

Population Structure & Genomic Diversity of the Gila Monster Reflect Ecoregional Patterns

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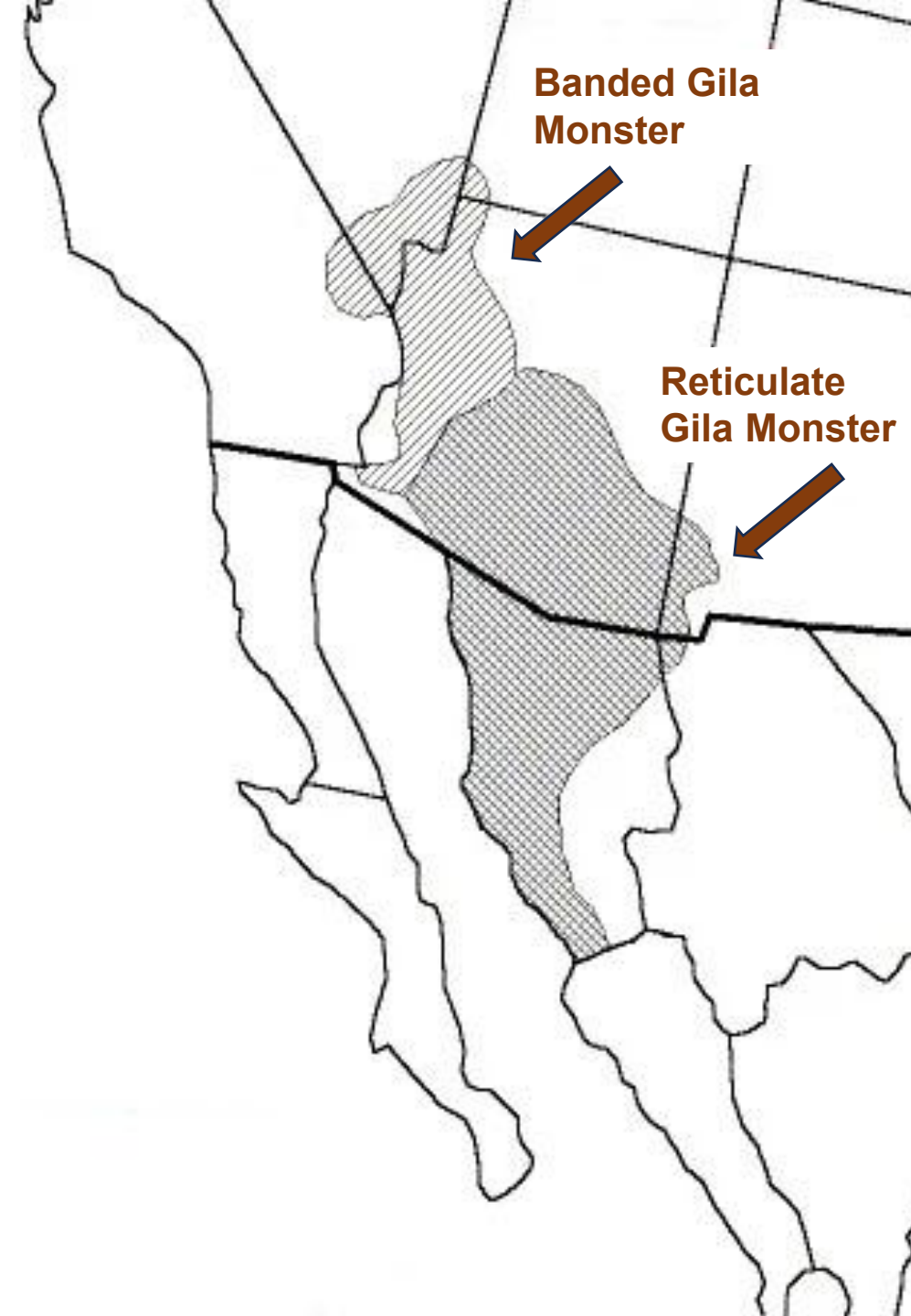


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Gila Monster (*Heloderma suspectum*)



- 1) Large venomous lizard native to the southwestern deserts.
- 2) Reclusive behavior, low tolerance for high temps, & patchy distribution make it notoriously difficult to study.
- 3) Much remains to be understood to better manage this species throughout the range

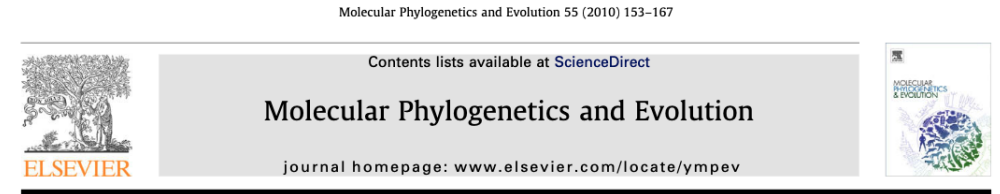


Previous genetic studies are limited



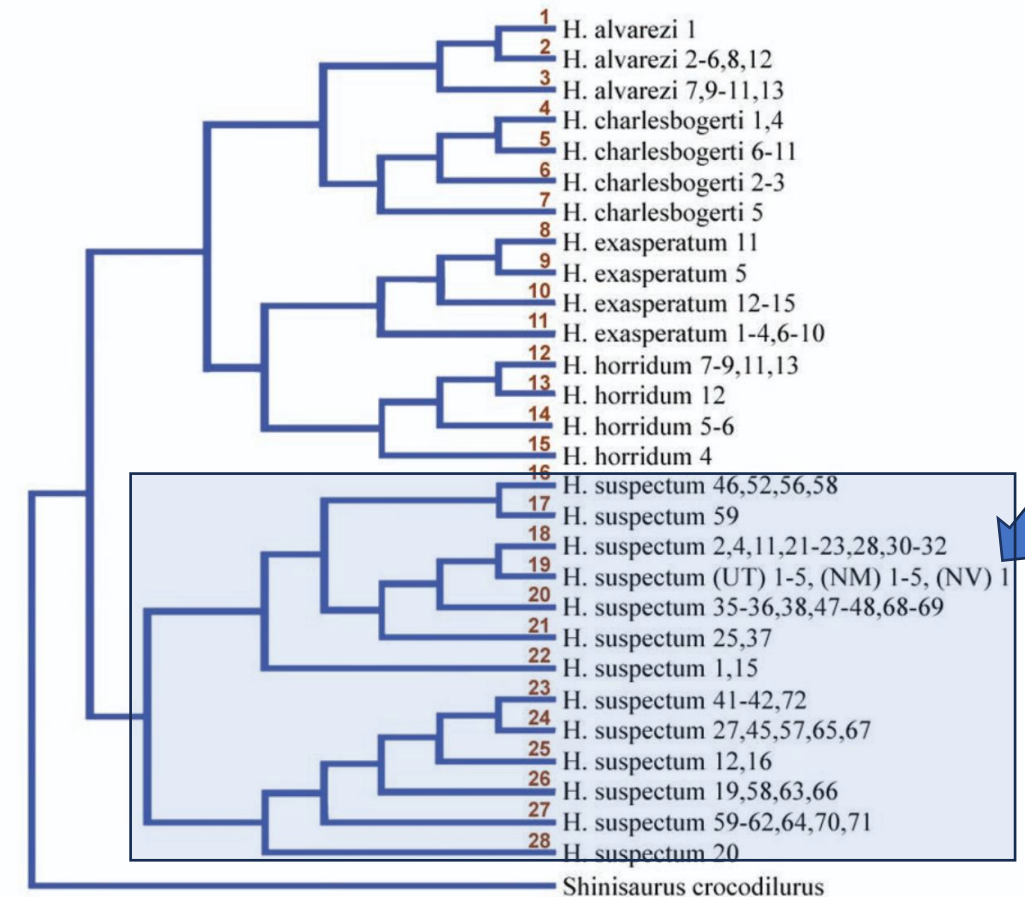
Main Conclusions:

