



# GENETIC CONNECTIVITY OF THE COASTAL CACTUS WREN

**Kelly Barr**

**Barbara Kus**

**Kris Preston**

**Amy Vandergast**



Photo by Alex Houston

# ACKNOWLEDGMENTS



## **NROC:**

**K. Moore & D. Kamada**

## **USGS:**

**S. Howell, A. Houston, M. Madden-Smith, L. Allen, A. Gallagher, P.J. Falatek, K. Allen**



# Overview

- Background
- Study Design
- Results & Analyses
- What's Next?



**Connectivity Monitoring Strategic Plan  
For the San Diego Preserve System**



Prepared for the San Diego Environmental Mitigation Program Working Group

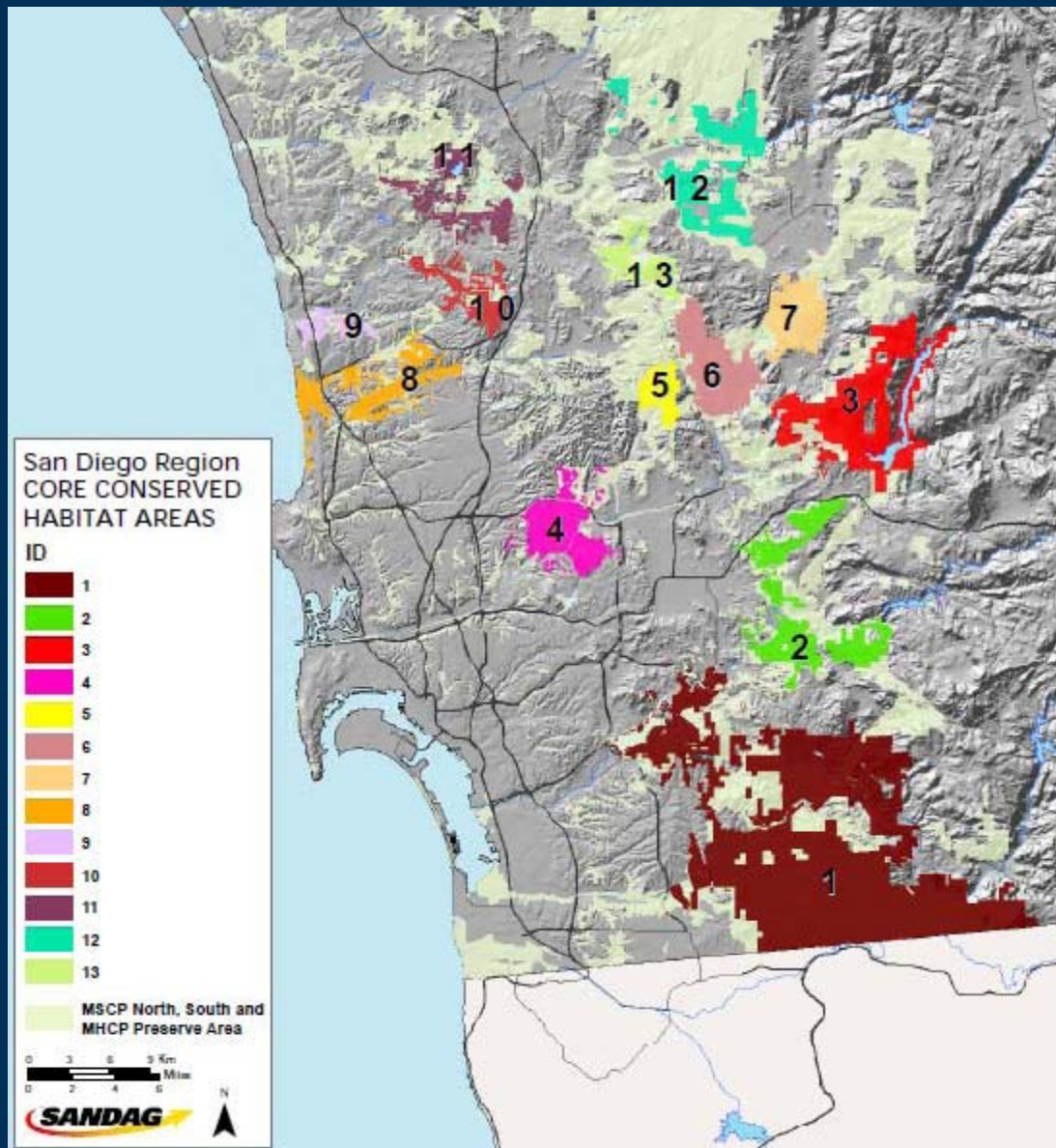
January 11, 2011

# Goal:

To identify and inform adaptive management actions to *maintain, restore or improve connectivity* between conserved core areas, and thereby:

- ensure persistence of species across preserve system
- preserve ecosystem function across the landscape





What is the functional connectivity among core areas for

- large animals
- small animals
- birds

Priority bird species:

- Coastal Cactus Wren
- California Gnatcatcher
- Least Bell's Vireo
- SW Willow Flycatcher

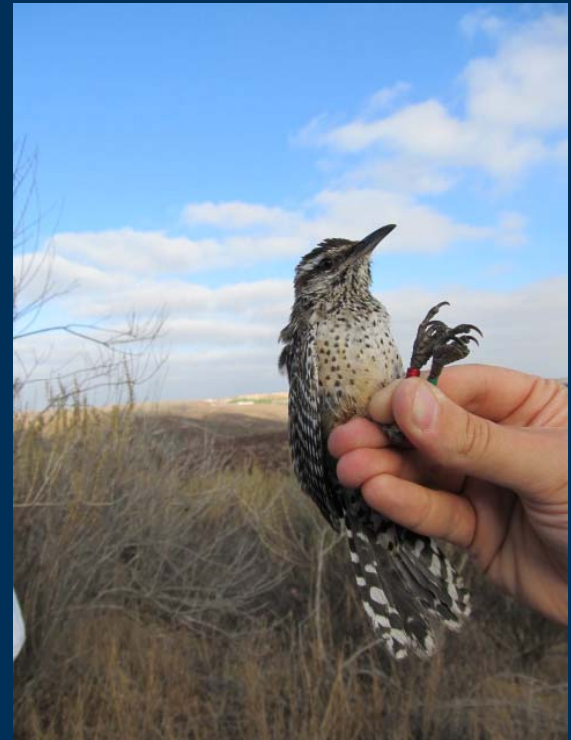
# Why Study Connectivity in Cactus Wrens?

- limited strictly to cactus habitat
- cactus highly fragmented by development & fire
- connectivity maintains genetic diversity within fragments & ensures recolonization after local extinctions
- understanding current connectivity would inform cactus restoration
  - How do Cactus Wrens utilize the landscape for movement?
  - identify connectivity trouble spots



# Genetic Approach

- genetic data provide information on gene flow (movement + successful breeding)
  - Dispersal = just movement
- determine natural and anthropogenic barriers that impede gene flow
- measures genetic diversity (the raw material for adaptation)



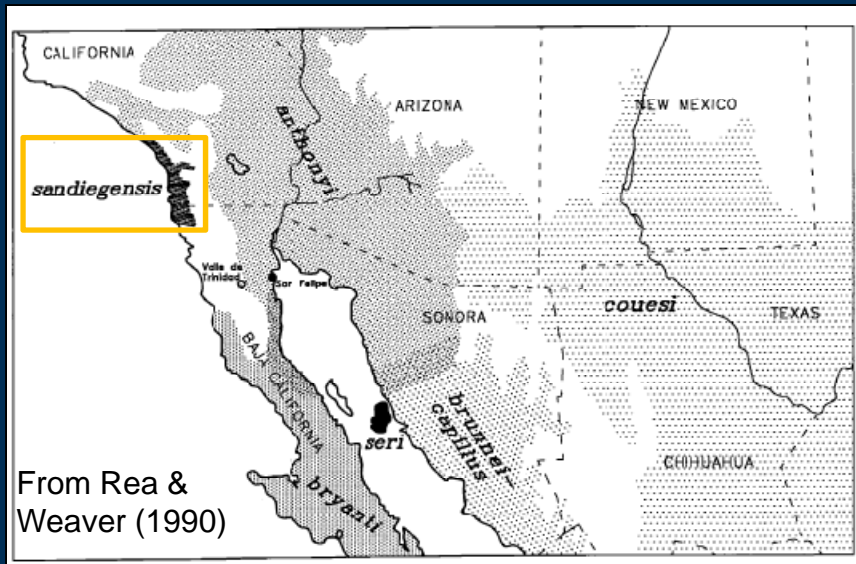


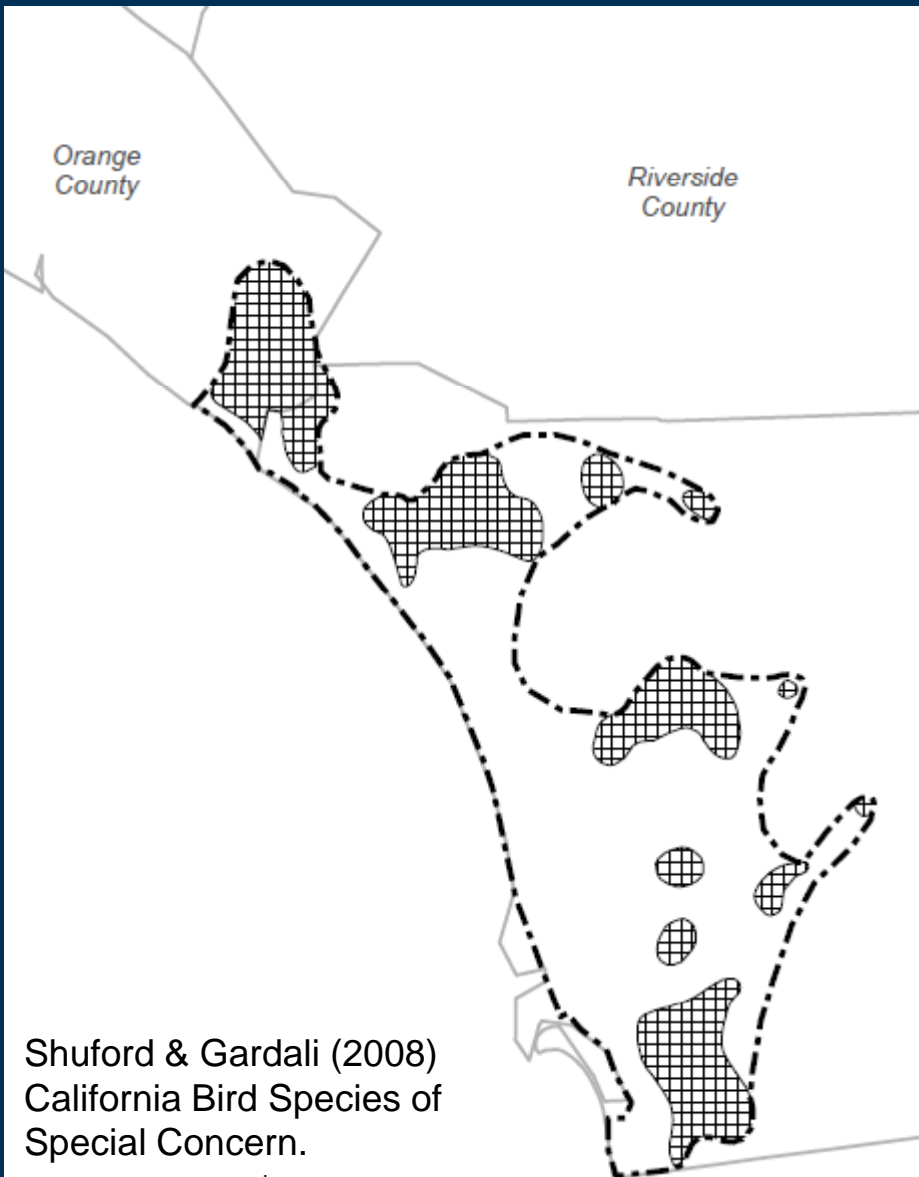
## Study Goals:

1. Are there limitations to gene flow?
2. Identify clusters (populations or gene pools).
3. What is the genetic diversity within clusters?



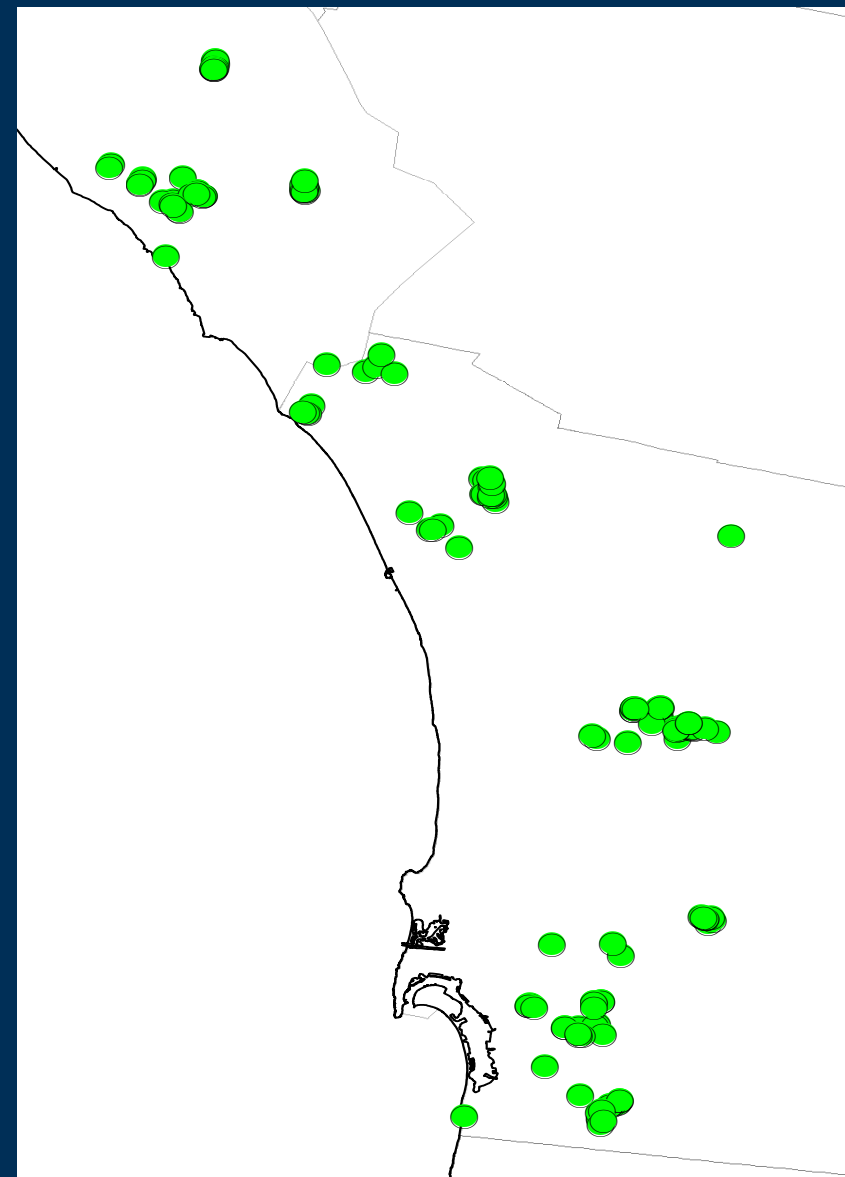
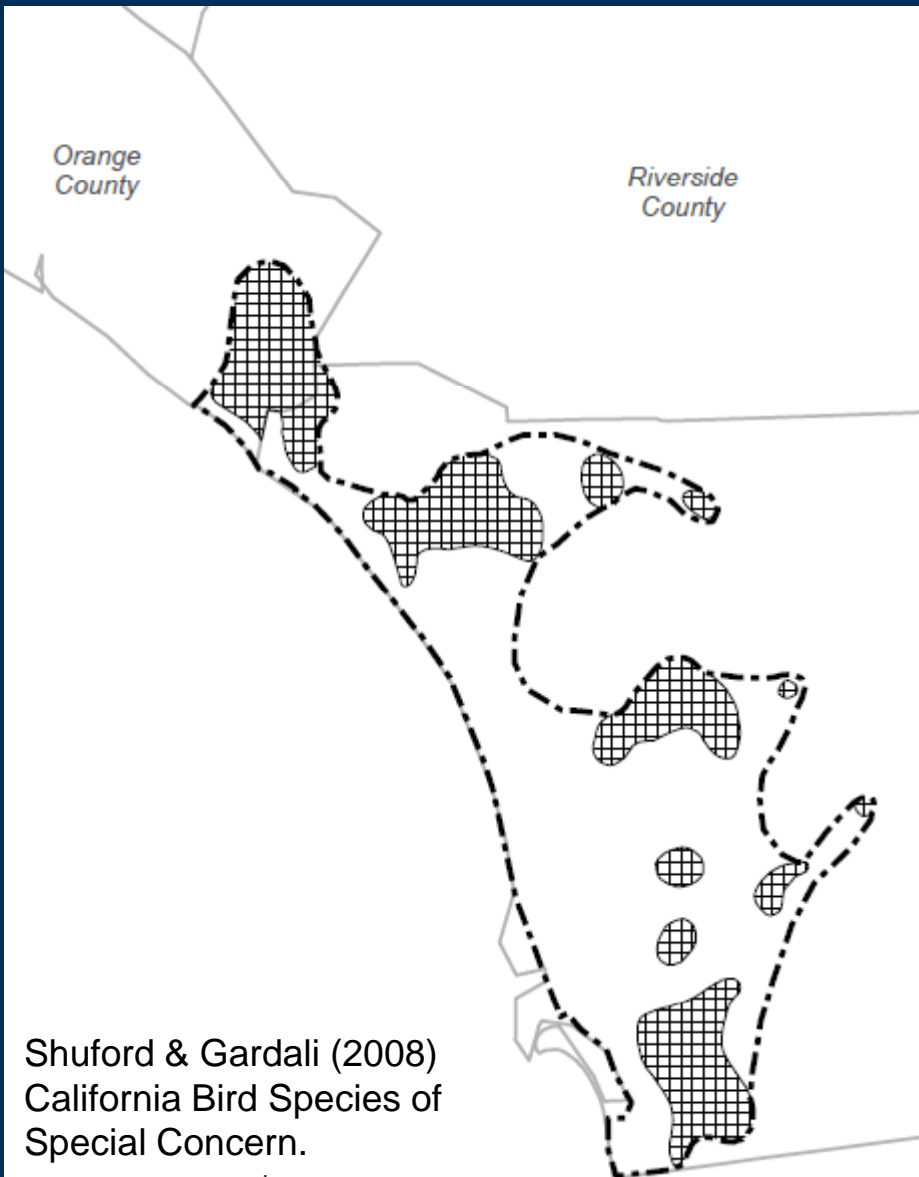


