DATA NOTE

The genome sequence of a black lacewing, *Nothochrysa capitata* (Fabricius, 1793) (Neuroptera: Chrysopidae)

[version 1; peer review: 2 approved]

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Abstract

We present a genome assembly from an individual female *Nothochrysa capitata* (a black lacewing; Arthropoda; Insecta; Neuroptera; Chrysopidae). The assembly contains two haplotypes with total lengths of 688.43 megabases and 587.48 megabases. Most of haplotype 1 (78.72%) is scaffolded into 8 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 16.43 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

Nothochrysa capitata; black lacewing; genome sequence; chromosomal; Neuroptera

This article is included in the Tree of Life gateway.

Open Peer Review

Approval Status ✓ ✓

	1	2
version 1 24 Nov 2025	✓ view	✓ view

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Species taxonomy

Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Neuropterida; Neuroptera; Hemerobiiformia; Chrysopidae; Nothochrysinae; *Nothochrysa*; *Nothochrysa capitata* (Fabricius, 1793) (NCBI:txid1504855)

Background

Nothochrysa capitata (Fabricius, 1793) is one of approximately 21 species of Chrysopidae in Britain and Ireland. This family is often referred to by the common name of the Green Lacewings, but the adults of the genus *Nothochrysa* are brown, rather than green. They share other characteristic traits with other members of the Chrysopidae such as holding their wings in a tent-like position over the body (Plant, 1997), having carnivorous larvae and laying stalked eggs on vegetation (Aspöck *et al.*, 1980).

N. capitata is primarily associated with conifers, where they lay their eggs on pine needles (Killington, 1937), however adults have also been found associated with oaks (Barnard *et al.*, 1986). It is widespread and common in England and Wales, with records from Scotland but not Ireland (NBN Atlas Partnership, 2025; Plant, 1994).

As well as their orange/brown colouration, *Nothochrysa* species differ from the remaining British and Irish Chrysopidae fauna by having the prominent Pseudomedia and Pseudocubitus veins running parallel to the hind wing margin, as apposed to reaching the wings at the rear margin. *N. capitata* is distinguished from the much less common *N. fulviceps* as it lacks the pale longitudinal stripe on the thorax, and the toothed base of the claw that *N. fulviceps* has. *N. capitata* is also a smaller species, with a wingspan of 20–35 mm, in comparison to excess of 40 mm in *N. fulviceps* (Plant, 1997).

No Chrysopidae from Europe have at this moment been assessed for risk of extinction by the IUCN, but this common, well researched species with a wide distribution has not been flagged as a conservation concern in the literature.

Much work has been conducted in recent years on the phylogeny of the Chrysopidae based on morphology (e.g. Breitkreuz *et al.*, 2021) and DNA sequences (e.g. Garzón-Orduña *et al.*, 2019). This work has provided support for many previously established relationships within the family while also initiating some areas of taxonomic reclassification. The publication of the first genome sequence of *Nothochrysa capitata* genome will facilitate further studies into the phylogeny and taxonomy of this family.

Methods

Sample acquisition and DNA barcoding

The specimen used for genome sequencing was an adult female *Nothochrysa capitata* (specimen ID NHMUK015060358, ToLID inNotCapi1; Figure 1), collected from Beinn Eighe National Nature Reserve, Scotland, United Kingdom (latitude 57.63, longitude –5.35) on 2022-08-23. The specimen was collected by Vladimir Blagoderov and identified by Gavin Broad. For the Darwin Tree of Life sampling and metadata approach, refer to Lawniczak *et al.* (2022).

Figure 1. Photographs of the *Nothochrysa capitata* (inNotCapi1) 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 inNotCapi1 sample was weighed and triaged to determine the appropriate extraction protocol. Tissue from the head and thorax 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 12.08 ng/μL and a yield of 567.76 ng, with a fragment size of 15.3 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 tissue from the head and thorax of the inNotCapi1 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 were created. 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 7 breaks and 39 joins, which reduced the scaffold count by 0.8% and increased the total assembly length by 0.6%. 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 *Nothochrysa capitata* specimen generated 20.95 Gb (gigabases) from 2.15 million reads, which were used to assemble the genome. GenomeScope2.0 analysis estimated the haploid genome size at 607.80 Mb, with a heterozygosity of 0.14% and repeat content of 29.82% (Figure 2). These estimates guided expectations for the assembly. Based on the estimated genome size, the sequencing data provided approximately 33× coverage. Hi-C sequencing produced 141.29 Gb from 935.68 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 688.43 Mb in 1 527 scaffolds, with 71 gaps, and a scaffold N50 of 61.89 Mb (Table 2).

