

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

Dustin A. Wood, Julia G. Smith, Jason L. Jones, Anthony Pawlicki, Dale DeNardo, Paul Maier, Cameron Rognan, Steve J. Hromada, Kenneth E. Nussear, Jocelyn Stalker, Collin Stratton, C.M. Gienger, and Amy G. Vandergast

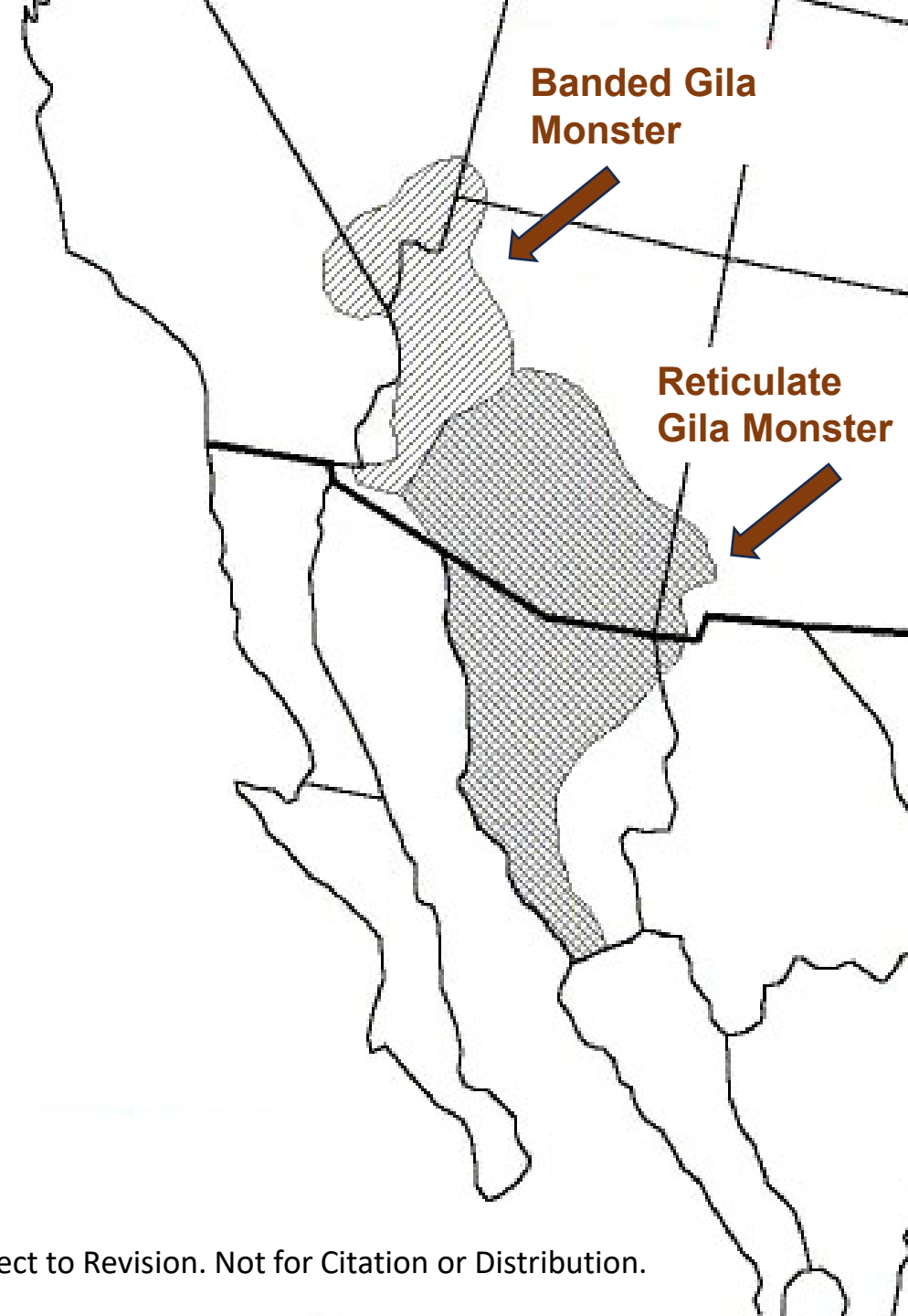


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Gila Monster (*Heloderma suspectum*)



- 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 regarding
 - Population structure & management units
 - Genetic Diversity
 - Landscape connectivity



