



Mapping Gene Flow of Colorado Whiptail Lizards

Katrina Smith and Christina Hupy PhD, University of Wisconsin Eau Claire, Department of Geography and Anthropology

ABSTRACT

The purpose of this study was to use a Geographic Information System (GIS) to map and analyze gene flow according to the spatial occurrences of three species of native Colorado lizards in the genus *Aspidoscelis*. The six-lined race runner, *Aspidoscelis sexlineatus*, is diploid and reproduces sexually, while the diploid checkered whiptail lizard, *Aspidoscelis tessellata*, is parthenogenic and produces female clones. The triploid checkered whiptail lizard, *Aspidoscelis neotesselata*, is also parthenogenic and is a hybrid of *A. sexlineatus* and *A. tessellata*. The spatial analysis conducted in this study produced a distribution map of *A. sexlineatus* and of the distinct clonal lines resulting from mutation in *A. tessellata* and *A. neotesselata*. From this map we concluded that the species do not disperse randomly but are restricted in location by undetermined environmental variables and competition for similar resources. The southeastern corner of Otero County was determined to be the site of the hybridization event that resulted in *A. neotesselata*. We also concluded that *A. neotesselata* pattern class A is a result of a mutation in *A. neotesselata* pattern class B; both classes moved northwest from the site of hybridization. *A. neotesselata* pattern class D moved due north from the site of hybridization. This study has effectively mapped the spatial movement of genes among these three lizard species throughout southeastern Colorado.

INTRODUCTION

Evolutionary events such as genetic divergence and hybridization of species determine the fate of local biological diversity and occur in areas where genetic diversity is high and many species are present. In order to locate the areas of genetic divergence and hybridization among three species of native Colorado lizards, we used a geographic information system (GIS) to determine the species' spatial distribution.

Two of the species (*Aspidoscelis tessellata* and *Aspidoscelis neotesselata*) are parthenogenic, which means the entire population consists of females that asexually reproduce new female clones. Each genetic mutation in a fertile individual results in a distinct clonal line. These clonal lines have been described within each species using dorsal scale patterns and are appropriately called pattern classes.

The diploid checkered whiptail lizard, *A. tessellata*, has two pairs of chromosomes per cell, and ranges through the Southwest in New Mexico, Texas, Oklahoma, and Colorado. This species likely moved into Colorado from the south.



The six-lined race runner, *Aspidoscelis sexlineatus*, is also diploid but reproduces sexually; the population consists of both males and females.

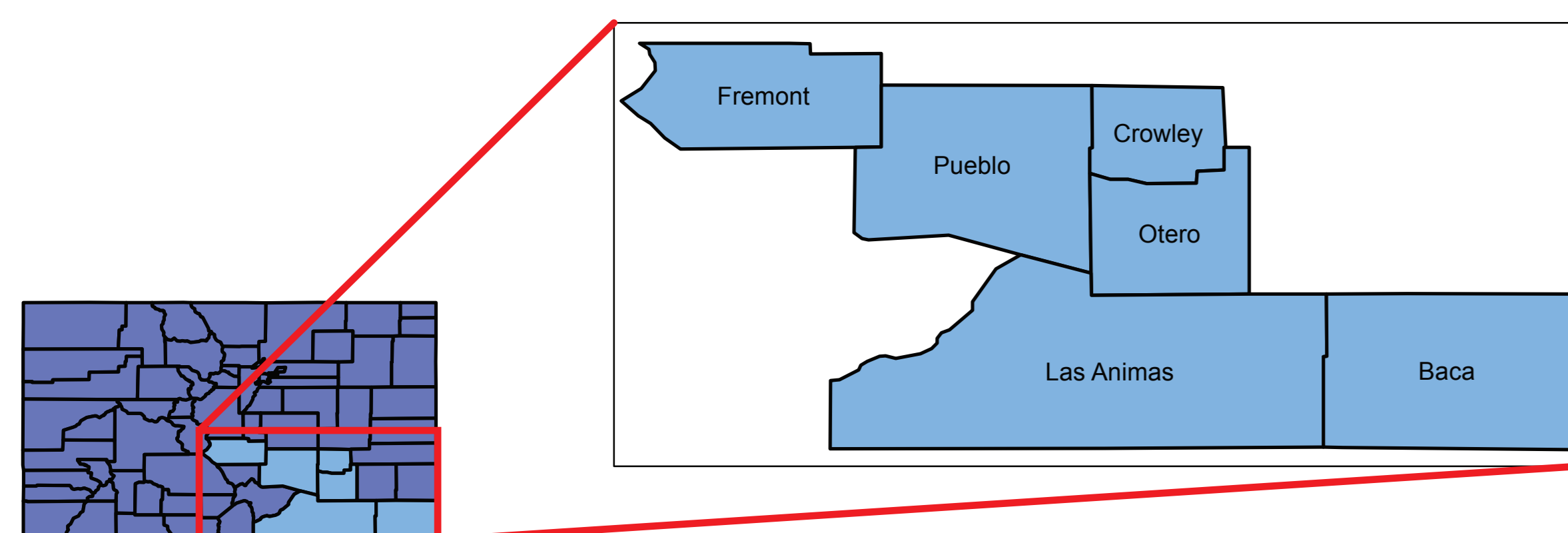
A. neotesselata is the result of a hybridization event between a female *A. tessellata* (diploid) and a male *A. sexlineatus* (sperm is haploid). Therefore the 2n egg from the female was fertilized by the 1n sperm resulting in a 3n offspring (*A. neotesselata*).