Most of the assembly sequence (78.72%) was assigned to 8 chromosomal-level scaffolds, representing 6 autosomes and the W and Z sex chromosomes. These chromosome-level scaffolds,

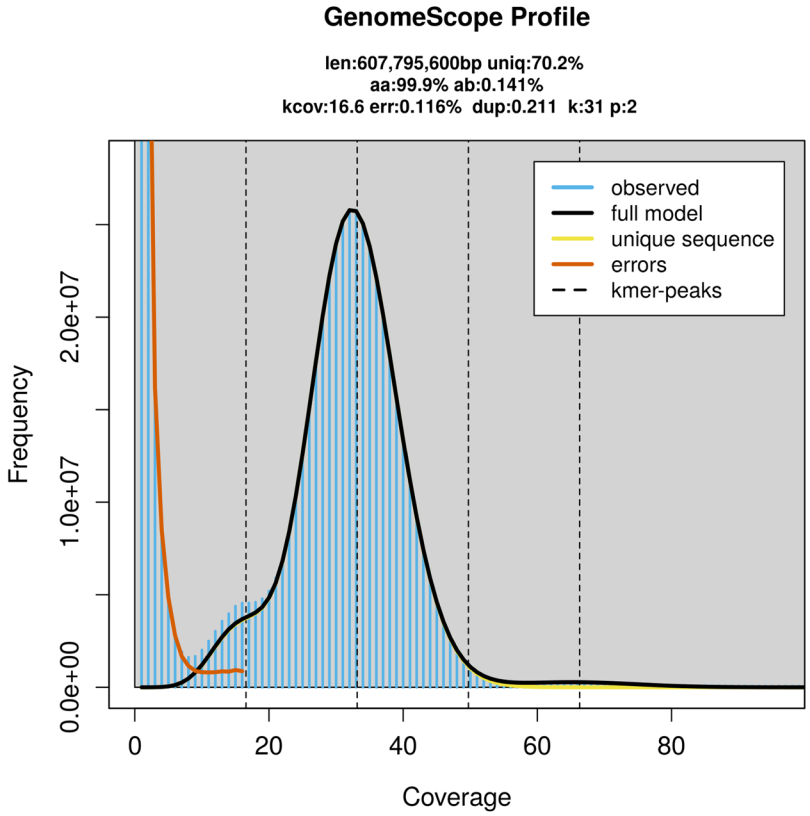

Figure 2. Frequency distribution of *k*-mers generated using GenomeScope2. The plot shows observed and modelled *k*-mer spectra, providing estimates of genome size, heterozygosity, and repeat content based on unassembled sequencing reads.

Table 1. **Specimen and sequencing data for BioProject PRJEB87451.**

Platform	PacBio HiFi	Hi-C
ToLID	inNotCapi1	inNotCapi1
Specimen ID	NHMUK015060358	NHMUK015060358
BioSample (source individual)	SAMEA115574593	SAMEA115574593
BioSample (tissue)	SAMEA115599612	SAMEA115599612
Tissue	head and thorax	head and thorax
Instrument	Revio	Illumina NovaSeq X
Run accessions	ERR14835536	ERR14782876
Read count total	2.15 million	935.68 million
Base count total	20.95 Gb	141.29 Gb

Table 2. **Genome assembly statistics.**

Metric	Haplotype 1	Haplotype 2
Assembly name	inNotCapi1.hap1.1	inNotCapi1.hap2.1
Assembly accession	GCA_965240235.1	GCA_965239645.1
Assembly level	chromosome	scaffold
Span (Mb)	688.43	587.48
Number of chromosomes	8	scaffold-level
Number of contigs	1 598	1 191
Contig N50	19.0 Mb	18.98 Mb
Number of scaffolds	1 527	1 145
Scaffold N50	61.89 Mb	93.13 Mb
Longest scaffold length (Mb)	123.56	-
Sex chromosomes	W and Z	-
Organelles	Mitochondrion: 16.43 kb	-

confirmed by Hi-C data, are named according to size (Figure 3; Table 3). The sex chromosomes Z and W were identified by copy number and read coverage. Contigs on chromosome Z (0–987 kbp) and chromosome W (2.8-8.1 Mbp) have uncertain order and orientation. Additional sequence of the W chromosome might be in the unscaffolded sequences.