- Diversification within the species is recent (~ late Pleistocene)
- Found little support for the two subspecies
- Presumed regional structure across the range was unlikely due to low diversity



Conservation phylogenetics of helodermatid lizards using multiple molecular markers and a supertree approach

Michael E. Douglas^{a,*}, Marlis R. Douglas^a, Gordon W. Schuett^b, Daniel D. Beck^c, Brian K. Sullivan^d

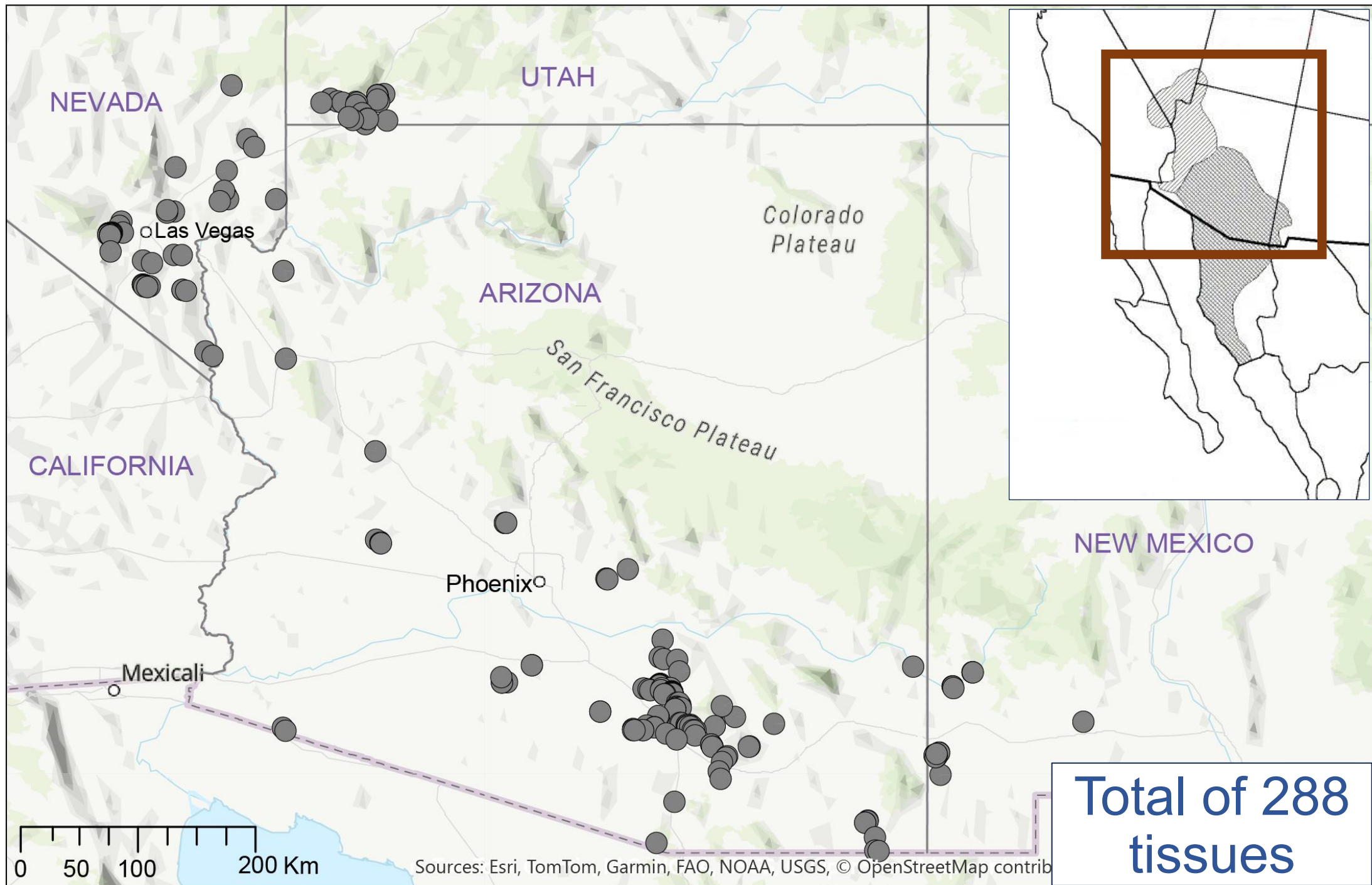


Why focus on genetic information?

Genetic diversity, connectivity & population size are positively linked to persistence and resilience to future environmental change

- These metrics are essential components for species management and recovery programs





Objectives

Provide a genomic reference point for ongoing management:

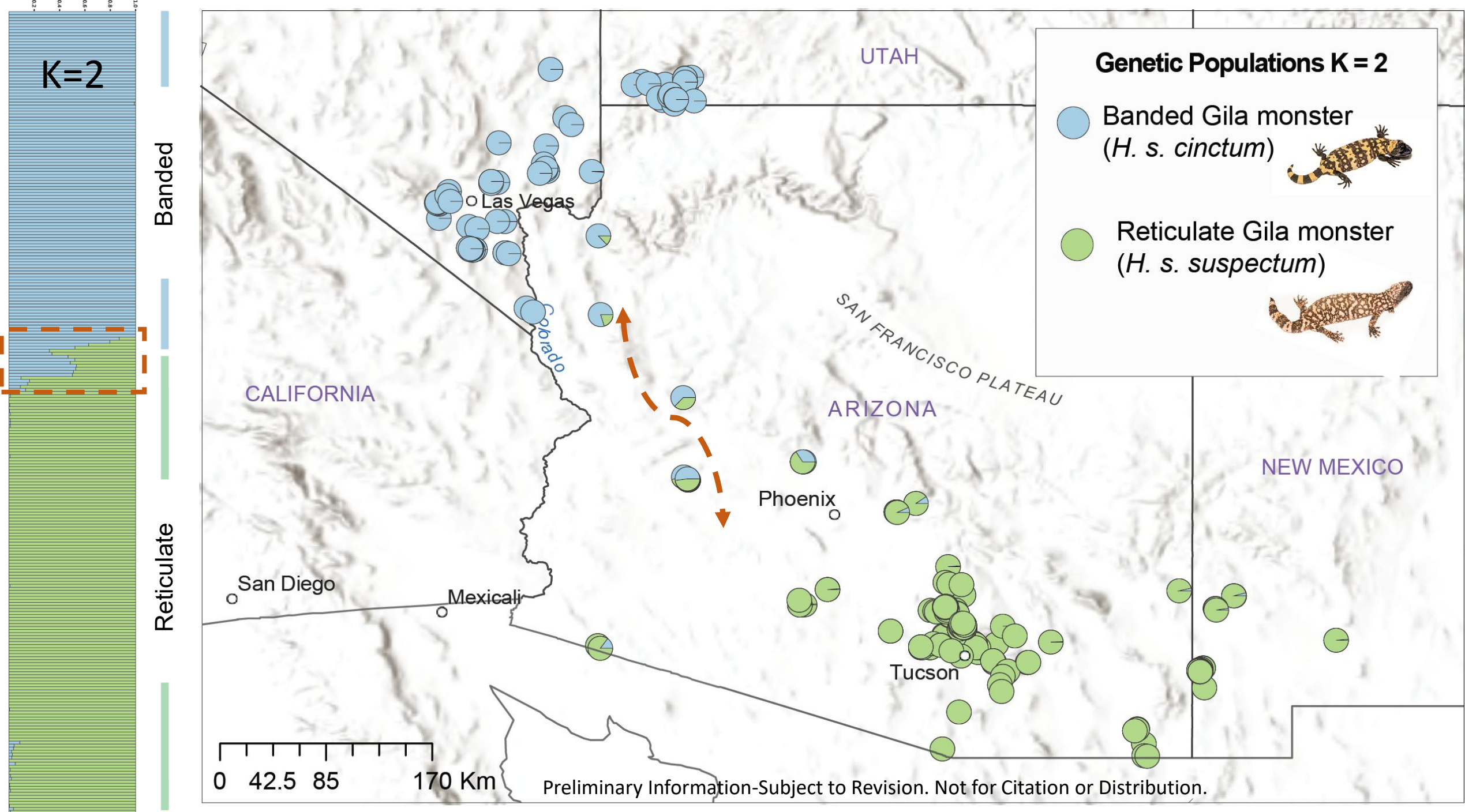
- 1) Determine if there is any regional genetic structure across the range
- 2) Estimate genetic diversity metrics & highlight any areas of concern
- 3) Determine genetic/environment associations to better understand habitat barriers

