DATA NOTE

The genome sequence of the Skin Moth, *Monopis laevigella* (Denis & Schiffermüller, 1775) [version 1; peer review: awaiting peer review]

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v1 **First published:** 21 Aug 2023, **8**:359
https://doi.org/10.12688/wellcomeopenres.19810.1
Latest published: 21 Aug 2023, **8**:359
https://doi.org/10.12688/wellcomeopenres.19810.1

Abstract

We present a genome assembly from two female *Monopis laevigella* specimens (the Skin Moth; Arthropoda; Insecta; Lepidoptera; Tineidae). The genome sequences are 632.6 and 625.5 megabases in span. For both genomes, most of the assembly is scaffolded into 25 chromosomal pseudomolecules, including the Z sex chromosome. The mitochondrial genomes were also assembled and are 18.9 and 18.89 kilobases in length.

Keywords

Monopis laevigella, Skin Moth, 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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Author roles: Boyes D: Investigation, Resources; **Hammond J**: Writing – Original Draft Preparation, Writing – Review & Editing;

Competing interests: No competing interests were disclosed.

Grant information: This work was supported by Wellcome through core funding to the Wellcome Sanger Institute (206194) and the Darwin Tree of Life Discretionary Award (218328).
The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

How to cite this article: Boyes D, Hammond J, University of Oxford and Wytham Woods Genome Acquisition Lab *et al.* **The genome sequence of the Skin Moth, *Monopis laevigella* (Denis & Schiffermüller, 1775) [version 1; peer review: awaiting peer review]** Wellcome Open Research 2023, **8**:359 https://doi.org/10.12688/wellcomeopenres.19810.1

First published: 21 Aug 2023, **8**:359 https://doi.org/10.12688/wellcomeopenres.19810.1

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; Tineoidea; Tineidae; Tineinae; *Monopis*; *Monopis laevigella* (Denis & Schiffermüller, 1775) (NCBI:txid691988).

Background

The Skin Moth *Monopis laevigella* (Denis & Schiffermüller, 1775) is a moth of the Tineidae family. Its English vernacular name is derived from the feeding habits of the larvae, which feed on a wide range of animal-derived matter such as bird nests, carrion, owl pellets, and bird guano (Boyes, 2018b; Pelham-Clinton, 1985). Consequently, the species is extremely widespread within the British Isles, even being found in the archipelagos of St Kilda, Orkney, and Shetland (Pelham-Clinton, 1985). Globally the species has a Holarctic distribution, being found in Europe, North America (formerly identified there as *M. rusticella*), and Asia, east to Shaanxi Province in China (Xiao & Houhun, 2006). The species is found widely in the north Atlantic, being abundant in Iceland and recorded from Greenland. In the Faroe Islands, the species is thought to be synanthropic, breeding on animal matter such as wool in unheated outbuildings (Kaaber, 2010). By contrast, the population in St Kilda appears to breed on the sea cliffs rather than around (former) human habitation, presumably feeding on the guano of seabirds (Pelham-Clinton, 1985).

Larvae feed within a silken tunnel on the larval foodstuff. Adults in the south of the British Isles can be found in two overlapping broods between April and September, however in Scotland there is typically just one brood, June to August (Boyes, 2018b). Adult moths typically have a blueish-grey appearance with irroration of paler scales, and a yellowish head. There is variation in the degree of irroration and St Kildan specimens show a brown head, a rare phenotype in the nearest landmass, the Outer Hebrides (Pelham-Clinton, 1985). Adults fly after dark and are often encountered at light, but the species can be bred in abundance (sometimes hundreds of adults emerging) from bird nests, apparently showing a preference for 'closed' nests such as those of tits (Paridae) (Boyes, 2018a; Boyes & Lewis, 2019). They can also be netted at dusk readily around rabbit warrens (J. Hammond, personal observation).

Monopis laevigella is not unique in its seemingly unusual choice of foodstuff and indeed many members of its family, including species of economic importance such as the *Tinea* and *Tineola* 'clothes moths', feed as larvae on non-vegetable matter such as fungi, lichens, and animal detritus. A genome of *Monopis laevigella* will contribute to our understanding of the evolution of the diversity of larval foodstuff in the Tineidae, and possibly reveal genes with biotechnological application involved in the digestion of animal polymers.

