



Genome Resources

Assembly of the largest squamate reference genome to date: The western fence lizard, *Sceloporus occidentalis*

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Abstract

Spiny lizards (genus *Sceloporus*) have long served as important systems for studies of behavior, thermal physiology, dietary ecology, vector biology, speciation, and biogeography. The western fence lizard, *Sceloporus occidentalis*, is found across most of the major biogeographical regions in the western United States and northern Baja California, Mexico, inhabiting a wide range of habitats, from grassland to chaparral to open woodlands. As small ectotherms, *Sceloporus* lizards are particularly vulnerable to climate change, and *S. occidentalis* has also become an important system for studying the impacts of land use change and urbanization on small vertebrates. Here, we report a new reference genome assembly for *S. occidentalis*, as part of the California Conservation Genomics Project (CCGP). Consistent with the reference genomics strategy of the CCGP, we used Pacific Biosciences HiFi long reads and Hi-C chromatin-proximity sequencing technology to produce a de novo assembled genome. The assembly comprises a total of 608 scaffolds spanning 2,856 Mb, has a contig N50 of 18.9 Mb, a scaffold N50 of 98.4 Mb, and BUSCO completeness score of 98.1% based on the tetrapod gene set. This reference genome will be valuable for understanding ecological and evolutionary dynamics in *S. occidentalis*, the species status of the California endemic island fence lizard (*S. becki*), and the spectacular radiation of *Sceloporus* lizards.

Key words: California Conservation Genomics Project, CCGP, de novo genome assembly, Iguania, Phrynosomatidae, reptile, Squamata

Introduction

The western fence lizard, *Sceloporus occidentalis*, is a widespread species found across most of the major biogeographical regions of the western United States (Fig. 1), ranging from northwestern Washington (United States) to northern Baja California (Mexico) and east to central Utah (United States). Western fence lizards occupy a correspondingly broad range of habitats, including grassland, chaparral, sagebrush, woodland, open coniferous forest, urban yards and landscapes, and farmland, from sea level to 3,350 m (Stebbins and McGinnis 2012). Their widespread distribution, often high local abundance, and easily observable nature have made *S. occidentalis* a model organism for research in areas including behavior, thermal physiology, dietary ecology, and disease vector biology,

among others, and it may be the most actively studied North American lizard (Marcellini and Mackey 1970; Goldberg 1974; Rose 1976; Adolph 1990; Sinervo and Losos 1991; Rochester et al. 2010). The species comprises 5 geographically structured subspecies, all of which occur in California, with 1 former subspecies (*S. o. becki*) recently elevated to species status (*S. becki*; Salerno et al. 2023). *S. occidentalis* also exhibits fine-scale genetic structure (Wishingrad and Thompson 2023) and a complex biogeographic history that includes divergence in a ring-like pattern as populations expanded northward across the Sierra Nevada and coast ranges (Bouzd et al. 2022).

The archetypal western fence lizard exhibits light brown to dark gray dorsal coloration with dark brown to black chevrons in two longitudinal lines down the back, yellow to

