DATA NOTE

The genome sequence of the Streamer, *Anticlea derivata* (Denis & Schiffermüller, 1775) [version 1; peer review: awaiting peer review]

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Abstract

We present a genome assembly from an individual female *Anticlea derivata* (the Streamer; Arthropoda; Insecta; Lepidoptera; Geometridae). The genome sequence is 355.8 megabases in span. Most of the assembly is scaffolded into 32 chromosomal pseudomolecules, including the W and Z sex chromosomes. The mitochondrial genome has also been assembled and is 17.39 kilobases in length.

Keywords

Anticlea derivata, the Streamer, 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; 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; *Anticlea*; *Anticlea derivata* (Denis & Schiffermüller, 1775) (NCBI:txid934824).

Background

Anticlea derivata, the Streamer, is an elegant and distinctive moth in the family Geometridae. The forewings are light silvery brown, suffused with violet in fresh specimens. This ground colour is overlain by a series of dark bands, the most distal of which has a sinuous river-like shape that gives the moth its common name. *A. derivata* has been recorded widely across Europe and east through Russia (GBIF Secretariat, 2022). In Britain, the species can be found throughout England, Scotland, Northern Ireland and Wales, although it is commoner in the south (NBN Atlas Partnership, 2021). In Ireland, *A. derivata* has been recorded in the west and south of the country (MothsIreland, 2023). The moth is found predominantly around woodland edges and on well-drained hillsides with abundant shrubs and bushes (Wagner, 2023).

In southern Britain and central Europe, the adult moth is on the wing in April and May, with larvae feeding from May to June or July on leaves of dog-rose *Rosa canina*. The larvae are green with a series of pale yellow hoops encircling the body, and brown diamond-shaped patches along the dorsal midline. The pupae overwinter (Wagner, 2023).

We present a complete genome sequence for *Anticlea derivata*, determined as part of the Darwin Tree of Life project. The assembled genome sequence will facilitate research into host plant adaptations in Lepidoptera and contribute to the growing set of resources for understanding molecular evolution in insects.

Genome sequence report

The genome was sequenced from one female *Anticlea derivata* (Figure 1) collected from Wytham Woods, Oxfordshire, UK (51.77, –1.34). A total of 67-fold coverage in Pacific Biosciences single-molecule HiFi long reads was generated. Primary assembly contigs were scaffolded with chromosome conformation Hi-C data. Manual assembly curation corrected 5 missing joins or mis-joins, reducing the scaffold number by 4.76%.

Figure 1. Photograph of the *Anticlea derivata* (ilAntDeri1) specimen used for genome sequencing.

The final assembly has a total length of 355.8 Mb in 39 sequence scaffolds with a scaffold N50 of 12.7 Mb (Table 1). Most (99.99%) of the assembly sequence was assigned to 32 chromosomal-level scaffolds, representing 30 autosomes and the W and Z sex chromosomes. Chromosome-scale scaffolds confirmed by the Hi-C data are named in order of size (Figure 2–Figure 5; Table 2). While not fully phased, the assembly deposited is of one haplotype. Contigs corresponding to the second haplotype have also been deposited. The mitochondrial genome was also assembled and can be found as a contig within the multifasta file of the genome submission.

The estimated Quality Value (QV) of the final assembly is 69.9 with *k*-mer completeness of 100%, and the assembly has a BUSCO v5.3.2 completeness of 98.1% (single = 97.7%, duplicated = 0.3%), using the lepidoptera_odb10 reference set (n = 5,286).

Metadata for specimens, spectral estimates, sequencing runs, contaminants and pre-curation assembly statistics can be found at https://links.tol.sanger.ac.uk/species/934824.

Methods

Sample acquisition and nucleic acid extraction

A female *Anticlea derivata* (ilAntDeri1) was collected from Wytham Woods, Oxfordshire (biological vice-county Berkshire), UK (latitude 51.77, longitude –1.34) on 2021-03-31, using a light trap. The specimen was collected and identified by Douglas Boyes (University of Oxford) and was snap-frozen on dry ice.