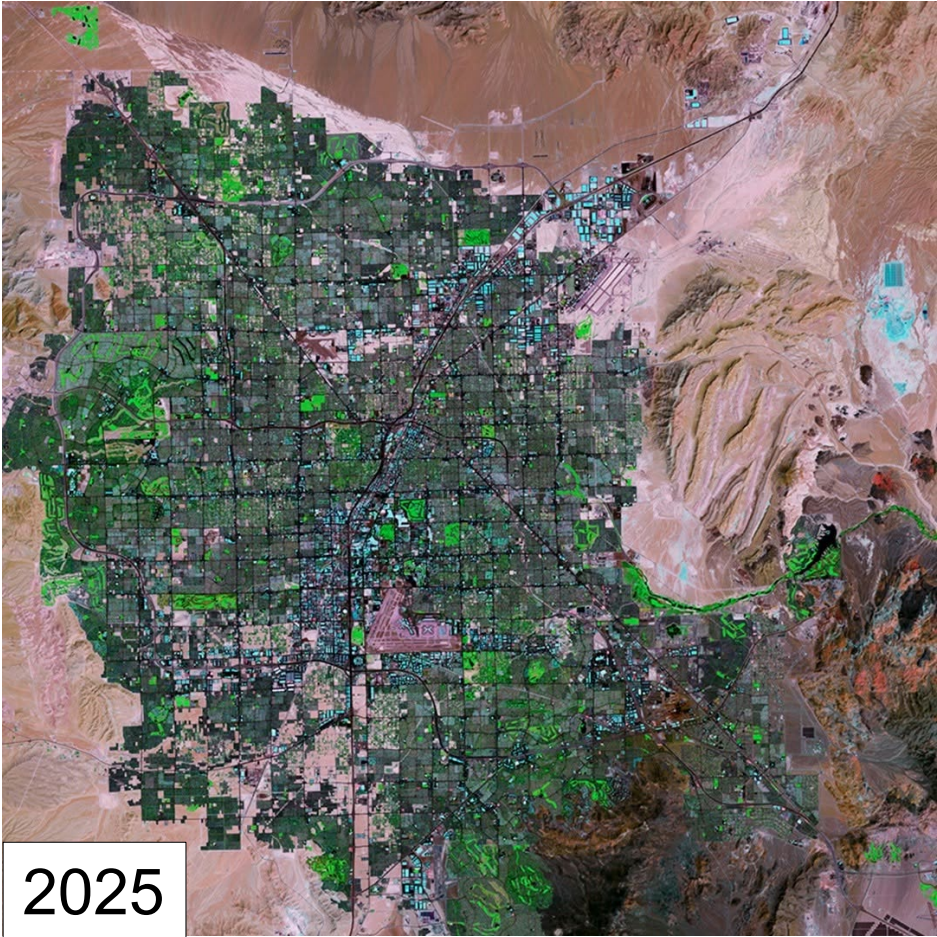
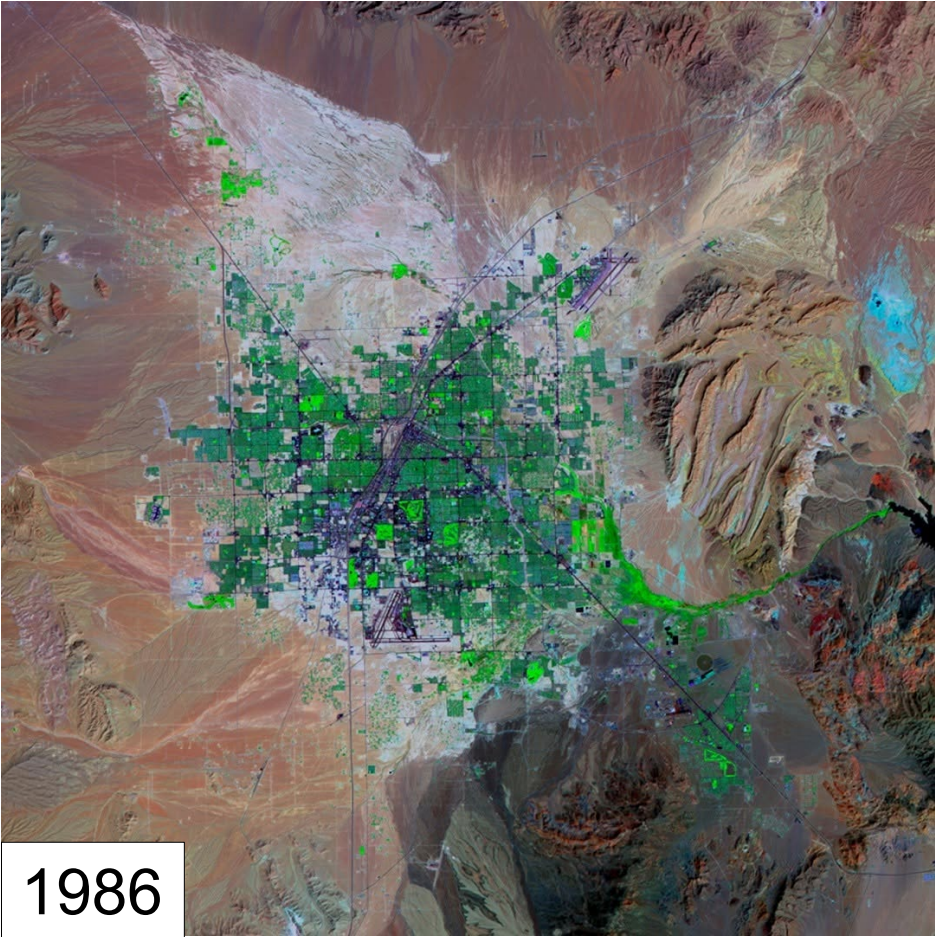
Why focus on genetic diversity?

Since **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



Rapid growth in Vegas Valley has contributed to habitat loss and fragmentation



Year	1965	1970	1980	1990	2000	2010	2015	2020	2024
Population (Est.)	150,000	240,000	450,000	700,000	1,300,000	1,900,000	2,300,000	2,700,000	3,000,000

Ref: <https://www.macrotrends.net/global-metrics/cities/23043/las-vegas/population>.

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Specific Objectives

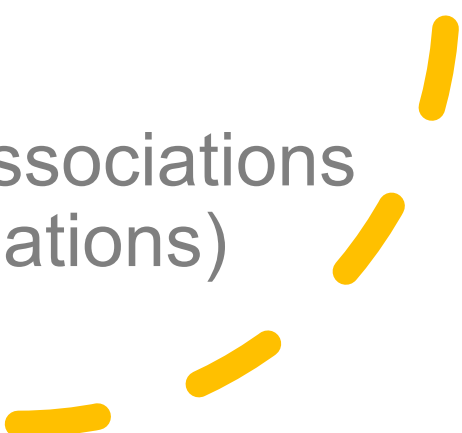
Provide a genomic reference point for ongoing management:

- 1) Collect tissue samples from throughout the Gila Monster's range & develop a genomic dataset
 - 2) Estimate the current population structure & genetic diversity
 - 3) Determine genetic/habitat associations (emphasis on Nevada populations)
- 
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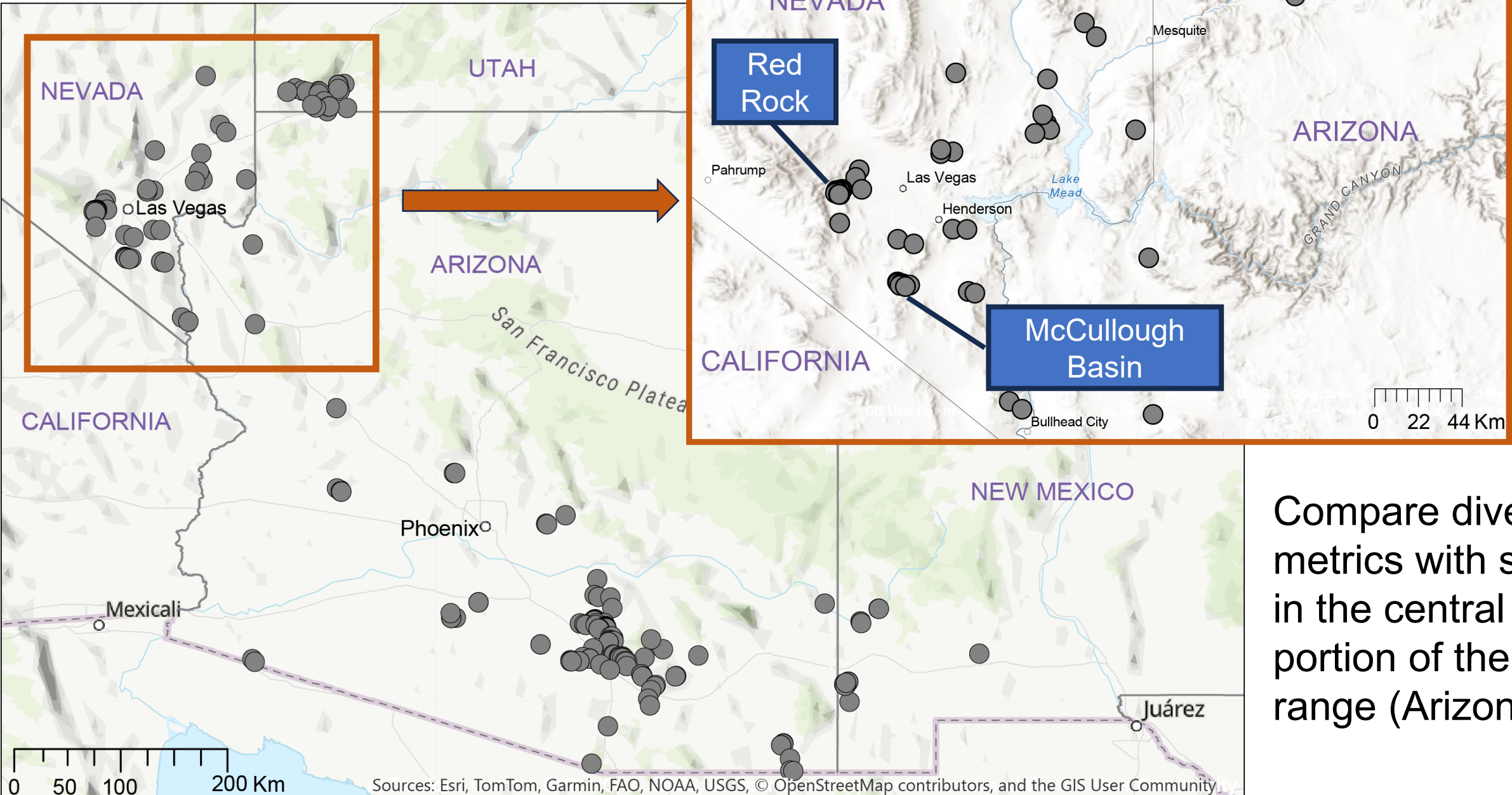
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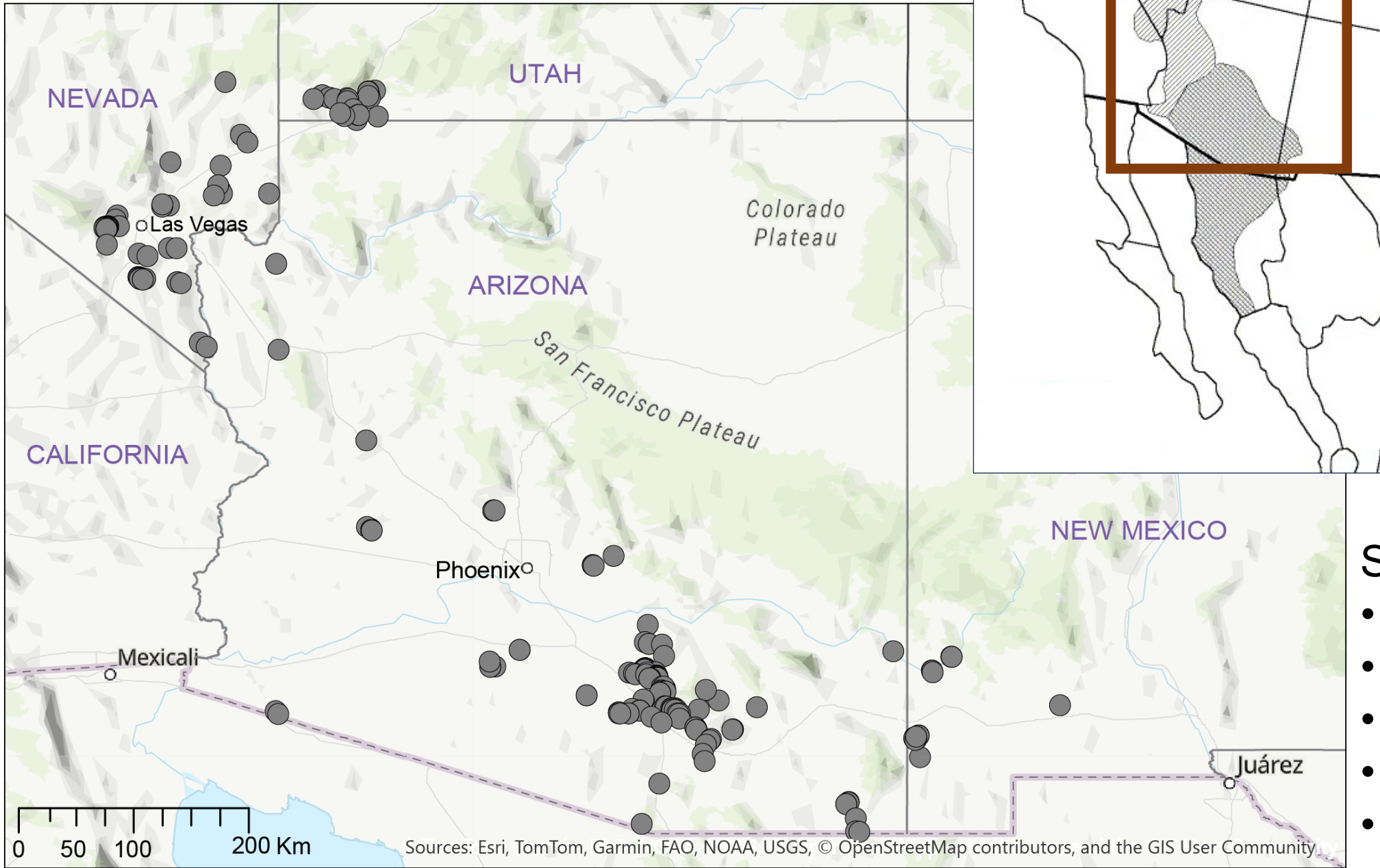
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Two Focal Sites (16+ samples)



Compare diversity metrics with sites in the central portion of the range (Arizona)

Sample Acquisition – 288 Tissues



Sources:

- Field work in NV
- ASU
- MVZ
- MSB
- CAS

Sample Acquisition & Sequencing

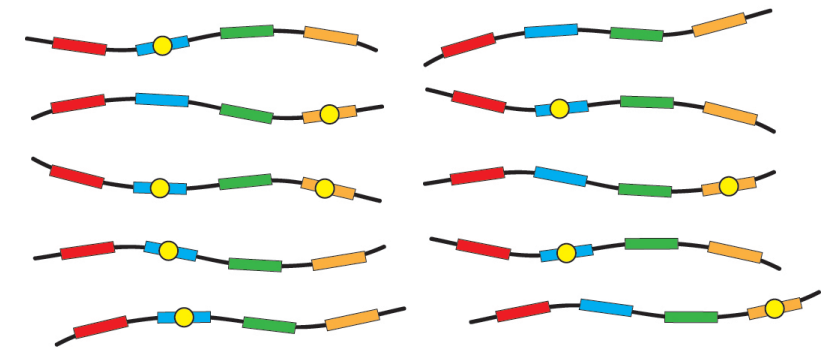
Completed next-generation sequencing (2RAD)
on all the DNA samples mentioned above



Markers

- 38,000 SNP markers
 - Excellent for assessing genome-wide diversity
 - Fine scale genetic structure
 - Genetic Population Size (N_e)

Single Nucleotide Polymorphisms (SNPs)

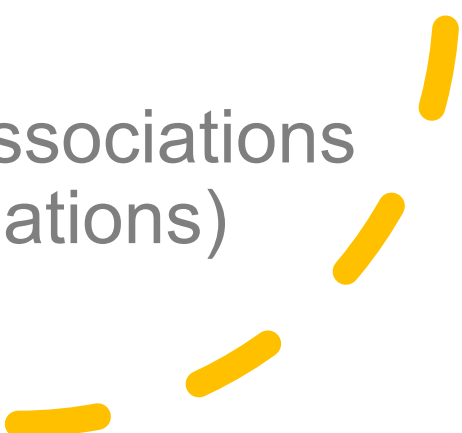


Many of the genetic differences are single nucleotide substitutions in the DNA sequence.

