DATA NOTE

The genome sequence of the Scarce Vapourer, *Orgyia recens* (Hübner, 1819) (Lepidoptera: Erebidae)

[version 1; peer review: 2 approved]

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Abstract

We present a genome assembly from an individual female *Orgyia recens* (Scarce Vapourer; Arthropoda; Insecta; Lepidoptera; Erebidae). The assembly contains two haplotypes with total lengths of 533.68 megabases and 485.54 megabases. Most of haplotype 1 (99.76%) is scaffolded into 31 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 15.47 kilobases. Gene annotation of this assembly on Ensembl identified 10 917 protein-coding genes. 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

Orgyia recens; Scarce Vapourer; genome sequence; chromosomal; Lepidoptera

This article is included in the Tree of Life gateway.

Open Peer Review

Approval Status ✓ ✓

	1	2
version 1 21 Oct 2025	✓ view	✓ view

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Any reports and responses or comments on the article can be found at the end of the article.

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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; Erebidae; Lymantriinae; Orgyia; *Orgyia recens* (Hübner, 1819) (NCBI:txid198700)

Background

Orgyia recens is a day-flying tussock moth with marked sexual dimorphism. Males are brown to orange-brown with a white mark near the tornus and an orange-and-white mark near the forewing apex. Females are entirely wingless, pale grey, and stout (Heath & Emmet, 1979; The Butterfly Foundation, 2025). Gravid females reach about 25 mm in length.

Adults emerge from late May through July, with a partial second generation reported from August to October (Heath & Emmet, 1979). Males fly during the day, while flightless females stay on or close to the pupal case. A newly emerged female emits pheromones immediately; the first male to arrive mates, after which the female lays up to ~350 eggs on or near the pupal case and then dies (Heath & Emmet, 1979).

Larvae are present from July onwards. They overwinter as larvae in a loose silk spinning between two leaves of the food plant, resume feeding in April, and pupate in May. Recorded host plants include broad-leaved trees and shrubs such as bramble (*Rubus fruticosus*), willows (*Salix* spp.; e.g. *S. cinerea* subsp. *oleifolia*, *S. caprea*), hawthorn (*Crataegus monogyna*), pedunculate oak (*Quercus robur*), and sessile oak (*Quercus petraea*) (Heath & Emmet, 1979; Wheeler, 2025).

In Great Britain, *O. recens* is a Red Data Book species, restricted to a few areas in north-east England and the Norfolk Broads (Kimber, 2025; Wheeler, 2025). Its wider range extends from the north of the Iberian Peninsula east across western and central Europe into East Asia (including Japan), north to southern Scandinavia and south to the Mediterranean (The Butterfly Foundation, 2025). The species is reported to be in decline across its range and it is listed as Endangered (EN) and considered Nationally Rare in Great Britain (Kimber, 2025).

We present a chromosome-level genome sequence for *Orgyia recens*, the Scarce Vapourer. The assembly was produced using the Tree of Life pipeline from a specimen collected in Sutton North Fen, England, UK (Figure 1).

Methods

Sample acquisition and DNA barcoding

The specimen used for genome sequencing was an adult female *Orgyia recens* (specimen ID NHMUK014584932, ToLID ilOrgRece1; Figure 1), collected from Sutton North Fen, England, UK (latitude 52.4, longitude 0.11) on 2022-09-07. The specimen was collected by Mick Acourt and formally 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).

Figure 1. Photograph of the *Orgyia recens* (ilOrgRece1) specimen used for genome sequencing.

The initial identification was verified by an additional DNA barcoding process according to the framework developed by Twyford *et al.* (2024). A small sample was dissected from the specimen and stored in ethanol, while the remaining parts were shipped on dry ice to the Wellcome Sanger Institute (WSI) (see the protocol). The tissue was lysed, the COI marker region was amplified by PCR, and amplicons were sequenced and compared to the BOLD database, confirming the species identification (Crowley *et al.*, 2023). Following whole genome sequence generation, the relevant DNA barcode region was also used alongside the initial barcoding data for sample tracking at the WSI (Twyford *et al.*, 2024). The standard operating procedures for Darwin Tree of Life barcoding are available on protocols.io.