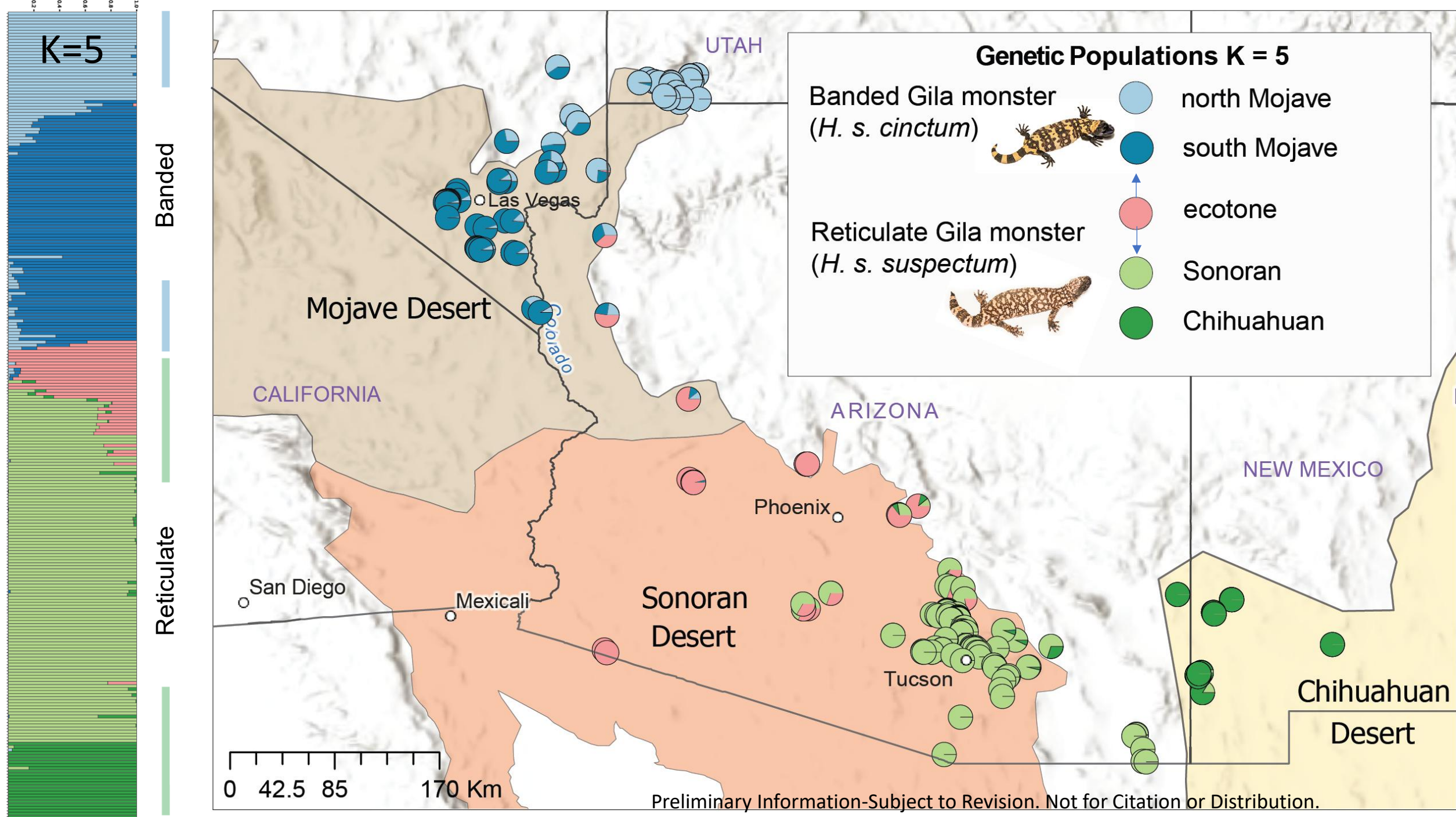
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Specific Objectives