The mitochondrial genome was also assembled (length 16.43 kb, OZ251095.1). 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 57.2, and for haplotype 2, 56.9. When the two haplotypes are combined, the assembly achieves an estimated QV of 57.1. The *k*-mer completeness is 96.74% for haplotype 1, 92.41% for haplotype 2, and 99.29% for the combined haplotypes (Figure 4).

BUSCO analysis using the endopterygota_odb10 reference set (n = 2 124) identified 97.2% of the expected gene set (single = 96.3%, duplicated = 0.9%) 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 **7.7.Q57**.

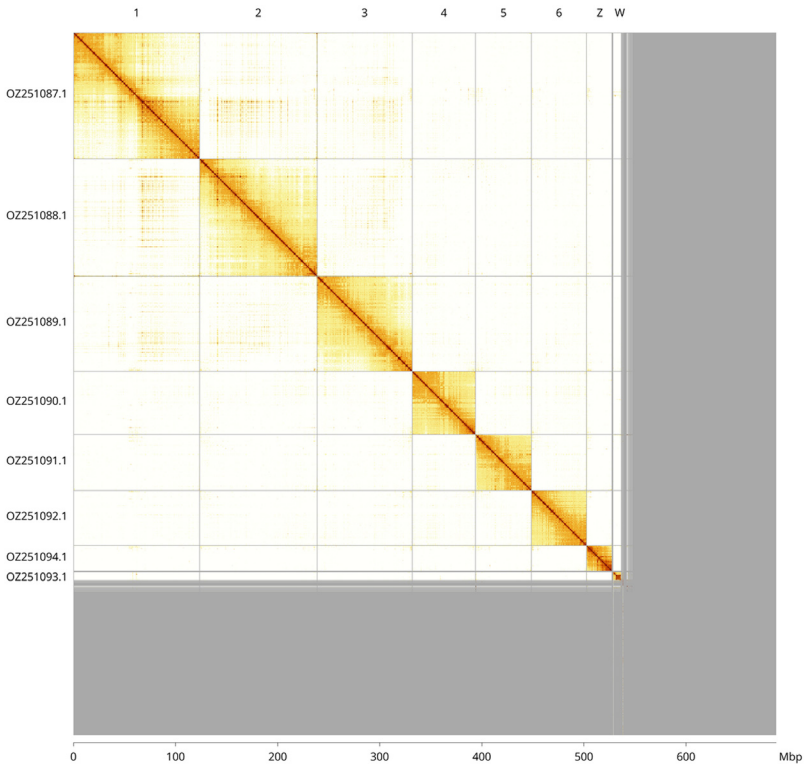

Figure 3. Hi-C contact map of the *Nothochrysa capitata* genome assembly. Assembled chromosomes are shown in order of size and labelled along the axes, with a megabase scale shown below. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *Nothochrysa capitata* inNotCapi1.

INSDC accession	Molecule	Length (Mb)	GC%
OZ251087.1	1	123.56	28.50
OZ251088.1	2	115.09	28.50
OZ251089.1	3	93.32	28.50
OZ251090.1	4	61.89	28.50
OZ251091.1	5	54.82	28.50
OZ251092.1	6	53.99	28.50
OZ251093.1	W	13.49	27.50
OZ251094.1	Z	25.80	29.50

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.

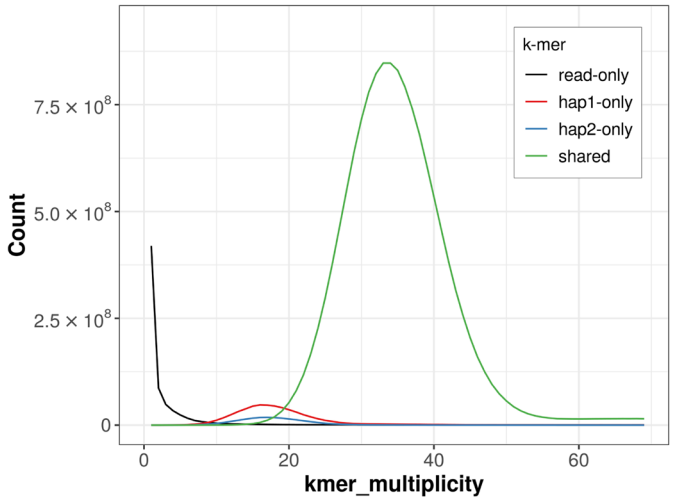

Figure 4. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the final assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers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