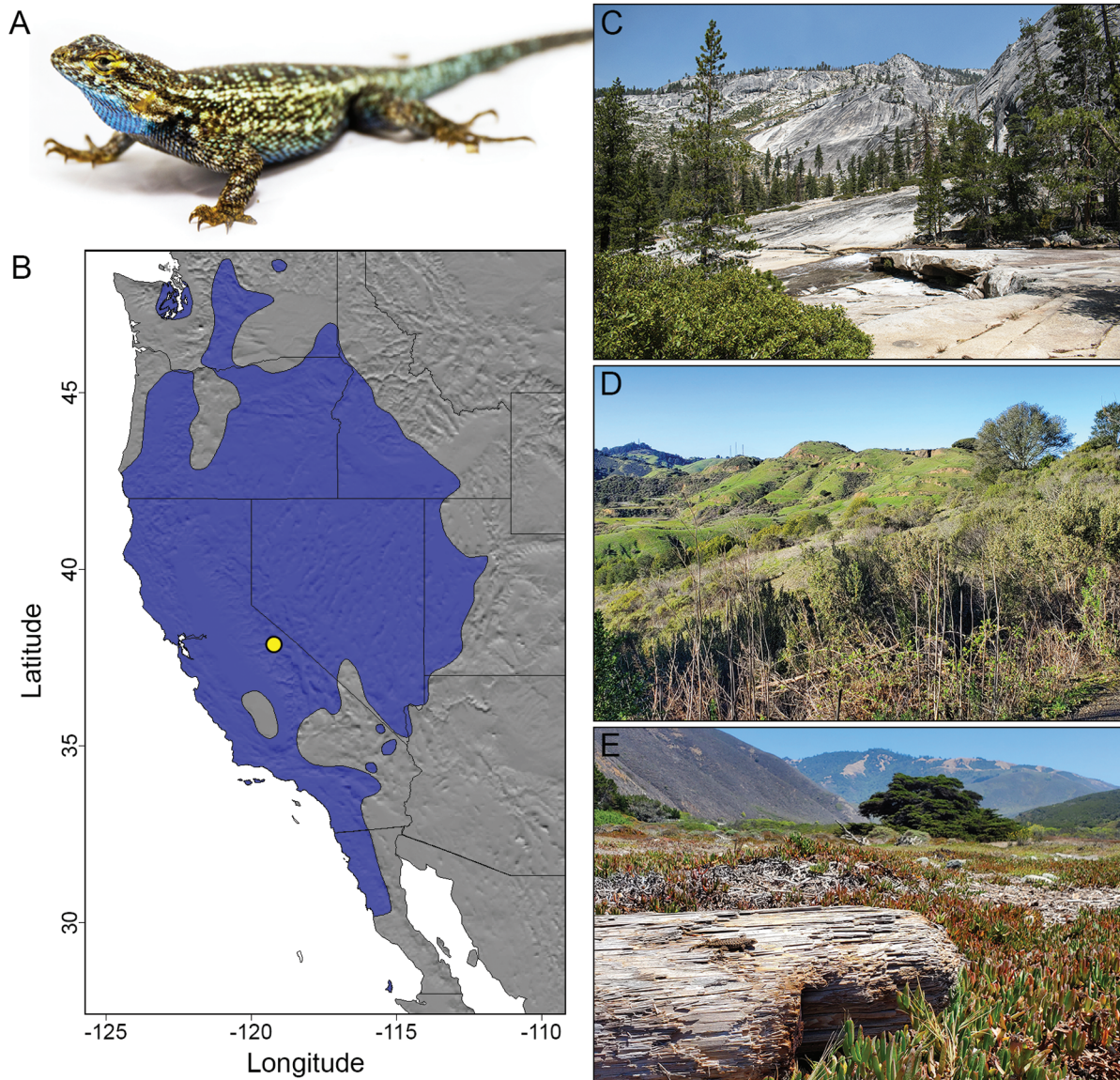


Fig. 1. Photo of the western fence lizard (*Sceloporus occidentalis*) used to generate the reference genome (A) and a range map (B) for *S. occidentalis* based on data from the Global Assessment of Reptile Distributions (Roll et al. 2017) with the location for the genome specimen indicated by the circle. Western fence lizards occupy habitat ranging from montane mixed conifer forest (C) to open woodland and grassland (D) to coastal scrub (E). Note the basking *S. occidentalis* on the log in the foreground of panel E.

orange coloration on the posterior of all limbs, and bright blue to blue-green ventral patches, particularly in adult males, that make them easily recognizable and have given them the colloquial name “blue-bellies.” However, they display phenotypic variation across their range, including distinct high elevation (Leaché et al. 2010) and urban (Putman et al. 2019) phenotypes, revealing the tight coupling between local environmental conditions and external traits. Despite their large range and ability to persist across many habitat types, as small ectotherms these lizards are sensitive to changes in their thermal environment, and spiny lizards (genus *Sceloporus*) are projected to experience significant declines due to climate change (Sinervo et al. 2010). *Sceloporus occidentalis* populations are also frequently affected by urbanization, land use conversion, and habitat fragmentation (Delaney et al. 2010, 2021), making the development of genomic resources in this system valuable for

studies of organismal responses to landscape alteration and climate change, for which *S. occidentalis* could serve as a model system.

