



DATA NOTE

The genome sequence of the Fern moth, *Horisme tersata* (Denis & Schiffermüller) , 1775 (Lepidoptera: Geometridae)

[version 1; peer review: 2 approved]

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V1 First published: 10 Oct 2025, 10:565
<https://doi.org/10.12688/wellcomeopenres.24980.1>

Latest published: 10 Oct 2025, 10:565
<https://doi.org/10.12688/wellcomeopenres.24980.1>

Abstract

We present a genome assembly from an individual male *Horisme tersata* (Fern moth; Arthropoda; Insecta; Lepidoptera; Geometridae). The assembly contains two haplotypes with total lengths of 558.12 megabases and 558.96 megabases. Most of haplotype 1 (99.71%) is scaffolded into 21 chromosomal pseudomolecules, including the Z sex chromosome. Haplotype 2 was assembled to scaffold level. The mitochondrial genome has also been assembled, with a length of 16.42 kilobases. This assembly was generated as part of the Darwin Tree of Life project, which produces reference genomes for eukaryotic species found in Britain and Ireland.

Keywords



Horisme tersata; Fern moth; genome sequence; chromosomal; Lepidoptera





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

Open Peer Review

Approval Status  

	1	2
version 1 10 Oct 2025	 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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Author roles: Crowley LM: Investigation, Resources;

Competing interests: No competing interests were disclosed.

Grant information: This work was supported by Wellcome through core funding to the Wellcome Sanger Institute (220540) and the Darwin Tree of Life Discretionary Award (218328).

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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How to cite this article: Crowley LM, University of Oxford and Wytham Woods Genome Acquisition Lab, Darwin Tree of Life Barcoding Collective *et al.* **The genome sequence of the Fern moth, *Horisme tersata* (Denis & Schiffermüller), 1775 (Lepidoptera: Geometridae) [version 1; peer review: 2 approved]** Wellcome Open Research 2025, 10:565

<https://doi.org/10.12688/wellcomeopenres.24980.1>

First published: 10 Oct 2025, 10:565 <https://doi.org/10.12688/wellcomeopenres.24980.1>

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; Obtectomera; Geometroidea; Geometridae; Larentiinae; *Horisme*; *Horisme tersata* (Denis & Schiffermüller, 1775 (NCBI:txid986989))

Background

Horisme tersata (Denis & Schiffermüller, 1775), the Fern moth, is a resident geometrid of calcareous hedgerows, scrub and open woodland in southern Britain. The adults fly mainly June to mid-August and come to light (Waring *et al.*, 2017).

A narrow black streak is visible at rest where the second forewing cross-line aligns with a dark dorsal line on the abdomen. (Waring *et al.*, 2017). The very similar *H. radicularia* (the Cryptic Fern) typically shows a black apical streak, a paler apical area and lacks a forewing discal spot; certain separation may require genitalia (Lepiforum e.V., 2025). Fern and Cryptic Fern larvae both feed on traveller's-joy (*Clematis vitalba*) (Waring *et al.*, 2017).

We present a chromosome-level genome sequence for *Horisme tersata*. The assembly was produced using the Tree of Life pipeline from a specimen collected in Wytham Woods, Oxfordshire, United Kingdom (Figure 1). This assembly was generated 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 (Blaxter *et al.*, 2022).

Methods

Sample acquisition and DNA barcoding

The specimen used for genome sequencing was an adult male *Horisme tersata* (specimen ID Ox003715, ToLID iHorTers1;



Figure 1. Photograph of the *Horisme tersata* (iHorTers1) specimen used for genome sequencing.

Figure 1), collected from Wytham Woods, Oxfordshire, UK (latitude 51.772, longitude -1.338) on 2023-06-20T12:00:00. The specimen was collected and identified by Liam Crowley (University of Oxford). For the Darwin Tree of Life sampling and metadata approach, refer to Lawniczak *et al.* (2022).

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) (see the protocol). 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 are available on protocols.io.

Nucleic acid extraction

Protocols for high molecular weight (HMW) DNA extraction developed at the Wellcome Sanger Institute (WSI) Tree of Life Core Laboratory are available on protocols.io (Howard *et al.*, 2025). The iHorTers1 sample was weighed and triaged to determine the appropriate extraction protocol. Tissue from the whole organism was homogenised by powermashing using a PowerMasher II tissue disruptor.