Nucleic acid extraction

Protocols for high molecular weight (HMW) DNA extraction developed at the Wellcome Sanger Institute (WSI) Tree of Life Core Laboratory are available on protocols.io (Howard *et al.*, 2025). The ilOrgRece1 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 18.1 ng/μL and a yield of 850.70 ng, with a fragment size of 10.4 kb.

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 ilOrgRece1 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 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 organelle genomes were assembled using MitoHiFi (Uliano-Silva *et al.*, 2023).

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 9 breaks, 169 joins, and removal of one haplotypic duplication. The curation process is documented 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 *Orgyia recens* specimen generated 71.19 Gb (gigabases) from 9.10 million reads, which were used to assemble the genome. GenomeScope2.0 analysis estimated the haploid genome size at 501.04 Mb, with a heterozygosity of 0.38% and repeat content of 26.03% (Figure 2). These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 139× coverage. Hi-C sequencing produced 126.59 Gb from 838.35 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 533.68 Mb in 84 scaffolds, with 250 gaps, and a scaffold N50 of 18.65 Mb (Table 2).

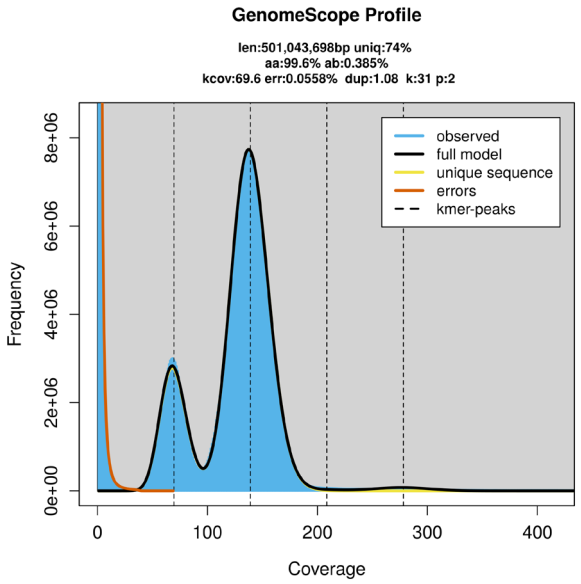

Figure 2. Frequency distribution of *k*-mers generated using GenomeScope2. The plot shows observed and modelled *k*-mer spectra, providing estimates of genome size, heterozygosity, and repeat content based on unassembled sequencing reads.

Table 1. Specimen and sequencing data for BioProject PRJEB83509.

Platform	PacBio HiFi	Hi-C
ToLID	ilOrgRece1	ilOrgRece1
Specimen ID	NHMUK014584932	NHMUK014584932
BioSample (source individual)	SAMEA114805682	SAMEA114805682
BioSample (tissue)	SAMEA114805801	SAMEA114805801
Tissue	whole organism	whole organism
Instrument	Revio	Illumina NovaSeq X
Run accessions	ERR14106127	ERR14075549
Read count total	9.10 million	838.35 million
Base count total	71.19 Gb	126.59 Gb

Table 2. Genome assembly statistics.

Assembly name	ilOrgRece1.hap1.1	ilOrgRece1.hap2.1
Assembly accession	GCA_965115965.1	GCA_965116105.1
Assembly level	chromosome	scaffold
Span (Mb)	533.68	485.54
Number of chromosomes	31	scaffold-level
Number of contigs	334	307
Contig N50	7.22 Mb	8.52 Mb
Number of scaffolds	84	231
Scaffold N50	18.65 Mb	18.14 Mb
Longest scaffold length (Mb)	29.18	-
Sex chromosomes	W and Z	-
Organelles	Mitochondrion: 15.47 kb	-

Most of the haplotype 1 assembly sequence (99.76%) was assigned to 31 chromosomal-level scaffolds, representing 29 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). Scaffolds on Chromosome W from ~1–26.33 Mb have uncertain order and orientation.