Here, we present the first assembled reference genome for *S. occidentalis*, produced as part of the California Conservation Genomics Project (CCGP; Shaffer et al. 2022; Toffelmier et al. 2022). The *S. occidentalis* genome assembly joins 42 other lizard reference genomes, including 4 others for Phrynosomatidae, a family with roughly 140 species. This genome assembly will contribute to our understanding of the ecology and evolution of this widespread, ecologically and scientifically important, charismatic species. Because *S. occidentalis* is an abundant member of most communities in California, this new resource will also contribute to several ongoing and future aspects of California habitat and biodiversity conservation (Amburgey et al. 2021; Fiedler et al. 2022).

Methods

Biological materials

We collected an adult male *S. occidentalis* (field number: IW3139) from Yosemite National Park, Mariposa County, California (37.72642, -119.38959), in August 2020. The specimen was collected under applicable state (SC-8436) and national park (YOSE-2020-SCI-0058) scientific research permits following a protocol approved by the UC Berkeley Animal Care and Use Committee (AUP-2016-02-8453-2). We removed liver tissue, immediately flash froze it in liquid nitrogen, and stored it at -80 °C until extraction of genomic DNA (gDNA).

DNA extraction

High molecular weight (HMW) gDNA was extracted from 30 mg of liver tissue using the Nanobind Tissue Big DNA kit following the manufacturer's instructions (Pacific BioSciences—PacBio, Menlo Park, California). DNA purity was estimated using absorbance ratios ($260/280 = 1.85$ and $260/230 = 2.40$) on a NanoDrop ND-1000 spectrophotometer. The final DNA yield (298 ng/μL; 37 μg) was quantified using a Quantus Fluorometer (QuantiFluor ONE dsDNA Dye assay; Promega, Madison, Wisconsin). The size distribution of the HMW DNA was estimated using the Femto Pulse system (Agilent, Santa Clara, California) which indicated that 63% of the fragments were 100 kb or longer.

HiFi library preparation and sequencing

The HiFi SMRTbell library was constructed using the SMRTbell Express Template Prep Kit v2.0 (PacBio, Cat. #100-938-900) according to the manufacturer's instructions. HMW gDNA was sheared to a target DNA size distribution between 15 and 20 kb. The sheared gDNA was concentrated using 0.45× of AMPure PB beads (PacBio, Cat. #100-265-900) for the removal of single-strand overhangs at 37 °C for 15 min, followed by further enzymatic steps of DNA damage repair at 37 °C for 30 min, end repair and A-tailing at 20 °C for 10 min and 65 °C for 30 min, ligation of overhang adapter v3 at 20 °C for 60 min and 65 °C for 10 min to inactivate the ligase, then nuclease treated at 37 °C for 1 h. The SMRTbell library was purified and concentrated with 0.45× Ampure PB beads (PacBio, Cat. #100-265-900) for size selection using the BluePippin/PippinHT system (Sage Science, Beverly, Massachusetts; Cat. #BLF7510/HPE7510) to collect fragments greater than 7 to 9 kb. The 15 to 20 kb average HiFi SMRTbell library was sequenced at the University of California Davis DNA Technologies Core (Davis, California) using five 8M SMRT cells, Sequel II sequencing chemistry 2.0, and 30-h movies each on a PacBio Sequel II sequencer.

Omni-C library preparation and sequencing

The Omni-C library was prepared using the Dovetail Omni-C Kit (Dovetail Genomics, California) according to the manufacturer's protocol with slight modifications. First, specimen tissue was thoroughly ground with a mortar and pestle while cooled with liquid nitrogen, after which chromatin was fixed in place in the nucleus. The suspended chromatin solution was then passed through 100 and 40 μm cell strainers to remove large debris. Fixed chromatin was digested under various conditions of DNase I until a suitable fragment length distribution of DNA molecules was obtained. Chromatin ends were repaired and ligated to a

biotinylated bridge adapter followed by proximity ligation of adapter-containing ends. After proximity ligation, crosslinks were reversed, and the DNA was purified from proteins. Purified DNA was treated to remove biotin that was not internal to ligated fragments. An NGS library was generated using an NEB Ultra II DNA Library Prep kit (New England Biolabs, Ipswich, Massachusetts) with an Illumina compatible y-adaptor. Biotin-containing fragments were then captured using streptavidin beads. The post-capture product was split into 2 replicates prior to PCR enrichment to preserve library complexity, with each replicate receiving unique dual indices. The library was sequenced at Vincent J. Coates Genomics Sequencing Lab (Berkeley, California) on an Illumina NovaSeq platform (Illumina, San Diego, California) to generate approximately 100 million 2×150 bp read pairs per GB of genome size.

