



DATA NOTE

The genome sequence of the Tortix moth, *Archips podanus* (Scopoli, 1763)

[version 1; peer review: 2 approved]

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Abstract

We present a genome assembly from a male specimen of *Archips podanus* (Tortix moth; Arthropoda; Insecta; Lepidoptera; Tortricidae). The genome sequence has a total length of 549.00 megabases. Most of the assembly (99.72%) is scaffolded into 30 chromosomal pseudomolecules, including the Z sex chromosome. The mitochondrial genome has also been assembled, with a length of 15.45 kilobases.

Keywords

Archips podanus, Tortix moth, genome sequence, chromosomal, Lepidoptera



This article is included in the [Tree of Life](#) gateway.

Open Peer Review

Approval Status

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Any reports and responses or comments on the article can be found at the end of the article.

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Species taxonomy

Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Apoditrysia; Tortricoidea; Tortricidae; Tortricinae; Archipini; *Archips*; *Archips podanus* (Scopoli, 1763) (NCBI:txid2655036)

Background

Archips podanus is a micro-moth in the family Tortricidae. It is common and widespread in Britain, although local in Scotland. It is present throughout Europe and Asia and has been recorded around Vancouver, Canada (GBIF Secretariat, 2025).

The adult moth is sexually dimorphic. The males are relatively brightly coloured with rich browns and yellowish patterning; the females are brown with a netted pattern (Sterling *et al.*, 2023). The males are polymorphic with a number of forms, recognised based on the structure of the adeagus (Kozlov & Motorkin, 1990). The forms differed in their response to sex pheromones (Safonkin, 1988).

The moth is polyphagous, laying its eggs in batches of 50 to 100 on the upper surface of a wide range of deciduous trees, and occasionally on conifers (Hancock *et al.*, 2015). The eggs are covered in a waxy secretion. The larvae hibernate when small, and then emerge to feed in buds and later in leaf or flower spinnings where it pupates (Langmaid *et al.*, 2018).

We present a chromosome-level genome sequence for *Archips podanus* based on a male specimen collected in Wytham Woods, Oxfordshire, UK and sequenced as part of the Darwin Tree of Life Project.

Genome sequence report

Sequencing data

The genome of a specimen of *Archips podanus* (Figure 1) was sequenced using Pacific Biosciences single-molecule HiFi long reads, generating 15.76 Gb (gigabases) from 1.19 million reads. GenomeScope analysis of the PacBio HiFi data estimated

the haploid genome size at 544.17 Mb, with a heterozygosity of 0.37% and repeat content of 39.31%. These values provide an initial assessment of genome complexity and the challenges anticipated during assembly. Based on this estimated genome size, the sequencing data provided approximately 27.0x coverage of the genome. Chromosome conformation Hi-C sequencing produced 112.92 Gb from 747.84 million reads. Table 1 summarises the specimen and sequencing information.

Assembly statistics

The primary haplotype was assembled, and contigs corresponding to an alternate haplotype were also deposited in INSDC databases. The assembly was improved by manual curation, which corrected 67 misjoins or missing joins and removed 22 haplotypic duplications. These interventions reduced the total assembly length by 1.59%, decreased the scaffold count by 8.33%, also decreasing the scaffold N50 by 3.71%. The final assembly has a total length of 549.00 Mb in 43 scaffolds, with 43 gaps, and a scaffold N50 of 19.64 Mb (Table 2).

The snail plot in Figure 2 provides a summary of the assembly statistics, indicating the distribution of scaffold lengths and other assembly metrics. Figure 3 shows the distribution of scaffolds by GC proportion and coverage. Figure 4 presents a cumulative assembly plot, with separate curves representing different scaffold subsets assigned to various phyla, illustrating the completeness of the assembly.

Most of the assembly sequence (99.62%) was assigned to 30 chromosomal-level scaffolds, representing 29 autosomes and the Z sex chromosome. These chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 5; Table 3). During curation, chromosome Z was assigned based on synteny with *Archips crataeganus* (GCA_947859365.1) (Boyes *et al.*, 2024).

The mitochondrial genome was also assembled. This sequence is included as a contig in the multifasta file of the genome submission and as a standalone record.

Assembly quality metrics

The estimated Quality Value (QV) and *k*-mer completeness metrics, along with BUSCO completeness scores, were calculated for each haplotype and the combined assembly. The QV reflects the base-level accuracy of the assembly, while *k*-mer completeness indicates the proportion of expected *k*-mers identified in the assembly. BUSCO scores provide a measure of completeness based on benchmarking universal single-copy orthologues.

The combined primary and alternate assemblies achieve an estimated QV of 63.7. The *k*-mer recovery for the primary haplotype is 87.46%, and for the alternate haplotype 1.73%; the combined primary and alternate assemblies have a *k*-mer recovery of 87.74%. BUSCO analysis using the lepidoptera_odb10 reference set (*n* = 5,286) identified 98.4% of the expected gene set (single = 97.8%, duplicated = 0.5%).



