



## Genome Resources

# Chromosome-level reference genome of stinkwort, *Dittrichia graveolens* (L.) Greuter: A resource for studies on invasion, range expansion, and evolutionary adaptation under global change

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## Abstract

*Dittrichia graveolens* (L.) Greuter, or stinkwort, is a weedy annual plant within the family Asteraceae. The species is recognized for the rapid expansion of both its native and introduced ranges: in Europe, it has expanded its native distribution northward from the Mediterranean basin by nearly 7 °C latitude since the mid-20th century, while in California and Australia the plant is an invasive weed of concern. Here, we present the first de novo *D. graveolens* genome assembly (1N = 9 chromosomes), including complete chloroplast (151,013 bp) and partial mitochondrial genomes (22,084 bp), created using Pacific Biosciences HiFi reads and Dovetail Omni-C data. The final primary assembly is 835 Mbp in length, of which 98.1% are represented by 9 scaffolds ranging from 66 to 119 Mbp. The contig N50 is 74.9 Mbp and the scaffold N50 is 96.9 Mbp, which, together with a 98.8% completeness based on the BUSCO embryophyta10 database containing 1,614 orthologs, underscores the high quality of this assembly. This pseudo-molecule-scale genome assembly is a valuable resource for our fundamental understanding of the genomic consequences of range expansion under global change, as well as comparative genomic studies in the Asteraceae.

**Key words:** Asteraceae, California, Dovetail Omni-C, organelle genomes, Pacific Biosciences HiFi, range shift

## Introduction

*Dittrichia graveolens* (L.) Greuter (stinkwort) is an annual plant in the Inulae tribe within the Asteraceae family (Fig. 1A–C), growing in open, disturbed habitat including roadsides, agricultural land, industrial lots, and hillsides (Brullo and de Marco 2000). The species' native distribution lies around the Mediterranean Basin, extending to the Middle East and India and northward to central France (Lustenhouwer and Parker 2022). Germinating in response to heavy rains, *D. graveolens* grows vegetatively as a rosette until bolting in late spring and summer and flowering in late summer and fall, producing up to several thousand seed heads per plant at the end of the growing season (USDA 2013; Lustenhouwer et al. 2018). Plants have yellow radiate flowers and wind-dispersed fruits (Brownsey et al. 2013b).

*D. graveolens* has expanded its native range northward by nearly 7 °C latitude since the mid-20th century, now occurring in the Netherlands, southern Sweden, and Poland (Kocián

2015; Lustenhouwer et al. 2018; Lustenhouwer and Parker 2022). Although the onset of this native range expansion coincided with climate change in central Europe (Lenoir et al. 2008), population spread extended far beyond expectations based on climate tracking alone, resulting in a niche expansion to more temperate climates (Lustenhouwer and Parker 2022). A common garden study showed that plants at the range edge rapidly evolved earlier flowering time than core populations in response to the shorter growing season in the north, increasing plant fitness and promoting further range expansion (Lustenhouwer et al. 2018). Existing genomic resources for *D. graveolens* consist of ddRAD sequencing data for 190 individuals originating along a latitudinal gradient from southern France to the Netherlands (European Nucleotide Archive accession PRJEB22978), used in reference-free analyses to characterize population structure in this common garden study. The results showed a decline in genetic diversity toward the northern range limit (Lustenhouwer et al. 2018).