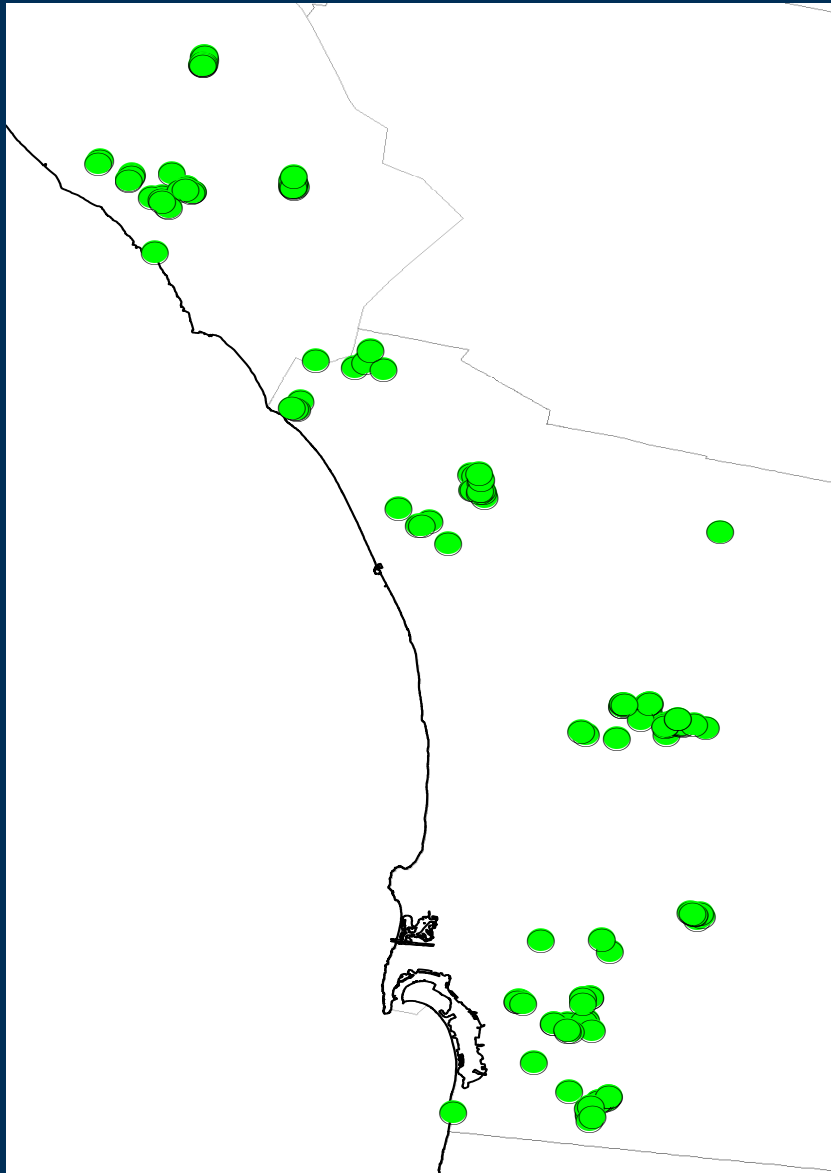




Shuford & Gardali (2008)  
California Bird Species of  
Special Concern.







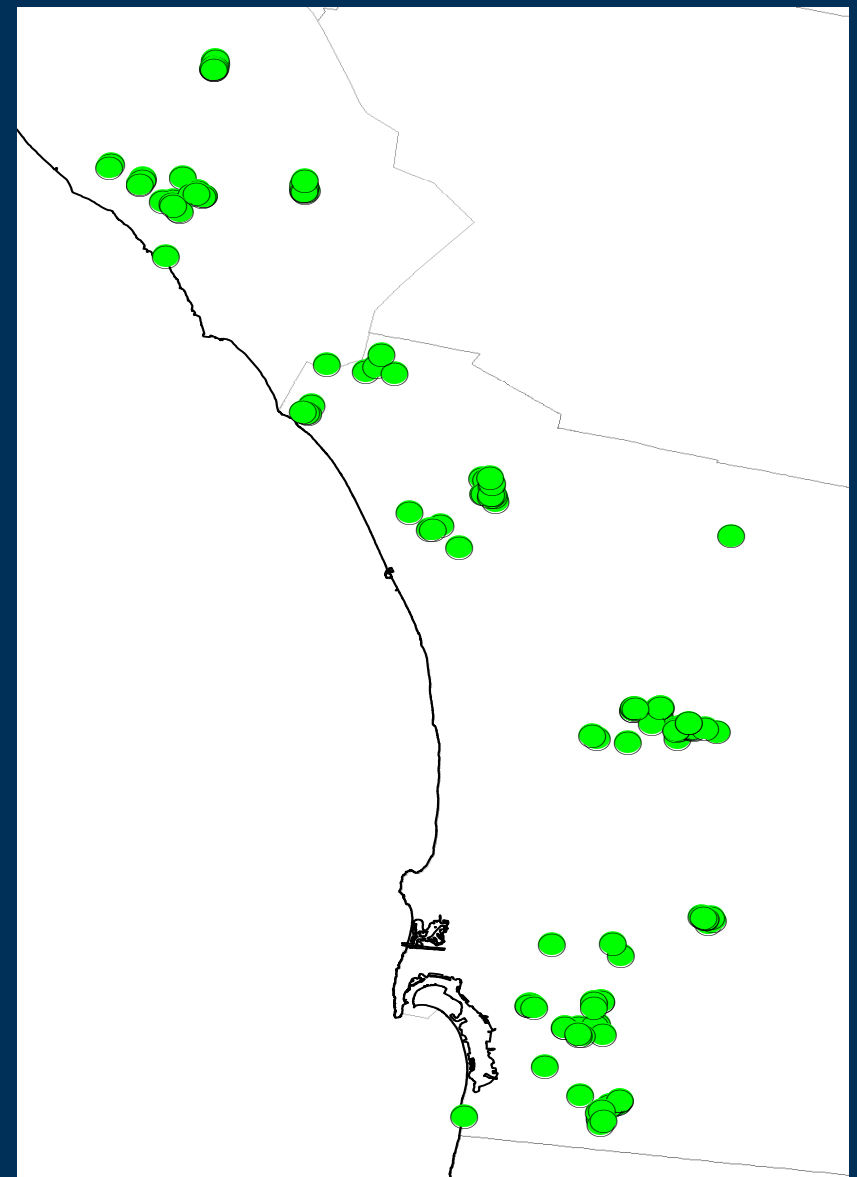
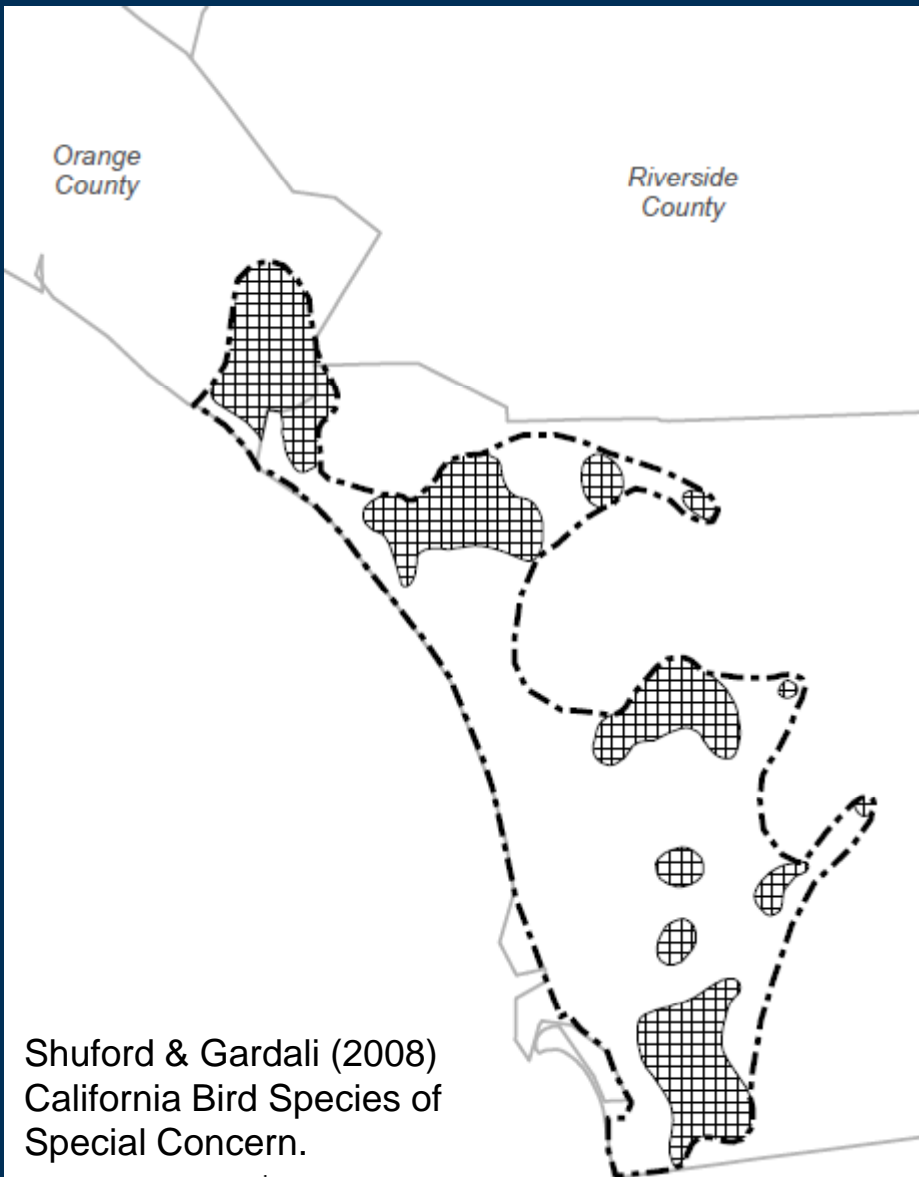
## Exhaustive sampling

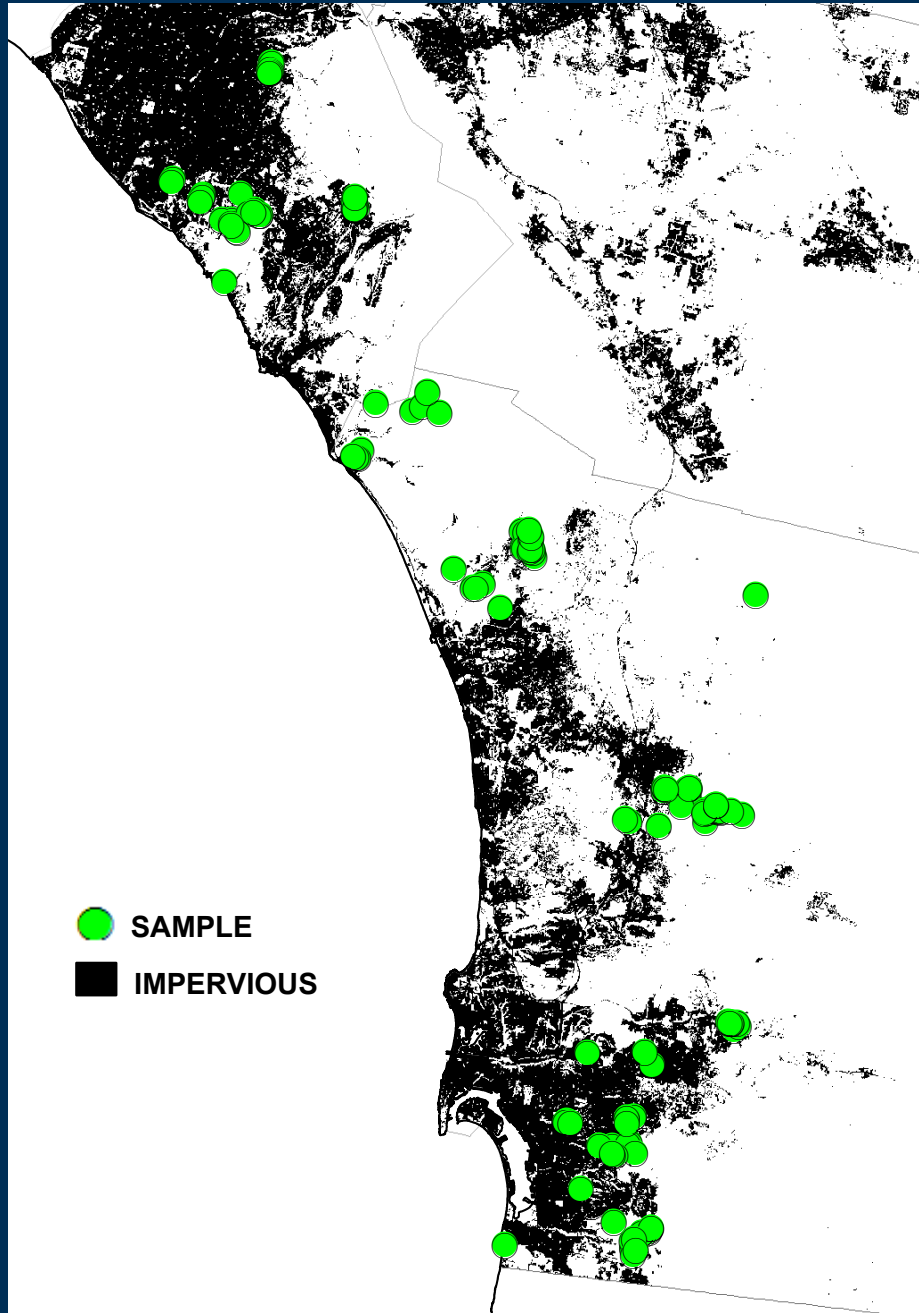
- USFWS cactus mapping
- SD Bird Atlas
- CACW working group