The mitochondrial genome was also assembled (length 15.47 kb, OZ220585.1). 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 60.4, and for haplotype 2, 60.3. When the two haplotypes are combined, the assembly achieves an estimated QV of 60.3. The *k*-mer completeness is 92.58% for haplotype 1, 88.14% for haplotype 2, and 99.85% for the combined haplotypes (Figure 4).

BUSCO analysis using the lepidoptera_odb10 reference set (n = 5 286) identified 98.8% of the expected gene set (single = 98.4%, duplicated = 0.5%) for haplotype 1. The snail plot in Figure 5 summarises the scaffold length distribution and other assembly statistics for haplotype 1. The blob plot in Figure 6 shows the distribution of scaffolds by GC proportion and coverage for haplotype 1.

Table 4 lists the assembly metric benchmarks adapted from Rhie *et al.* (2021) and the Earth BioGenome Project Report on Assembly Standards September 2024. The EBP metric, calculated for the haplotype 1, is **6.C.Q60**, meeting the recommended reference standard.

Genome annotation report

The *Orgyia recens* genome assembly (GCA_965115965.1) was annotated by Ensembl at the European Bioinformatics Institute (EBI). This annotation includes 19 832 transcribed mRNAs from 10 917 protein-coding and 1 860 non-coding genes. The average transcript length is 14 118.14 bp, with an average of 1.55 coding transcripts per gene and 6.73 exons per transcript. For further information about the annotation, please refer to the annotation page on Ensembl.

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

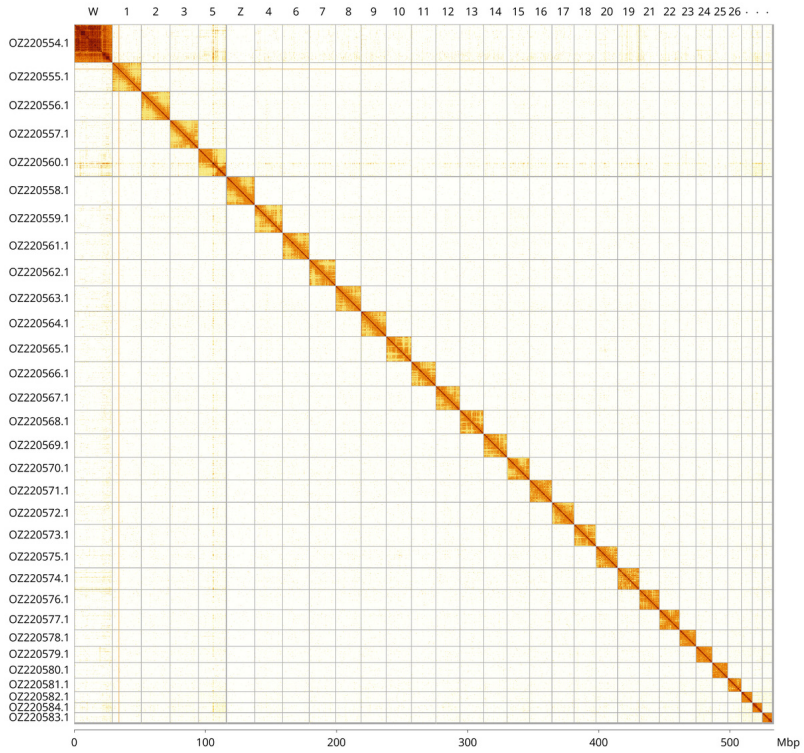

Figure 3. Hi-C contact map of the *Orgyia recens* genome assembly. Assembled chromosomes are shown in order of size (including unlocalised sequence assigned to each chromosome) and labelled along the axes, with a megabase scale shown below. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *Orgyia recens* ilOrgRece1.