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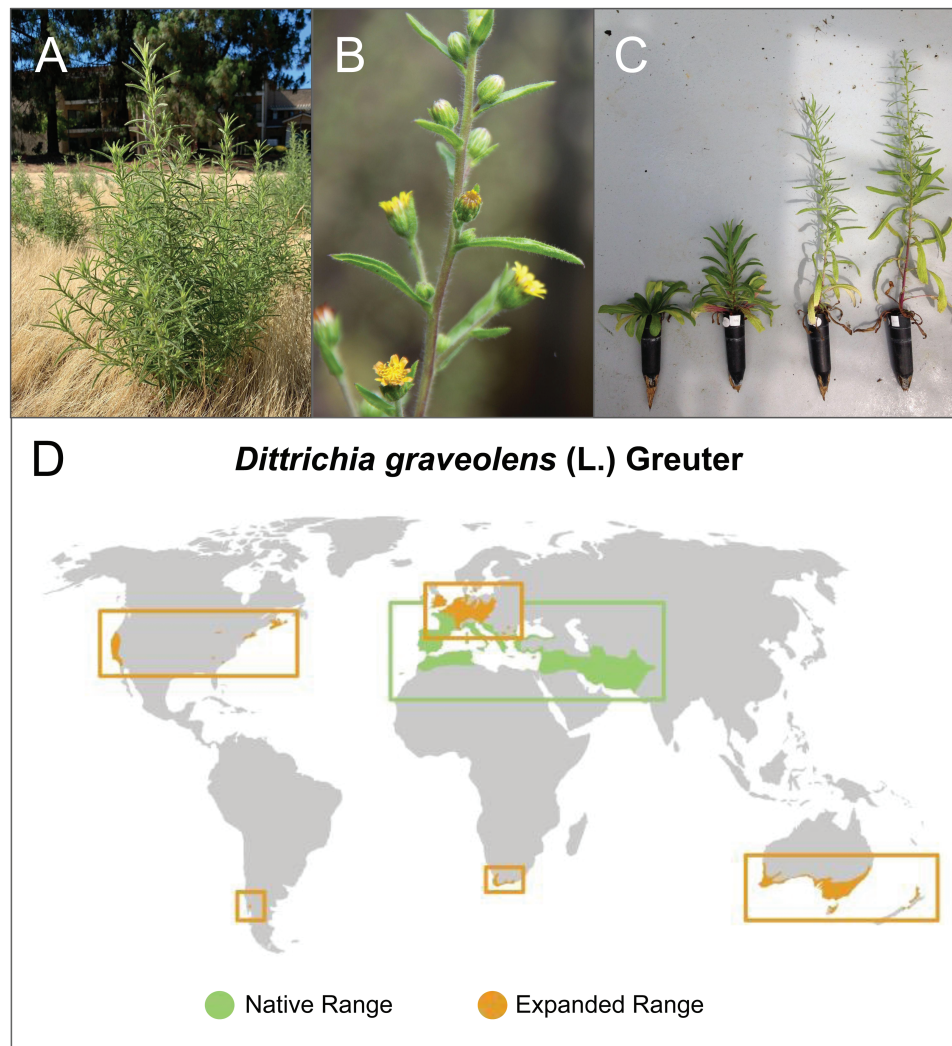
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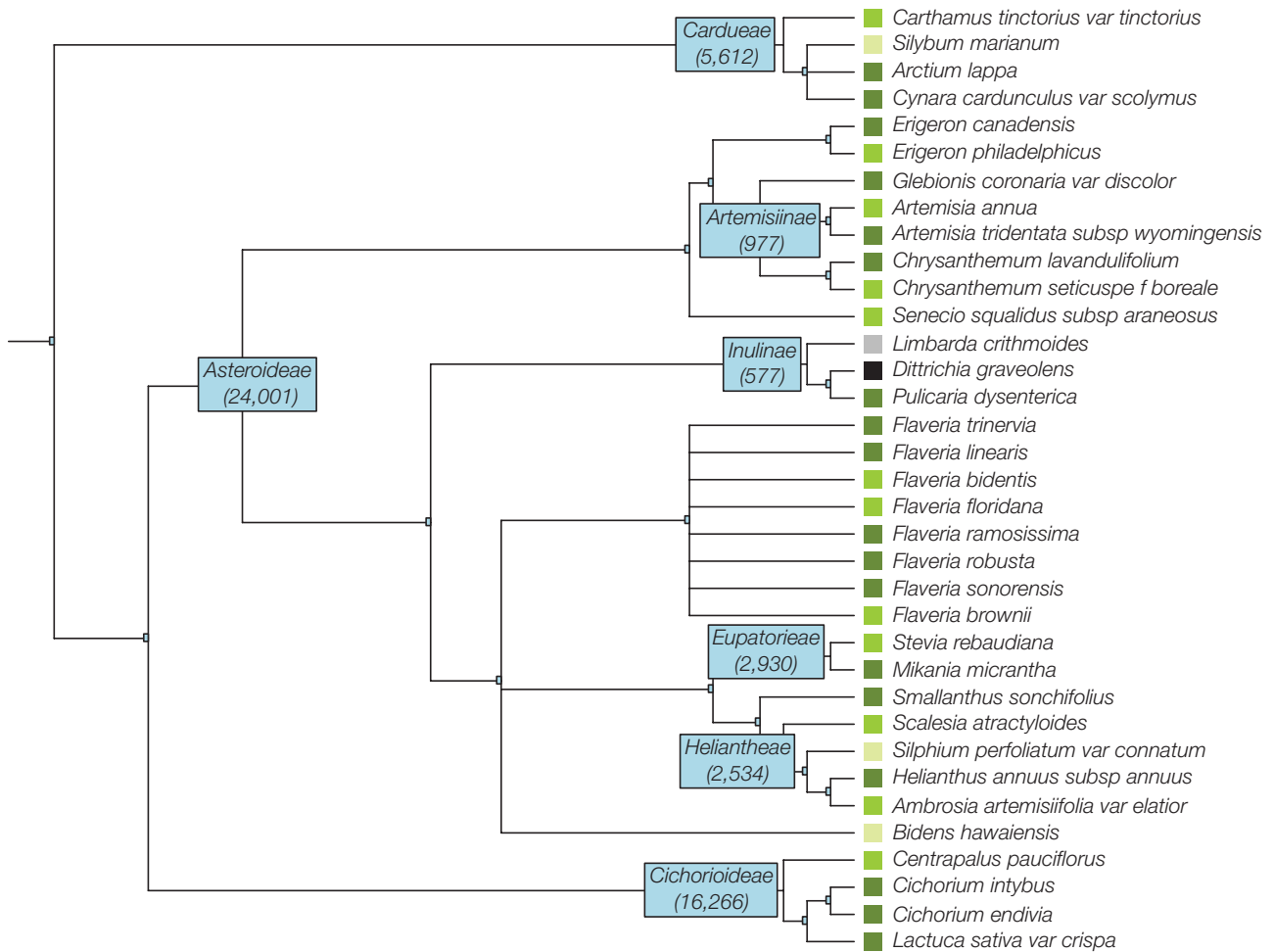
Outside its native range, *D. graveolens* has been introduced and successfully established elsewhere around the world, including Australia and New Zealand, South Africa, and North and South America (Parsons and Cuthbertson 2001; Brownsey 2012; DiTomaso and Brownsey 2013; Santilli et al. 2021; Fig. 1D). In California and Australia, the species is considered a noxious weed (Parsons and Cuthbertson 2001; California Department of Food and Agriculture 2021); it contains a sesquiterpene lactone that causes contact dermatitis in humans (Thong et al. 2008; Ponticelli et al. 2022), and its seeds have a barbed pappus that can damage the intestines of livestock (Philbey and Morton 2000). The combination of high spread capacity (short generation time, high fecundity, and dispersal ability) and high potential impact on agricultural and restoration land makes *D. graveolens* an invasive species of particular concern (USDA 2013). No niche shifts beyond the Mediterranean climate of the historic native range have yet been identified in California or Australia (Lustenhauer and Parker 2022). Nonetheless, given the high evolutionary potential of the species in its native range, it is possible that genomic changes driving other traits play a role in the ongoing invasions.