DNA was extracted at the Tree of Life laboratory, Wellcome Sanger Institute (WSI). The ilAntDeri1 sample was weighed and dissected on dry ice with tissue set aside for Hi-C sequencing. Head and thorax tissue was disrupted using a Nippi Powermasher fitted with a BioMasher pestle. High molecular weight (HMW) DNA was extracted using the Qiagen MagAttract HMW DNA extraction kit. HMW DNA was sheared into an average fragment size of 12–20 kb in a Megaruptor 3 system with speed setting 30. Sheared DNA was purified by solid-phase reversible immobilisation using AMPure PB beads with a 1.8X ratio of beads to sample to remove the shorter fragments and concentrate the DNA sample. The concentration of the sheared and purified DNA was assessed using a Nanodrop spectrophotometer and Qubit Fluorometer and Qubit dsDNA High Sensitivity Assay kit. Fragment size distribution was evaluated by running the sample on the FemtoPulse system.

Sequencing

Pacific Biosciences HiFi circular consensus DNA sequencing libraries were constructed according to the manufacturers'

Table 1. Genome data for *Anticlea derivata*, ilAntDeri1.1.

Project accession data		
Assembly identifier	ilAntDeri1.1	
Species	*Anticlea derivata*	
Specimen	ilAntDeri1	
NCBI taxonomy ID	934824	
BioProject	PRJEB55883	
BioSample ID	SAMEA10107024	
Isolate information	ilAntDeri1 ilAntDeri1	
Assembly metrics*		***Benchmark***
Consensus quality (QV)	69.9	*≥ 50*
k-mer completeness	100%	*≥ 95%*
BUSCO**	C:98.1%[S:97.7%,D:0.3%], F:0.6%,M:1.3%,n:5,286	*C ≥ 95%*
Percentage of assembly mapped to chromosomes	99.99%	*≥ 95%*
Sex chromosomes	W and Z	*localised homologous pairs*
Organelles	Mitochondrial genome assembled	*complete single alleles*
Raw data accessions		
PacificBiosciences SEQUEL II	ERR10224851	
Hi-C Illumina	ERR10177757	
Genome assembly		
Assembly accession	GCA_947579855.1	
Accession of alternate haplotype	GCA_947579405.1	
Span (Mb)	355.8	
Number of contigs	78	
Contig N50 length (Mb)	7.5	
Number of scaffolds	39	
Scaffold N50 length (Mb)	12.7	
Longest scaffold (Mb)	15.0	

* Assembly metric benchmarks are adapted from column VGP-2020 of "Table 1: Proposed standards and metrics for defining genome assembly quality" from (Rhie *et al.*, 2021).

** BUSCO scores based on the lepidoptera_odb10 BUSCO set using v5.3.2. C = complete [S = single copy, D = duplicated], F = fragmented, M = missing, n = number of orthologues in comparison. A full set of BUSCO scores is available at https://blobtoolkit.genomehubs.org/view/ilAntDeri1.1/dataset/CANPUU01/busco.

instructions. DNA sequencing was performed by the Scientific Operations core at the WSI on Pacific Biosciences SEQUEL II (HiFi) instrument. Hi-C data were also generated from head and thorax tissue of ilAntDeri1 that had been set aside, using the Arimav2 kit and sequenced on the Illumina NovaSeq 6000 instrument.

Genome assembly, curation and evaluation

Assembly was carried out with Hifiasm (Cheng *et al.*, 2021) and haplotypic duplication was identified and removed with purge_dups (Guan *et al.*, 2020). The assembly was then scaffolded with Hi-C data (Rao *et al.*, 2014) using YaHS (Zhou *et al.*, 2023). The assembly was checked for

