

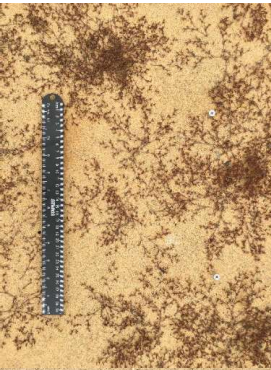
Genomic structure of *Chorizantho orcuttiana*

Jyotsna Sharma and Jaspreet Kaur

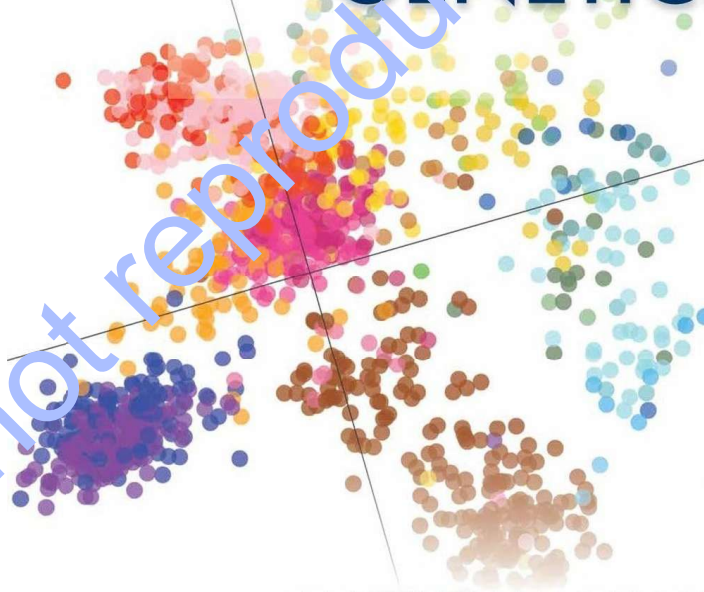
Texas Tech University

Wednesday, 24 June 2026

Chorizantho orcuttiana



MOLECULAR
POPULATION
GENETICS



Major Topics

1. Introduction to the species and our conservation research that inspired the population genetics questions.
2. Genetic investigations



Chorizanthe orcuttiana

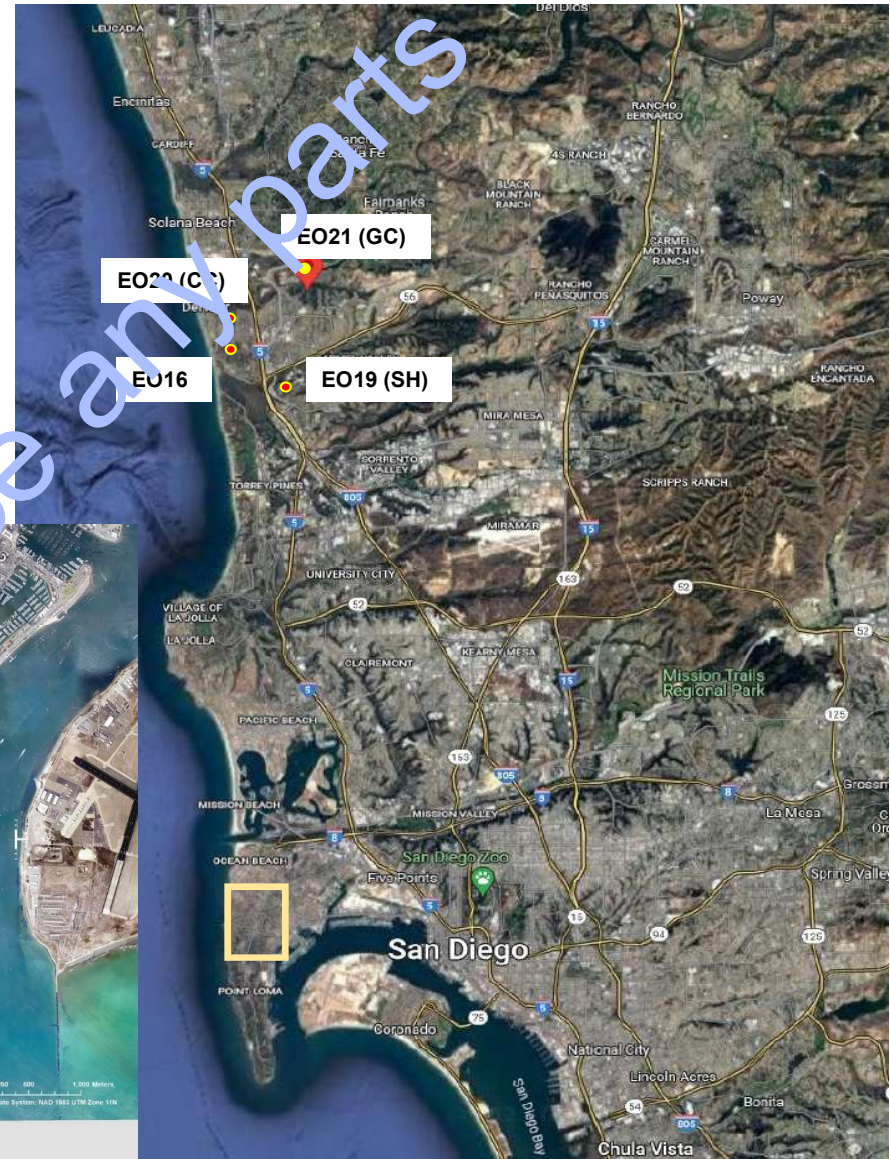
- Polygonaceae
- Listed Endangered (October 7, 1996) by the federal Endangered Species Act; endemic to San Diego County, CA
- Nine (9) extant natural populations
- A polyploid that exhibits allopoloidy (chromosomes from different parental species), is an octoploid, and can be an aneuploid (abnormal no. of chromosomes)
- Exhibits demographic and phenotypic variation in fitness across space and time
- Appears to respond to targeted, intensive, strategic management



Known extant occurrences - nine

NBPL - 1,918 acres

527 acres - Point Loma Ecological
Conservation Area (**PLECA**)

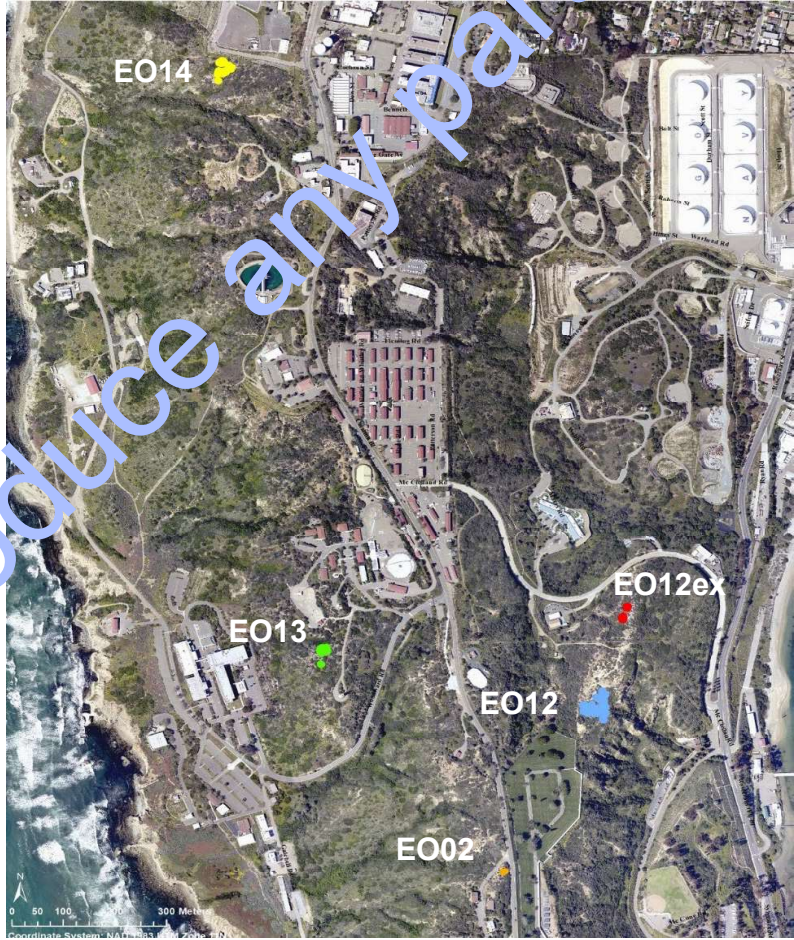
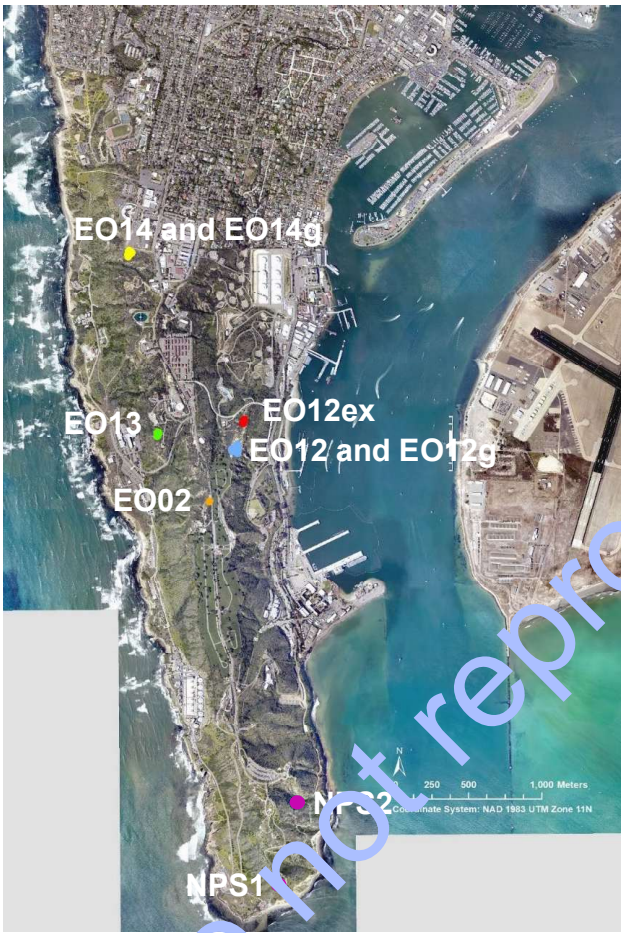


Geographic distances (Km) among populations

	EO12	EO14	EO13	EO16	EO20	EO21	EO02
EO12	00.0						
EO14	01.6	00.0					
EO13	00.6	01.3	00.0				
EO16	27.6	26.2	27.5	00.0			
EO20	28.8	27.4	28.7	01.3	00.0		
EO21	30.2	28.8	30.1	03.6	03.1	00.0	
EO02	00.4	01.8	00.6	28.0	29.2	30.5	00.0



Point Loma Peninsula



What we inherited

April 2016



Where we are now

May 2025



Rare Plant Research & Management at Naval Base Point Loma

Jyotsna Sharma, Ph.D.
Professor of Plant & Microbial Ecology and Conservation
Texas Tech University

Chorizanthe orcuttiana population illustrating a 'carpet' of plants as a result of adaptive management and efforts by Texas Tech University (PI J. Sharma). Adaptive management strategies have allowed natural populations to become more sustained and persistent through the years when exposed to temporal weather-related pressures. Plants and populations, however, exhibit high sensitivity to lack of appropriate management and / or timely adaptive intervention.