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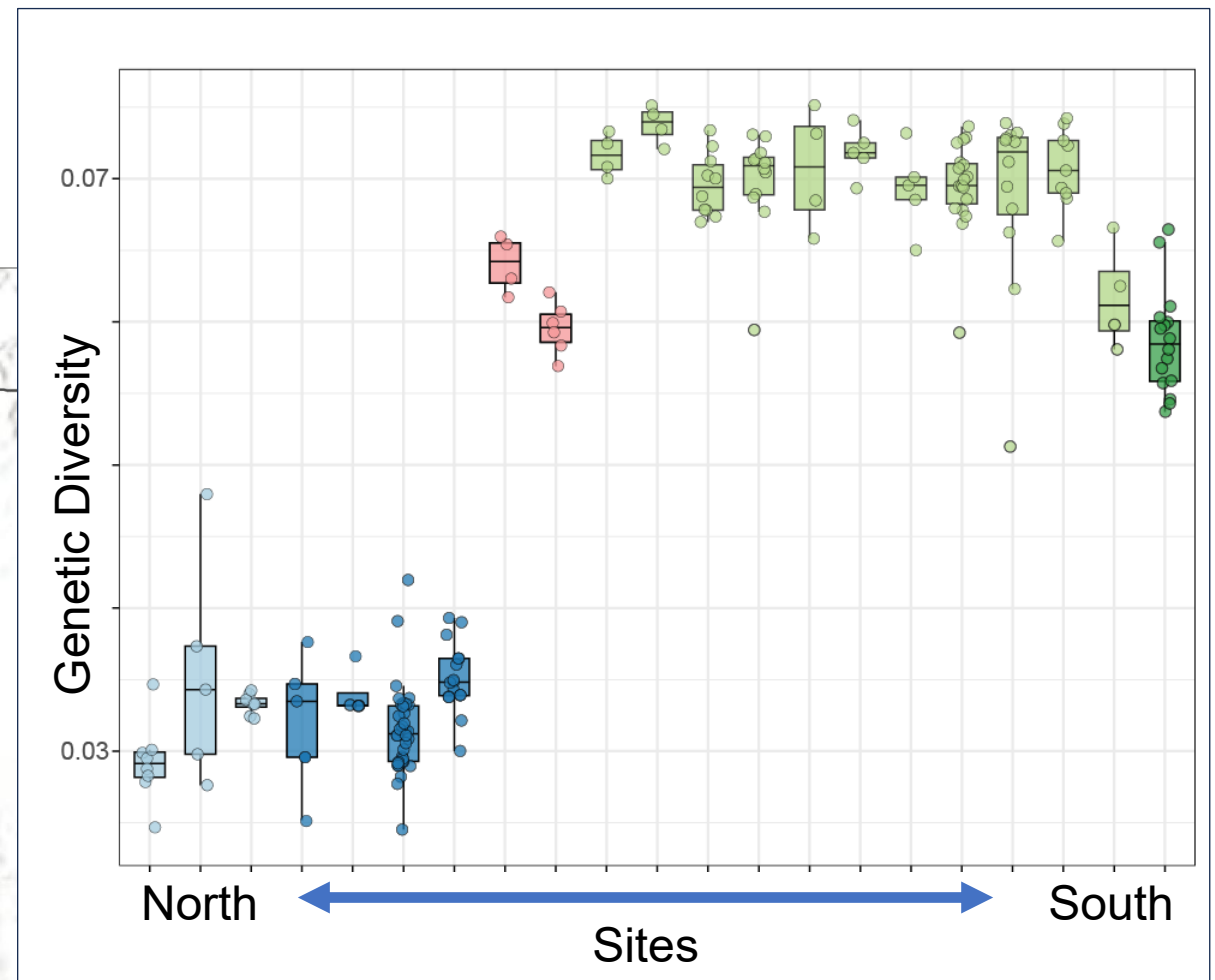
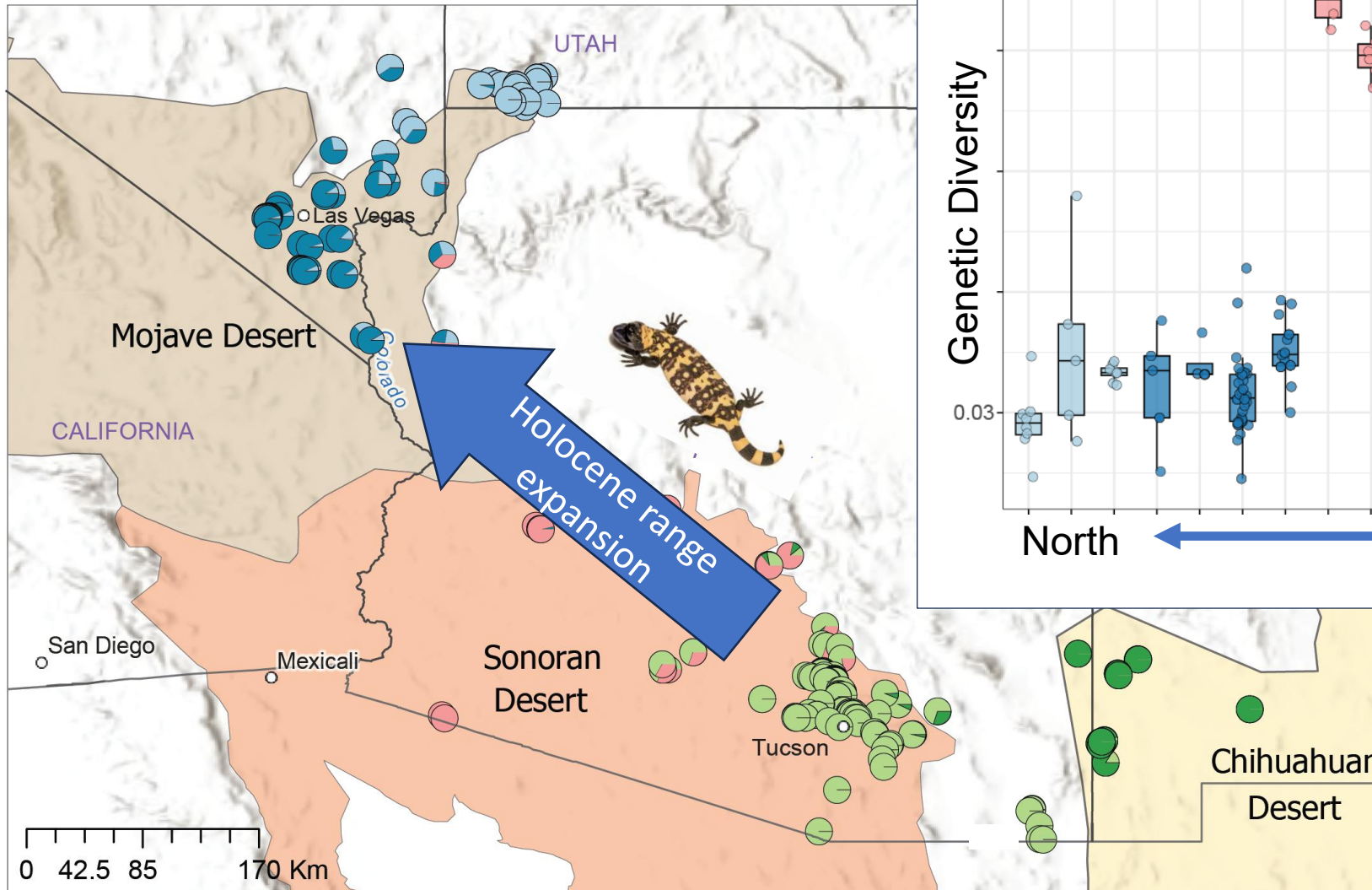
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Rangewide Genetic Diversity



Latitudinal shift in diversity

Effective Population Size – N_e

- Relevant metric in conservation biology
- N_e is proportional to genetic diversity & rate of inbreeding
 - $N_e < 50$ -100 threshold of concern

Region	Samples	N_e	95% CI
North Mojave	34	25	13 – 61
South Mojave	74	37	27 – 52
Ecotone	19	71	20 – Inf
Sonoran	113	190	117 – 419
Chihuahuan	26	50	26 – 192



Why lower diversity in this portion of the range?