Nuclear genome assembly

We assembled the *S. occidentalis* genome following the CCGP assembly pipeline Version 4, which uses PacBio HiFi reads and Omni-C data to produce high-quality and highly contiguous genome assemblies while minimizing manual curation (outlined in Table 1). We removed remnant adapter sequences from the PacBio HiFi dataset using HiFiAdapterFilt (Sim et al. 2022) and obtained the initial dual or partially phased diploid assembly (<http://lh3.github.io/2021/10/10/introducing-dual-assembly>) using HiFiasm (Cheng et al. 2021) with the filtered PacBio HiFi reads and the Omni-C dataset. We tagged output haplotype 1 as the primary assembly and output haplotype 2 as the alternate assembly. We identified sequences corresponding to haplotypic duplications, contig overlaps, and repeats on the primary assembly with purge_dups (Guan et al. 2020) and transferred them to the alternate assembly. We scaffolded both assemblies using the Omni-C data with SALSA (Ghurye et al. 2017, 2018).

We generated Omni-C contact maps by aligning the Omni-C data against both assemblies with BWA-MEM (Li 2013) and identified ligation junctions and generated Omni-C pairs using pairtools (Goloborodko et al. 2018). We generated a multiresolution Omni-C matrix with cooler (Abdennur an Mirny 2020) and balanced it with HiCExplorer (Ramírez et al. 2018). We used HiGlass [Version 2.1.11] (Kerpedjiev et al. 2018) and the PretextView (<https://github.com/wtsi-hpag/PretextView>); <https://github.com/wtsi-hpag/PretextView>; <https://github.com/wtsi-hpag/PretextView>) to visualize the contact maps. We checked the contact maps for major misassemblies, cutting the scaffolds where misassemblies were identified. No further joins were made after this step. Using the PacBio HiFi reads and YAGClosier (<https://github.com/merlyescalona/yagcloser>) we closed some of the remaining gaps generated during scaffolding. We then checked for contamination using the BlobToolKit framework (Challis et al. 2020). Finally, we trimmed remnants of sequence adaptors and mitochondrial contamination identified during NCBI contamination screening.

Mitochondrial genome assembly

We assembled the mitochondrial genome of *S. occidentalis* from the PacBio HiFi reads using the reference-guided pipeline MitoHiFi (<https://github.com/marcelauliano/MitoHiFi>; Allio et al. 2020). An existing mitochondrial sequence for *S. occidentalis* (NCBI:AB079242.1) was used as the starting

Table 1. Assembly pipeline and software used.

Assembly	Software and options	Version
Filtering PacBio HiFi adapters	HiFiAdapterFilt	Commit 64d1c7b
K-mer counting	Meryl (k = 21)	1
Estimation of genome size and heterozygosity	GenomeScope	2
De novo assembly (contigging)	HiFiasm (Hi-C Mode, -primary, output p_ctg.hap1, p_ctg.hap2)	0.16.1-r375
Remove low-coverage, duplicated contigs	purge_dups	1.2.6
Scaffolding		
Omni-C scaffolding	SALSA (-DNASE, -i 20, -p yes)	2
Gap closing	YAGCloser (-mins 2 -f 20 -mcc 2 -prt 0.25 -eft 0.2 -pld 0.2)	Commit 0e34c3b
Omni-C contact map generation		
Short-read alignment	BWA-MEM (-5SP)	0.7.17-r1188
SAM/BAM processing	samtools	1.11
SAM/BAM filtering	pairtools	0.3.0
Pairs indexing	pairix	0.3.7
Matrix generation	cooler	0.8.10
Matrix balancing	hicExplorer (hicCorrectmatrix correct --filterThreshold -2 4)	3.6
Contact map visualization	HiGlass	2.1.11
	PretextView	0.1.4
	PretextView	0.1.5
	PretextViewSnapshot	0.0.3
Organelle assembly		
Mitogenome assembly	MitoHiFi (-r, -p 50, -o 1)	2 Commit c06ed3e
Genome quality assessment		
Basic assembly metrics	QUAST (--est-ref-size)	5.0.2
Assembly completeness	BUSCO (-m geno, -l tetrapoda)	5.0.0
	Mercury	2020-01-29
Contamination screening		
Local alignment tool	BLAST+	2.1
General contamination screening	BlobToolKit	2.3.3