The purpose of this study was to investigate the spatial distribution of *A. sexlineatus* and each pattern class of *A. tessellata* and *A. neotesselata* to determine areas of overlap where genetic divergence and hybridization may have occurred.

OBJECTIVES

- Expand and compile a more complete distribution of each pattern class within Colorado.
- Organize the data and build a geodatabase using ArcGIS.
- Analyze the pattern class distribution map to explore relationships between spatial distribution and genetic phylogeny of *Aspidoscelis* lizards.
- Determine the likely region of origin of each clonal line.
- Determine if competition among *Aspidoscelis* species may affect distribution.



METHODS

Our study area includes Fremont, Pueblo, Crowley, Otero, Las Animas, and Baca Counties of southeastern Colorado. A total of 754 lizard records were compiled with locality and taxonomic information. Sixty-nine lizards were captured, euthanized, and preserved while exact locations of capture were determined using a GPS. The species and pattern class (when applicable) of each sample were also determined and noted. Locality information for the remaining 685 lizards was collected from museum records. Using ArcGIS software, the data set of collected geographic locations of *Aspidoscelis* was geocoded and mapped. Two GIS tools were used to analyze the distribution of lizards exhibited a directional trend, while the standard distance tool measured the degree to which the lizards were concentrated or dispersed around the mean center point.