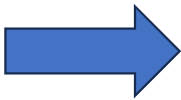
Chorizanthe orcuttiana plants at NBPL exhibit the potential to grow larger in size (i.e., increased plant fitness leading to higher seed production) because of the management activities PI J. Sharma of Texas Tech University



Adaptive management works



Adaptive management works



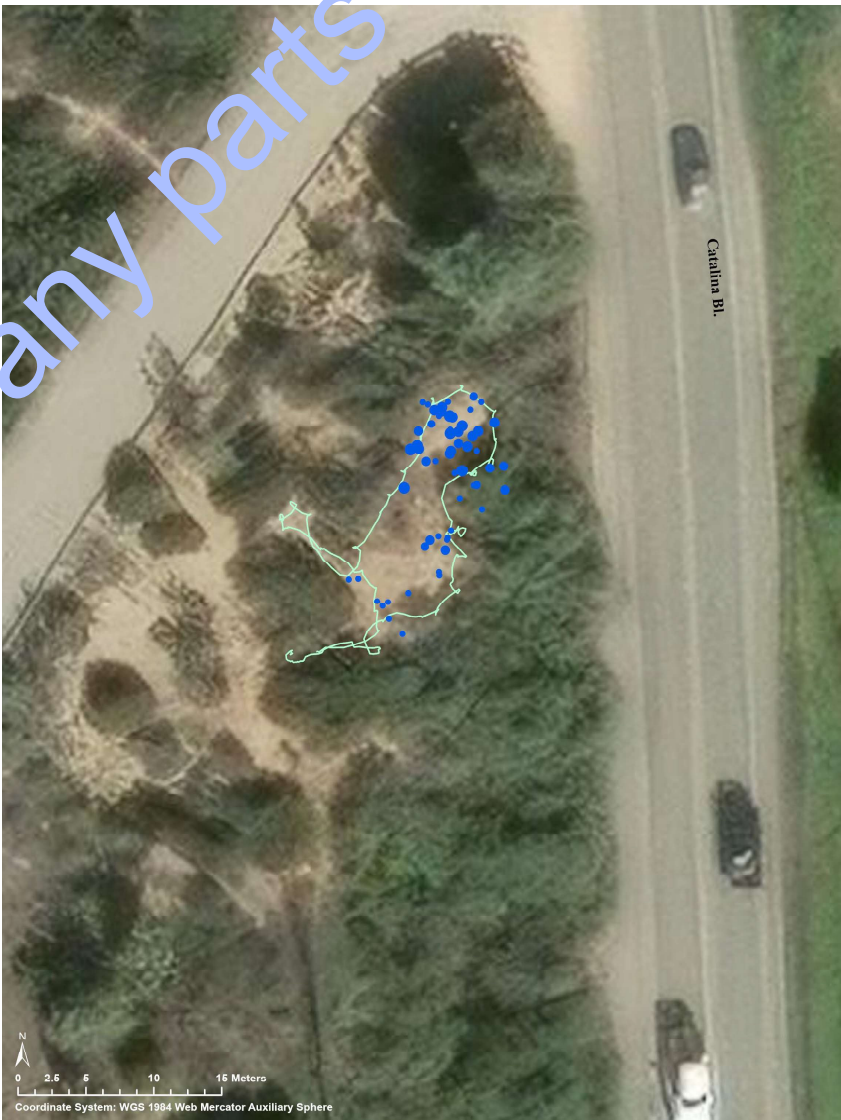
Year	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
Site												
EO02	n/a	n/a	n/a	n/a	n/a	n/a	98	12	-	556	882	3908
EO12	246	1102	622	2490	3629	2955	7973	187	-	2140	4837	20449
EO12ex	0	-	2	-	-	265	874	242	-	246	140	115
EO13	0	61	42	50	291	326	1130	504	-	712	1737	6484
EO14	0	171	76	219	177	571	2255	2458	-	5122	16854	66210

Chorizanthe orcuttiana

2025 EO02 census map
Area of active management = $\geq 650 \text{ m}^2$



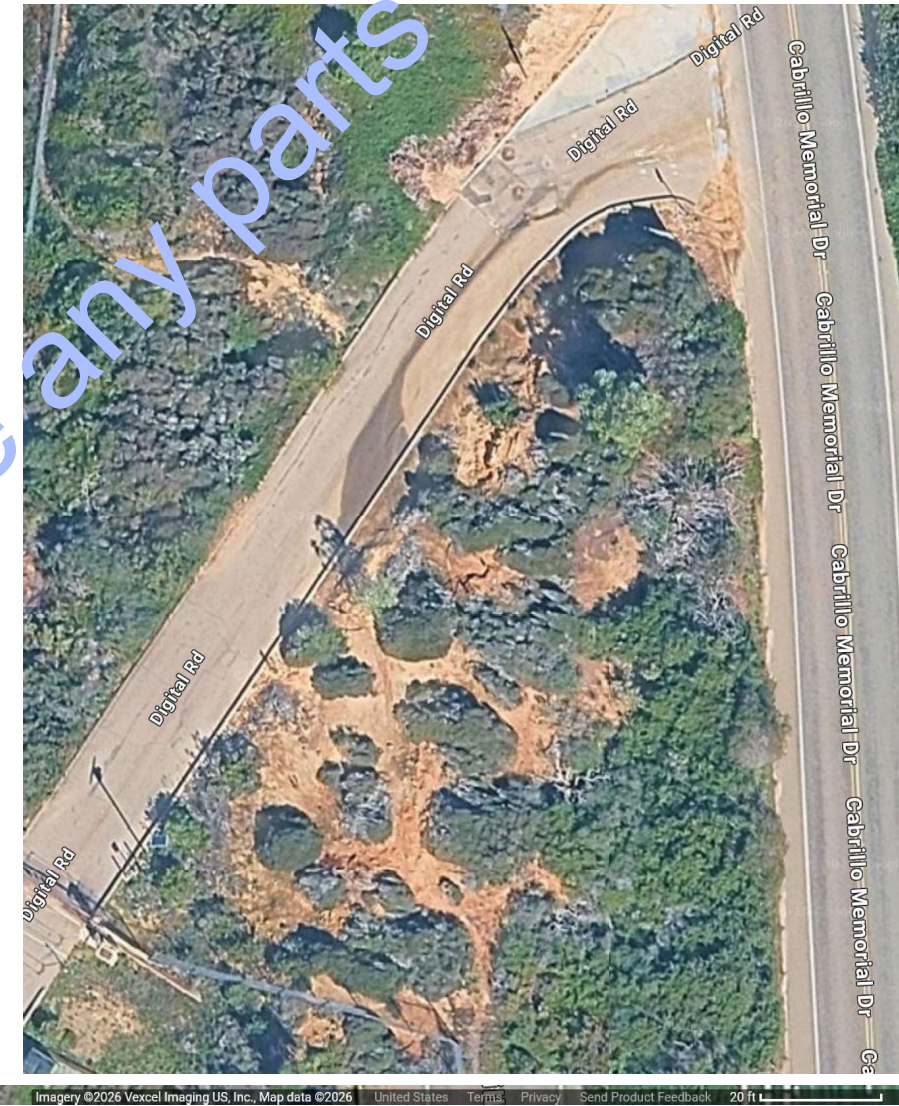
- 1-25
- 26-50
- 51-80
- 80-150
- 151-270
- EO02 survey tracks



Chorizanthe orcuttiana

2025 EO02

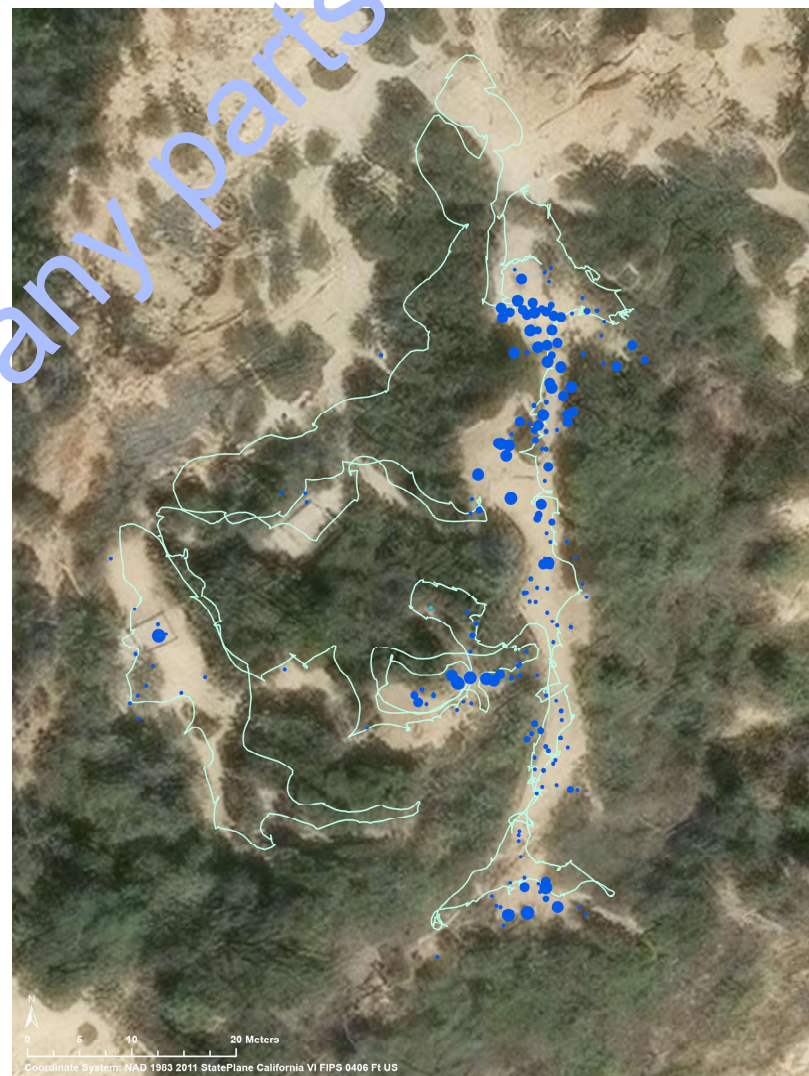
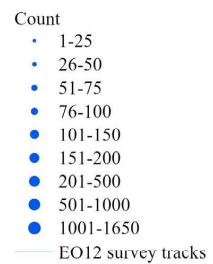
Increased area of active management by ~ 65m²



Chorizanthe orcuttiana

2025 EO12 census map

Area of active management = $\geq 4000 \text{ m}^2$



Chorizanthe orcuttiana

2025 EO12ex census map

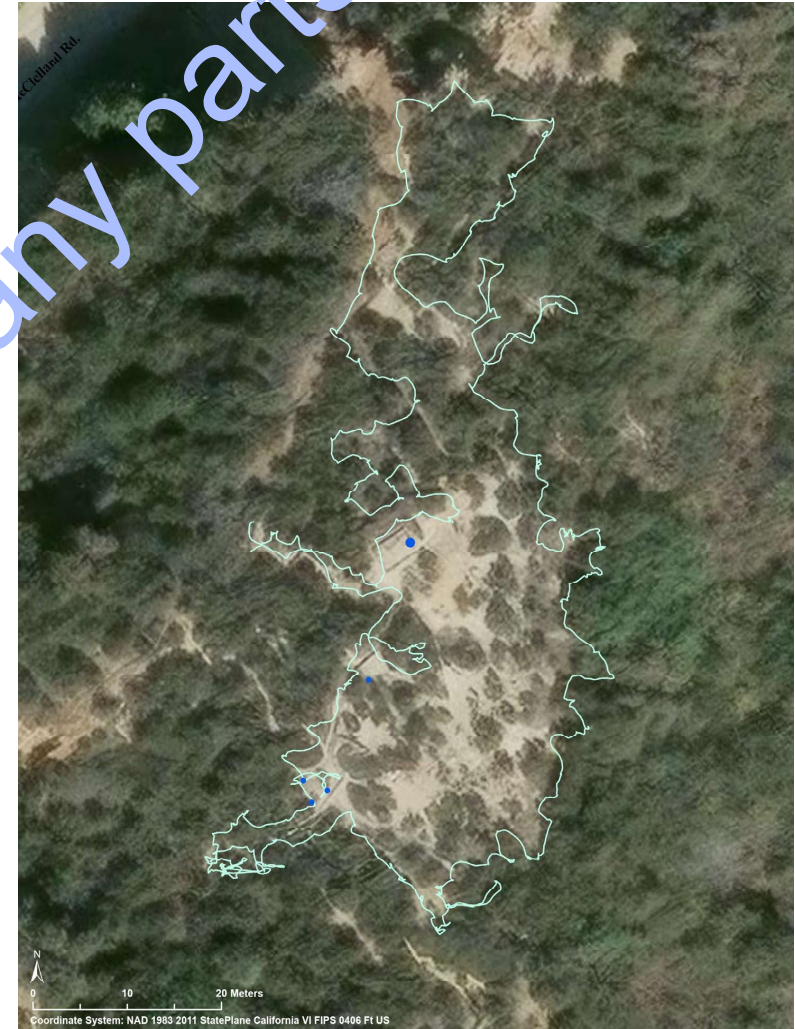
Area of active management = $\geq 2500 \text{ m}^2$



