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DATA NOTE

The genome sequence of the Golden Plusia, *Polychrysia moneta* (Fabricius, 1787) (Lepidoptera: Noctuidae)

[version 1; peer review: 2 approved]

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Abstract

We present a genome assembly from a male specimen of *Polychrysia moneta* (Golden Plusia; Arthropoda; Insecta; Lepidoptera; Noctuidae). The assembly contains two haplotypes with total lengths of 430.64 megabases and 425.60 megabases. Most of haplotype 1 (98.46%) is scaffolded into 31 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 15.26 kilobases. This work is part of Project Psyche, a collaborative programme generating genomes for European butterflies and moths.

Keywords

Polychrysia moneta; Golden Plusia; genome sequence; chromosomal; Lepidoptera

This article is included in the Tree of Life gateway.

Open Peer Review

Approval Status ✓ ✓

	1	2
version 1 23 Jan 2026	✓ view	✓ view

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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; Obtectomera; Noctuoidea; Noctuidae; Plusiinae; *Polychrysia*; *Polychrysia moneta* (Fabricius, 1787) (NCBI:txid1870248)

Background

Polychrysia moneta (Golden Plusia) is a noctuid moth associated with montane and riparian habitats across southern and central Europe, extending eastwards into Asia (*Polychrysia moneta (fabricius, 1787) on GBIF*, 2025; Wagner, 2025). Reported habitats include riparian forests, ravine woodlands and alpine forb communities (to >2 000 m), as well as gardens close to woodland where the larval host grows (Wagner, 2025).

Adults are distinctive: forewings are broad golden-yellow with fine patterning and a large kidney-shaped mark edged in silvery white, and the thorax has prominent fan-like scale tufts. The gold can vary from paler, greyer individuals to darker, browner ones (Waring & Townsend, 2017).

Larvae feed on *Aconitum* spp., including *A. vulparia* and *A. variegatum* or *A. napellus*. The species overwinters as an early instar; larvae are typically found from late April or May to late June or July in the Alps (Wagner, 2025). Adults fly mainly in July to August, with occasional records in late June or September. Local declines have been linked to dark, even-aged conifer or dense beech/maple plantations in riverine and ravine forests, which reduce suitable host-plant stands (Wagner, 2025).

We report a chromosome-level genome sequence for *P. moneta*, sequenced as part of Project Psyche. The sequence data were derived from a male specimen (Figure 1) collected from Unterschächen, Switzerland.

Figure 1. Voucher photograph of the *Polychrysia moneta* (ilPolMone1) specimen used for genome sequencing.

Methods

Sample acquisition

The specimen used for genome sequencing was an adult male *Polychrysia moneta* (specimen ID SAN28000110, ToLID ilPolMone1; Figure 1), collected from Unterschächen, Switzerland (latitude 46.8641, longitude 8.7826; elevation 1 053 m) on 2023-08-11. The specimen was collected and identified by Ashwini Mohan (University of Neuchâtel).

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 ilPolMone1 sample was weighed and triaged to determine the appropriate extraction protocol. Tissue from the thorax 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 62.44 ng/μL and a yield of 2 934.68 ng, with a fragment size of 13.2 kb. The 260/280 spectrophotometric ratio was 1.9, and the 260/230 ratio was 2.69.

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), according to 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.

Specimen details, sequencing platforms, and data yields are summarised in Table 1.

Hi-C

Sample preparation and crosslinking

The Hi-C sample was prepared from 20–50 mg of frozen tissue from the head of the ilPolMone1 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 Diagnocine 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 to create 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.

Specimen details, sequencing platforms, and data yields are summarised in Table 1.

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 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. TreeVal was used to generate the flat files and maps for use in curation.

Table 1. Specimen and sequencing data for BioProject PRJEB80108.

Platform	PacBio HiFi	Hi-C
ToLID	ilPolMone1	ilPolMone1
Specimen ID	SAN28000110	SAN28000110
BioSample (source individual)	SAMEA115109944	SAMEA115109944
BioSample (tissue)	SAMEA115109985	SAMEA115109983
Tissue	thorax	head
Instrument	Revio	Illumina NovaSeq X
Run accessions	ERR13698292	ERR13670056
Read count total	4.24 million	812.82 million
Base count total	39.42 Gb	122.74 Gb

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 four breaks and 61 joins. This reduced the scaffold count by 9.5% and increased scaffold N50 by 0.9%. The curation process is described at https://gitlab.com/wtsi-grit/rapid-curation. PretextSnapshot was used to generate a Hi-C contact map of the final assembly.