Figure 1. Photograph of the *Archips podanus* (ilArcPodn1) specimen used for genome sequencing.

Table 1. Specimen and sequencing data for *Archips podanus*.

Project information			
Study title	Archips podanus (large fruit-tree tortrix)		
Umbrella BioProject	PRJEB55946		
Species	<i>Archips podanus</i>		
BioSpecimen	SAMEA7701540		
NCBI taxonomy ID	2655036		
Specimen information			
Technology	ToLID	BioSample accession	Organism part
PacBio long read sequencing	ilArcPodn1	SAMEA7701729	whole organism
Hi-C sequencing	ilArcPodn2	SAMEA114805821	head and thorax
Sequencing information			
Platform	Run accession	Read count	Base count (Gb)
Hi-C Illumina NovaSeq X	ERR13389719	7.48e+08	112.92
PacBio Sequel IIe	ERR10224898	1.19e+06	15.76

Table 2 provides assembly metric benchmarks adapted from Rhie *et al.* (2021) and the Earth BioGenome Project (EBP) Report on Assembly Standards September 2024. The assembly achieves the EBP reference standard of 7.C.Q63.

Methods

Sample acquisition and DNA barcoding

An adult male *Archips podanus* (specimen ID Ox000679, ToLID ilArcPodn1) was collected from Wytham Woods, Oxfordshire, United Kingdom (latitude 51.77, longitude -1.34) on 2020-07-20, using a light trap. The specimen was collected and identified by Douglas Boyes (University of Oxford) and preserved on dry ice.

The specimen used for Hi-C sequencing (specimen ID NHMUK015054684, ToLID ilArcPodn2) was collected from Bure Marshes National Nature Reserve Fen, England, United Kingdom (latitude 52.7, longitude 1.46) on 2022-06-28, using a light trap. The specimen was collected by Chris Fletcher, Dominic Phillips and Laura Sivess, and identified by David Lees (all from the Natural History Museum) and preserved by dry freezing (-80 °C).

The initial identification was verified by an additional DNA barcoding process according to the framework developed by Twyford *et al.* (2024). A small sample was dissected from the specimen and stored in ethanol, while the remaining parts were shipped on dry ice to the Wellcome Sanger Institute (WSI) (Pereira *et al.*, 2022). The tissue was lysed, the COI marker region was amplified by PCR, and amplicons were sequenced and compared to the BOLD database, confirming

the species identification (Crowley *et al.*, 2023). Following whole genome sequence generation, the relevant DNA barcode region was also used alongside the initial barcoding data for sample tracking at the WSI (Twyford *et al.*, 2024). The standard operating procedures for Darwin Tree of Life barcoding have been deposited on protocols.io (Beasley *et al.*, 2023).

Metadata collection for samples adhered to the Darwin Tree of Life project standards described by Lawniczak *et al.* (2022).

Nucleic acid extraction

The workflow for high molecular weight (HMW) DNA extraction at the Wellcome Sanger Institute (WSI) Tree of Life Core Laboratory includes a sequence of procedures: sample preparation and homogenisation, DNA extraction, fragmentation and purification. Detailed protocols are available on protocols.io (Denton *et al.*, 2023b). The ilArcPodn1 sample was prepared for DNA extraction by weighing and dissecting it on dry ice (Jay *et al.*, 2023). Tissue from the whole organism was homogenised using a PowerMasher II tissue disruptor (Denton *et al.*, 2023a).

HMW DNA was extracted using the Automated MagAttract v1 protocol (Sheerin *et al.*, 2023). DNA was sheared into an average fragment size of 12–20 kb in a Megaruptor 3 system (Todorovic *et al.*, 2023). Sheared DNA was purified by solid-phase reversible immobilisation, using AMPure PB beads to eliminate shorter fragments and concentrate the DNA (Strickland *et al.*, 2023). The concentration of the sheared and purified DNA was assessed using a Nanodrop spectrophotometer

Table 2. Genome assembly data for *Archips podanus*.

Genome assembly		
Assembly name	ilArcPodn1.1	
Assembly accession	GCA_964237515.1	
Alternate haplotype accession	GCA_964237425.1	
Assembly level for primary assembly	chromosome	
Span (Mb)	549.00	
Number of contigs	86	
Number of scaffolds	43	
Longest scaffold (Mb)	44.8	
Assembly metric	Measure	Benchmark
Contig N50 length	13.58 Mb	≥ 1 Mb
Scaffold N50 length	19.64 Mb	= chromosome N50
Consensus quality (QV)	Primary: 63.7; alternate: 67.2; combined: 63.7	≥ 40
<i>k</i> -mer completeness	Primary: 87.46%; alternate: 1.73%; combined: 87.74%	$\geq 95\%$
BUSCO*	C:98.4%[S:97.8%,D:0.5%], F:0.3%,M:1.3%,n:5,286	$S > 90\%$; $D < 5\%$
Percentage of assembly mapped to chromosomes	99.62%	$\geq 90\%$
Sex chromosomes	Z	localised homologous pairs
Organelles	Mitochondrial genome: 15.45 kb	complete single alleles

* BUSCO scores based on the lepidoptera_odb10 BUSCO set using version 5.5.0. C = complete [S = single copy, D = duplicated], F = fragmented, M = missing, n = number of orthologues in comparison.

and a Qubit Fluorometer using the Qubit dsDNA High Sensitivity Assay kit. The fragment size distribution was evaluated by running the sample on the FemtoPulse system.

