



GENOME NOTE

The genome sequence of the Star Sedge, *Carex echinata*

Murray (Poales: Cyperaceae)

[version 1; peer review: 1 approved]

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Abstract

We present a genome assembly of *Carex echinata* (Star Sedge; Streptophyta; Magnoliopsida; Poales; Cyperaceae). The assembly consists of two haplotypes with total lengths of 378.73 megabases and 369.81 megabases. Most of the haplotype 1 assembly (99.91%) was scaffolded into 29 chromosomal pseudomolecules. Haplotype 2 was assembled to scaffold level. The mitochondrial genome assembly has a length of 1637.33 kilobases and the plastid genome assembly has a length of 179.09 kilobases. Gene annotation of the haplotype 1 assembly by Ensembl identified 27,157 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

Carex echinata, Star Sedge, genome sequence, chromosomal, Poales



This article is included in the [Tree of Life gateway](#).

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Species taxonomy

Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Cyperaceae; Cyperoideae; Cariceae; *Carex*; *Carex* subgen. *Vignea*; *Carex echinata* Murray (NCBI:txid234467)

Background

The Star Sedge, *Carex echinata* Murray (Figure 1), has a wide native distribution across the temperate Northern Hemisphere, as well as in Sumatra, New Guinea, south-eastern Australia, New Zealand and southern Chile (POWO, 2026).

It is a perennial sedge that grows in seasonally or permanently waterlogged habitats on acidic to base-rich substrates. In Britain and Ireland, it grows in mires, wet heaths, upland flushes and springs, as well as rush-pastures, wet meadows and flushed grassland on hill slopes. It is also found, rarely, in wet woodland rides. It occurs from sea level to 1,166 m on Ben More in Mid Perthshire (Porter & Foley, 2023).

The species was lost from many 10 km squares (hectads) in lowland England during the nineteenth century through drainage and agricultural improvement of wetlands. These losses continued through much of the twentieth century. However, it is still abundant in upland regions elsewhere in Britain and Ireland, where suitable habitat persists (Porter & Foley, 2023).

Reported chromosome counts vary, but most records in the Chromosome Counts Database (CCDB) give sporophytic counts of $2n = 56$ or 58 (Rice *et al.*, 2015).

We sequenced the genome of *Carex echinata* as part of the Darwin Tree of Life Project, which aims to generate high-quality reference genomes for all named eukaryotic species in Britain and Ireland to support research, conservation, and the sustainable use of biodiversity. The sequenced specimen was collected from Balavil Fen, Insh Marshes, East Inverness-Shire, Scotland, UK.



Figure 1. Photograph of *Carex echinata* from Gniewino Commune, NW Poland; this is not the sequenced specimen.

Photograph: Krzysztof Ziarnek, CC BY-SA 4.0.

Methods

Sample acquisition, flow cytometry and DNA barcoding

A specimen of *C. echinata* (specimen ID EDTOL06281, ToLID lpCarEchi2) was used for genome sequencing. It was collected from Balavil Fen, Insh Marshes, East Inverness-Shire, Scotland, UK (latitude 57.099, longitude -3.9789) on 2023-07-19. The specimen was collected by José Ignacio Márquez-Corro and Andy Griffiths and identified by José Ignacio Márquez-Corro. The herbarium voucher for the sequenced plant (collector number DAG13) is deposited at Edinburgh ([E01358572](#)).

The genome size was estimated by flow cytometry following the ‘one-step’ method outlined in [Pellicer et al. \(2021\)](#) and using propidium iodide as the fluorochrome. The General Purpose Buffer (GPB) supplemented with 3% PVP was used for isolation of nuclei ([Loureiro et al., 2007](#)), and the internal calibration standard was *Solanum lycopersicum* L. ‘Stupické polní rané’ with an assumed 1C-value of 968 Mb ([Doležel et al., 2007](#)).

The initial identification was verified by an additional DNA barcoding process according to the framework developed by [Twyford et al. \(2024\)](#). Part of the plant specimen was preserved in silica gel desiccant ([Chase & Hills, 1991](#)). DNA extracted from the dried plant was amplified by PCR for standard barcode markers, with the amplicons sequenced and compared to public sequence databases including GenBank and the Barcode of Life Database (BOLD) ([Ratnasingham & Hebert, 2007](#)). Following whole-genome sequencing, 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

High molecular weight (HMW) DNA extraction protocols developed by the Tree of Life Core Laboratory at the Wellcome Sanger Institute (WSI) are available on [protocols.io](#) ([Howard et al., 2025](#)). Tissue from the lpCarEchi2 sample was weighed and [triaged](#) to select the appropriate extraction workflow. Tissue from the leaf and stem was homogenised by [cryogenic bead beating](#). HMW DNA was extracted using the [Automatic Sorbitol Washing + Plant Organic Extraction](#) 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), using AMPure PB beads (Pacific Biosciences) and the Thermo Fisher KingFisher™ Apex to eliminate shorter fragments and concentrate the DNA.

