DATA NOTE

The genome sequence of the Cistus Forester, *Adscita geryon* (Hübner, [1813]) (Lepidoptera: Zygaenidae)

[version 1; peer review: 4 approved]

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Abstract

We present a genome assembly from an individual female *Adscita geryon* (Cistus Forester; Arthropoda; Insecta; Lepidoptera; Zygaenidae). The assembly contains two haplotypes with total lengths of 764.63 megabases and 670.15 megabases. Most of haplotype 1 (99.63%) is scaffolded into 32 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 15.32 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

Adscita geryon; Cistus Forester; genome sequence; chromosomal; Lepidoptera

This article is included in the Tree of Life gateway.

Open Peer Review

Approval Status ✓ ✓ ✓ ✓

	1	2	3	4
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Species taxonomy

Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Apoditrysia; Zygaenoidea; Zygaenidae; Procridinae; *Adscita*; *Adscita geryon* (Hübner) (NCBI:txid287208)

Background

Adscita geryon (Hübner, [1813]), also known as the Cistus Forester, is a moth in the family Zygaenidae with a forewing length of 9–12 mm, with males relatively larger (Waring *et al.*, 2017). The wings are metallic green and the species is not easy to distinguish from other species of *Adscita*, but it is on average the smallest of the three species in the United Kingdom, and the male antenna has only seven, not ten, segments which are not tapered towards the base and strongly pectinate unlike the Scarce Forester, *Jordanita globulariae* (Hübner, 1793).

In the United Kingdom (1 787 records on NBN Trust (2025)) the Cistus Forester ranges from southern England to Cumbria and Durham in the north but does not range southwest of Dorset (Randle *et al.*, 2019), nor to Ireland. In Wales it occurs on the Great Orme (Randle *et al.*, 2019). The Cistus Forester has disappeared from the former eastern parts of its range (Randle *et al.*, 2019). In the Palaearctic, the species ranges from the north of the Iberian Peninsula through central Europe, although is absent from higher latitudes such as Scandinavia (GBIF Secretariat, 2025) (ignoring false New World records belonging to mis-ascribed Sphingidae), it occurs in Ukraine, European Russia and north-west Turkey (Efetov & Tarmann, 1999),

Adscita geryon occurs on calcareous grasslands, favouring south facing slopes (Waring *et al.*, 2017), and this diurnal moth, although quite localised, can be locally abundant (Randle *et al.*, 2019). In the United Kingdom it flies from early May to mid-July with a peak in early June (Randle *et al.*, 2019), rarely August (Waring *et al.*, 2017). The adult is fond of flowers of various trefoils and thyme (Waring *et al.*, 2017). In Europe, the larva feeds principally on Common Rock Rose *Helianthemum nummularium* (L.) Mill. and other species of *Helianthemum*, while in captivity it is known to feed on species of Geraniaceae and, for the first instar only, *Rumex* L. (Polygonaceae) (Efetov & Tarmann, 1999). The hairy larva, with darker brown longitudinal stripes, feeds from July to May, overwintering low down and pupating on a cocoon on the ground (Waring *et al.*, 2017). See Lepiforum (2025) for pictures of its early stages.

The DNA barcode from the present *A. geryon* mitogenome assembly (OZ193787.1) represents the COI-5P cluster Barcode Index Number (BIN) BOLD:ABY4365, with up to 2.25% variability (n = 75), on BOLD (29/07/2025). It is identical to a haplotype from Europe. This mitochondrial cluster also includes *Adscita albanica* (Naufock, 1926) and the nearest neighbour is *A. capitalis* (Staudinger, 1879) (BOLD:ACE3127) lwhich has a *p*-distance of 1.2% from OZ193787.1. In contrast, there are two other clusters on BOLD – both identified as *A. geryon* – BOLD:ABY8878 (Italy; about 3.06% *p*-distant) and BOLD:ABY8876 (North Macedonia, Serbia and Italy; about 3.6% *p*-distant), either of which might approximate to *A. geryon* sspp. *acutafibra* Verity, 1946 or *orientalis* Alberti, 1938. The genus *Adscita* Retzius, 1783, feeding on Cistaceae and Polygonaceae is sister to + *Jordanita* Verity, 1946, feeding on Asteraceae (Miric *et al.*, 2024).