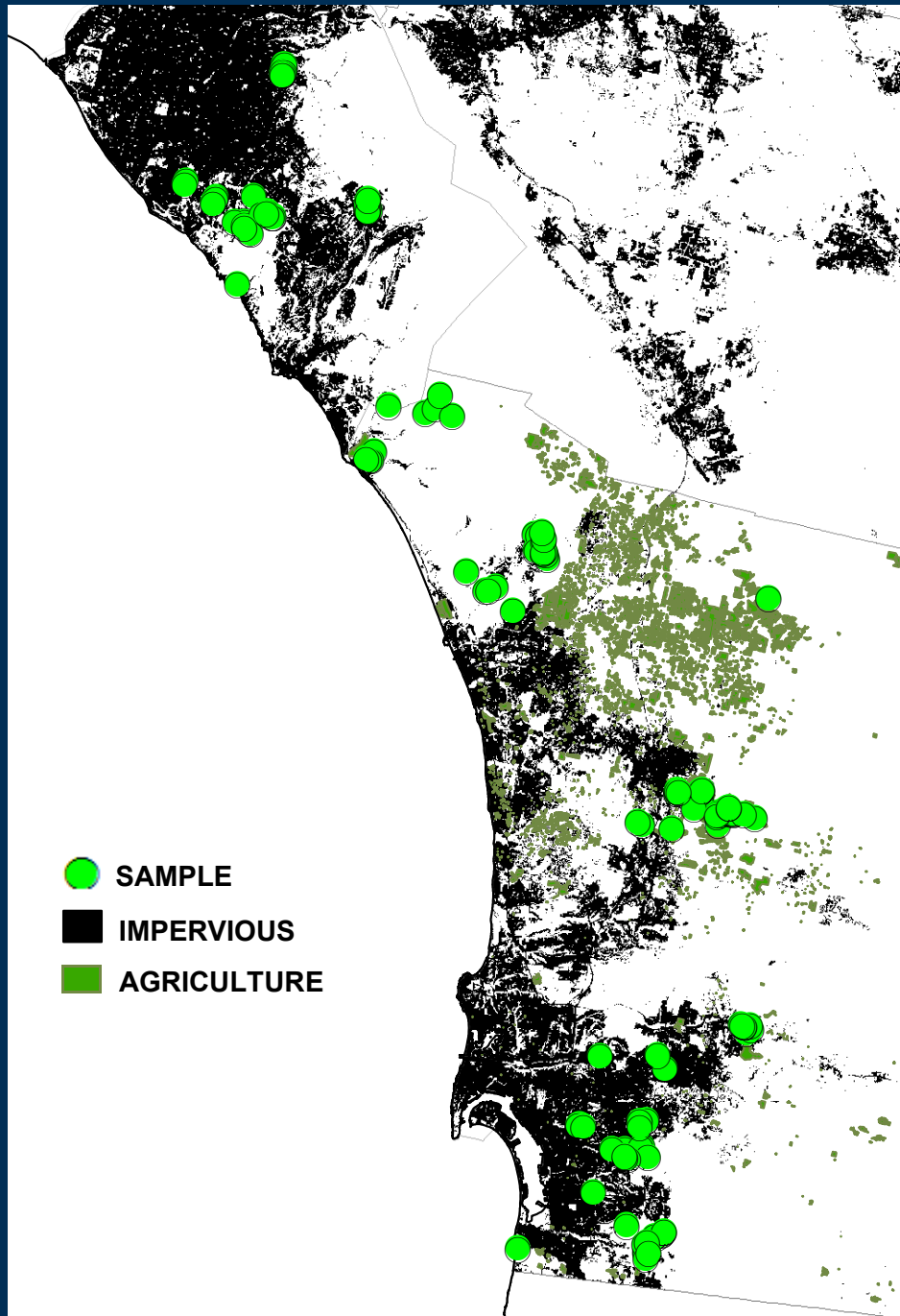
## Partners & cooperators

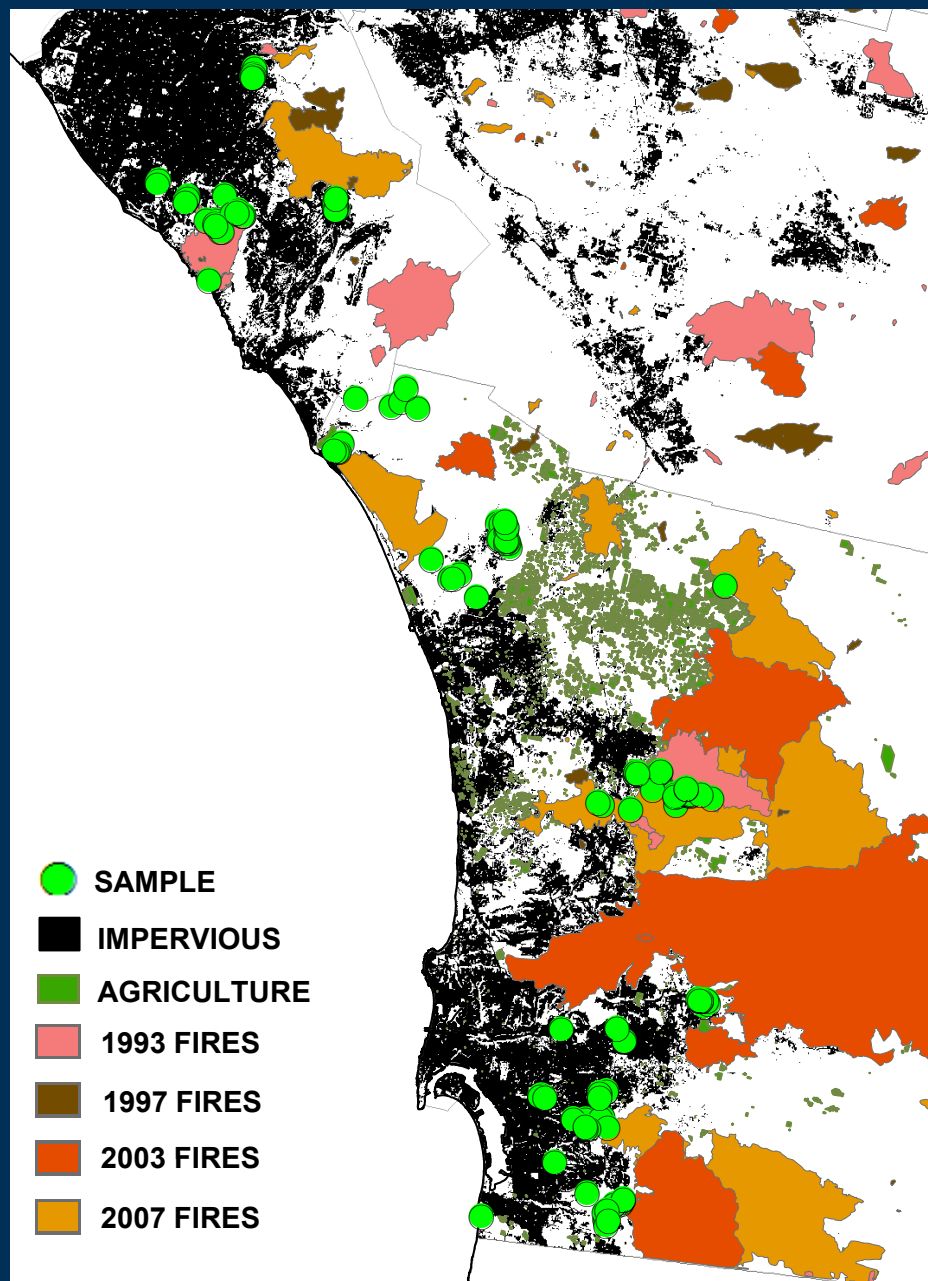
- USFWS
- SDNWR
- CDFG
- ICR Safari Park
- CBI
- TNC
- AECOM
- Fallbrook NWC
- MCB Camp Pendleton
- SD Audobon Society
- Sweetwater Authority
- SDMMP
- San Dieguito River Valley Conservancy



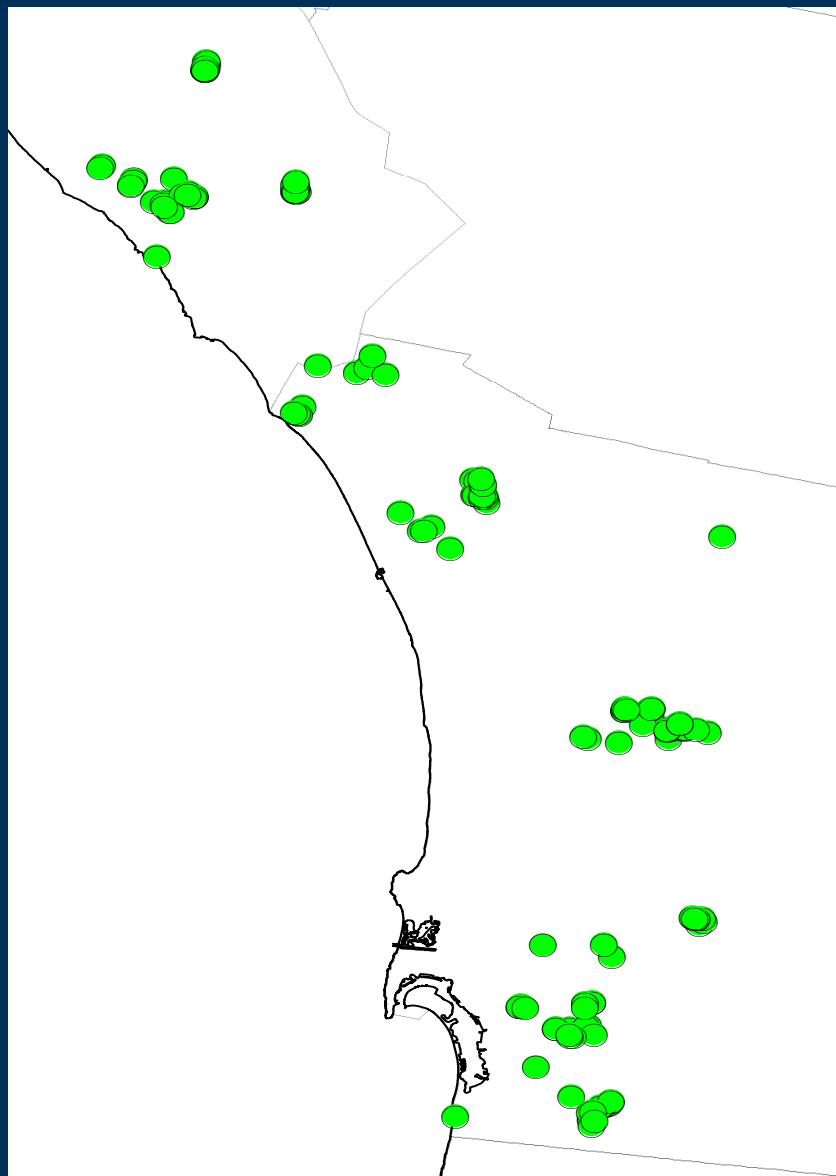












420 TOTAL BIRDS SAMPLED  
165 INDIVIDUALS ANALYZED

- 1 NESTLING
- 1-2 ADULTS



## Nestling feathers

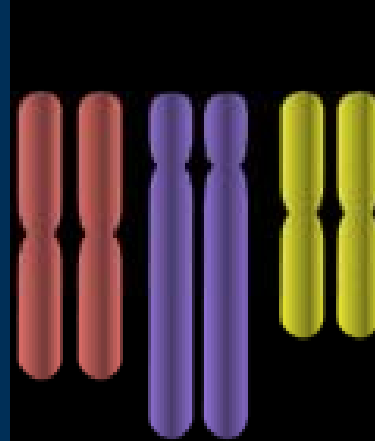
# Toenail clip





# A Little Genetics....

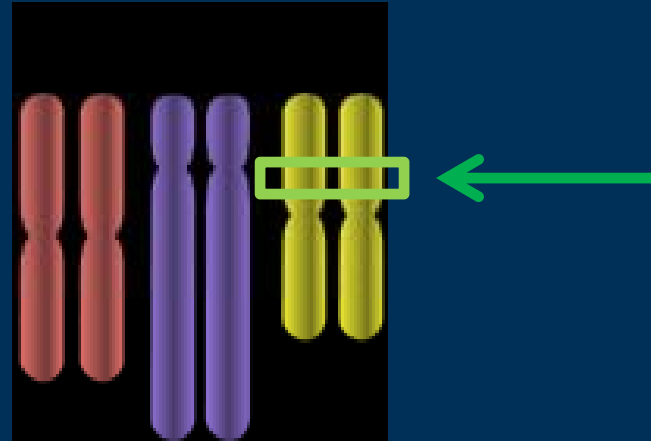
- Diploid





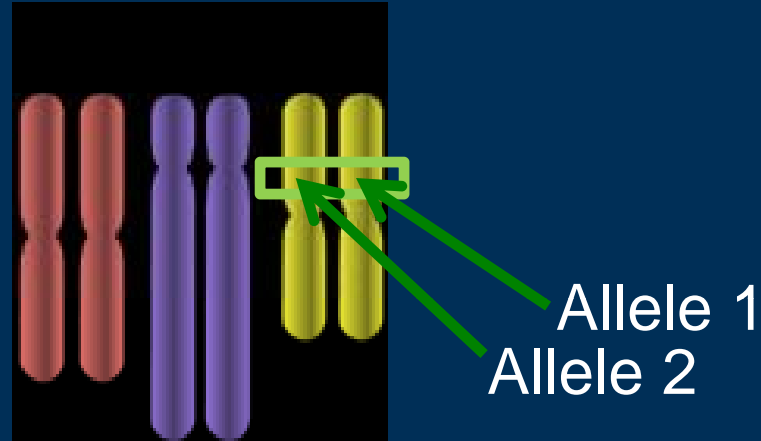
# A Little Genetics....

- Diploid
- Locus (loci)



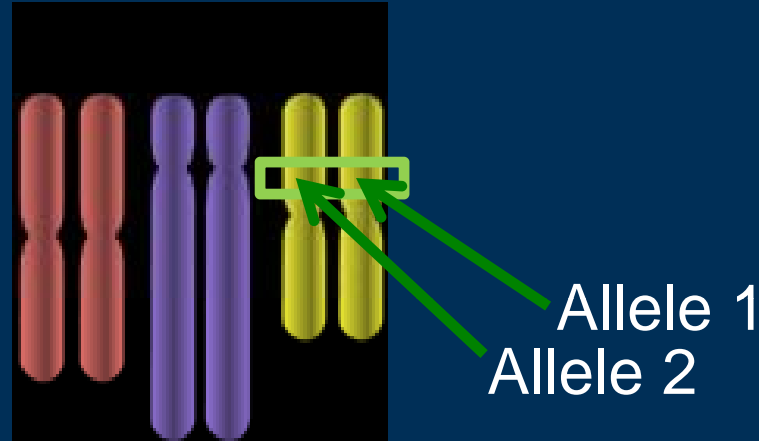
# A Little Genetics....

- Diploid
- Locus (loci)
- Alleles



# A Little Genetics....

- Diploid
- Locus (loci)
- Alleles
- Homozygous:
  - Allele 1 = Allele 2
- Heterozygous:
  - Allele 1  $\neq$  Allele 2



# Types of Markers...

- DNA Sequence
- SNPs
- Microsatellites
  - High mutation rate = high polymorphism
  - Selectively neutral
  - Using many markers covers more genome
  - 20 microsatellites analyzed here

# Classes of Analyses

- **Cluster analyses**
  - Individual-based
  - Infers number of clusters (K)
  - Multiple methods used to confirm results
    - STRUCTURE
    - GENELAND
- **Landscape analyses**
  - Groups of individuals
  - Genetic distance versus geographic distance
  - Intervening habitat
- **Genetic diversity within clusters**



# STRUCTURE

Individual 1
Individual 2
Individual 3
Individual 4

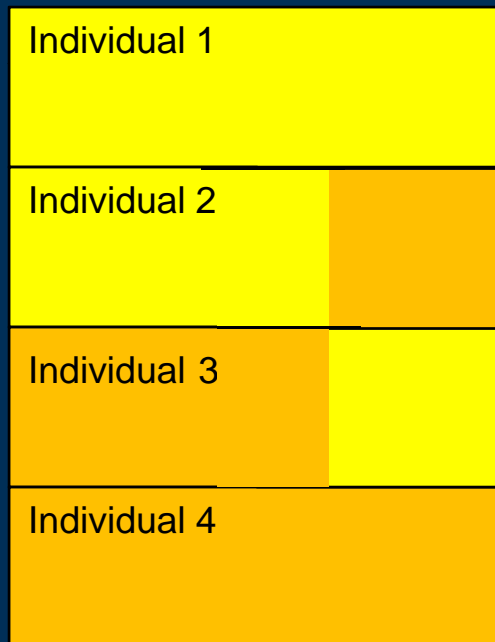
$$K = 1$$

# STRUCTURE

Individual 1
Individual 2
Individual 3
Individual 4

$$K = 2$$

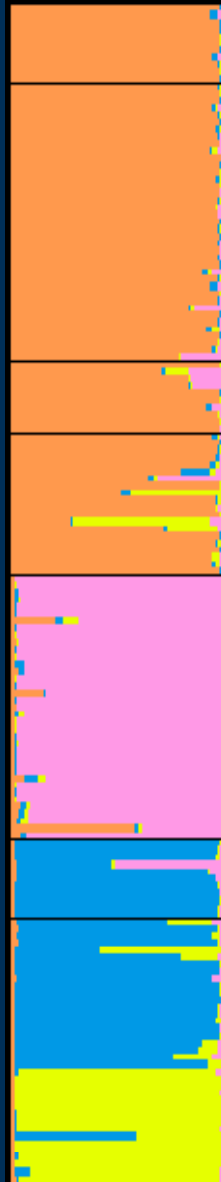
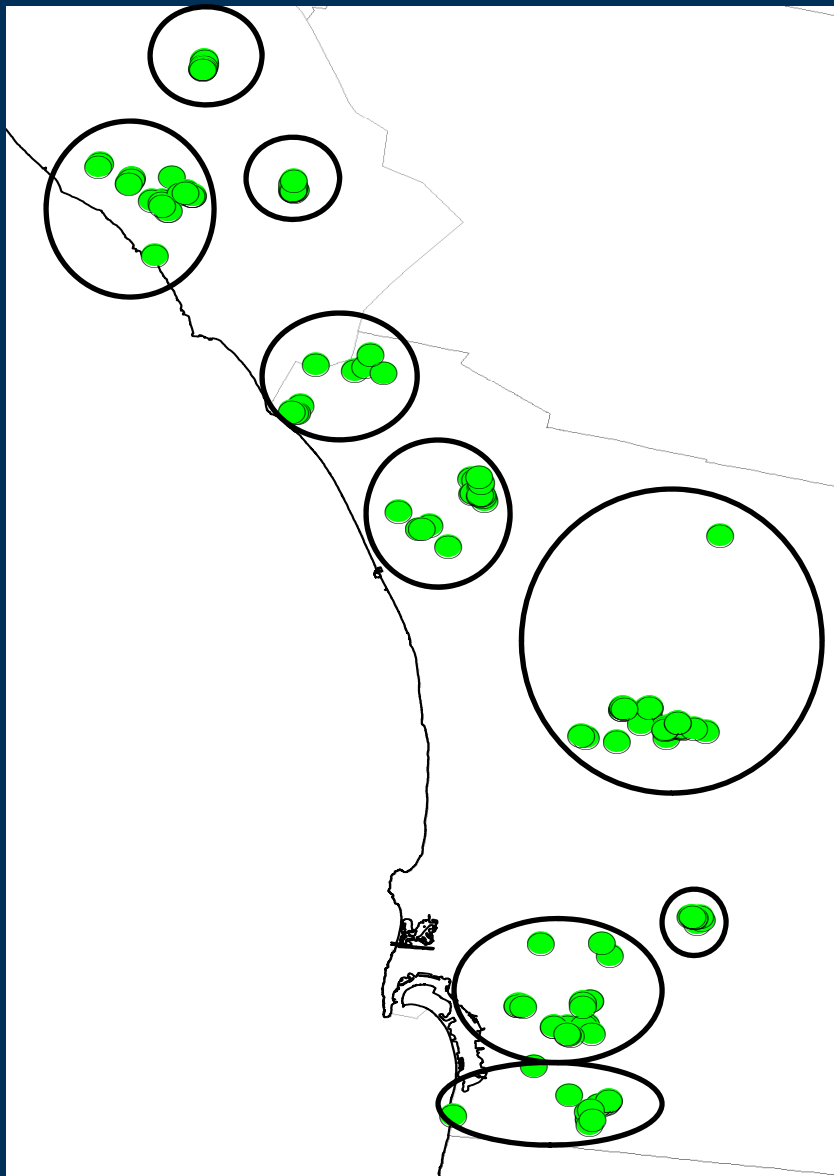
# STRUCTURE