The concentration of the sheared and purified DNA was assessed with a NanoDrop spectrophotometer and a Qubit Fluorometer using the Qubit dsDNA High Sensitivity Assay kit. Fragment size distribution was evaluated by running the sample on the Femto Pulse system. For this sample, final post-shearing DNA measurements included a Qubit concentration of 17.7 ng/μL, an average fragment size of 18.4 kb and a yield of 917.80 ng.

PacBio HiFi library preparation and sequencing

Library DTOL15205173 was prepared with the SMRTbell Prep Kit 3.0 (Pacific Biosciences) according to 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 with a Qubit Fluorometer v4.0 (Thermo Fisher 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 library was sequenced on a Revio instrument (Pacific Biosciences, California, USA). The prepared libraries selected for multiplexing were pooled based on genome size, library molarity, and the intended plex level. Primers were annealed and polymerases were bound to generate circularised complexes, following the manufacturer’s instructions. Complexes were purified using SMRTbell beads, diluted to the Revio loading concentration, and spiked with a Revio sequencing internal control. The pooled libraries were sequenced on a Revio 25M Plex SMRT cell in a 4-plex run.

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

Hi-C data were generated from the lpCarEchi2 leaf | stem sample using the Arima-HiC v2 kit (Arima Genomics). Tissue was finely ground using the Covaris cryoPREP Dry Pulverizer (Covaris), and then subjected to nuclei isolation. Nuclei were isolated using

a modified protocol based on the Qiagen QProteome Cell Compartment Kit (Qiagen), in which only the Lysis and CE2 buffers were used, with QIAshredder spin columns. After isolation, nuclei were fixed using formaldehyde to a final concentration of 2% to crosslink the DNA. The crosslinked DNA was then digested and biotinylated according to the manufacturer's instructions. A clean-up step was performed with SPRIselect beads before library preparation. DNA concentration was quantified using the Qubit Fluorometer v4.0 (Thermo Fisher Scientific) and the Qubit HS Assay Kit, following the manufacturer's instructions.

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. Libraries were amplified with 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 to create 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. Libraries were sequenced on the Illumina NovaSeq X, generating paired-end 150-bp reads.

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](#). The k -mer frequency distribution was analysed with GenomeScope (version 2.1.0) ([Ranallo-Benavidez et al., 2020](#)), providing fitted point estimates of haploid genome size, heterozygosity and repeat content.

The HiFi reads were assembled using Hifiasm in Hi-C phasing mode ([Cheng et al., 2021, 2022](#)), producing two haplotypes. Hi-C reads ([Rao et al., 2014](#)) were mapped to 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](#); [Tegenfeldt et al., 2025](#)) and MerquyFK ([Rhie et al., 2020](#)). The organelle genomes were assembled using OATK ([Zhou et al., 2025](#)). The comparator for the mitochondrial assembly was the mitochondrial genome of *Carex neurocarpa* (OQ834962.1). The comparator for the plastid assembly was the chloroplast genome of *Carex paxii* (PP790563.1).

Assembly curation

The assembly was decontaminated using the Assembly Screen for Cobionts and Contaminants (ASCC) pipeline. The flat files and maps for curation were generated with [TreeVal](#). 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. \(2021\)](#). The two haplotype assemblies were combined for curation. Manual corrections included 29 breaks and 83 joins. This reduced the scaffold count by 52.5% and increased the scaffold N50 by 1.9%. The curation process is described at [sanger-tol/curation-resources](#). A Hi-C contact map of the haplotype 1 assembly was generated with PretextViewSnapshot.

Assembly quality assessment

The MerquyFK 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 database ($k = 31$) computed prior to genome assembly. The analysis outputs included assembly QV scores and completeness statistics.

The haplotype 1 assembly was assessed using BlobToolKit ([Challis et al., 2020](#)). PacBio reads were mapped to the assembly to derive sequence coverage, and BUSCO ([Manni et al., 2021](#)) was used to assess gene-set completeness. DIAMOND BLASTp searches of extracted BUSCO proteins and DIAMOND BLASTx searches of assembly sequences against UniProt Reference Proteomes ([Buchfink et al., 2021](#)), followed by BLASTn searches of sequences without DIAMOND BLASTx hits against the NCBI nt database ([Altschul et al., 1990](#)), supported taxonomic assignment. Coverage, sequence composition, taxonomic assignment and BUSCO results were integrated into a BlobDir for interactive inspection and visualisation. The snail and blob plots were rendered locally from this hosted BlobDir using BlobTk v0.8.3. The scaffold-length radial scale function for the snail plot was set to linear ([Challis & Blaxter, 2026](#)). The blob plot used circular markers with area proportional to scaffold length ([Challis et al., 2020](#)).

