DATA NOTE

The genome sequence of the Brown Moss-moth, *Bryotropha terrella* (Denis & Schiffermüller), 1775

[version 1; peer review: 3 approved]

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Abstract

We present a genome assembly from a female specimen of *Bryotropha terrella* (Brown Moss-moth; Arthropoda; Insecta; Lepidoptera; Gelechiidae). The genome sequence has a total length of 756.35 megabases. Most of the assembly (99.62%) is scaffolded into 31 chromosomal pseudomolecules, including the W and Z sex chromosomes. The mitochondrial genome has also been assembled, with a length of 15.29 kilobases.

Keywords

Bryotropha terrella, Brown Moss-moth, genome sequence, chromosomal, Lepidoptera

This article is included in the Tree of Life gateway.

Open Peer Review

Approval Status ✓ ✓ ✓

	1	2	3
version 1 04 Jun 2025	✓ view	✓ view	✓ view

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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; Gelechioidea; Gelechiidae; Anomologinae; *Bryotropha*; *Bryotropha terrella* (Denis & Schiffermüller), 1775 (NCBI:txid1280429)

Background

As part of the Darwin Tree of Life Project – which aims to generate high-quality reference genomes for all named eukaryotic species in Britain and Ireland to support research, conservation, and the sustainable use of biodiversity – we present a chromosomally complete genome sequence for the Brown Mossmoth, *Bryotropha terrella*. This genome was assembled using the Tree of Life pipeline from a specimen collected in Wytham Woods, Oxfordshire, United Kingdom (Figure 1).

Genome sequence report

Sequencing data

The genome of a specimen of *Bryotropha terrella* (Figure 1) was sequenced using Pacific Biosciences single-molecule HiFi long reads, generating 30.83 Gb (gigabases) from 3.40 million reads, which were used to assemble the genome. GenomeScope analysis estimated the haploid genome size at 740.34 Mb, with a heterozygosity of 1.72% and repeat content of 45.63%. These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 41 coverage. Hi-C sequencing produced 96.60 Gb from 639.73 million reads, used to scaffold the assembly. Table 1 summarises the specimen and sequencing details.

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 34 misjoins or missing joins and removed 7 haplotypic duplications. These interventions decreased the scaffold count by 18.18%. The final assembly has a total length of 756.35 Mb in 53 scaffolds, with 98 gaps, and a scaffold N50 of 24.17 Mb (Table 2).

Figure 1. Photograph of the *Bryotropha terrella* (ilBryTerr3) specimen used for genome sequencing.

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 31 chromosomal-level scaffolds, representing 29 autosomes and the W and Z sex chromosomes. These chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 5; Table 3).

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 64.8. The *k*-mer completeness is 73.13% for the primary haplotype and 68.97% for the alternate haplotype; and 99.65% for the combined primary and alternate assemblies. BUSCO v.5.5.0 analysis using the lepidoptera_odb10 reference set (n = 5,286) identified 97.8% of the expected gene set (single = 96.8%, duplicated = 1.0%).

Table 2 provides assembly metric benchmarks adapted from Rhie *et al.* (2021) and the Earth BioGenome Project Report on Assembly Standards September 2024. The primary assembly achieves the EBP reference standard of **7.C.Q67**.

Methods

Sample acquisition and DNA barcoding

The specimen used for genome sequencing was an adult female *Bryotropha terrella* (specimen ID Ox003086, ToLID ilBryTerr3), collected from Wytham Woods, Oxfordshire, United Kingdom (latitude 51.772, longitude –1.338) on 2022-07-22, using a light trap. The specimen was collected by Finley Hutchinson and Liam Crowley (University of Oxford), identified by Finley Hutchinson and preserved on dry ice.

Table 1. **Specimen and sequencing data for *Bryotropha terrella*.**

Project information			
Study title	Bryotropha terrella (cinerous neb)		
Umbrella BioProject	PRJEB74972		
Species	*Bryotropha terrella*		
BioSpecimen	SAMEA113425689		
NCBI taxonomy ID	1280429		
Specimen information			
Technology	**ToLID**	**BioSample accession**	**Organism part**
PacBio long read sequencing	ilBryTerr3	SAMEA113425870	whole organism
Hi-C sequencing	ilBryTerr2	SAMEA111458783	whole organism
Sequencing information			
Platform	**Run accession**	**Read count**	**Base count (Gb)**
Hi-C Illumina NovaSeq X	ERR12945472	6.40e+08	96.6
PacBio Revio	ERR12921318	3.40e+06	30.83