Software citations are listed in the text.

sequence. After completion of the nuclear genome, we searched for matches of the resulting mitochondrial assembly sequence in the nuclear genome assembly using BLAST+ (Camacho et al. 2009) and filtered out contigs and scaffolds from the nuclear genome with a percentage of sequence identity >99% and size smaller than the mitochondrial assembly sequence.

Genome size estimation and quality assessment

We generated k-mer counts from the PacBio HiFi reads using meryl (<https://github.com/marbl/meryl>). The k-mer database was then used in GenomeScope2.0 (Ranallo-Benavidez et al. 2020) to estimate genome features including genome size, heterozygosity, and repeat content. To obtain general contiguity metrics, we ran QUAST (Gurevich et al. 2013). To evaluate genome quality and completeness we used BUSCO (Manni et al. 2021) with the Tetrapoda ortholog database (tetrapoda_odb10), which contains 5,310 genes. Assessments of base-level accuracy (QV) and k-mer completeness were performed using the previously generated meryl database and mercury (Rhie et al. 2020). We further estimated genome assembly accuracy via BUSCO gene set frameshift analysis using the pipeline described in Korlach et al. (2017).

Measurements of the size of the phased blocks are based on the size of the contigs generated by HiFiasm in Hi-C mode. We followed the quality metric nomenclature established by Rhie et al. (2021), with the genome quality code $x \cdot y \cdot P \cdot Q \cdot C$, where $x = \log_{10}[\text{contig NG50}]$; $y = \log_{10}[\text{scaffold NG50}]$; $P = \log_{10}[\text{phased block NG50}]$; $Q = \text{Phred base accuracy QV (quality value)}$; and $C = \% \text{ genome represented by the first "n" scaffolds, following a known karyotype of } 2n = 2 \cdot 2 \text{ for } S. occidentalis \text{ (Jackson and Hunsacker 1970)}$. Quality metrics for the notation were calculated on the primary assembly.

Results

The Omni-C and PacBio HiFi sequencing libraries generated 290 million read pairs and 5.3 million reads, respectively. The latter yielded 29.94-fold coverage (N50 read length 16,535 bp; minimum read length 45 bp; mean read length 16,088 bp; maximum read length of 63,768 bp) based on the GenomeScope2.0 genome size estimation of 2.8 Gb. Based on PacBio HiFi reads, we estimated 0.168% sequencing error rate and 0.521% nucleotide heterozygosity rate. The k-mer spectrum based on PacBio HiFi reads

show a bimodal distribution with a major peak at ~29-fold coverage (Fig. 2A), which supports that of a low heterozygosity profile.

The final assembly (rSceOcc1) consists of two pseudo haplotypes, primary and alternate. Genome size for the primary assembly is similar to the estimated value from GenomeScope2.0 (Fig. 2A), but the alternate is ~400 Mb

larger. The primary assembly consists of 608 scaffolds spanning 2.8 Gb with contig N50 of 18.9 Mb, scaffold N50 of 98.4 Mb, longest contig of 124.1 Mb and largest scaffold of 320.8 Mb. The alternate assembly consists of 1,822 scaffolds, spanning 3.2 Gb with contig N50 of 17.6 Mb, scaffold N50 of 38.7 Mb, largest contig 115.5 Mb, and largest scaffold of 309.6 Mb. Detailed assembly statistics