Count

- 1-25
- 106

— EO12ex survey tracks



Chorizanthe orcuttiana

2025 EO13 census map

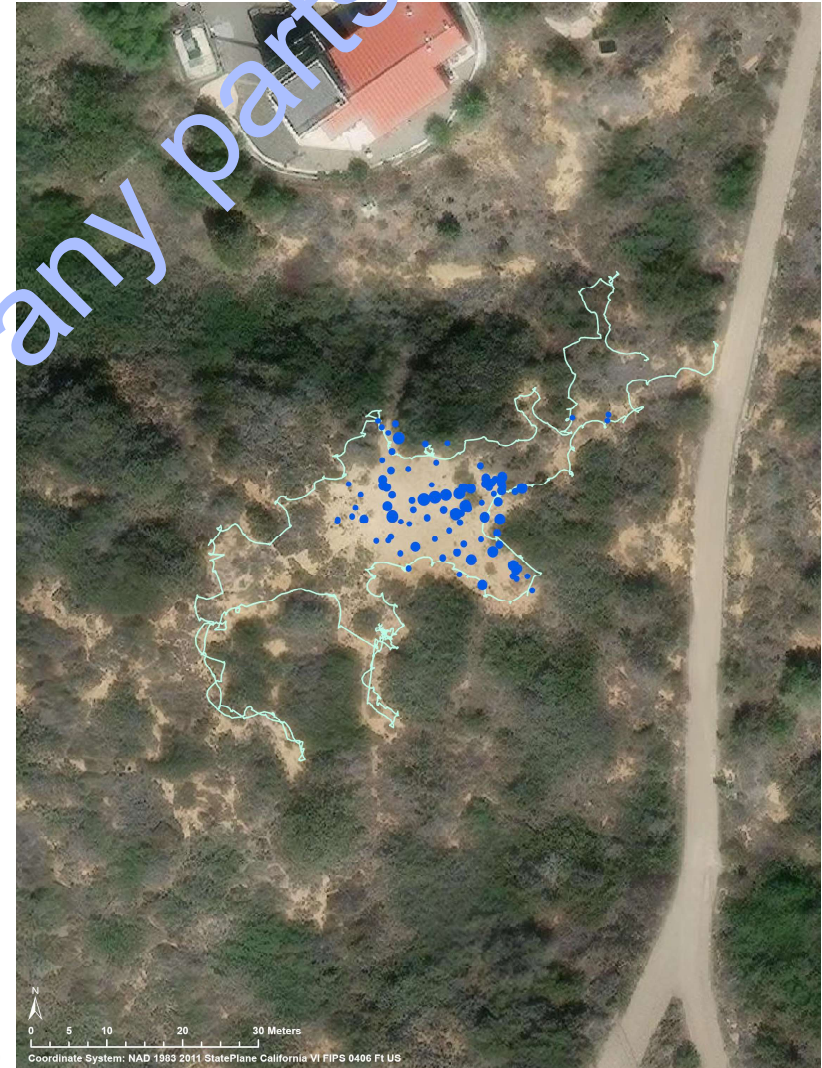
Area of active management = $\geq 2700 \text{ m}^2$



Count

- 1-25
- 26-50
- 51-75
- 76-100
- 101-150
- 151-200
- 201-300
- 301-410

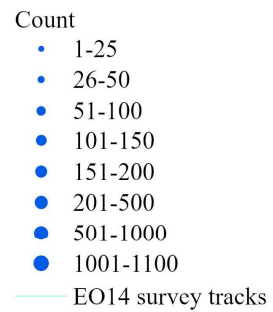
— EO13 survey tracks



Chorizanthe orcuttiana

2025 EO14 census map

Area of active management = $\geq 4000 \text{ m}^2$



Adaptive management

Empirical data and intensive, strategic interventions (i.e., management)

Understanding population dynamics, demography, and plant fitness



Microclimate (soil edaphic, microbial, environmental variables); recruitment, mortality, plant fitness, population size

Coupled approaches:
natural, and manipulative experiments

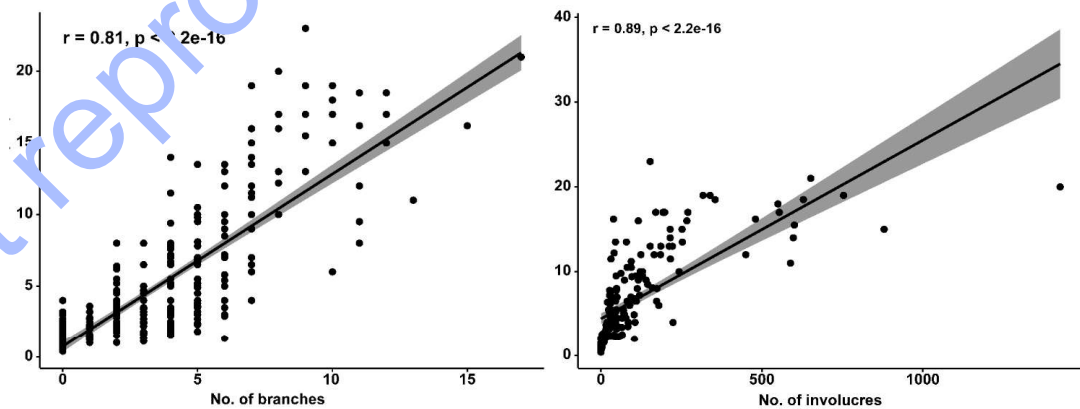
PLANT SPECIES BIOLOGY

ORIGINAL ARTICLE |  Full Access

Seed germination and plant fitness response of a narrowly endemic, rare winter annual to spatial heterogeneity in microenvironment

Jaspreet Kaur✉, Dylan Schwilk, Jyotsna Sharma

Plant fitness - plant width, number of stems, and number of involucre were measured. (Plant width was a strong indicator of plant fitness)



Spearman's correlation between plant width, number of branches, and number of involucre

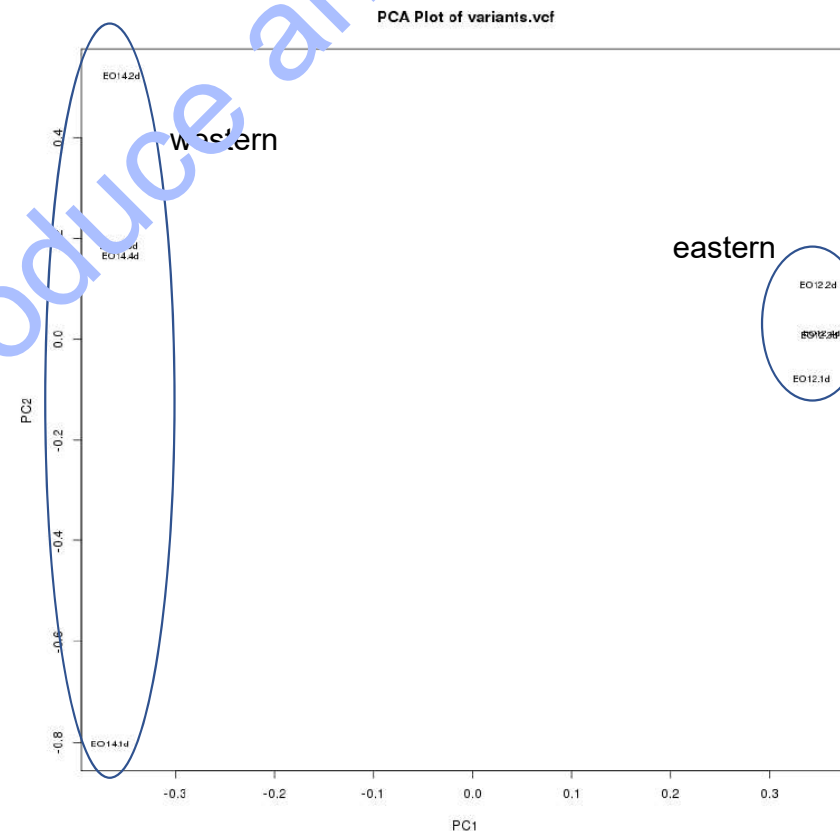
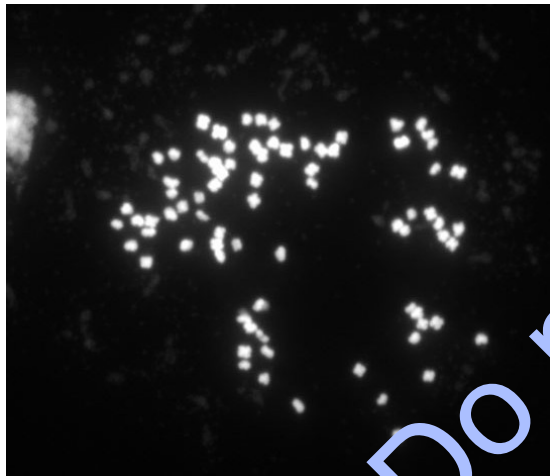
Given the observations, curiosity about patterns of genetic variation (relation to phenotypic variation, gene expression, epigenetics...)

- 1) Created 8 dual-indexed GBS libraries using enzyme combination PstI+MspI.
- 2) Combined all libraries into a single pool and sequenced on a NextSeq HO 1x150-bp run.
- 3) Generated ≥ 32 M reads for the pool.
- 4) All expected barcodes and samples detected.
- 5) Mean quality scores $\approx Q30$ for all libraries.

genome size $\sim 1\text{-}1.5\text{Gb}$
 $n=(18\text{--}19)20(21)$

Reads_per_sample	Filtered_marker_number	Filtered_loci_number
500000	2238	1425
1000000	2655	1747
2000000	3115	2090
4000000	3426	2343

***Chorizanthe orcuttiana* karyotyping**
Range 62 to 78 chromosomes (this individual)

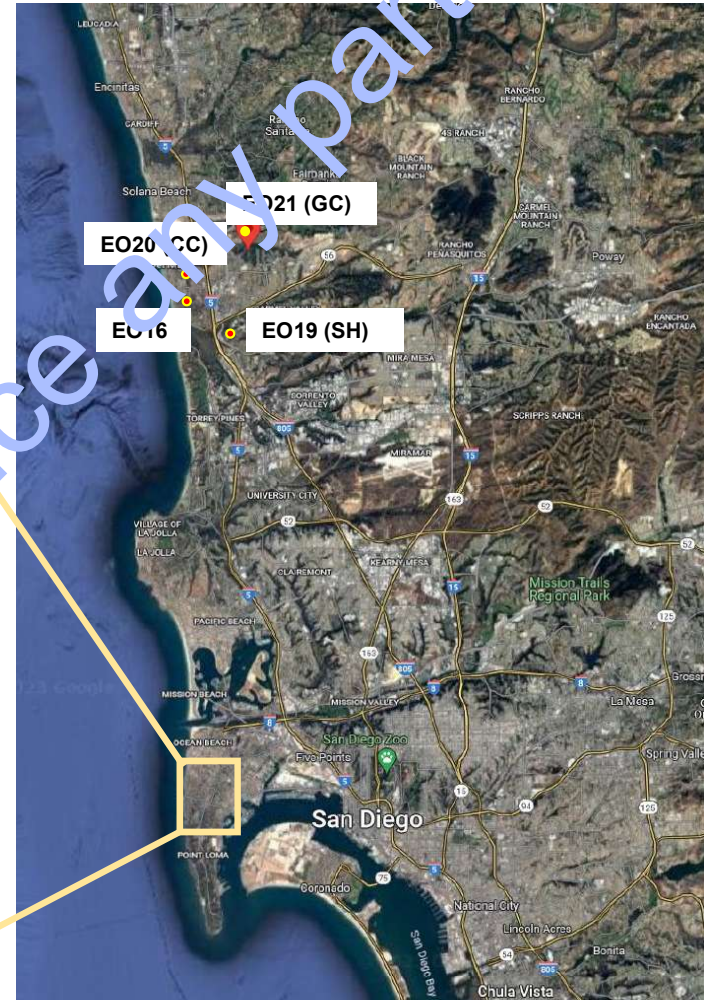
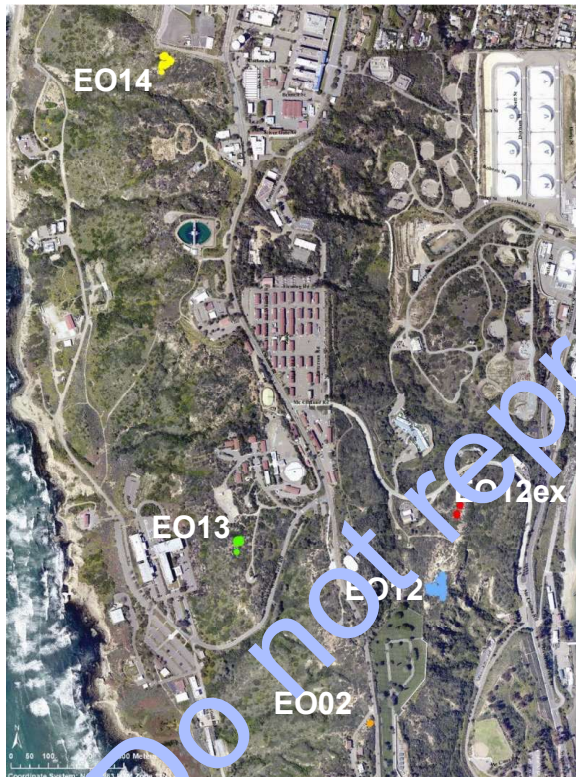