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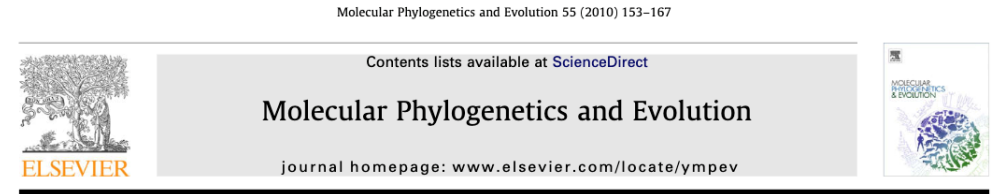
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Previous genetic studies are limited



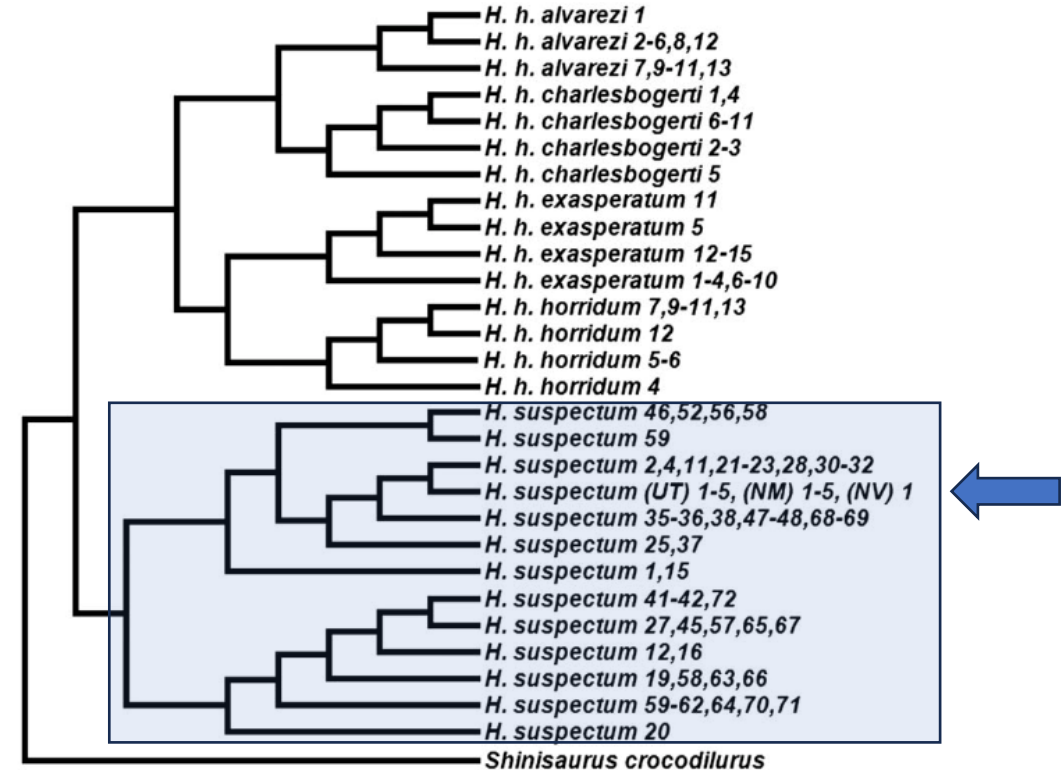
Main Conclusions:

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

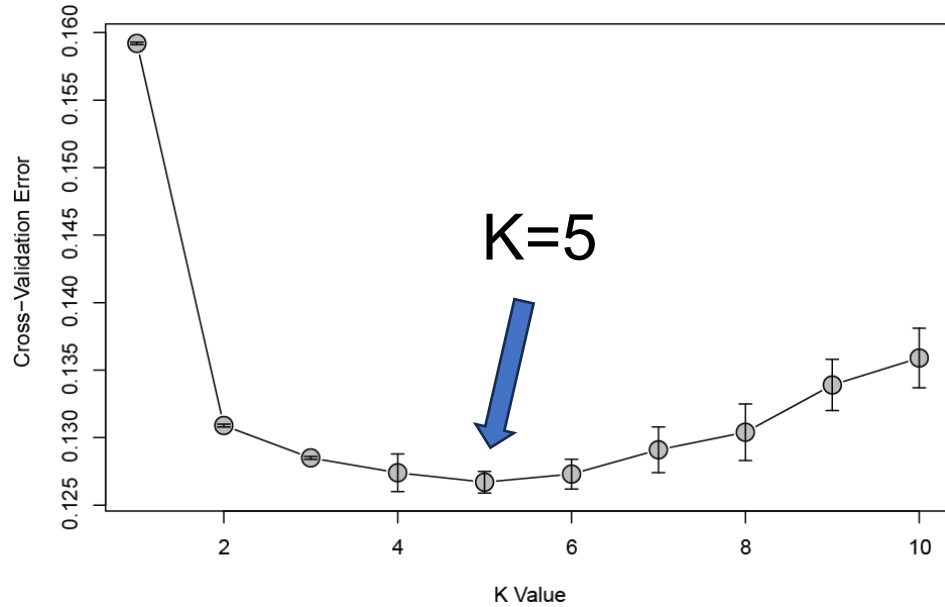


Conservation phylogenetics of helodermatid lizards using multiple molecular markers and a supertree approach