Asteraceae is a superfamily comprising 20,000 to 30,000 species (~5% to 10% of angiosperm species), many of which are economically useful and/or ecologically important. Reference genomes are currently available for 33 taxa in Asteraceae, representing 1% of genera in the family (22/2,128 genera per Open Tree of Life phylogeny ott3.3). Assembly level varies between species, with 18 chromosome-level, 12 scaffold-level, and 3 contig-level genomes (Fig. 2). The available genomes are primarily species of great agricultural importance such as *Helianthus annuus* (sunflower) and *Lactuca sativa* (lettuce), several medicinal aromatic species (*Artemisia annua*, *Erigeron breviscapus*, *Centaurea cyanus*, *Glebionis coronaria*), as well as fellow invasive annuals *Ambrosia artemisiifolia* and *Erigeron canadensis*. Within the Inuleae tribe, the only species with a reference genome is *Pulicaria dysenterica* (Genbank accession GCA\_947179395.2). The closest relative to *D. graveolens* with a high-quality chloroplast assembly is *Limbarda crithmoides* (Genbank accession NC\_066031.1; Fig. 2).

Asteraceae species have high sequence diversity, low synteny, and evidence of ancient whole-genome duplication or triplication at different points in time (Fan et al. 2022). This sequence



**Fig. 1.** Photos of *D. graveolens* and its global range: A) growing along a footpath in Santa Clara County, California, USA; B) closeup of leaves, buds, and flowers; C) life stages: juvenile rosette through reproductive adult; D) map of global distribution of *D. graveolens* with both native and expanded ranges. Data sources detailed in Lustenhauer and Parker (2022), GBIF (2020), and Santilli et al. (2021). Photo sources: A) Andrew Lopez, B) Nicky Lustenhauer, and C) Miranda K. Melen. Map projection: Robinson.



**Fig. 2.** Taxa in the Asteraceae family for which reference genomes are available. Colors indicate assembly level (light green: contig, medium green: scaffold, dark green: chromosome). *D. graveolens* is labeled in black and the closest relative with a chloroplast assembly (*L. crithmoides*) is in gray. Numbers at each node (blue boxes) indicate the total number of taxa descending from that subfamily/tribe/subtribe. Taxonomy from Open Tree of Life ott3.3 (OpenTreeofLife et al. 2019; in agreement with Mandel et al. 2019).

divergence impedes using confamilial species as reference genomes for mapping. Greater species-level resolution in the Asteraceae is necessary to support quality conservation and population genomics and the discovery of genetic mechanisms of secondary metabolite diversity. Asteraceae are well known for including many of the world's worst invasive species (Baker 1974; Hodgins et al. 2016). The reasons for *D. graveolens*' rapid range expansion and invasion success are as yet undetermined, and the genetic consequences of that range expansion remain to be studied. Here, we present the first high-quality de novo genome assembly of *D. graveolens* based on Pacific Biosciences (PacBio) HiFi long reads and scaffolded with Dovetail Omni-C data. This genome will help fill gaps in comparative genomic resources for the Inulae tribe and the Asteraceae, and it will be used in planned molecular ecological and functional analysis along range expansion gradients in *D. graveolens*' Mediterranean home range and along its invasion path in California.