Range-wide genetic structure

5 peninsular populations

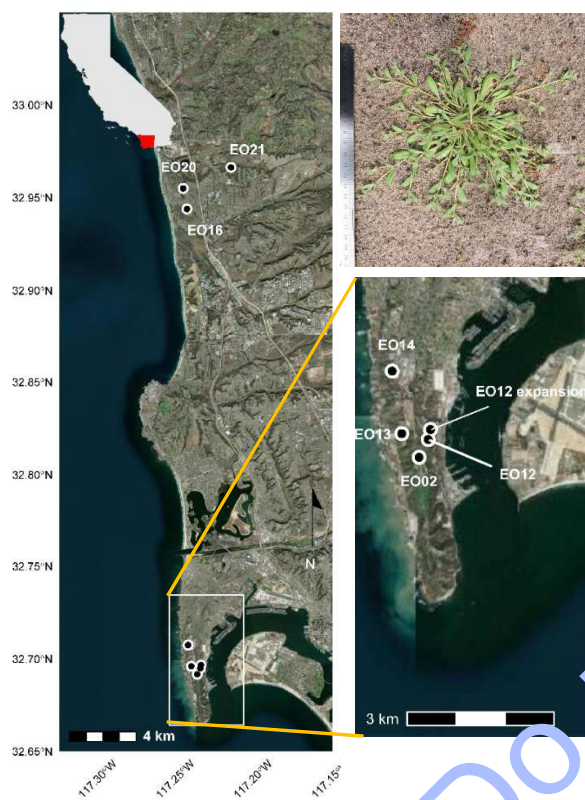
3 non-peninsular (northern) populations

Plants sampled in 2020 and 2021



Population genetics of *Chorizanthe orcuttiana*: questions that we addressed

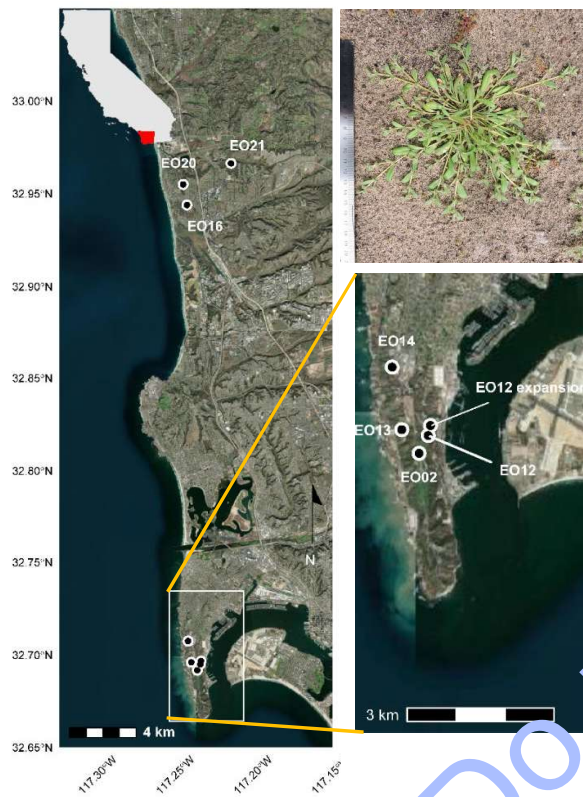
5 peninsular populations, 3 non-peninsular (northern) populations



1. Is there spatial genetic structure across *Chorizanthe orcuttiana* populations?
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Population genetics of *Chorizanthe orcuttiana*: questions that we addressed

5 peninsular populations, 3 non-peninsular (northern) populations



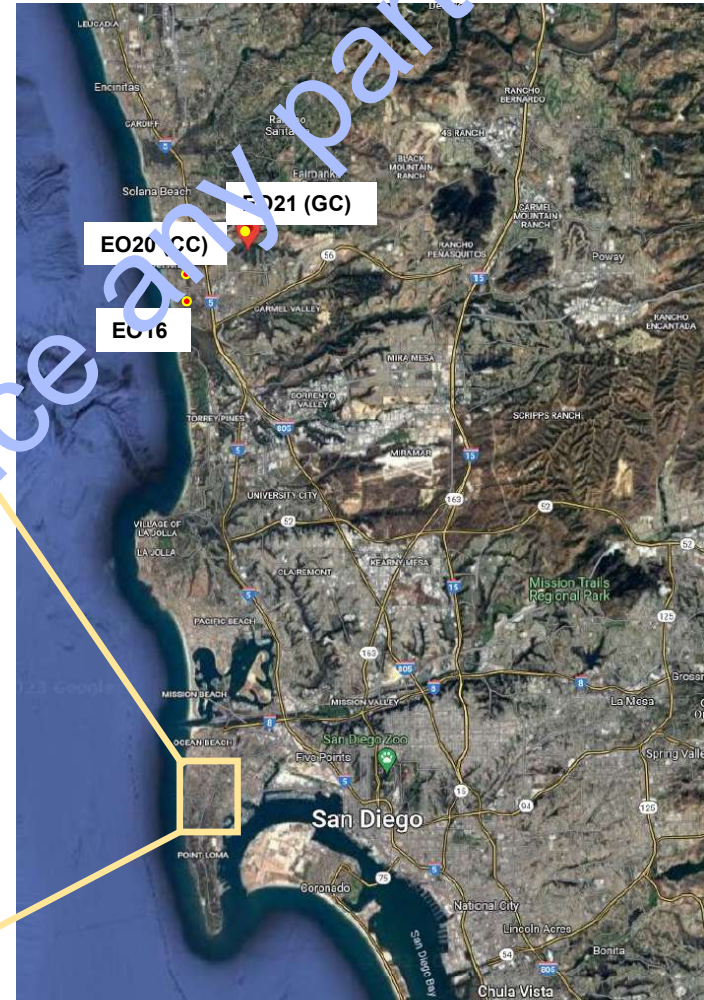
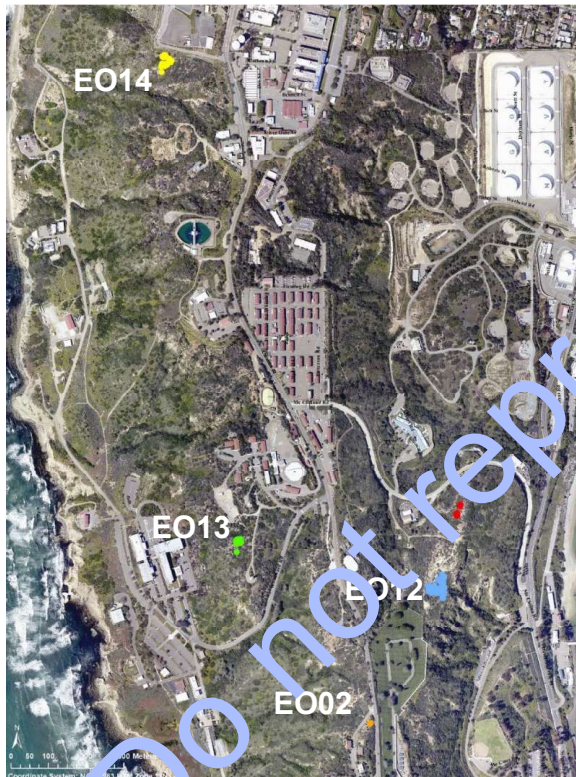
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Range-wide genetic structure

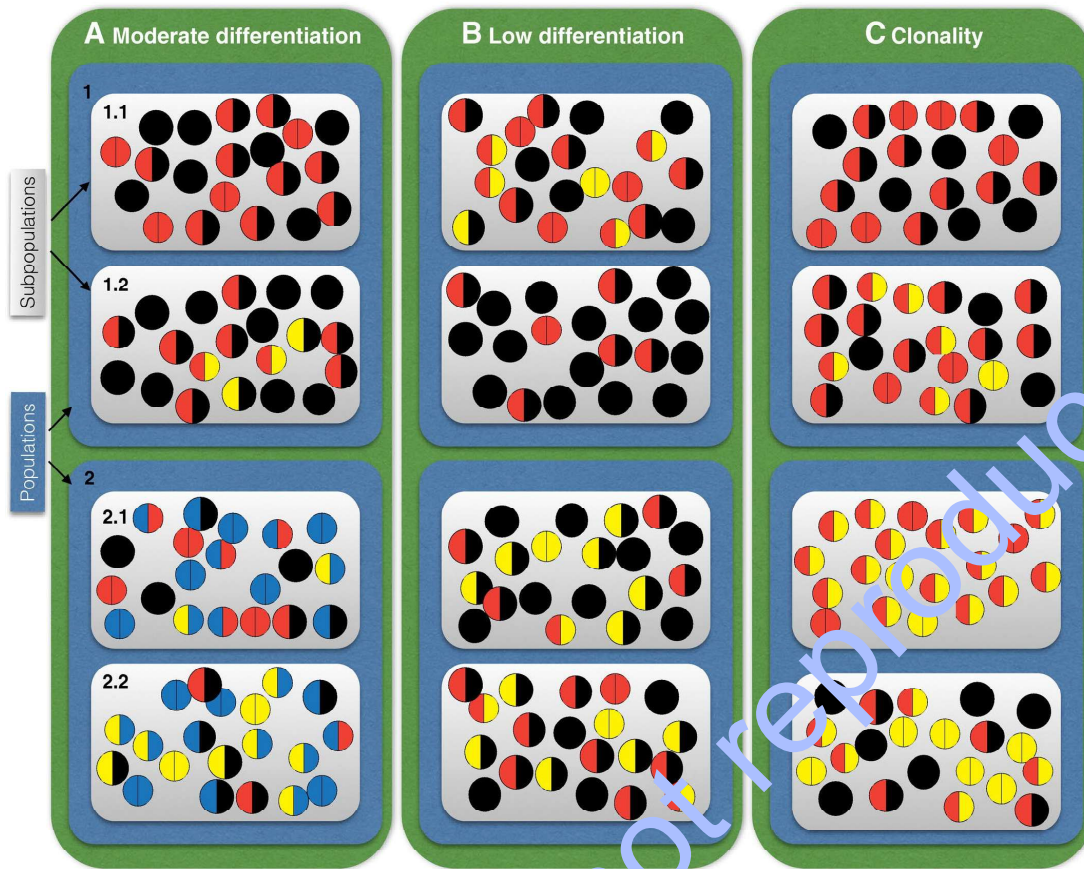
5 peninsular populations

3 non-peninsular (northern) populations

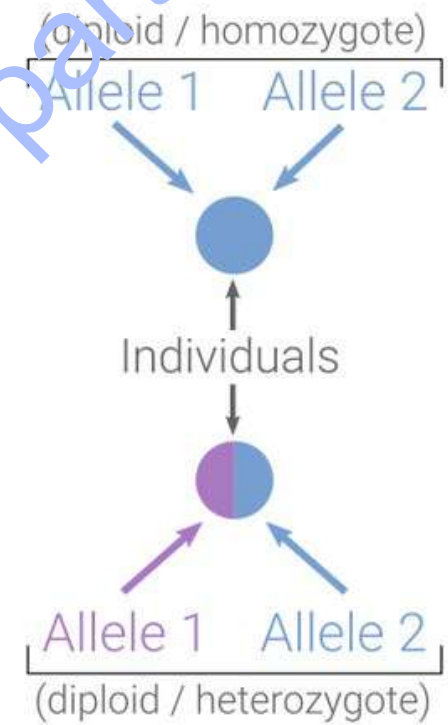
Plants sampled in 2020 and 2021



Allelic diversity

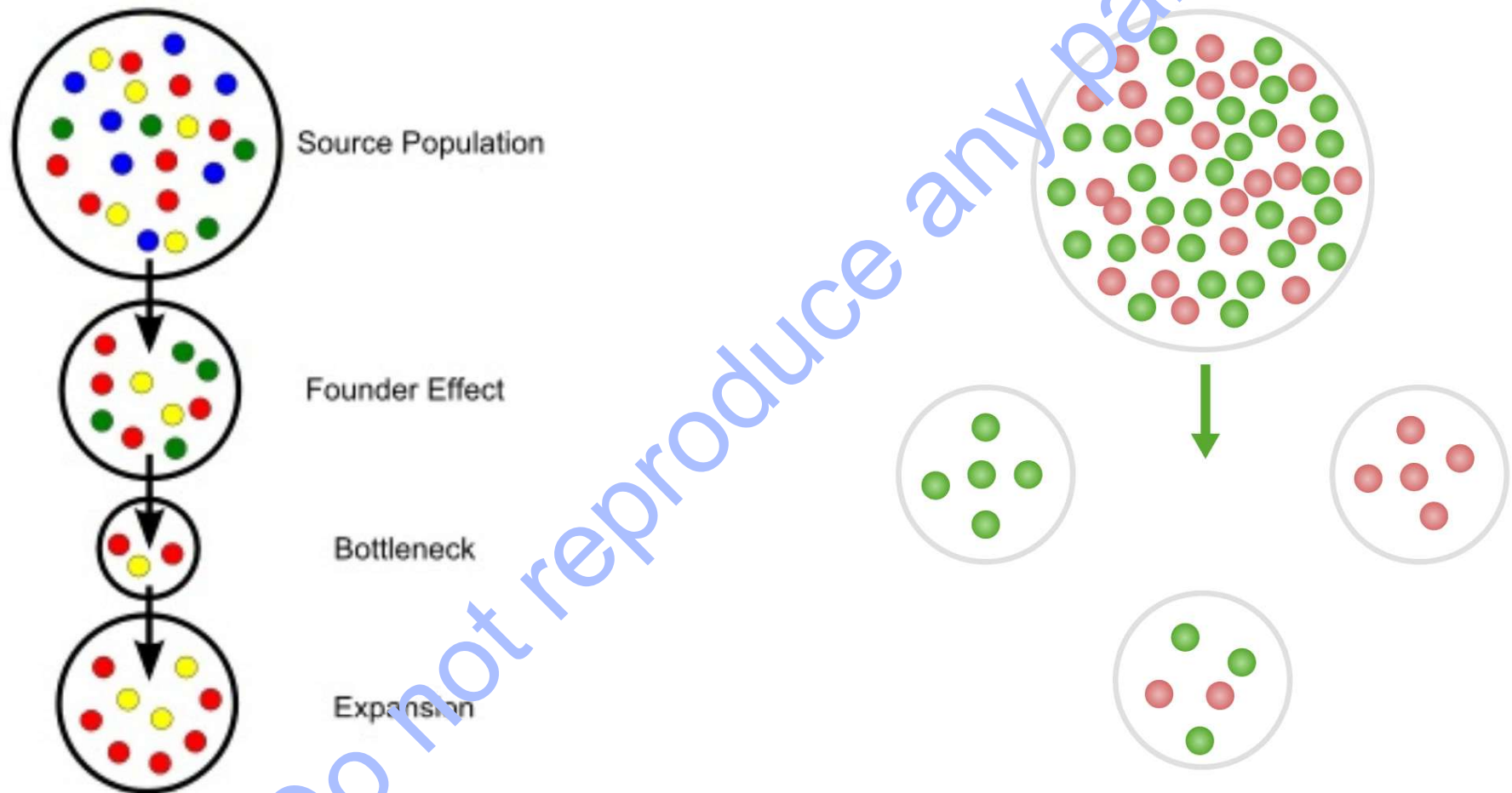


Diploid organism with up to four alleles (black, blue, red, and yellow) per locus



Chorizanthe orcuttiana (octoploid) analyses based on 32,512 loci and 102,640 alleles

Allelic diversity



Spatial genetic structure: Summary statistics

- 372 individuals, eight populations, two years; 32,512 loci and 102,640 alleles
- Restriction site-associated DNA sequencing (RAD-Seq) single nucleotide polymorphisms (SNPs)
- Data subsampled to hexaploidy in GenoDive (i.e, likely an underestimation still)
- Similar yet relatively high heterozygosity in each population. All populations exhibit comparable expected and observed heterozygosities and consequently low levels of inbreeding.

