GENOME NOTE

The genome sequence of Slender Tare, *Vicia parviflora* Cav. (Fabales: Fabaceae)

[version 1; peer review: 1 approved]

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Abstract

We present a genome assembly of *Vicia parviflora* (Slender Tare; Streptophyta; Magnoliopsida; Fabales; Fabaceae). The primary assembly has a total length of 2,826.49 megabases. Most of the primary assembly (99.62%) is scaffolded into 7 chromosomal pseudomolecules. The mitochondrial sequences have lengths of 341.49 and 64.57 kilobases and the plastid genome assembly has a length of 122.23 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

Vicia parviflora, slender tare, genome sequence, chromosomal, Fabales

This article is included in the Tree of Life gateway.

Open Peer Review

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	1
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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; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade; NPAAA clade; Hologalegina; IRL clade; Fabeae; *Vicia*; *Vicia parviflora* Cav. (NCBI:txid1053407)

Background

Vicia parviflora Cav., the Slender Tare, is an aptly named annual vetch in the family Fabaceae, native to Britain. This species sprawls over other vegetation or climbs using its simple leaf-tip tendrils to a height of about 60 cm. The stems and inflorescences are very slender, reminiscent of its more widespread relative, *Vicia tetrasperma* (L.) Schreb. (also known as *Ervum tetraspermum* L.). The two species are very similar, but *V. parviflora* generally has more flowers per inflorescence, larger flowers and fruits, and often more than four seeds per fruit (Stace, 2019).

Vicia parviflora grows on heavy calcareous clay soils that are frequently wet in winter but baked dry in summer. Its habitats include arable field margins, sunny banks, tracksides, woodland margins and urban waste ground. It also occurs in municipal flower beds (Stroh *et al.*, 2019).

In Britain, its native distribution is largely restricted to lowland southern England. It is absent from Wales, Scotland and Ireland, although it may be under-recorded because of confusion with *Vicia tetrasperma*. A BSBI species account published in 2015 lists it as Vulnerable in Great Britain.

Molecular evidence places *V. parviflora* and *V. tetrasperma* in a distinct clade for which recognition as the genus *Ervum* L. has been proposed (Schaeffer *et al.*, 2012). Under this classification, *V. parviflora* is treated as *Ervum gracile* DC., as adopted by Stace (2019).

Vicia parviflora is a diploid species with a chromosome count of $2n = 14$ (Henniges *et al.*, 2022).

We sequenced the genome of *Vicia parviflora* 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 Wytham Wood, Oxfordshire, UK (Figure 1).

Figure 1. The sequenced specimen of *Vicia parviflora*. Left: flowering plant in its habitat. Top right: developing pods, narrow leaflets and tendrils. Bottom right: detail of the pale purple flowers.

Methods

Sample acquisition, flow cytometry and DNA barcoding

A specimen of *V. parviflora* (specimen ID KDTOL10859, ToLID drVicParv1) was used for genome sequencing. It was collected from Wytham Wood, Oxfordshire, UK (latitude 51.7697, longitude −1.3302) on 2023-06-25. The specimen was collected by Maarten Christenhusz, Keith Kirby, Paul Kersey, José Ignacio Márquez-Corro and Ilia Leitch and identified by Maarten Christenhusz. A second specimen was used for Hi-C and RNA sequencing (specimen ID KDTOL10896, ToLID drVicParv2). It was collected from Wytham Wood, Oxfordshire, UK (latitude 51.7697, longitude −1.3302) on 2023-06-26. The specimen was collected by Maarten Christenhusz, Keith Kirby, Paul Kersey, José Ignacio Márquez-Corro and Ilia Leitch and identified by Maarten Christenhusz. The herbarium voucher for the sequenced plant (collector number MC9565) is deposited in the Herbarium, Royal Botanic Gardens, Kew (K), as specimen K001527197.

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 *Petroselinum crispum* 'Champion Moss Curled' with an assumed 1C-value of 2,200 Mb (Obermayer *et al.*, 2002).