Genome sequence report

Sequence data

The genome of a specimen of *C. echinata* was sequenced using Pacific Biosciences single-molecule HiFi long reads, generating 16.97 Gb (gigabases) from 1.37 million reads. These reads were used to assemble the genome. GenomeScope analysis using a $p = 2$ model gave a k -mer-based haploid genome size estimate of 375.10 Mb, with heterozygosity of 0.16% and repeat content of 30.76%; the full-model fit was 96.56% (Figure 2). Using flow cytometry, the genome size (1C-value) of the sample was estimated to be 0.46 pg, equivalent to 450.00 Mb. These estimates guided expectations for the assembly. The NCBI assembly record reports 43× genome coverage. Hi-C sequencing produced 118.12 Gb from 391.13 million read pairs, which were used to scaffold the haplotype 1 assembly. Table 1 summarises the specimen and sequencing details.

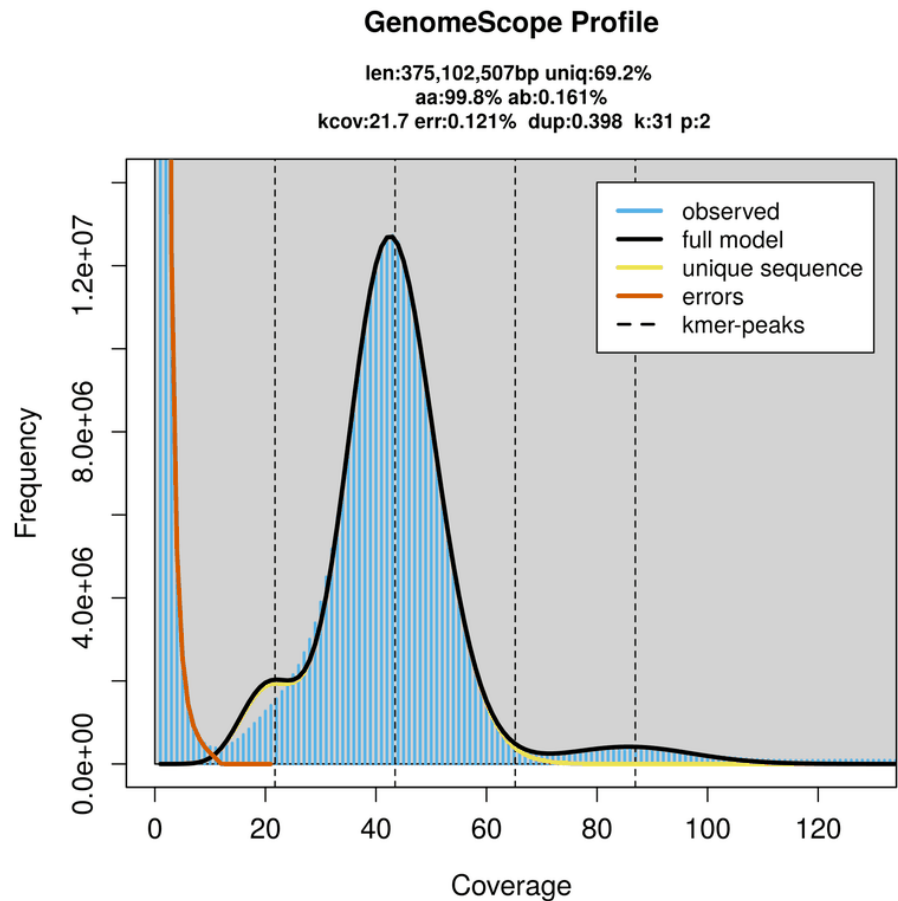


Figure 2. GenomeScope model fitted to the k -mer frequency distribution. The plot shows the observed and modelled k -mer spectra used to estimate haploid genome size, heterozygosity and repeat content from unassembled sequencing reads.

Table 1. Specimen and sequencing data for *C. echinata* (BioProject [PRJEB88758](#))

Platform	PacBio HiFi	Hi-C
ToLID	lpCarEchi2	lpCarEchi2
Specimen ID	EDTOL06281	EDTOL06281
BioSample (source individual)	SAMEA114782725	SAMEA114782725
BioSample (tissue)	SAMEA114788133	SAMEA114788133
Tissue	leaf, stem	leaf stem

Platform	PacBio HiFi	Hi-C
Instrument	Revio	Illumina NovaSeq X
Library ID & run accession(s)	DTOL15205173: ERR14886543	SQPP-59463-T:C6: ERR14895954
Read count total	1.37 million reads	391.13 million read pairs
Base count total	16.97 Gb	118.12 Gb

Assembly statistics

The genome was assembled into two haplotypes using Hi-C phasing. The haplotype 1 assembly was curated to chromosome level, while haplotype 2 was assembled to scaffold level. The haplotype 1 assembly, which is proposed as the reference assembly for this species, has a total length of 378.73 Mb in 36 scaffolds (excluding organelle sequences), with 47 gaps, and its scaffold N50 is 13.58 Mb (Table 2). The scaffold auN for the haplotype 1 assembly is 13.4 Mb.