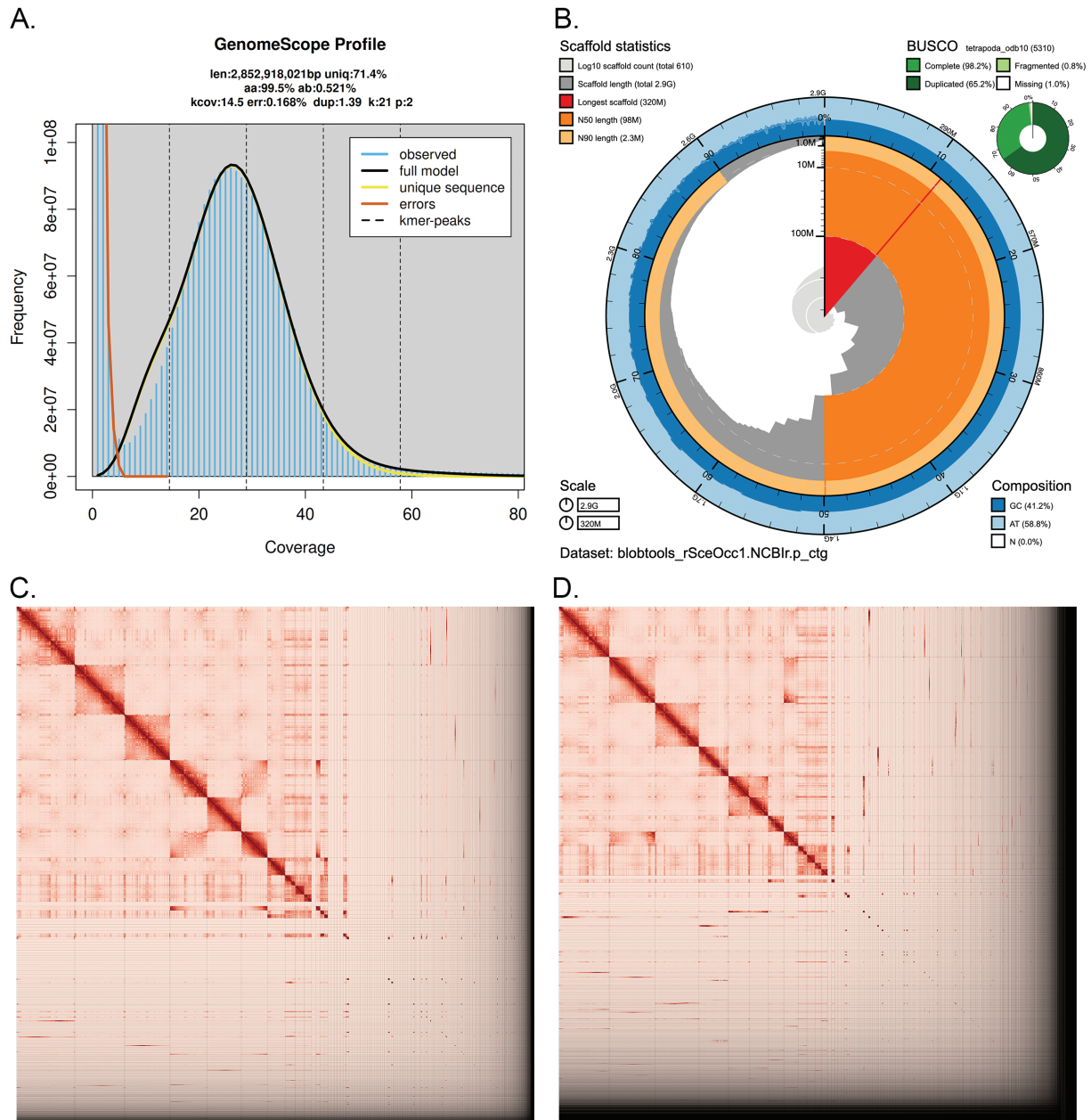


Fig. 2. Visual overview of genome assembly metrics. A) K-mer spectrum output generated from PacBio HiFi data without adapters using GenomeScope2.0. B) BlobToolKit Snail plot showing a graphical representation of the quality metrics presented in Table 2 for the *S. occidentalis* primary assembly (rSceOcc1). The plot circle represents the full size of the assembly. From the inside out, the central plot covers length-related metrics. The red line represents the size of the longest scaffold; all other scaffolds are arranged in size-order moving clockwise around the plot and drawn in gray, starting from the outside of the central plot. Dark and light orange arcs show the scaffold N50 and scaffold N90 values. The central light gray spiral shows the cumulative scaffold count with a white line at each order of magnitude. White regions in this area reflect the proportion of Ns in the assembly; the dark vs. light blue area around it shows mean, maximum, and minimum GC vs. AT content at 0.1% intervals (Challis et al. 2020). Hi-C contact maps for the primary (C) and alternate (D) genome assembly were generated with PretextSnapshot. Hi-C contact maps translate proximity of genomic regions in 3D space to contiguous linear organization. Each cell in the contact map corresponds to sequencing data supporting the linkage (or join) between 2 such regions. Scaffolds are separated by black lines, and higher density corresponds to higher levels of fragmentation.

Table 2. Sequencing and assembly statistics and accession numbers.

BioProjects and Vouchers	CCGP NCBI BioProject	PRJNA720569
	Genus NCBI BioProject	PRJNA765857
	Species NCBI BioProject	PRJNA777217
	NCBI Bio-sample	SAMN27480378
	Specimen identification number	IW3139
Genome Sequence	PacBio HiFi long read runs	1 PacBio SMRT Sequel II run: 5.7 M spots, 85.9 Gbp, 57.2 Gb
	OmniC Illumina sequencing	1 Illumina NovaSeq 6000 run: 290 M spots, 87.5 Gbp, 28 Gb
	PacBio HiFi NCBI SRA Accession	SRX15651255
	OmniC Illumina NCBI SRA Accession	SRX15651256, SRX15651257