Hi-C sample preparation

Tissue from the head and thorax of the ilArcPodn2 sample was processed for Hi-C sequencing at the WSI Scientific Operations core, using the Arima-HiC v2 kit. In brief, 20–50 mg of frozen tissue (stored at -80°C) was fixed, and the DNA crosslinked using a TC buffer with 22% formaldehyde concentration. After crosslinking, the tissue was homogenised using the Diagnocine Power Masher-II and BioMasher-II tubes and pestles. Following the Arima-HiC v2 kit manufacturer's instructions, crosslinked DNA was digested using a restriction enzyme master mix. The 5'-overhangs were filled in and labelled with biotinylated nucleotides and proximally ligated. An overnight incubation was carried out for enzymes to digest remaining proteins and for crosslinks to reverse. A clean up was performed with SPRIselect beads prior to

library preparation. Additionally, the biotinylation percentage was estimated using the Qubit Fluorometer v4.0 (Thermo Fisher Scientific) and Qubit HS Assay Kit and Arima-HiC v2 QC beads.

Library preparation and sequencing

Library preparation and sequencing were performed at the WSI Scientific Operations core.

PacBio HiFi

At a minimum, samples were required to have an average fragment size exceeding 8 kb and a total mass over 400 ng to proceed to the low input SMRTbell Prep Kit 3.0 protocol (Pacific Biosciences, California, USA), depending on genome size and sequencing depth required. Libraries were prepared using the SMRTbell Prep Kit 3.0 (Pacific Biosciences, California, USA) as per the manufacturer's instructions. The kit includes the reagents required for end repair/A-tailing, adapter ligation, post-ligation SMRTbell bead cleanup, and nuclease treatment.