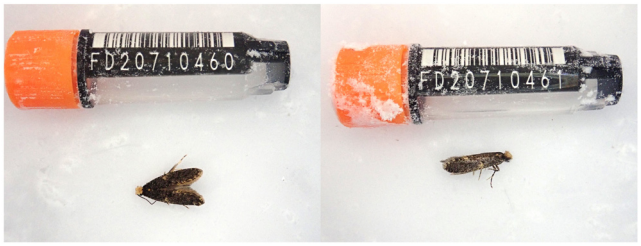

Figure 1. Photographs of the *Monopis laevigella* specimens used for genome sequencing.

Genome sequence report

The genome was sequenced from one female *Monopis laevigella* (Figure 1) collected from Wytham Woods, Oxfordshire. A total of 40-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 11 missing joins or mis-joins and removed 10 haplotypic duplications, reducing the assembly length by 0.55% and the scaffold number by 28%, and increasing the scaffold N50 by 8.75%.

The final ilMonLaev1.1 assembly has a total length of 632.1 Mb in 36 sequence scaffolds with a scaffold N50 of 26.5 Mb and the ilMonLaev2.1 assembly has a total length of 625.5 Mb in 55 sequence scaffolds with a scaffold N50 of 24.6 Mb (Table 1). For both assemblies, most of the assembly sequence was assigned to 25 chromosomal-level scaffolds, representing 24 autosomes and the Z sex chromosome. Chromosome-scale scaffolds confirmed by the Hi-C data are named in order of size (Figure 2–Figure 5; Table 2 and Table 3). Both specimens have ZO karyotype. 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 ilMonLaev1.1 assembly is 68.5 with *k*-mer completeness of 100%, and the assembly has a BUSCO v5.3.2 completeness of 95.5% (single = 94.6%, duplicated = 0.9%), using the lepidoptera_odb10 reference set (n = 5,286).

The estimated Quality Value (QV) of the final ilMonLaev2.1 assembly is 67.1 with *k*-mer completeness of 100%, and the assembly has a BUSCO v5.3.2 completeness of 95.4% (single = 94.4%, duplicated = 1.0%), 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/691988.

Table 1. Genome data for *Monopis laevigella*.

Project accession data		
Assembly identifier	ilMonLaev1.1	ilMonLaev2.1
Species	*Monopis laevigella*	*Monopis laevigella*
Specimen	ilMonLaev1.1	ilMonLaev2
NCBI taxonomy ID	691988	691988
BioProject	PRJEB56368	PRJEB56368
BioSample ID	SAMEA10979206	SAMEA10979208
Isolate information	ilMonLaev1, female	ilMonLaev2, female
Assembly metrics*	**ilMonLaev1.1**	**ilMonLaev2.1**
Consensus quality (QV) (≥ *50)*	68.5	67.1
k-mer completeness (≥ *95%)*	100%	100%
BUSCO** (*C* ≥ *95%)*	C:95.5%[S:94.6%,D:0.9%], F:0.8%,M:3.7%,n:5,286	C:95.4%[S:94.4%,D:1.0%],F:0.9%,M:3.7%,n:5,286
Percentage of assembly mapped to chromosomes (≥ *95%)*	99.92%	99.68%
Sex chromosomes (*localised homologous pairs)*	Z chromosome	Z chromosome
Organelles (*complete single alleles)*	Mitochondrial genome assembled	Mitochondrial genome assembled
Raw data accessions		
PacificBiosciences SEQUEL II	ERR10395967	ERR10355983, ERR10395967
Hi-C Illumina	ERR10313051	Data from ilMonLaev1
Genome assembly		
Assembly accession	GCA_947458855.1	GCA_947359445.1
Accession of alternate haplotype	GCA_947458865.1	GCA_947359455.1
Span (Mb)	632.1	625.5
Number of contigs	109	149
Contig N50 length (Mb)	12.8	11.6
Number of scaffolds	36	55
Scaffold N50 length (Mb)	26.5	24.6
Longest scaffold (Mb)	37.4	37.1

* 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/ilMonLaev1.1/dataset/CANHBR01/busco.

Methods

Sample acquisition and nucleic acid extraction

Bird's nest material was collected from Wytham Woods, Oxfordshire (biological vice-county: Berkshire), UK (latitude 51.77, longitude –1.34) by Douglas Boyes (University of Oxford) on 2021-06-16. Two *Monopis laevigella* specimens (specimen numbers Ox001943 and Ox001944; individuals ilMonLaev1 and ilMonLaev2) were reared from birds' nest material and identified by Douglas Boyes. The specimens were preserved on dry ice.