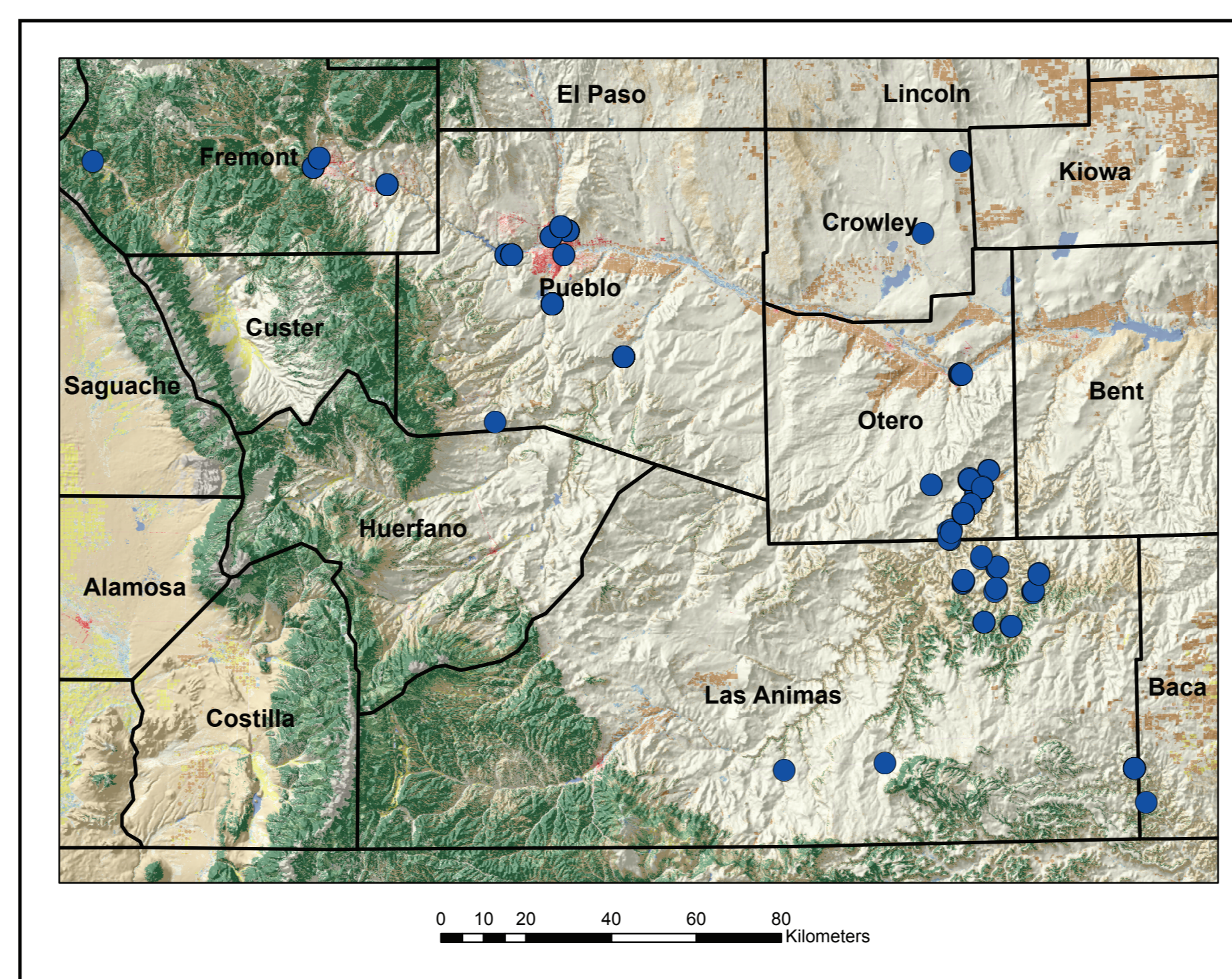


Figure 1. Point locations of 754 lizards at 90 different locations throughout the study area in southeastern Colorado. Lizards are not grouped by species and pattern class because scale does not allow for accurate representation.

RESULTS

Pattern Class Overlap	Polygon Area (km ²)	Percent Total Area
A	482.96	10.60
B	1889.79	41.47
BC	2.93	0.06
BCS	86.62	1.90
BS	589.47	12.94
C	393.11	8.63
CS	186.80	4.10
D	21.26	0.47
DBCS	30.34	0.67
DCS	103.85	2.28
DS	25.74	0.56
ND	8.05	0.18
S	735.93	16.15

Table 1. Areas described as polygons where one or more pattern classes overlap in distribution. Pattern class code is as follows: A=*A. neotesselata* A; B=*A. neotesselata* B; C=*A. tessellata* C; D=*A. tessellata* D; ND=*A. neotesselata* D; S=*A. sexlineatus*.