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

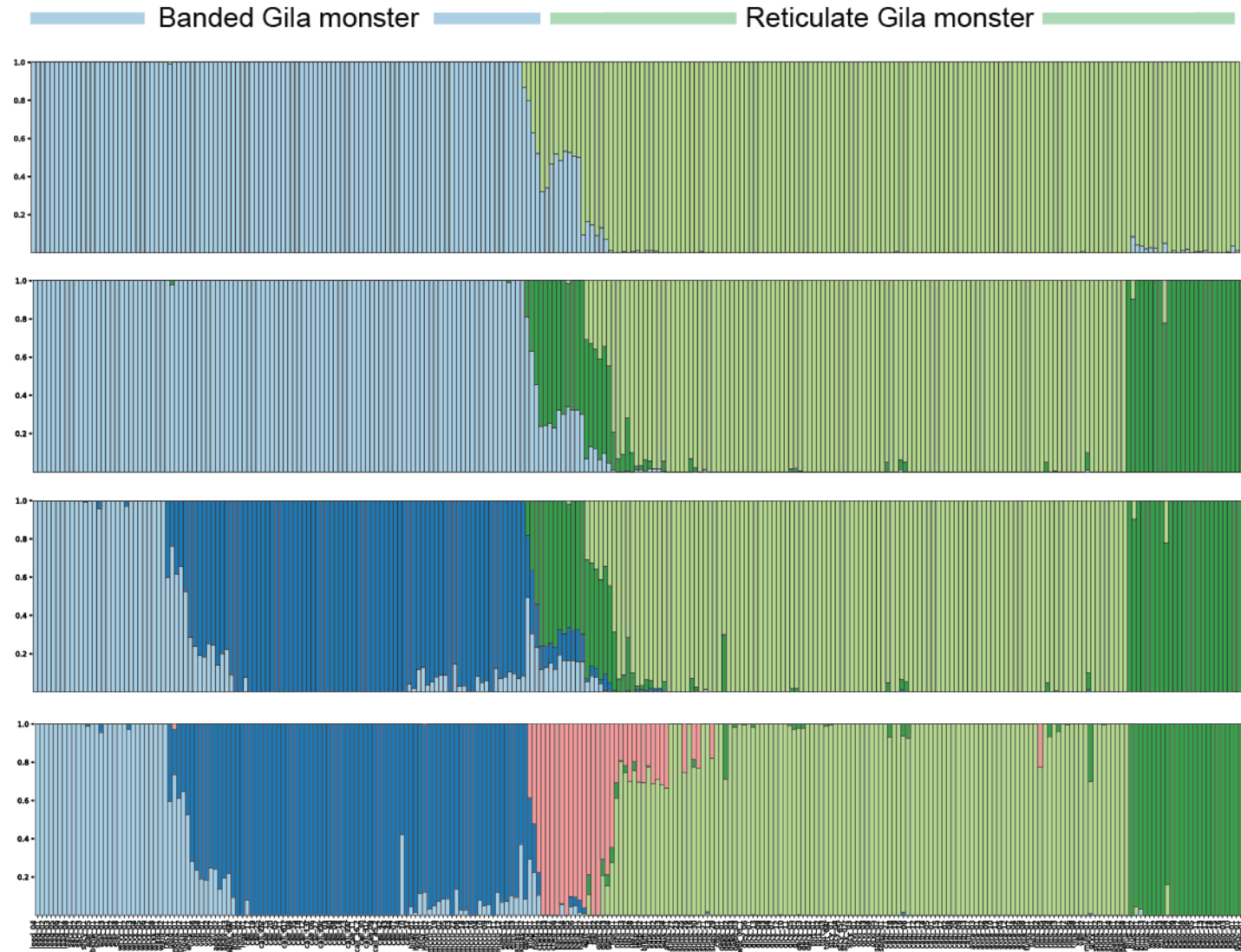


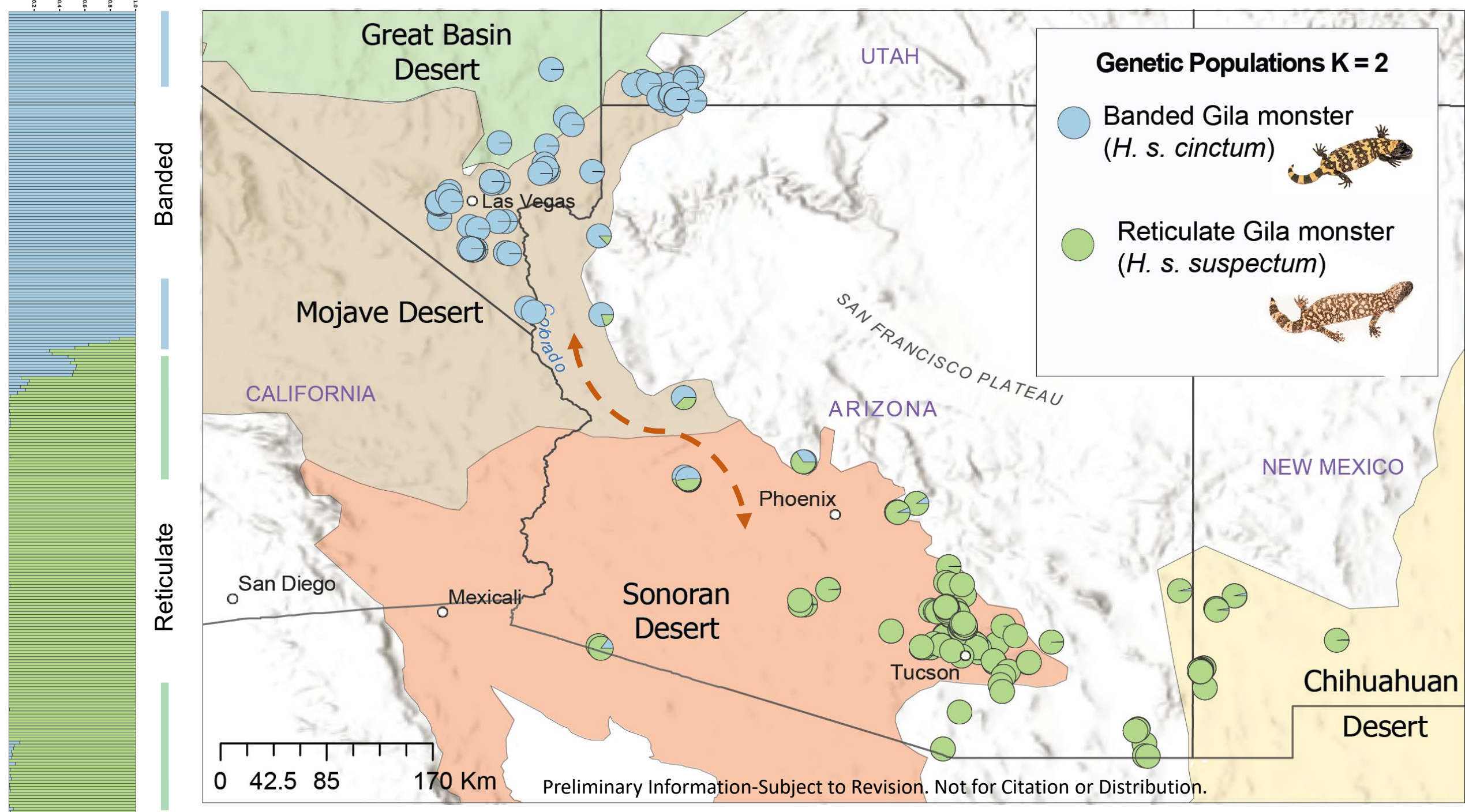
Population Structure Analyses

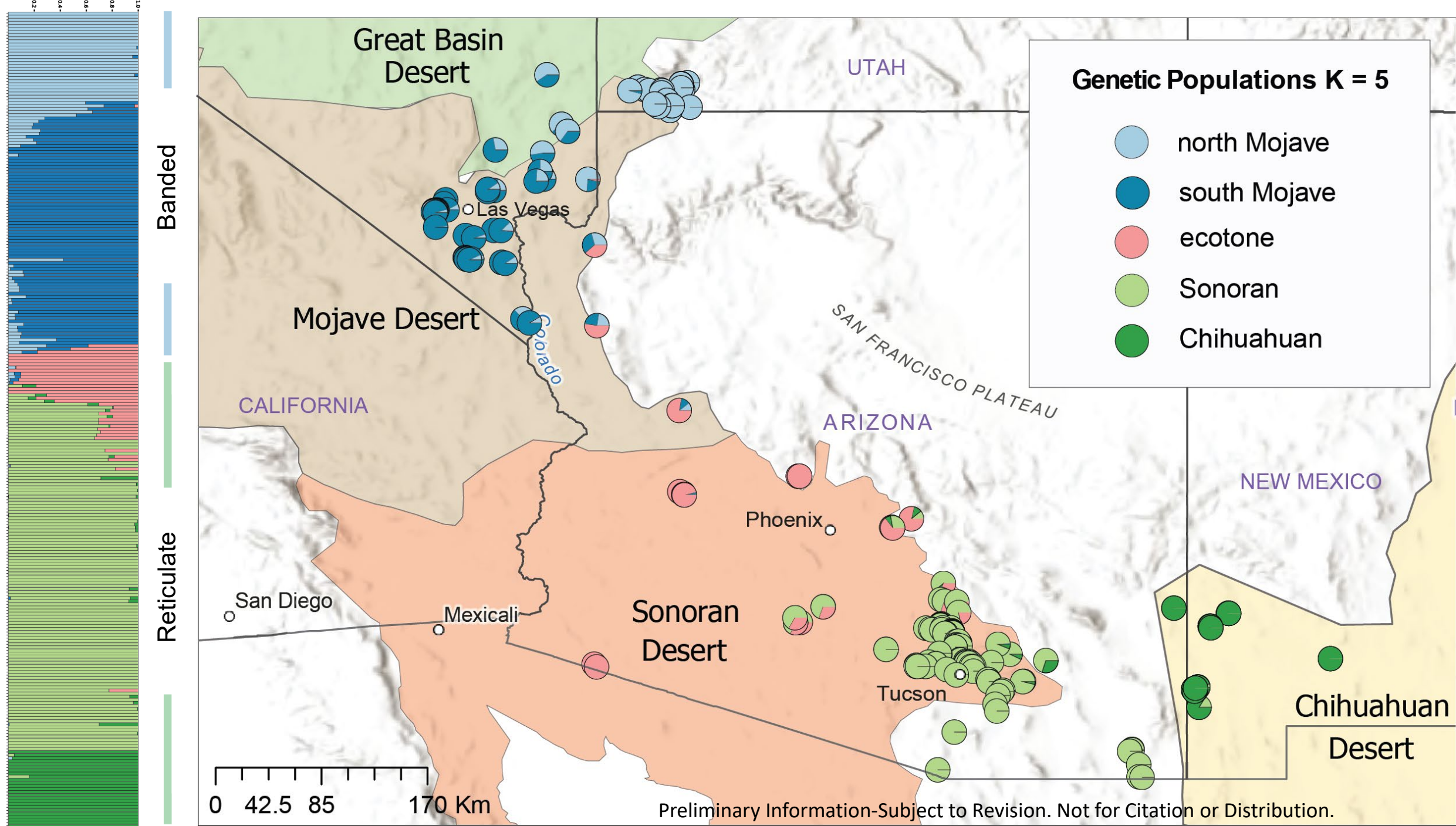


Admixture (Alexander et al. 2009)