We present a chromosomally complete genome sequence for *Adscita geryon*, the Cistus Forester. The assembly was produced using the Tree of Life pipeline from a specimen collected in Aston Rowant, England, United Kingdom (Figure 1), as part of the Darwin Tree of Life project. The genome will be useful not only for studies of species phylogeography but for phylogenetics. The branching pattern of *Adscita*, which included as exemplars *A. geryon* and an early branching species, *Adscita mauretanica* (Naufock, 1932) based on one mitochondrial and seven nuclear gene fragments, has so far proved hard to resolve considering an inferred shallow radiation in the last 15 million years (Miric *et al.*, 2024).

Methods

Sample acquisition and DNA barcoding

The specimen used for genome sequencing was an adult female *Adscita geryon* (specimen ID NHMUK013698373, ToLID ilAdsGery1; Figure 1), collected from Aston Rowant, England, United Kingdom (latitude 51.67, longitude –0.95) on 2022-06-04. The specimen was collected and identified by David Lees (Natural History Museum). Sample metadata were collected in line with the Darwin Tree of Life project standards described by 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

Figure 1. Photograph of *Adscita geryon* on Chiltern Gentian (not the specimen used for genome sequencing).

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 ilAdsGery1 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 57.82 ng/μL and a yield of 2 717.54 ng, with a fragment size of 16.4 kb. The 260/280 spectrophotometric ratio was 1.88, and the 260/230 ratio was 2.31.

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 whole organism tissue of the ilAdsGery1 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 to 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 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 19 breaks and 215 joins. 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) 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 *Adscita geryon* specimen generated 63.36 Gb (gigabases) from 5.39 million reads, which were used to assemble the genome. GenomeScope2.0 analysis estimated the haploid genome size at 711.56 Mb, with a heterozygosity of 0.82% and repeat content of 44.21% (Figure 2).

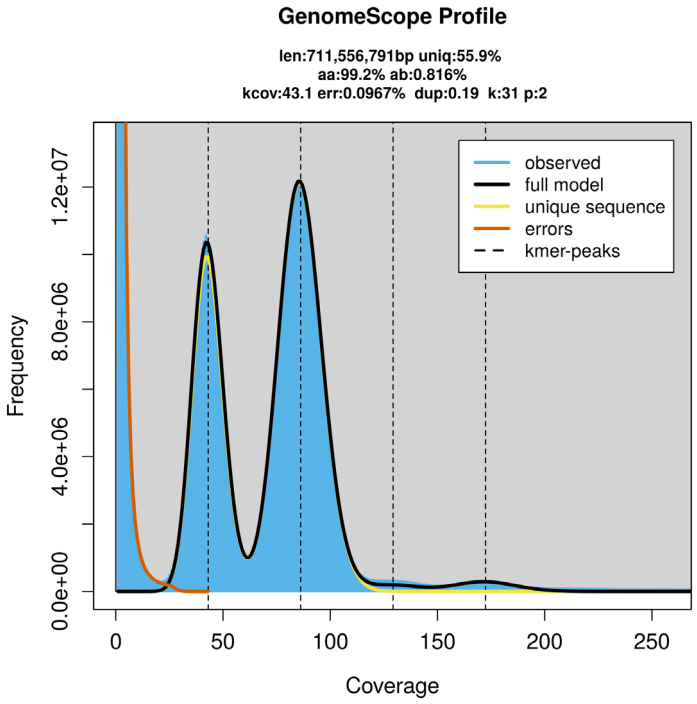

Figure 2. Frequency distribution of *k*-mers generated using GenomeScope2. The plot shows observed and modelled *k*-mer spectra, providing estimates of genome size, heterozygosity, and repeat content based on unassembled sequencing reads.

These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 86× coverage. Hi-C sequencing produced 97.99 Gb from 648.94 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 764.63 Mb in 114 scaffolds, with 273 gaps, and a scaffold N50 of 24.94 Mb (Table 2).

Most of the assembly sequence (99.63%) was assigned to 32 chromosomal-level scaffolds, representing 30 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). Chromosomes Z and W were assigned by HiC signal.