INSDC accession	Molecule	Length (Mb)	GC%
OZ220555.1	1	22.07	33.50
OZ220556.1	2	21.76	34
OZ220557.1	3	21.71	34
OZ220559.1	4	21.34	34
OZ220560.1	5	21.48	35
OZ220561.1	6	20.30	33.50
OZ220562.1	7	20.12	33.50
OZ220563.1	8	19.38	33.50
OZ220564.1	9	19.23	34
OZ220565.1	10	19.16	33.50
OZ220566.1	11	18.68	33.50
OZ220567.1	12	18.27	33.50
OZ220568.1	13	18.02	34
OZ220569.1	14	17.94	33.50
OZ220570.1	15	17.31	34
OZ220571.1	16	17.04	33.50
OZ220572.1	17	16.79	34
OZ220573.1	18	16.72	34
OZ220574.1	19	16.47	34.50
OZ220575.1	20	16.56	34
OZ220576.1	21	15.42	34
OZ220577.1	22	15.20	34.50
OZ220578.1	23	12.62	34
OZ220579.1	24	12.46	34.50
OZ220580.1	25	11.79	34.50
OZ220581.1	26	10.37	34.50
OZ220582.1	27	8.34	35
OZ220583.1	28	7.59	35
OZ220584.1	29	7.65	35.50
OZ220554.1	W	29.18	37
OZ220558.1	Z	21.45	33.50

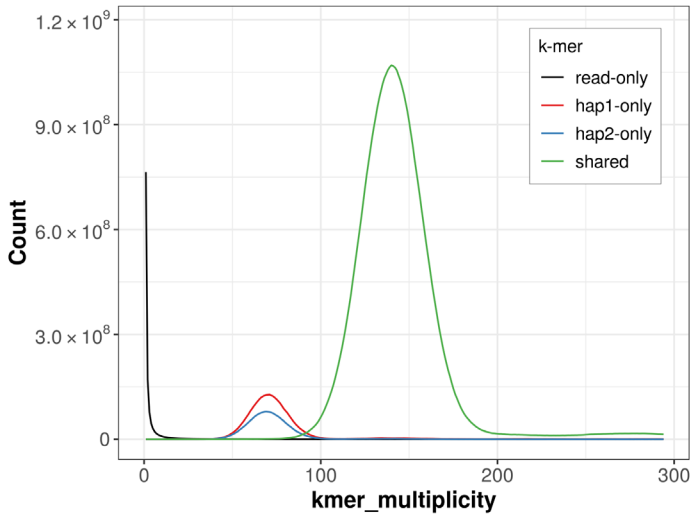

Figure 4. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the final assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers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