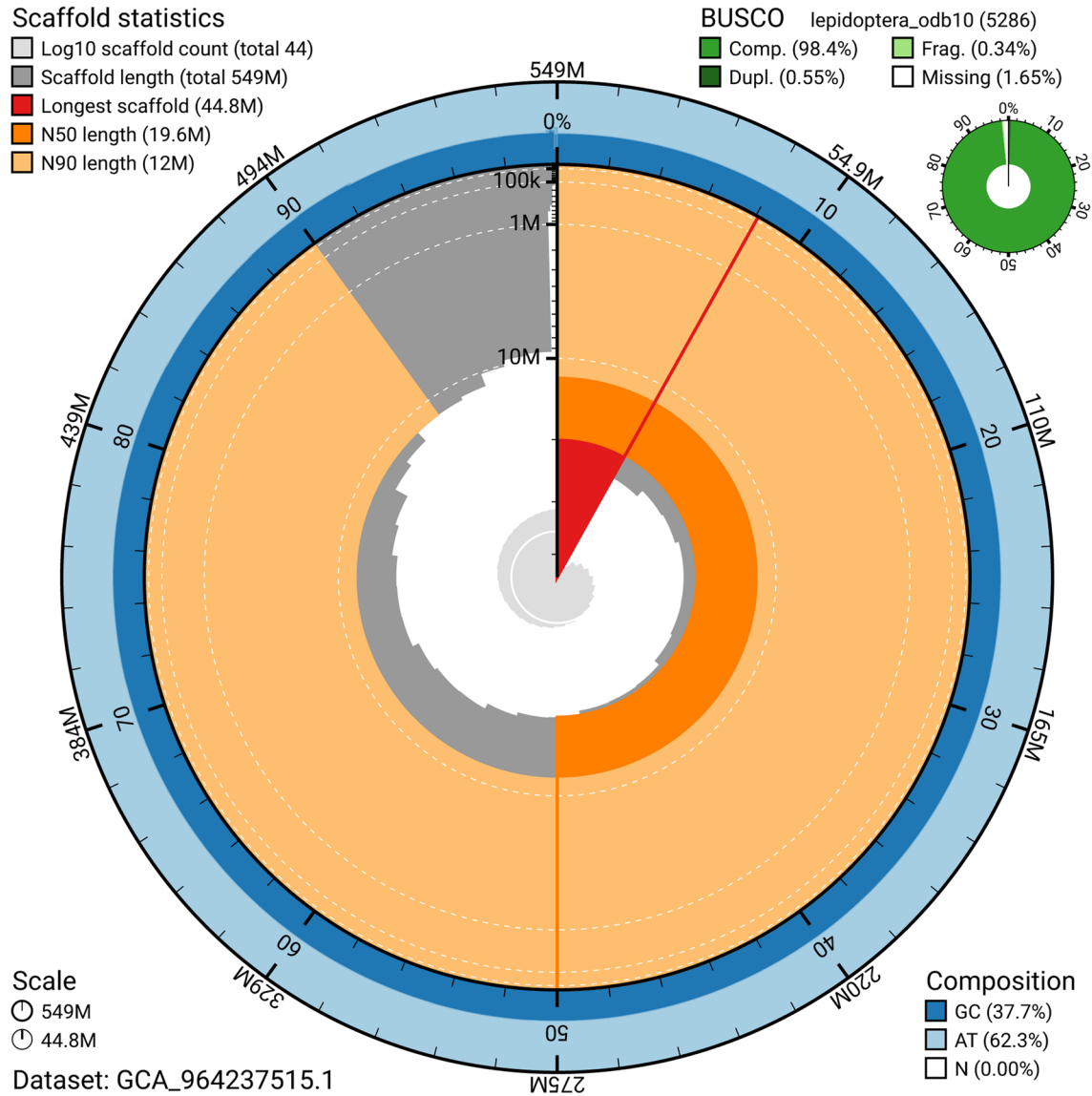


Figure 2. Genome assembly of *Archips podanus*, ilArcPodn1.1: metrics. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1,000 bins around the circumference. The outermost blue tracks display the distribution of GC, AT, and N percentages across the bins. Scaffolds are arranged clockwise from longest to shortest and are depicted in dark grey. The longest scaffold is indicated by the red arc, and the deeper orange and pale orange arcs represent the N50 and N90 lengths. A light grey spiral at the centre shows the cumulative scaffold count on a logarithmic scale. A summary of complete, fragmented, duplicated, and missing BUSCO genes in the lepidoptera_odb10 set is presented at the top right. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/GCA_964237515.1/dataset/GCA_964237515.1/snail.

Following the manufacturer's instructions, size selection and clean up was carried out using diluted AMPure PB beads (Pacific Biosciences, California, USA). DNA concentration was quantified using the Qubit Fluorometer v4.0 (Thermo Fisher Scientific) with Qubit 1X dsDNA HS assay kit and the final library fragment size analysis was carried out using the

Agilent Femto Pulse Automated Pulsed Field CE Instrument (Agilent Technologies) and gDNA 55kb BAC analysis kit.

Samples were sequenced using the Sequel IIe system (Pacific Biosciences, California, USA). The concentration of the library loaded onto the Sequel IIe was in the range 40–135 pM.