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 both haplotypes using the *k*-mer database (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 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).

We used lep_busco_painter to paint Merian elements along chromosomes (Wright *et al.*, 2024). Merian elements represent the 32 ancestral linkage groups in Lepidoptera. The painting process utilised BUSCO gene locations from the lepidoptera_odb10 set (Kriventseva *et al.*, 2019) and chromosome lengths from NCBI Datasets. Each complete BUSCO gene (both single-copy and duplicated) was assigned to a Merian element based on a reference database, then plotted along chromosomes drawn to scale.

Genome sequence report

Sequence data

PacBio sequencing of the *Polychrysia moneta* specimen generated 39.42 Gb (gigabases) from 4.24 million reads, which were used to assemble the genome. GenomeScope2.0 analysis estimated the haploid genome size at 428.92 Mb, with a heterozygosity of 1.89% and repeat content of 22.82% (Figure 2). These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 89× coverage. Hi-C sequencing produced 122.74 Gb from 812.82 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 430.64 Mb in 285 scaffolds, with 108 gaps, and a scaffold N50 of 14.44 Mb (Table 2).

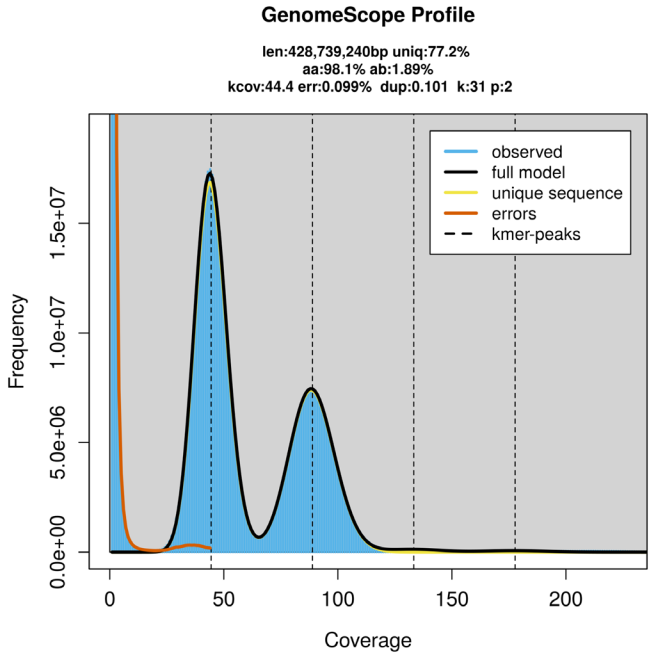

Figure 2. Frequency distribution of *k*-mers generated using GenomeScope2. The plot shows observed and modelled *k*-mer spectra, providing estimates of genome size, heterozygosity, and repeat content based on unassembled sequencing reads.

Most of the assembly sequence (98.46%) was assigned to 31 chromosomal-level scaffolds, representing 30 autosomes and the Z sex chromosome. These chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 3; Table 3). Chromosome painting with Merian elements illustrates the distribution of orthologues along chromosomes

Table 2. Genome assembly statistics.

Assembly name	ilPolMone1.hap1.1	ilPolMone1.hap2.1
Assembly accession	GCA_964276815.1	GCA_964276775.1
Assembly level	chromosome	scaffold
Span (Mb)	430.64	425.60
Number of chromosomes	31	scaffold-level
Number of contigs	393	197
Contig N50	6.07 Mb	6.21 Mb
Number of scaffolds	285	89
Scaffold N50	14.44 Mb	14.34 Mb
Longest scaffold length (Mb)	26.67	-
Sex chromosomes	Z	-
Organelles	Mitochondrion: 15.26 kb	-