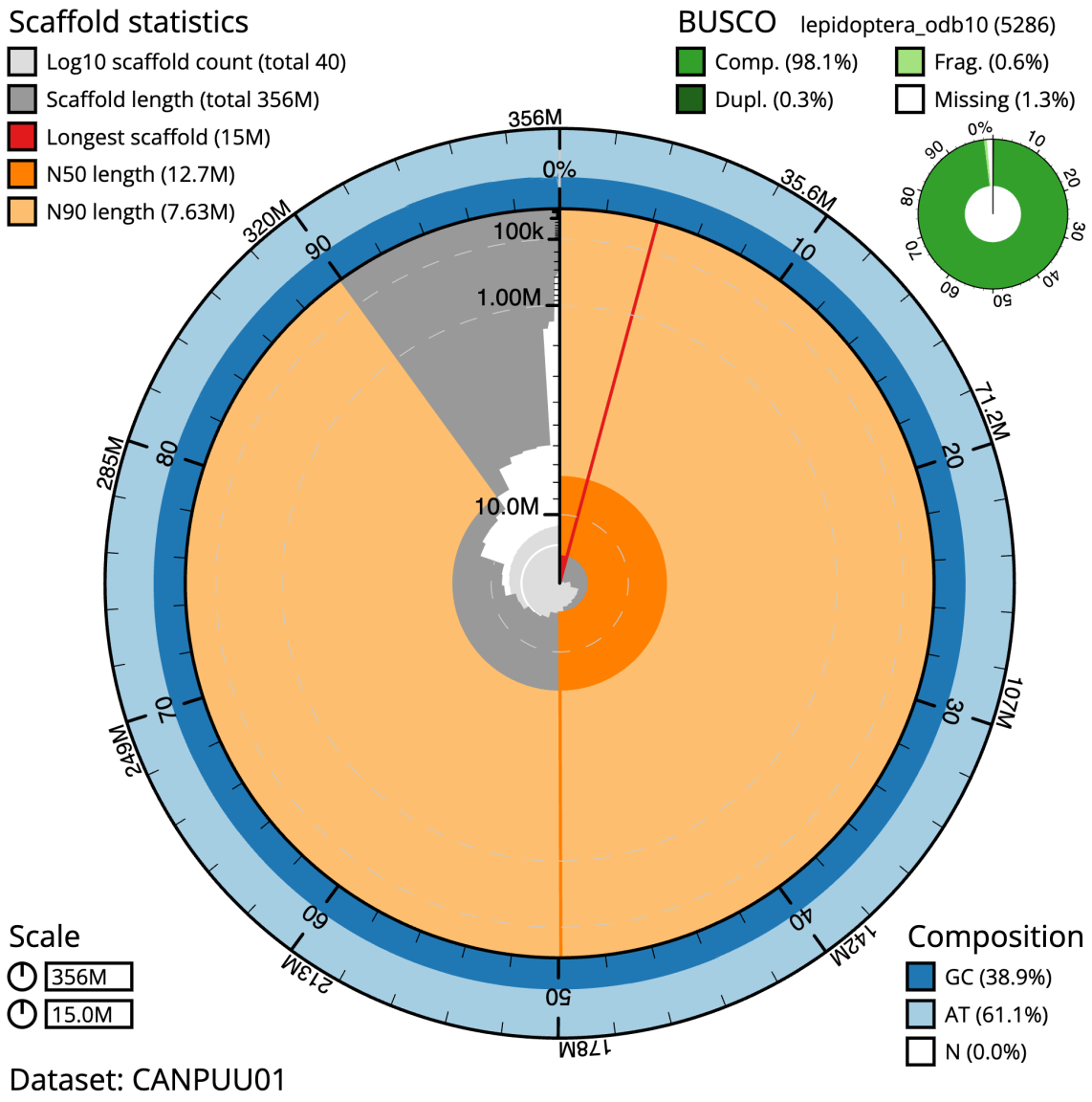

Figure 2. Genome assembly of *Anticlea derivata*, ilAntDeri1.1: metrics. The BlobToolKit Snailplot shows N50 metrics and BUSCO gene completeness. The main plot is divided into 1,000 size-ordered bins around the circumference with each bin representing 0.1% of the 355,821,062 bp assembly. The distribution of scaffold lengths is shown in dark grey with the plot radius scaled to the longest scaffold present in the assembly (14,989,189 bp, shown in red). Orange and pale-orange arcs show the N50 and N90 scaffold lengths (12,706,007 and 7,626,879 bp), respectively. The pale grey spiral shows the cumulative scaffold count on a log scale with white scale lines showing successive orders of magnitude. The blue and pale-blue area around the outside of the plot shows the distribution of GC, AT and N percentages in the same bins as the inner plot. A summary of complete, fragmented, duplicated and missing BUSCO genes in the lepidoptera_odb10 set is shown in the top right. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/ilAntDeri1.1/dataset/CANPUU01/snail.