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 62.4, and for haplotype 2, 62.9. When the two haplotypes are combined, the assembly achieves an estimated QV of 62.6. The *k*-mer completeness is 83.82% for haplotype 1, 79.84% for haplotype 2, and 99.40% for the combined haplotypes (Figure 4).

BUSCO analysis using the lepidoptera_odb10 reference set (n = 5 286) identified 98.0% of the expected gene set (single = 97.3%, duplicated = 0.8%) for haplotype 1. The snail plot in Figure 5 summarises the scaffold length distribution and other assembly statistics for haplotype 1. The blob

Table 1. Specimen and sequencing data for BioProject PRJEB78782.

Platform	PacBio HiFi	Hi-C
ToLID	ilAdsGery1	ilAdsGery1
Specimen ID	NHMUK013698373	NHMUK013698373
BioSample (source individual)	SAMEA114805667	SAMEA114805667
BioSample (tissue)	SAMEA114805786	SAMEA114805786
Tissue	whole organism	whole organism
Instrument	Revio	Illumina NovaSeq X
Run accessions	ERR13485737	ERR13493994
Read count total	5.39 million	648.94 million
Base count total	63.36 Gb	97.99 Gb

Table 2. Genome assembly statistics.

Assembly name	ilAdsGery1.hap1.1	ilAdsGery1.hap2.1
Assembly accession	GCA_964275185.1	GCA_964275195.1
Assembly level	chromosome	scaffold
Span (Mb)	764.63	670.15
Number of chromosomes	32	N/A
Number of contigs	387	177
Contig N50	9.27 Mb	10.38 Mb
Number of scaffolds	114	82
Scaffold N50	24.94 Mb	24.71 Mb
Longest scaffold length (Mb)	62.18	N/A
Sex chromosomes	W and Z	N/A
Organelles	Mitochondrion: 15.32 kb	N/A

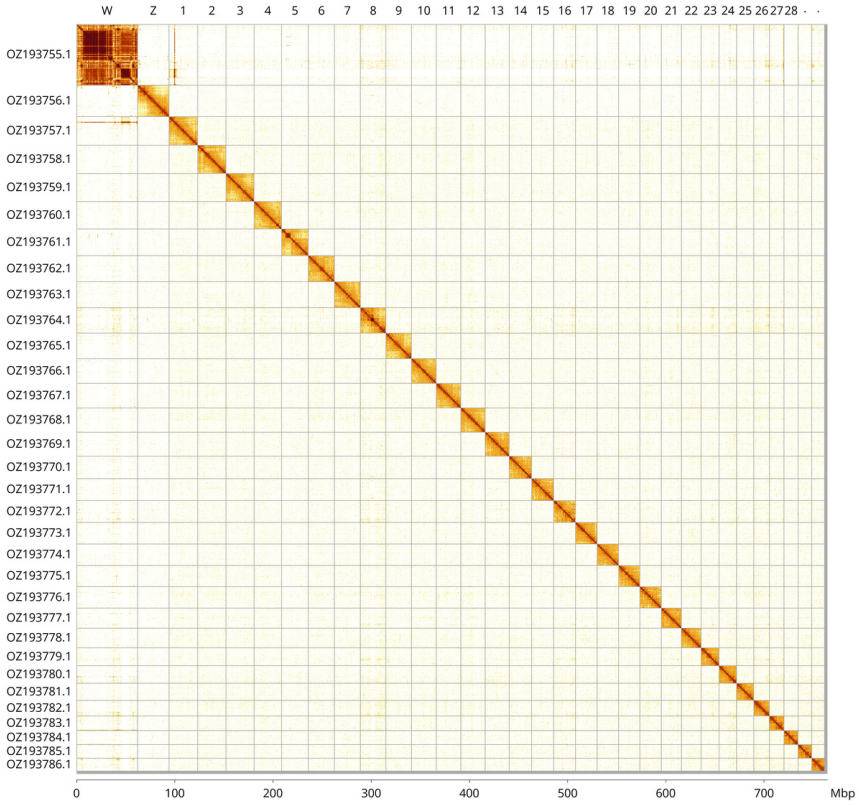

Figure 3. Hi-C contact map of the *Adscita geryon* genome assembly. Assembled chromosomes are shown in order of size and labelled along the axes, with a megabase scale shown below. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *Adscita geryon* ilAdsGery1.