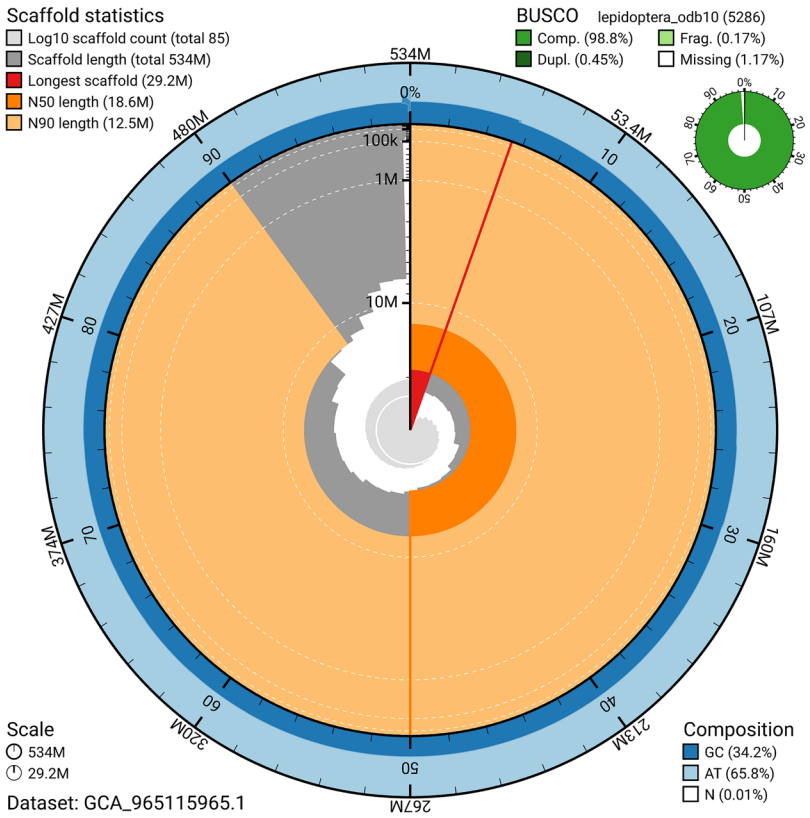

Figure 5. Assembly metrics for ilOrgRece1.hap1.1. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1 000 bins around the circumference. The outermost blue tracks display the distribution of GC, AT, and N percentages across the bins. Scaffolds are arranged clockwise from longest to shortest and are depicted in dark grey. The longest scaffold is indicated by the red arc, and the deeper orange and pale orange arcs represent the N50 and N90 lengths. A light grey spiral at the centre shows the cumulative scaffold count on a logarithmic scale. A summary of complete, fragmented, duplicated, and missing BUSCO genes in the set is presented at the top right. An interactive version of this figure can be accessed on the BlobToolKit viewer.