contamination and corrected as described previously (Howe *et al.*, 2021). Manual curation was performed using HiGlass (Kerpedjiev *et al.*, 2018) and Pretext (Harry, 2022). The mitochondrial genome was assembled using MitoHiFi (Uliano-Silva *et al.*, 2022), which runs MitoFinder (Allio *et al.*, 2020) or MITOS (Bernt *et al.*, 2013) and uses these annotations to select the final mitochondrial contig and to ensure the general quality of the sequence.

A Hi-C map for the final assembly was produced using bwa-mem2 (Vasimuddin *et al.*, 2019) in the Cooler file format (Abdennur & Mirny, 2020). To assess the assembly metrics,

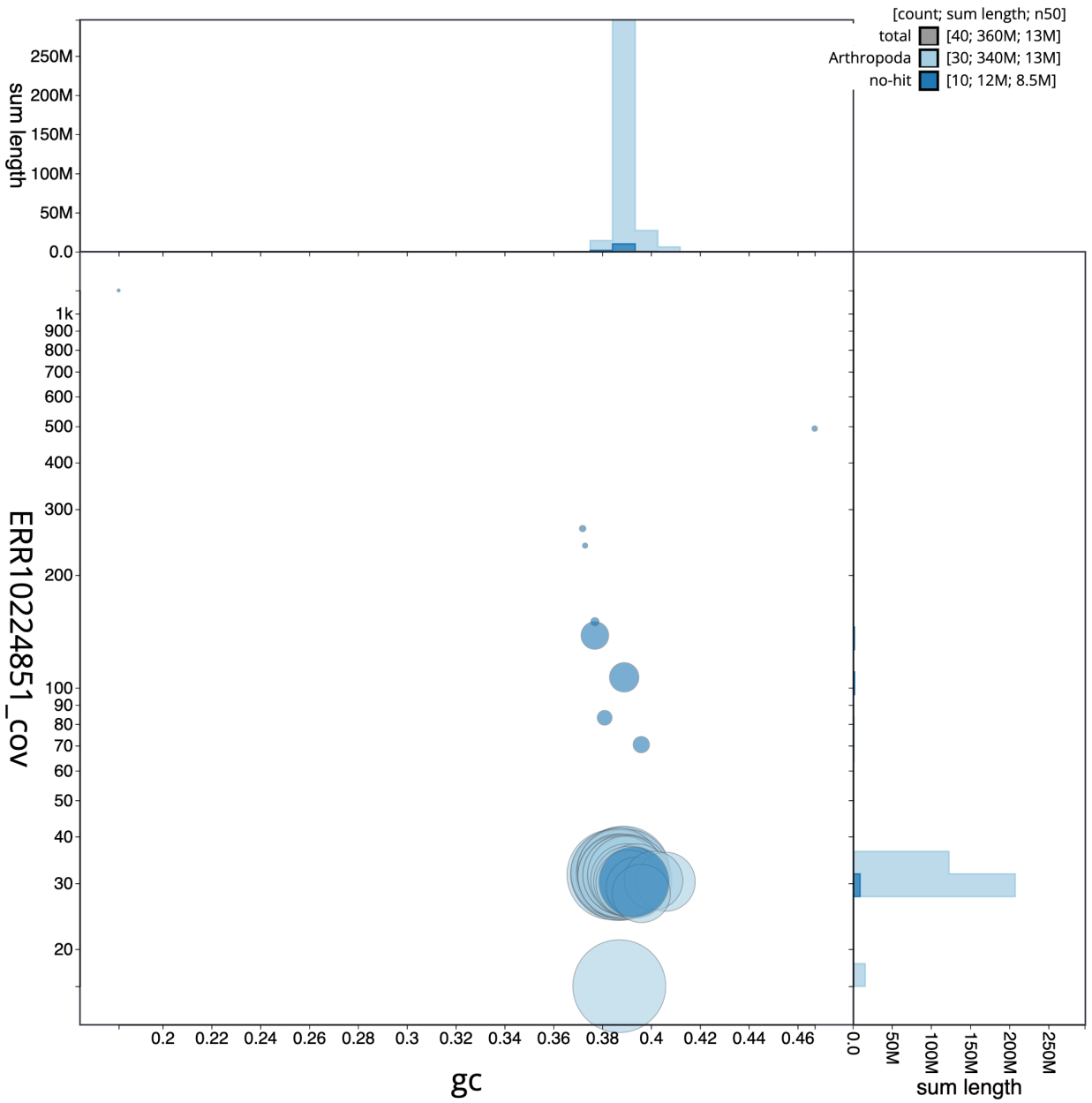

Figure 3. Genome assembly of *Anticlea derivata*, ilAntDeri1.1: BlobToolKit GC-coverage plot. Scaffolds are coloured by phylum. Circles are sized in proportion to scaffold length. Histograms show the distribution of scaffold length sum along each axis. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/ilAntDeri1.1/dataset/CANPUU01/blob.

the *k*-mer completeness and QV consensus quality values were calculated in Merqury (Rhie *et al.*, 2020). This work was done using Nextflow (Di Tommaso *et al.*, 2017) DSL2 pipelines "sanger-tol/readmapping" (Surana *et al.*, 2023a) and "sanger-tol/genomenote" (Surana *et al.*, 2023b). The genome was analysed within the BlobToolKit environment (Challis *et al.*, 2020) and BUSCO scores (Manni *et al.*, 2021; Simão *et al.*, 2015) were calculated.

Table 3 contains a list of relevant software tool versions and sources.

Wellcome Sanger Institute – Legal and Governance

The materials that have contributed to this genome note have been supplied by a Darwin Tree of Life Partner. The submission of materials by a Darwin Tree of Life Partner is subject to the **'Darwin Tree of Life Project Sampling Code**