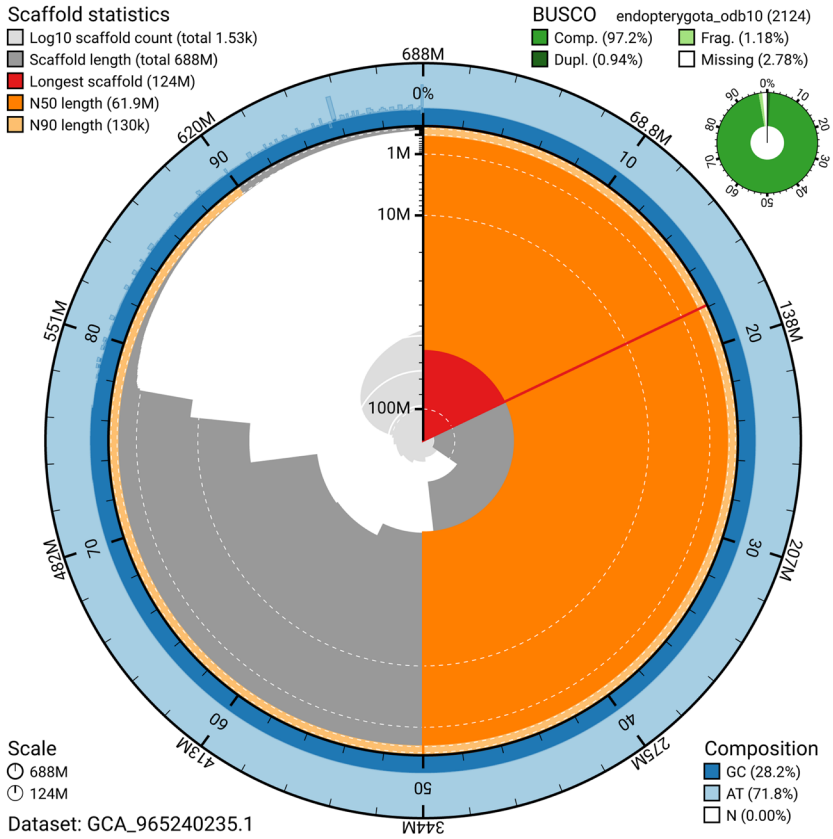

Figure 5. Assembly metrics for inNotCapi1.hap1.1. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the whole genome sequence, and the main plot is divided into 1 000 bins around the circumference. The outermost 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.

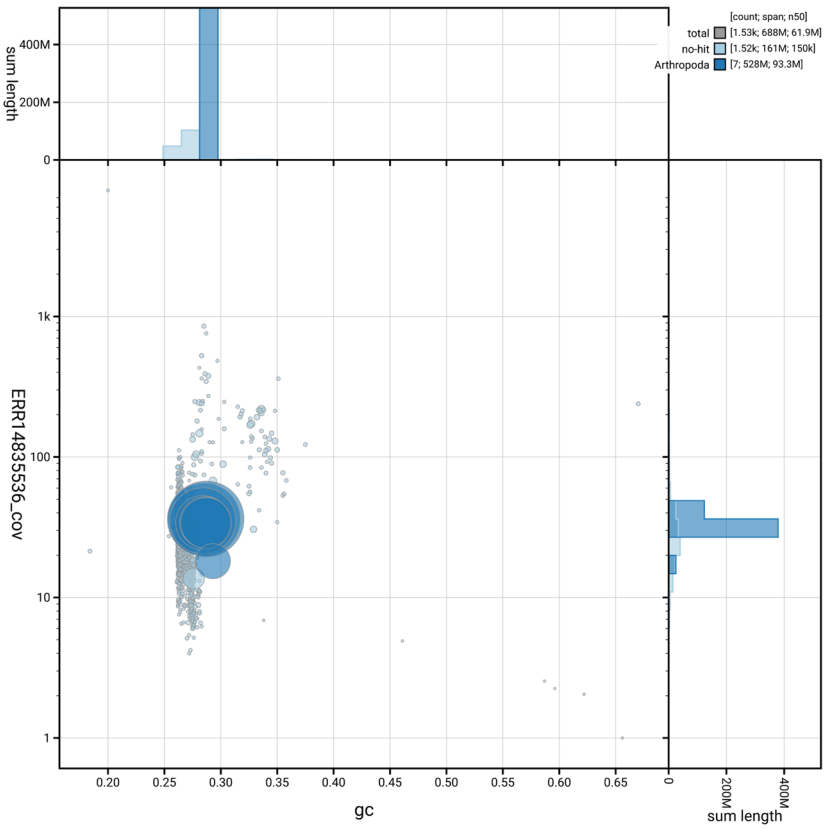

Figure 6. BlobToolKit GC-coverage plot for inNotCapi1.hap1.1. Blob plot showing sequence coverage (vertical axis) and GC content (horizontal axis). The circles represent scaffolds, with the size proportional to scaffold length and the colour representing phylum membership. The histograms along the axes 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 *Nothochrysa capitata* assembly.