DNA was extracted at the Tree of Life laboratory, Wellcome Sanger Institute (WSI). The ilMonLaev1 sample was weighed and dissected on dry ice with tissue set aside for Hi-C sequencing.

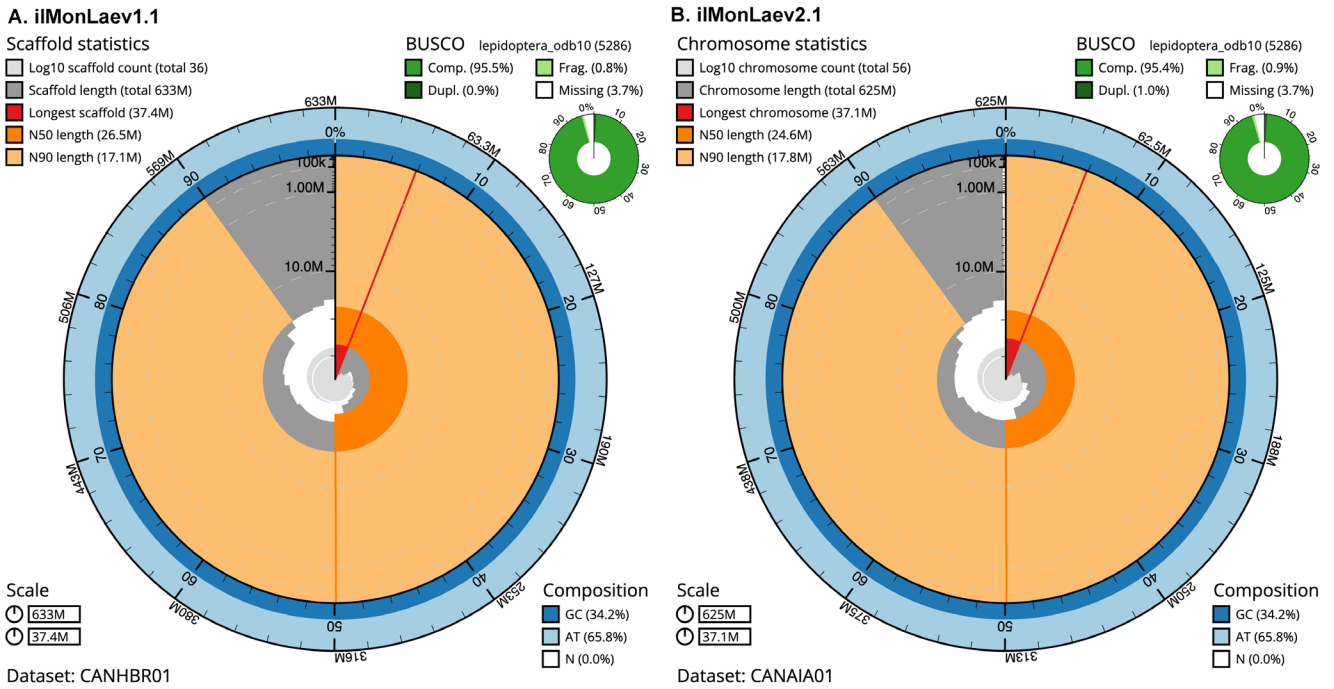

Figure 2. Genome assembly of *Monopis laevigella:* metrics for **A**. ilMonLaev1.1 and **B**. ilMonLaev2.1. The BlobToolKit Snailplot shows N50 metrics and BUSCO gene completeness. The main plot is divided into 1,000 size-ordered bins around the circumference with each bin representing 0.1% of the assembly. The distribution of scaffold lengths is shown in dark grey with the plot radius scaled to the longest scaffold present in the assembly shown in red. Orange and pale-orange arcs show the N50 and N90 scaffold lengths 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. Interactive versions of these figures may be viewed for ilMonLaev1.1 and ilMonLaev2.1.