## Methods

### Biological materials

The plant used for this reference genome originates from a population located in the native range of *D. graveolens* in southern France. Seeds were sampled from a highway service

station, Aire du Merle Sud, along the A54 near Salon-de-Provence (43.63790 N, 4.98474 E) on 1 November 2018. The Nagoya Protocol was followed to collect genetic resources in France (certificate of compliance TREL2302365S/653). The collected seeds were used in a greenhouse common garden experiment at the University of California, Santa Cruz (UCSC), in February to December 2019. Plants were bagged with a light-permeable mesh prior to budding to ensure self-fertilization. Seeds produced by these plants were then used to grow a second generation of this experiment in March to December 2020, which provided the biological material for this study (plant identifier in experiment: id 3264, maternal family 2 from population FS-MER). The reference genome specimen is thus a direct descendant of field-collected seeds after 1 generation of selfing. A tissue voucher specimen of this plant is stored in a frozen collection at the UCSC Department of Ecology and Evolutionary Biology, and is cross-listed at the Norris Center (UCSC\_NL\_FS-MER\_Block4\_2020\_SAMPLE3264).

Additional short-read sequencing from a different sample was used for the mitochondrial genome assembly (sample reference CEJES6B739). This plant was grown from seed collected at a roadside population along California State Route 26 near the community of Mokelumne Hill (38.3176 N, 120.6525 W) at the invasion front in California on 2

December 2018. *D. graveolens* is classed as a noxious weed by the California Department of Food and Agriculture (California Code of Regulations 4500) and such plant material may be collected from state highways for research without additional permissions.

### Short-read mitogenome sequencing

To prepare Illumina short-read libraries for sample CEJES6B739, DNA was extracted from fresh leaf tissue using the Qiagen DNeasy Plant DNA Kit (Qiagen Inc, Valencia, CA), mixing the leaf in the lysis buffer in a microcentrifuge tube using a scored micropestle. A Tn5-based tagmentation and dual-indexed DNA library were made following the method described in [Russell et al. \(2020\)](#), and this was sequenced with  $2 \times 150$  bp reads on an Illumina NextSeq 550 (Illumina, San Diego, CA) at the UCSC Paleogenomics Laboratory.

### Omni-C library preparation and sequencing

We used the Dovetail Omni-C Kit (Dovetail Genomics, Scotts Valley, CA) following the manufacturer's protocol with slight modifications to prepare the Omni-C library. Young leaf tissue was ground with a mortar and pestle in liquid nitrogen. Nuclear chromatin was fixed in place and then digested under different conditions of DNase and a suitable fragment length distribution of DNA molecules was chosen. Chromatin end-repair was followed by biotinylated bridge adapter ligation and then proximity ligation of adapter-containing ends. Crosslinks were reversed, DNA purified from proteins, and biotin that was not internal to the ligated fragments was removed. The library was enriched using the NEB Ultra II DNA Library Prep Kit (New England Biolabs, Ipswich, MA) with Illumina-compatible  $\gamma$ -adaptor, then split and separately indexed to increase complexity. Biotin-containing fragments were captured using streptavidin beads and size selection was performed to remove fragments  $>1,000$  bp. Both size-selected libraries were sequenced at the UCLA Technology Center for Genomics and Bioinformatics (Los Angeles, CA) on an Illumina NovaSeq S4 aiming to generate 100 million  $2 \times 150$  bp reads.

### HMW DNA extraction for PacBio

High molecular weight (HMW) genomic DNA (gDNA) was extracted from a single individual (190 mg; sample 3,264) using the method described in [Inglis et al. \(2018\)](#), with the following modifications. Sodium metabisulfite (1%, w/v) was used instead of 2-mercaptoethanol (1%, v/v) in the sorbitol wash buffer and the lysis buffer. Using a mortar and pestle, frozen tissue was pulverized in liquid nitrogen for 15 min and gently resuspended in 10 mL of sorbitol wash buffer. The suspension was centrifuged at  $3,500 \times g$  for 5 min at room temperature, and the supernatant was discarded. The ground tissue pellet was gently resuspended using a paintbrush in 10 mL of sorbitol wash buffer. The wash step was repeated 5 times to remove potential contaminants that may coprecipitate with DNA. Instead of the standard  $65^\circ\text{C}$ , the lysis step was performed at  $45^\circ\text{C}$  for 1 h with gentle inversion every 15 min. The DNA purity was estimated using absorbance ratios ( $260/280 = 1.80$  and  $260/230 = 2.45$ ) on a NanoDrop ND-1000 spectrophotometer. The final DNA yield (26  $\mu\text{g}$ ) was quantified using a Quantus Fluorometer (QuantiFluor ONE dsDNA Dye assay; Promega, Madison, WI). The size distribution of the HMW DNA was estimated

using the Femto Pulse system (Agilent, Santa Clara, CA), where 38% of the DNA fragments were found to be 50 kb or longer.

