DATA NOTE

The genome sequence of the Cardinal, *Argynnis pandora* (Denis & Schiffermüller, 1775) (Lepidoptera: Nymphalidae)

[version 1; peer review: awaiting peer review]

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Abstract

We present a genome assembly from a female specimen of *Argynnis pandora* (Cardinal; Arthropoda; Insecta; Lepidoptera; Nymphalidae). The assembly contains two haplotypes with total lengths of 451.40 megabases and 390.99 megabases. Most of haplotype 1 (98.93%) is scaffolded into 30 chromosomal pseudomolecules, including the W and Z sex chromosomes. Haplotype 2 was assembled to scaffold level. The mitochondrial genome has also been assembled, with a length of 15.15 kilobases.

Keywords

Argynnis pandora; Cardinal; genome sequence; chromosomal; Lepidoptera

This article is included in the Tree of Life gateway.

Open Peer Review

Approval Status *AWAITING PEER REVIEW*

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; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Argynnini; *Argynnis*; *Argynnis pandora* (Denis & Schiffermüller, 1775) (NCBI:txid405018)

Background

The Cardinal, *Argynnis pandora* ([Denis & Schiffermüller], 1775), is a butterfly species of the family Nymphalidae. It is distributed across the western Palaearctic, from north Africa and southern Europe to Pakistan and India. *Argynnis pandora* prefers arid environments but can also occur in humid mountain regions, inhabiting areas from sea level up to an altitude of approximately 2 000 m (García-Barros *et al.*, 2013). Adults can be encountered far from stable populations because of their strong dispersal capabilities, particularly in late summer (Hensle, 1995).

With a wingspan of 64–80 mm, *A. pandora* is the largest species of the genus *Argynnis*. Females are easily distinguished from males by lacking androconial spots and having more pronounced silver markings (García-Barros *et al.*, 2013).

The species is univoltine and adults are long-lived, with a flight period spanning from May to September (García-Barros *et al.*, 2013; Tolman & Lewington, 2009). Eggs are deposited on dead vegetation (García-Barros, 2000) and, once hatched, larvae move to the host plants (*Viola* spp.). It hibernates as a first instar larva and the development is concentrated in the following spring (García-Barros *et al.*, 2013). In the Iberian Peninsula, pupae are parasitised by *Pteromalus puparum* (Chalcidoidea: Pteromalidae) (Shaw *et al.*, 2009).

The variation of the mitochondrial genome within the species is moderate, but clear spatial structuring is absent (Dapporto *et al.*, 2022). The species is currently listed as Least Concern in the IUCN Red List of Europe (Van Swaay *et al.*, 2025). The karyotype of *A. pandora* is 29 (de Lesse, 1970). The first reference genome for *A. pandora* presented here provides a fundamental resource for exploring the species' evolutionary history and clarifying its phylogenetic relationship with the sister genera *Fabriciana* and *Speyeria* (De Moya *et al.*, 2017). This genome sequence is based on a female specimen (Figure 1) collected from Măcin, Romania.

Methods

Sample acquisition

The specimen used for genome sequencing was an adult female *Argynnis pandora* (specimen ID SAN28000265, ToLID ilArgPand1; Figure 1), collected from Măcin, Romania (latitude 45.2449, longitude 28.1897; elevation 90 m) on 2021-09-08. The specimen was collected and identified by Roger Vila (Institut de Biologia Evolutiva).

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 ilArgPand1 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 20.91 ng/μL and a yield of 982.77 ng, with a fragment size of 15.6 kb.