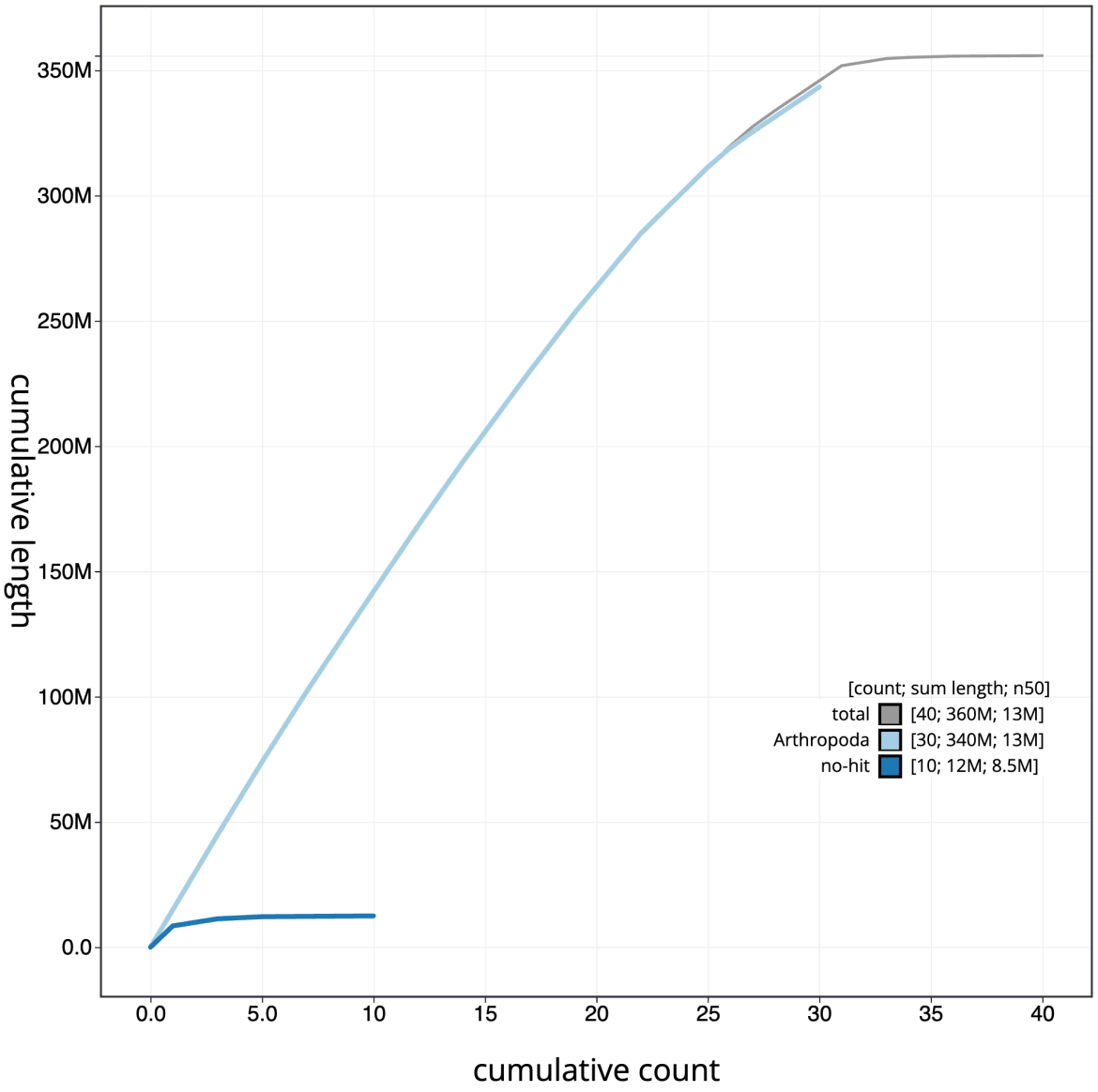

Figure 4. Genome assembly of *Anticlea derivata*, ilAntDeri1.1: BlobToolKit cumulative sequence plot. The grey line shows cumulative length for all scaffolds. Coloured lines show cumulative lengths of scaffolds assigned to each phylum using the buscogenes taxrule. An interactive version of this figure is available at https://blobtoolkit.genomehubs.org/view/ilAntDeri1.1/dataset/CANPUU01/cumulative.

of Practice', which can be found in full on the Darwin Tree of Life website here. By agreeing with and signing up to the Sampling Code of Practice, the Darwin Tree of Life Partner agrees they will meet the legal and ethical requirements and standards set out within this document in respect of all samples acquired for, and supplied to, the Darwin Tree of Life Project.

Further, the Wellcome Sanger Institute employs a process whereby due diligence is carried out proportionate to the nature of the materials themselves, and the circumstances under 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