Table 2. Genome assembly statistics for *C. echinata*

Genome assembly	Haplotype 1	Haplotype 2
Assembly name	lpCarEchi2.hap1.1	lpCarEchi2.hap2.1
Assembly accession	GCA_965279795.1	GCA_965279845.1
Assembly level	chromosome	scaffold
Span (Mb)	378.73	369.81
Number of chromosomes	29	-
Number of contigs	83	88
Contig N50 (Mb)	11.29	9.09
Number of scaffolds (excluding organelle sequences)	36	31
Scaffold N50 (Mb)	13.58	13.32
Scaffold auN (Mb)	13.4	13.2
Longest scaffold length (Mb)	18.19	18.28
Organelles	Mitochondrial genome: 1,637.33 kb; - Plastid genome: 179.09 kb	

Most of the haplotype 1 assembly sequence (99.91%) was assigned to 29 chromosome-level scaffolds. These chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 3; Table 3).

The mitochondrial genome (length 1637.33 kb, OZ257389.1) and plastid genome (length 179.09 kb, OZ257390.1) were also assembled. These sequences are included as contigs in the multifasta file of the haplotype 1 genome submission and as standalone records.

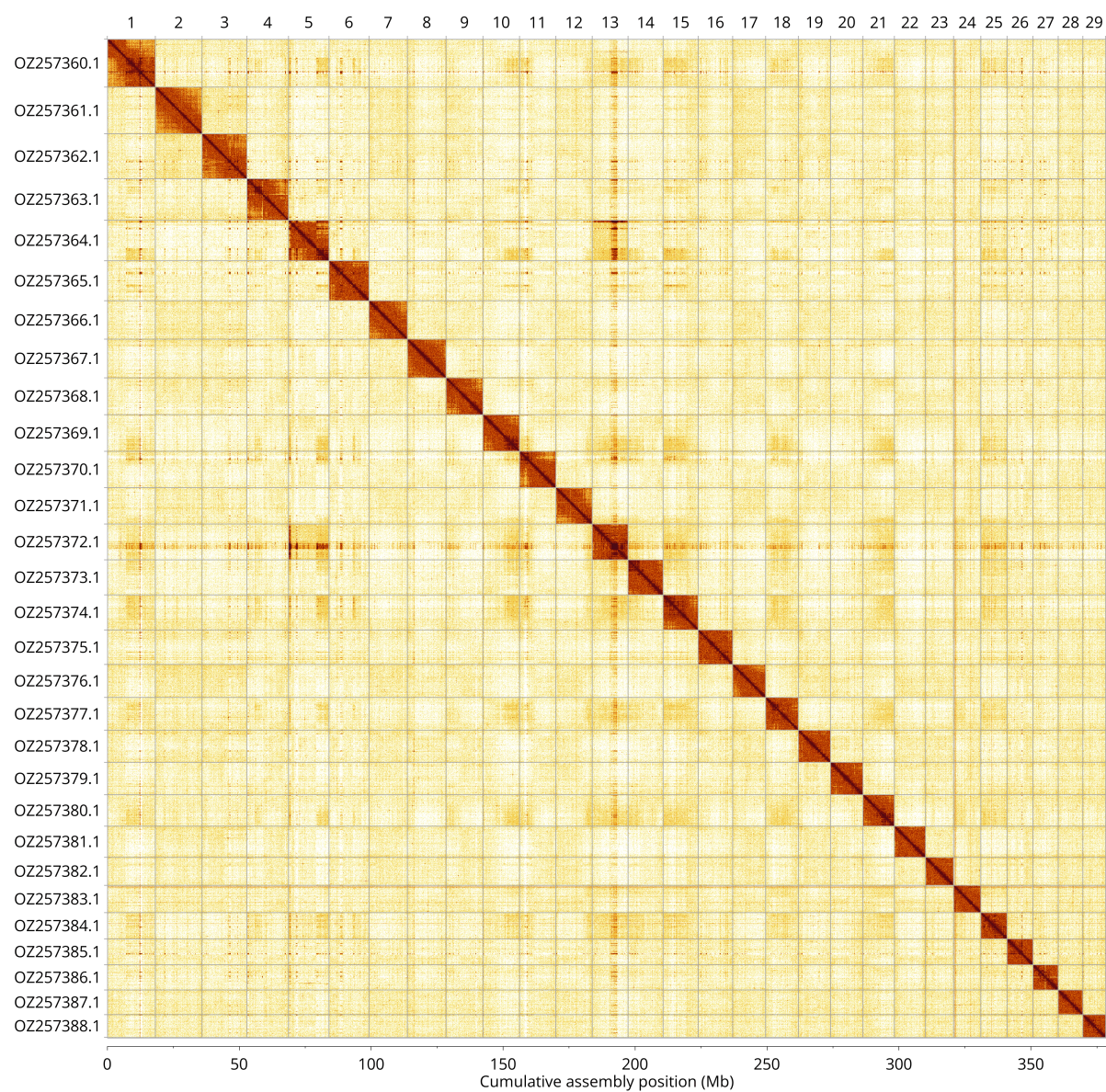


Figure 3. Hi-C contact map of the *C. echinata* haplotype 1 assembly. Assembled chromosomes are shown in order of size and labelled along the axes, with a megabase scale shown below. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the haplotype 1 genome assembly of *C. echinata* IpCarEchi2