The PacBio HiFi data generation was performed at UC Davis DNA Technologies Core (Davis, CA). The HiFi SMRTbell library was constructed using the SMRTbell Express Template Prep Kit v2.0 (Pacific Biosciences, Menlo Park, CA; Cat. #100-938-900) according to the manufacturer's instructions (PN 101-853-100 Version 05, August 2021). HMW gDNA was sheared using Diagenode's Megaruptor 3 system (Diagenode, Belgium; Cat. B06010003) to the size distribution mode between 15 and 20 kb. The sheared gDNA was then put through the following enzymatic steps: single-strand overhangs removal, DNA damage repair, end-repair and A-tailing, overhang adapter v3 ligation, and nuclease treatment. AMPure PB Beads (Pacific Biosciences, Menlo Park, CA; Cat. #100-265-900) were used for all purification steps for sheared gDNA and SMRTbell library. Size selection for the SMRTbell library was done using the PippinHT system (Sage Science, Beverly, MA; Cat. #HPE7510) to collect fragments greater than 7 to 9 kb. Finally, the HiFi SMRTbell library was sequenced using one 8M SMRT cell, Sequel II sequencing chemistry 2.0, and 30-h movies on a PacBio Sequel II sequencer. Quality control of reads was conducted with FastQC ([Andrews 2010](#)) and LongQC ([Fukasawa et al. 2020](#)).

### Genome size and ploidy estimation

Raw PacBio HiFi reads were provided as input to KMC to count k-mers ( $k = 21$ ) and create a histogram ([Kokot et al. 2017](#)). The histogram was used for estimation of genome size, heterozygosity, and repeat content in GenomeScope 2.0, and Smudgeplot v0.2.2 was used for ploidy estimation with  $L = 16$  and  $U = 1,800$  ([Ranallo-Benavidez et al. 2020](#)).

### Nuclear genome assembly

HiFi reads were filtered for HiFi-specific adapters using HiFiAdapterFilt ([Sim et al. 2022](#)). Filtered reads were checked for contaminants using Centrifuge ([Kim et al. 2016](#)) with an index containing archaea, bacteria, fungi, and virus according to NCBI taxonomy ([Schoch et al. 2020](#)). No contaminants were filtered out as those identified were minimal and primarily bacterial taxa with sequence similarity to chloroplast. Adapter-filtered HiFi reads were used to create a draft assembly in hifiasm using the  $-l0$  parameter due to the estimated low heterozygosity ([Cheng et al. 2021](#)). Raw Omni-C reads ( $--h1$  and  $--h2$ ) were also included to aid in primary and alternate haplotype organization. The resulting draft assemblies, primary (hap1) and alternate (hap2), were filtered for chloroplast sequence with BLAST ([Camacho et al. 2009](#)) using the publicly available *L. crithmoides* ([Sayers et al. 2021](#)), the closest related chloroplast genome assembly available. Scaffolding followed previously described methods ([https://aidenlab.org/assembly/manual\\_180322.pdf](https://aidenlab.org/assembly/manual_180322.pdf)). Omni-C reads were aligned to the primary draft assembly with BWA ([Li and Durbin 2009](#)) and used to create a pairs file filtered for duplicates with Juicer ([Durand et al. 2016](#)). 3D-DNA ([Dudchenko et al. 2017](#)) default parameters were used for scaffolding, as it leverages the long-distance read pair alignments to order and orient contigs. Results were visualized in JuiceBox ([Dudchenko et al. 2018](#)) followed by YAGCloser to close gaps with support of HiFi reads (<https://github.com/merlyescalona/>

yagcloser). The resulting gap-filled scaffolds were sorted in order of decreasing size and named/numbered accordingly. Scaffolding of the alternate draft assembly followed identical methods. The partial mitochondrial genome was identified within a scaffold in both nuclear assemblies and removed by breaking the scaffolds at those coordinates (Table 1).

### Assembly quality assessment

At each step in the assembly and scaffolding process, assembly statistics and completeness were tracked with QUAST (Gurevich et al. 2013) and BUSCO (Manni et al. 2021). Final genomes were further evaluated by aligning the HiFi reads used to generate the assembly to the resulting assembly with Minimap2 (Li 2018). The Omni-C reads filtered for adapters with Cutadapt v1.18 (Martin 2011) were used to obtain the quality value (QV) with Merqury (Rhie et al. 2020).