HMW DNA was extracted in the WSI Scientific Operations core using the Automated MagAttract v2 protocol. DNA was sheared into an average fragment size of 12–20 kb following the Megaruptor@3 for LI PacBio protocol. Sheared DNA was purified by automated SPRI (solid-phase reversible immobilisation). 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. For this sample, the final post-shearing DNA had a Qubit concentration of 45 ng/μL and a yield of 2 115.00 ng, with a fragment size of 15.2 kb. The 260/280 spectrophotometric ratio was 1.94, and the 260/230 ratio was 1.77.

PacBio HiFi library preparation and sequencing

Library preparation and sequencing were performed at the WSI Scientific Operations core. Libraries were prepared using the SMRTbell Prep Kit 3.0 (Pacific Biosciences, California, USA), following the manufacturer's instructions. The kit includes reagents for end repair/A-tailing, adapter ligation, post-ligation SMRTbell bead clean-up, and nuclease treatment. Size selection and clean-up were performed using diluted AMPure PB beads (Pacific Biosciences). DNA concentration was quantified using a Qubit Fluorometer v4.0 (ThermoFisher Scientific) and the Qubit 1X dsDNA HS assay kit. Final library fragment size was assessed with the Agilent Femto Pulse Automated Pulsed Field CE Instrument (Agilent Technologies) using the gDNA 55 kb BAC analysis kit.

The sample was sequenced on a Revio instrument (Pacific Biosciences). The prepared library was normalised to 2 nM, and 15 µL was used for making complexes. Primers were annealed and polymerases bound to generate circularised complexes, following the manufacturer's instructions. Complexes were purified using 1.2X SMRTbell beads, then diluted to the Revio loading concentration (200–300 pM) and spiked with a Revio sequencing internal control. The sample was sequenced on a Revio 25M SMRT cell. The SMRT Link software (Pacific Biosciences), a web-based workflow manager, was used to configure and monitor the run and to carry out primary and secondary data analysis.

Hi-C

Sample preparation and crosslinking

The Hi-C sample was prepared from 20–50 mg of frozen tissue from the ilHorTers1 sample using the Arima-HiC v2 kit (Arima Genomics). Following the manufacturer's instructions, tissue was fixed and DNA crosslinked using TC buffer to a final formaldehyde concentration of 2%. The tissue was homogenised using the Diagenode Power Masher-II. Crosslinked DNA was digested with a restriction enzyme master mix, biotinylated, and ligated. Clean-up was performed with SPRISelect beads before library preparation. DNA concentration was measured with the Qubit Fluorometer (Thermo Fisher Scientific) and Qubit HS Assay Kit. The biotinylation percentage was estimated using the Arima-HiC v2 QC beads.

Hi-C library preparation and sequencing

Biotinylated DNA constructs were fragmented using a Covaris E220 sonicator and size selected to 400–600 bp using SPRISelect beads. DNA was enriched with Arima-HiC v2 kit Enrichment beads. End repair, A-tailing, and adapter ligation were carried out with the NEBNext Ultra II DNA Library Prep Kit (New England Biolabs), following a modified protocol where library preparation occurs while DNA remains bound to the Enrichment beads. Library amplification was performed using KAPA HiFi HotStart mix and a custom Unique Dual Index (UDI) barcode set (Integrated DNA Technologies). Depending on sample concentration and biotinylation percentage determined at the crosslinking stage, libraries were amplified with 10–16 PCR cycles. Post-PCR clean-up was performed with SPRISelect beads. Libraries were quantified using the AccuClear Ultra High Sensitivity dsDNA Standards Assay Kit (Biotium) and a FLUOstar Omega plate reader (BMG Labtech).

Prior to sequencing, libraries were normalised to 10 ng/µL. Normalised libraries were quantified again and equimolar and/or weighted 2.8 nM pools. Pool concentrations were checked using the Agilent 4200 TapeStation (Agilent) with High Sensitivity D500 reagents before sequencing. Sequencing was performed using paired-end 150 bp reads on the Illumina NovaSeq X.