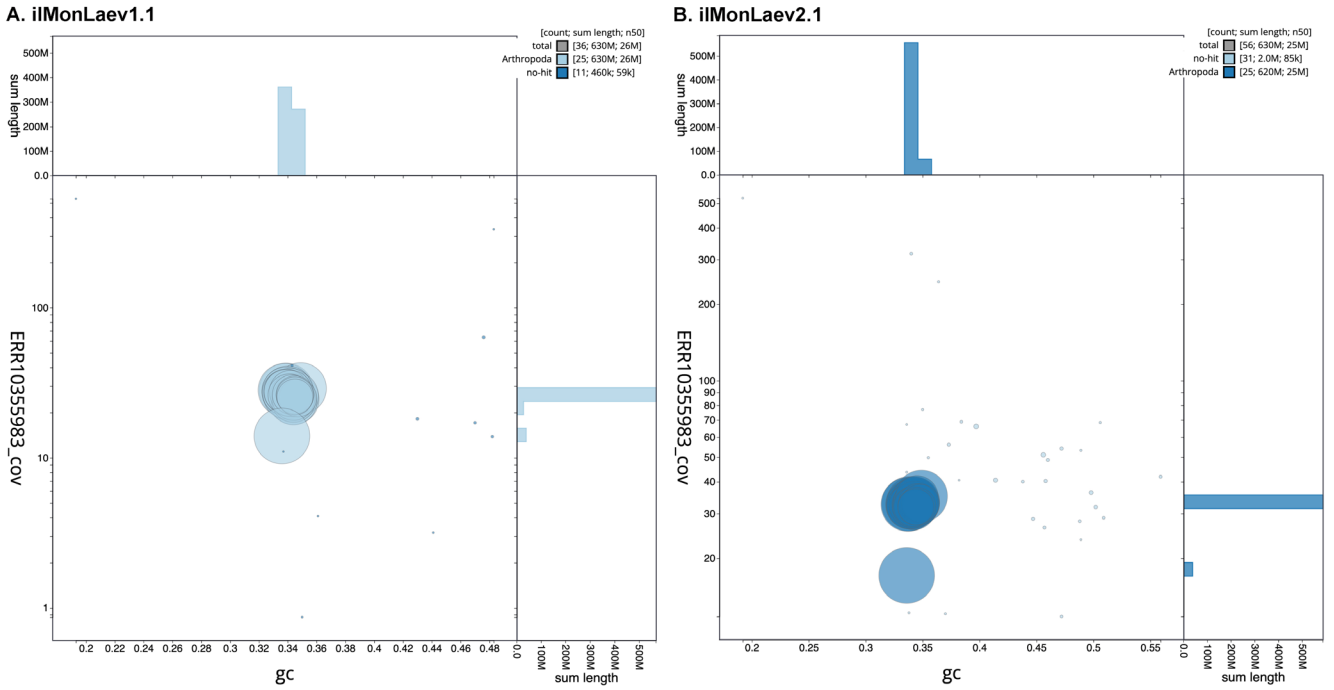

Figure 3. Genome assembly of *Monopis laevigella*: BlobToolKit GC-coverage plots for **A**. ilMonLaev1.1 and **B**. ilMonLaev2.1. Scaffolds are coloured by phylum. Circles are sized in proportion to scaffold length. Histograms show the distribution of scaffold length sum along each axis. Interactive versions of these figures may be viewed for ilMonLaev1.1 and ilMonLaev2.1.