Population	No. of individuals	No. of alleles	No. of private alleles	Expected heterozygosity (H_e)	Observed heterozygosity (H_o)	Inbreeding coefficient (G_{is})
EO02	10	78617	7	0.34	0.37	-0.10
EO12	83	100293	14	0.40	0.36	0.11
EO12exp	29	86517	35	0.30	0.32	-0.05
EO13	60	97449	53	0.36	0.36	0.01
EO14	74	99439	90	0.39	0.36	0.09
EO16	59	99205	40	0.37	0.34	0.09
EO20	30	94485	5	0.35	0.34	0.01
EO21	27	96058	1	0.39	0.35	0.09

Spatial genetic structure: Analysis of the Molecular Variance (AMOVA)

Partitioning of genetic variation (%var) within individuals, among individuals nested within populations and among populations is shown alongside the associated fixation indices F_{it} (overall inbreeding), F_{is} (within-population inbreeding) and F_{st} (fixation index or genetic differentiation) and a standardized or corrected measure of F_{st} (F'). Statistical significance was determined using 999 permutations in GenoDive.

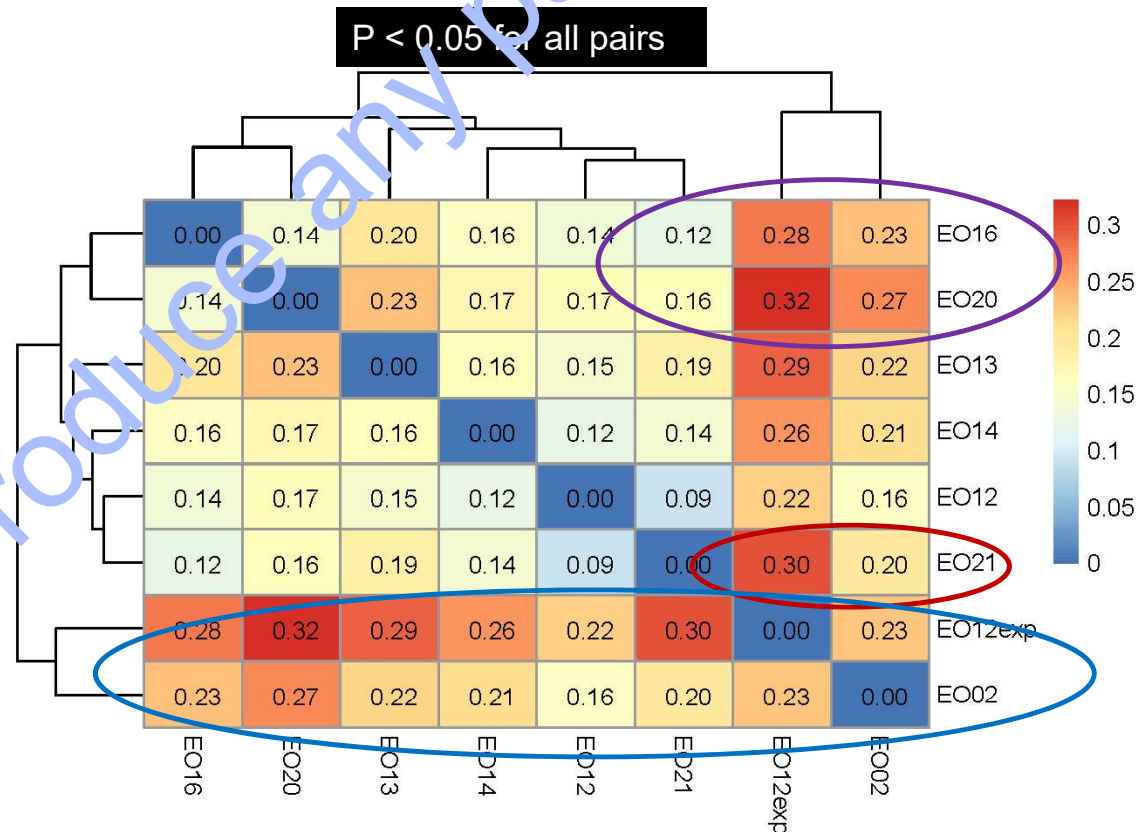
Source of Variation	Nested in	%var	F statistics	P	F'
Within Individual	--	0.769	$F_{it} = 0.231$	--	--
Among Individual	location	0.024	$F_{is} = 0.030$	0.001	--
Among locations	population	0.046	$F_{st} = 0.055$	0.001	0.09
Among populations		0.161	$F_{st} = 0.161$	0.001	0.26

- Population differentiation among eight populations as population groupings explain 16% of the genetic variation in *C. orcuttiana* ($P = 0.001$). The genetic differentiation among population is even higher (26%) when F_{st} values are standardized for the high internal diversity within populations.
- Small (5%) yet significant variation was also detected among individuals within populations ($P = 0.001$) where most genetic variation is at the individual level (77%).

Spatial genetic structure: Cluster analyses

- 372 individuals, eight populations, two years; 32,512 loci and 102,640 alleles

- Hierarchical clustering of populations based on pairwise F_{st} values.
- Ranged from 0.09 to 0.32 differentiation
- EO12exp and EO02 highest differentiation from the remaining 6 populations.
- EO16 and EO20 are a next pair that shows high divergence from the remaining populations - explained by the distance.
- Yet, EO21 which should cluster with EO16 and EO20 is more closely related to the peninsular populations. (See PCA and STRUCTURE)

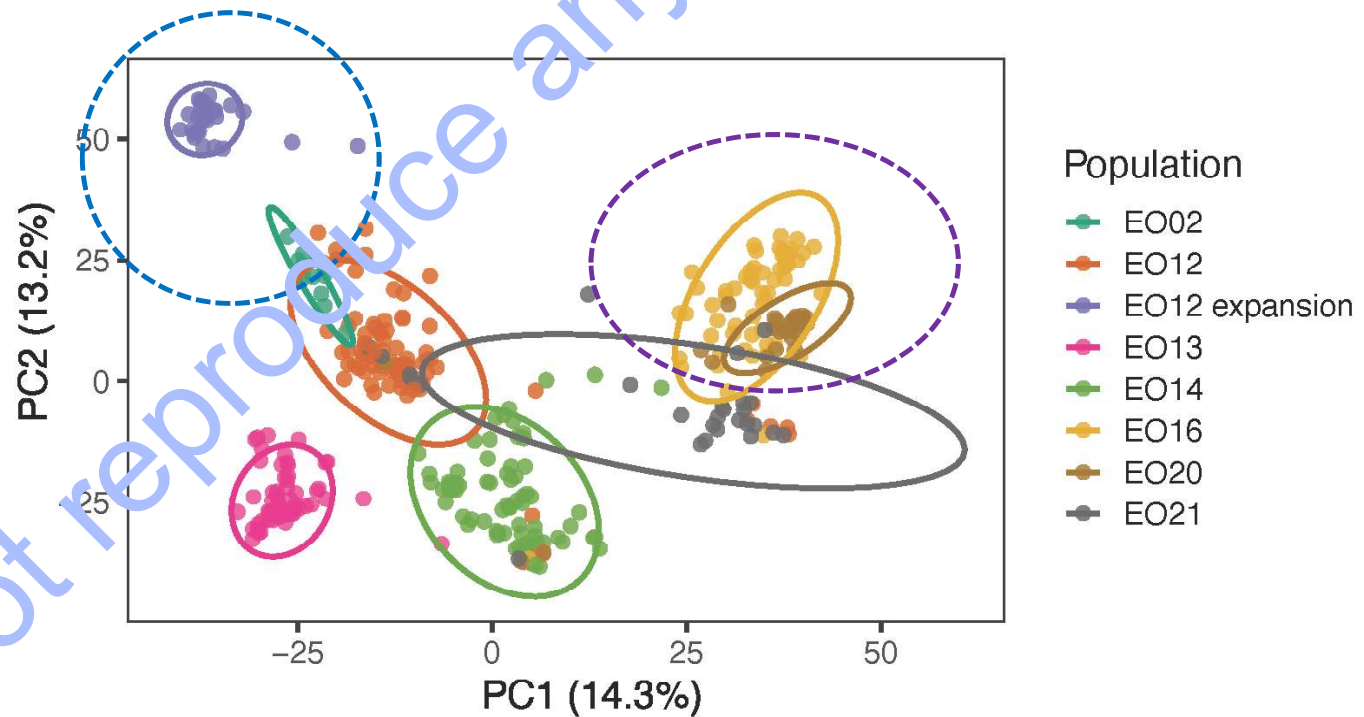


Pairwise comparison of genetic differentiation among populations

Spatial genetic structure: Principal component analysis based on allelic frequencies

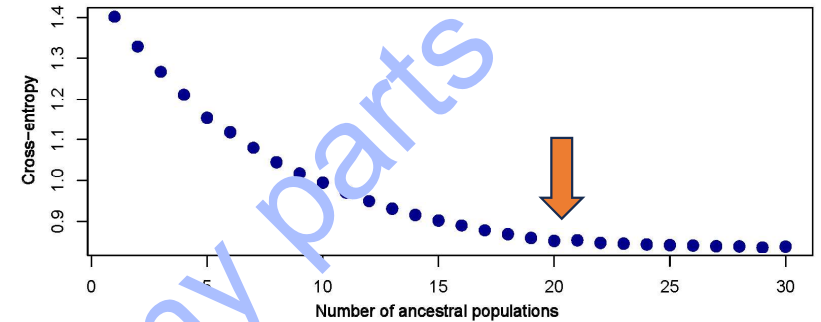
- 372 individuals, eight populations, two years; 32,512 loci and 102,640 alleles

- EO12exp is the most diverged. EO02 proximal with both EO12exp and EO12.
- EO16 and EO20 have close clustering with each other and farther from the others.
- EO12 and EO21 exhibit wide spread of points. The likely reason of association of non-peninsular EO21 to the peninsular populations.