Table 2. **Genome assembly data for *Bryotropha terrella*.**

Genome assembly		
Assembly name	ilBryTerr3.1	
Assembly accession	GCA_964059635.1	
Alternate haplotype accession	*GCA_964059585.1*	
Assembly level for primary assembly	chromosome	
Span (Mb)	756.35	
Number of contigs	151	
Number of scaffolds	53	
Longest scaffold (Mb)	82.39	
Assembly metric	**Measure**	***Benchmark***
Contig N50 length	10.89 Mb	*≥ 1 Mb*
Scaffold N50 length	24.17 Mb	*= chromosome N50*
Consensus quality (QV)	Primary: 67.3; alternate: 64.0; combined: 64.8	*≥ 40*
k-mer completeness	Primary: 73.13%; alternate: 68.97%; combined: 99.65%	*≥ 95%*
BUSCO*	C:97.8%[S:96.8%,D:1.0%], F:0.4%,M:1.8%,n:5,286	*S > 90%; D < 5%*
Percentage of assembly assigned to chromosomes	99.62%	*≥ 90%*
Sex chromosomes	W and Z	*localised homologous pairs*
Organelles	Mitochondrial genome: 15.29 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.

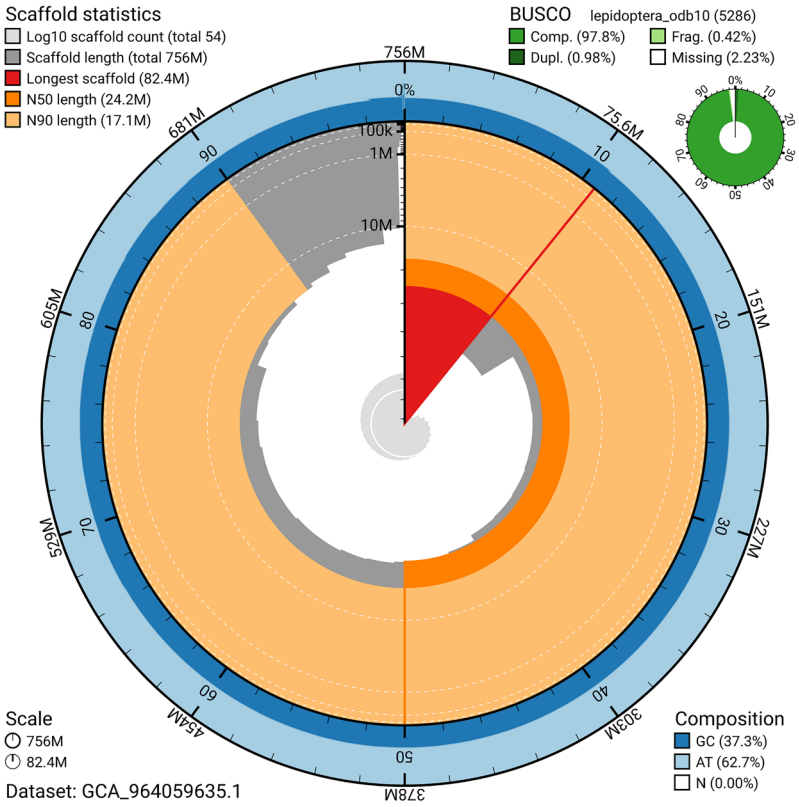

Figure 2. Genome assembly of *Bryotropha terrella*, ilBryTerr3.1: metrics. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1,000 bins around the circumference. 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_964059635.1/dataset/GCA_964059635.1/snail.

A second specimen, used for Hi-C sequencing (specimen ID NHMUK014425923, ToLID ilBryTerr2), was collected from Tonbridge, England, United Kingdom (latitude 51.18, longitude 0.29) on 2021-08-16 by actinic light. The specimen was collected and identified by Gavin Broad (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 each 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 (Howard *et al.*, 2025). Detailed protocols are available on protocols.io (Denton *et al.*, 2023b). The ilBryTerr3 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 in the WSI Scientific Operations core using the Automated MagAttract v2 protocol (Oatley *et al.*, 2023). The DNA was sheared into an average fragment size of 12–20 kb in a Megaruptor 3 system (Bates *et al.*, 2023). Sheared DNA was purified by solid-phase reversible immobilisation, using AMPure PB beads to eliminate shorter fragments