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 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

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 drVicParv1 sample was weighed and triaged to select the appropriate extraction workflow. HMW DNA was prepared for one PacBio HiFi library: DTOL14860954. Tissue 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 following the Sanger Tree of Life Fragmented DNA clean up: Automated SPRI protocol.

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 196.0 ng/μL, and an average fragment size of 18.8 kb. The 260/280 spectrophotometric ratio was 1.86, and the 260/230 ratio was 2.35.

RNA was extracted from leaf tissue of drVicParv2 in the Tree of Life Laboratory at the WSI using the RNA Extraction: Automated MagMax™ *mir*Vana protocol. The RNA concentration was assessed with a NanoDrop spectrophotometer and a Qubit Fluorometer using the Qubit RNA Broad-Range Assay kit. RNA integrity was assessed using the Agilent RNA 6000 Pico Kit and Eukaryotic Total RNA assay.

PacBio HiFi library preparation and sequencing

Library preparation and sequencing took place in the WSI Scientific Operations core. Library DTOL14860954 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 in two runs on a Revio instrument (Pacific Biosciences, California, USA). Prepared libraries with a molarity greater than 2 nM were normalised to 2 nM, and 15 μL was used for making complexes. For libraries with a molarity below 2 nM, the available 10 μL library volume was used without normalisation. Primers were annealed and polymerases were bound to generate circularised complexes, following the manufacturer's instructions. Complexes were purified using 1.2× SMRTbell beads, diluted to the Revio loading concentration of 200–300 pM, and spiked with a Revio sequencing internal control. Sequencing used Revio 25M SMRT cells. SMRT Link software (Pacific Biosciences), a web-based workflow manager, was used to configure and monitor the runs and to carry out primary and secondary data analysis.

Hi-C

Sample preparation and crosslinking

Hi-C data were generated from the drVicParv2 leaf 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.

RNA library preparation and sequencing

Libraries were prepared with the NEBNext® Ultra II Directional RNA Library Prep Kit for Illumina (New England Biolabs), following the manufacturer's instructions. Poly(A) mRNA was isolated from 100 ng of total RNA using oligo(dT) beads, converted to cDNA, and uniquely indexed; 14 PCR cycles were performed. Libraries were prepared with an intended average fragment size of 100–300 bp. Libraries were quantified, normalised, and pooled equimolarly to a final concentration of 2.8 nM before dilution to 150 pM for loading. Sequencing was carried out on the Illumina NovaSeq X, generating paired-end 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 genome size, heterozygosity and repeat content.

The HiFi reads were assembled using Hifiasm (Cheng *et al.*, 2021) with the --primary option. The Hi-C reads (Rao *et al.*, 2014) were mapped to contigs using bwa-mem2 (Vasimuddin *et al.*, 2019), and the contigs were scaffolded in YaHS (Zhou *et al.*, 2023) with the --break option for handling potential misassemblies. The scaffolded assemblies were evaluated using Gfastats (Formenti *et al.*, 2022), BUSCO (Manni *et al.*, 2021) and MerquryFK (Rhie *et al.*, 2020).

The organelle genomes were assembled using OATK (Zhou *et al.*, 2025).

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). Manual corrections included 17 breaks and 36 joins. This reduced the scaffold count by 8.7% and reduced the scaffold N50 by 74.4%. The curation process is described at sanger-tol/curation-resources. A Hi-C contact map of the primary assembly was generated with PretextSnapshot.

Assembly quality assessment

The MerquryFK tool (Rhie *et al.*, 2020) was run in a Singularity container (Kurtzer *et al.*, 2017) to evaluate *k*-mer completeness and assembly quality for the primary and alternate haplotypes using the *k*-mer database ($k = 31$) computed prior to genome assembly. The analysis outputs included assembly QV scores and completeness statistics.