INSDC accession	Molecule	Length (Mb)	GC%
OZ257360.1	1	18.19	35
OZ257361.1	2	17.71	34.50
OZ257362.1	3	17.01	34.50
OZ257363.1	4	15.78	35.50
OZ257364.1	5	15.32	36.50
OZ257365.1	6	15.14	35
OZ257366.1	7	14.61	34.50

INSDC accession	Molecule	Length (Mb)	GC%
OZ257367.1	8	14.59	34.50
OZ257368.1	9	13.98	34.50
OZ257369.1	10	13.92	35
OZ257370.1	11	13.76	34.50
OZ257371.1	12	13.73	34.50
OZ257372.1	13	13.58	37.50
OZ257373.1	14	13.33	34.50
OZ257374.1	15	13.28	35
OZ257375.1	16	13.03	34.50
OZ257376.1	17	12.48	34.50
OZ257377.1	18	12.38	34.50
OZ257378.1	19	12.27	34.50
OZ257379.1	20	12.22	34.50
OZ257380.1	21	11.90	35
OZ257381.1	22	11.86	34.50
OZ257382.1	23	10.59	34.50
OZ257383.1	24	10.40	34.50
OZ257384.1	25	9.85	35
OZ257385.1	26	9.85	34.50
OZ257386.1	27	9.59	35
OZ257387.1	28	9.32	35
OZ257388.1	29	8.72	34.50

Assembly quality metrics

For the haplotype 1 assembly, the estimated QV is 66.1, and for the haplotype 2 assembly, 65.3. When the two haplotypes are combined, the assembly achieves an estimated QV of 65.7. The *k*-mer completeness is 98.07% for the haplotype 1 assembly, 96.57% for the haplotype 2 assembly, and 99.27% for the combined haplotypes (Figure 4).

BUSCO analysis using the poales_odb12 reference set ($n = 6,282$) identified 97.9% of the expected gene set (single = 94.7%, duplicated = 3.2%) in the haplotype 1 assembly using BUSCO v.6.1.0. For the haplotype 2 assembly, BUSCO v.6.0.0 analysis using poales_odb12 identified 97.2% of the expected gene set (single = 93.7%, duplicated = 3.5%).

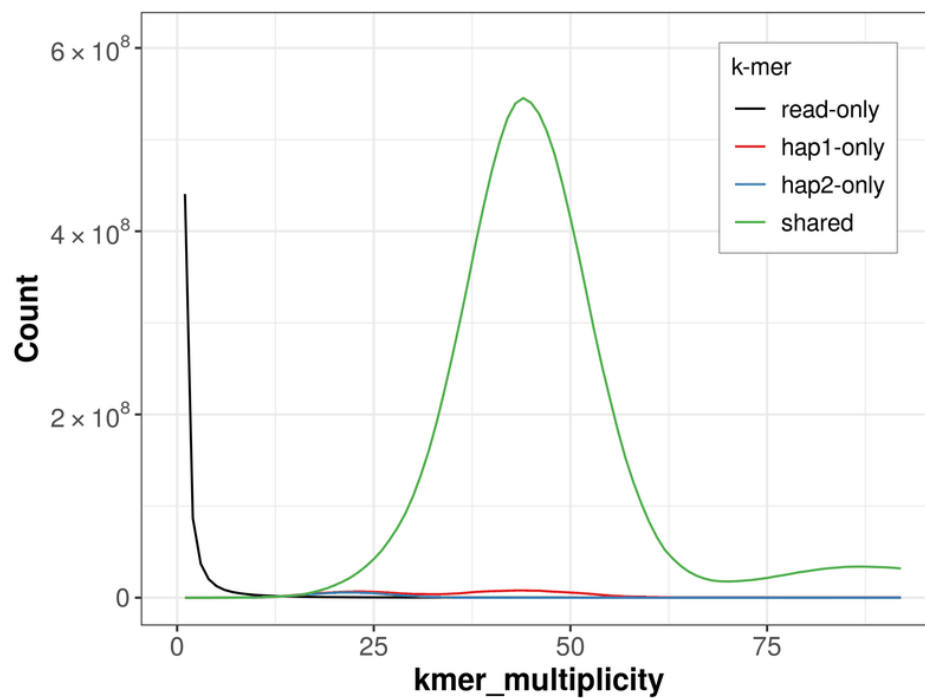


Figure 4. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the haplotype 1 assembly, the haplotype 2 assembly and the combined haplotypes. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers that appear in the reads but are not assembled, while the remaining curves correspond to *k*-mers recovered in the assemblies shown.