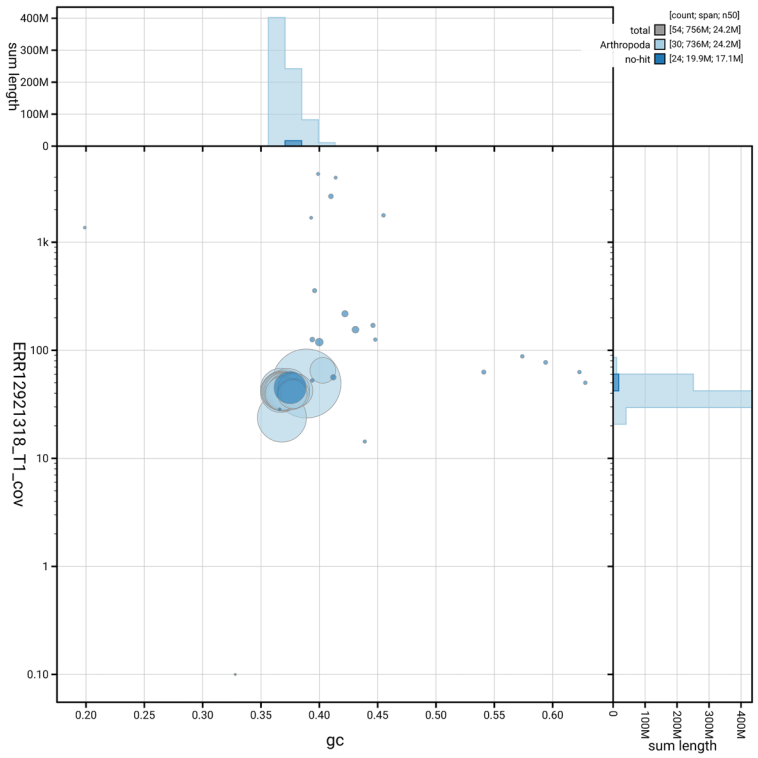

Figure 3. Genome assembly of *Bryotropha terrella*, ilBryTerr3.1: BlobToolKit GC-coverage plot. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. 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_964059635.1/dataset/GCA_964059635.1/blob.

and concentrate the DNA (Strickland *et al.*, 2023). The concentration of the sheared and purified DNA was assessed using a Nanodrop spectrophotometer and Qubit Fluorometer using the Qubit dsDNA High Sensitivity Assay kit. Fragment size distribution was evaluated by running the sample on the FemtoPulse system.

Hi-C sample preparation and crosslinking

Hi-C data were generated from the whole organism of the ilBryTerr2 sample using the Arima-HiC v2 kit (Arima Genomics) with 20–50 mg of frozen tissue (stored at –80 °C). As per manufacturer's instructions, tissue was fixed, and the DNA crosslinked using a TC buffer with 22% formaldehyde concentration, and a final formaldehyde concentration of 2%. The tissue was then homogenised using the Diagnocine Power Masher-II. The crosslinked DNA was digested using a restriction enzyme master mix, then biotinylated and ligated. A clean up was performed with SPRIselect beads prior to library preparation. DNA concentration was quantified using the Qubit Fluorometer v4.0 (Thermo Fisher Scientific) and Qubit HS Assay Kit, and sample biotinylation percentage was estimated using the 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), depending on genome size and sequencing depth required. Libraries were prepared using the SMRTbell Prep Kit 3.0 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. Size-selection and clean-up were carried out using diluted AMPure PB beads (Pacific Biosciences). DNA concentration was quantified using the Qubit Fluorometer v4.0 (ThermoFisher 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 the gDNA 55kb BAC analysis kit.

Samples were sequenced on a Revio instrument (Pacific Biosciences, California, USA). Prepared libraries were normalised to 2 nM, and 15 µL was used for making complexes. Primers were annealed and polymerases were bound to create circularised complexes according to manufacturer's instructions. The complexes were purified with the 1.2X clean up with SMRTbell beads. The purified complexes were then diluted to the Revio loading concentration (in the range 200–300 pM), and spiked with a Revio sequencing internal control. Samples were