- Due to recent range expansion (Holocene) as aridification occurred in the Mojave Desert region
- Fewer adults contributing to breeding per generation in this portion of the range
 - This is the range limit for the species, colder and drier.
 - Food availability and habitat heterogeneity likely reduce densities
- Habitat fragmentation and loss in certain areas
 - Urbanization, roads, and associated infrastructure

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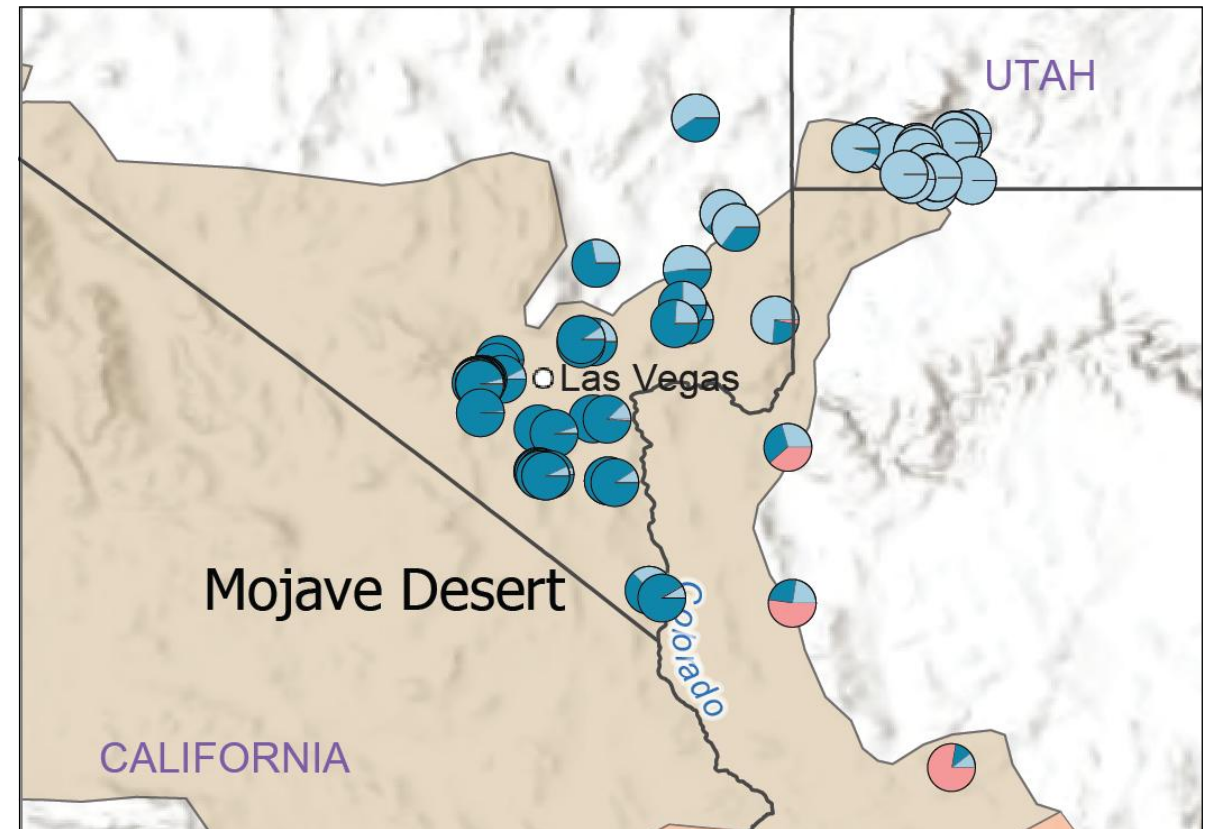
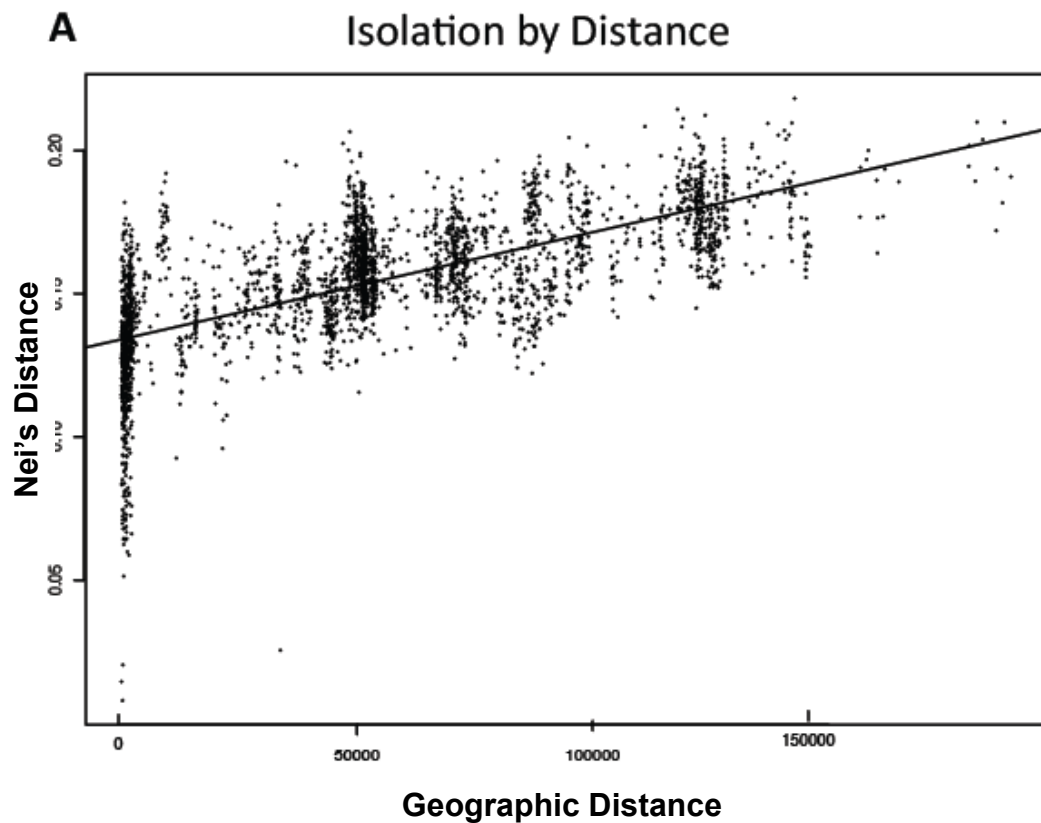
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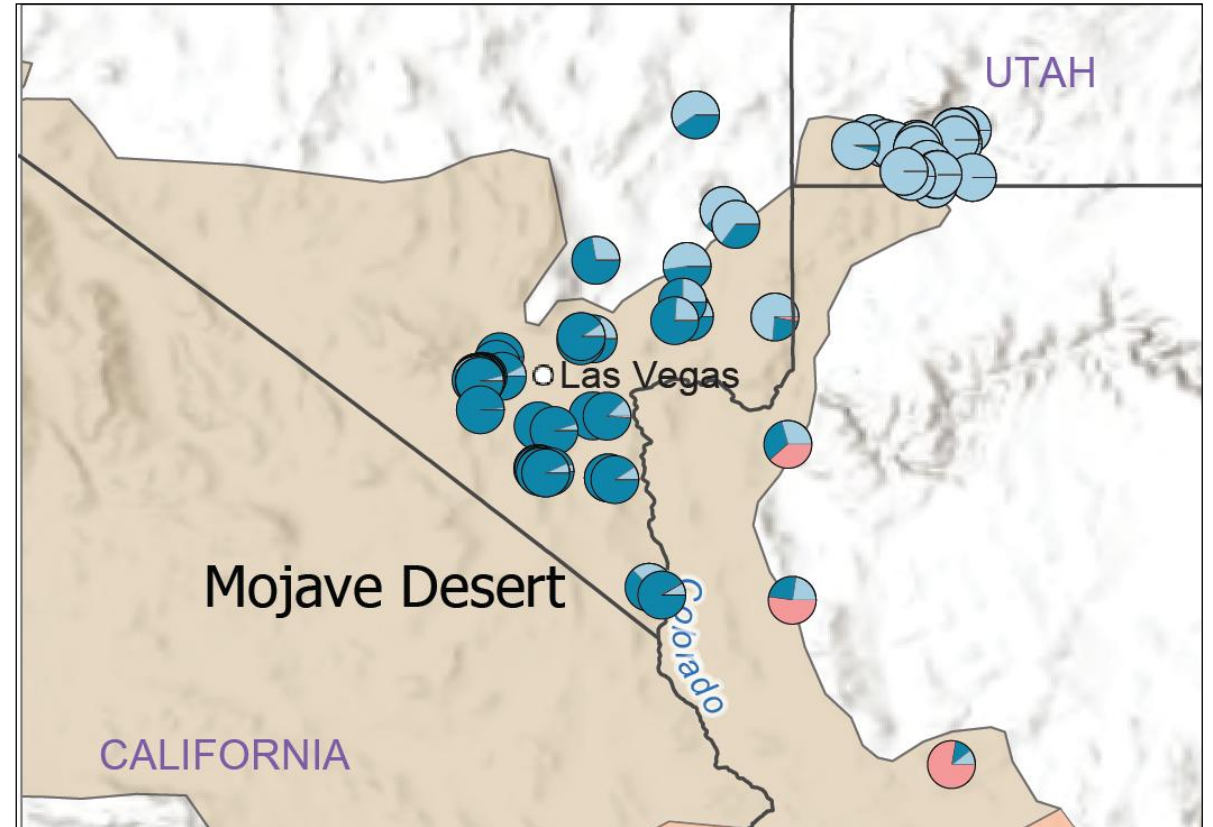
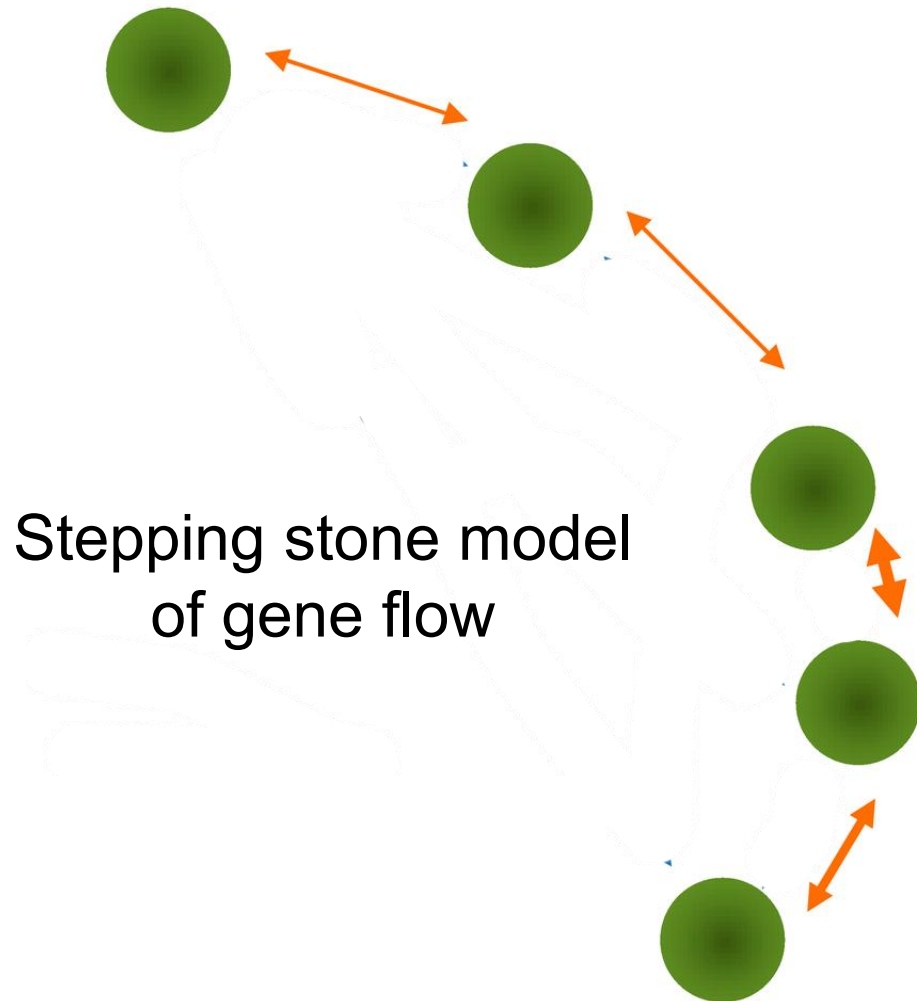
Genetic Connectivity – Banded Gila Monster