INSDC accession	Molecule	Length (Mb)	GC%
OZ193757.1	1	29.14	35.50
OZ193758.1	2	28.80	35
OZ193759.1	3	28.67	35.50
OZ193760.1	4	27.86	35
OZ193761.1	5	27.35	34.50
OZ193762.1	6	26.46	35.50
OZ193763.1	7	26.40	35
OZ193764.1	8	26.17	37.50
OZ193765.1	9	25.98	35.50
OZ193766.1	10	25.22	35.50
OZ193767.1	11	24.94	35.50
OZ193768.1	12	24.77	35.50
OZ193769.1	13	24.59	35.50
OZ193770.1	14	22.86	35
OZ193771.1	15	22.44	35
OZ193772.1	16	22.11	35.50
OZ193773.1	17	22.01	35
OZ193774.1	18	21.88	35
OZ193775.1	19	21.76	35.50
OZ193776.1	20	21.74	35.50
OZ193777.1	21	20.46	35.50
OZ193778.1	22	20.21	35.50
OZ193779.1	23	18.17	36
OZ193780.1	24	17.91	35.50
OZ193781.1	25	17.53	35.50
OZ193782.1	26	15.85	36.50
OZ193783.1	27	14.83	36
OZ193784.1	28	14.41	35.50
OZ193785.1	29	13.72	35.50
OZ193786.1	30	13.26	36
OZ193755.1	W	62.18	40.50
OZ193756.1	Z	32.15	35.50

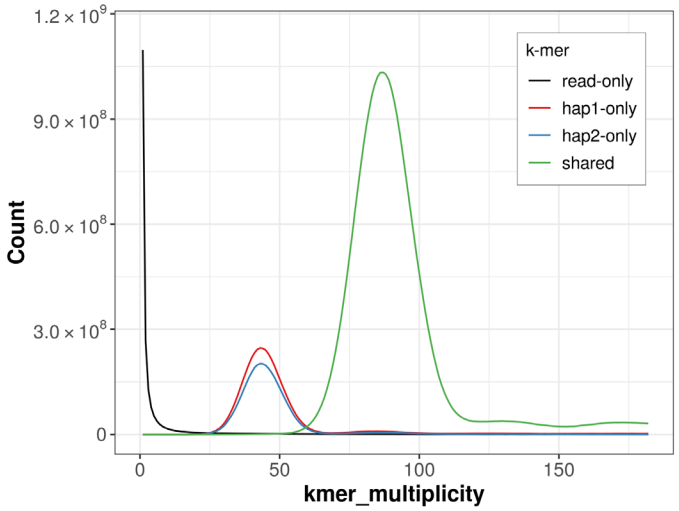

Figure 4. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the final assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers 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.