Measure	Value	Benchmark
EBP summary (haplotype 1)	7.7.Q57	6.C.Q40
Contig N50 length	19 Mb	≥ 1 Mb
Scaffold N50 length	61.89 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 57.2; haplotype 2: 56.9; combined: 57.1	≥ 40
k-mer completeness	Haplotype 1: 96.74%; Haplotype 2: 92.41%; combined: 99.29%	≥ 95%
BUSCO	C:97.2% [S:96.3%; D:0.9%]; F:1.2%; M:1.6%; n:2 124	S > 90%; D < 5%
Percentage of assembly assigned to chromosomes	78.72%	≥ 90%

Data availability

European Nucleotide Archive: Nothochrysa capitata. Accession number PRJEB87451. The genome sequence is released openly for reuse. The *Nothochrysa capitata* genome sequencing initiative is part of the Darwin Tree of Life Project (PRJEB40665) and the Sanger Institute Tree of Life Programme (PRJEB43745). 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	4.4.5	https://github.com/blobtoolkit/blobtoolkit
BUSCO	5.7.1	https://gitlab.com/ezlab/busco
bwa-mem2	2.2.1	https://github.com/bwa-mem2/bwa-mem2
Cooler	0.8.11	https://github.com/open2c/cooler
DIAMOND	2.1.8	https://github.com/bbuchfink/diamond
fasta_windows	0.2.4	https://github.com/tolkit/fasta_windows
FastK	1.1	https://github.com/thegenemyers/FASTK
GenomeScope2.0	2.0.1	https://github.com/tbenavi1/genomescope2.0
Gfastats	1.3.6	https://github.com/vgl-hub/gfastats
Hifiasm	0.19.8-r603	https://github.com/chhylp123/hifiasm
HiGlass	1.13.4	https://github.com/higlass/higlass
MerquryFK	1.1.2	https://github.com/thegenemyers/MERQURY.FK
Minimap2	2.28-r1209	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	24.10.4	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	1.21	https://github.com/samtools/samtools
sanger-tol/ascc	0.1.0	https://github.com/sanger-tol/ascc
sanger-tol/blobtoolkit	v0.7.1	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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PubMed Abstract | Publisher Full Text | Free Full Text

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Reference Source

Barnard PC, Brooks SJ, Stork NE: **The seasonality and distribution of Neuroptera, Raphidioptera and Mecoptera on oaks in Richmond Park, Surrey, as revealed by insecticide knock-down sampling.** *Journal of Natural History.* 1986; **20**(6): 1321–1331.
Publisher Full Text

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Version 1

Reviewer Report 14 January 2026

https://doi.org/10.21956/wellcomeopenres.27775.r143569

✔ **Jan Veenstra**
University of Bordeaux, Pessac, France

This is yet another high quality genome assembly from Welcome Open Research. It is sometimes annoying that you have to write something, as in general the comments could be as simple as: "Great work, thanks a lot for doing this". This time I actually have a, really minor, comment to make. So here it comes:

The "but" in the sentence: "No Chrysopidae from Europe have at this moment been assessed for risk of extinction by the IUCN, but this common, well researched species with a wide distribution has not been flagged as a conservation concern in the literature." seems weird to me, as I do not see a contrast between the first and second part of the sentence.

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: Insect neuropeptides

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 13 January 2026

https://doi.org/10.21956/wellcomeopenres.27775.r143567

Matsapume Detcharoen
Division of Biological Science, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla, Thailand, Hat Yai, Thailand

This note reports a high-quality genome assembly of Nothochrysa capitata, generated using PacBio HiFi and Hi-C data as part of the Darwin Tree of Life project. The authors produce a chromosome-level assembly for one haplotype, including identification of the W and Z sex chromosomes, and provide extensive quality metrics demonstrating high completeness and consensus accuracy.

The manuscript is clearly written. Assembly quality is high, with BUSCO completeness >97% and transparent reporting of curation steps.

A brief explanatory sentence on the chromosome assignment benchmark in Table 4 between 78.72% vs 90% target would improve clarity for readers.

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, applied biology

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.