Geographic Distance correlated with genetic distance (R 0.684, p-value 0.001)



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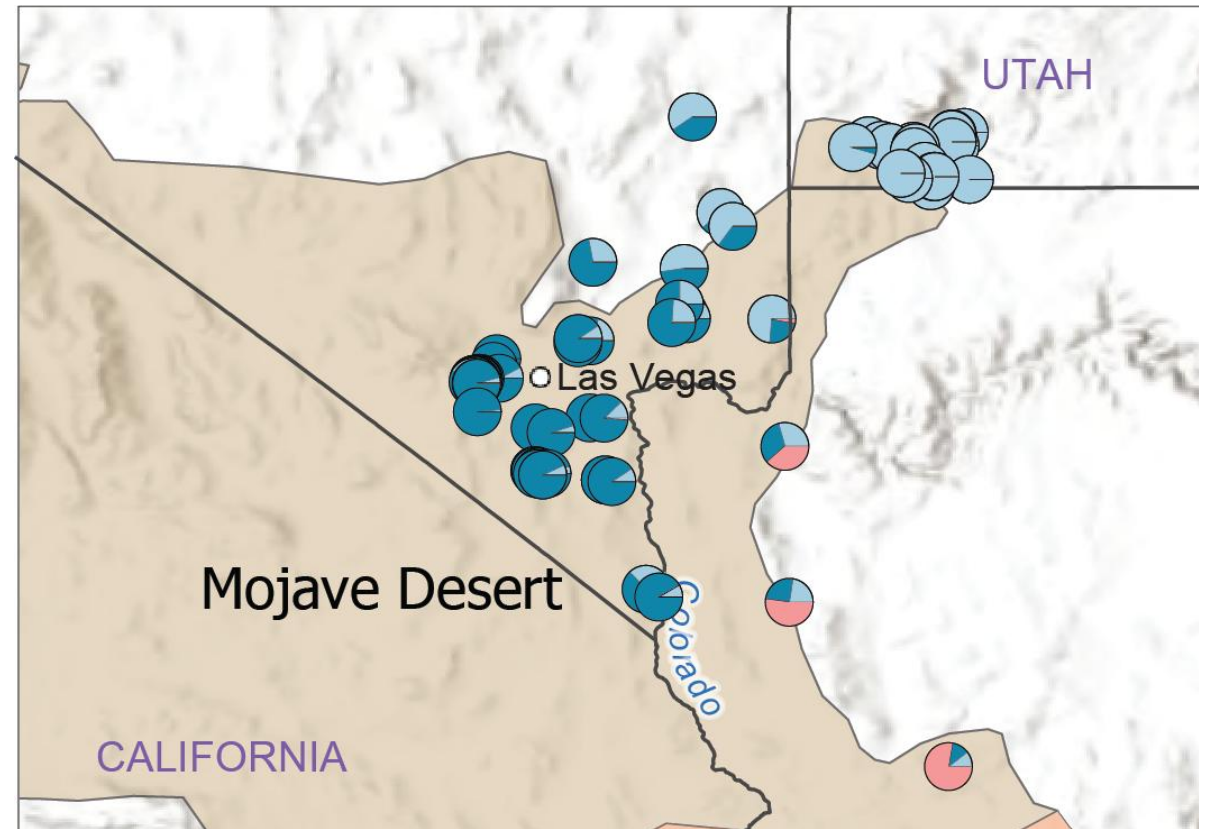
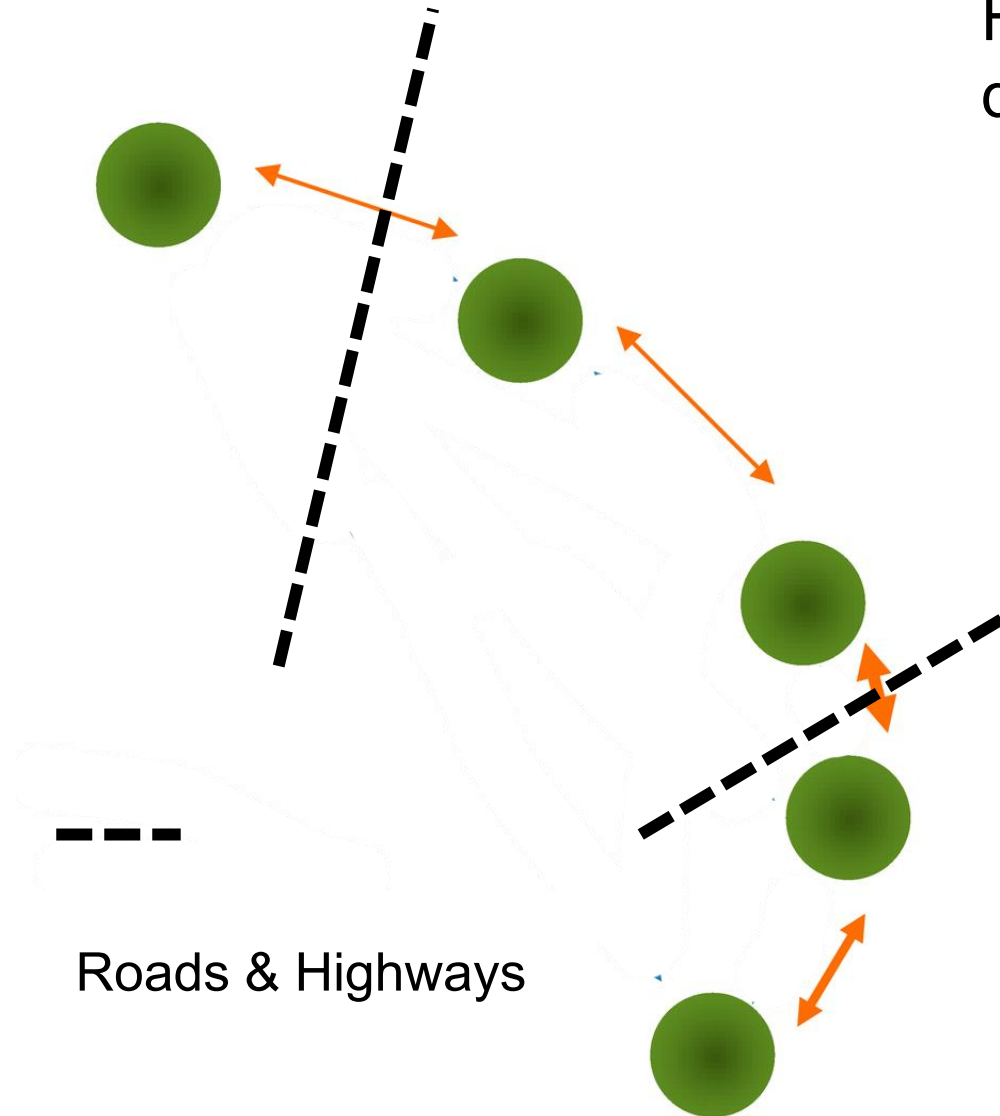
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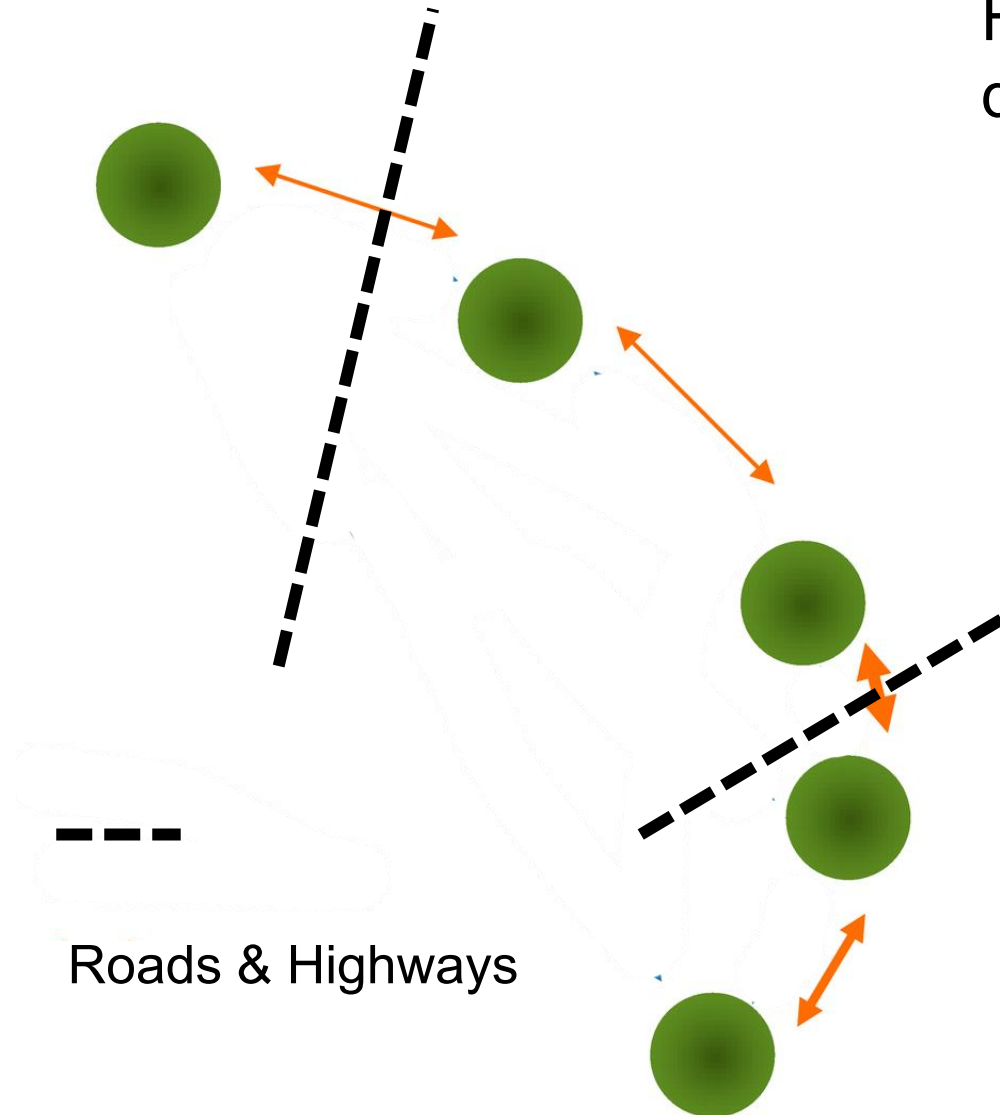
Highways were correlated with genetic distances ($R = 0.606$; $p = 0.001$).