**Table 1.** Assembly pipeline and software used.

Nuclear assembly	Software	Version
Read Quality control	FastQC	0.11.8
Read Quality control	LongQC	1.2.0c
Omni-C adapter trimming	Cutadapt	1.18
K-mer counting	KMC	3.1.1
Estimation of genome size and heterozygosity	GenomeScope	2
Filtering PacBio HiFi adapters	HiFiAdapterFilt	2.0.1
Identifying contaminants		
Contaminant identification	Centrifuge	1.0.4
De novo assembly (contigging)	Hifiasm	0.16.1-r375
Contig detection of organelle sequence	BLAST	2.13.0
Omni-C mapping and pairing	BWA-MEM	0.7.17-r1188
	Samtools	1.9.1.16.1
	Juicer	1.6
	Juicer Tools	2.20.00
Scaffolding	3D-DNA	180922
Assembly visualization	JuiceBox	1.11.08
Gap closing	YAGCloser	Commit
	<a href="https://github.com/merlyescalona/yagcloser">https://github.com/merlyescalona/yagcloser</a>	0e34c3b
Benchmarking		
Basic assembly stats	QUAST	5.2.0
Assembly completeness	BUSCO	5.4.3
	Minimap2	2.24-r1122
	Meryl	1.3
	Merqury	1.3
Organelle assemblies		
Chloroplast	Seqtk	1.3-r106
	Flye	2.9
	GetOrganelle	1.7.4
Mitochondria	NOVOPlasty	4.3.1
	BLAST	2.13.0

Software citations are listed in the text.

### Organelle genome assemblies

Adapter-filtered HiFi reads were aligned to the *L. crithmoides* chloroplast with minimap2 (-ax map-hifi) and filtered for Q20 (samtools view -F4 -q20). These reads were subset with seqtk subseq and contigged with Flye (Kolmogorov et al. 2019). A circular assembly was achieved using the assembly graph from Flye as input for GetOrganelle (Jin et al. 2020) using the *L. crithmoides* chloroplast as a reference (--genes).

We used short-read sequencing of sample CEJES6B739 to construct a partial mitochondrial genome in NOVOPlasty (Dierckxsens et al. 2017) with the *Cox1* gene from GetOrganelleDB as a seed. We used this mitochondrial genome as a BLAST query to identify the corresponding mitochondrial genome in a contig of the nuclear genome of the reference individual.