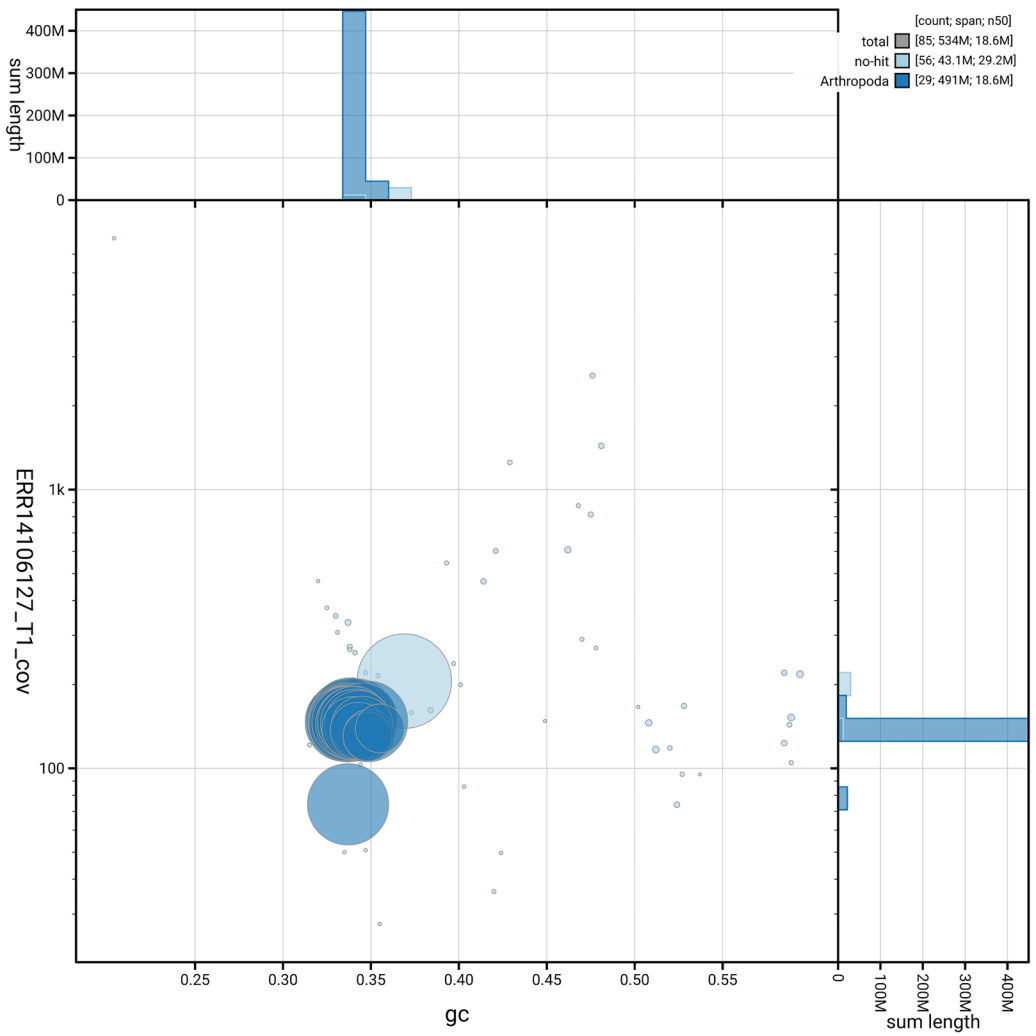

Figure 6. BlobToolKit GC-coverage plot for ilOrgRece1.hap1.1. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes 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 *Orgyia recens* assembly.

Measure	Value	Benchmark
EBP summary (haplotype 1)	6.C.Q60	6.C.Q40
Contig N50 length	7.22 Mb	≥ 1 Mb
Scaffold N50 length	18.65 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 60.4; haplotype 2: 60.3; combined: 60.3	≥ 40
k-mer completeness	Haplotype 1: 92.58%; Haplotype 2: 88.14%; combined: 99.85%	≥ 95%
BUSCO	C:98.8% [S:98.4%; D:0.5%]; F:0.2%; M:1.0%; n:5 286	S > 90%; D < 5%
Percentage of assembly assigned to chromosomes	99.76%	≥ 90%

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: Orgyia recens (scarce vapourer). Accession number PRJEB83509. The genome sequence is released openly for reuse. The *Orgyia recens* 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. **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
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

Software	Version	Source
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	-	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	1.2.2	https://github.com/c-zhou/yahs

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Open Peer Review

Current Peer Review Status: ✔ ✔

Version 1

Reviewer Report 24 January 2026

https://doi.org/10.21956/wellcomeopenres.27629.r144410

✔ **Peter Huemer**
Tyrolean Federal State Museums, Innsbruck, Austria

A well-written data note, which, however, from the reviewer's perspective, contains a somewhat geographically unbalanced background description of the species. References from continental Europe would be very helpful here, for example:

- Reference to additional larval host plants such as *Betula* spp. (Ebert 1994)
- High level of threat and inclusion in Red Lists (Ebert 1994, Huemer 2007)

Specific remark:
"Larvae are present from July onwards. They overwinter as larvae in a loose silk spinning between two leaves of the food plant, resume feeding in April, and pupate in May."
This sentence describes only the first generation.
In addition, due to the risk of confusion for this species, it would seem sensible to include a note on morphological differences compared with the widely distributed European species *Orgyia antiqua.*

Ebert, G. (ed.) (1994): Die Schmetterlinge Baden-Württembergs. Band 4: Nachtfalter II. Eugen Ulmer, Stuttgart, 536 pp.

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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: Integrative taxonmic expertise in European Lepidoptera

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 22 November 2025

https://doi.org/10.21956/wellcomeopenres.27629.r136934

Josephine R Paris
University of Exeter Library, Devon, UK

This a good Data Note, which contains good background information for the species (the Scarce Vapourer). The methods contain a thorough description of the library preparation and bioinformatics methods. The genome quality is very good and it's nice that both sex chromosomes were sequenced and assembled.

Small comments to improve readability:
It seems as though commas have been replaced by a space in all numbers in the thousands, e.g. in the abstract describing the number of protein-coding genes identified in the abstract: 10 917 and in the description of the Genome annotation report. This may be a rendering issue, but fixing this would be appreciated to improve readability.

In the background section, my preference would be to present the species' overall distribution first, i.e. "Its wider range extends from the north of the Iberian Peninsula east across western and central Europe into East Asia (including Japan), north to southern Scandinavia and south to the Mediterranean (The Butterfly Foundation, 2025)." before making specific references to it's restricted distribution in Great Britain (leading it to be listed as a Red Data Book species).

Datasets are available via the links given in the text.

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 genomics of non-models, genome assembly and annotation

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.