THE SHAPE OF THINGS TO COME

a window into desert tortoise connectivity in a changing landscape

(2015-UNR-1580A-Desert Tortoise Connectivity Modeling)

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Overview

(a) Genetic connectivity & modeling

(b) Setting up predictive models

(c) Direction of preliminary data

(d) Work to be done

MSHCP Objective D.4.2

Identify critical connectivity corridors for covered species, prioritize conservation and/or acquisition of corridors, and increase permeability for species movement where feasible


Photo courtesy of USGS


Photo courtesy bing images

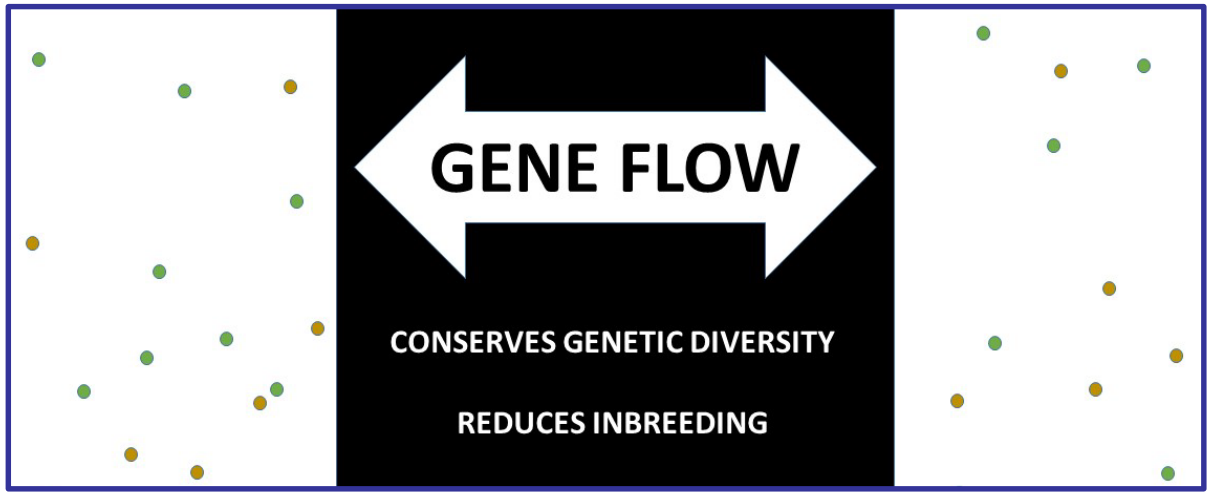
Habitat loss & Connectivity

In areas subject to anthropogenic pressures, connectivity corridors improve opportunities for individual contact and gene flow