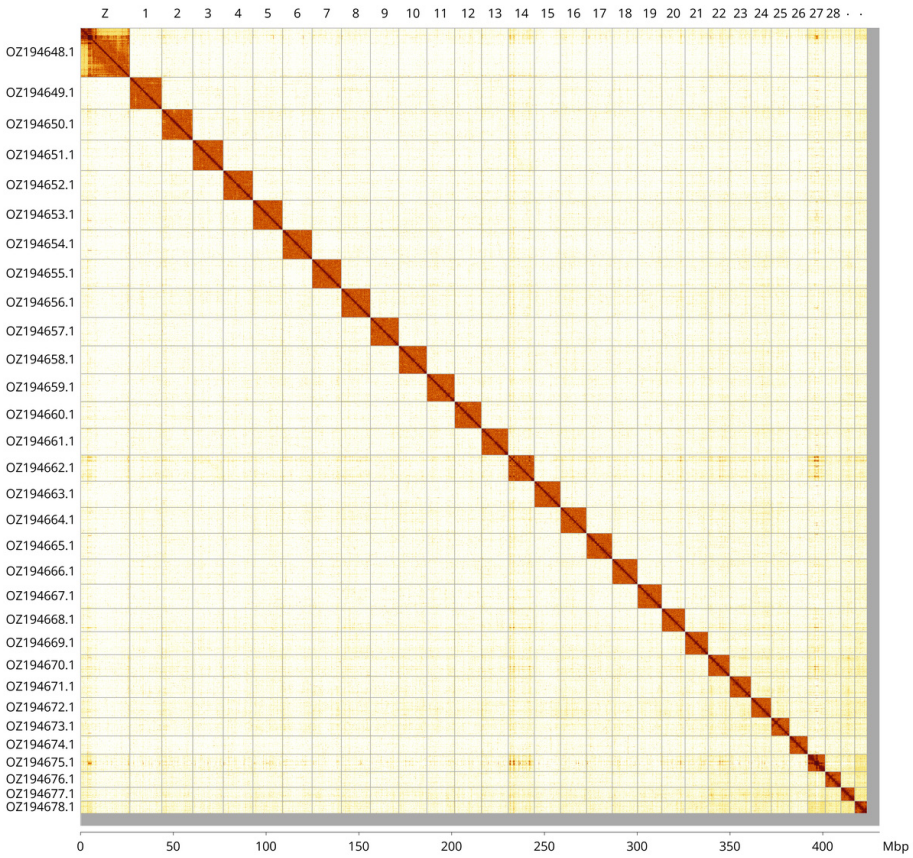

Figure 3. Hi-C contact map of the *Polychrysia moneta* genome assembly. Assembled chromosomes are shown in order of size and labelled along the axes, with a megabase scale shown below. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *Polychrysia moneta* ilPolMone1.

INSDC accession	Molecule	Length (Mb)	GC%	Assigned Merian elements
OZ194649.1	1	17.23	35	M2
OZ194650.1	2	16.69	35.50	M17;M20
OZ194651.1	3	16.41	35	M1
OZ194652.1	4	16.02	35	M3
OZ194653.1	5	15.95	34.50	M5
OZ194654.1	6	15.90	34.50	M9
OZ194655.1	7	15.78	34.50	M8
OZ194656.1	8	15.63	34.50	M7
OZ194657.1	9	15.31	34.50	M12
OZ194658.1	10	15.10	34.50	M16
OZ194659.1	11	15.04	34.50	M18
OZ194660.1	12	14.44	35	M4
OZ194661.1	13	14.40	35	M6
OZ194662.1	14	14.14	35	M23
OZ194663.1	15	14.07	34.50	M21
OZ194664.1	16	14.03	34.50	M22
OZ194665.1	17	13.84	35	M15
OZ194666.1	18	13.67	35	M10
OZ194667.1	19	13.01	35.50	M11
OZ194668.1	20	12.55	35	M13
OZ194669.1	21	12.44	35	M14
OZ194670.1	22	11.67	35	M19
OZ194671.1	23	11.43	34.50	M24
OZ194672.1	24	10.84	34.50	M26
OZ194673.1	25	9.88	35	M27
OZ194674.1	26	9.83	34.50	M28
OZ194675.1	27	9.41	37.50	M30
OZ194676.1	28	8.56	36	M25
OZ194677.1	29	7.34	35.50	M29
OZ194678.1	30	6.72	36	M31
OZ194648.1	Z	26.67	36	MZ

and highlights patterns of chromosomal evolution relative to Lepidopteran ancestral linkage groups (Figure 4). The Z chromosome was identified by synteny analysis with the genome of *Acronicta aceris* (GCA_910591435.1) (Boyes *et al.*, 2021). During curation, we noted that contigs on chromosome Z (4.1- 6.0 Mbp) have uncertain order and orientation.