Genome 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 assembled using Hifiasm in Hi-C phasing mode (Cheng *et al.*, 2021; Cheng *et al.*, 2022), producing two haplotypes. Hi-C reads (Rao *et al.*, 2014) were mapped to the primary contigs using bwa-mem2 (Vasimuddin *et al.*, 2019). Contigs were further scaffolded with Hi-C data 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 (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. **TreeVal** was used to generate the flat files and maps for use in curation. Manual curation was conducted primarily in **PretextView** and **HiGlass** (Kerpedjiev *et al.*, 2018). Scaffolds were visually inspected and corrected as described by Howe *et al.* (2021). Manual corrections included 10 breaks and 28 joins. The curation process is documented at <https://gitlab.com/wtsi-grit/rapid-curation>. PretextViewSnapshot was used to generate a Hi-C contact map of the final assembly.

Assembly quality assessment

The Merquery.FK tool (Rhie *et al.*, 2020) was run in a Singularity container (Kurtzer *et al.*, 2017) to evaluate k -mer completeness and assembly quality for both 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 implementation of the earlier Snakemake version (Challis *et al.*, 2020). The pipeline aligns PacBio reads using minimap2 (Li, 2018) and SAMtools (Danecek *et al.*, 2021) to generate coverage tracks. It runs BUSCO (Manni *et al.*, 2021) using lineages identified from the NCBI Taxonomy (Schoch *et al.*, 2020). For the three domain-level 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 containerisation through Docker (Merkel, 2014) and Singularity (Kurtzer *et al.*, 2017).

Genome sequence report

Sequence data

PacBio sequencing of the *Horisme tersata* specimen generated 39.67 Gb (gigabases) from 3.55 million reads, which were used to assemble the genome. GenomeScope2.0 analysis estimated the haploid genome size at 551.84 Mb, with a heterozygosity of 0.90% and repeat content of 33.27% (Figure 2). These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 70x coverage. Hi-C sequencing produced 96.11 Gb from 636.48 million reads, which were used to scaffold the assembly. Table 1 summarises the specimen and sequencing details.

Assembly statistics

The genome was assembled into two haplotypes using Hi-C phasing. Haplotype 1 was curated to chromosome level, while haplotype 2 was assembled to scaffold level. The final assembly has a total length of 558.12 Mb in 60 scaffolds, with 183 gaps, and a scaffold N50 of 28.02 Mb (Table 2).

Most of the assembly sequence (99.71%) was assigned to 21 chromosomal-level scaffolds, representing 20 autosomes and the Z sex chromosome. These chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 3; Table 3). Z chromosome identified based BUSCO gene painting with ancestral Merian elements (Wright *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.

For haplotype 1, the estimated QV is 62.6, and for haplotype 2, 62.4. When the two haplotypes are combined, the assembly achieves an estimated QV of 62.5. The *k*-mer completeness is 80.73% for haplotype 1, 80.70% for haplotype 2, and 99.65% for the combined haplotypes (Figure 4).

BUSCO analysis using the lepidoptera_odb10 reference set ($n = 5286$) identified 98.4% of the expected gene set (single = 98.0%, duplicated = 0.4%) for haplotype 1. The snail plot in Figure 5 summarises the scaffold length distribution and other assembly statistics for haplotype 1. The blob plot in Figure 6 shows the distribution of scaffolds by GC proportion and coverage for haplotype 1.

Table 4 lists the assembly metric benchmarks adapted from Rhie *et al.* (2021) the Earth BioGenome Project Report on Assembly Standards September 2024. The EBP metric, calculated for the haplotype 1, is **6.C.Q62**, meeting the recommended reference standard.

