI Genbank Data identification number: OM478592 Direct URL to data: https://www.ncbi.nlm.nih.gov/nucleotide/OM478592

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 Noctuoidea. 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	
trnI(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
trnL2(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
CYTB	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).

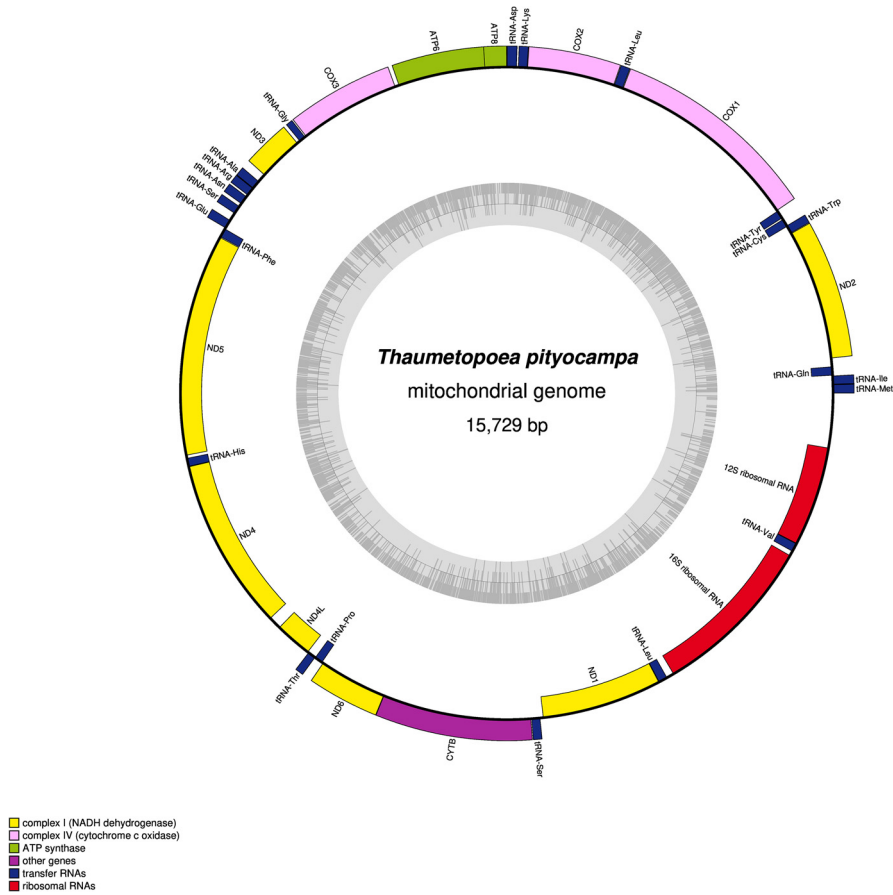


Fig. 1. Map of the *T. pityocampa* SP mitogenome generated with OGDRAW. Annotated genes are highlighted.

12S rRNA-15,310-
T**ATTT**TATTACAAAATTTCAAGA**ATAGAT**TTTTTTTTTTTTTTTTT
TATATTAAATT**ATTTA**ATGTAAATTAAT**ATTTA**ATTTATTAAT
TATAGTATTATAAAA**ATTTA**ATATAAATTATTAAATATTAAAT
ATTTTCTTTTATTCTTTTTTTCATAATATTGTATTAAATACAA
ACTTGGAAATTAAAATTTTATAATTCAAATATTTTAC**ATTTAA**
TTATAAATATATT**ATTTA**TATTTTTTCATAAATTAATGTATTAT
TAAATTGAATAATAAATTAATT**ATTTA**AATAAATATAAATATA
AATAATAAATTAAAT**ATTTA**ATATATATATATATATATAT**GTATA**
TTTATATGTATACATGTATATAATTAATTTTTTCAAACC**ATTTT**
TTATAATTTTTATATAAAATATATAAAATATATC
-15,729-trnM

Fig. 2. Characteristics of the AT-rich region of the *T. pityocampa* SP mitogenome. The AT-rich region consists of an ATAGA (red) motif followed by a 17 bp poly-T 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).

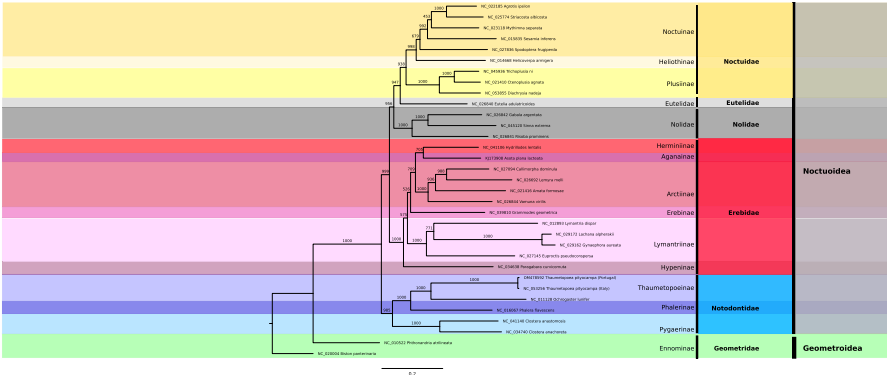


Fig. 3. Phylogenetic tree built on concatenated alignments of the nucleotide sequences of the 13 protein-coding and both rRNA genes applying a Maximum Likelihood approach with PHYML. For both *T. pityocampa* populations the countries are given.

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	Herminiinae	<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 adulatricoides</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 flaves cens</i>	NC_016067
Noctuoidea	Notodontidae	Pygaerinae	<i>Clostera anachoreta</i>	NC_034740
Noctuoidea	Notodontidae	Pygaerinae	<i>Clostera 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 mitochondrion 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 nucleotide sequences of the 13 PCGs and 2 rRNA genes from the NCBI ‘nucleotide’ database (<https://www.ncbi.nlm.nih.gov/nucleotide>, 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 and 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, diagfreq=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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