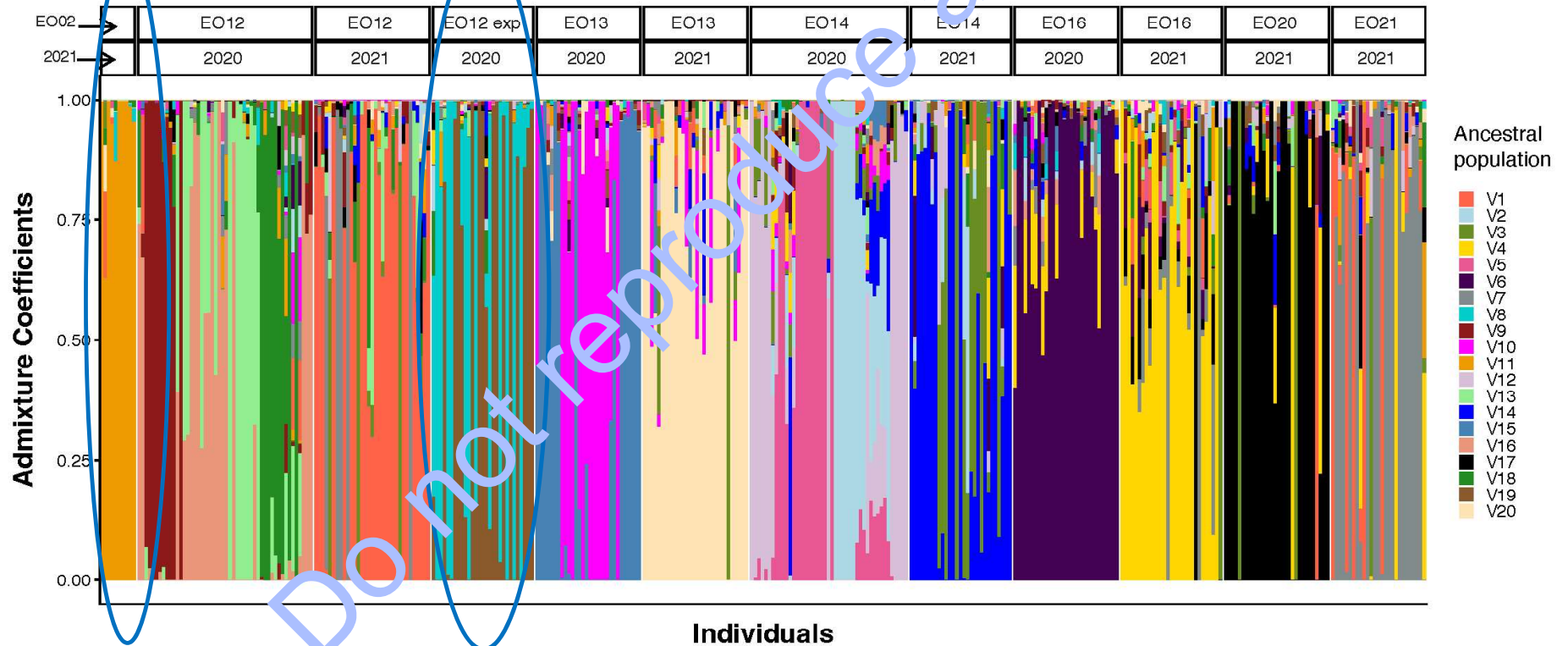


Genetic admixture

- All 20 ancestral populations were represented in each extant populations although their proportions varied considerably.
- The temporal structure is also evident



Cross-entropy measure for conducting structure analysis



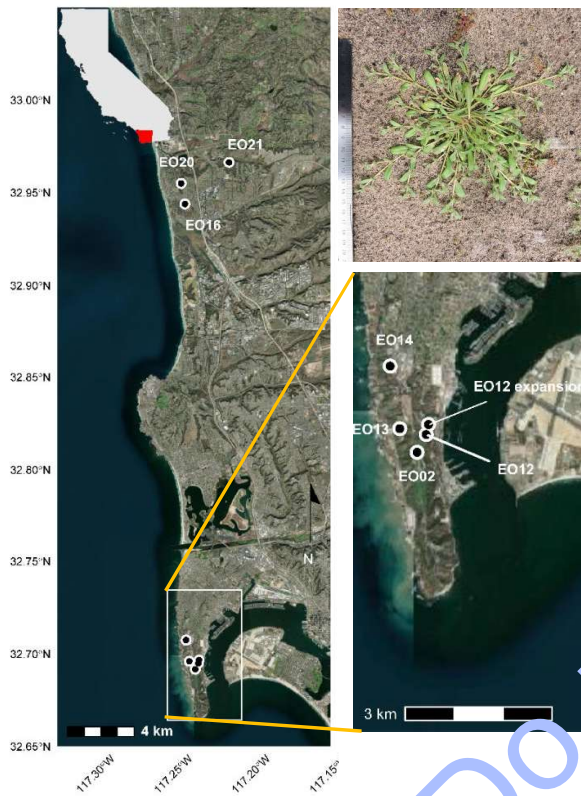
Genetic admixture

Admixture categories based on the proportions of ancestral populations. The pure category included plants with $\geq 95\%$ representation of a single ancestral population while low, moderate and high admixture categories included individuals with 95-70%, 70-50% and $<50\%$, maximum representation of any given ancestral population, respectively. Percentage of individuals in each category is presented.

Population	No. of individuals	Pure (%)	Low admixture (%)	Moderate admixture (%)	High admixture (%)
EO02	10	70.00	20.00	10.00	00.00
EO12	83	33.73	36.14	13.25	16.87
EO12exp	29	58.62	34.48	03.45	03.45
EO13	60	40.00	36.67	15.00	08.33
EO14	74	36.49	29.73	13.51	20.27
EO16	59	44.07	27.12	16.95	11.86
EO20	30	43.33	50.00	03.33	03.33
EO21	27	29.63	59.26	07.41	03.70

Population genetics of *Chorizanthe orcuttiana*: questions that we addressed

5 peninsular populations, 3 non-peninsular (northern) populations



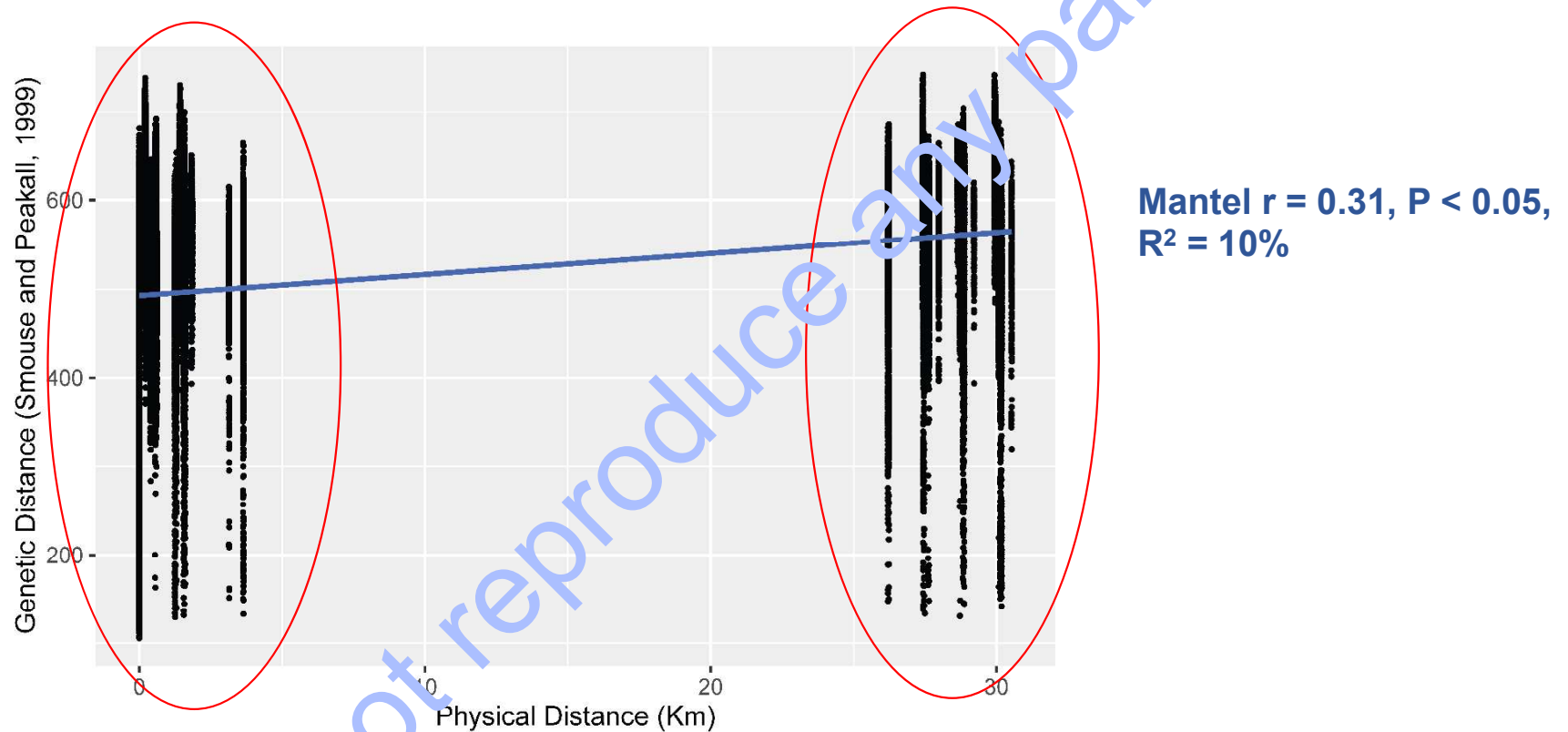
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Geographic distances (Km) among populations

	EO12	EO14	EO13	EO16	EO20	EO21	EO02
EO12	00.0						
EO14	01.6	00.0					
EO13	00.6	01.3	00.0				
EO16	27.6	26.2	27.5	00.0			
EO20	28.8	27.4	28.7	01.3	00.0		
EO21	30.2	28.8	30.1	03.6	03.1	00.0	
EO02	00.4	01.8	00.6	28.0	29.2	30.5	00.0



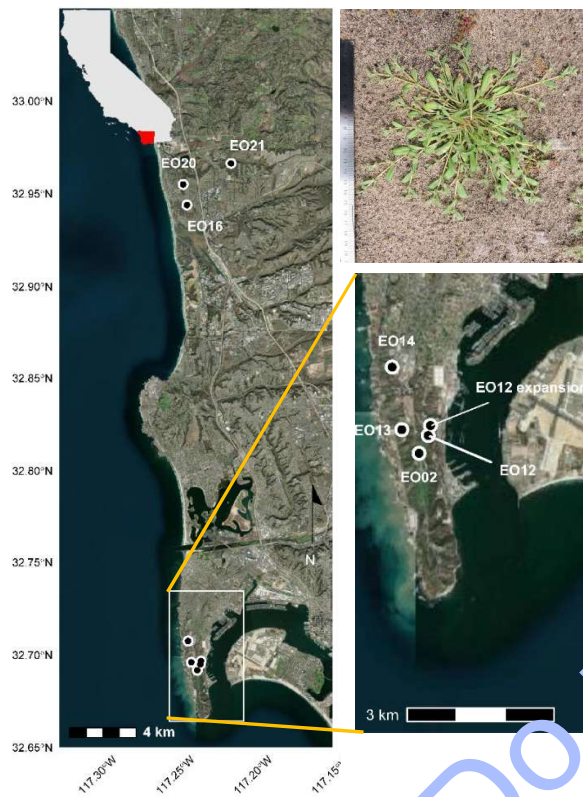
Are geographic and genetic distances correlated? – Isolation by distance analyses



Although Mantel detected moderate differentiation based on geographic distances, much of the variation resides within populations (within individuals, in fact).

Population genetics of *Chorizanthe orcuttiana*: questions that we addressed

5 peninsular populations, 3 non-peninsular (northern) populations



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Temporal genetic structure: summary statistics

- 276 individuals, four populations, two years; 32,512 loci and 102,040 alleles
- Similar yet relatively high heterozygosity in each population in each year. All populations exhibit comparable expected and observed heterozygosities and consequently low levels of inbreeding.

Population	Year	No. of individuals	No. of alleles	No. of private alleles	Expected heterozygosity (H_e)	Observed heterozygosity (H_o)	Inbreeding coefficient (G_{is})
EO12	2020	50	96914	64	0.38	0.35	0.085
EO13	2020	30	91163	20	0.33	0.35	-0.002
EO14	2020	45	97229	83	0.38	0.33	0.135
EO16	2020	30	91791	46	0.31	0.33	-0.048
EO12	2021	33	95699	43	0.40	0.38	0.048
EO13	2021	30	92649	30	0.37	0.39	-0.060
EO14	2021	29	93079	14	0.38	0.40	-0.046
EO16	2021	29	97047	37	0.39	0.36	0.087

Temporal genetic structure: Analysis of the Molecular Variance (AMOVA)