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

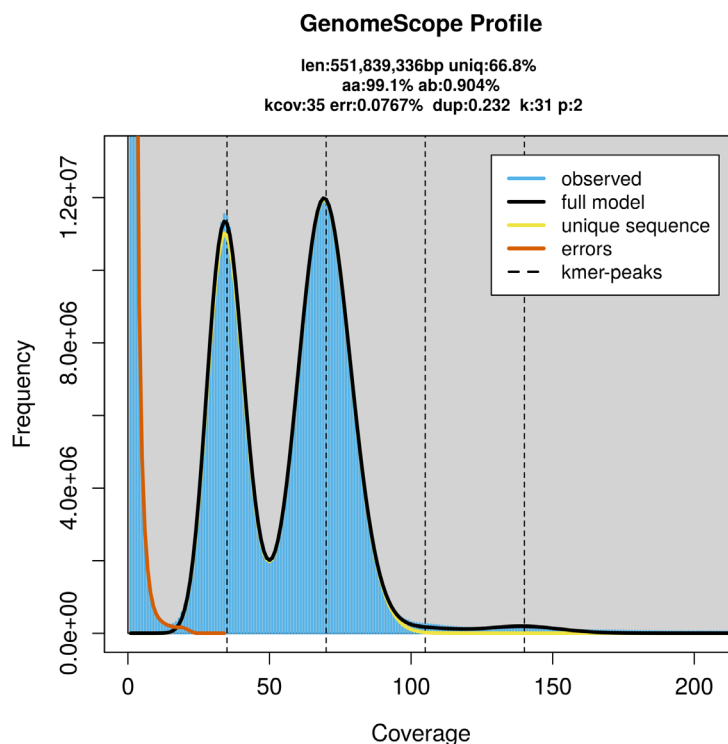


Figure 2. Frequency distribution of *k*-mers generated using GenomeScope2. The plot shows observed and modelled *k*-mer spectra, providing estimates of genome size, heterozygosity, and repeat content based on unassembled sequencing reads.

Table 1. Specimen and sequencing data for BioProject PRJEB82379.

Platform	PacBio HiFi	Hi-C
ToLID	ilHorTers1	ilHorTers1
Specimen ID	Ox003715	Ox003715
BioSample (source individual)	SAMEA114644767	SAMEA114644767
BioSample (tissue)	SAMEA114645396	SAMEA114645396
Tissue	whole organism	whole organism
Instrument	Revio	Illumina NovaSeq X
Run accessions	ERR13957076	ERR13947550
Read count total	3.55 million	636.48 million
Base count total	39.67 Gb	96.11 Gb

Table 2. Genome assembly statistics.

Assembly name	ilHorTers1.hap1.1	ilHorTers1.hap2.1
Assembly accession	GCA_964341575.1	GCA_964341595.1
Assembly level	chromosome	scaffold
Span (Mb)	558.12	558.96
Number of chromosomes	21	N/A
Number of contigs	243	294
Contig N50	4.57 Mb	4.4 Mb
Number of scaffolds	60	123
Scaffold N50	28.02 Mb	28.07 Mb
Longest scaffold length (Mb)	52.22	N/A
Sex chromosomes	Z	N/A
Organelles	Mitochondrion: 16.42 kb	N/A

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](#). 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 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.