The snail plot in Figure 5 provides a summary of assembly contiguity, cumulative scaffold count, sequence composition and BUSCO completeness for the haplotype 1 assembly (Challis & Blaxter, 2026). The relative sizes of the longest scaffold, scaffold N50 and N90, together with the dark-grey scaffold-length distribution, show how much of the assembly is contained in long scaffolds. The outer composition track shows variation in GC, AT and N content, while the central track shows the cumulative scaffold count and the BUSCO inset summarises gene-set completeness. The BlobToolKit snail plot retains the earlier poales_odb10 assessment (80.0% complete), whereas the updated haplotype 1 result reported here uses poales_odb12 (97.9% complete).

The blob plot in Figure 6 displays scaffolds from the haplotype 1 assembly by GC proportion and base coverage. Marker area is proportional to scaffold length, and colour indicates taxonomic assignment (Challis *et al.*, 2020).

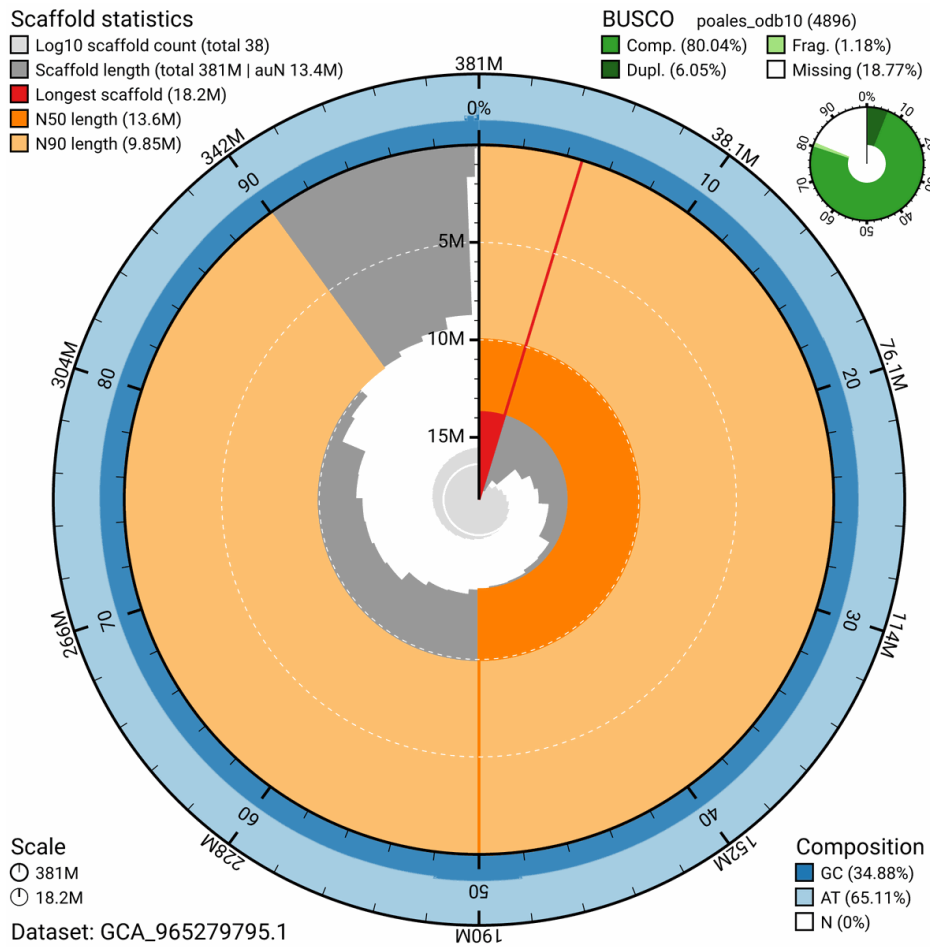


Figure 5. Assembly metrics for IpCarEchi2.hap1.1, the haplotype 1 assembly. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the haplotype 1 assembly, and the main plot is divided into 1,000 bins around the circumference. 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. Scaffold length is shown on a linear radial scale, scaled to the longest scaffold. Red shading indicates the longest scaffold, and the deeper orange and pale orange shading represent the N50 and N90 lengths. The summary statistics include scaffold auN, the area under the scaffold Nx curve. The 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 poales_odb10 set is presented at the top right. The assembly can be explored interactively in the [BlobToolKit viewer](#).