- 276 individuals, four populations, two years
- 32,512 loci and 102,640 alleles

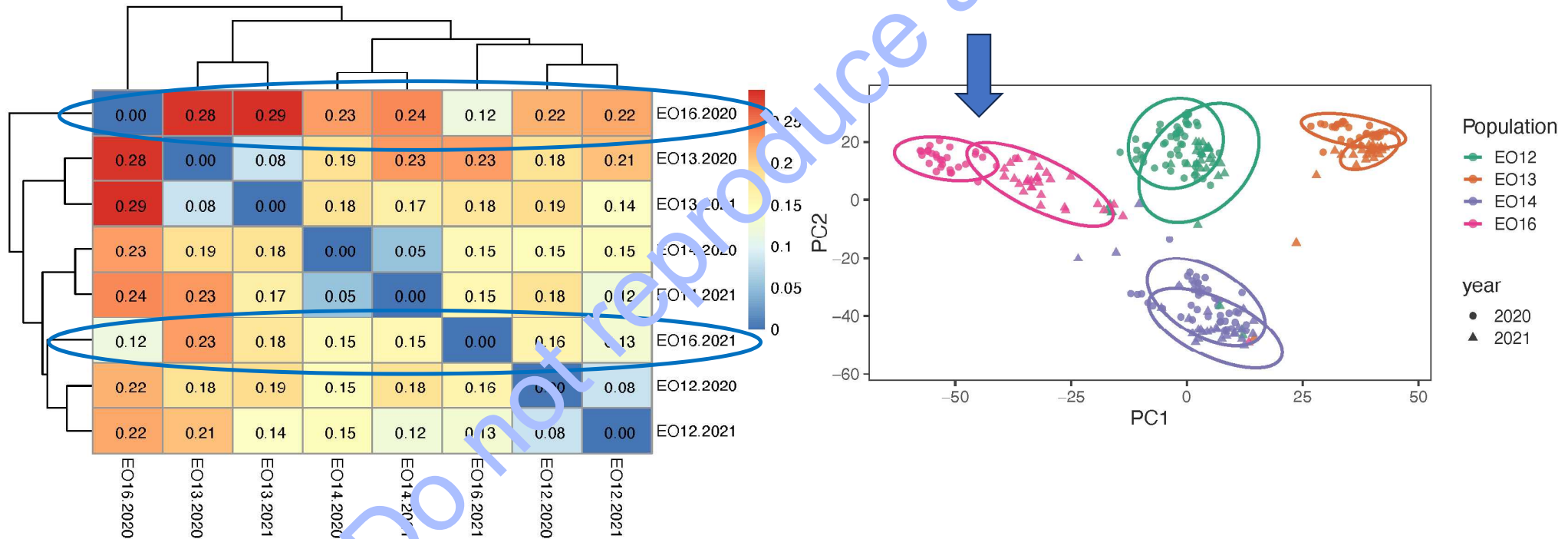
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Source of Variation	Nested in	%var	F statistics	P	F'
Within Individual	--	0.781	$F_{it} = 0.219$	--	--
Among Individuals	Year	0.032	$F_{is} = 0.039$	0.001	--
Among Years	Population	0.072	$F_{st} = 0.082$	0.001	0.13
Among Populations		0.115	$F_{st} = 0.115$	0.001	0.19

Temporal genetic structure: Cluster analyses

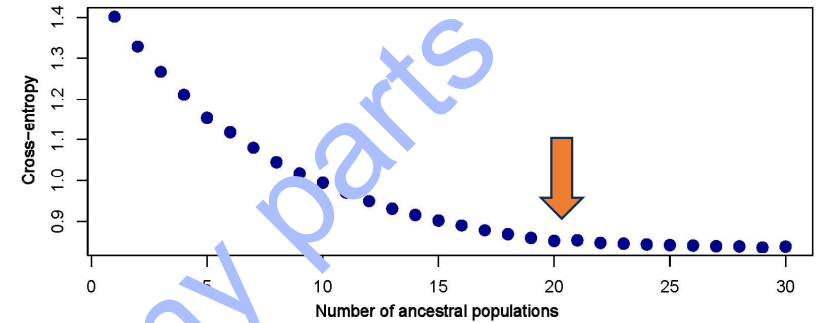
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Differentiation across years: populations cluster together but show variation. EO16 dispersion.

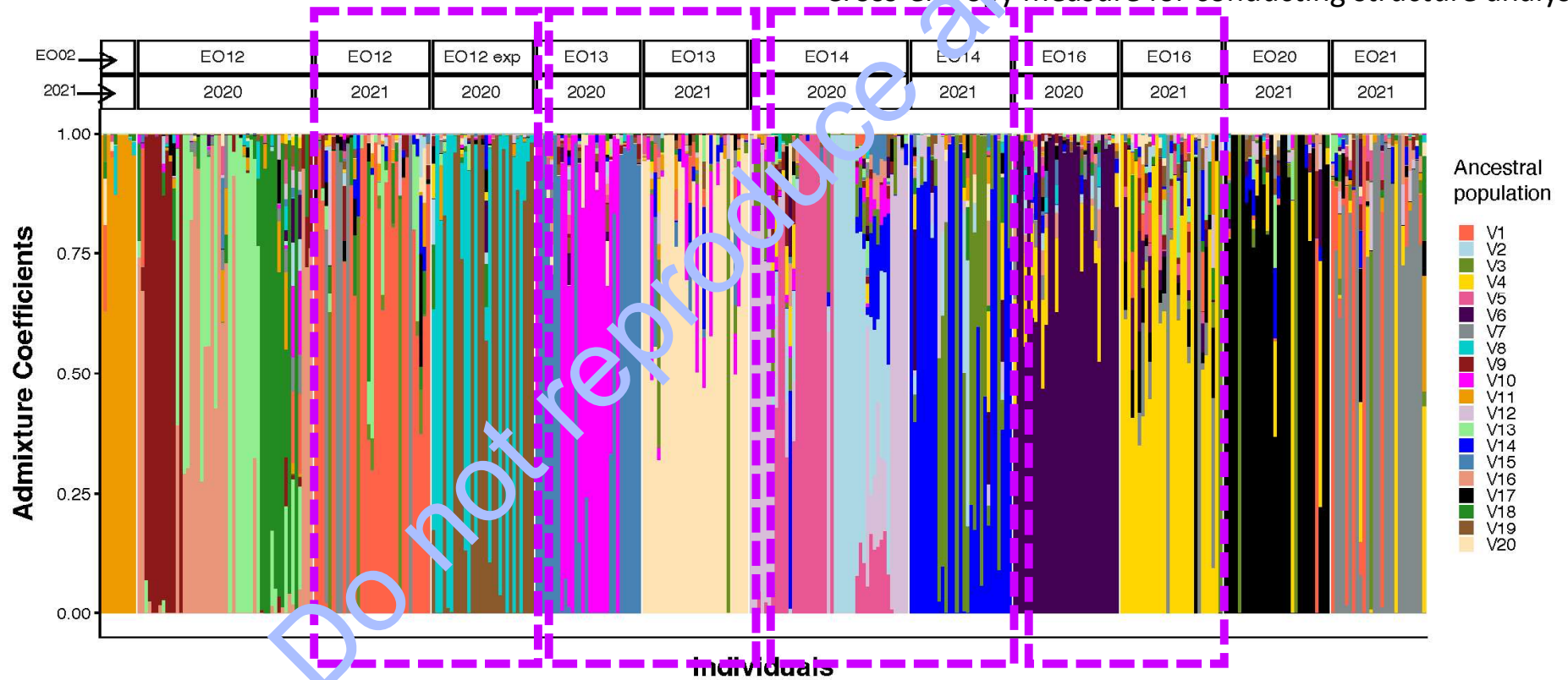


Genetic admixture

Signal for temporal variation is detectable in each population that was sampled in 2020 and 2021

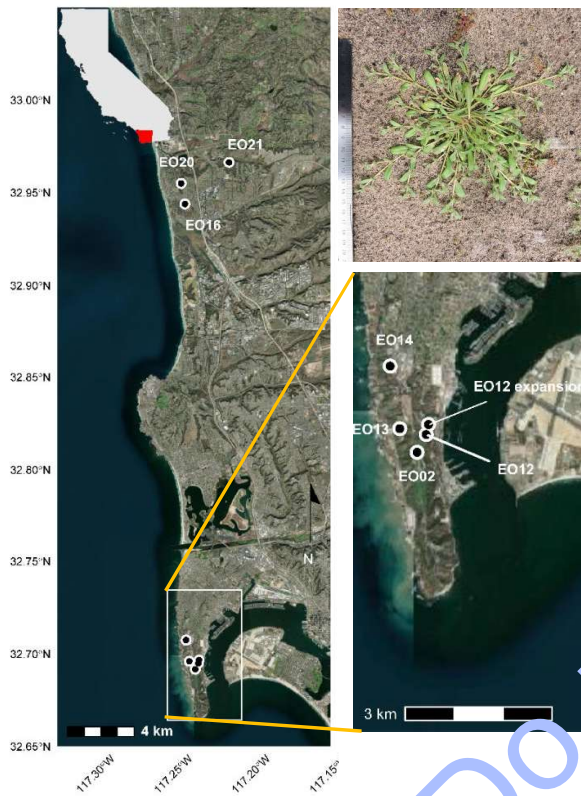


Cross-entropy measure for conducting structure analysis



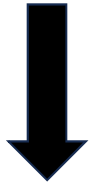
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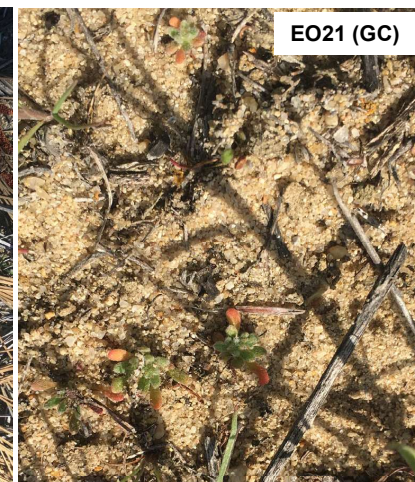
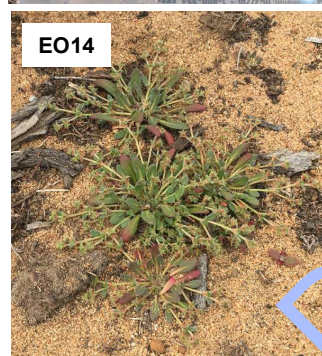


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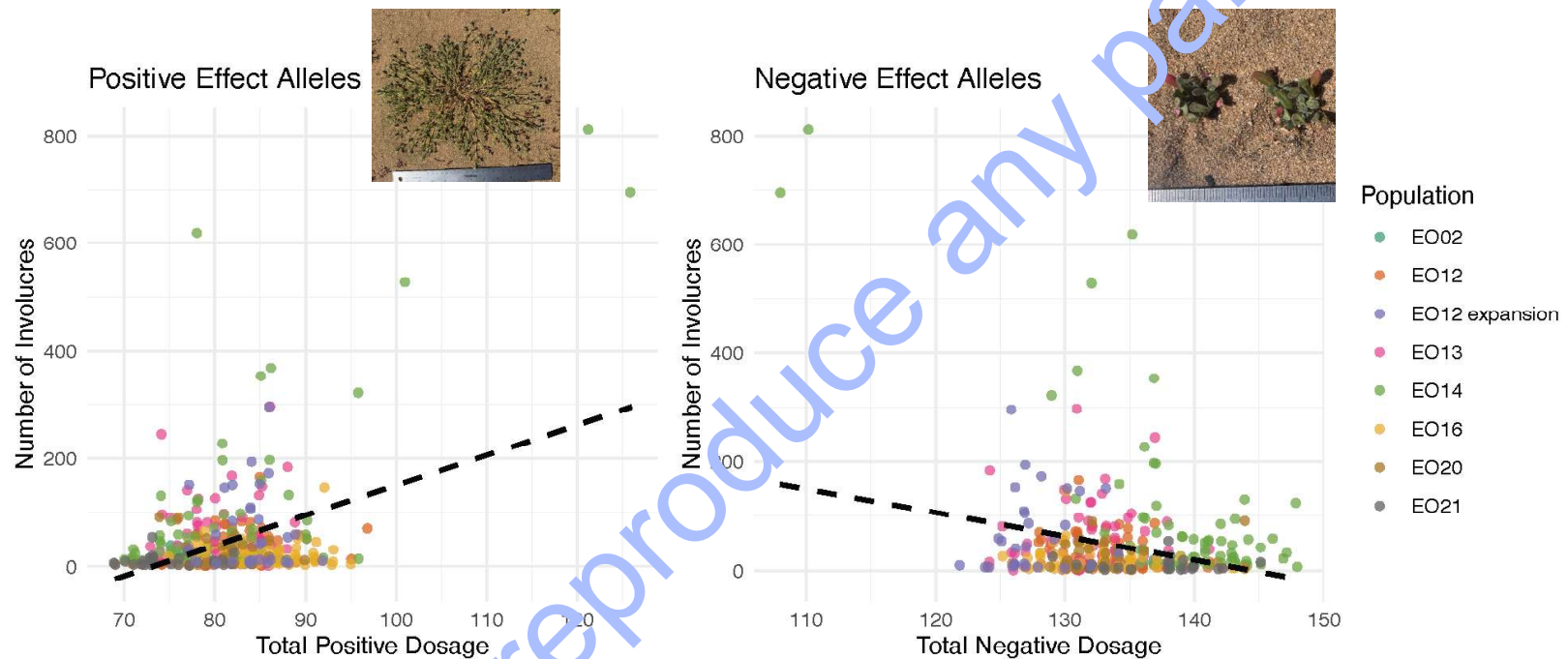
Phenotype-Genotype Association



Population	Mean # of involucres per plant	
EO02	66.0	21.0
EO12		15.6
EO13		19.5
EO14		208.0
EO16	14.5	14.0
EO20		20.0
EO21		9.4