$$K = 2$$

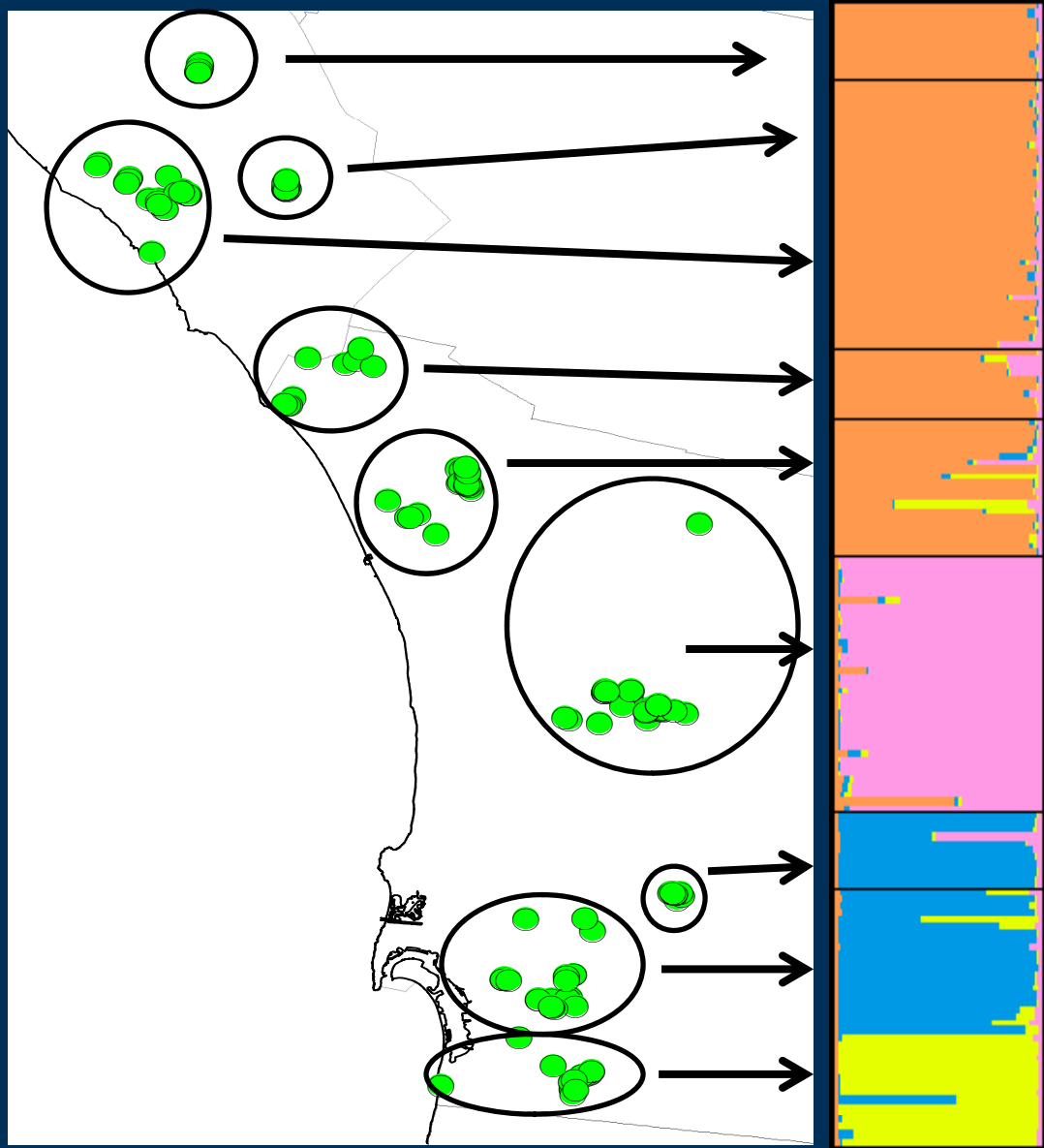
Admixture:

- Recent gene flow
- Common ancestry



 USGS

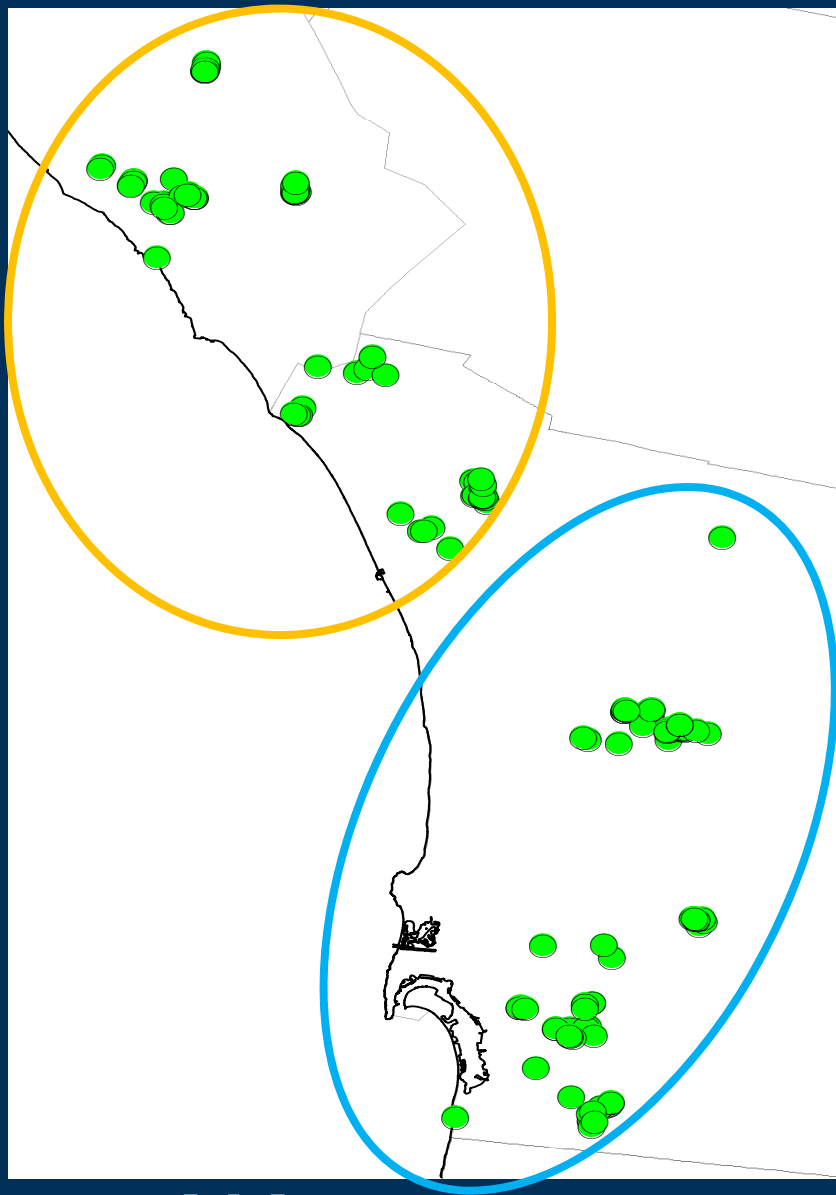
$K = 4$



 USGS

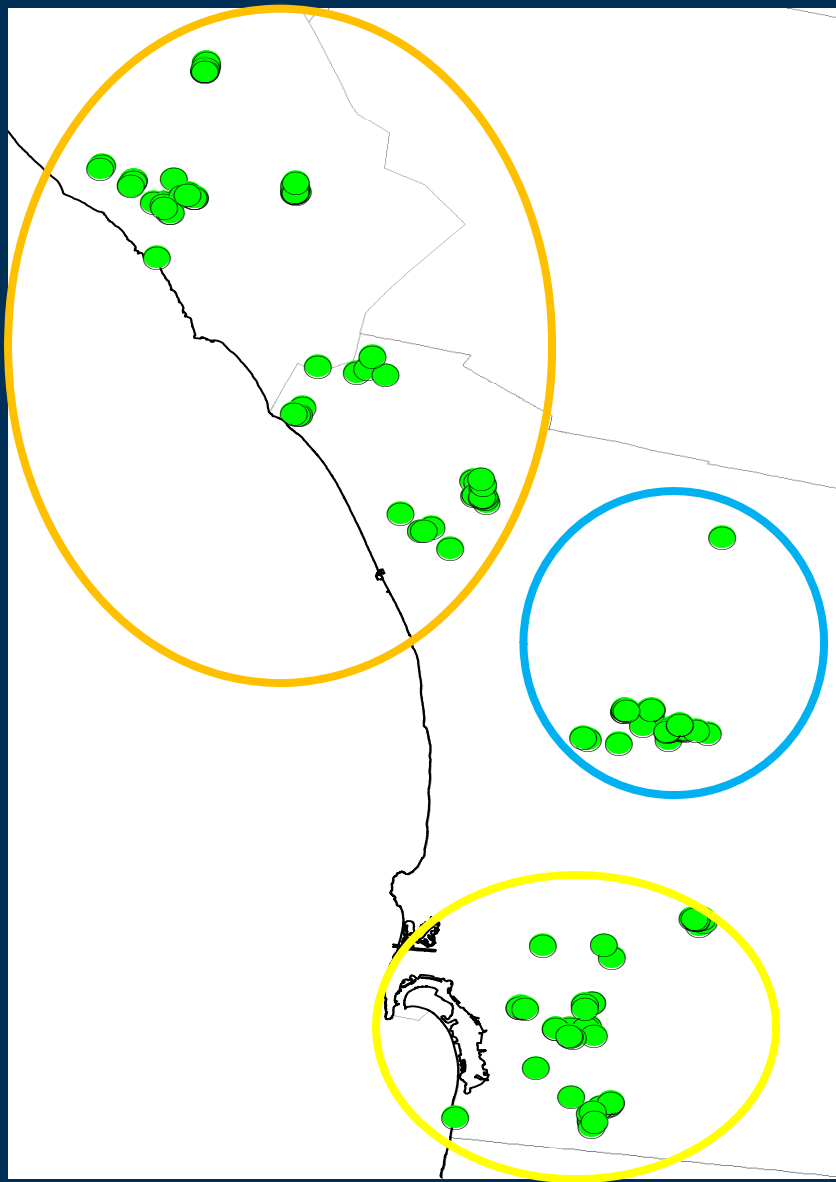
$K = 4$





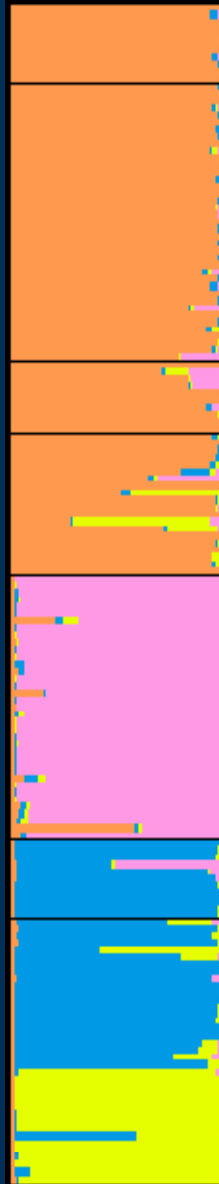
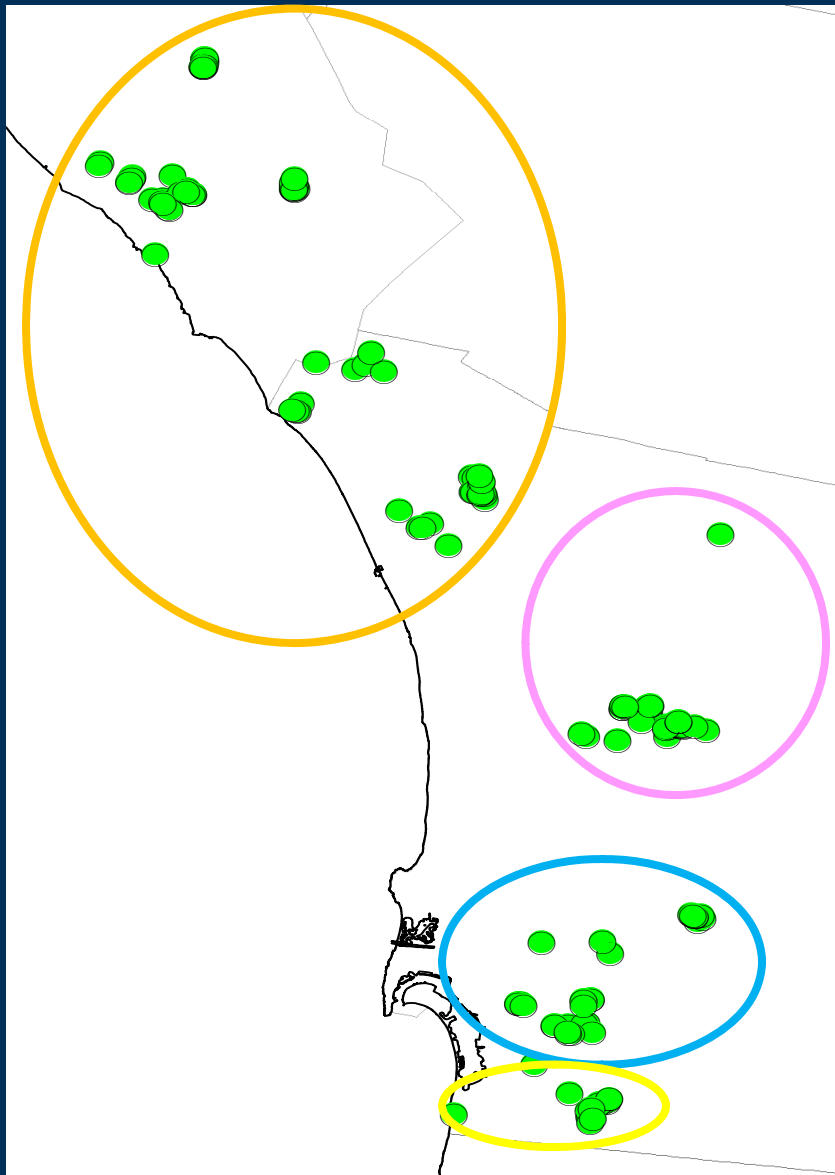
 USGS