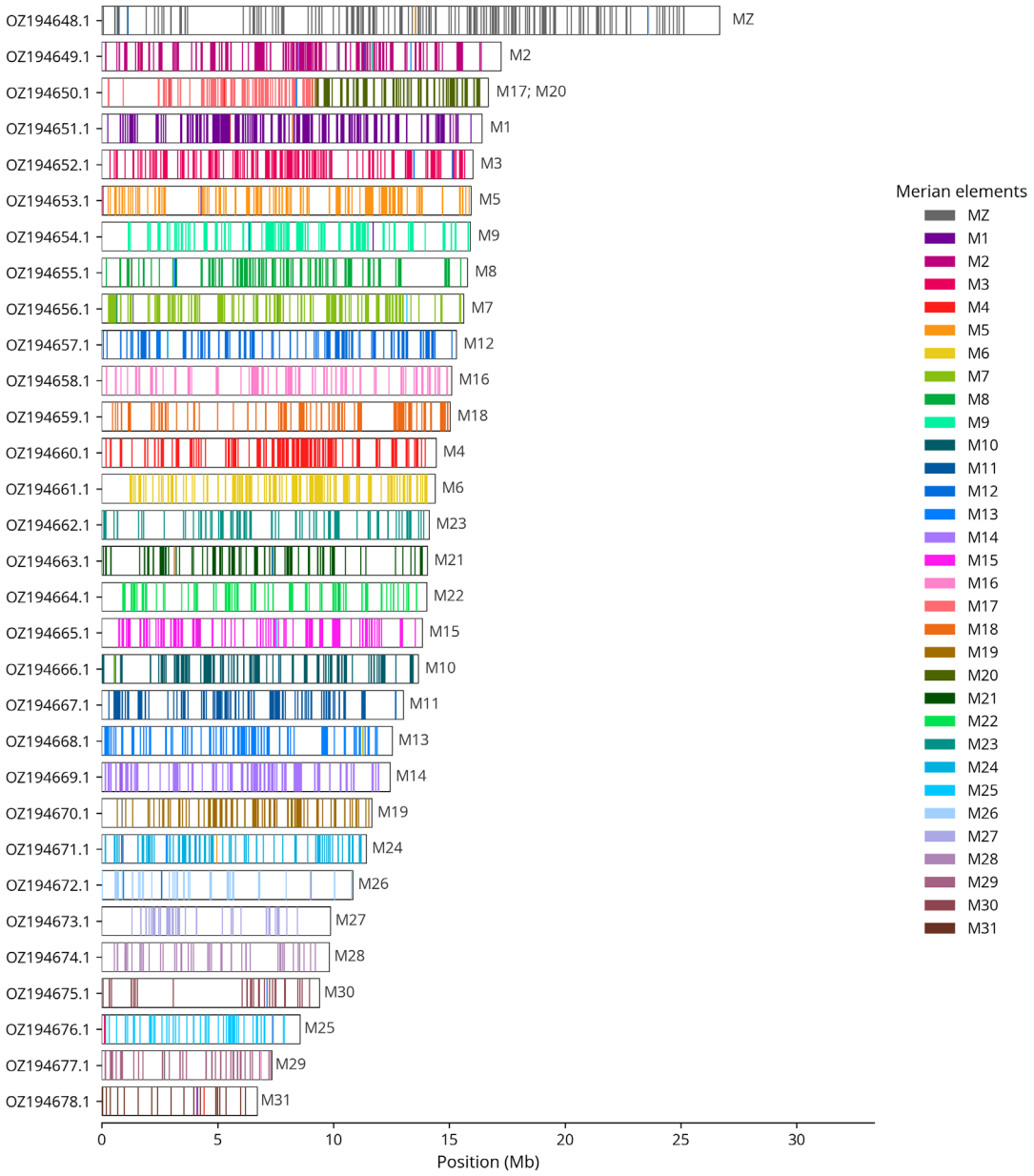

Figure 4. Merian elements painted across chromosomes in the ilPolMone1.hap1.1 assembly of *Polychrysia moneta*. Chromosomes are drawn to scale, with the positions of orthologues shown as coloured bars. Each orthologue is coloured by the Merian element that it belongs to. All orthologues which could be assigned to Merian elements are shown.