- Maximum-likelihood clustering method
- Cross-validation is used to identify the number of populations for which the data have best predictive accuracy







Phylogenetic Analysis

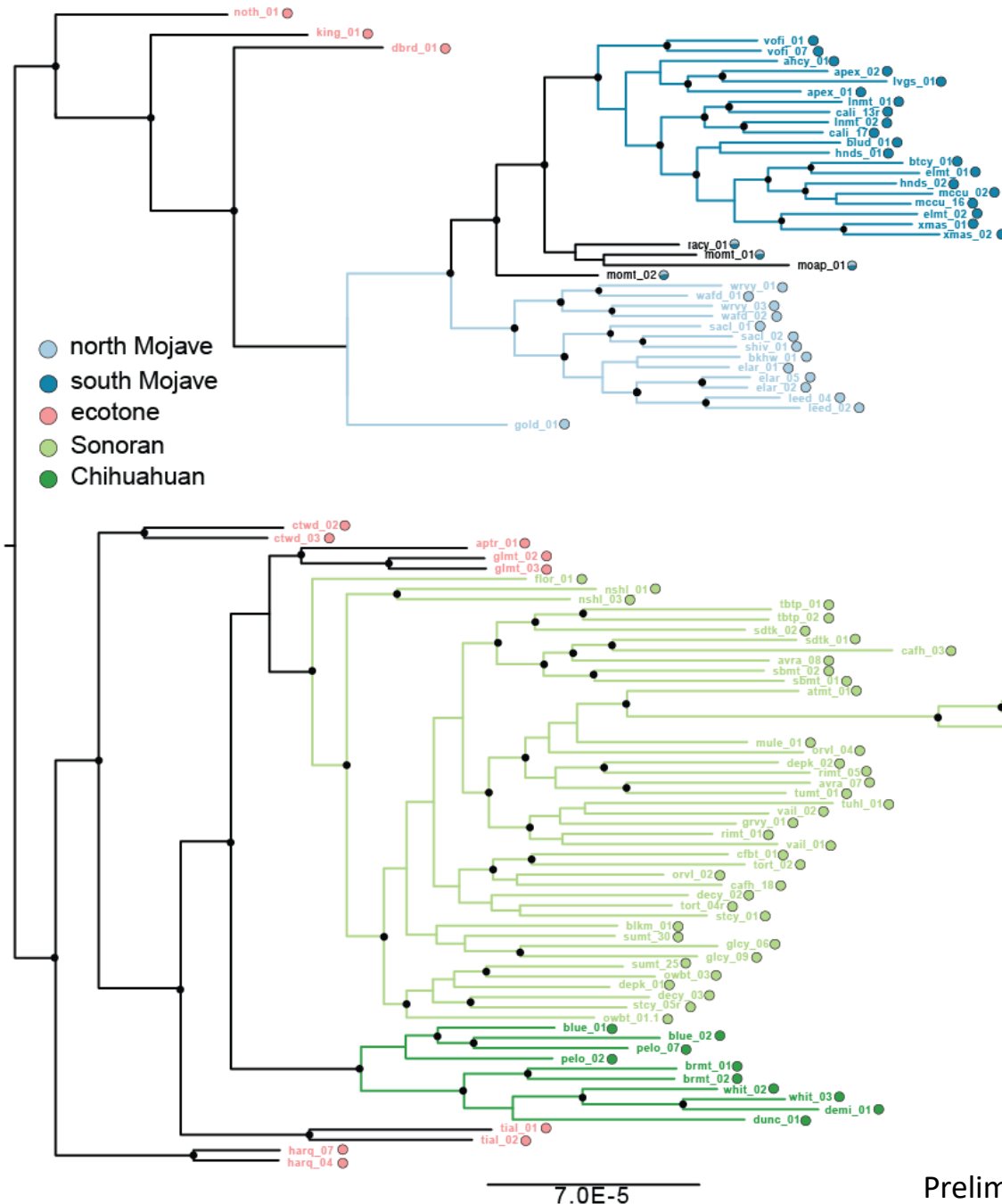
Banded Gila monster
(*H. s. cinctum*)