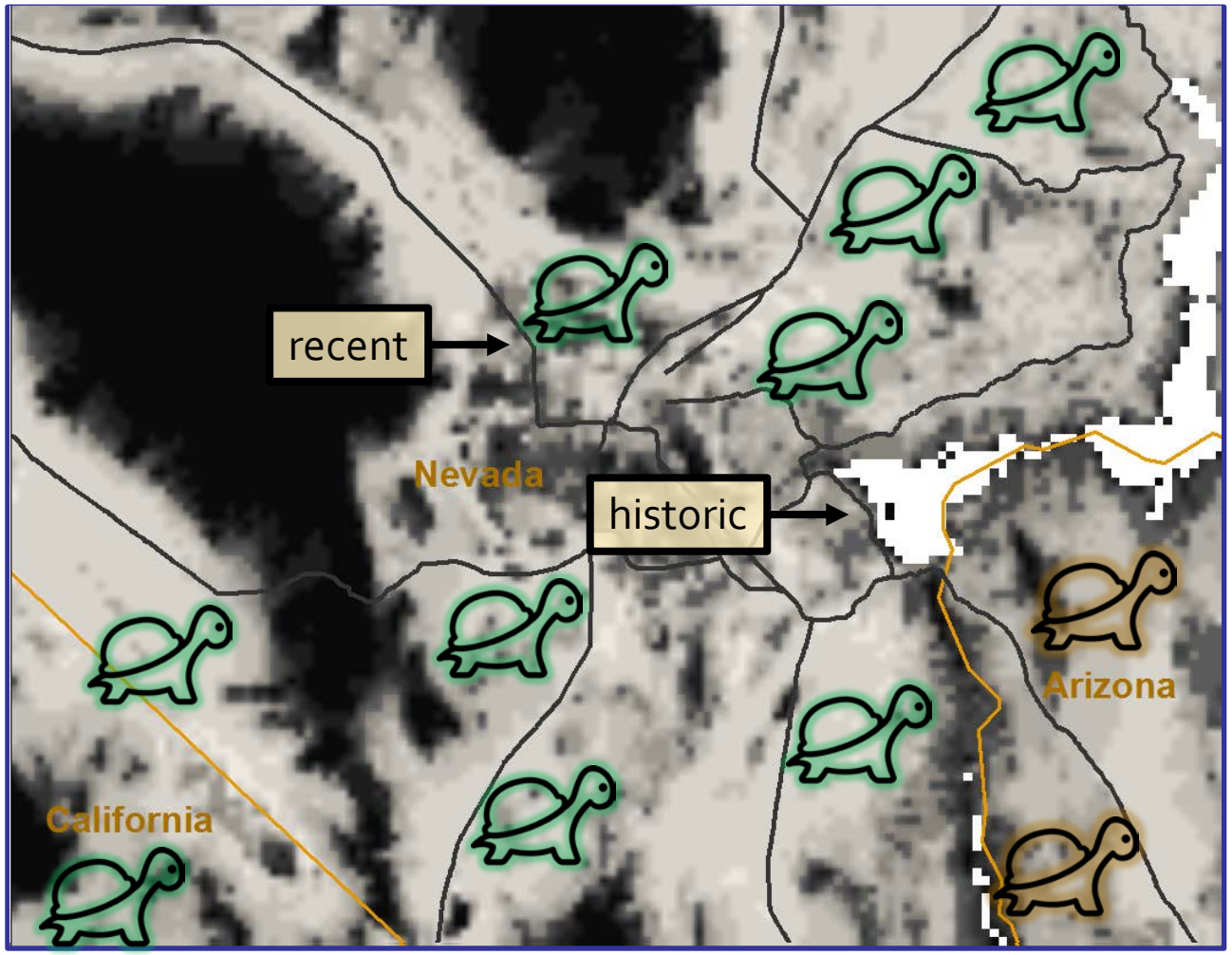
Measuring Connectivity

DEMOGRAPHIC CONNECTIVITY

GENETIC CONNECTIVITY



The Genetic Time Lag



Forward-In-Time Modeling

linear barriers limit dispersal

GRASSHOPPER

stepping-stone populations are needed

ASIATIC CHEETAH