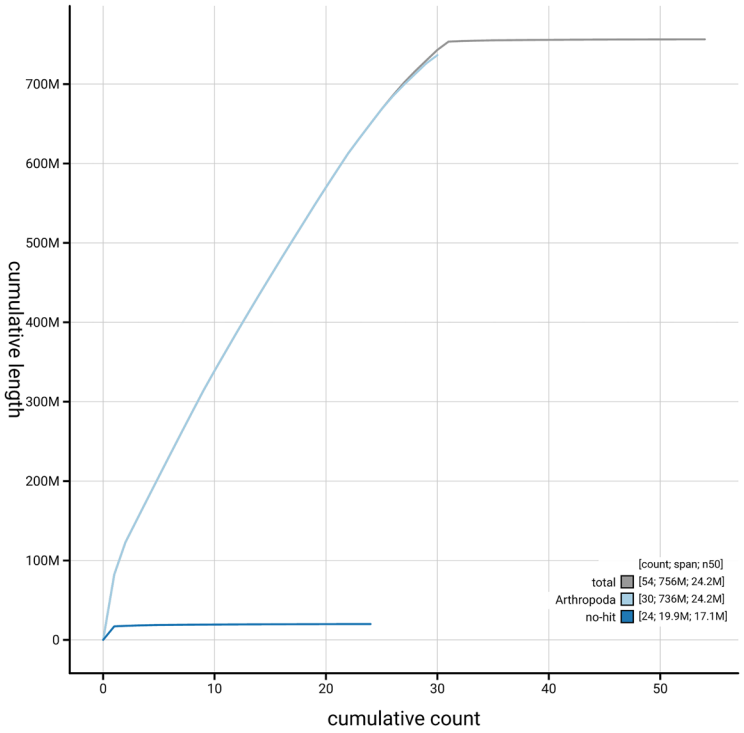

Figure 4. Genome assembly of *Bryotropha terrella*, ilBryTerr3.1: BlobToolKit cumulative sequence plot. The grey line shows cumulative length for all scaffolds. Coloured lines show cumulative lengths of scaffolds assigned to each phylum using the buscogenes taxrule. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/GCA_964059635.1/dataset/GCA_964059635.1/cumulative.

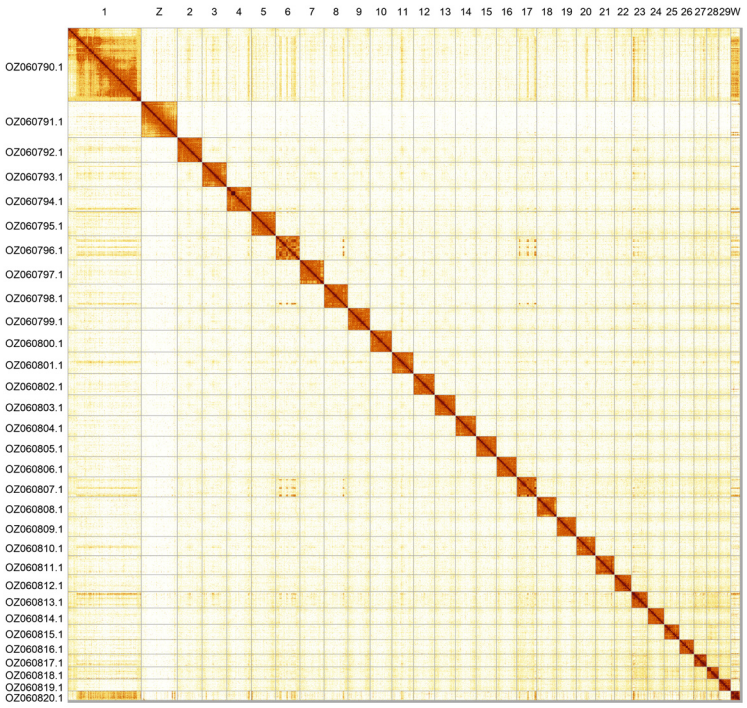

Figure 5. Genome assembly of *Bryotropha terrella*: Hi-C contact map of the ilBryTerr3.1 assembly, generated using PretextSnapshot. Chromosomes are shown in order of size and labelled along the axes.

Table 3. Chromosomal pseudomolecules in the genome assembly of *Bryotropha terrella*, ilBryTerr3.