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

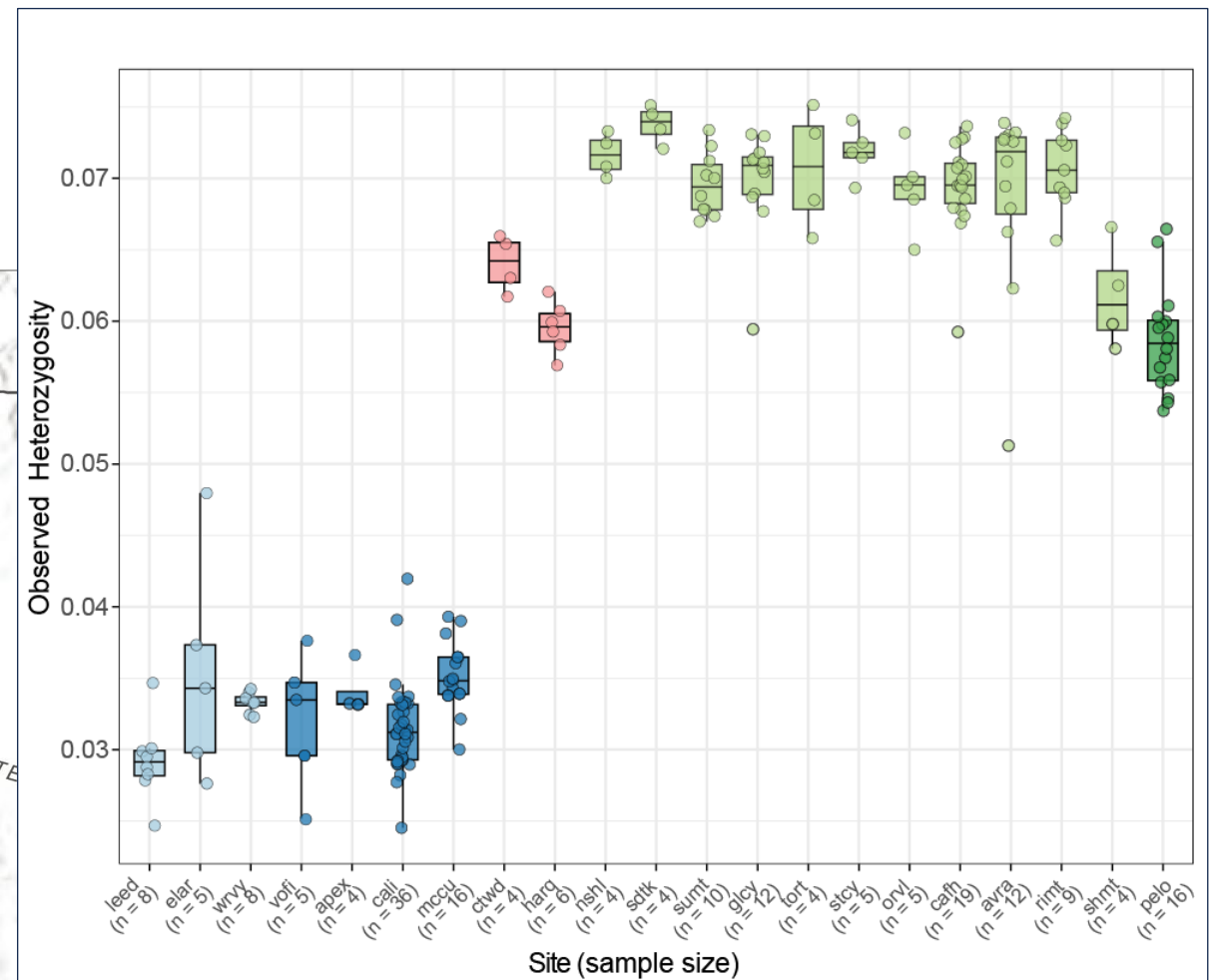
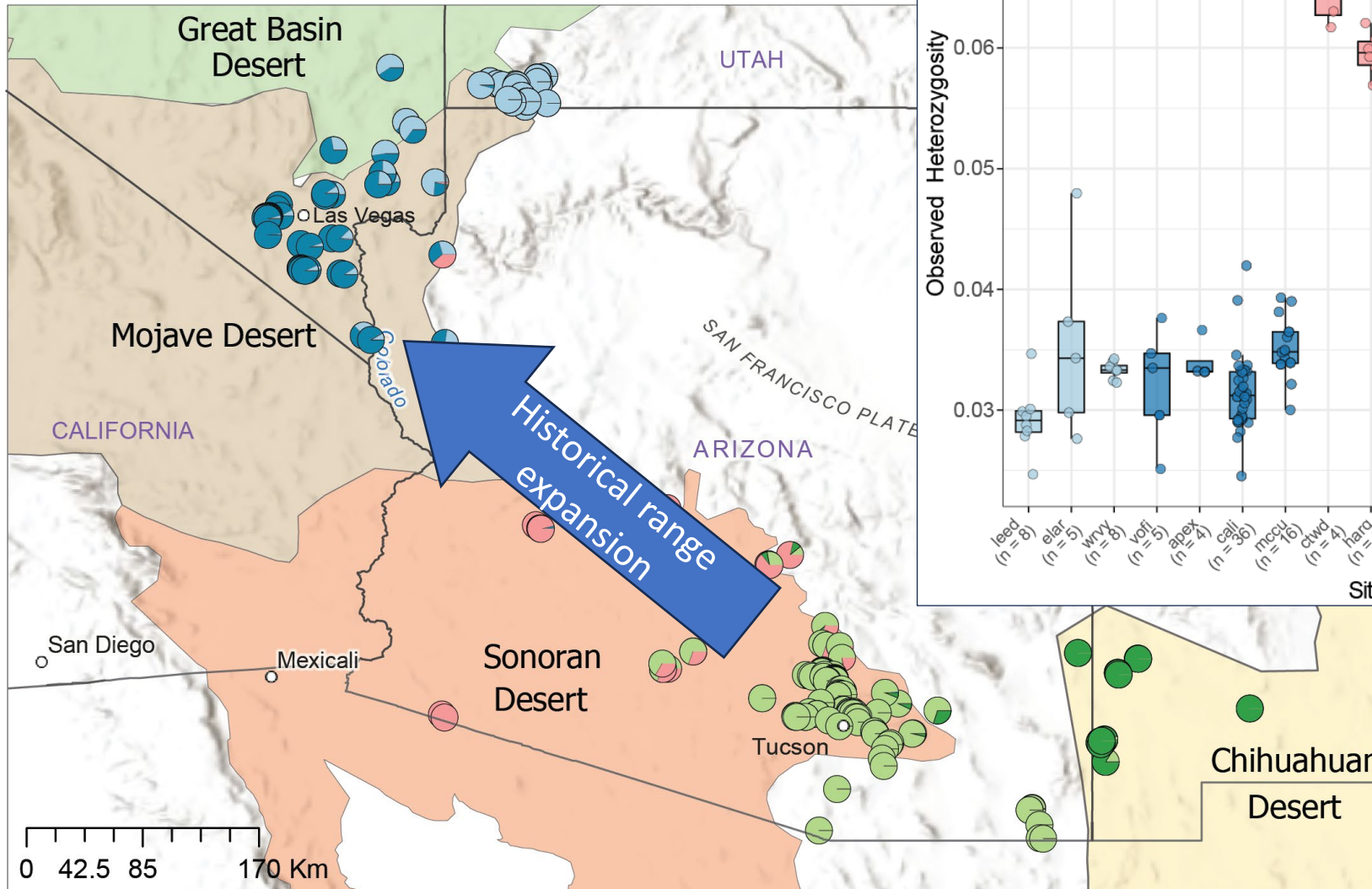


IQ-Tree3 - 32,422
parsimony informative
sites



Preliminary Information-Subject to Revision. Not for Citation or Distribution.