The mitochondrial genome was also assembled (length 15.26 kb, OZ194679.1). This sequence is included as a contig in the multifasta file of the genome submission and as a standalone record.

Assembly quality metrics

For haplotype 1, the estimated QV is 63.8, and for haplotype 2, 66.1. When the two haplotypes are combined, the assembly achieves an estimated QV of 64.8. The *k*-mer completeness is 69.30% for haplotype 1, 69.21% for haplotype 2, and 99.60% for the combined haplotypes (Figure 5). BUSCO analysis using the lepidoptera_odb10 reference set (n = 5 286) identified 98.9% of the expected gene set (single = 98.6%, duplicated = 0.3%) in haplotype 1. For haplotype 2, BUSCO analysis identified 99.0% of the expected gene set (single = 98.6%, duplicated = 0.4%). The snail plot in Figure 6 summarises the scaffold length distribution and other assembly statistics for haplotype 1. The blob plot in Figure 7 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) and the Earth BioGenome Project Report on Assembly Standards September 2024. The EBP metric, calculated for the haplotype 1, is **6.C.Q63**, meeting the recommended reference standard.

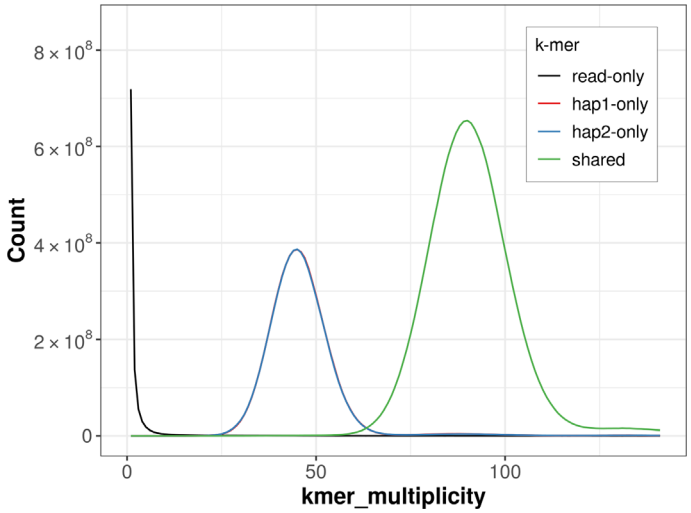

Figure 5. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the final assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers that appear in the reads but are not assembled. The green curve (the homozygous peak) corresponds to *k*-mers shared by both haplotypes and the red and blue curves (the heterozygous peaks) show *k*-mers found only in one of the haplotypes.