water bodies & roads reduce gene flow

MASSASSAUGA

Project Goals

I) Model genetic connectivity scenarios forward-in-time:

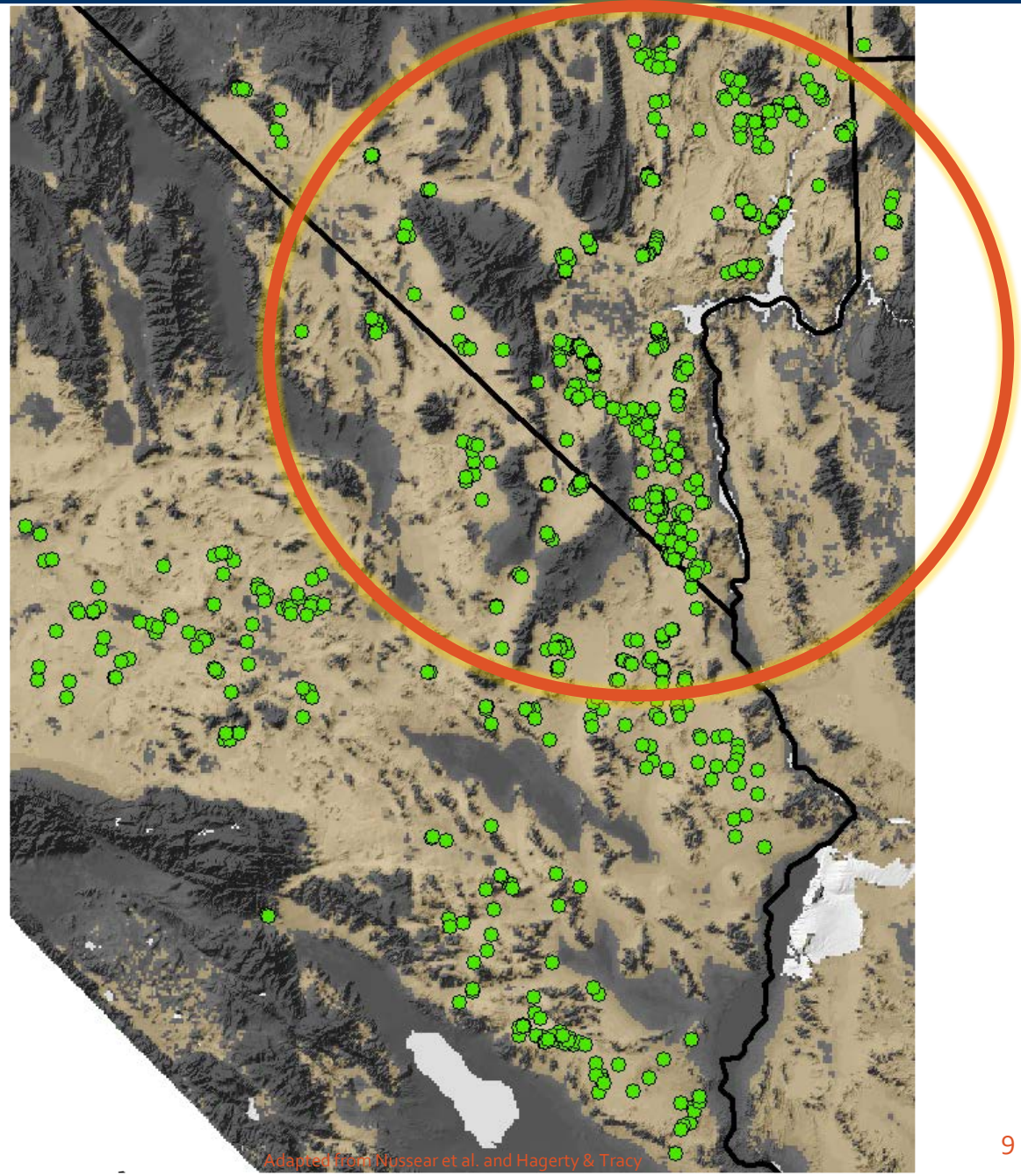
1) Undisturbed habitat
2) Current levels of landscape disturbance
3) Future estimates of landscape disturbance