Rangewide Genetic Diversity



Latitudinal shift in
diversity –
Lower in Mojave
Desert Region

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



Effective Population Size – Ne

- Differences in habitat, resource availability, and genetic connectivity to neighboring sites may drive the disparity here.
- Both below $N_e < 50$ -100 threshold

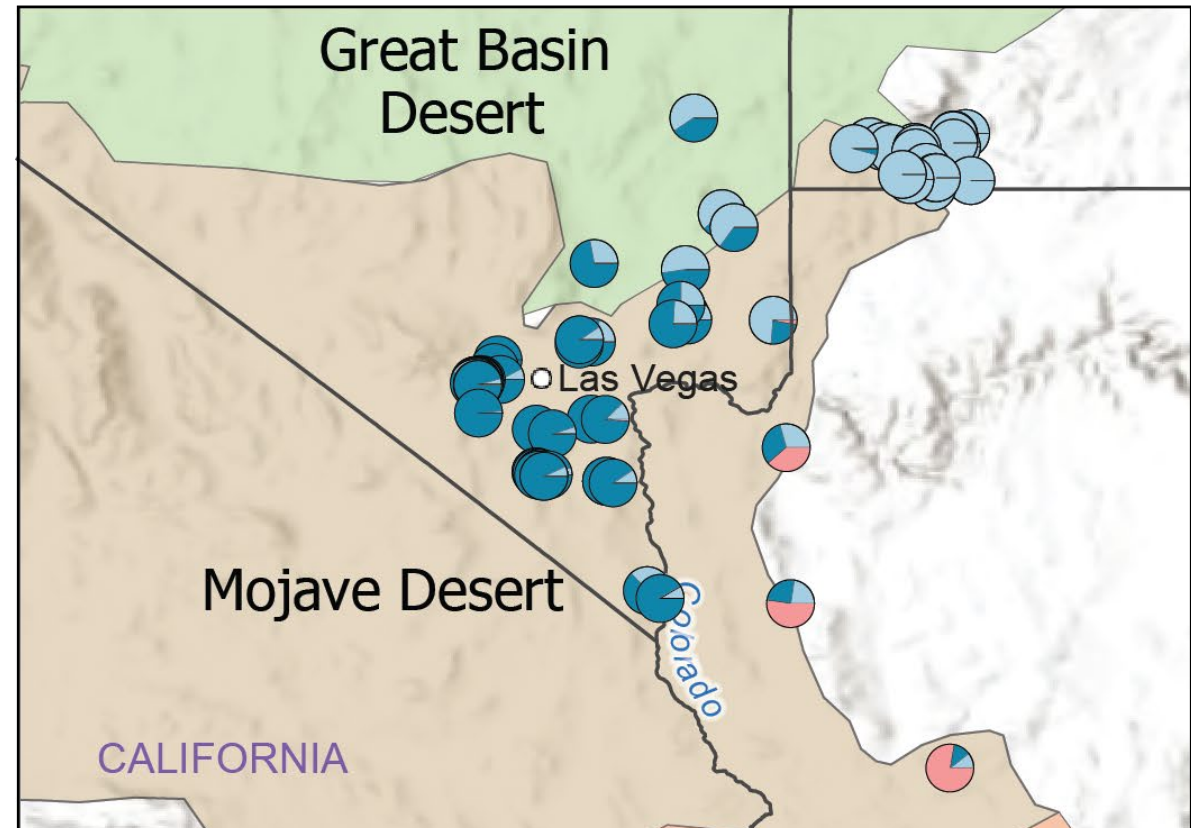
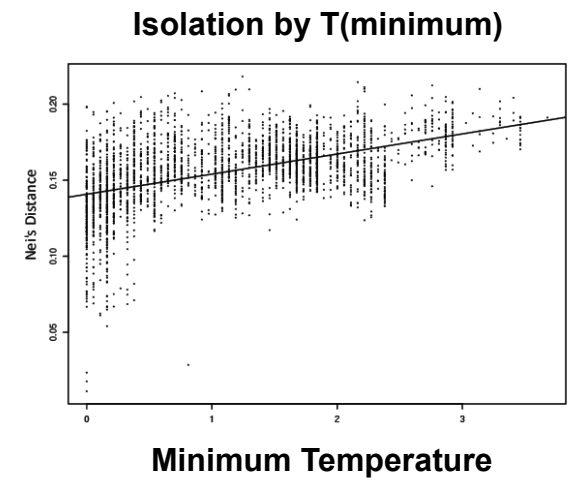
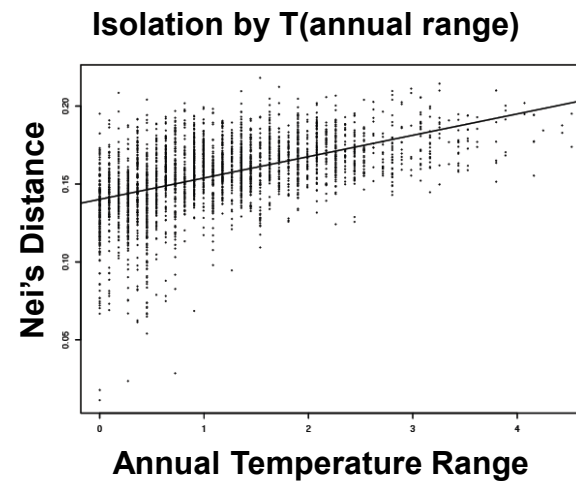
Two Focal Sites in Clark Co, NV	Samples	Ne	95% CI
Red Rock	36	16	10 – 26
McCullough Basin	16	22	9 – 245

Genetic/Climate Associations

Temperature associated with genetic diversity may drive regional differentiation

- South Mojave Population (Dark Blue)
 - Have lower annual temperature (5°C)
 - Higher minimum temperatures (7°C)
- Consistent with narrow thermal tolerances & may be of adaptive significance

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Management Implications

Regional Structure highlights that each desert ecoregion contains unique components of the overall genetic diversity with Gila Monsters

- Nevada & Utah contains a genetically distinct subspecies, Banded Gila Monster (*H. s. cinctum*).
- Genetic groups in Nevada may have adaptive significance tied to climate variables
- Protecting habitats in both regions may be crucial to ensure the representation of diversity in this subspecies

The northern edge of the range shows low genetic diversity, which may partially result from historical range expansion

- ongoing habitat loss and fragmentation in this area could be contributing to even lower diversity.



Acknowledgements

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Museum of Southwestern Biology

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desert conservation
PROGRAM