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Sonoran Desert Study (Kwiatkowski et al 2008)

- Reported no difference in movement patterns or home range size in areas with high urbanization
- These same pops had female-skewed sex ratios
 - Higher male mortality rates

Management Implications

- Genomic support for the two subspecies
 - Banded Gila Monster (*H. s. cinctum*) is almost entirely contained within Utah and Nevada.
- Desert ecoregions contain unique components of the overall genetic diversity of Gila Monsters
 - Protecting habitats and connectivity in these regions may be crucial to maintain diversity in this subspecies



Acknowledgements

Contribution to Tissues & Field Data

University of Texas Arlington

California Academy of Sciences

Museum of Vertebrate Zoology

Museum of Southwestern Biology

Photos from Paul Maier

Funding

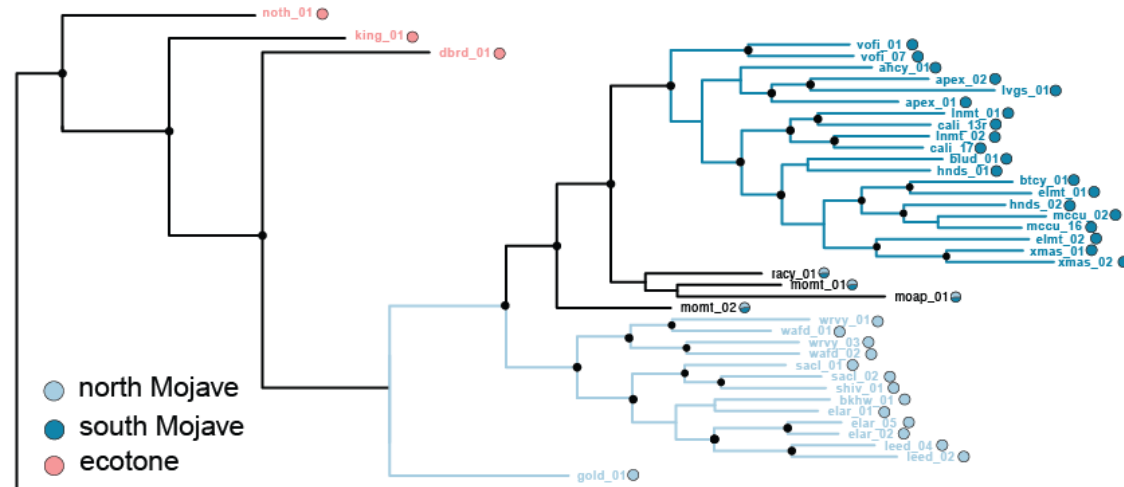


desert conservation
PROGRAM



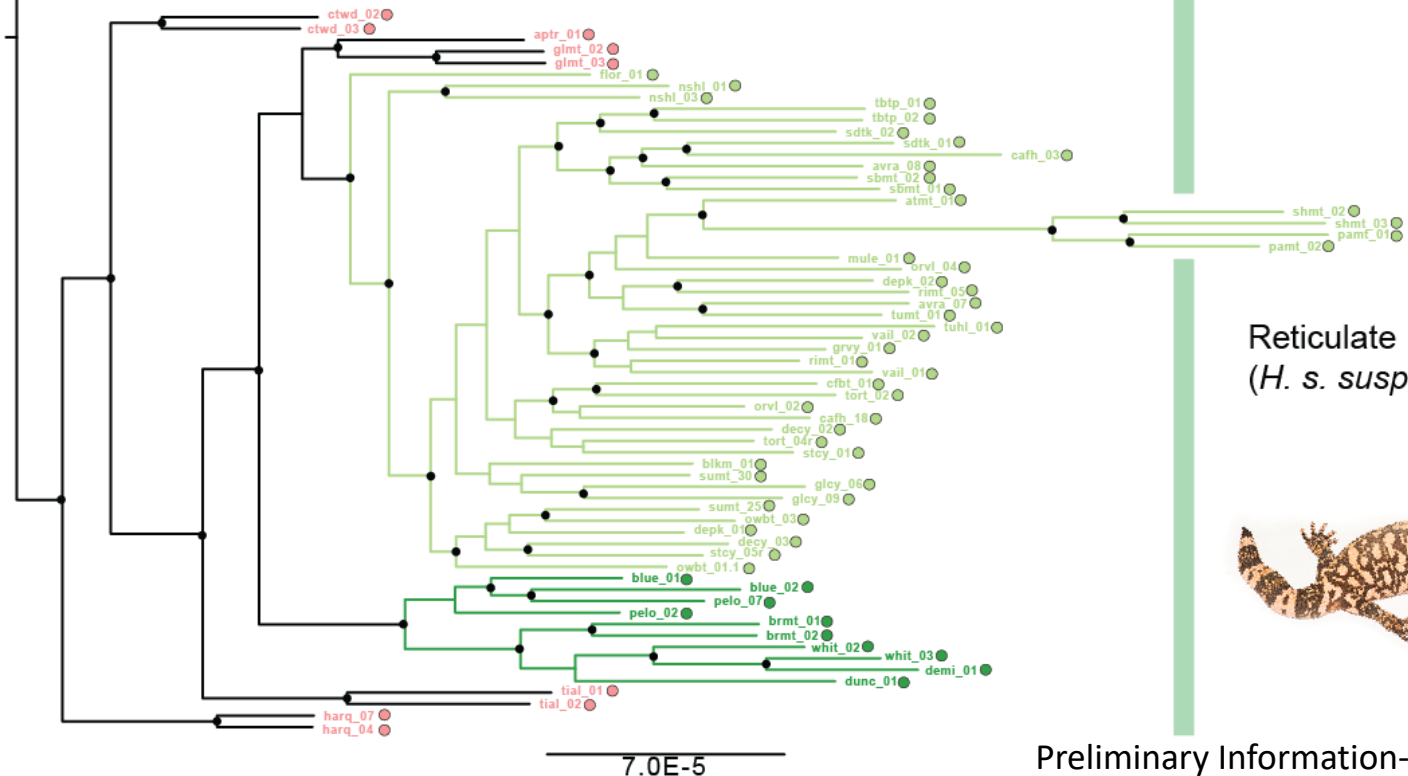
Phylogenetic Analysis

Banded Gila monster
(*H. s. cinctum*)



- north Mojave
- south Mojave
- ecotone
- Sonoran
- Chihuahuan

Reticulate Gila monster
(*H. s. suspectum*)



IQ-Tree3 - 32,422
parsimony informative
sites