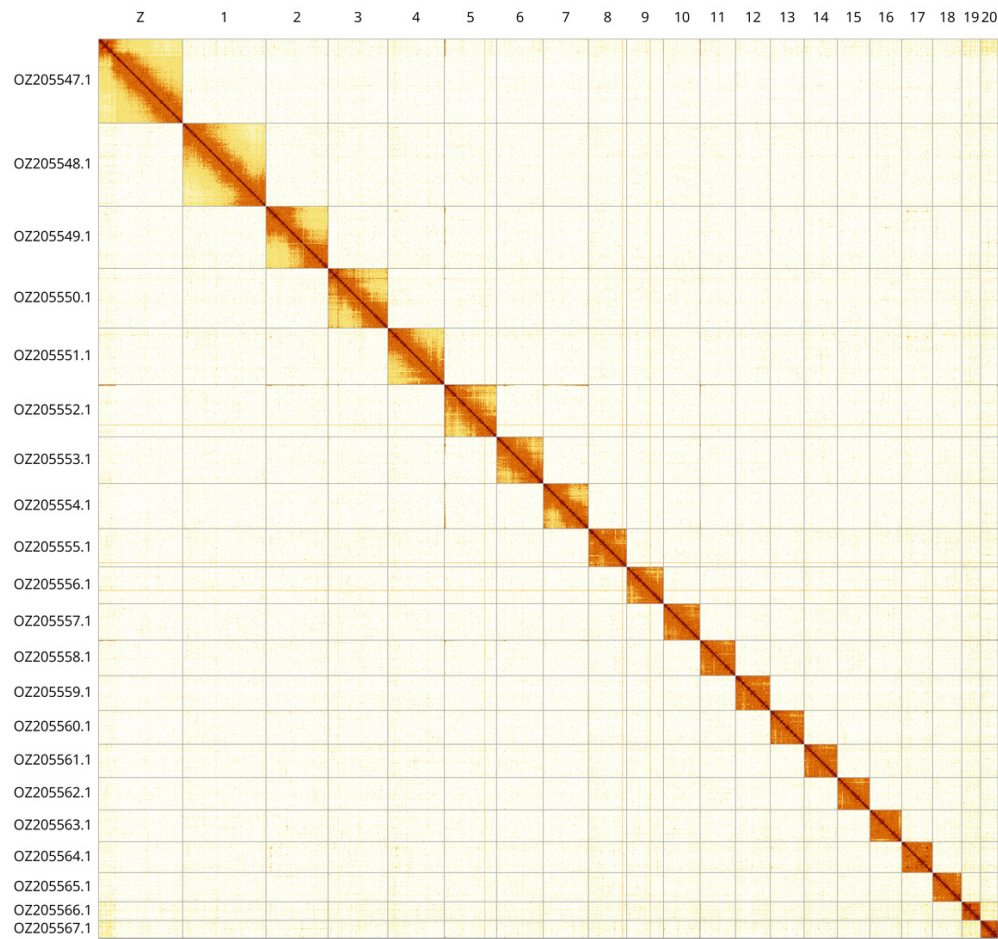


Figure 3. Hi-C contact map of the *Horisme tersata* genome assembly. Assembled chromosomes are shown in order of size and labelled along the axes. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *Horisme tersata* iHorTers1.

INSDC accession	Molecule	Length (Mb)	GC%
OZ205548.1	1	51.46	38
OZ205549.1	2	38.42	38
OZ205550.1	3	37.04	38
OZ205551.1	4	34.91	38
OZ205552.1	5	32.31	38
OZ205553.1	6	28.85	38
OZ205554.1	7	28.02	38
OZ205555.1	8	23.59	38
OZ205556.1	9	22.83	38

INSDC accession	Molecule	Length (Mb)	GC%
OZ205557.1	10	22.56	38
OZ205558.1	11	21.92	37.50
OZ205559.1	12	21.40	37.50
OZ205560.1	13	21.07	38
OZ205561.1	14	20.50	38
OZ205562.1	15	20.05	38
OZ205563.1	16	19.80	38
OZ205564.1	17	19.03	38.50
OZ205565.1	18	18.04	38.50
OZ205566.1	19	11.53	38.50
OZ205567.1	20	10.96	40
OZ205547.1	Z	52.22	38

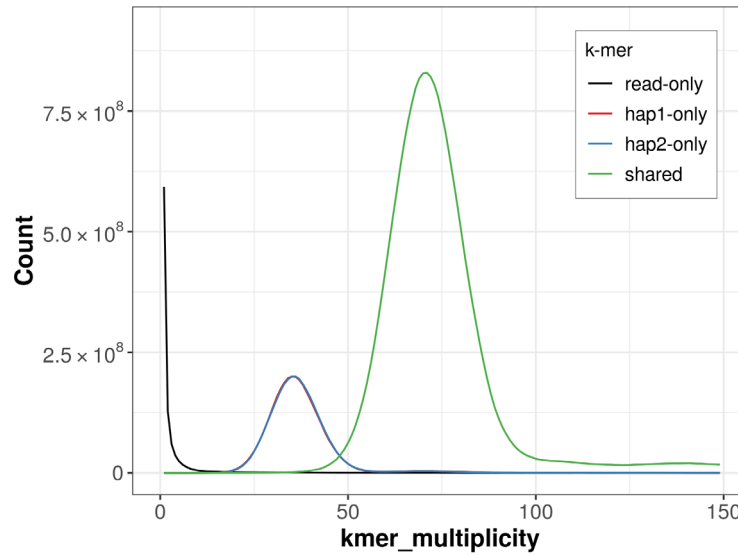


Figure 4. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the final assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers that appear in the reads but are not assembled. The green curve corresponds to *k*-mers shared by both haplotypes, and the red and blue curves show *k*-mers found only in one of the haplotypes.