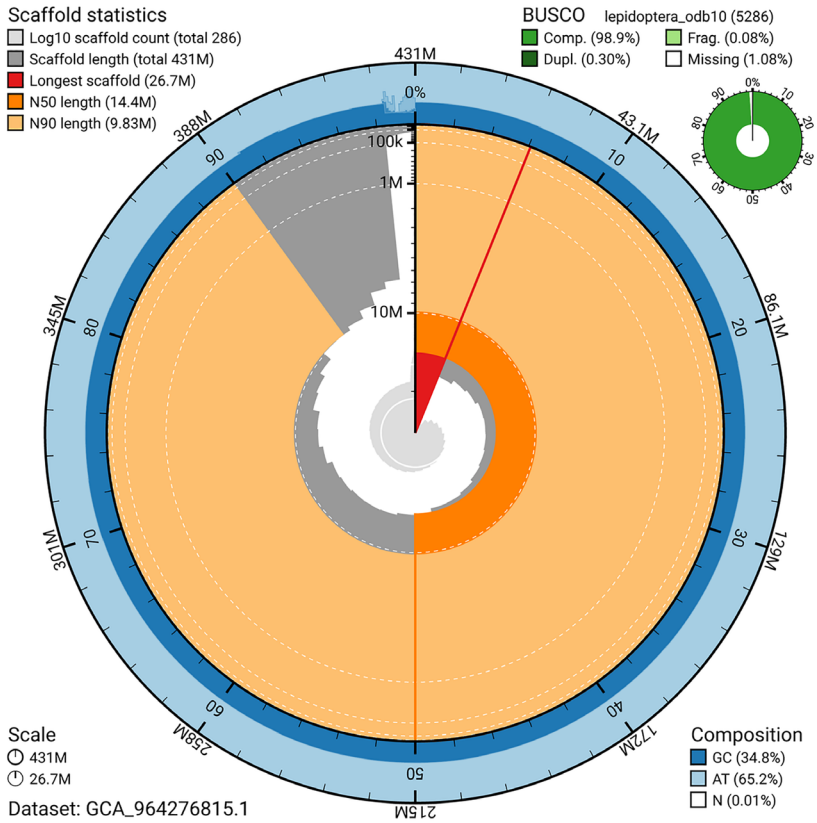

Figure 6. Assembly metrics for ilPolMone1.hap1.1. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1,000 bins around the circumference. The outermost 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.

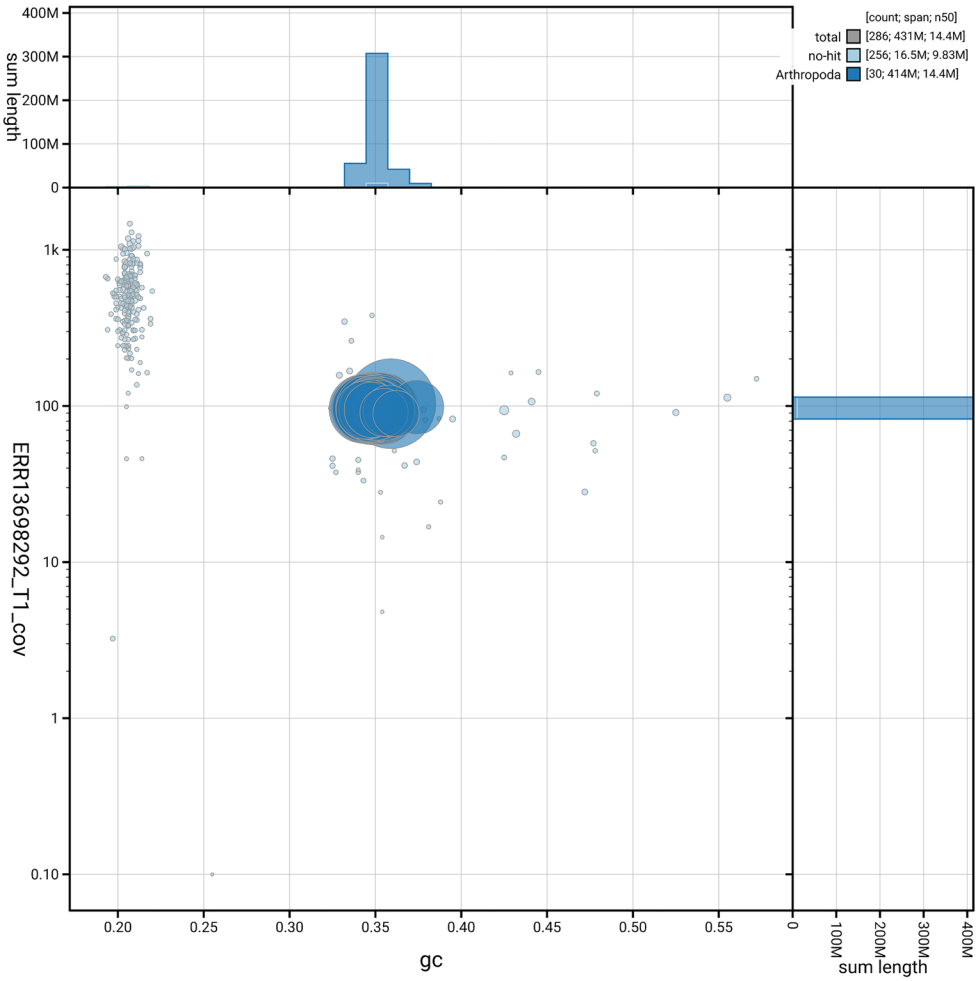

Figure 7. BlobToolKit GC-coverage plot for ilPolMone1.hap1.1. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes 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 *Polychrysia moneta* assembly.