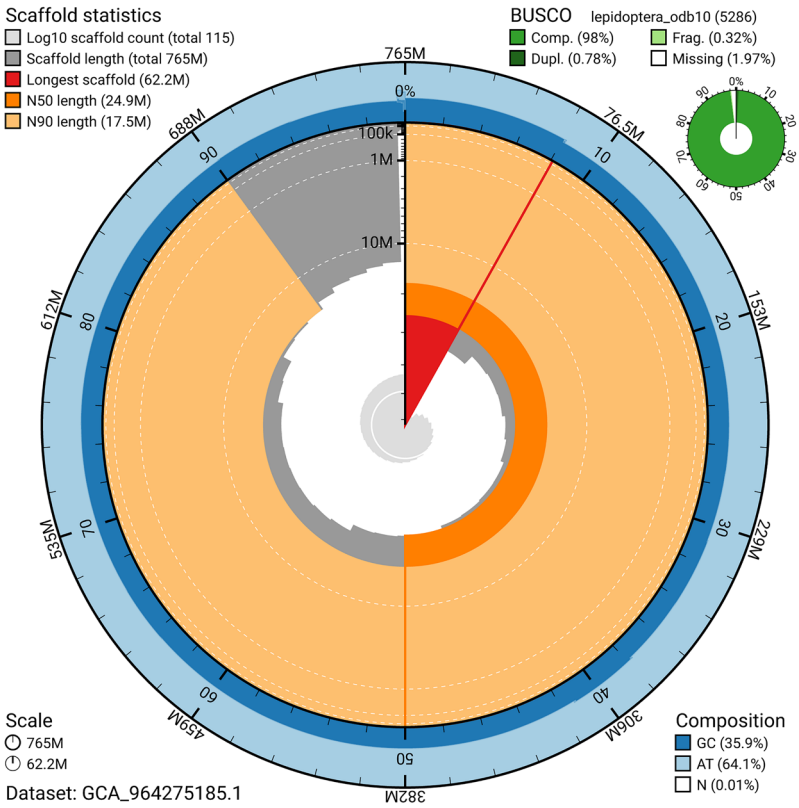

Figure 5. Assembly metrics for ilAdsGery1.hap1.1. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1 000 bins around the circumference. The outermost 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.

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

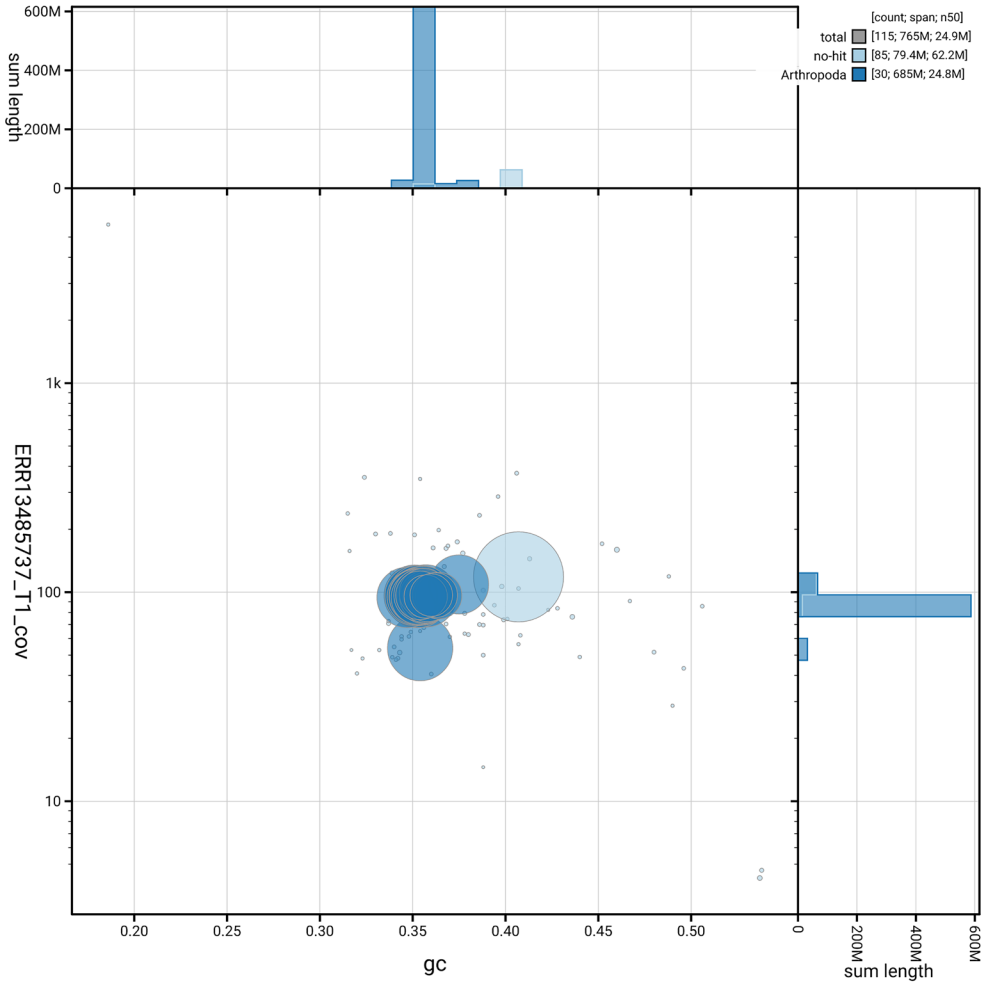

Figure 6. BlobToolKit GC-coverage plot for ilAdsGery1.hap1.1. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes 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 *Adscita geryon* assembly.