The primary assembly was assessed using BlobToolKit (Challis *et al.*, 2020). PacBio reads were mapped to the primary 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 *V. parviflora* was sequenced using Pacific Biosciences single-molecule HiFi long reads, generating 103.10 Gb (gigabases) from 6.88 million reads. We assembled the genome from these reads. GenomeScope analysis using a $p = 2$ model gave a *k*-mer-based haploid genome size estimate of 2,864.67 Mb, with heterozygosity of 0.05% and repeat content of 57.48%; the full-model fit was 98.50% (Figure 2). Using flow cytometry, the genome size (1C-value) of the sample was estimated to

be 3.26 pg, equivalent to 3,190.00 Mb. These estimates guided expectations for the assembly. The sequencing data provided reported coverage of 35× coverage of the genome. Hi-C sequencing produced 374.21 Gb from 1,239.11 million read pairs, which were used to scaffold the primary assembly. RNA sequencing data were also generated and are available in public sequence repositories. Table 1 summarises the specimen and sequencing details.

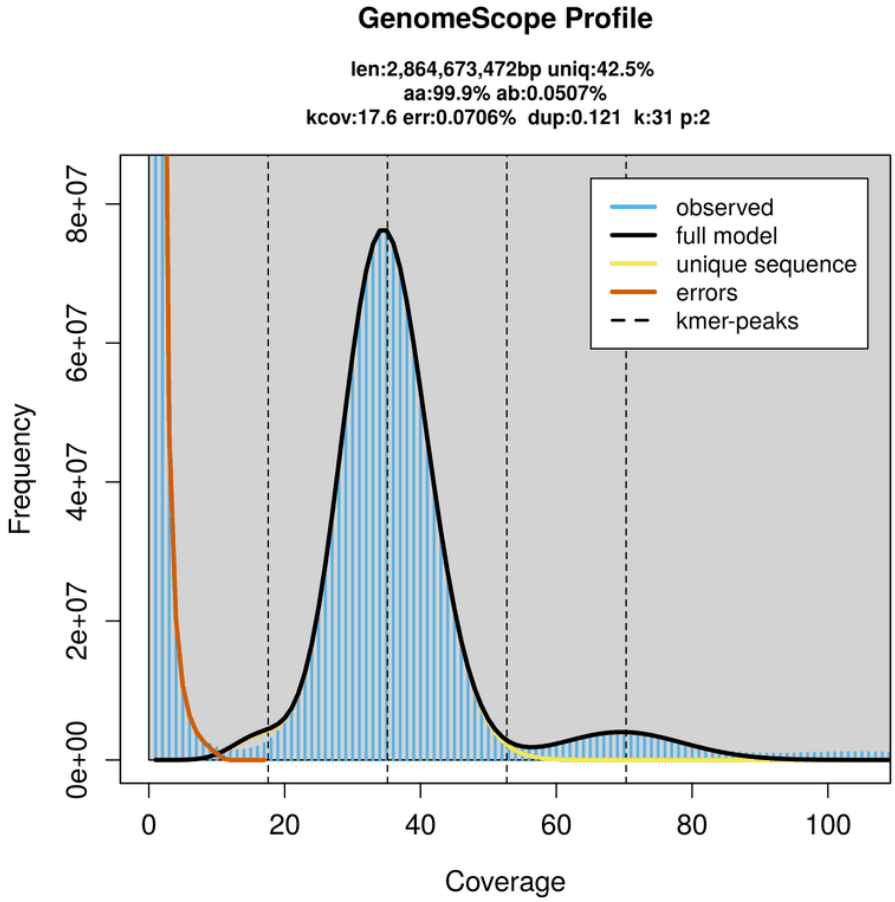

Figure 2. GenomeScope model fitted to the *k*-mer frequency distribution. The plot shows the observed and modelled *k*-mer spectra used to estimate genome size, heterozygosity and repeat content from unassembled sequencing reads.