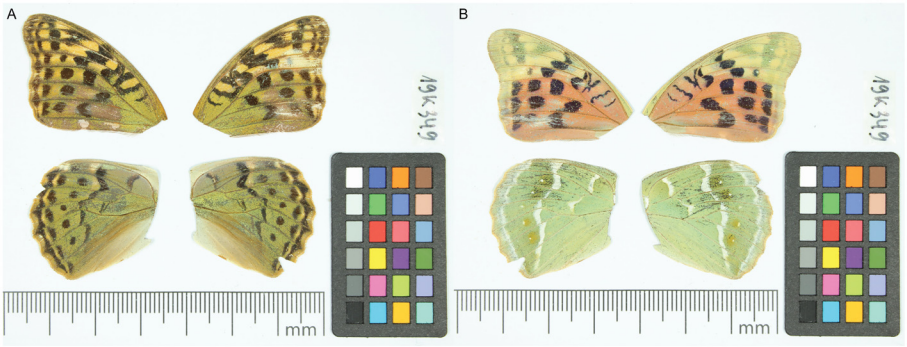

Figure 1. Voucher photographs of the *Argynnis pandora* (ilArgPand1) specimen used for genome sequencing: **A.** dorsal (upperside), **B.** ventral (underside).

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 whole organism of the ilArgPand1 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 Accu-Clear 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)

Table 1. Specimen and sequencing data for BioProject PRJEB81909.

Platform	PacBio HiFi	Hi-C
ToLID	ilArgPand1	ilArgPand1
Specimen ID	SAN28000265	SAN28000265
BioSample (source individual)	SAMEA115768764	SAMEA115768764
BioSample (tissue)	SAMEA115768844	SAMEA115768844
Tissue	whole organism	whole organism
Instrument	Revio	Illumina NovaSeq X
Run accessions	ERR13917225	ERR13925947
Read count total	1.44 million	760.17 million
Base count total	16.68 Gb	114.79 Gb

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. 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 24 breaks and 126 joins. This reduced the scaffold count by 40.1%, increased scaffold N50 by 3.3%, and increased the total assembly length by 1.1%. 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 coloured and plotted along chromosomes drawn to scale.

Genome sequence report

Sequence data

PacBio sequencing of the *Argynnis pandora* specimen generated 16.68 Gb (gigabases) from 1.44 million reads, which were used to assemble the genome. GenomeScope2.0 analysis estimated the haploid genome size at 409.48 Mb, with a heterozygosity of 1.82% and repeat content of 17.97% (Figure 2). These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 39× coverage. Hi-C sequencing produced 114.79 Gb from 760.17 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 451.40 Mb in 238 scaffolds, with 224 gaps, and a scaffold N50 of 15.07 Mb (Table 2).

Most of the assembly sequence (98.93%) was assigned to 30 chromosomal-level scaffolds, representing 28 autosomes and the W and Z sex chromosomes. 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 and highlights patterns of chromosomal evolution relative to Lepidopteran ancestral linkage groups (Figure 4). Chromosome Z and W were assigned by read coverage and presence as single copy in the diploid assembly, and Merian elements were also mapped to Chromosome Z for confirmation. During curation, we noted that scaffolds making up Chromosome W have uncertain order and orientation. The mitochondrial genome was also assembled (length 15.15 kb, OZ203742.1). 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 57.1, and for haplotype 2, 57.7. When the two haplotypes are combined, the assembly achieves an estimated QV of 57.4. The *k*-mer completeness is 72.49% for haplotype 1, 67.42% for haplotype 2, and 99.73% for the combined haplotypes (Figure 5).

BUSCO analysis using the lepidoptera_odb10 reference set (n = 5 286) identified 99.0% of the expected gene set (single = 98.2%, duplicated = 0.8%) in haplotype 1. For haplotype 2, BUSCO analysis identified 93.4% of the expected gene set (single = 92.7%, duplicated = 0.7%).