Measure	Value	Benchmark
EBP summary (haplotype 1)	6.C.Q62	6.C.Q40
Contig N50 length	9.27 Mb	≥ 1 Mb
Scaffold N50 length	24.94 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 62.4; haplotype 2: 62.9; combined: 62.6	≥ 40
k-mer completeness	Haplotype 1: 83.82%; Haplotype 2: 79.84%; combined: 99.40%	≥ 95%
BUSCO	C:98.0% [S:97.3%; D:0.8%]; F:0.3%; M:1.6%; n:5 286	S > 90%; D < 5%
Percentage of assembly assigned to chromosomes	99.63%	≥ 90%

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 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.

Data availability

European Nucleotide Archive: Adscita geryon. Accession number PRJEB78782. The genome sequence is released openly for reuse. The *Adscita geryon* 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 Natural History Museum 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

Software	Version	Source
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
Seqtk	1.3	https://github.com/lh3/seqtkext-link
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

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Open Peer Review

Current Peer Review Status: ✔ ✔ ✔ ✔

Version 1

Reviewer Report 27 December 2025

https://doi.org/10.21956/wellcomeopenres.27487.r137601

✔ **Aleksandra Gwiazdowska**
Polish Academy of Sciences, Twarda, Poland

The authors described the genome of the Cistus Forester (Adscita geryon). The introduction contained information about the species. The photograph of the Cistus Forester in nature was fine, but I would like to see a photograph of the voucher that the authors used to do a genome or I would like to have information where I can find a photograph of the voucher. The methods are described in great detail, and each part has a link to see the details on the web side. The pipeline is also available online.
In summary, the results and methods are available and reproducible. The reference genome will help for future studies.

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: Population Genetics, Conservation 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 24 November 2025

https://doi.org/10.21956/wellcomeopenres.27487.r138610

Henk den Bakker
University of Georgia, Griffin, Griffin, USA

This manuscript describes the sequencing of the genome of the Cistus Forester moth, Adscita geryon. It provides an introduction to the natural history of the species and a detailed description of the genome sequencing and associated bioinformatics protocols.

I have a few small suggested edits:

1. Can the author address what the rationale was for sequencing A. geryon, and not the more common species Adscita statices.

2. In the last paragraph of the back ground section ...The branching pattern of Adscita,.. please change to ...The phylogeny of Adscita...

3. In the Nucleic acid extraction subsection of the Methods section, in the sentence before the last sentence of the second paragraph ...and a yield of 2 717.54 ng, with a fragment size of 16.4 kb. I assume it is an average fragment size. Please correct if that assumption is correct.

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: Bioinformatics, phylogenetics, systematics

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 24 November 2025

https://doi.org/10.21956/wellcomeopenres.27487.r138612

Pritha Dey
National Centre for Biological Sciences-TIFR, Bengaluru, India

The manuscript is overall well-written, concise. Here are a few comments:

1) While the technical details are adequate, the manuscript will benefit from a brief understanding of why Adscita geryon is evolutionarily relevant-with details about habitat specificity and phylogenetic placement with the Zygaenidae family

2) It would help the readers if the biological relevance of retaining two haplotypes of different lengths is highlighted.
Also, would subsequent genomic analysis use Haplotype 1 over Haplotype 2, if yes, why

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: Taxonomy, evolutionary ecology

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 06 November 2025

https://doi.org/10.21956/wellcomeopenres.27487.r135946

Abdoallah Sharaf
University of Konstanz, Konstanz, Germany

The article is scientifically sound in its current form, with no major flaws in rationale, methods, reproducibility, or data presentation. All evaluation questions can confidently be answered “Yes,” indicating high technical quality, methodological transparency, and data integrity.
The work aligns with the standards and best practices of the *Darwin Tree of Life* (DToL) and *Earth BioGenome Project* initiatives, delivering a reference-quality genome for *Adscita geryon*. The assembly achieves excellent metrics (N50 = 24.94 Mb, BUSCO completeness = 98.0%), demonstrating careful experimental design, data handling, and quality control.
No substantive revisions are required for scientific soundness. The article represents a valuable and well-executed contribution to biodiversity genomics and Lepidopteran research.

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, and biodiversity research

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.