➤ **Genetics based differences in plant fitness are evident**

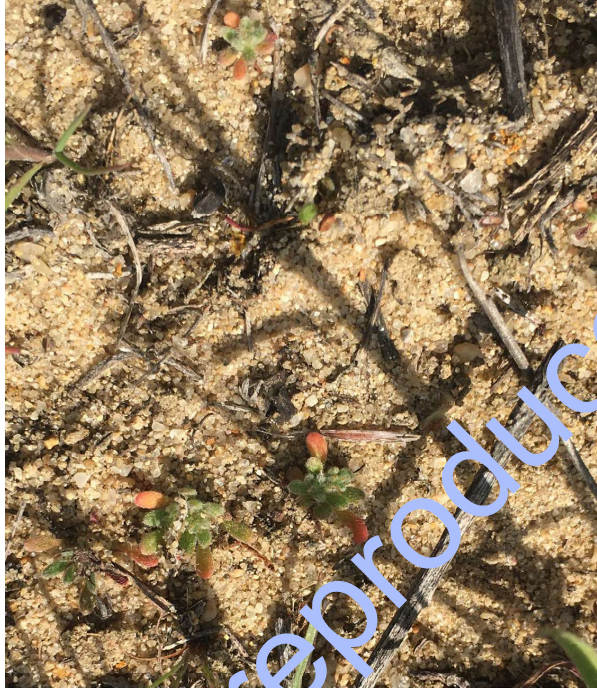


Latent factor mixed model (LFMM) analysis for genotype-phenotype interactions in *Chorizanthe orcuttiana*. LFMM identified **71 alleles significantly associated with number of involucre**, a measure of reproductive fitness for the species. The figure shows the relationship between number of involucre and cumulative dosages of negative and positively associated alleles across study populations. **26 had a negative effect and the remanning 45 had a positive effect.**

EO16



EO21



EO14



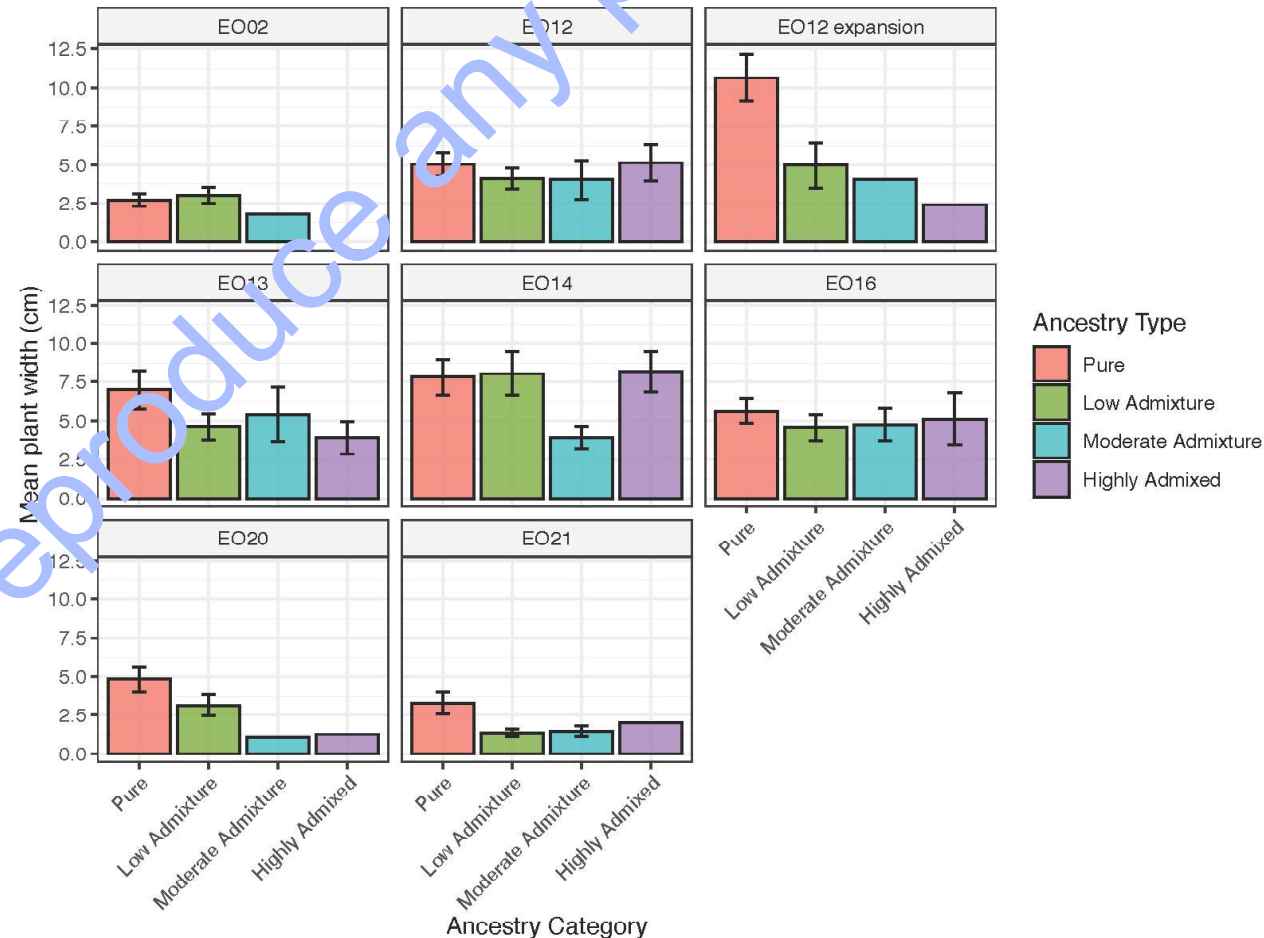
26 loci associated with a negative effect and 45 with a positive effect on plant fitness.

Does admixture (ancestry) affect plant fitness?

- Effect of ancestry type on plant width and number of involucre was not detected though there is a signal in several populations

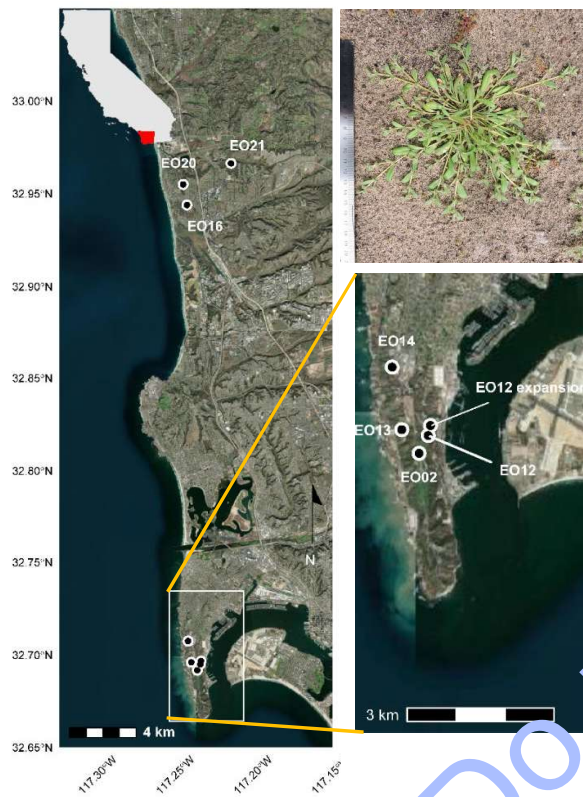
Relationship between ancestry admixture levels and plant fitness of *Chorizanthe orcuttiana*.

Higher fitness of pure individuals (with minimal admixture) combined with higher frequency of pure genotypes across populations suggests purifying selection.



Population genetics of *Chorizanthe orcuttiana*: questions that we addressed

5 peninsular populations, 3 non-peninsular (northern) populations



1. Is there spatial genetic structure across *Chorizanthe orcuttiana* populations?
2. Are geographic and genetic distances correlated?
3. Is there a temporal signal in the genetic structure in *Chorizanthe orcuttiana* populations?
4. Is the phenotypic (plant fitness) variation among populations more likely a result of divergent natural selection or neutral evolutionary divergence such as genetic drift?
5. What is the genetic relationship between *C. orcuttiana* and *C. procumbens*?

Genetic relationship between *C. orcuttiana* and *C. procumbens*

56,810 loci and 205,694 alleles



C. orcuttiana

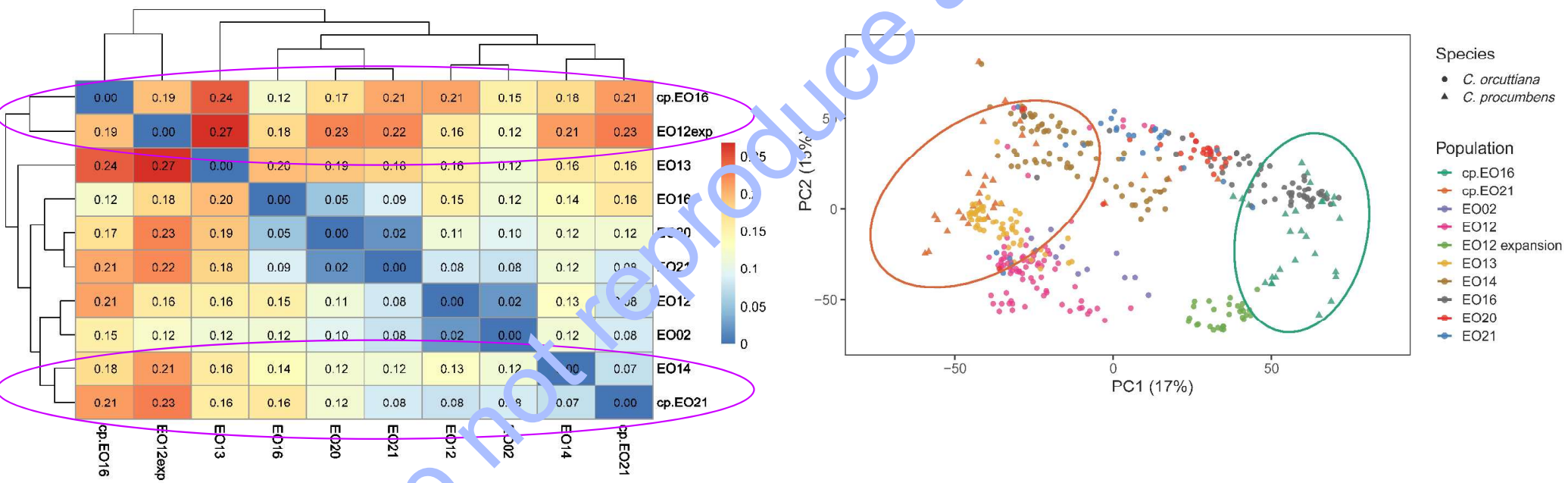


C. procumbens

Genetic relationship between *C. orcuttiana* and *C. procumbens*

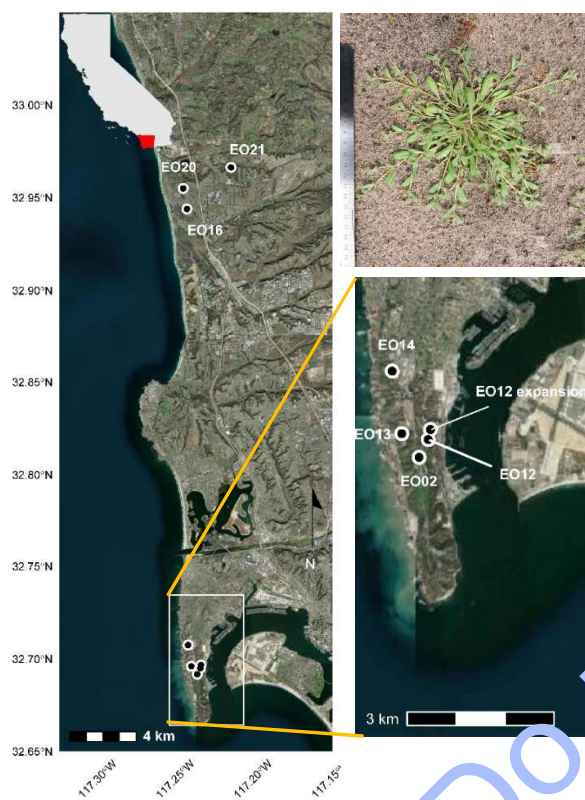
Lack of species-specific clustering for *C. orcuttiana* and *C. procumbens* suggests an incomplete or ongoing lineage sorting between two species, with shared polymorphism persisting and active gene flow.

P < 0.05 for all comparisons



Population genetics of *Chorizanthe orcuttiana*: questions that we addressed

5 peninsular populations, 3 non-peninsular (northern) populations



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Implications for conservation

High polymorphism, high heterozygosity in each population



High potential for generating unique allelic diversity across space / time.

Smaller populations (EO02 and EO12exp)



Lower allelic diversity despite proximity to diverse populations



Likely to be founder populations
- Or bottlenecks / remanent seedbanks
- Yet, High H_o , -ve inbreeding, and diverged.

Evolutionary potential of an annual octoploid with high H is a strong point for this taxon but fitness seems to suffer, and local adaptation in fitness is detectable.



Implications for conservation

Spatial segregation among natural populations dominant over temporal variation.

Size of population is a genetic fitness indicator. Geographic distance not so much.

Genetic intervention such as genetic rescue is not required for *C. orcuttiana* management.

Ideally, seeds from different populations should not be intermixed to allow natural selection and local adaptation.

Temporal variation adds to the genetic heterogeneity to provide genetic buffering – seed banks should represent multiple years.

Adaptive management appears to be the key to success for this taxon that has the genetic potential (for now!).



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- California State Parks
- San Diego Natural History Museum
- California Department of Fish and Wildlife
- The City of San Diego

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