Table 1. Specimen and sequencing data for *V. parviflora* (BioProject PRJEB80417)

Platform	PacBio HiFi	Hi-C	RNA-seq
ToLID	drVicParv1	drVicParv2	drVicParv2
Specimen ID	KDTOL10859	KDTOL10896	KDTOL10896
BioSample (source individual)	SAMEA114563337	SAMEA114563338	SAMEA114563338
BioSample (tissue)	SAMEA114563426	SAMEA114563427	SAMEA114563427
Tissue	leaf	leaf	leaf
Instrument	Revio (2 runs)	Illumina NovaSeq X	Illumina NovaSeq X
Library ID & run accession(s)	DTOL14860954: ERR13725956, ERR13725957	ERR13732198	ERR13962545
Read count total	6.88 million reads	1,239.11 million read pairs	42.26 million read pairs

Platform	PacBio HiFi	Hi-C	RNA-seq
Base count total	103.10 Gb	374.21 Gb	12.76 Gb

Assembly statistics

The primary assembly was generated and an alternate haplotype assembly was also deposited at contig level in INSDC databases. The primary assembly is proposed as the reference assembly for this species. It has a total length of 2,826.49 Mb in 164 scaffolds (excluding organelle sequences), with 1,128 gaps, and a scaffold N50 of 399.06 Mb (Table 2). The primary assembly has a scaffold auN of 405 Mb.

Table 2. Genome assembly statistics for *V. parviflora*

Genome assembly	Primary assembly	Alternate haplotype assembly
Assembly name	drVicParv1.1	drVicParv1.1 alternate haplotype
Assembly accession	GCA_965231315.1	GCA_965231235.1
Assembly level	chromosome	contig
Span (Mb)	2,826.49	40.44
Number of chromosomes	7	-
Number of contigs	1,292	1,025
Contig N50 (Mb)	4.2	0.04
Number of scaffolds (excluding organelle sequences)	164	1,025
Scaffold N50 (Mb)	399.06	0.04
Scaffold auN (Mb)	405	-
Longest scaffold length (Mb)	481.76	0.88
Organelles	Mitochondrial genomes: 341.49 and 64.57 kb; Plastid genome: 122.23 kb	-

Most of the primary assembly sequence (99.62%) was assigned to 7 chromosome-level scaffolds. These chromosome-level scaffolds, confirmed by Hi-C data, are named according to size (Figure 3; Table 3).

Two mitochondrial genomes (lengths 341.49 kb [OZ246708.1] and 64.57 kb [OZ246709.1]) and the plastid genome (length 122.23 kb, OZ246710.1) were also assembled. These sequences are included as contigs in the multifasta file of the primary genome submission and as standalone records.