### Results

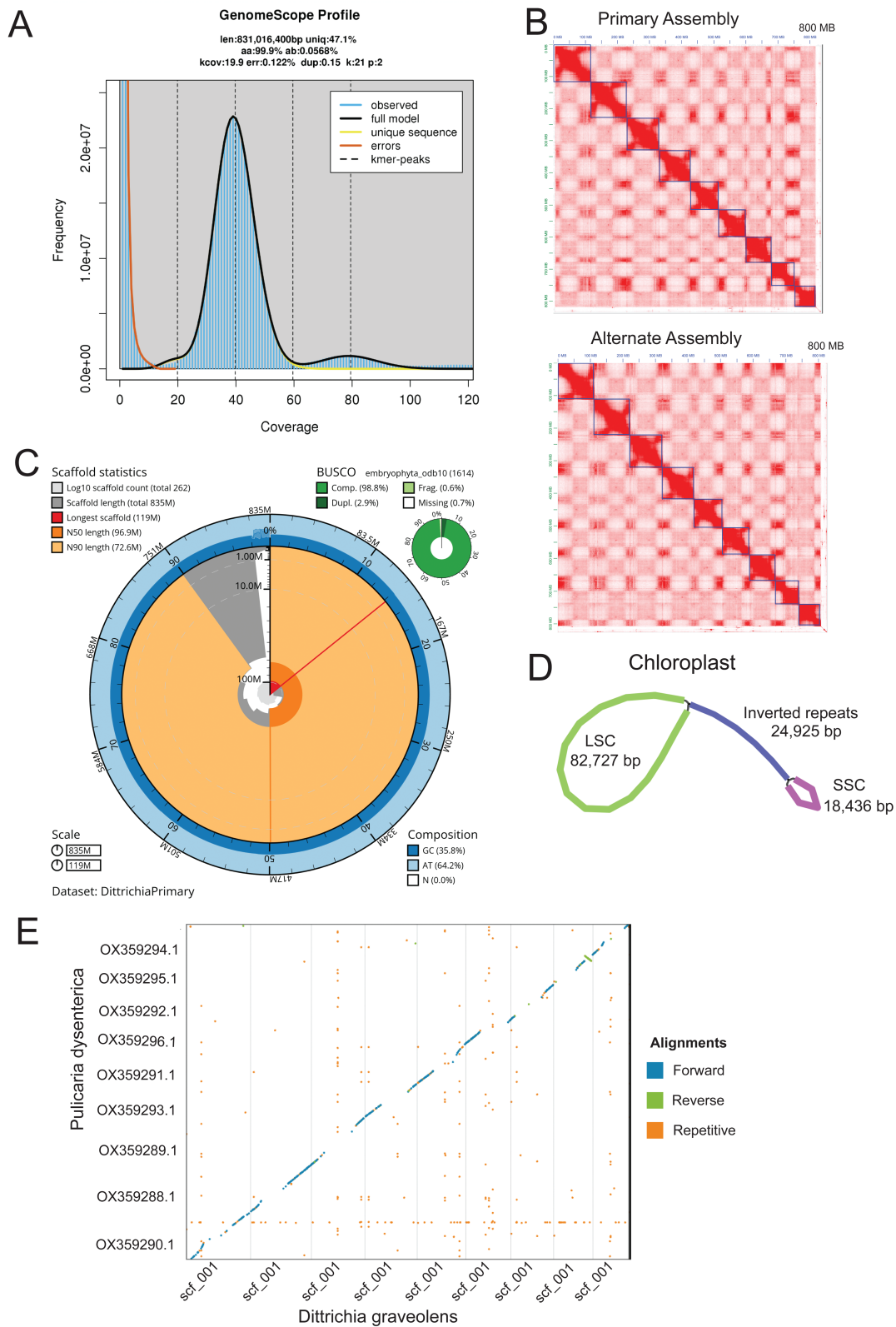
HiFi sequencing produced 2.4 M reads with an N50 of 14 kb and approximately 41× coverage. From this sequencing, the genome length estimate was 831 Mbp, 47.1% of which is unique, non-repetitive sequence, with a heterozygosity of 0.0568% (Fig. 3A). Omni-C sequencing produced 84 M 150 bp paired-end reads totaling 15× in coverage. HiFi sequencing with Omni-C for phasing generated primary and alternate draft assemblies ~835 Mbp in length with contig N50s of ~75 Mbp. After scaffolding with Omni-C and gap closing with HiFi, the final primary genome was 835 Mbp long, with an N50 of 96.9 Mb and 98.1% of its sequence organized into 9 pseudo-molecules, and with an average of 8.69 Ns per 100 kb (Fig. 3B and C). The BUSCO score was 98.8% complete (2.9% duplicates; Fig. 3C) and the QV score was 34.2913. The alternate genome was 824 Mbp long, with an N50 of 96.4 Mb 97.8% organized into 9 pseudo-molecules, and 6.49 Ns per 100 kb. The alternate BUSCO was 98.6% (2.9% duplicate), with 2 extra genes missing that were complete in the primary genome.

The chloroplast assembly produced a circular assembly 151,013 bp in length (Fig. 3D). Illumina short-read paired-end sequencing used for the mitochondrial assembly consisted of 14.2 M reads and the resulting contig was 22,084 bp. Only 1 contig was produced by NOVOPlasty, but this likely does not represent the complete mitogenome.

Detailed statistics for each assembly are summarized in Table 2.

### Discussion

Prior to our sequencing effort, the genome size of *D. graveolens* was estimated to be 2C = 1.99 pg, consisting of 18 chromosomes (Zonneveld 2019). Our results are in concordance with these estimates as 835 Mbp and 9 base chromosomes (2n = 18). This is a relatively small and simple genome compared with others in the Asteraceae (Garcia et al. 2013) but similar in size and synteny to the closest relative with a reference genome, *P. dysenterica* (Fig. 3E). Our heterozygosity is 0.0568%, lower than that of sequenced medicinal plants *A. annua* at 1% to 1.5% (Shen et al. 2018), and *E. breviscapus* (2.04%; He et al. 2021), but the individual we selected was grown from seed produced after 1 generation of selfing. Re-analysis of published ddRAD-seq data



**Fig. 3.** A) K-mer spectra created with HiFi reads,  $k = 21$ , to estimate genome size. B) Contact map of primary and alternate assemblies showing 9 pseudo-molecules ordered largest to smallest. C) Snail plot visualizing the primary assembly contiguity and completeness metrics. D) Assembly graph of the complete chloroplast genome. E) Whole-genome alignment of *P. dysenterica* to *D. graveolens*.

for *D. graveolens* from the same source region in southern France (Lustenhauer et al. 2018), corrected for fragment length, shows an average observed heterozygosity of 0.12%

(Appendix 1). Given that 1 generation of selfing would result in halved heterozygosity, this value closely corresponds to the reference genome presented here.