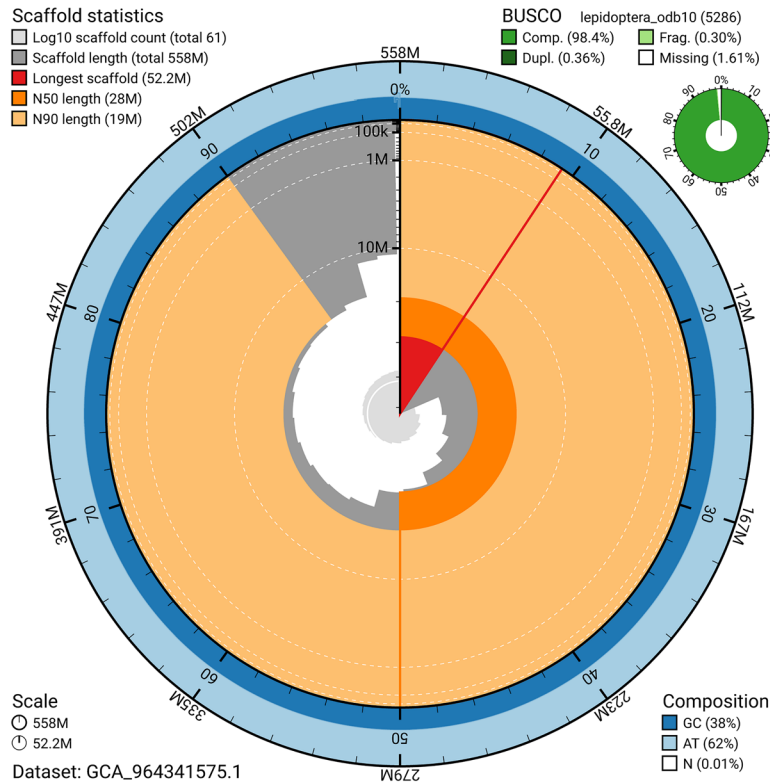


Figure 5. Assembly metrics for ilHorTers1.hap1.1. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1 000 bins around the circumference. The outermost 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 set is presented at the top right. An interactive version of this figure can be accessed on the [BlobToolKit viewer](#).

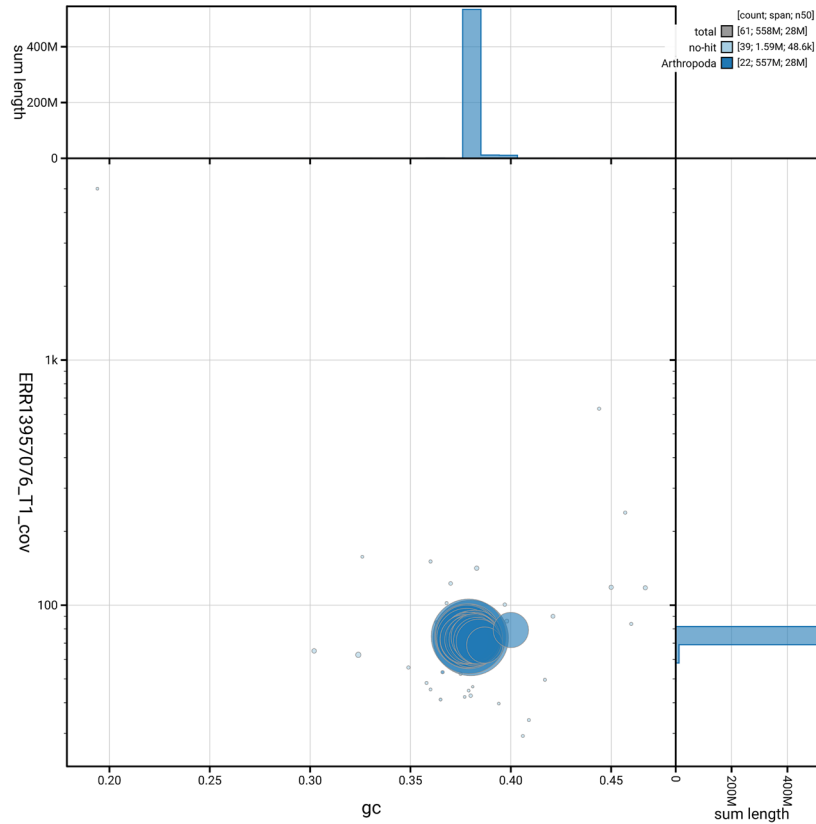


Figure 6. BlobToolKit GC-coverage plot for ilHorTers1.hap1.1. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes display the total length of sequences distributed across different levels of coverage and GC content. An interactive version of this figure is available on the [BlobToolKit viewer](#).

Table 4. Earth Biogenome Project summary metrics for the *Horisme tersata* assembly.