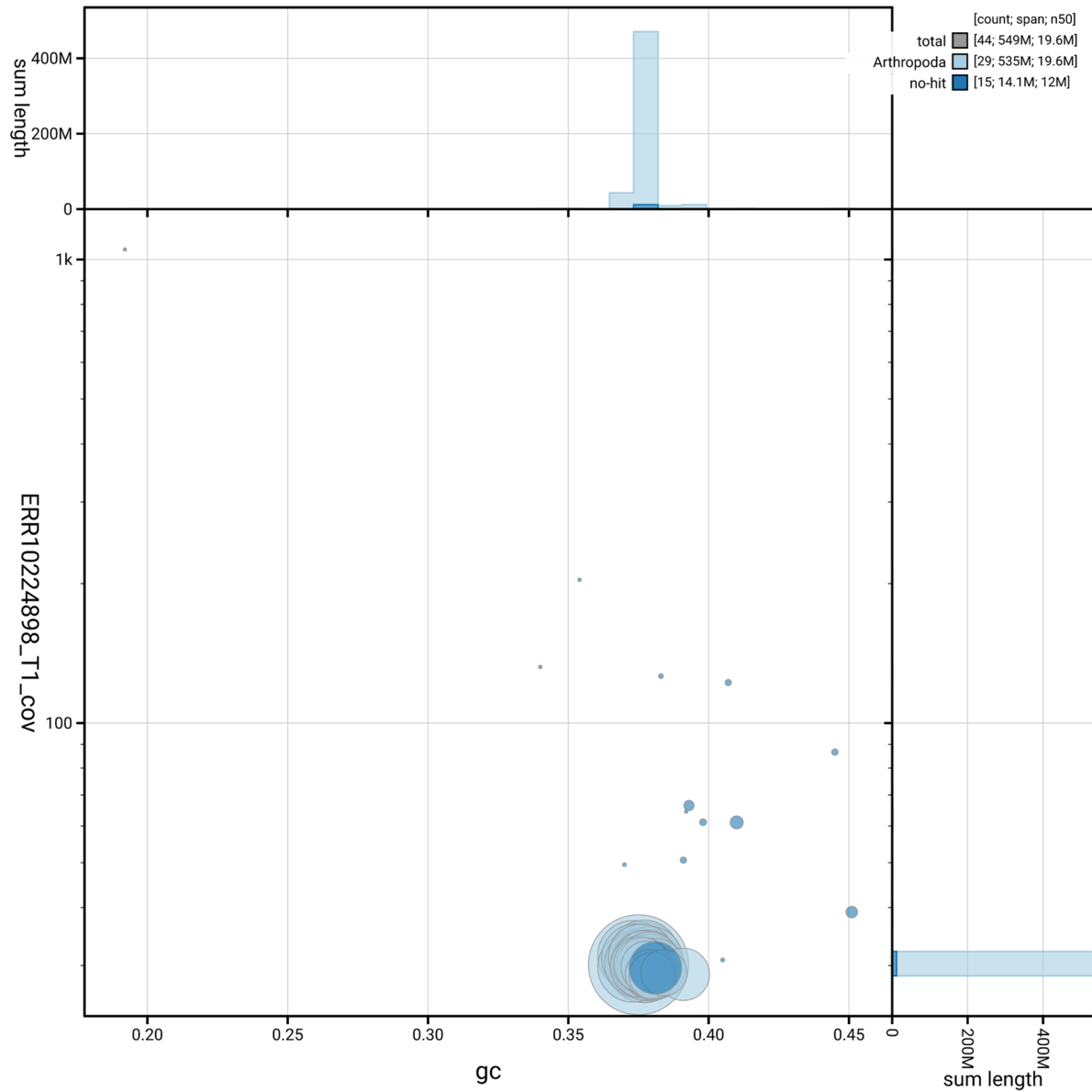


Figure 3. Genome assembly of *Archips podanus*, ilArcPodn1.1: BlobToolKit GC-coverage plot. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes display the total length of sequences distributed across different levels of coverage and GC content. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/GCA_964237515.1/blob.

The SMRT link software, a PacBio web-based end-to-end workflow manager, was used to set-up and monitor the run, as well as perform primary and secondary analysis of the data upon completion.

Hi-C

For Hi-C library preparation, DNA was fragmented using the Covaris E220 sonicator (Covaris) and size selected using

SPRIselect beads to 400 to 600 bp. The DNA was then enriched using the Arima-HiC v2 kit Enrichment beads. Using the NEBNext Ultra II DNA Library Prep Kit (New England Biolabs) for end repair, A-tailing, and adapter ligation. This uses a custom protocol which resembles the standard NEBNext Ultra II DNA Library Prep protocol but where library preparation occurs while DNA is bound to the Enrichment beads. For library amplification, 10 to 16 PCR cycles were required,