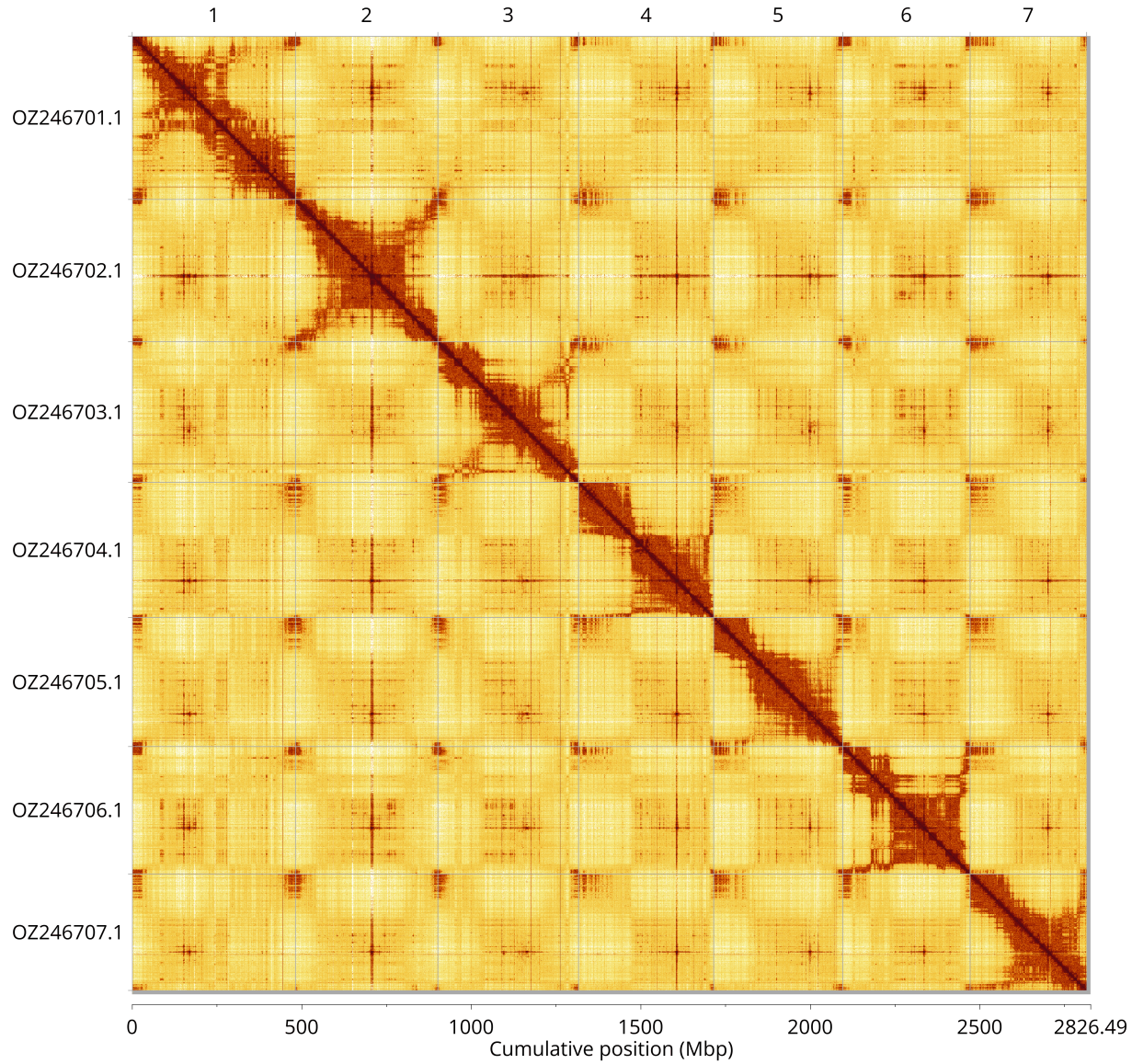

Figure 3. Hi-C contact map of the *V. parviflora* primary assembly. Assembled chromosomes are shown in order of size and labelled along the axes, with a megabase scale shown below. The plot was generated using PretextSnapshot.

Table 3. Chromosomal pseudomolecules in the primary genome assembly of *V. parviflora* drVicParv1

INSDC accession	Molecule	Length (Mb)	GC%
OZ246701.1	1	481.76	35.50
OZ246702.1	2	420.55	35.50
OZ246703.1	3	414.38	35.50
OZ246704.1	4	399.06	35.50
OZ246705.1	5	379.59	35.50
OZ246706.1	6	376.15	35.50
OZ246707.1	7	344.40	35.50

Assembly quality metrics

The combined primary and alternate assemblies achieve an estimated QV of 61.7. The *k*-mer completeness is 99.02% for the primary assembly, 1.80% for the alternate haplotype, and 99.38% for the combined assemblies (Figure 4).

BUSCO v.5.7.1 analysis of the primary assembly using the fabales_odb10 reference set (n = 5,366) identified 97.6% of the expected gene set (single = 94.3%, duplicated = 3.3%).