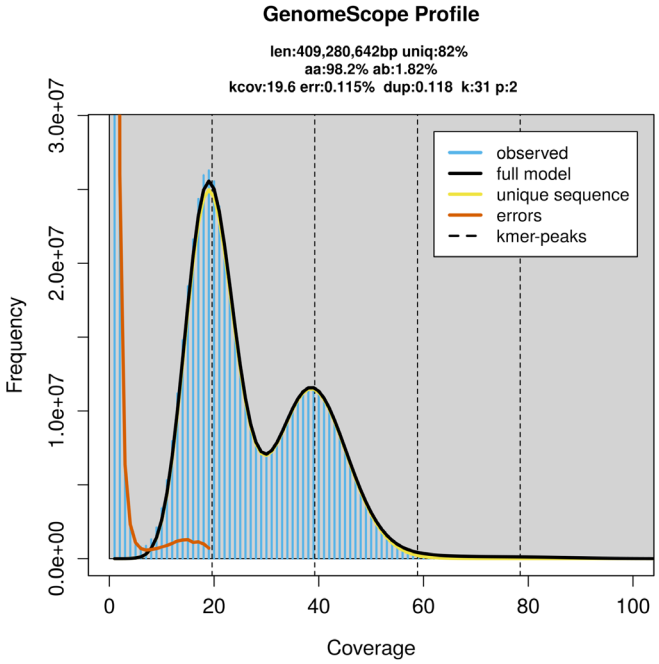

Figure 2. Frequency distribution of *k*-mers generated using GenomeScope2. The plot shows observed and modelled *k*-mer spectra, providing estimates of genome size, heterozygosity, and repeat content based on unassembled sequencing reads.

Table 2. Genome assembly statistics.

Assembly name	ilArgPand1.hap1.1	ilArgPand1.hap2.1
Assembly accession	GCA_964340695.1	GCA_964340615.1
Assembly level	chromosome	scaffold
Span (Mb)	451.40	390.99
Number of chromosomes	30	scaffold-level
Number of contigs	462	321
Contig N50	4.37 Mb	4.71 Mb
Number of scaffolds	238	219
Scaffold N50	15.07 Mb	14.75 Mb
Longest scaffold length (Mb)	36.25	-
Sex chromosomes	W and Z	-
Organelles	Mitochondrion: 15.15 kb	-

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.Q57**, 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 Tree of Life collaborator. The Wellcome

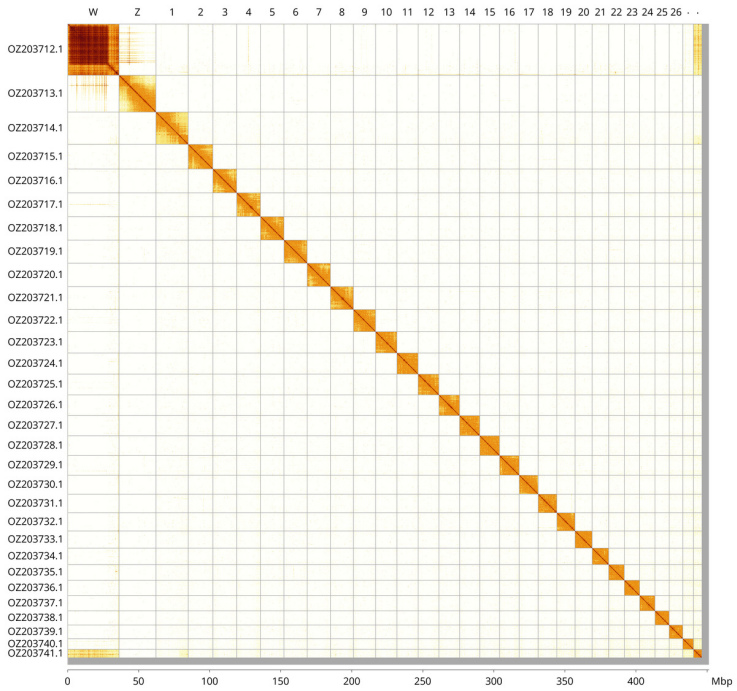

Figure 3. Hi-C contact map of the *Argynnis pandora* genome assembly. Assembled chromosomes are shown in order of size and labelled along the axes. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *Argynnis pandora* ilArgPand1.