$K = 2$



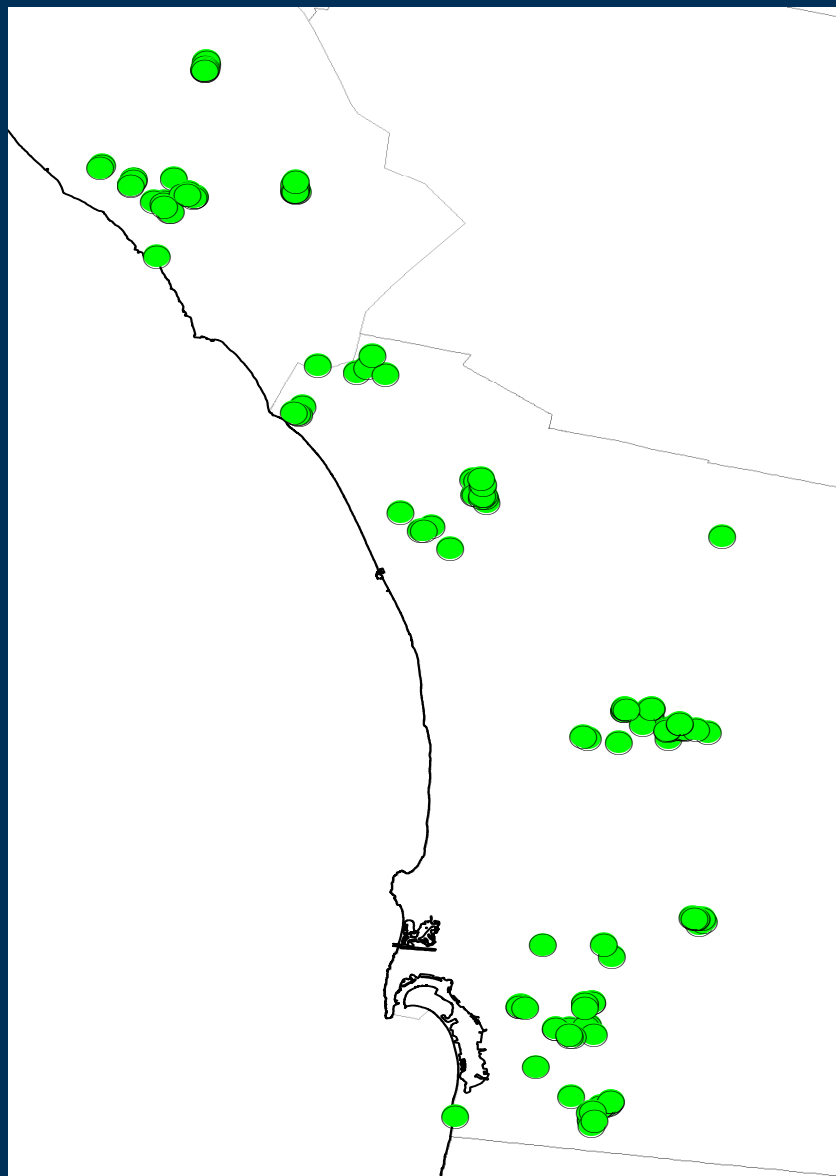
 USGS

$K = 3$



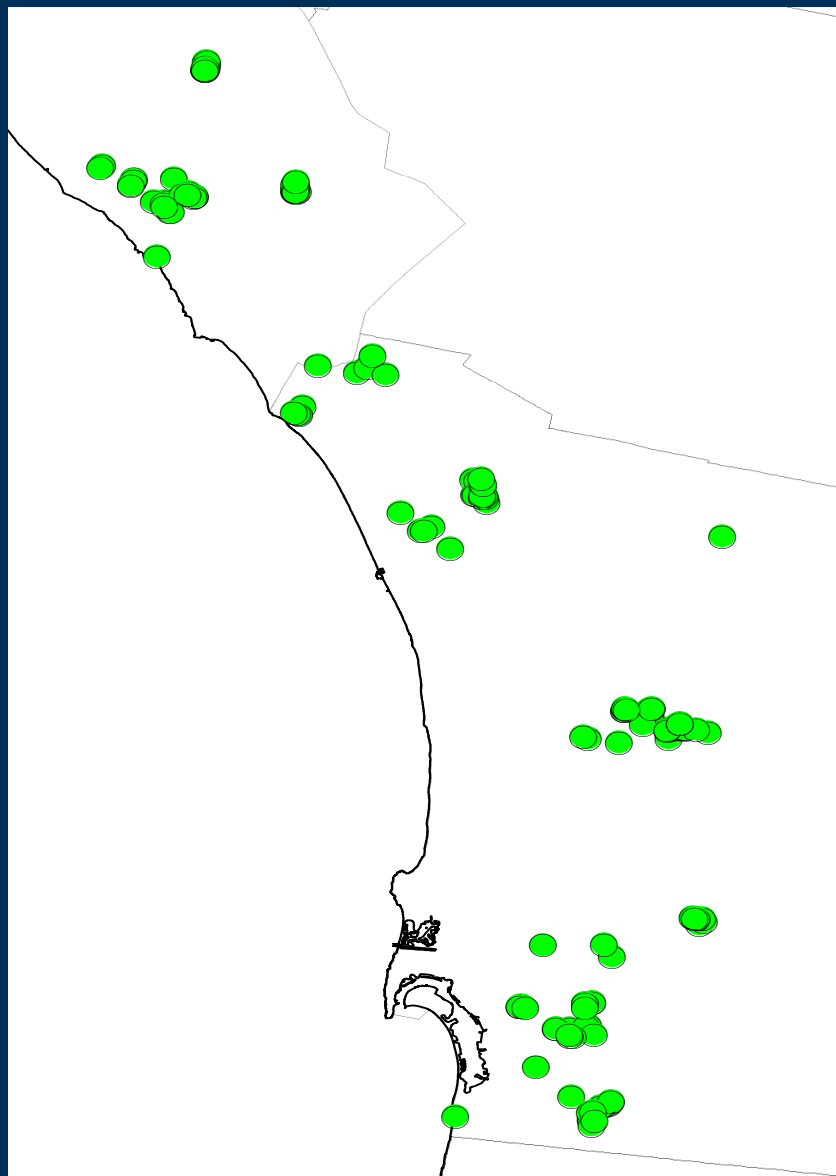
 USGS

$K = 4$



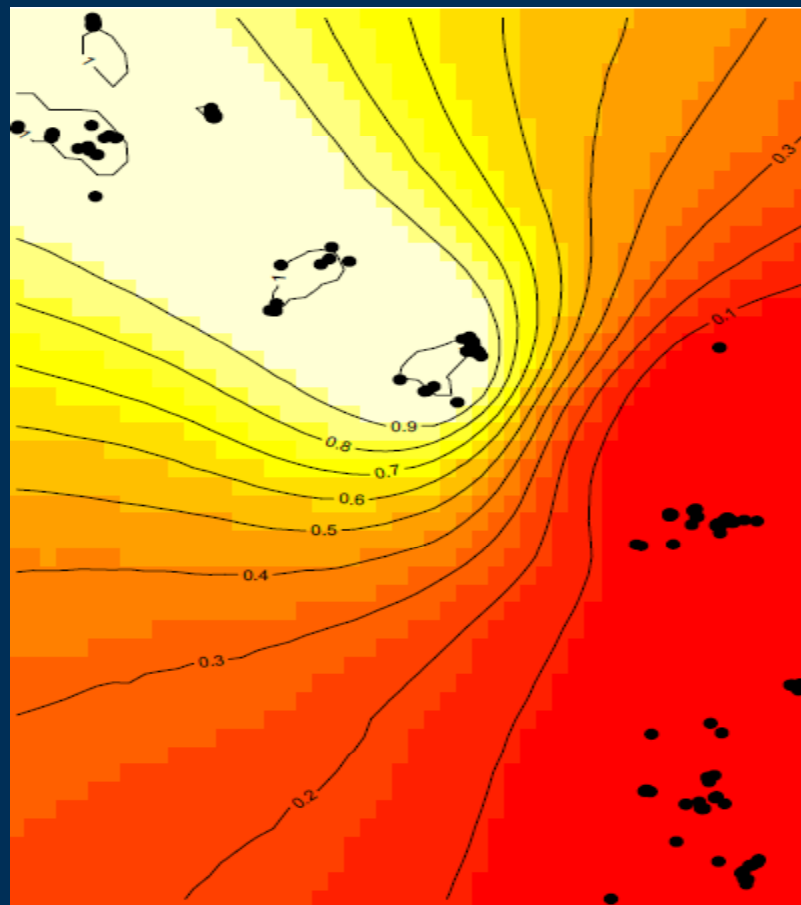
## GENELAND

- Individual-based cluster analysis
- Considers a spatial component

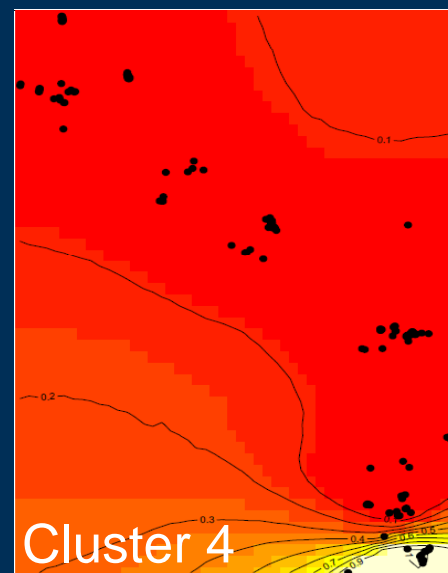
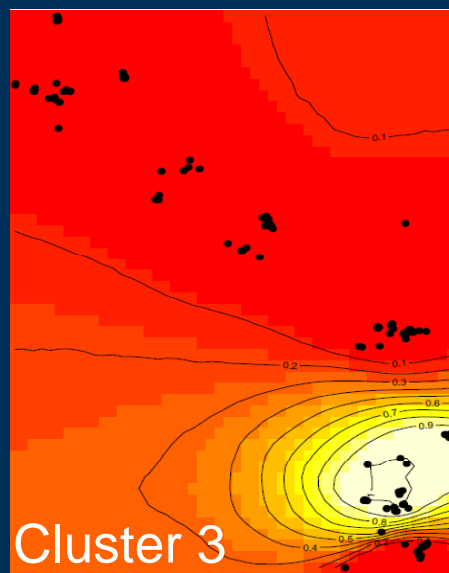
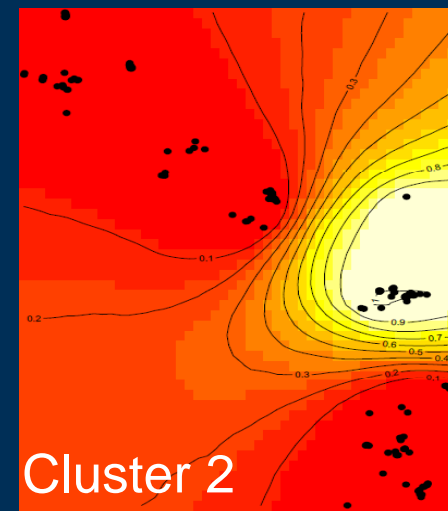
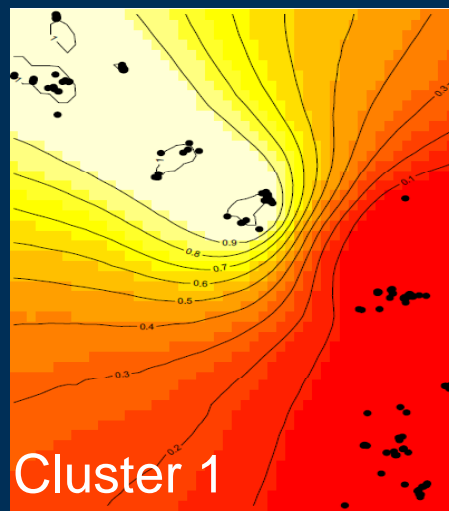
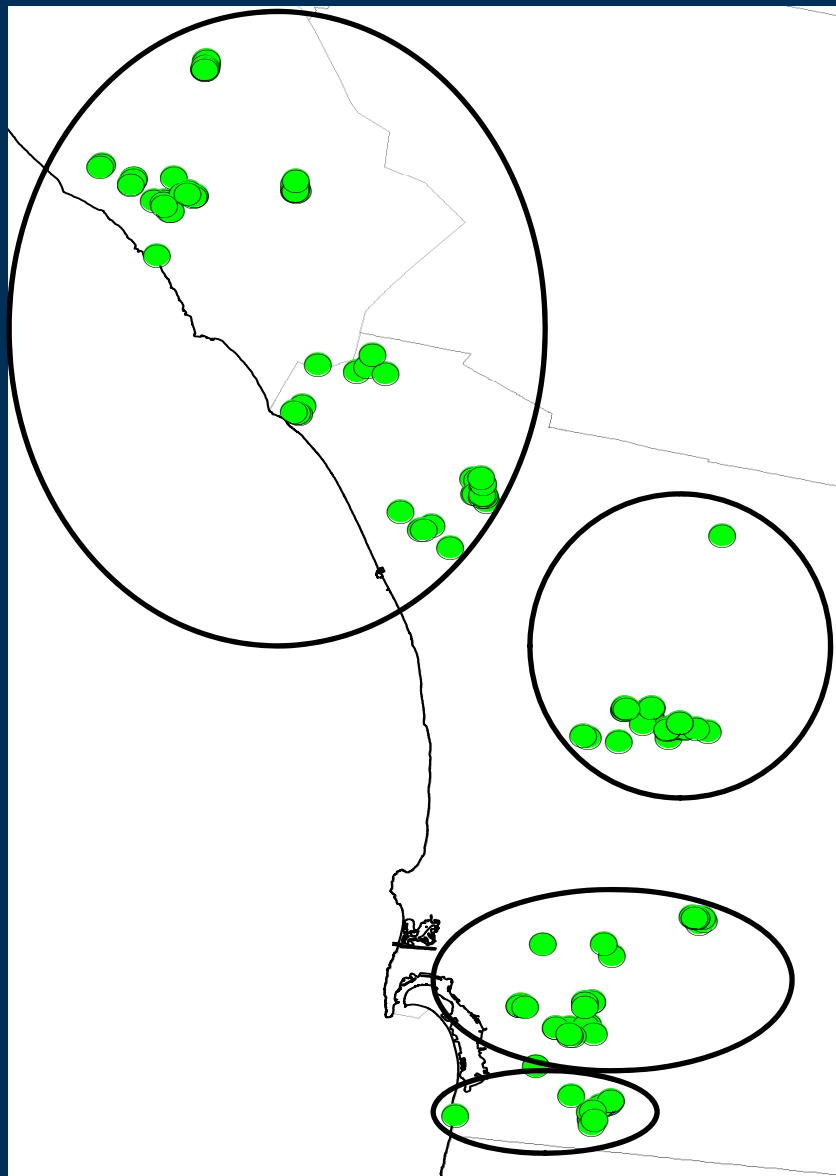