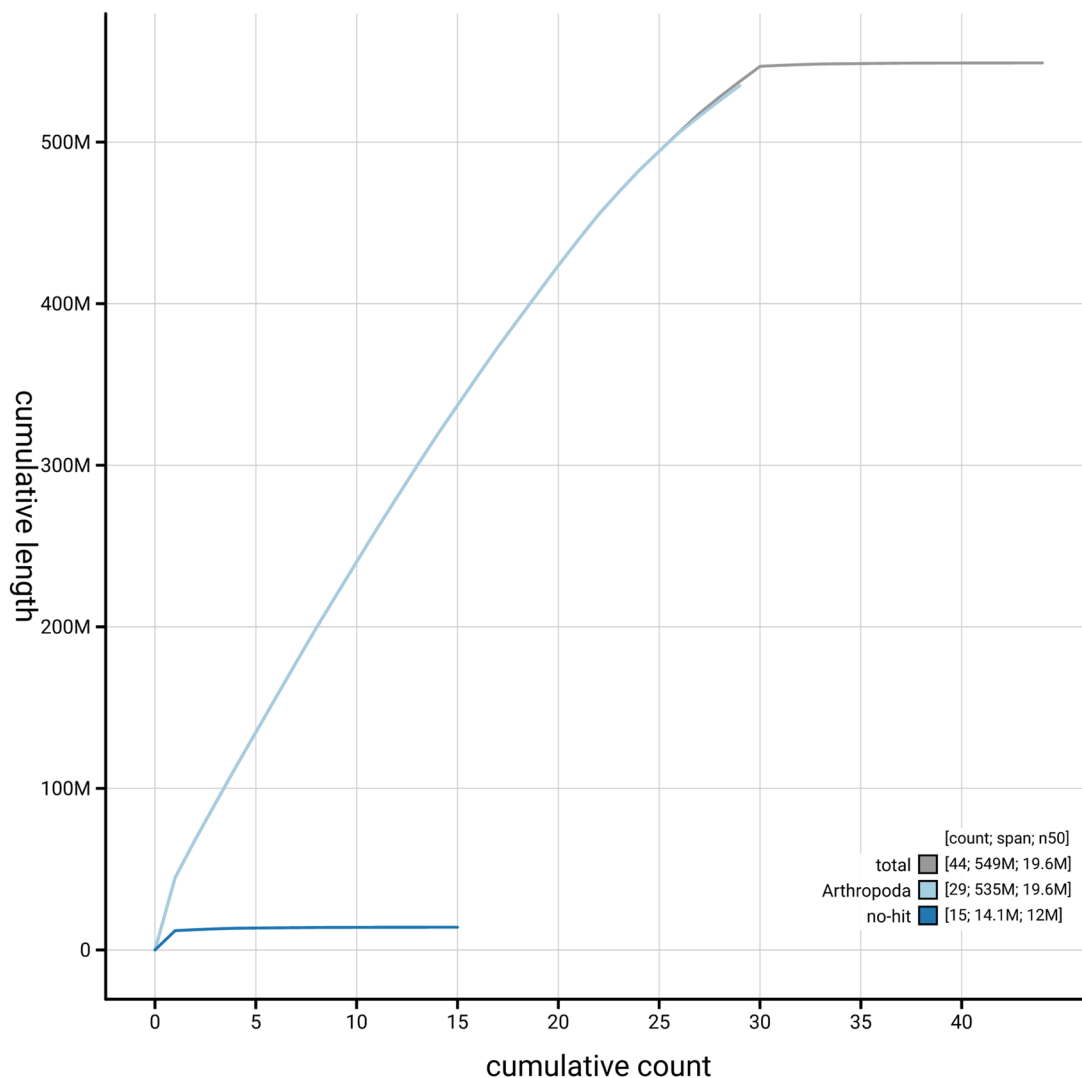


Figure 4. Genome assembly of *Archips podanus*, ilArcPodn1.1: BlobToolKit cumulative sequence plot. The grey line shows cumulative length for all scaffolds. Coloured lines show cumulative lengths of scaffolds assigned to each phylum using the buscogenes taxrule. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/GCA_964237515.1/dataset/GCA_964237515.1/cumulative.

determined by the sample biotinylation percentage. The Hi-C sequencing was performed using paired-end sequencing with a read length of 150 bp on an Illumina NovaSeq X instrument.

Genome assembly, curation and evaluation

Assembly

Prior to assembly of the PacBio HiFi reads, a database of *k*-mer counts ($k = 31$) was generated from the filtered reads using FastK. GenomeScope2 (Ranallo-Benavidez *et al.*, 2020) was used to analyse the *k*-mer frequency distributions, providing estimates of genome size, heterozygosity, and repeat content.

The HiFi reads were first assembled using Hifiasm (Cheng *et al.*, 2021) with the --primary option. Haplotypic duplications were identified and removed using purge_dups (Guan *et al.*, 2020). The Hi-C reads were mapped to the primary contigs using bwa-mem2 (Vasimuddin *et al.*, 2019). The contigs were further scaffolded using the provided Hi-C data (Rao *et al.*, 2014) in YaHS (Zhou *et al.*, 2023) using the --break option for handling potential misassemblies. The scaffolded assemblies were evaluated using Gfastats (Formenti *et al.*, 2022), BUSCO (Manni *et al.*, 2021) and MERQUERY.FK (Rhie *et al.*, 2020).

The mitochondrial genome was assembled using MitoHiFi (Uliano-Silva *et al.*, 2023), which runs MitoFinder

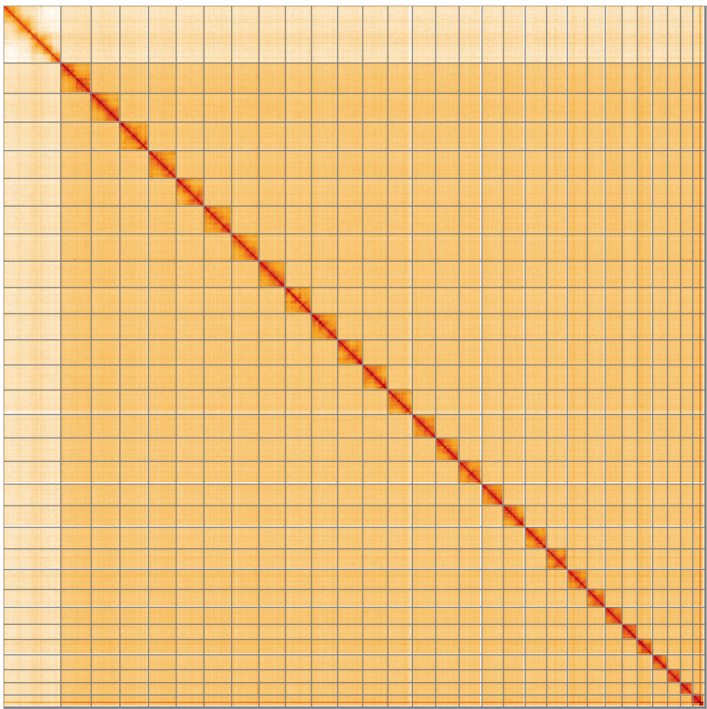


Figure 5. Genome assembly of *Archips podanus*: Hi-C contact map of the ilArcPodn1.1 assembly, visualised using HiGlass. Chromosomes are shown in order of size from left to right and top to bottom. An interactive version of this figure may be viewed at <https://genome-note-higlass.tol.sanger.ac.uk/l/?d=C-jvG7tgS3WKVwIBiqT8oQ>.

Table 3. Chromosomal pseudomolecules in the genome assembly of *Archips podanus*, ilArcPodn1.