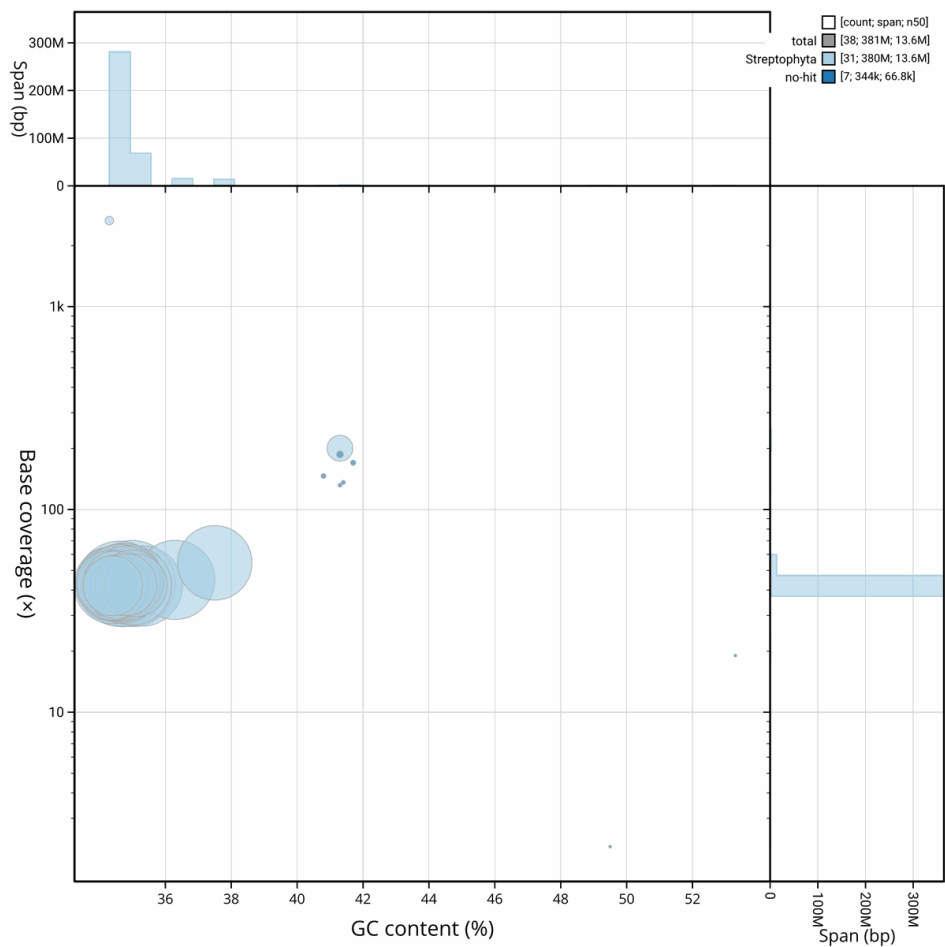


Figure 6. BlobToolKit blob plot for IpCarEchi2.hap1.1, the haplotype 1 assembly. The plot shows base coverage (vertical axis) and GC content (horizontal axis). Circles represent scaffolds; marker area is proportional to scaffold length, and colour indicates taxonomic assignment. The histograms along the axes display the total length of sequences distributed across different levels of coverage and GC content. The assembly can be explored interactively in the [BlobToolKit viewer](#).

Table 4 presents assembly quality metrics alongside the Earth BioGenome Project (EBP) benchmarks described by [Howe et al.. \(2026\)](#). The three-part EBP metric calculated for the haplotype 1 assembly is **7.C.Q66**.

Table 4. Earth BioGenome Project summary metrics for the *C. echinata* assembly

Measure	Value	Benchmark
EBP summary (haplotype 1)	7.C.Q66	6.C.Q40
Contig N50 length	11.29 Mb	> 1 Mb
Scaffold N50 length	13.58 Mb	= chromosome N50
Consensus quality (QV)	Haplotype 1: 66.1; haplotype 2: 65.3; combined: 65.7	# 40
k-mer completeness	Haplotype 1: 98.07%; Haplotype 2: 96.57%; combined: 99.27%	> 90% (combined assembly)
BUSCO	Haplotype 1: C:97.9% [S:94.7%, D:3.2%], F:0.7%, M:1.3%, n:6,282;	C > 90%

Measure	Value	Benchmark
Percentage of assembly assigned to chromosomes	Haplotype 2: C:97.2% [S:93.7%, D:3.5%], F:0.7%, M:2.0%, n:6,282 99.91%	# 90%

Notes: The EBP summary uses log10(Contig N50); chromosome-level (C) or log10(Scaffold N50); Q (Mercury QV). For *k*-mer completeness, the benchmark is assessed using the combined assembly value. Haplotype 1: BUSCO v6.1.0 using the poales_odb12 lineage dataset; Haplotype 2: BUSCO v6.0.0 using the poales_odb12 lineage dataset: C=complete; S=single-copy; D=duplicated; F=fragmented; M=missing; n=orthologues. The BUSCO benchmark for plants uses total completeness (C) to accommodate biological duplication, as an adaptation of the EBP single-copy benchmark.