INSDC accession	Name	Length (Mb)	GC%
OZ060790.1	1	82.39	39
OZ060792.1	2	27.71	37
OZ060793.1	3	27.66	37
OZ060794.1	4	27.46	36.5
OZ060795.1	5	27.43	36.5
OZ060796.1	6	27.16	37.5
OZ060797.1	7	26.93	37
OZ060798.1	8	26.76	37
OZ060799.1	9	24.99	37
OZ060800.1	10	24.31	36.5
OZ060801.1	11	24.17	37
OZ060802.1	12	23.77	37
OZ060803.1	13	23.45	37
OZ060804.1	14	23.03	36.5
OZ060805.1	15	22.97	36.5
OZ060806.1	16	22.51	37
OZ060807.1	17	22.46	37.5
OZ060808.1	18	22.45	37
OZ060809.1	19	21.95	37
OZ060810.1	20	21.46	37.5
OZ060811.1	21	21.43	37
OZ060812.1	22	18.82	37
OZ060813.1	23	18.48	38
OZ060814.1	24	18.3	37
OZ060815.1	25	17.07	37.5
OZ060816.1	26	16.16	38
OZ060817.1	27	14.48	37.5
OZ060818.1	28	13.47	38
OZ060819.1	29	13.39	37.5
OZ060820.1	W	10.39	40.5
OZ060791.1	Z	40.49	37
OZ060821.1	MT	0.02	20

sequenced on Revio 25M SMRT cells (Pacific Biosciences, California, USA). 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, the biotinylated DNA constructs were fragmented using a Covaris E220 sonicator and size-selected to 400–600 bp using SPRISelect beads. DNA was then enriched using Arima-HiC v2 Enrichment beads. The NEBNext Ultra II DNA Library Prep Kit (New England Biolabs) was used for end repair, A-tailing, and adapter ligation, following a modified protocol in which library preparation is carried out while the DNA remains bound to the enrichment beads. PCR amplification was performed using KAPA HiFi HotStart mix and custom dual-indexed adapters (Integrated DNA Technologies) in a 96-well plate format. Depending on sample concentration and biotinylation percentage determined at the crosslinking stage, samples were amplified for 10–16 PCR cycles. Post-PCR clean-up was carried out using SPRISelect beads. The libraries were quantified using the Accuclear Ultra High Sensitivity dsDNA Standards Assay kit (Biotium) and normalised to 10 ng/μL before sequencing. Hi-C sequencing was performed on the 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 (Rao *et al.*, 2014) were mapped to the primary contigs using bwa-mem2 (Vasimuddin *et al.*, 2019), and the contigs were scaffolded 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 MERQURY.FK (Rhie *et al.*, 2020).

The mitochondrial genome was assembled using MitoHiFi (Uliano-Silva *et al.*, 2023), which runs MitoFinder (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. 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) computed prior to genome assembly. The analysis outputs included assembly QV scores and completeness statistics.

The genome was analysed using the BlobToolKit pipeline, a Nextflow (Di Tommaso *et al.*, 2017) implementation of the earlier Snakemake BlobToolKit pipeline (Challis *et al.*, 2020). The pipeline aligns PacBio reads using minimap2 (Li, 2018) and SAMtools (Danecek *et al.*, 2021) to generate coverage tracks. Simultaneously, it queries the GoaT database (Challis *et al.*, 2023) to identify relevant BUSCO lineages and runs BUSCO (Manni *et al.*, 2021). For the three domain-level BUSCO lineages, BUSCO genes are aligned to the UniProt Reference Proteomes database (Bateman *et al.*, 2023) using DIAMOND blastp (Buchfink *et al.*, 2021). The genome is divided into chunks based on the density of BUSCO genes from the closest taxonomic lineage, and each chunk is aligned to the UniProt Reference Proteomes database with DIAMOND blastx. Sequences without hits are chunked using seqtk and aligned to the NT database with blastn (Altschul *et al.*, 1990). The BlobToolKit suite consolidates all 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), with package management via Conda and Bioconda (Grüning *et al.*, 2018), and containerisation through Docker (Merkel, 2014) and Singularity (Kurtzer *et al.*, 2017).

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.

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

Table 4. Software tools: versions and sources.

Software tool	Version	Source
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
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
GoaT CLI	0.2.5	https://github.com/genomehubs/goat-cli
Hifiasm	0.19.8-r603	https://github.com/chhylp123/hifiasm
HiGlass	44086069ee7d4d3f6f3f0012569789ec138f42b84a a44357826c0b6753eb28de	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

Software tool	Version	Source
PretextSnapshot	-	https://github.com/sanger-tol/PretextSnapshot
samtools	1.19.2	https://github.com/samtools/samtools
sanger-tol/ascc	0.1.0	https://github.com/sanger-tol/ascc
sanger-tol/blobtoolkit	0.6.0	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

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: Bryotropha terrella (cinerous neb). Accession number PRJEB74972; https://identifiers.org/ena.embl/PRJEB74972. The genome sequence is released openly for reuse. The *Bryotropha terrella* genome sequencing initiative is part of the Darwin Tree of Life Project (PRJEB40665), the Sanger Institute Tree of Life Programme (PRJEB43745) and Project Psyche (PRJEB71705). 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 University of Oxford and Wytham Woods Genome Acquisition Lab are listed here: https://doi.org/10.5281/zenodo.12157525.