INSDC accession	Molecule	Length (Mb)	GC%	Assigned Merian elements
OZ203714.1	1	22.78	32	M12;M30
OZ203715.1	2	17.37	31.50	M2
OZ203716.1	3	16.76	32	M1
OZ203717.1	4	16.73	32	M17;M20
OZ203718.1	5	16.47	31.50	M8
OZ203719.1	6	16.38	32	M5
OZ203720.1	7	16.33	31.50	M9
OZ203721.1	8	16.19	32	M3
OZ203722.1	9	15.62	31.50	M7
OZ203723.1	10	15.07	31.50	M16
OZ203724.1	11	14.90	31.50	M18
OZ203725.1	12	14.59	32	M6
OZ203726.1	13	14.49	31.50	M4
OZ203727.1	14	14.25	31.50	M21
OZ203728.1	15	13.90	31.50	M22
OZ203729.1	16	13.85	32	M10
OZ203730.1	17	13.42	31.50	M15

INSDC accession	Molecule	Length (Mb)	GC%	Assigned Merian elements
OZ203731.1	18	13.12	32	M11
OZ203732.1	19	12.81	32.50	M14
OZ203733.1	20	12.03	31.50	M13
OZ203734.1	21	11.60	32	M23
OZ203735.1	22	11.01	31.50	M26
OZ203736.1	23	10.83	32	M19
OZ203737.1	24	10.79	31.50	M24
OZ203738.1	25	9.97	32	M28
OZ203739.1	26	9.62	31.50	M27
OZ203740.1	27	7.48	33	M29
OZ203741.1	28	5.97	33.50	M31
OZ203712.1	W	36.25	36	-
OZ203713.1	Z	25.97	32	M25;MZ