II) Quantify corridor conditions

Genetic Data

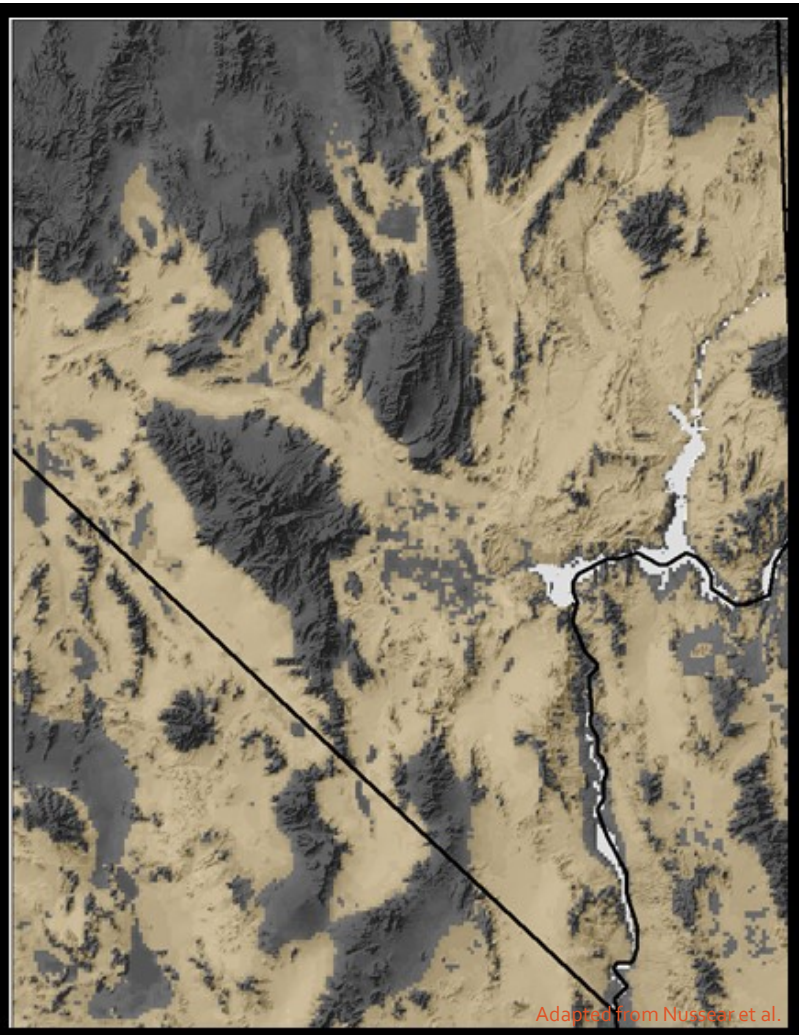
N = 744

loci = 20



Adapted from Nussear et al. and Hagerty & Tracy

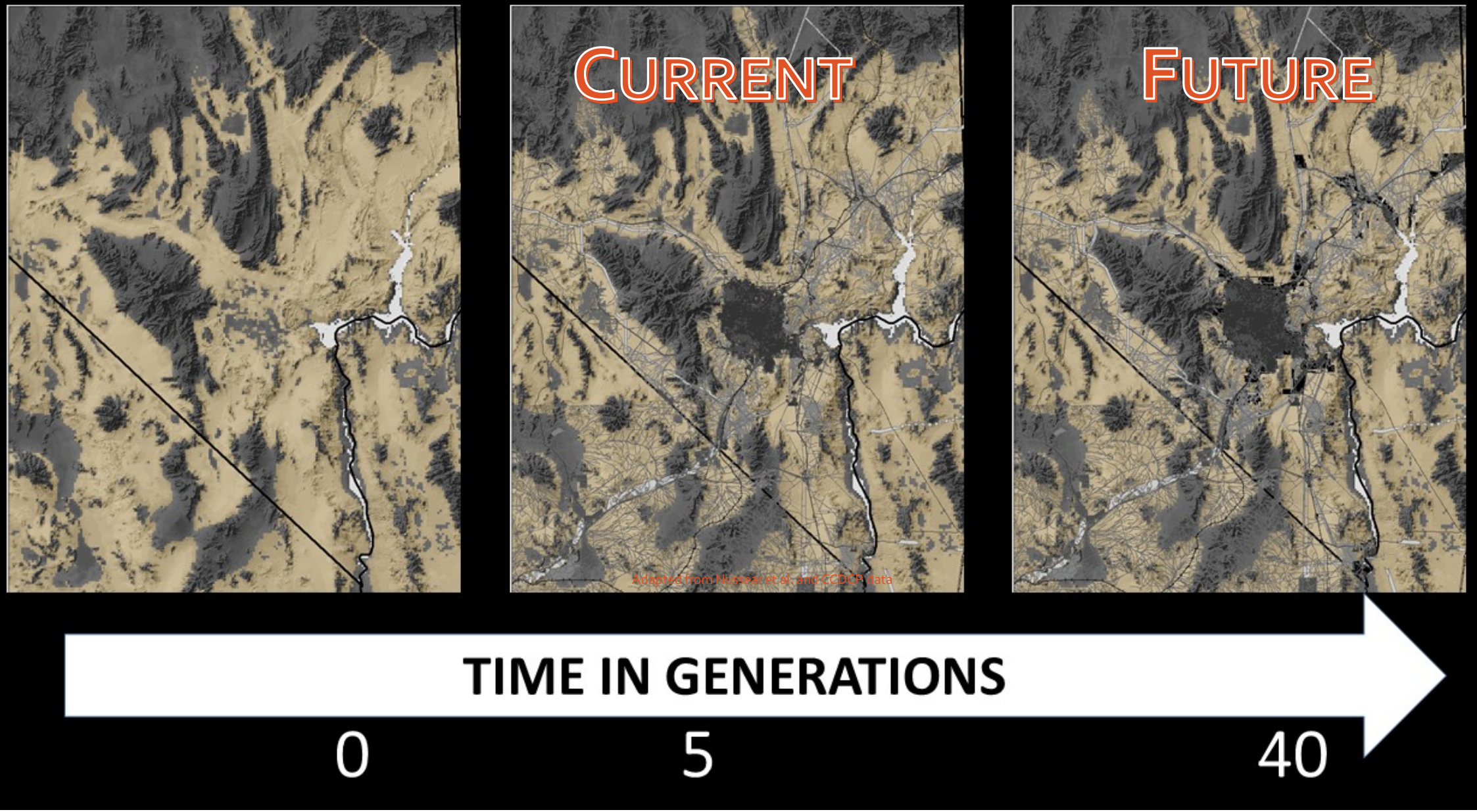
Modeling Undisturbed Habitat



Adapted from Nussear et al.

TIME IN GENERATIONS

0 5 40

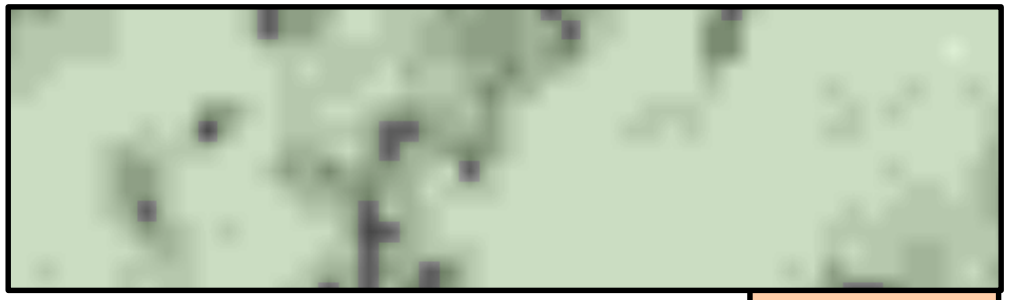

CURRENT
FUTURE
Adapted from Nusseaux et al. and CCDCP data
TIME IN GENERATIONS
0
5
40