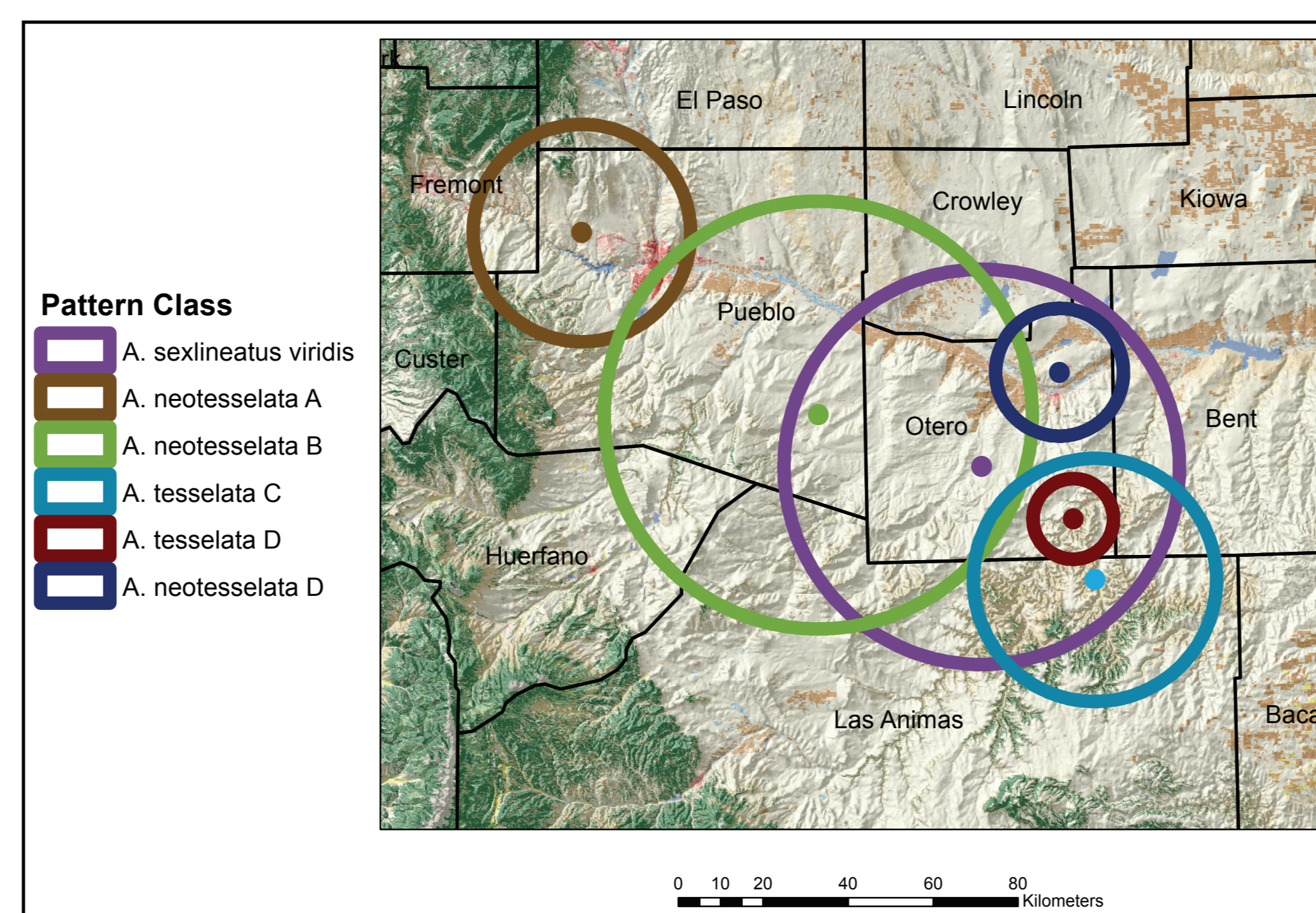


Figure 2. Standard distribution of 754 lizards at 90 different locations throughout the study area. All lizards are from the genus *Aspidoscelis* and are grouped by species and pattern class.