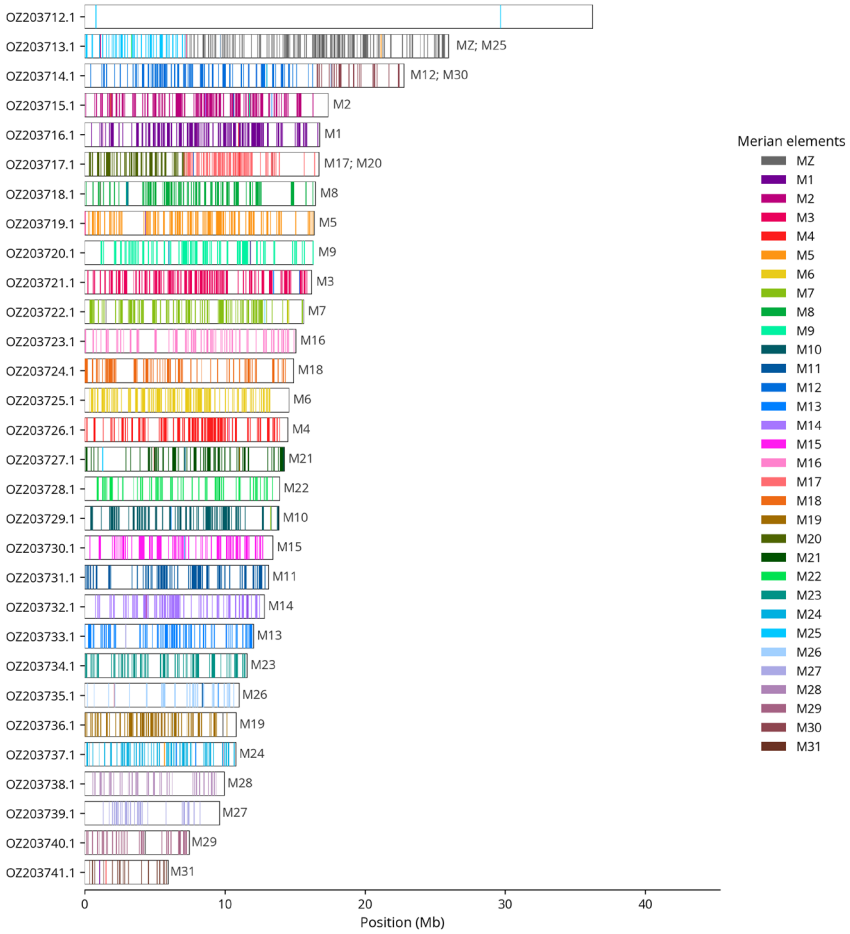

Figure 4. Merian elements painted across chromosomes in the ilArgPand1.hap1.1 assembly of *Argynnis pandora*. Chromosomes are drawn to scale, with the positions of orthologues shown as coloured bars. Each orthologue is coloured by the Merian element that it belongs to. All orthologues which could be assigned to Merian elements are shown.

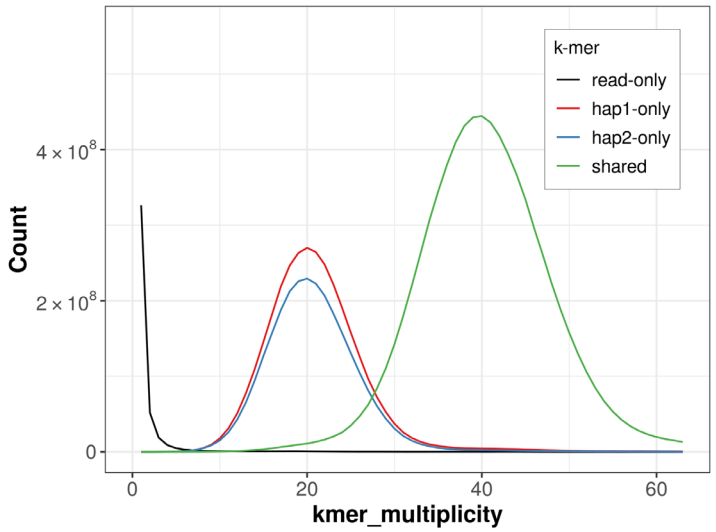

Figure 5. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the final assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers 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.

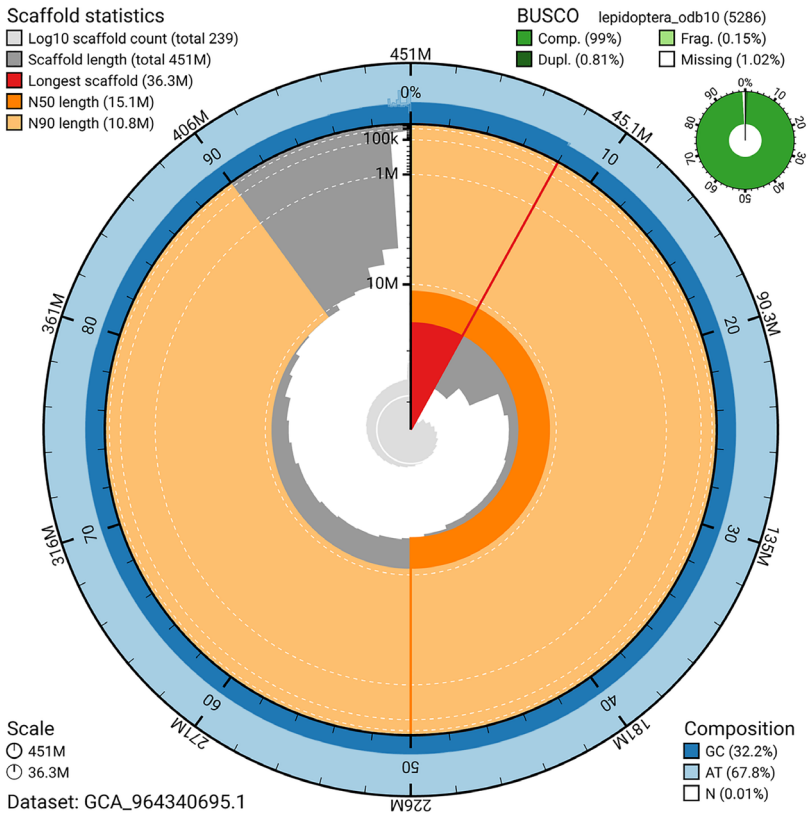

Figure 6. Assembly metrics for ilArgPand1.hap1.1. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1,000 bins around the circumference. The outermost 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.