## GENELAND

- Individual-based cluster analysis
- Considers a spatial component

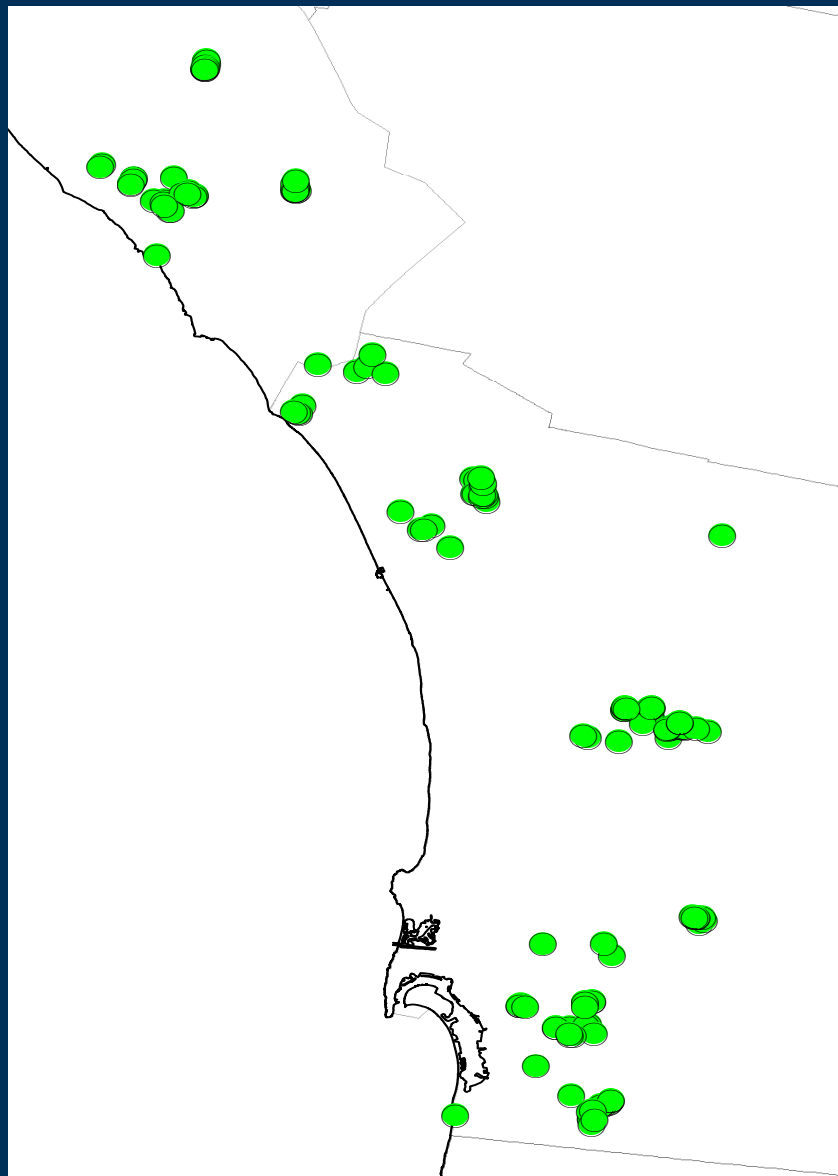


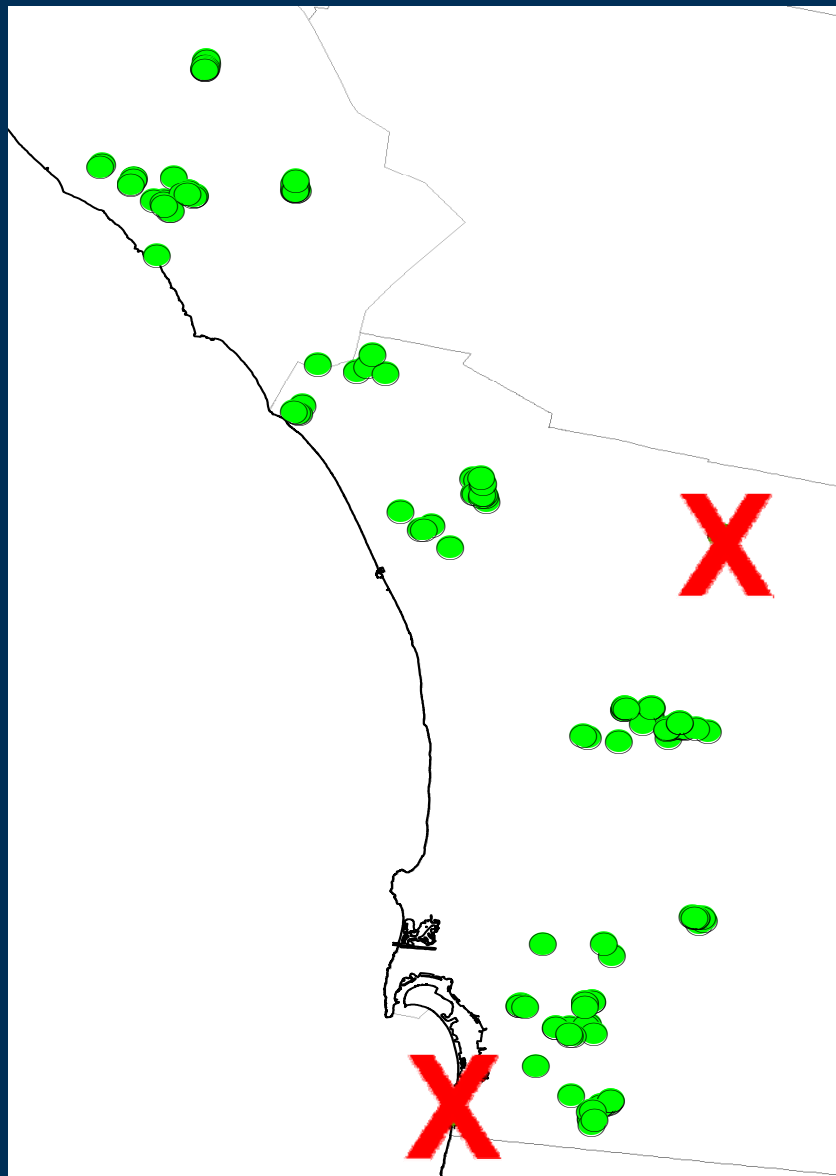


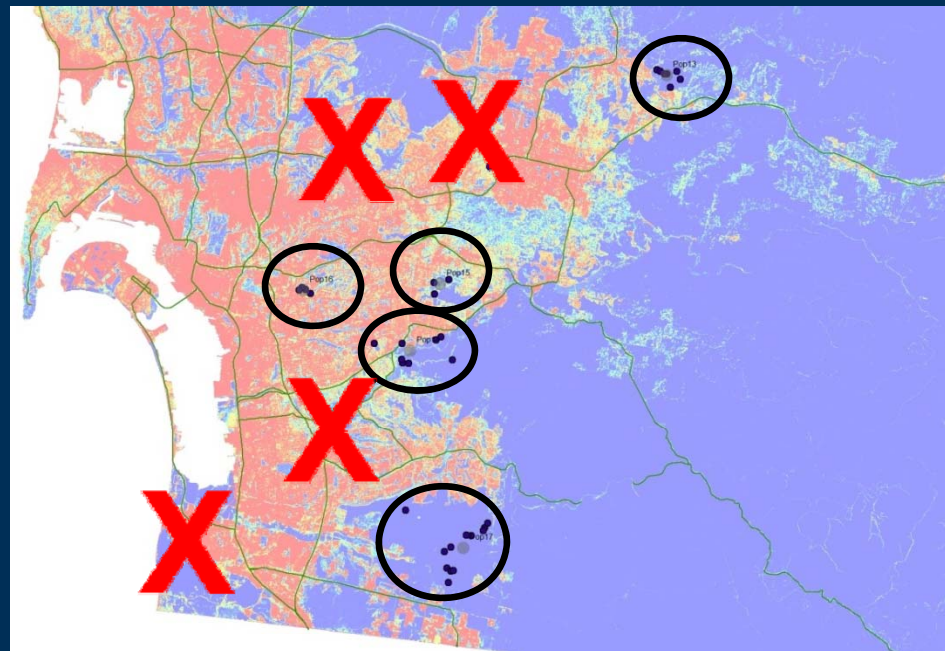
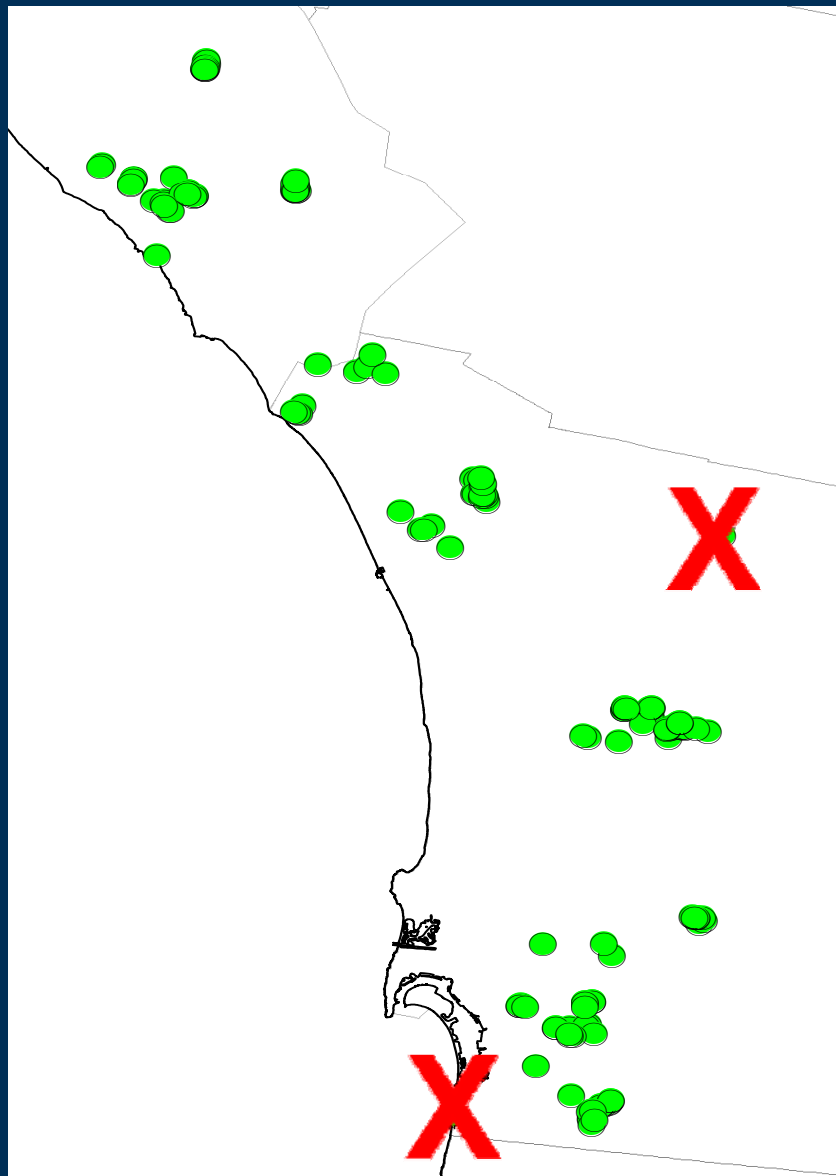


# Landscape Perspective?

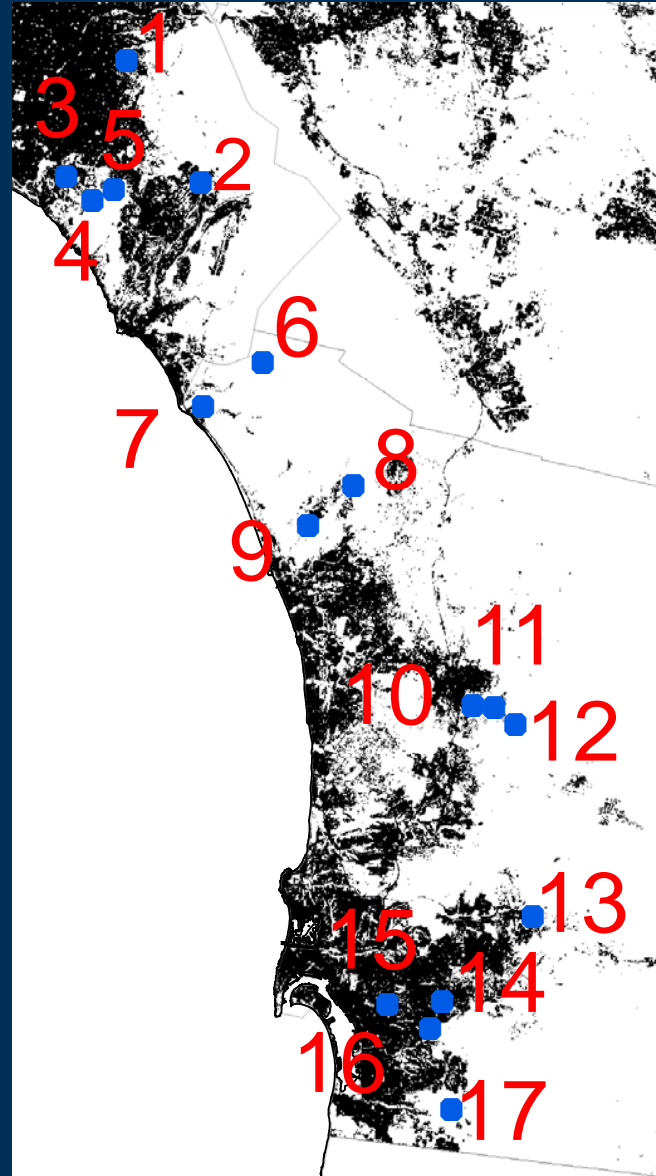
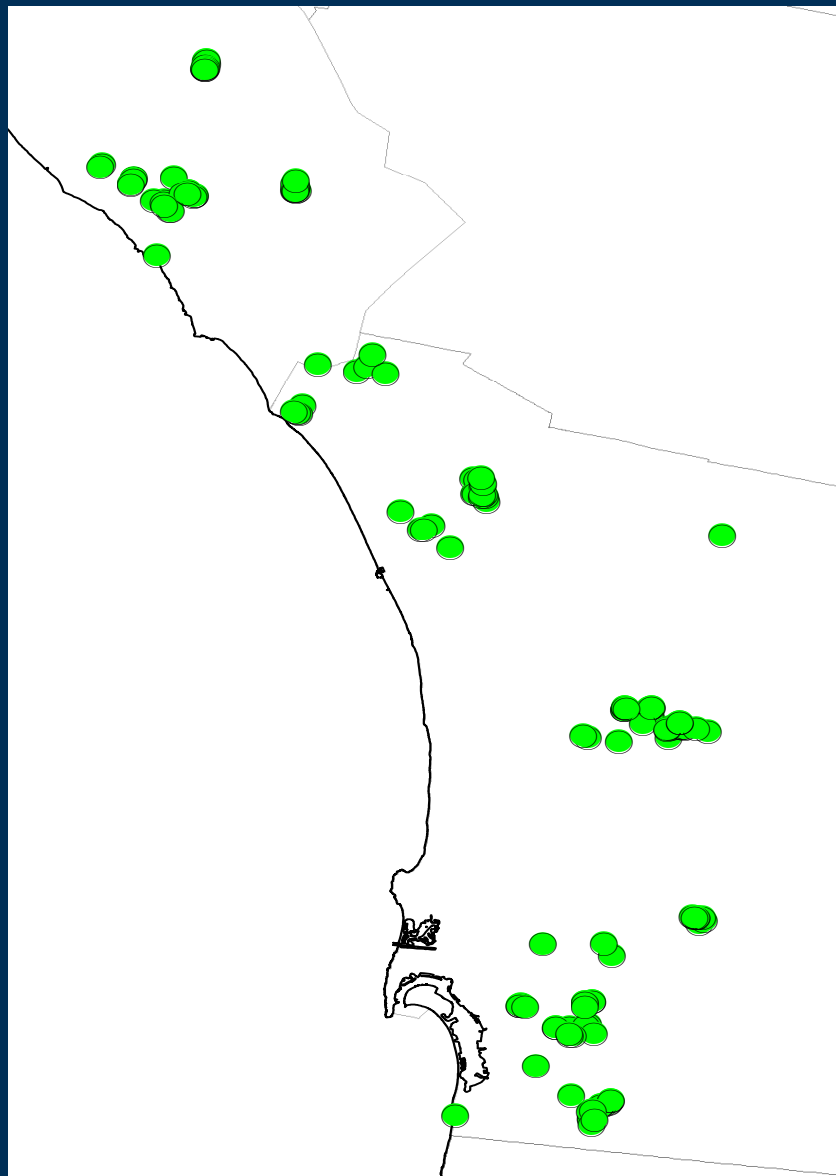
- $F_{ST}$ 
  - Genetic differentiation between groups
  - Scales 0 to 1
    - 0 = no genetic differences



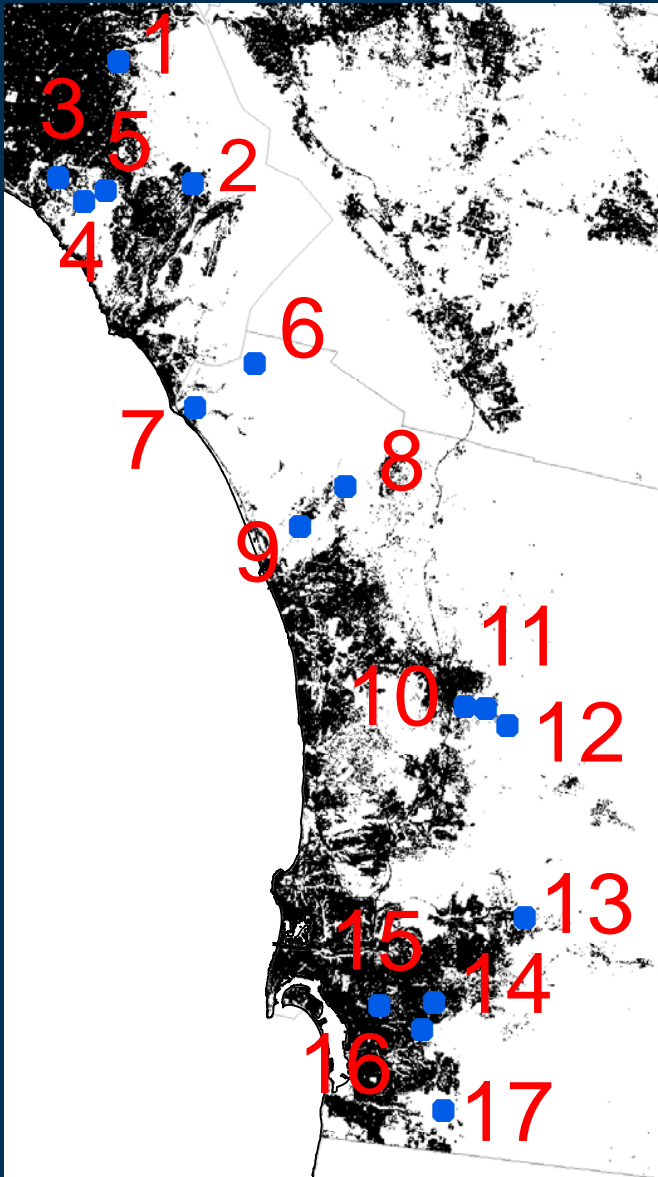




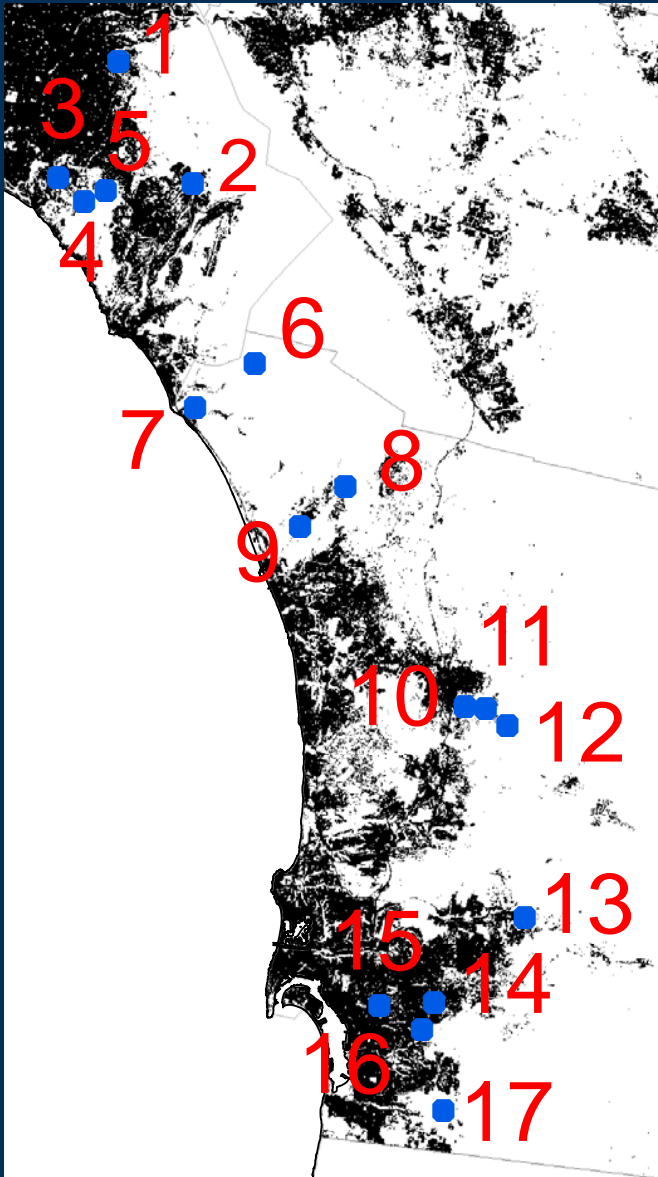


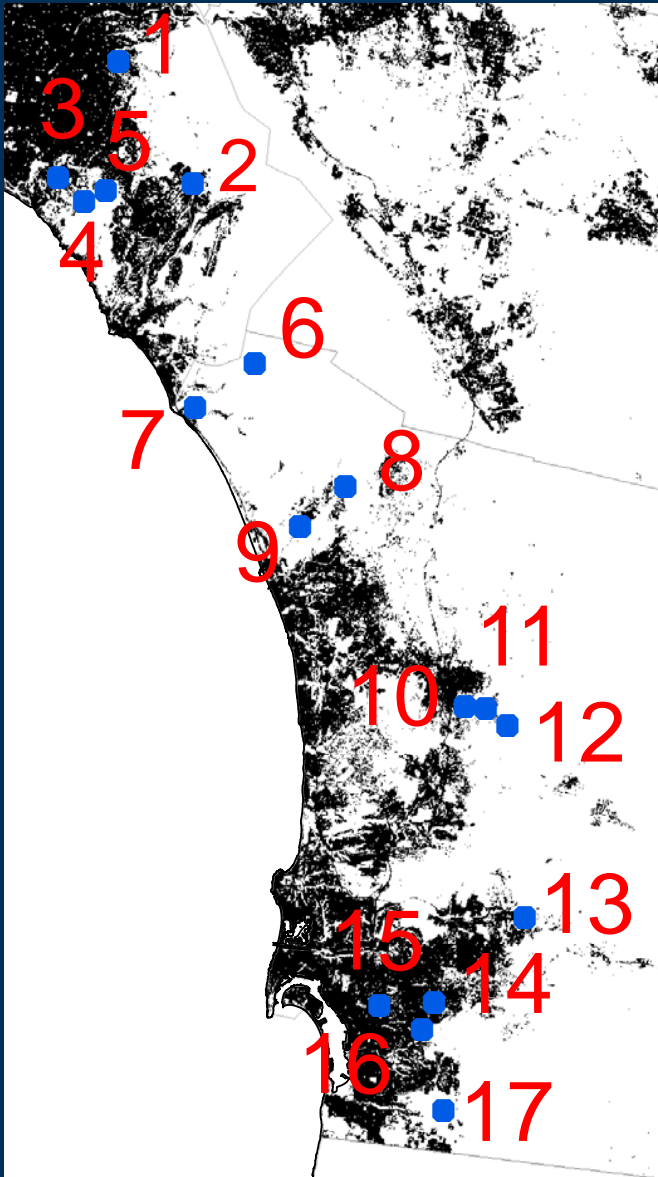


$F_{ST}$ ?