Model Parameters

INPUT
habitat suitability model
reproductive age
clutch size
mortality rate

Genetic Data & Corridor Success

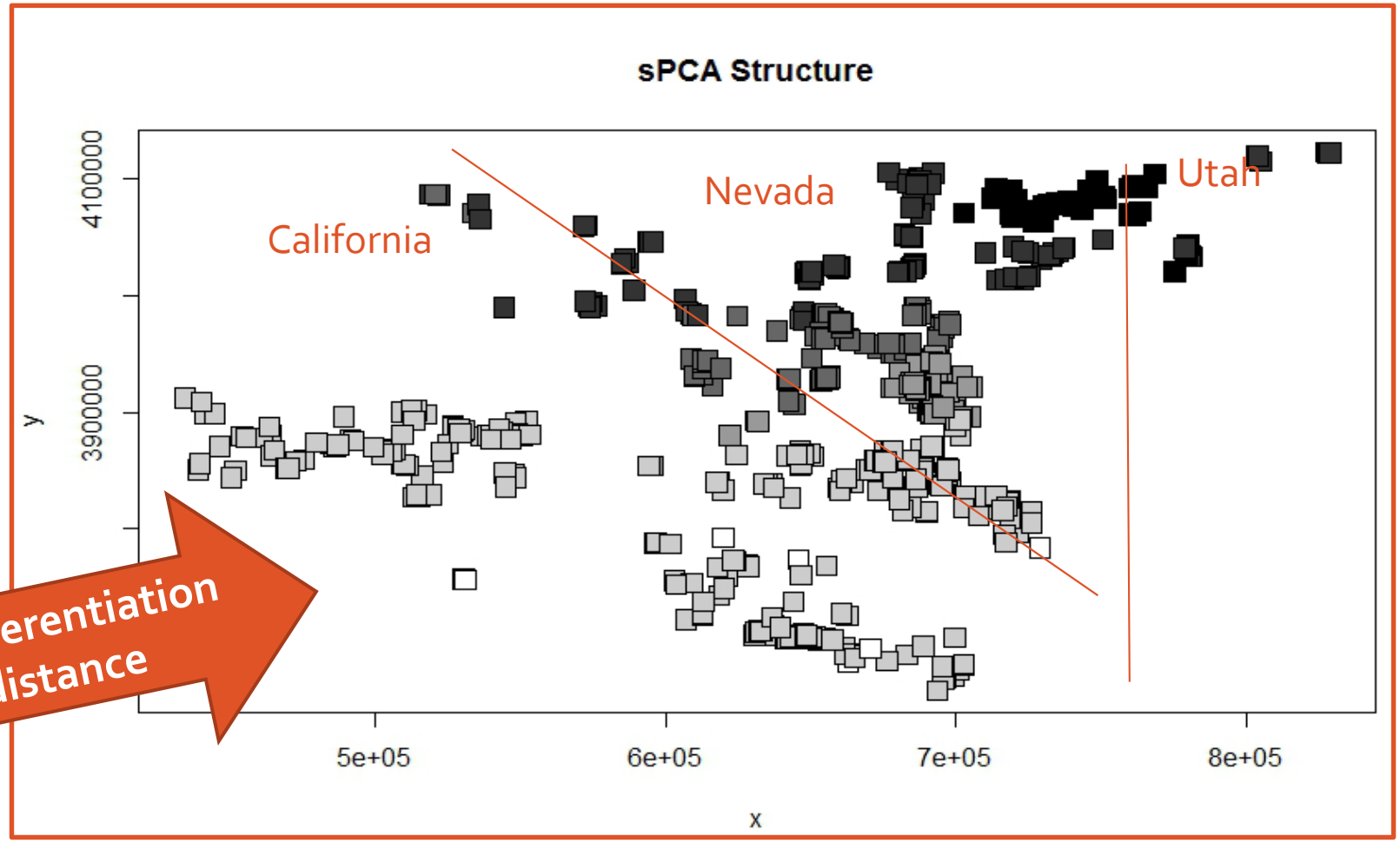
CSI = 0



CSI = 1

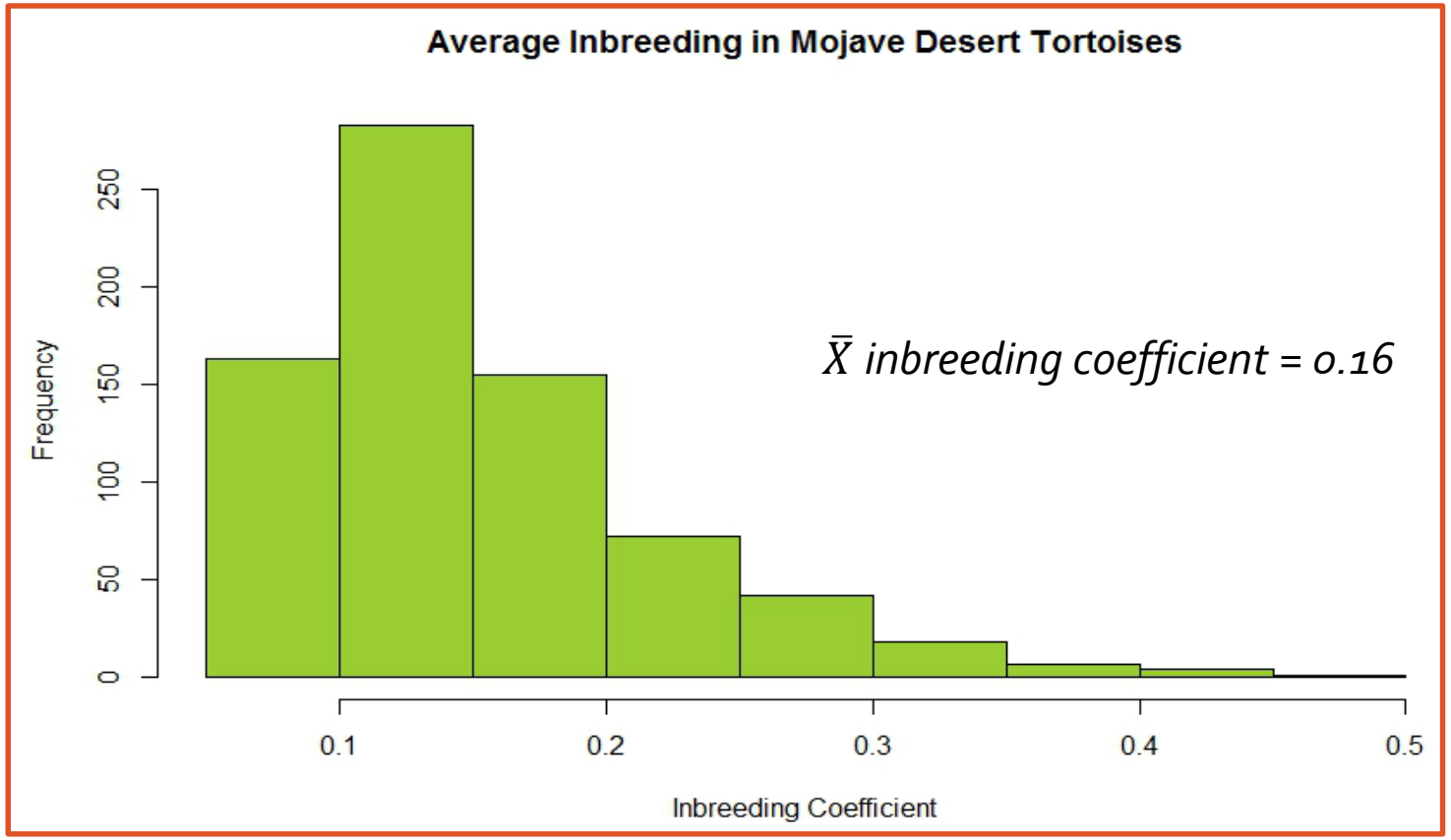
CSI = ?