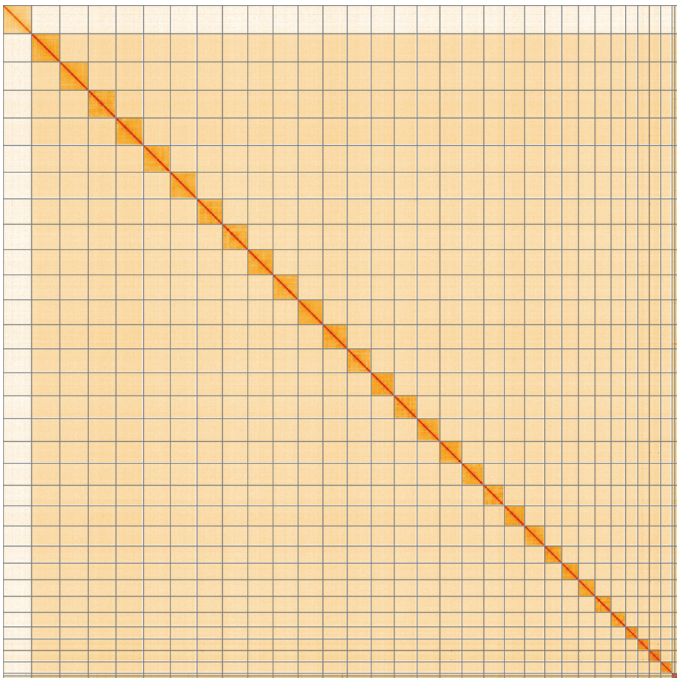

Figure 5. Genome assembly of *Anticlea derivata*, ilAntDeri1.1: Hi-C contact map of the ilAntDeri1.1 assembly, visualised using HiGlass. Chromosomes are shown in order of size from left to right and top to bottom. An interactive version of this figure may be viewed at https://genome-note-higlass.tol.sanger.ac.uk/l/?d=TfZJxD6HQtCEgkJVe2Q2ZA.

Table 2. Chromosomal pseudomolecules in the genome assembly of *Anticlea derivata*, ilAntDeri1.

INSDC accession	Chromosome	Length (Mb)	GC%
OX388258.1	1	14.89	39.0
OX388259.1	2	14.87	38.5
OX388260.1	3	14.61	39.0
OX388261.1	4	14.53	39.0
OX388262.1	5	14.07	38.5
OX388263.1	6	14.02	38.5
OX388264.1	7	13.38	38.5
OX388265.1	8	13.34	38.5
OX388266.1	9	13.3	38.5
OX388267.1	10	13.16	38.5
OX388268.1	11	13.07	39.0
OX388269.1	12	12.71	38.5
OX388270.1	13	12.61	39.0
OX388271.1	14	12.16	38.5
OX388272.1	15	12.03	38.5
OX388273.1	16	11.98	38.5
OX388274.1	17	11.61	39.0
OX388275.1	18	11.53	39.0
OX388276.1	19	10.8	39.0
OX388277.1	20	10.65	39.0
OX388278.1	21	10.6	39.0
OX388279.1	22	8.97	39.0
OX388280.1	23	8.73	39.5
OX388281.1	24	8.71	39.0
OX388282.1	25	8.48	39.5
OX388283.1	26	7.63	39.0
OX388284.1	27	6.39	39.5
OX388285.1	28	6.07	40.5
OX388286.1	29	5.99	40.0
OX388287.1	30	5.91	39.5
OX388288.1	W	1.5	39.0
OX388257.1	Z	14.99	38.5
OX388289.1	MT	0.02	18.5

Table 3. Software tools: versions and sources.

Software tool	Version	Source
BlobToolKit	4.1.5	https://github.com/blobtoolkit/blobtoolkit
BUSCO	5.3.2	https://gitlab.com/ezlab/busco
Hifiasm	0.16.1-r375	https://github.com/chhylp123/hifiasm
HiGlass	1.11.6	https://github.com/higlass/higlass
Merqury	MerquryFK	https://github.com/thegenemyers/MERQURY.FK
MitoHiFi	2	https://github.com/marcelauliano/MitoHiFi
PretextView	0.2	https://github.com/wtsi-hpag/PretextView
purge_dups	1.2.3	https://github.com/dfguan/purge_dups
sanger-tol/genomenote	v1.0	https://github.com/sanger-tol/genomenote
sanger-tol/readmapping	1.1.0	https://github.com/sanger-tol/readmapping/tree/1.1.0
YaHS	yahs-1.1.91eebc2	https://github.com/c-zhou/yahs

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: *Anticlea derivata* (streamer). Accession number PRJEB55883; https://identifiers.org/ena.embl/PRJEB55883. (Wellcome Sanger Institute, 2022)

The genome sequence is released openly for reuse. The *Anticlea derivata* genome sequencing initiative is part of the Darwin Tree of Life (DToL) project. 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.

Author information

Members of the University of Oxford and Wytham Woods Genome Acquisition Lab are listed here: https://doi.org/10.5281/zenodo.4789928.

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Members of the Wellcome Sanger Institute Tree of Life programme are listed here: https://doi.org/10.5281/zenodo.4783585.

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Members of the Tree of Life Core Informatics collective are listed here: https://doi.org/10.5281/zenodo.5013541.

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

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