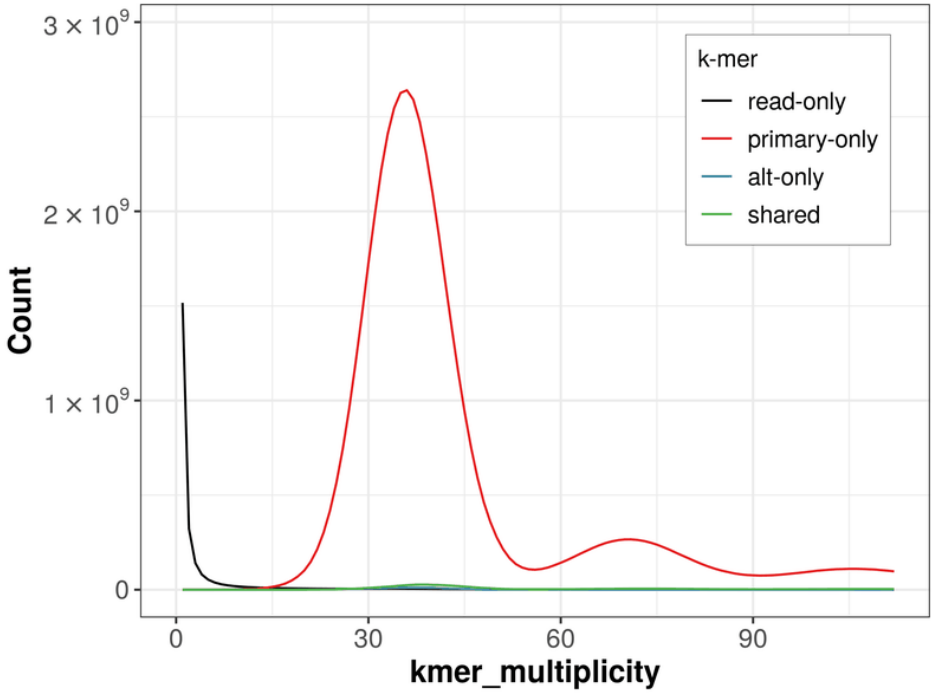

Figure 4. Evaluation of *k*-mer completeness using MerquryFK. This plot illustrates the recovery of *k*-mers from the original read data in the primary assembly, the alternate haplotype assembly and the combined assemblies. The horizontal axis represents *k*-mer multiplicity, and the vertical axis shows the number of *k*-mers. The black curve represents *k*-mers that appear in the reads but are not assembled, 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 primary 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 blob plot in Figure 6 displays scaffolds from the primary assembly by GC proportion and base coverage. Marker area is proportional to scaffold length, and colour indicates taxonomic assignment (Challis *et al.*, 2020).