Measure	Value	Benchmark
EBP summary (haplotype 1)	6.C.Q63	6.C.Q40
Contig N50 length	6.07 Mb	≥ 1 Mb
Scaffold N50 length	14.44 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 63.8; haplotype 2: 66.1; combined: 64.8	≥ 40
k-mer completeness	Haplotype 1: 69.30%; Haplotype 2: 69.21%; combined: 99.60%	≥ 95%
BUSCO	C:98.9% [S:98.6%; D:0.3%]; F:0.1%; M:1.0%; n:5 286	S > 90%; D < 5%
Percentage of assembly assigned to chromosomes	98.46%	≥ 90%

Notes: EBP summary uses log10(Contig N50); chromosome-level (C) or log10(Scaffold N50); Q (Merqury QV). BUSCO: C=complete; S=single-copy; D=duplicated; F=fragmented; M=missing; n=orthologues

Wellcome Sanger Institute – Legal and Governance

The materials that have contributed to this genome note have been supplied by a Tree of Life collaborator. 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 undertaken according to a Research Collaboration Agreement or Material Transfer Agreement entered into by the Tree of Life collaborator, Genome Research Limited (operating as the Wellcome Sanger Institute), and in some circumstances, other Tree of Life collaborators.

Data availability

European Nucleotide Archive: Polychrysia moneta (golden plusia). Accession number PRJEB80108. The genome sequence is released openly for reuse. The *Polychrysia moneta* genome sequencing initiative is part of 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 Ensembl at the European Bioinformatics Institute. Raw data and assembly accession identifiers are reported in Table 1 and Table 2.

Pipelines used for genome assembly at the WSI Tree of Life are available at https://pipelines.tol.sanger.ac.uk/pipelines. Table 5 lists software versions used in this study.

Author information

Contributors are listed at the following links:

- 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 Project Psyche Community

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
Hifiasm	0.19.8-r603	https://github.com/chhylp123/hifiasm
HiGlass	1.13.4	https://github.com/higlass/higlass
lep_busco_painter	1.0.0	https://github.com/charlottewright/lep_busco_painter
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

Software	Version	Source
MultiQC	1.14; 1.17 and 1.18	https://github.com/MultiQC/MultiQC
Nextflow	23.10.0	https://github.com/nextflow-io/nextflow
PretextSnapshot	0.0.5	https://github.com/sanger-tol/PretextSnapshot
PretextView	1.0.3	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
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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✔ **Sarah Inwood**
University of Otago, Dunedin, New Zealand

This data note described a chromosome-level genome for *Polychrysia moneta.* This high-quality genome was assembled from PacBio HiFi and Illumina Hi-C reads from a male specimen, and contains two haplotypes and a mitochondrial genome. This genome has not yet been annotated, but will be in future using RNA-seq data.

Minor comments:

- The Blob toolkit GC-coverage graph showed a number of short scaffolds with much lower GC content and slightly higher read depth, with their phylum membership having no hit. Did the authors explore what these shorter low-GC content scaffolds are likely to correspond to?
- Mitofinder was mentioned in text but a version was not provided in the software table. Conversely, bedtools, cooler, fasta_windows, and sanger-tol/curationpretext were all in the software table but not mentioned in text - what were these tools used for?

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, host-parasite interactions, parasitoid wasps, insects, viruses, biocontrol

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 12 March 2026

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Melody Clark
Natural Environment Research Council, Cambridge, UK

This brief Data Note describes the genome sequence of a male Golden Plusia moth. The assembly is at haplotype level with scaffolds comprising 31 chromosomal pseudochromosomes including the Z sex chrosomome and the mitochondrial genome. The biology and habitat of this species is described, with the sequencing impetus provided by Project Psyche under the auspices of the WSI Tree of Life. DNA extraction and PacBio/Hi-C sequencing were conducted using standard protocols with assembly generated using WSI Tree of Life pipelines with some manual curation. Thus the genome is of very high quality. Chromosome painting has also been performed using Merian elements identifying ancestral linkage groups. Annotation is currently pending on RNA-seq data.

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: Transcriptomics and genomics of non-model species

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.