Genome Assembly Primary (Alternate)	Assembly identifier	rSceOcc1
	HiFi read coverage	37.14x
	Number of contigs (primary/alternate)	659/1,822
	Contig N50 (bp)	18,989,278/17,628,953
	Contig NG50 ^b (bp)	18,989,278/20,278,101
	Longest contigs (primary/alternate)	124,125,603/115,579,027
	Number of scaffolds (primary/alternate)	608/1,771
	Scaffold N50 (bp)	98,418,489/38,771,511
	Scaffold NG50 ^b	98,418,489/88,220,525
	Size of final assembly (bp)	2,856,356,971/3,186,658,811
	Gaps per Gbp (# gaps)	18 (51)/16 (51)
	NCBI Genome Assembly Accession	GCA_000XXXXXX.1
	Assembly quality identifier ^a	7.7.P7.Q61.C57
	Base pair QV (mercury)	P: Q 61.6835, A: Q 61.4466
	Assembly Quality ^c	Indel QV (frameshift analysis)
K-mer completeness		P: 92.8931%, A: 93.6217%
BUSCO completeness		98.10%:32.90%:65.20%:0.80%:1.10%
Primary (C:S:D:F:M)		98.30%:31.90%:66.40%:0.70%:1.00%
Alternate (C:S:D:F:M)		
Organelles	1 complete mitochondrial sequence CM041364.1	

^aAssembly quality code $x \cdot y \cdot P \cdot Q \cdot C$ derived notation, from [Rhie et al. \(2021\)](#). $x = \log_{10}[\text{contig NG50}]$; $y = \log_{10}[\text{scaffold NG50}]$; $P = \log_{10}[\text{phased block NG50}]$; $Q = \text{Phred base accuracy QV (quality value)}$; $C = \% \text{ genome represented by the first "n" scaffolds, following a known karyotype for SPECIES of 2n} = 22$. Quality code for all the assembly denoted by primary assembly (rSceOcc1.0.p).

^bRead coverage and NGx statistics have been calculated based on the estimated genome size of 2.85 Gb.

^c(P)primary and (A)lternate assembly values.

are reported in [Table 2](#) and graphical representation for the primary assembly in [Fig. 2B](#) (see Supplementary Fig. 1 for the alternate assembly). The primary assembly has a BUSCO completeness score of 98.1% using the Tetrapoda gene set, a per-base quality (QV) of 61.68, a k-mer completeness of 92.89 and a frameshift indel QV of 48.71, while the alternate assembly has a BUSCO completeness score of 98.3% using the same gene set, a per-base quality (QV) of 61.39, a k-mer completeness of 93.62 and a frameshift indel QV of 49.12.