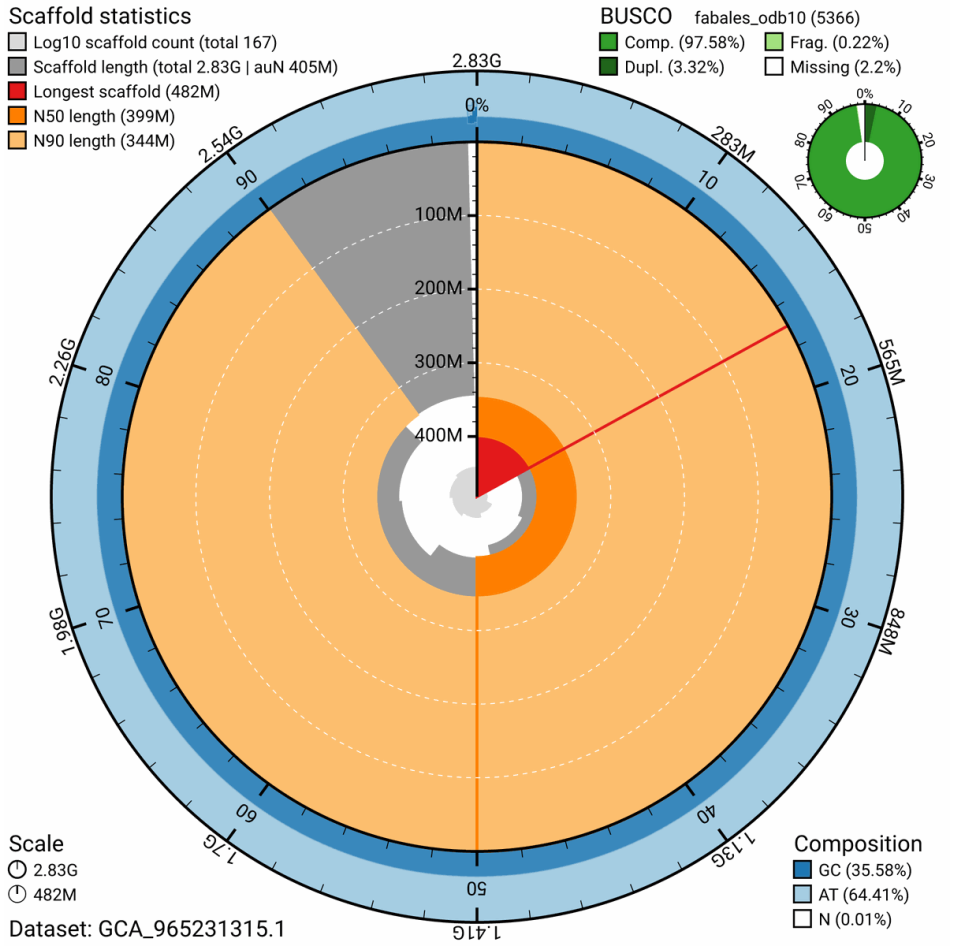

Figure 5. Assembly metrics for drVicParv1.1, the primary assembly. The BlobToolKit snail plot provides an overview of assembly metrics and BUSCO gene completeness. The circumference represents the length of the primary assembly, and the main plot is divided into 1,000 bins around the circumference. The 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 fabales_odb10 set is presented at the top right. The assembly can be explored interactively in the BlobToolKit viewer.