**Table 2.** Sequencing and assembly statistics, and accession numbers.

BioProjects & Vouchers	
CCGP NCBI BioProject	PRJNA720569
Species NCBI BioProject	PRJNA919063
NCBI BioSample	SAMN32619994
Specimen identification number	UCSC_NL_FS-MER_Block4_2020_SAMPLE3264
Genome sequence	
PacBio HiFi reads	1 PACBIO_SMRT (Sequel II) run: 2433439 spots, 34.0 G bases
Omni-C Illumina sequencing	6 Illumina NextSeq 550 runs: 11.9 M spots, 3.6 G bases 11.5 M spots, 3.4 G bases 12.2 M spots, 3.7 G bases 3.5 M spots, 1.0 G bases 2.7 M spots, 818 M bases
Illumina PE 150 bp	1 Illumina NextSeq 550 run: 7.1 M spots, 2.1 M bases
PacBio HiFi NCBI SRA	SRR23002284
Omni-C Illumina NCBI SRA	SRR23002279-83
Illumina PE SRA	SRR23255570
Genome assembly—primary (alternate)	
Assembly identifier	Dgra_v1_pri_scf_ (Dgra_v1_alt_scf_)
HiFi read coverage	41x
Number of contigs	235 (158)
Contig N50 (bp)	74,911,303 (74,485,925)
Longest contigs	111,114,853 (110,676,008)
Number of scaffolds	262 (292) <sup>a</sup>
Scaffold N50 (bp)	96,898,007 (96,379,130)
Size of final assembly (bp)	834,904,512 (824,346,690)
N's per 100 kbp	8.68 (6.49)
Base pair QV (Mercury)	P: 34.2913, A: 34.2439
k-mer completeness	P: 93.41%, A: 93.34%
BUSCO completeness	Embryophyta_obd10 ( <i>n</i> : 1,614)
Primary (C:S:D:F:M)	98.8%:95.9%:2.9%:0.6%:0.6%
Alternate (C:S:D:F:M)	98.6%:95.7%:2.9%:0.6%:0.6%
Assigned chromosomes %	98.1% (97.8%)
Organelles	1 complete chloroplast (in primary assembly) 2 partial mitochondria (primary and alternate)

<sup>a</sup>The number of scaffolds is higher than contigs due to small fragments created during misassembly correction in 3D-DNA.

The rapid population spread of *D. graveolens* in new areas is aided by its annual lifecycle, self-compatibility, high fecundity, wind dispersal, and high germination rate (Rameau et al. 2008; Brownsey et al. 2013a; Lustenhouwer et al. 2018). The species thrives in human-disturbed habitat such as roadsides and industrial sites which is facilitated by tolerance to environmental stressors such as high salinity (Grašič et al. 2016; Šajna et al. 2017), heavy metals (Shallari et al. 1998), and possibly to arsenic as found in *D. viscosa* (De Paolis et al. 2022). It has a high secondary metabolite diversity and toxicology with 262 compounds discovered to date (Ponticelli et al. 2022). Along with its small diploid genome, these traits

make *D. graveolens* a candidate model in the Inulae for studying the genetic basis of invasiveness in the Asteraceae.

*D. graveolens* is a particularly successful example of apparently climate-driven poleward range expansion, which will be key for many native species to persist under climate change (Urban et al. 2016). *D. graveolens*' rapid native range expansion is associated with the evolution of earlier phenology at the range limit and a niche expansion toward more temperate climates, enabling spread well beyond the expectation under climate tracking alone (Lustenhouwer et al. 2018; Lustenhouwer and Parker 2022). The reference genome presented here provides an opportunity to study the genomic basis of these impactful eco-evolutionary processes and will advance the emerging field of climate change genomics in plants (Lancaster et al. 2022).

In less than 40 years, *D. graveolens* has spread rapidly across California and is a potential threat to rangelands and wildlands undergoing fire recovery and restoration. There is now a strong urgency to understand and control the rapid spread of *D. graveolens* in its invaded range (Brownsey et al. 2013b). Comparative, population and landscape genomic analyses will indicate patterns of selection and evolution in these invading populations, and will help determine how evolution may contribute to invasion risk and impact on both wild and managed ecosystems. We are actively researching these topics and encourage community development and collaboration across the field of invasive species genomics.

## Supplementary material

Supplementary material is available at *Journal of Heredity* online.

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## Conflict of interest

The authors declare that they have no conflicts of interest.

## Data availability

Data generated for this study are available under NCBI BioProject PRJNA919063. Raw sequencing data for sample DitGraRef (NCBI BioSample SAMN32619994) are deposited in the NCBI Short Read Archive (SRA) under SRR23002279-84. Primary and alternate genome assemblies are available in PRJNA919087-8. Raw sequencing data for sample DitGraMitoRef used in the mitochondrial genome assembly is under SRR23255570. Assembly scripts and other data for the analyses presented can be found at the following GitHub repository: <https://doi.org/10.5281/zenodo.7508737>.

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