INSDC accession	Name	Length (Mb)	GC%
OZ174849.1	1	23.6	37.5
OZ174850.1	2	22.44	37.5
OZ174851.1	3	22.22	37.5
OZ174852.1	4	21.65	37.5
OZ174853.1	5	21.65	37.5
OZ174854.1	6	21.61	37.5
OZ174855.1	7	21.35	37.5
OZ174856.1	8	20.51	37.5
OZ174857.1	9	20.4	37.5
OZ174858.1	10	20.33	37.5
OZ174859.1	11	19.64	37.5
OZ174860.1	12	19.56	38
OZ174861.1	13	19.06	37.5
OZ174862.1	14	18.27	38

INSDC accession	Name	Length (Mb)	GC%
OZ174863.1	15	18.2	38
OZ174864.1	16	17.8	37.5
OZ174865.1	17	16.89	37.5
OZ174866.1	18	16.85	38
OZ174867.1	19	16.78	38
OZ174868.1	20	16.05	38
OZ174869.1	21	15.59	38
OZ174870.1	22	13.89	37.5
OZ174871.1	23	13.23	37.5
OZ174872.1	24	11.95	38
OZ174873.1	25	11.9	39
OZ174874.1	26	11.57	38
OZ174875.1	27	10.2	38
OZ174876.1	28	9.54	38
OZ174877.1	29	9.34	38.5
OZ174848.1	Z	44.8	37.5
OZ174878.1	MT	0.02	19.5

(Allio *et al.*, 2020) and uses these annotations to select the final mitochondrial contig and to ensure the general quality of the sequence.

Assembly curation

The assembly was decontaminated using the Assembly Screen for Cobionts and Contaminants (ASCC) pipeline. Flat files and maps used in curation were generated via the TreeVal pipeline (Pointon *et al.*, 2023). Manual curation was conducted primarily in PretextView (Harry, 2022) and HiGlass (Kerpedjiev *et al.*, 2018), with additional insights provided by JBrowse2 (Diesh *et al.*, 2023). Scaffolds were visually inspected and corrected as described by Howe *et al.* (2021). Any identified contamination, missed joins, and mis-joins were amended, and duplicate sequences were tagged and removed. Sex chromosomes were identified by synteny analysis. The curation process is documented at <https://gitlab.com/wtsi-grit/rapid-curation>.

Assembly quality assessment

The Merqury.FK tool (Rhie *et al.*, 2020), run in a Singularity container (Kurtzer *et al.*, 2017), was used to evaluate *k*-mer completeness and assembly quality for the primary and alternate haplotypes using the *k*-mer databases (*k* = 31) that were computed prior to genome assembly. The analysis outputs included assembly QV scores and completeness statistics.

A Hi-C contact map was produced for the final version of the assembly. The Hi-C reads were aligned using bwa-mem2 (Vasimuddin *et al.*, 2019) and the alignment files were combined using SAMtools (Danecek *et al.*, 2021). The Hi-C alignments were converted into a contact map using BEDTools (Quinlan & Hall, 2010) and the Cooler tool suite (Abdennur & Mirny, 2020). The contact map was visualised in HiGlass (Kerpedjiev *et al.*, 2018).

The blobtoolkit pipeline is a Nextflow (Di Tommaso *et al.*, 2017) port of the previous Snakemake Blobtoolkit pipeline

(Challis *et al.*, 2020). It aligns the PacBio reads in SAMtools and minimap2 (Li, 2018) and generates coverage tracks for regions of fixed size. In parallel, it queries the GoAT database (Challis *et al.*, 2023) to identify all matching BUSCO lineages to run BUSCO (Manni *et al.*, 2021). For the three domain-level BUSCO lineages, the pipeline aligns the BUSCO genes to the UniProt Reference Proteomes database (Bateman *et al.*, 2023) with DIAMOND blastp (Buchfink *et al.*, 2021). The genome is also divided into chunks according to the density of the BUSCO genes from the closest taxonomic lineage, and each chunk is aligned to the UniProt Reference Proteomes database using DIAMOND blastx. Genome sequences without a hit are chunked using seqtk and aligned to the NT database with blastn (Altschul *et al.*, 1990). The blobtools suite combines all these outputs into a blobdir for visualisation.

The blobtoolkit pipeline was developed using nf-core tooling (Ewels *et al.*, 2020) and MultiQC (Ewels *et al.*, 2016), relying on the Conda package manager, the Bioconda initiative (Grüning *et al.*, 2018), the Biocontainers infrastructure (da Veiga Leprevost *et al.*, 2017), as well as the Docker (Merkel, 2014) and Singularity (Kurtzer *et al.*, 2017) containerisation solutions.

Table 4 contains a list of relevant software tool versions and sources.

Wellcome Sanger Institute – Legal and Governance

The materials that have contributed to this genome note have been supplied by a Darwin Tree of Life Partner. The submission of materials by a Darwin Tree of Life Partner is subject to the ‘**Darwin Tree of Life Project Sampling Code of Practice**’, which can be found in full on the Darwin Tree of Life website [here](#). By agreeing with and signing up to the Sampling Code of Practice, the Darwin Tree of Life Partner agrees they will meet the legal and ethical requirements and standards set out within this document in respect of all samples acquired for, and supplied to, the Darwin Tree of Life Project.