We identified 2 misassemblies on the alternate assembly and broke the corresponding joins made by SALSA. We were able to close a total of 9 gaps, 7 on the primary assembly and 2 on the alternate. Finally, we filtered out 34 contigs, 2 from the primary and 32 from the alternate assembly, corresponding to mitochondrial contamination. No further contigs were removed. We have deposited both assemblies on NCBI (see [Table 2](#) and Data Availability for details).

We assembled a mitochondrial genome using MitoHiFi. The final mitochondrial genome assembly size is 14,426 bp. The final assembly version has a base composition of A = 39.95%, C = 17.11%, G = 10.38%, T = 32.56% and

consists of 20 unique transfer RNAs and 12 protein-coding genes.

Discussion

There are currently 89 other squamate genomes, including 42 lizards and 47 snakes, available on NCBI, ranging in size from 1.13 to 2.74 Gb (mean = 1.64 Gb), making the *S. occidentalis* genome the largest squamate reference genome assembled so far. At 2.86 Gb, the *S. occidentalis* genome is 4.2% larger than the next largest, the Japanese gecko, *Gekko gekko* ([Liu et al. 2015](#)). The 89 other squamate reference genomes have an average contig N50 of 14.5 Mb (ranging from 1.1 kb to 127.8 Mb), placing the contig N50 of 19.0 Mb for our *S. occidentalis* assembly in the upper end of this range, below only 17 other reference genomes.

Three of these existing 89 reference genomes are also phrynosomatid lizards, including two other *Sceloporus* species (*S. tristichus* and *S. undulatus*). The genome assembly sizes of these other species range from 1.82 Gb to 1.91 Gb (mean = 1.87 Gb), so the *S. occidentalis* genome is considerably larger than those of its congeners. Both of these species

and *S. occidentalis* are members of the same phylogenetic clade within *Sceloporus*, the *undulatus* group, which has a crown age of 15 to 20 million years (Leaché et al. 2016). Until recently *S. tristichus* and *S. undulatus* were considered conspecific lineages, and so their very similar genome assembly sizes are not surprising. However, the differences in putative genome sizes between these two close relatives and *S. occidentalis* suggest either substantial genome size evolution within the genus or the under- or overestimation of genome size for one or more of these species. The C value for *S. occidentalis* is 2.36 Gb, based on Feulgen densitometry (Olmo 1981), suggesting a genome size larger than the 1.82 Gb *S. tristichus* (Bedoya and Leaché 2021) and 1.91 Gb *S. undulatus* (Westfall et al. 2021) genome assemblies. The description of the *S. undulatus* genome indicates that the assembly may be missing some data or has repeat regions condensed (Westfall et al. 2021). It is also possible that our current assembly overestimates the size of the *S. occidentalis* genome, although this seems unlikely given the high BUSCO completeness (98.4%, see Table 2) and the relatively large estimate based on Feulgen densitometry (Olmo 1981).

The *S. occidentalis* reference genome provides a valuable resource for studying the conservation, ecology, and evolutionary dynamics of this species and other spiny lizards. The genus *Sceloporus* constitutes a rapid radiation containing more than 100 species, and the *Sceloporus* phylogeny as currently understood is characterized by high levels of gene tree discordance (Leaché et al. 2016). This reference genome can help to further resolve the species relationships in this speciose clade of lizards. It will also contribute to understanding patterns of speciation in this group, identifying regions of the genome involved in adaptation to environmental variation and rapid speciation, and examining the evolutionary dynamics in the complex biogeographic history of *S. occidentalis*.

Supplementary material

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

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Data availability

Data generated for this study are available under NCBI BioProject PRJNA720569. Raw sequencing data for sample IW3139 (NCBI BioSample SAMN27480378) are deposited in the NCBI Short Read Archive (SRA) under SRX15651255, SRX15651256, and SRX15651257. Assembly scripts and other data for the analyses presented can be found at the following GitHub repository: www.github.com/ccgproject/ccgp_assembly.

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