Genetic Structure

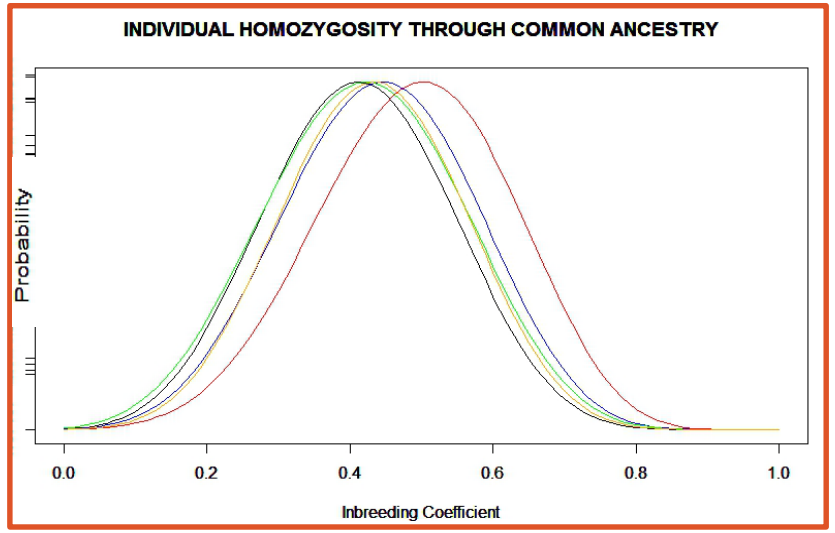


IBD increases genetic differentiation (F_{ST}) by geographic distance

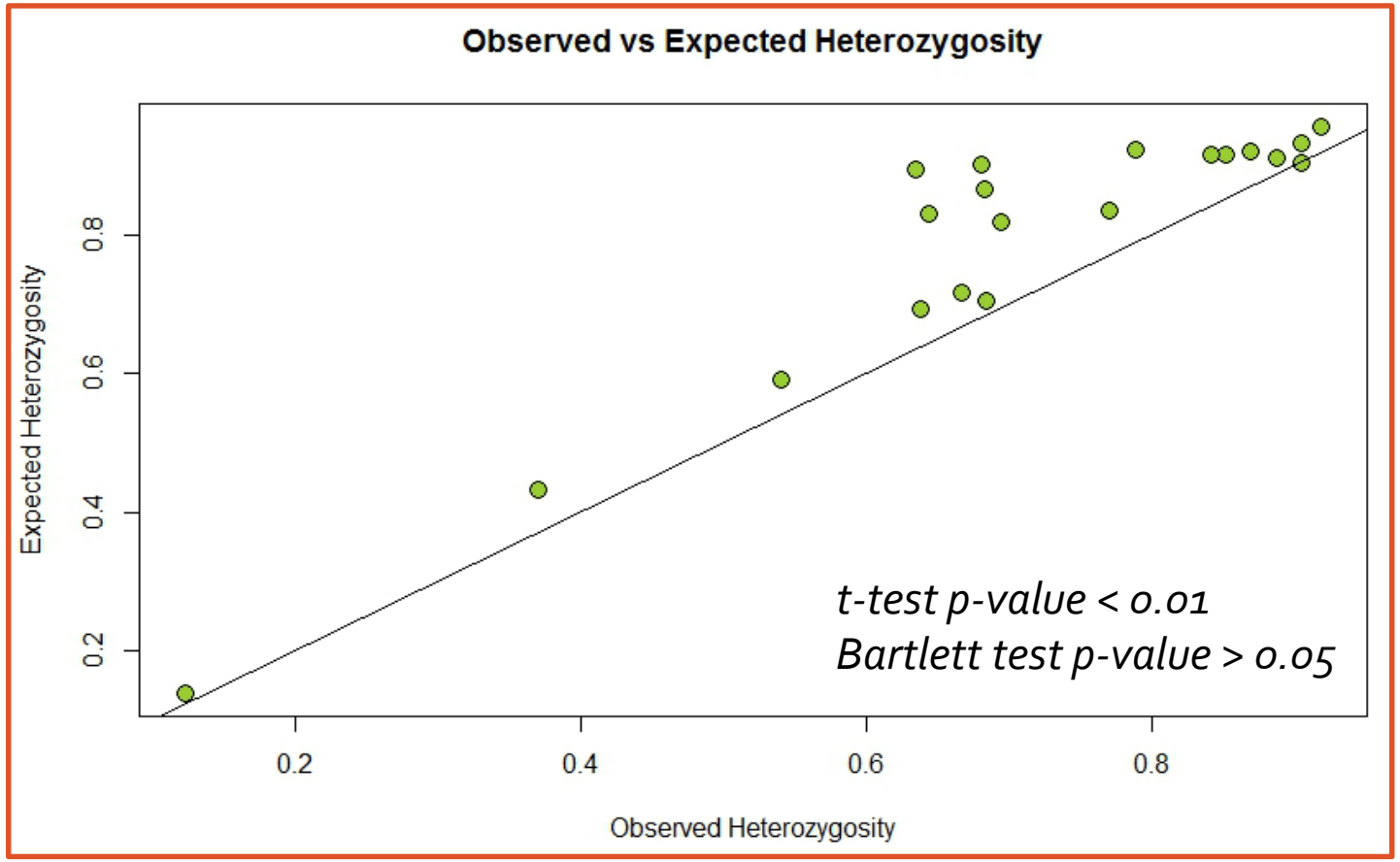
Genetic Structure

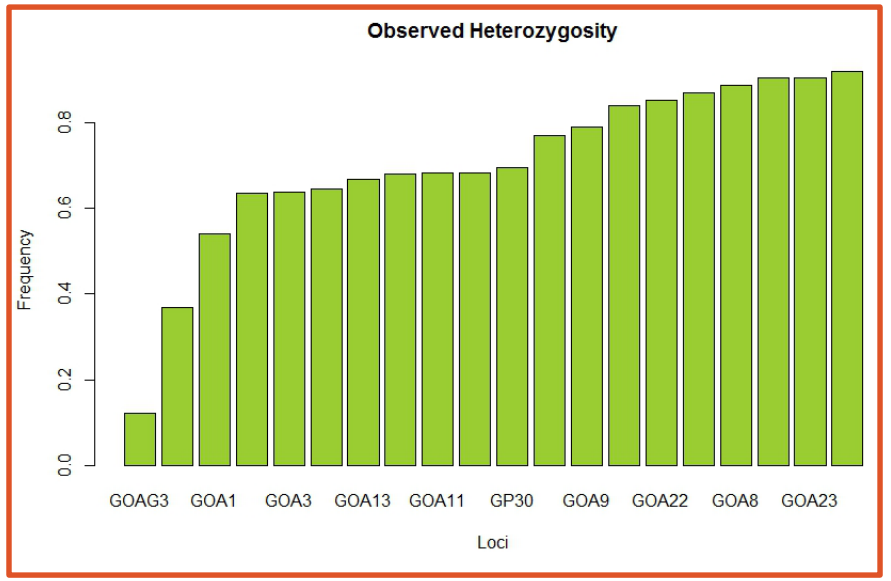