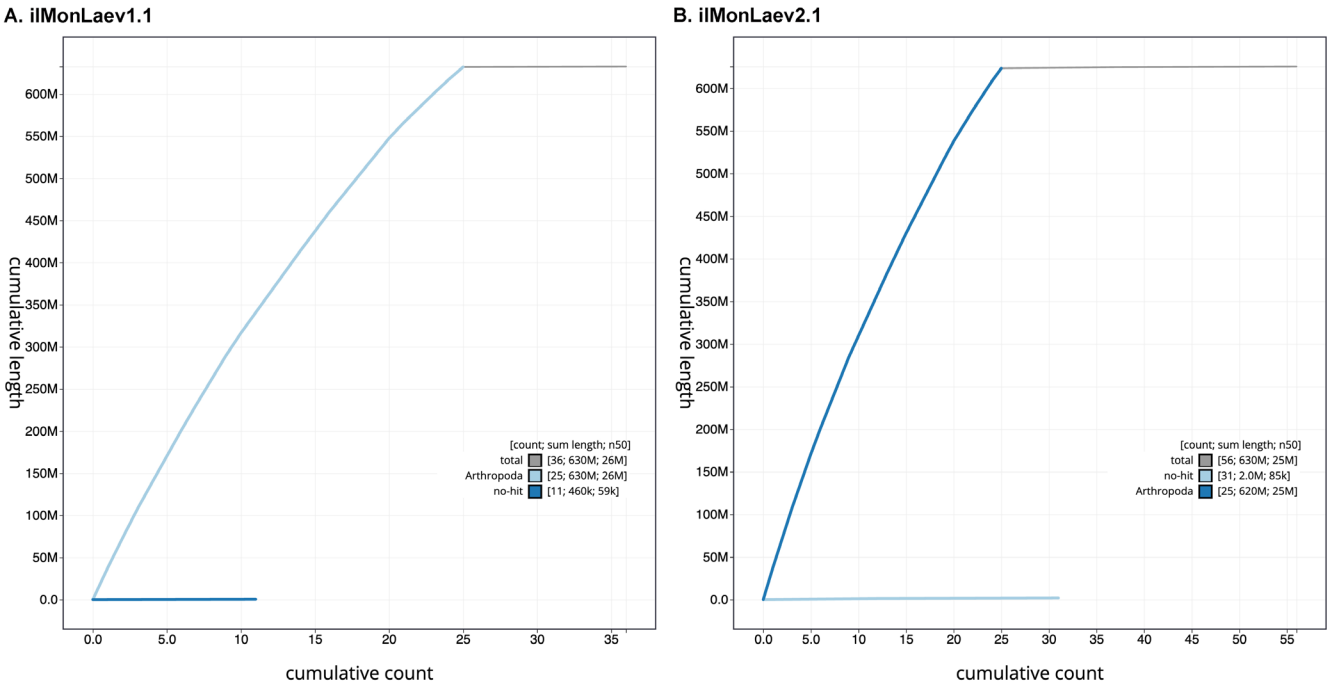

Figure 4. Genome assembly of *Monopis laevigella* for **A**. ilMonLaev1.1 and **B**. ilMonLaev2.1: BlobToolKit cumulative sequence plot. The grey line shows cumulative length for all scaffolds. Coloured lines show cumulative lengths of scaffolds assigned to each phylum using the buscogenes taxrule. Interactive versions of these figures may be viewed for ilMonLaev1.1 and ilMonLaev2.1.