Table 4. Software tools: versions and sources.

Software tool	Version	Source
BEDTools	2.30.0	https://github.com/arq5x/bedtools2
BLAST	2.14.0	ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/
BlobToolKit	4.3.9	https://github.com/blobtoolkit/blobtoolkit
BUSCO	5.5.0	https://gitlab.com/ezlab/busco
bwa-mem2	2.2.1	https://github.com/bwa-mem2/bwa-mem2
Cooler	0.8.11	https://github.com/open2c/cooler
DIAMOND	2.1.8	https://github.com/bbuchfink/diamond
fasta_windows	0.2.4	https://github.com/tolkit/fasta_windows
FastK	666652151335353eef2fcd58880bcef5bc2928e1	https://github.com/thegenemyers/FASTK
Gfastats	1.3.6	https://github.com/vgl-hub/gfastats

Software tool	Version	Source
GoaT CLI	0.2.5	https://github.com/genomehubs/goat-cli
Hifiasm	0.19.8-r603	https://github.com/chhyllp123/hifiasm
HiGlass	44086069ee7d4d3f6f3f0012569789ec138f42b84aa44357826c0b6753eb28de	https://github.com/higlass/higlass
MerquryFK	d00d98157618f4e8d1a9190026b19b471055b22e	https://github.com/thegenemyers/MERQURY.FK
Minimap2	2.24-r1122	https://github.com/lh3/minimap2
MitoHiFi	3	https://github.com/marcelauliano/MitoHiFi
MultiQC	1.14, 1.17, and 1.18	https://github.com/MultiQC/MultiQC
Nextflow	23.10.0	https://github.com/nextflow-io/nextflow
PretextView	0.2.5	https://github.com/sanger-tol/PretextView
samtools	1.19.2	https://github.com/samtools/samtools
sanger-tol/ascc	-	https://github.com/sanger-tol/ascc
sanger-tol/blobtoolkit	0.5.1	https://github.com/sanger-tol/blobtoolkit
Seqtk	1.3	https://github.com/lh3/seqtk
Singularity	3.9.0	https://github.com/sylabs/singularity
TreeVal	1.2.0	https://github.com/sanger-tol/treeval
YaHS	1.2a.2	https://github.com/c-zhou/yahs

Further, the Wellcome Sanger Institute employs a process whereby due diligence is carried out proportionate to the nature of the materials themselves, and the circumstances under which they have been/are to be collected and provided for use. The purpose of this is to address and mitigate any potential legal and/or ethical implications of receipt and use of the materials as part of the research project, and to ensure that in doing so we align with best practice wherever possible. The overarching areas of consideration are:

- Ethical review of provenance and sourcing of the material
- Legality of collection, transfer and use (national and international)

Each transfer of samples is further undertaken according to a Research Collaboration Agreement or Material Transfer Agreement entered into by the Darwin Tree of Life Partner, Genome Research Limited (operating as the Wellcome Sanger Institute), and in some circumstances other Darwin Tree of Life collaborators.

Data availability

European Nucleotide Archive: *Archips podanus* (large fruit-tree tortrix). Accession number PRJEB55946; <https://identifiers.org/ena.embl/PRJEB55946>. The genome sequence is released openly for reuse. The *Archips podanus* genome sequencing initiative is part of the Darwin Tree of Life (DTOL) project. All raw sequence data and the assembly have been

deposited in INSDC databases. The genome will be annotated using available RNA-Seq data and presented through the [Ensembl](#) pipeline at the European Bioinformatics Institute. Raw data and assembly accession identifiers are reported in [Table 1](#) and [Table 2](#).

Author information

Members of the Natural History Museum Genome Acquisition Lab are listed here: <https://doi.org/10.5281/zenodo.12159242>.

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Kay Lucek 

University of Neuchâtel, Neuchâtel, Switzerland

The authors present the chromosome level genome assembly of a male specimen of the Tortix moth *Archips podanus*. The assembly consists of 30 chromosomes and is not annotated for genes. The assembly is highly complete as revealed by the high BUSCO score but not phased. Sequencing and genome assembly follow the current state of the art and use established methods. The assembly has been generated using the established pipelines of the Darwin Tree of Life Consortium.

This is a very complete genome note and the genome will be of great value to study this holarctic species across the Northern Hemisphere, including within its introduced range in North America. The methods sections are very detailed, making the approaches reproducible.

Is the rationale for creating the dataset(s) clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of methods and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Speciation genomics

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 27 May 2025

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Michal Rindoš 

University of South Bohemia, Ceske Budejovice, Czech Republic

The *Note* contains basic information on the distribution and sexual dimorphism of the species.

In the abstract I would delete "Tortrix moth" in *Tortix moth; Arthropoda; Insecta; Lepidoptera; Tortricidae*

and also give examples of the host plants on which the species feeds. Otherwise I think the note is suitable for indexing.

Is the rationale for creating the dataset(s) clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of methods and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Biodiversity and systematics of Lepidoptera

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.