Measure	Value	Benchmark
EBP summary (haplotype 1)	6.C.Q62	6.C.Q40
Contig N50 length	4.57 Mb	≥ 1 Mb
Scaffold N50 length	28.02 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 62.6; haplotype 2: 62.4; combined: 62.5	≥ 40
<i>k</i> -mer completeness	Haplotype 1: 80.73%; Haplotype 2: 80.70%; combined: 99.65%	≥ 95%
BUSCO	C:98.4% [S:98.0%; D:0.4%]; F:0.3%; M:1.3%; n:5 286	S > 90%; D < 5%
Percentage of assembly assigned to chromosomes	99.71%	≥ 90%

Data availability

European Nucleotide Archive: *Horisme tersata* (the fern). Accession number [PRJEB82379](#). The genome sequence is released openly for reuse. The *Horisme tersata* 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](#).

Production code used in genome assembly at the WSI Tree of Life is available at <https://github.com/sanger-tol>. [Table 5](#) lists software versions used in this study.

Author information

Contributors are listed at the following links:

- Members of the [University of Oxford and Wytham Woods Genome Acquisition Lab](#)

- Members of the [Darwin Tree of Life Barcoding collective](#)
- Members of the [Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory team](#)
- Members of [Wellcome Sanger Institute Scientific Operations – Sequencing Operations](#)
- Members of the [Wellcome Sanger Institute Tree of Life Core Informatics team](#)
- Members of the [Tree of Life Core Informatics collective](#)
- Members of the [Darwin Tree of Life Consortium](#)

Table 5. Software versions and sources.

Software	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	1.1	https://github.com/thegenemyers/FASTK
GenomeScope2.0	2.0.1	https://github.com/tbenavi1/genomescope2.0
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	1.13.4	https://github.com/higlass/higlass
MerquryFK	1.1.2	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
PretextSnapshot	N/A	https://github.com/sanger-tol/PretextSnapshot
PretextView	0.2.5	https://github.com/sanger-tol/PretextView
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

Software	Version	Source
sanger-tol/curationpretext	1.4.2	https://github.com/sanger-tol/curationpretext
Seqtk	1.3	https://github.com/lh3/seqtk
Singularity	3.9.0	https://github.com/sylabs/singularity
TreeVal	1.4.0	https://github.com/sanger-tol/treeval
YaHS	1.2a.2	https://github.com/c-zhou/yahs

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Open Peer Review

Current Peer Review Status:  

Version 1

Reviewer Report 11 December 2025

<https://doi.org/10.21956/wellcomeopenres.27515.r140355>

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Niclas Backström 

Uppsala University, Uppsala, Sweden

The report presents a high quality genome assembly of a male fern moth (*Horisme tersata*) and the procedures for data generation, assembly, quality assessment and report writing follow the standards of DTOL. There are no major concerns regarding the methods or the assembly per se, I only have a couple of minor questions / suggestions (see below).

Is this species only found in Britain - if not, maybe its worth mentioning briefly what the entire distribution range is?

Second paragraph under Hi-C library preparation and sequencing. The second sentence (starting with "Normalised libraries were....") seems to be missing some information?

Is the chromosome number expected based on karyotype information? 21 chromosomes is a small number compared to e.g. the ancestral lepidopteran karyotype, but maybe this is expected. A brief comment on this would be informative.

What was the rationale behind selecting a male individual for sequencing? To get similar coverage between the Z and the autosomes?

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

Partly

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: Evolutionary genetics

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 October 2025

<https://doi.org/10.21956/wellcomeopenres.27515.r135921>

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Marko Mutanen 

University of Oulu, Oulu, Northern Ostrobothnia, Finland

This report introduces a genome sequence for a Geometrid moth *Horisme tersata*. The genome is read from a male specimen, and while this is fine, a female specimen should be preferred to with species like this where obtaining a female is rather straightforward.

The species introduction is a bit brief and nation (UK) focussed. It shortly introduces the species' appearance and makes a short account of the species' habitats and food plant. The food plant information is not accurate in the wider perspective as the species is common in some areas where all *Clematis* spp. are absent. It has actually been documented to feed e.g. on *Anemone nemorosa*. Like usually (but in my opinion not desirably), the species' systematics or phylogenetics affinities are not touched, although its close relatedness to *H. radicaria* is discussed.

The genome is clearly of good quality, as indicated e.g. by the high recovery rate of USCO loci. I have no reservations on that part.

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

Partly

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: Lepidoptera systematics and taxonomy, DNA barcoding, species delimitation, species identification, dark taxa, phylogenetics

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.