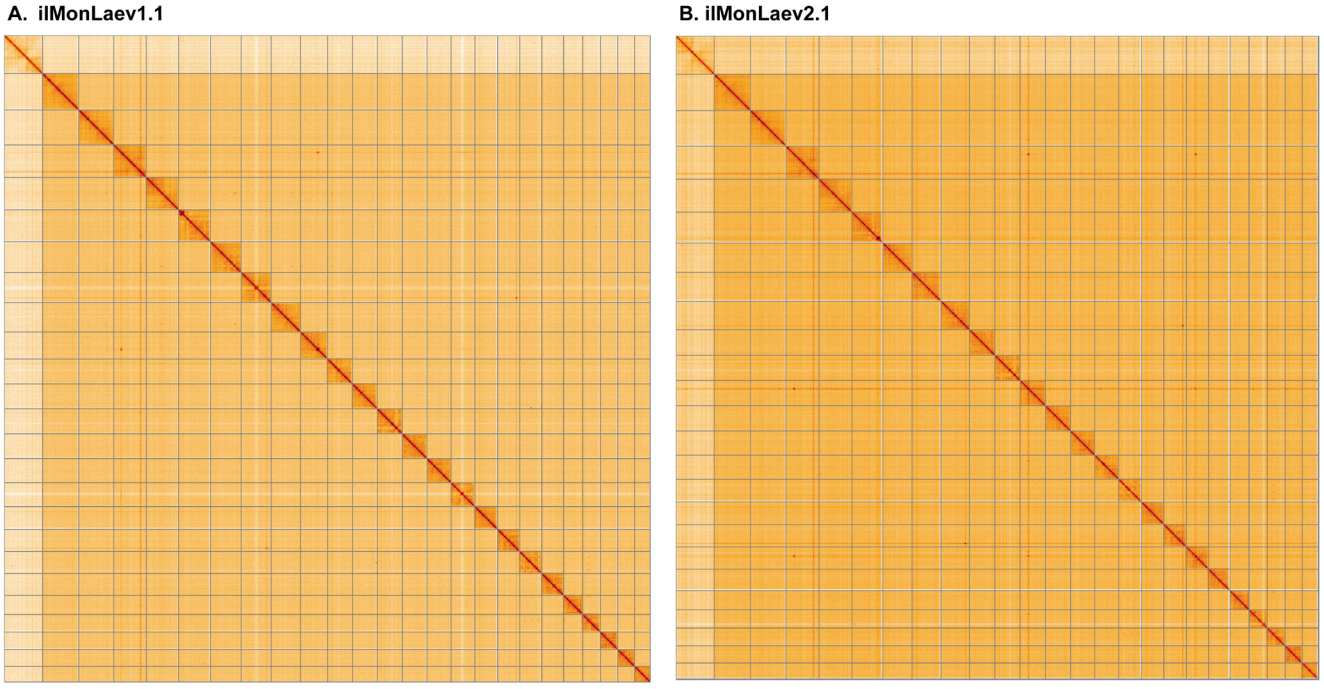

Figure 5. Genome assembly of *Monopis laevigella*: Hi-C contact map of **A**. ilMonLaev1.1 and **B**. ilMonLaev2.1 assemblies visualised using HiGlass. Chromosomes are shown in order of size from left to right and top to bottom. Interactive versions of these figures may be viewed for ilMonLaev1.1 and ilMonLaev2.1.

Table 2. Chromosomal pseudomolecules in the genome assembly of *Monopis laevigella*, ilMonLaev1.

INSDC accession	Chromosome	Size (Mb)	GC%
OX381577.1	1	35.39	33.9
OX381578.1	2	34.37	33.8
OX381579.1	3	31.71	34.9
OX381580.1	4	31.59	34
OX381581.1	5	31.24	34.4
OX381582.1	6	30.03	34.4
OX381583.1	7	29.42	34.2
OX381584.1	8	28.76	33.9
OX381585.1	9	26.46	34.4
OX381586.1	10	24.38	33.9
OX381587.1	11	24.34	34.2
OX381588.1	12	24.32	33.8
OX381589.1	13	24.28	33.9
OX381590.1	14	23.58	33.9
OX381591.1	15	23.38	34.4
OX381592.1	16	22.17	34.3
OX381593.1	17	21.68	34.2
OX381594.1	18	21.55	34.4
OX381595.1	19	21.43	34.1
OX381596.1	20	18.71	34.3
OX381597.1	21	17.1	34.7
OX381598.1	22	17.02	34.5
OX381599.1	23	16.47	34.5
OX381600.1	24	15.32	34.5
OX381576.1	Z	37.43	33.6
OX381601.1	MT	0.02	19.3

Table 3. Chromosomal pseudomolecules in the genome assembly of *Monopis laevigella*, ilMonLaev2.

INSDC accession	Chromosome	Length (Mb)	GC%
OX375840.1	1	35.34	34.0
OX375841.1	2	34.35	33.5
OX375842.1	3	32.14	35.0
OX375843.1	4	31.96	34.0
OX375844.1	5	29.84	34.5
OX375845.1	6	28.43	34.0
OX375846.1	7	28.05	34.5
OX375847.1	8	27.72	34.5
OX375848.1	9	24.71	34.0
OX375849.1	10	24.56	34.0
OX375850.1	11	24.49	34.5
OX375851.1	12	24.37	34.0
OX375852.1	13	23.54	34.0
OX375853.1	14	23.33	34.0
OX375854.1	15	21.92	34.5
OX375855.1	16	21.89	34.0
OX375856.1	17	21.82	34.5
OX375857.1	18	21.51	34.5
OX375858.1	19	20.81	34.0
OX375859.1	20	18.53	34.0
OX375860.1	21	17.75	34.5
OX375861.1	22	17.3	35.0
OX375862.1	23	16.65	34.5
OX375863.1	24	15.39	34.5
OX375839.1	Z	37.09	33.5
OX375864.1	MT	0.02	19.0

Whole organism 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' 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 tissue of ilMonLaev1 that had been set aside, using the Arima2 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 contamination and corrected using the gEVAL system (Chow *et al.*, 2016) as described previously (Howe *et al.*, 2021). Manual curation was performed using gEVAL, HiGlass (Kerpedjiev *et al.*, 2018) and Pretext (Harry, 2022). The mitochondrial genome was assembled using MitoHiFi (Uliano-Silva *et al.*, 2023), 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, 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 4 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 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)

Table 4. Software tools: versions and sources.

Software tool	Version	Source
BlobToolKit	4.0.7	https://github.com/blobtoolkit/blobtoolkit
BUSCO	5.3.2	https://gitlab.com/ezlab/busco
gEVAL	N/A	https://geval.org.uk/
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

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: *Monopis laevigella* (skin moth). Accession number PRJEB56368; https://identifiers.org/ena.embl/PRJEB56368. (Wellcome Sanger Institute, 2022)

The genome sequence is released openly for reuse. The *Monopis laevigella* 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

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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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