Genome annotation report

The *C. echinata* genome assembly (GCA_965279795.1) was annotated by Ensembl at the European Bioinformatics Institute (EBI). The annotation comprises 61,701 transcripts from 27,157 protein-coding genes and 13,585 non-coding genes. The average transcript length is 3,180.77 bp, with an average of 1.51 coding transcripts per gene and 4.90 exons per transcript. For further information about the annotation, please refer to the [annotation page](#) on Ensembl.

Data availability

European Nucleotide Archive: *Carex echinata* (star sedge). Accession number [PRJEB88758](#); <https://identifiers.org/ena.embl/PRJEB88758>. The genome sequence is released openly for reuse. The *C. echinata* genome sequencing initiative is part of the Darwin Tree of Life Project ([PRJEB40665](#)), Sanger Institute Tree of Life Programme ([PRJEB43745](#)) and AEGIS ([PRJEB80366](#)). All raw sequence data and the haplotype assemblies have been deposited in INSDC databases. Raw data and assembly accession identifiers are reported in Table 1 and Table 2.

Pipelines used for genome assembly at the WSI Tree of Life are available at <https://pipelines.tol.sanger.ac.uk/pipelines>. Table 5 lists software versions used in this study.

Table 5. Software versions and sources

Software	Version	Source
BLAST	2.14.0	https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/
BlobToolKit	4.4.6	https://github.com/genomehubs/blobtoolkit
BlobTk (hosted BlobDir)	0.5.1	https://github.com/genomehubs/blobtk
BlobTk (snail and blob plot renderer)	0.8.3	https://github.com/genomehubs/blobtk
BUSCO	5.8.3; 6.0.0; 6.1.0	https://gitlab.com/ezyab/busco
bwa-mem2	2.2.1	https://github.com/bwa-mem2/bwa-mem2
DIAMOND	2.1.8	https://github.com/bbuchfink/diamond
fasta_windows	0.2.4	https://github.com/tolkit/fasta_windows
FastK	1.2	https://github.com/thegenemyers/FASTK
GenomeScope	2.1.0	https://github.com/tbenavi1/genomescope2.0
Gfastats	1.3.6	https://github.com/vgl-hub/gfastats
Hifiasm	0.19.8-r603	https://github.com/chhyllp123/hifiasm
HiGlass	1.13.4	https://github.com/higlass/higlass

Software	Version	Source
MercuryFK	1.1.0-c1	https://github.com/thegenemyers/MERQUERY.FK
Minimap2	2.28-r1209	https://github.com/lh3/minimap2
Oatk	0.9	https://github.com/c-zhou/oatk
MultiQC	1.14; 1.17 and 1.18	https://github.com/MultiQC/MultiQC
Nextflow	24.10.4	https://github.com/nextflow-io/nextflow
PretextSnapshot	0.0.6	https://github.com/sanger-tol/PretextSnapshot
PretextView	1.0.3	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	v0.8.0	https://github.com/sanger-tol/blobtoolkit
sanger-tol/curationpretext	1.4.2	https://github.com/sanger-tol/curationpretext
Seqtk	1.4-r122	https://github.com/lh3/seqtk
Singularity	3.9.0	https://github.com/sylabs/singularity
TreeVal	1.3.0	https://github.com/sanger-tol/treeval
YaHS	1.2.2	https://github.com/c-zhou/yahs

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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.

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Automated Benchmarking

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As this article is a Genome Note, Automated Benchmarking has been used to determine whether the reported assembly passes four defined checks established by the Earth BioGenome Project: the raw and assembled data are publicly available, the Earth BioGenome Project three-part metric is met, the k-mer completeness exceeds 90%, and the BUSCO score passes the stated threshold.

For *Carex echinata* (lpCarEchi2), all four checks passed.

Data available: pass. ENA study PRJEB88758, raw-read accessions ERR14886543 and ERR14895954, and assembly accessions GCA_965279795.1 and GCA_965279845.1 are public.

Earth BioGenome Project three-part metric: pass. Haplotype 1 is reported as 7.C.Q66, meeting the 6.C.Q40 reference standard.

k-mer completeness: pass. The combined haplotype assemblies have 99.27% k-mer completeness, exceeding the Earth BioGenome Project target of 90%.

BUSCO: pass. Haplotype 1, which is proposed as the reference assembly for this species, has 97.9% complete BUSCOs (94.7% single-copy and 3.2% duplicated). BUSCO software version: 6.1.0; lineage dataset: poales_odb12. It meets the plant-specific target of greater than 90% complete BUSCOs.

This decision uses values reported in the Genome Note and public accession records.

Competing Interests: This Automated Benchmarking peer-review report was generated automatically and relies on analyses performed by the Tree of Life programme, which also produced the Genome Note under review.

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.