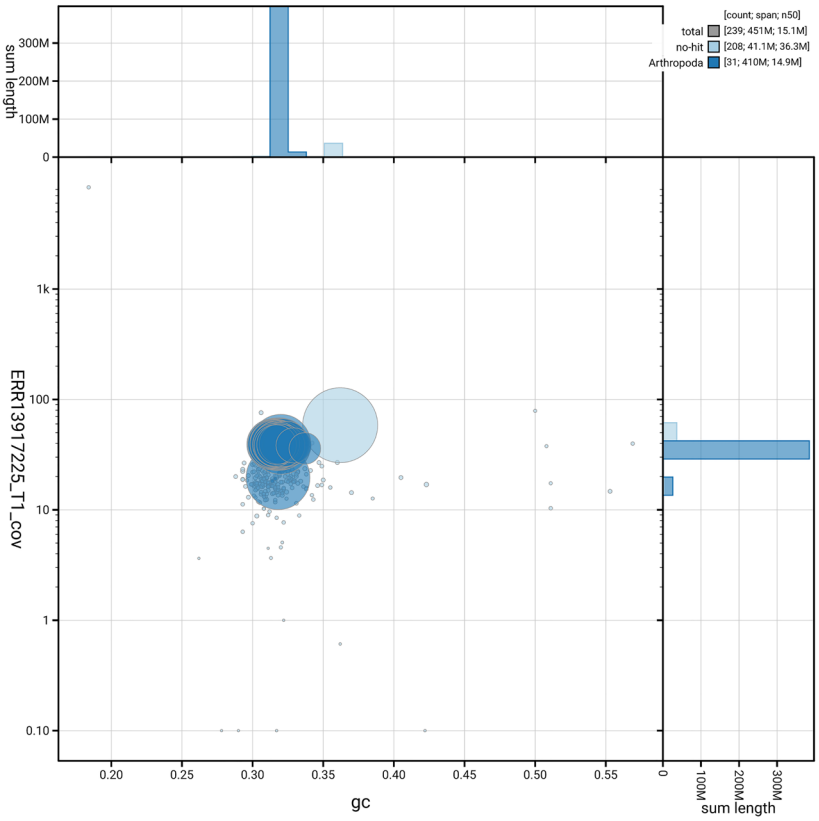

Figure 7. BlobToolKit GC-coverage plot for ilArgPand1.hap1.1. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes 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 *Argynnis pandora* assembly.

Measure	Value	Benchmark
EBP summary (haplotype 1)	6.C.Q57	6.C.Q40
Contig N50 length	4.37 Mb	≥ 1 Mb
Scaffold N50 length	15.07 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 57.1; haplotype 2: 57.7; combined: 57.4	≥ 40
k-mer completeness	Haplotype 1: 72.49%; Haplotype 2: 67.42%; combined: 99.73%	≥ 95%
BUSCO	C:99.0% [S:98.2%; D:0.8%]; F:0.2%; M:0.9%; n:5 286	S > 90%; D < 5%
Percentage of assembly assigned to chromosomes	98.93%	≥ 90%

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: Argynnis pandora (cardinal fritillary). Accession number PRJEB81909. The genome sequence is released openly for reuse. The *Argynnis pandora* 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.

Table 5. Software versions and sources.

Software	Version	Source
BEDTools	2.30.0	https://github.com/arq5x/bedtools2
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
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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