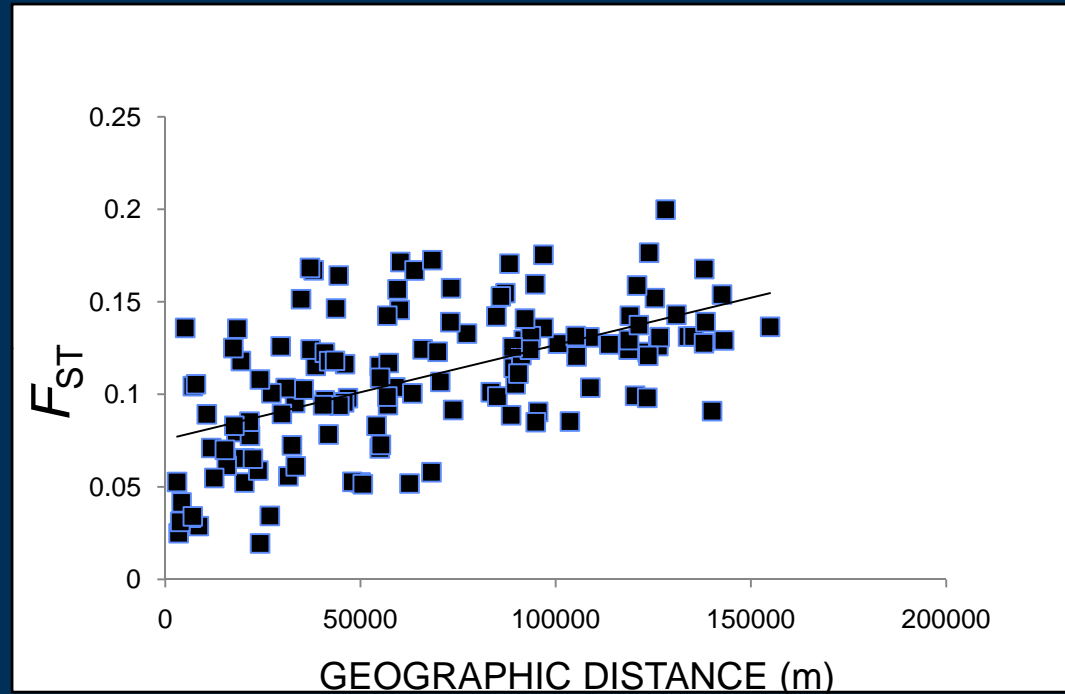


$$F_{ST} = 0.019 \text{ to } 0.2$$

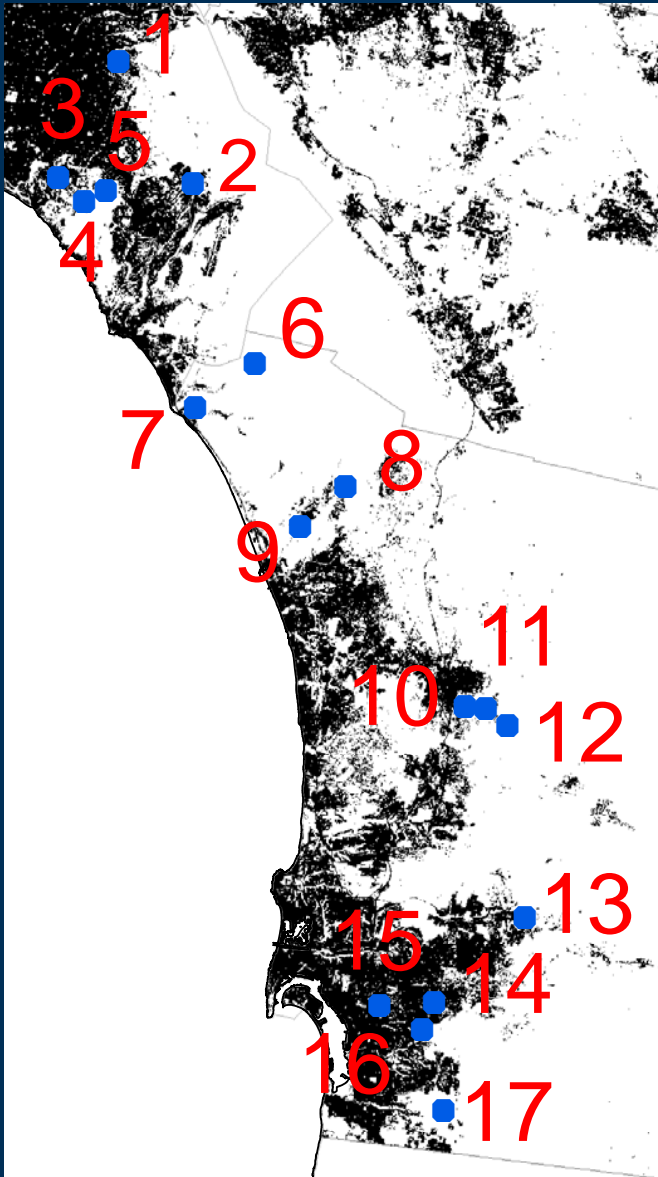




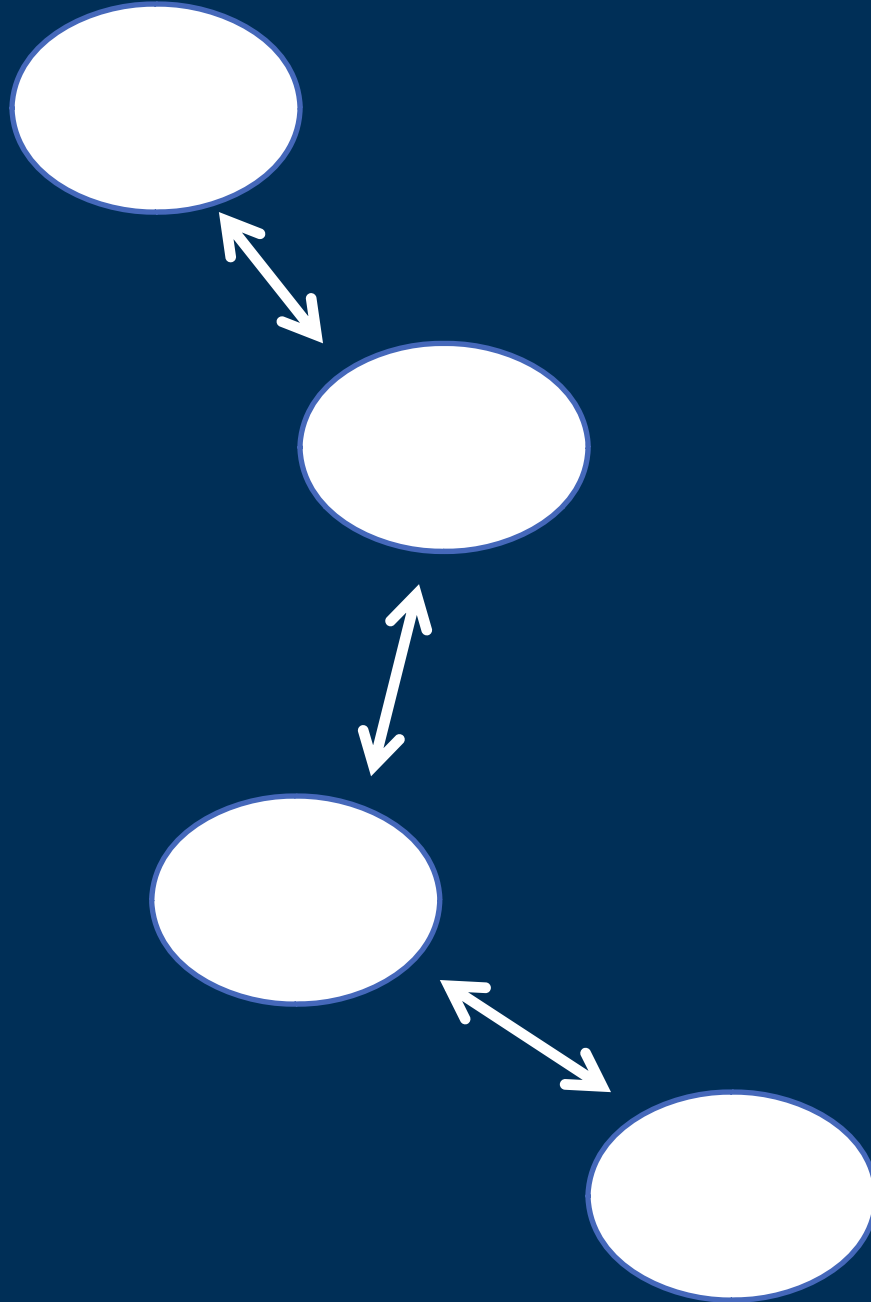
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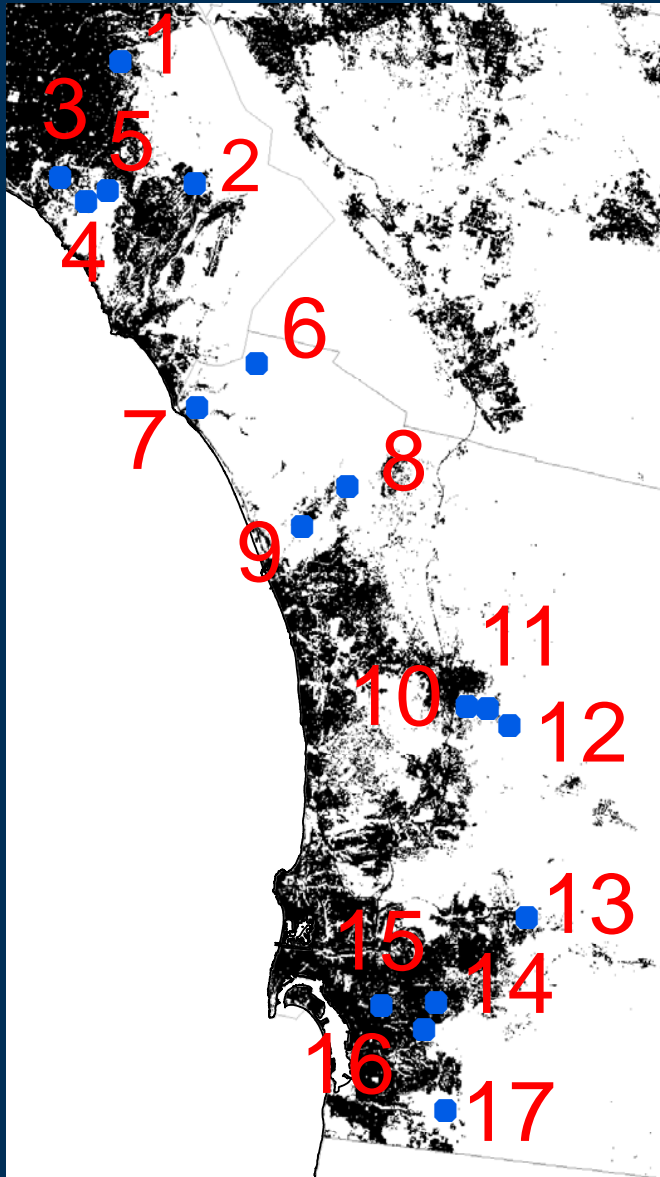


$$P < 0.001$$

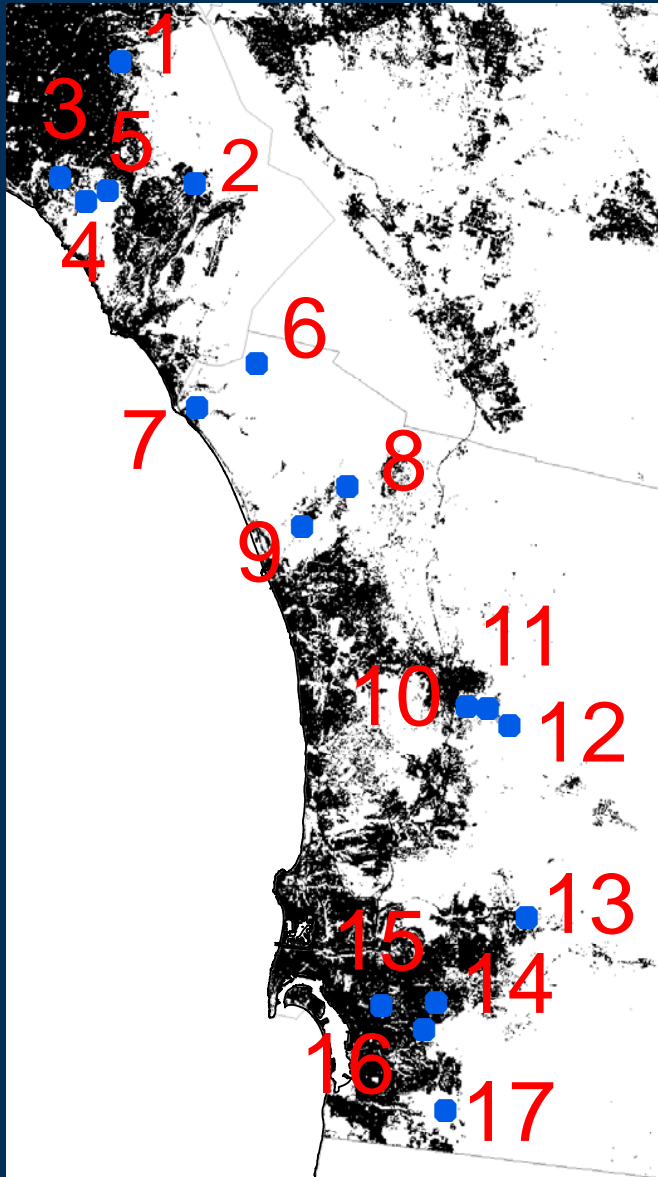


## STEPPING STONE GENE FLOW





Does anything else explain differentiation other than geographic distance?



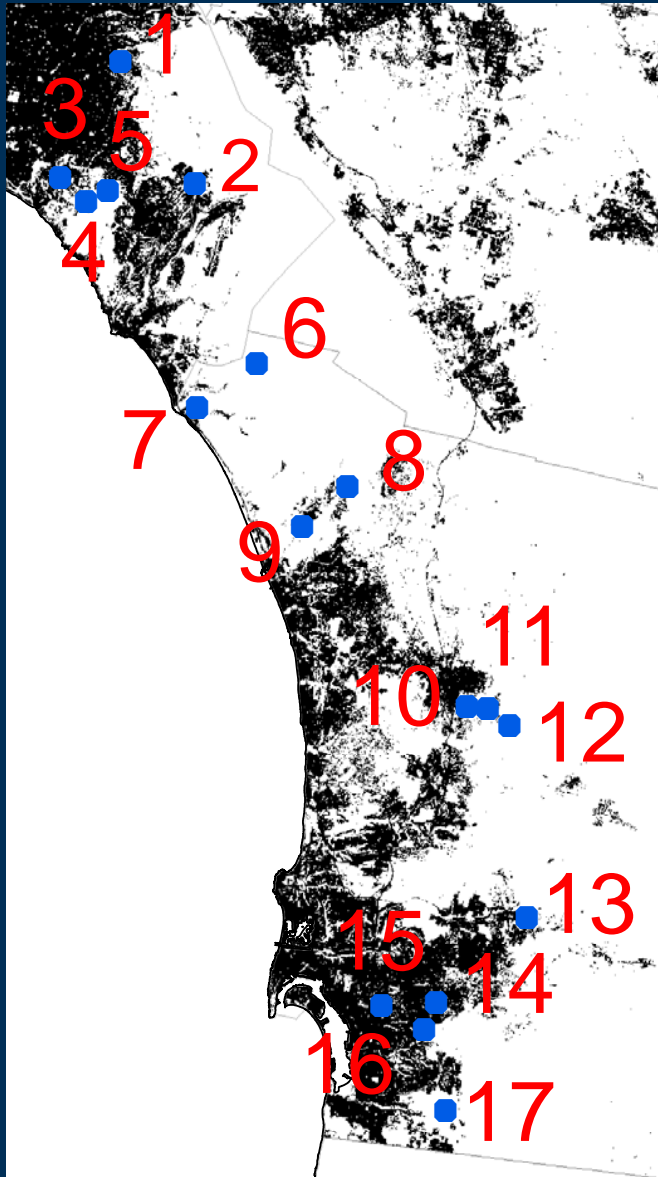
Does anything else explain differentiation other than geographic distance?

Pairwise matrix

0 = no fragmentation

1 = fragmented





Does anything else explain differentiation other than geographic distance?

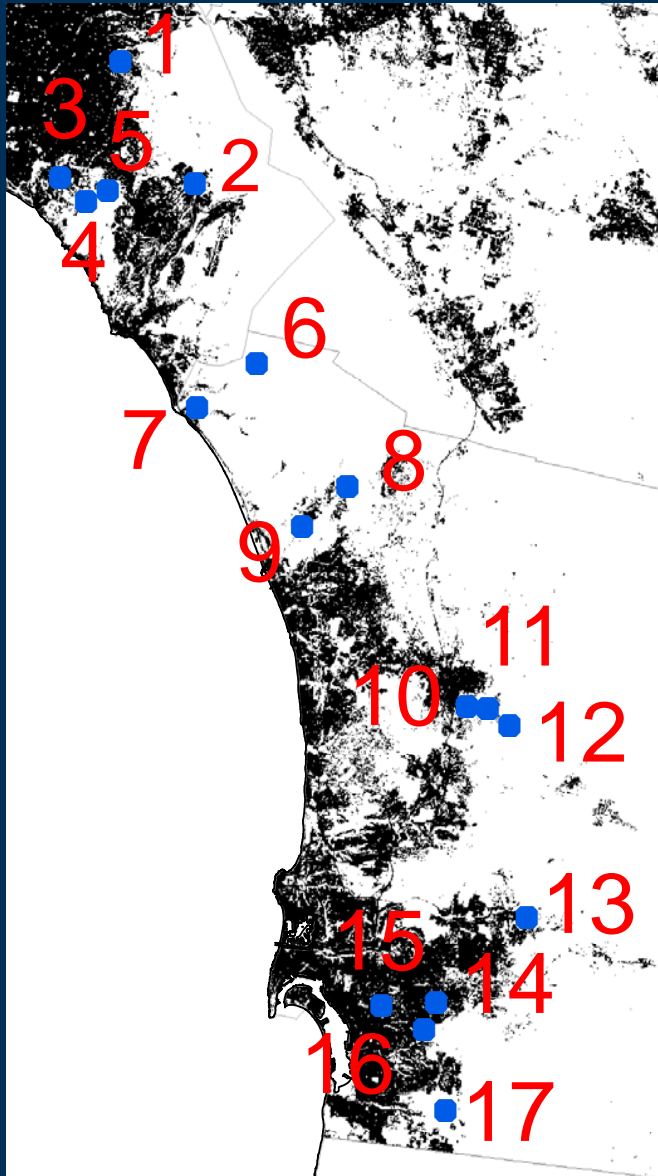
Pairwise matrix

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Differentiation versus geo dist:

$p < 0.001$



Does anything else explain differentiation other than geographic distance?