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

Members of the Darwin Tree of Life Barcoding collective are listed here: https://doi.org/10.5281/zenodo.12158331.

Members of the Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory team are listed here: https://doi.org/10.5281/zenodo.12162482.

Members of Wellcome Sanger Institute Scientific Operations: Sequencing Operations are listed here: https://doi.org/10.5281/zenodo.14870789.

Members of the Wellcome Sanger Institute Tree of Life Core Informatics team are listed here: https://doi.org/10.5281/zenodo.12160324.

Members of the Tree of Life Core Informatics collective are listed here: https://doi.org/10.5281/zenodo.12205391.

Members of the Darwin Tree of Life Consortium are listed here: https://doi.org/10.5281/zenodo.4783558.

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Open Peer Review

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Version 1

Reviewer Report 01 September 2025

https://doi.org/10.21956/wellcomeopenres.26825.r127593

✔ **Annabel Whibley**
Grapevine Improvement, Bragato Research Institute, Lincoln, New Zealand

In this Data Note, Hutchinson, Crowley, Broad and colleagues report the genome assembly of the Brown Moss-moth, *Bryotropha terrella.* No genome annotation is presented. I will note, really as a counterpoint to other data notes I have reviewed or read, that this makes little comment on the natural history of the species, including only the Darwin Tree of Life goals as justification for the work. At the very least I would like some steer as to whether this is due to lack of knowledge or lack of interest.

The quality of the assembly is excellent, with very few contigs and >99.6% of the assembly scaffolded into chromosomes, and impressive QV and completeness metrics. Chromosome 1 is markedly larger than the Z and other autosomal scaffolds, which strikes me as unusual, and I would be interested to view this alongside other related species: it shows some HiC interactions with the W chromosome and is perhaps enriched in repeat elements?

The methods and reporting follow standard Darwin Tree of Life templates. The links to publicly available datasets are functional, and report of methods and metadata is comprehensive and well-structured.

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: Genomics, Bioinformatics, Evolution

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 01 September 2025

https://doi.org/10.21956/wellcomeopenres.26825.r127587

Panagiotis Ioannidis
Foundation for Research & Technology - Hellas, Crete, Greece

This manuscript describes the sequencing and assembly of the genome of the lepidopteran Bryotropha terrela. The methodology used is the standard methodology used in all DToL samples, which is producing high quality genome assemblies. Such assemblies are suitable for any type of comparative analyses that aim to elucidate the ecology and evolution of this organism.

More specifically, assembly contiguity is very good since virtually all contigs were assigned to a chromosome. Additionally, BUSCO scores suggest that the content of the contigs is excellent.

My only comment has to do with the blobplot. Looking at it (figure 3) I noticed that there are quite a few small contigs either of low coverage, or of high GC content. All of them are annotated as "no-hit". Also, there is a couple of large contigs that are annotated as "no-hit". Could the authors comment on the origin of these contigs? Could they be symbiont related?

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: insect genomics, bioinformatics

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 25 June 2025

https://doi.org/10.21956/wellcomeopenres.26825.r125101

Sivasankaran Kuppusamy
Loyola College, Chennai, Tamil Nadu, India

Authors have done the chromosome-level genome sequence of *Bryotropha terrella* ([Denis & Schiffermüller], 1775). They have observed 31 chromosomal pseudomolecules in the assembly.

Minor comments on the Manuscript

Authors haven't given the proper taxonomic parenthesis of the describer of the species in the title. The title can be modified as "The genome sequence of the Brown Moss-moth, *Bryotropha terrella* ([Denis & Schiffermüller], 1775)"

Authors can include brief bionomics of the sequenced species in the background of the article. Authors have used the full form of Genus name *Bryotropha* throughout the text. The genus name can be used in full form first time and the can be a short form like *B. terrella.*

Authors have produced 100.43 Gb comprehensive sequences through the Hi-C illumina platform and PacBio. After the assembly they received 756.35 megabases. But authors haven't observed the protein-coding genes, non-coding genes and gene transcripts. Any reason?

The research article was well prepared and the manuscript meets the necessary scientific standard and 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: Phylogenetic analysis of Noctuoidea moths using mitogenome sequence

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.