$\bar{X}$ *inbreeding coefficient = 0.16*

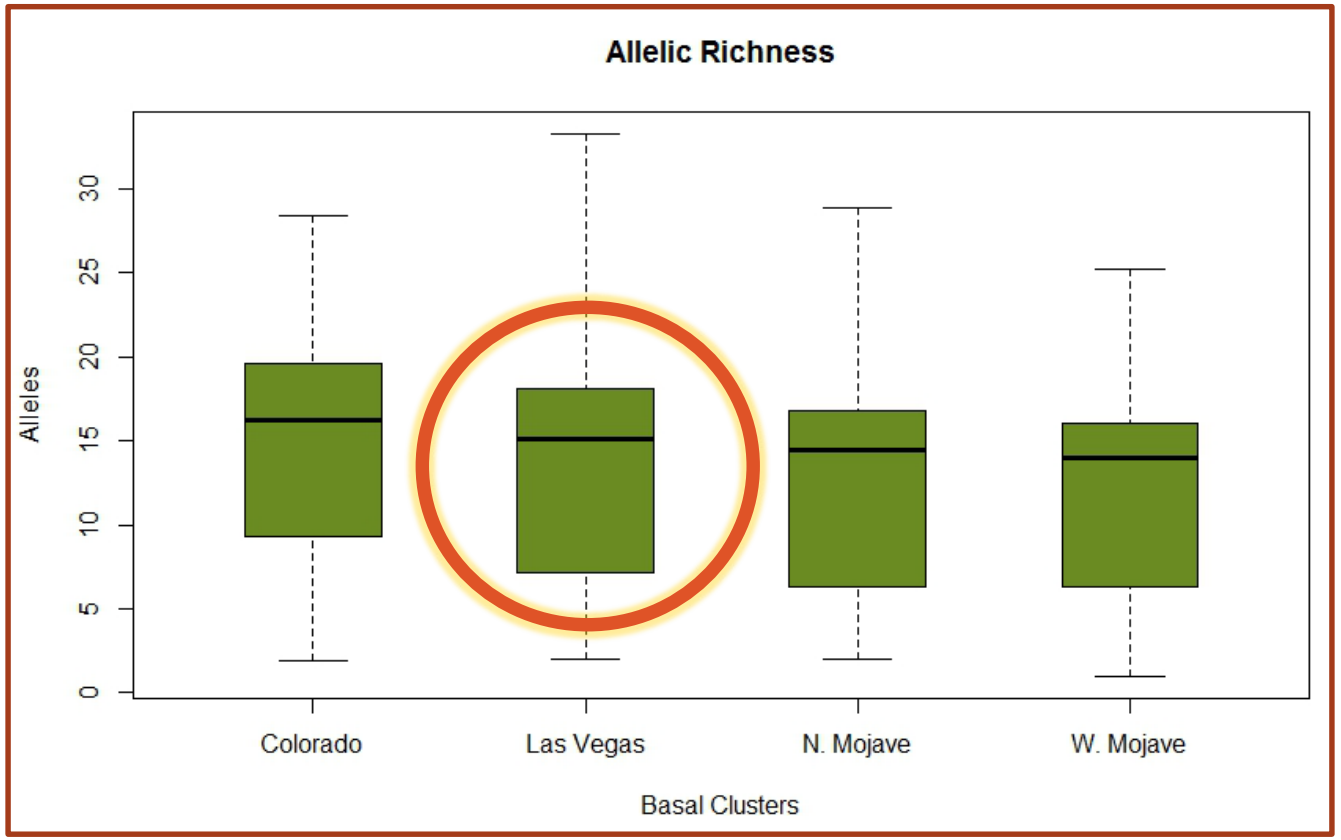


EVOLUTIONARY POTENTIAL





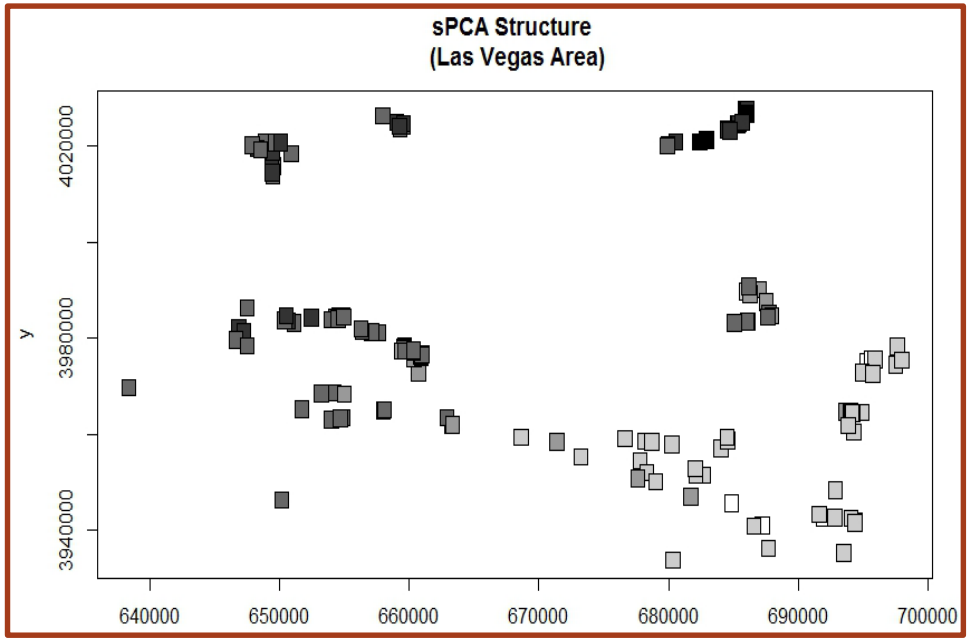
Evolutionary potential



Kruskal-Wallis p-value > 0.05

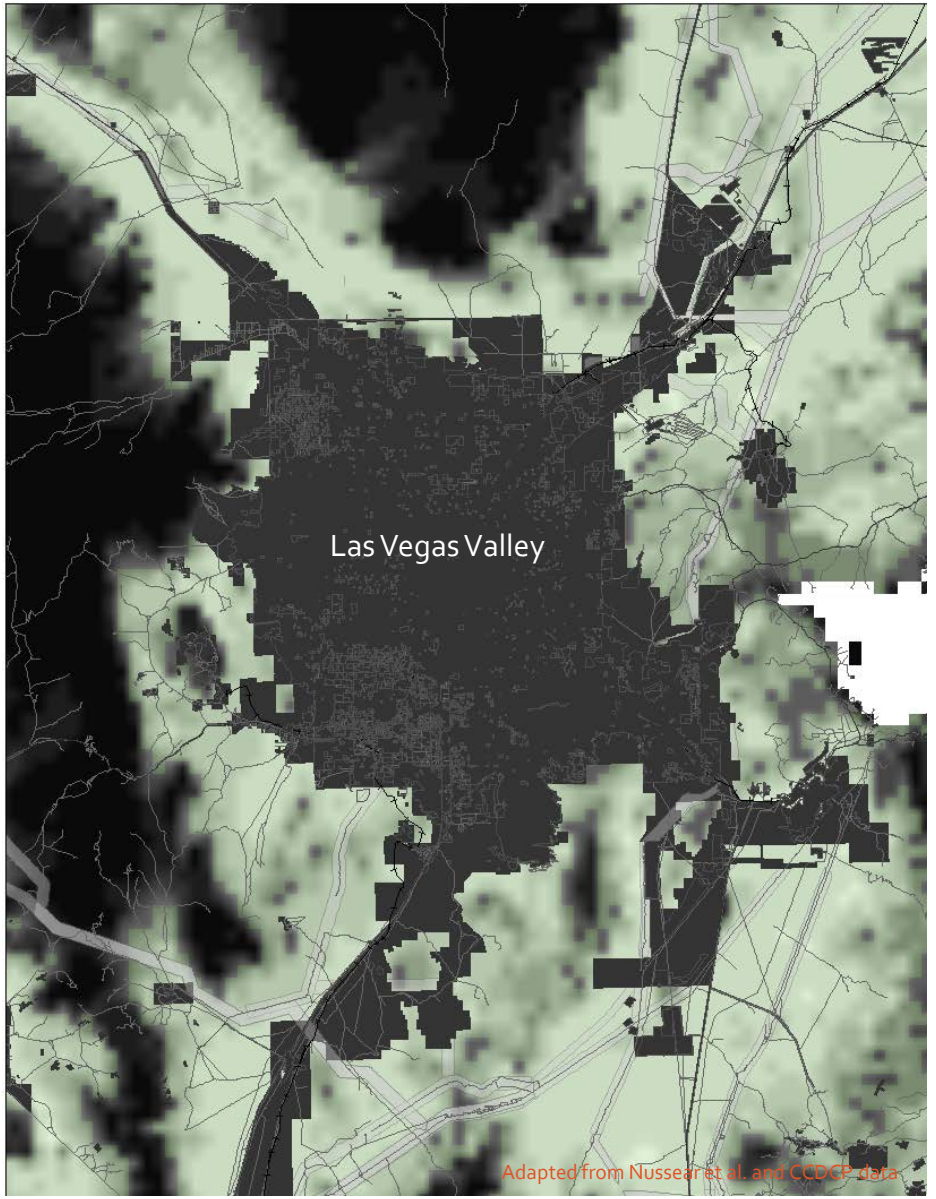
$\bar{X}$ *alleles per locus* ≈ *20*
range = 2 – 47

Las Vegas Valley



$\bar{X}$ *alleles per locus ≈ 16, range = 2 – 42*

pairwise F_{ST} *= 0.013*



Interested?

Stay tuned...

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