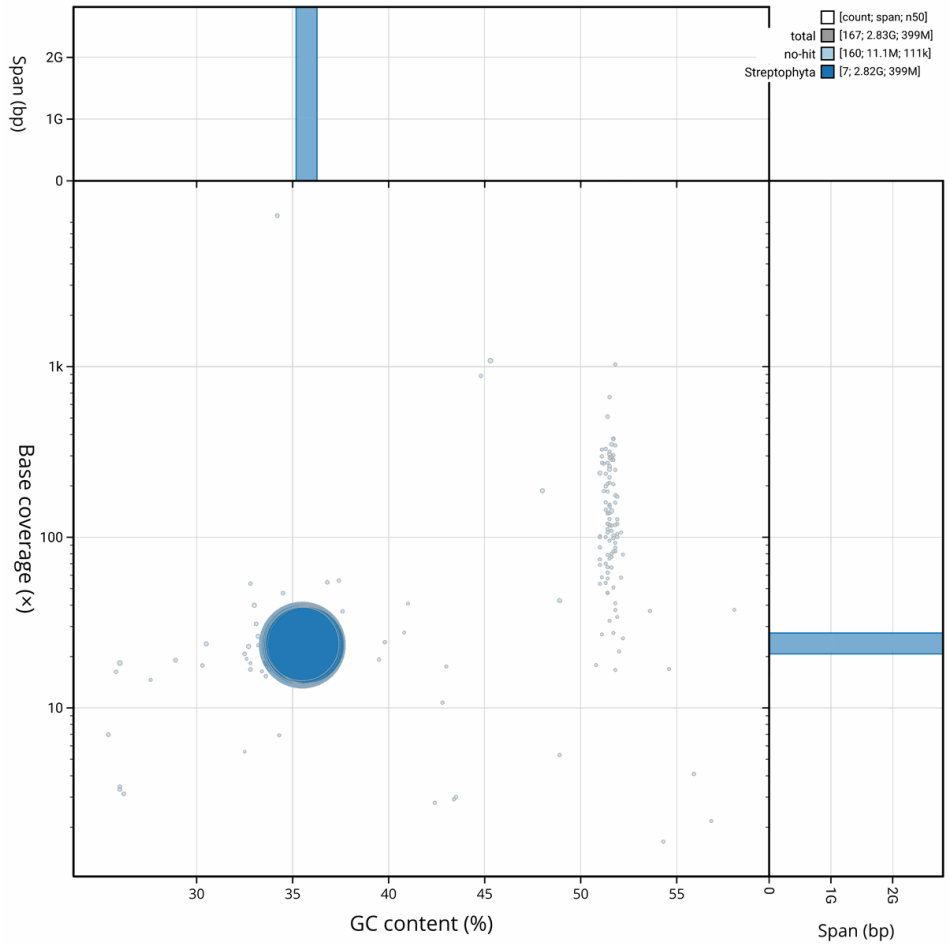

Figure 6. BlobToolKit blob plot for drVicParv1.1. The plot shows base coverage (vertical axis) and GC content (horizontal axis). Circles represent scaffolds; marker area is proportional to scaffold length, and colour indicates taxonomic assignment. The histograms along the axes display the total length of sequences distributed across different levels of coverage and GC content. The assembly can be explored interactively in the BlobToolKit viewer.

Table 4 lists the assembly metric benchmarks adapted from Rhie *et al.*. (2021) and the Earth BioGenome Project (EBP) Report on Assembly Standards. The three-part EBP metric calculated for the primary assembly is **6.C.Q62**.

Table 4. Earth BioGenome Project summary metrics for the *V. parviflora* assembly

Measure	Value	*Benchmark*
EBP summary (primary)	6.C.Q62	*6.C.Q40*
Contig N50 length	4.20 Mb	*> 1 Mb*
Scaffold N50 length	399.06 Mb	*= chromosome N50*
Consensus quality (QV)	Primary: 62.1; alternate: 53.3; combined: 61.7	*# 40*
k-mer completeness	Primary: 99.02%; alternate: 1.80%; combined: 99.38%	*> 90%*
BUSCO	C:97.6% [S:94.3%, D:3.3%], F:0.2%, M:2.2%, n:5,366	*S > 90%; D < 5%*

Measure	Value	*Benchmark*
Percentage of assembly assigned to chromosomes	99.62%	*# 90%*

Notes: The EBP summary uses log10(Contig N50); chromosome-level (C) or log10(Scaffold N50); Q (Merqury QV). BUSCO v5.7.1 using the fabales_odb10 lineage dataset: C=complete; S=single-copy; D=duplicated; F=fragmented; M=missing; n=orthologues.

Data availability

European Nucleotide Archive: Vicia parviflora. Accession number PRJEB80417; https://identifiers.org/ena.embl/PRJEB80417. The genome sequence is released openly for reuse. The *V. parviflora* 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 primary and alternate assemblies 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.

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	4.4.5	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	5.7.1; 6.1.0	https://gitlab.com/ezlab/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/chhylp123/hifiasm
HiGlass	1.13.4	https://github.com/higlass/higlass
MerquryFK	1.1.0-c1	https://github.com/thegenemyers/MERQURY.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

Software	Version	Source
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	1.4-r122	https://github.com/lh3/seqtk
Singularity	3.9.0	https://github.com/sylabs/singularity
TreeVal	1.1.1	https://github.com/sanger-tol/treeval
YaHS	1.2a.2	https://github.com/c-zhou/yahs

Author information

- Members of the Royal Botanic Gardens Kew Genome Acquisition Lab
- Members of the Plant Genome Sizing Collective
- 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
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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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Open Peer Review

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✔ **Automated Benchmarking**

Wellcome Sanger Institute, Hinxton, UK

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 Vicia parviflora (drVicParv1), all four checks passed.

Data available: pass. ENA study PRJEB80417, raw-read accessions ERR13725956, ERR13725957, ERR13732198, and ERR13962545, and assembly accessions GCA_965231315.1 and GCA_965231235.1 are public.

Earth BioGenome Project three-part metric: pass. The primary assembly is reported as 6.C.Q62, meeting the 6.C.Q40 reference standard.

k-mer completeness: pass. The combined haplotype assemblies have 99.38% k-mer completeness, exceeding the Earth BioGenome Project target of 90%.

BUSCO: pass. The primary assembly, which is proposed as the reference assembly for this species, has 97.6% complete BUSCOs (94.3% single-copy and 3.3% duplicated). BUSCO software version: 5.7.1; lineage dataset: fabales_odb10. 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.