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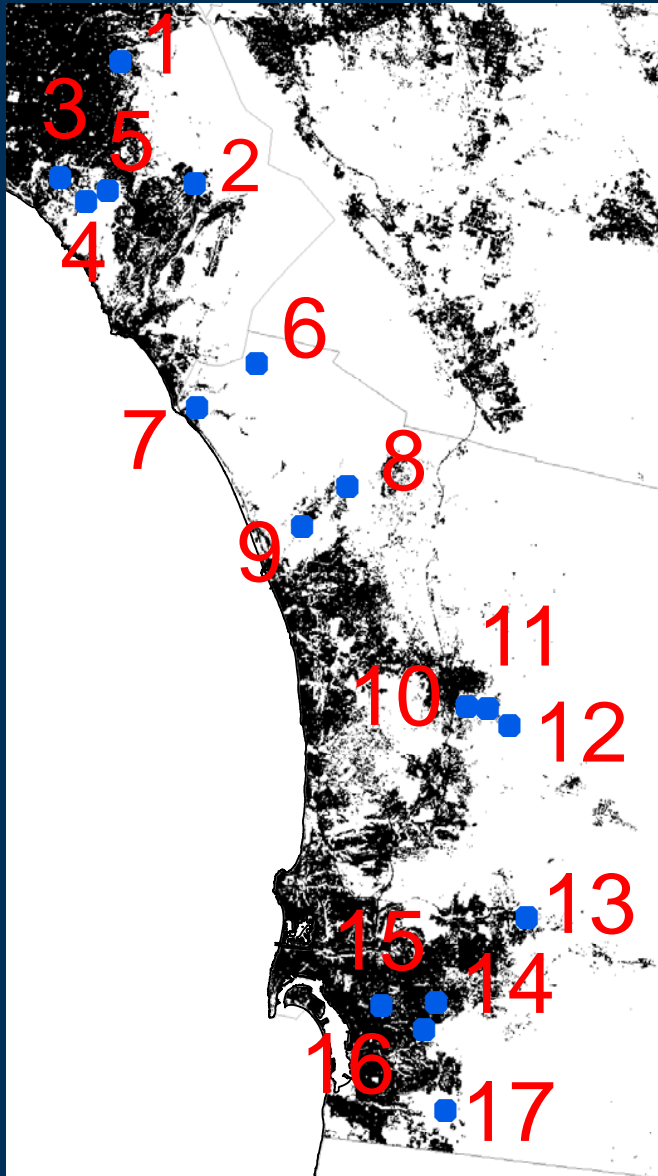
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Differentiation versus geo dist:

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Pairwise matrix

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Differentiation versus geo dist:

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Differentiation versus fragmentation:

$p < 0.001$

Differentiation vs. frag. (controlling for geo dist):

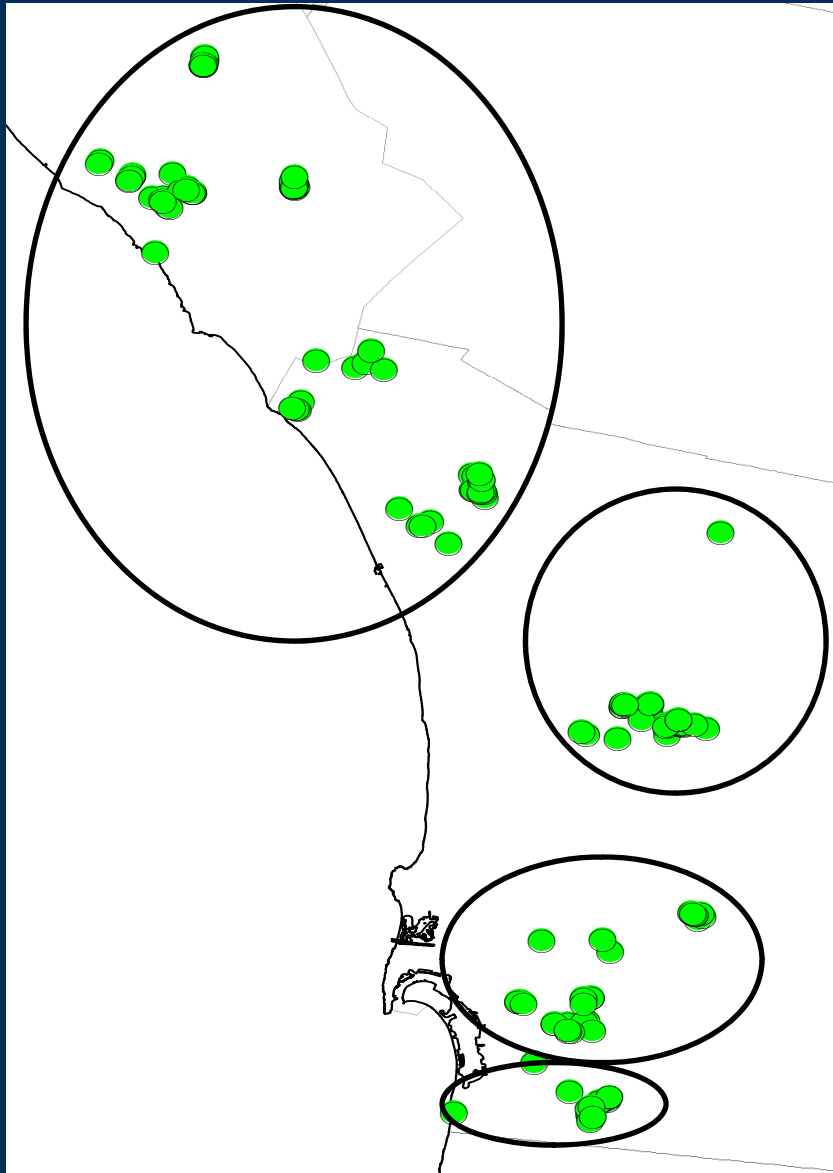
$p = 0.0001$

# GENETIC DIVERSITY



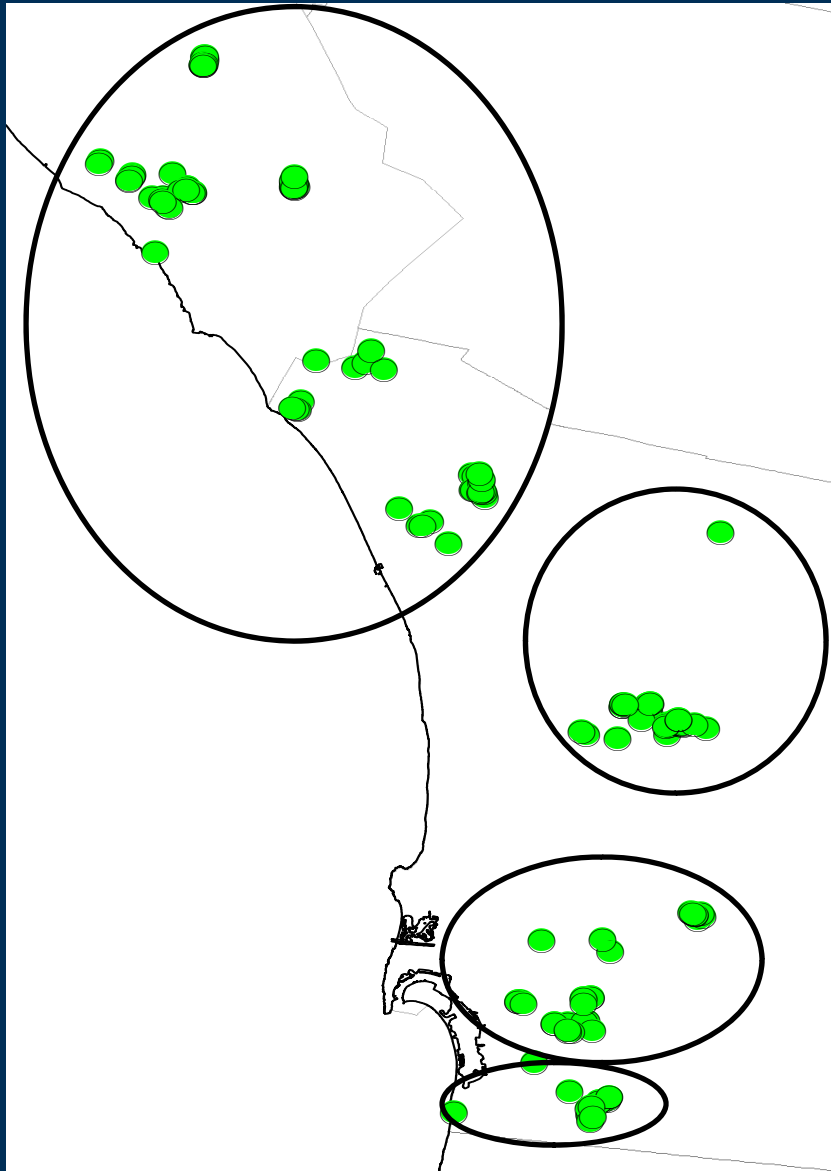
Cluster	Samples
OC-PEN	80
PASQUAL	37
SD	32
OTAY	16

# GENETIC DIVERSITY



Cluster	Samples	$H_E$	A
OC-PEN	80	0.64	5.5
PASQUAL	37	0.66	5.1
SD	32	0.63	5.4
OTAY	16	0.65	5.0

# GENETIC DIVERSITY



Cluster	Samples	$H_E$	A	$N_e$
OC-PEN	80	0.64	5.5	94 (68 - 129)
PASQUAL	37	0.66	5.1	52 (33 - 84)
SD	32	0.63	5.4	59 (40 - 91)
OTAY	16	0.65	5.0	34 (18 - 92)

$N_e \ll N_c$

# GENETIC DIVERSITY



Cluster	Samples	$H_E$	A	Ne
OC-PEN*	80	0.64	5.5	94 (68 - 129)
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Bottleneck\*

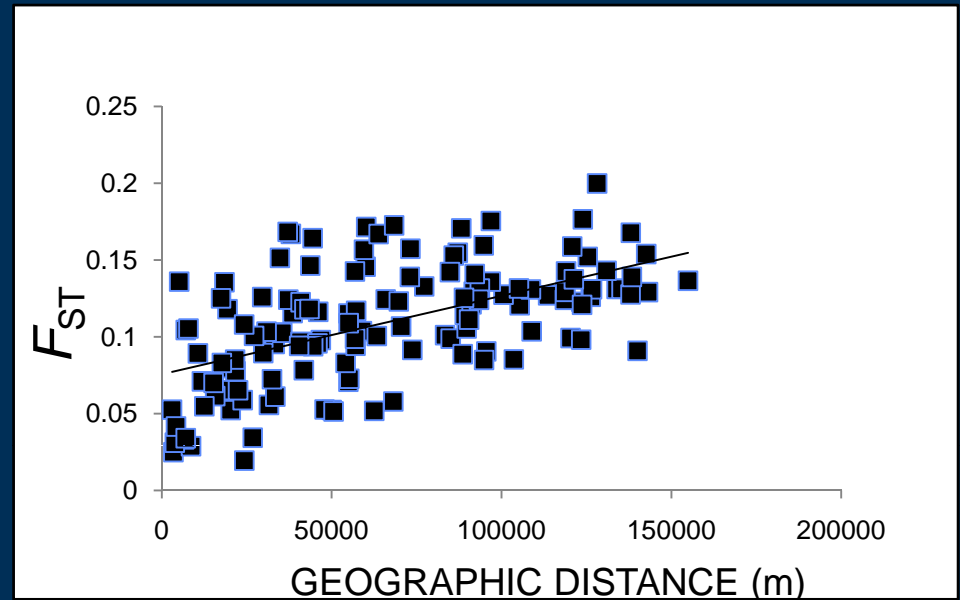
# TAKE HOME MESSAGES.....



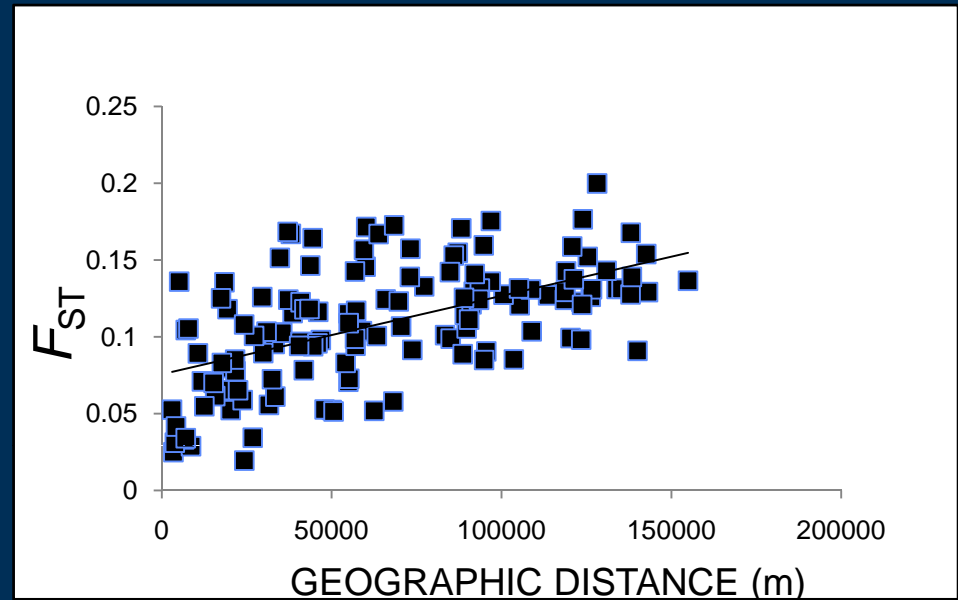
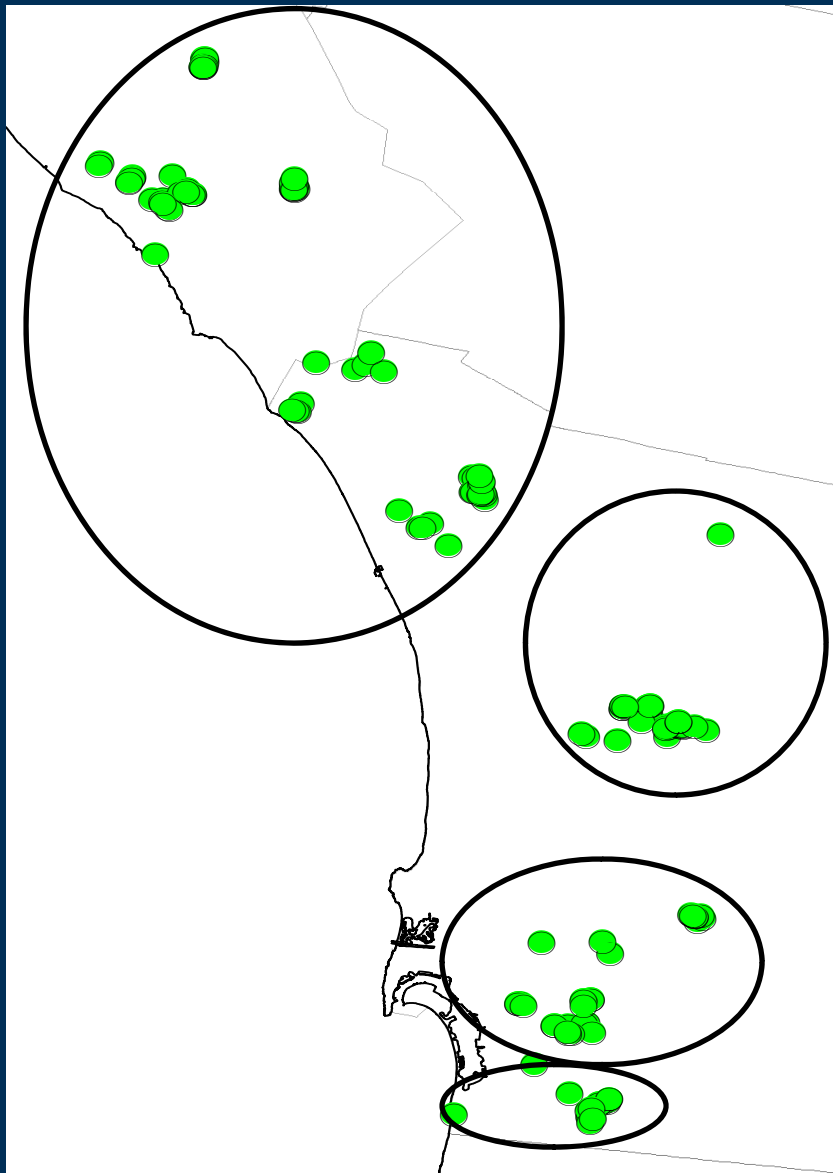
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# NEXT?

- Resighting study
- Expanding sampling into San Bernardino, LA, Ventura, and additional Orange County sites
  - CDFG
- Cactus habitat model & deeper landscape analyses
- Individual-based genetic distances
- Museum samples
- California Gnatcatcher genetic connectivity