RESULTS CONT'D

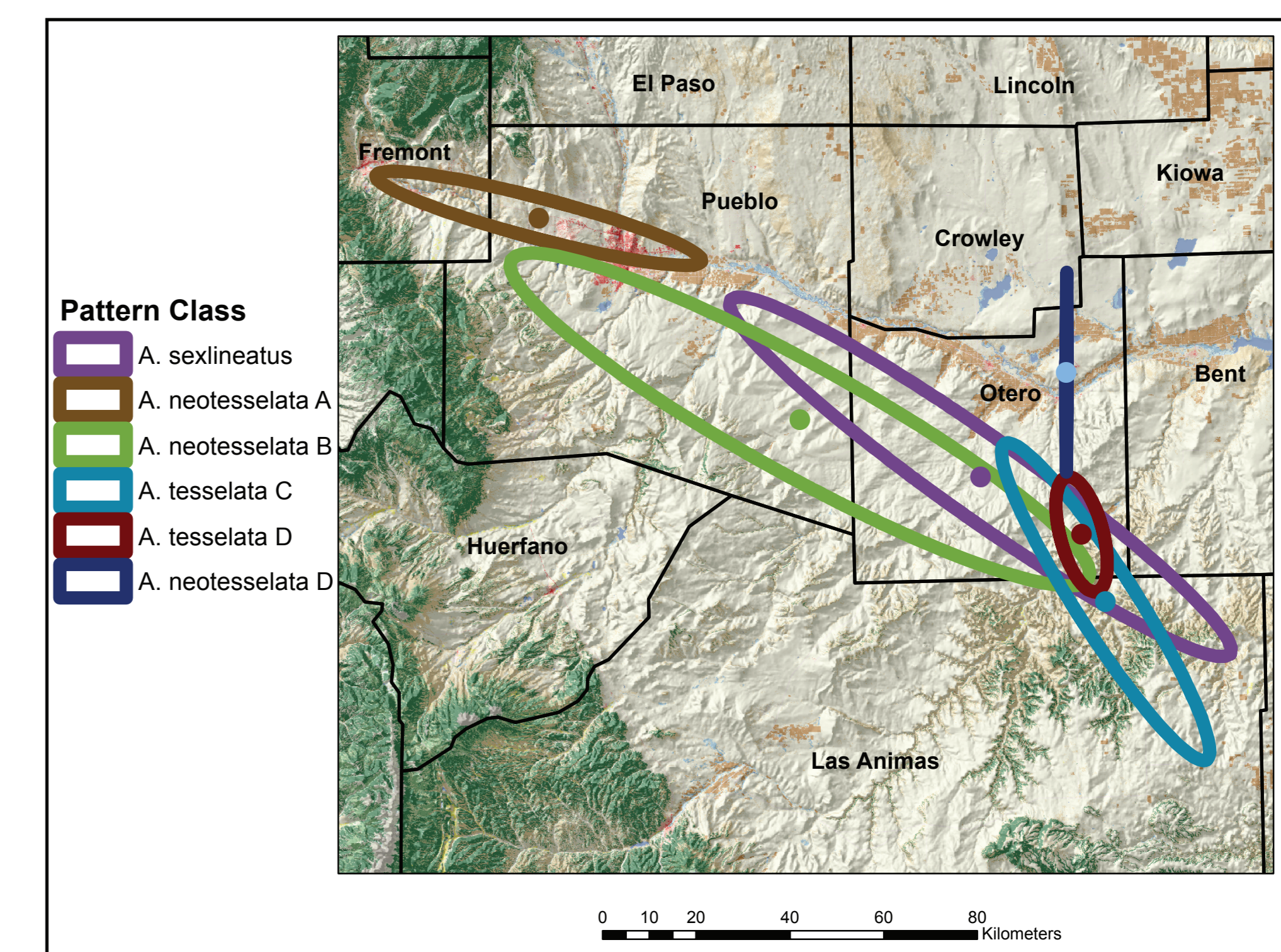


Figure 3. Directional distribution of 754 lizards at 90 different locations throughout the study area. All lizards are from the genus *Aspidoscelis* and are grouped by species and pattern class.

DISCUSSION

The directional distribution map (Fig. 3) indicates where the groups are located, while the standard distribution map (Fig. 2) indicates where the groups would be if they were dispersed randomly from the population's center point. The dissimilarity in these two maps indicates that these groups are not dispersing randomly but are constrained by some aspect of their environment. These constraints are likely a combination of abiotic and biotic variables, such as water availability, soil moisture, temperature, elevation, slope, and aspect, as well as vegetation type and cover, food resources, predator presence, and competition level. We expect that competition is a strong driver in the scattered distribution of the pattern class groups because all three species require similar habitats and food resources.

The southeastern corner of Otero County contains a 103.85 km² area of overlap in the distribution of *A. sexlineatus* and both pattern classes of *A. tessellata* suggesting that this is the most likely site of the hybridization event that resulted in *A. neotesselata*. This area represents only 2.28% of the total area occupied by all *Aspidoscelis* populations, suggesting further evidence that competition is high because pattern class populations spread out across Colorado to gain access to adequate and favorable habitat and resources.

Both *A. neotesselata* pattern class A and *A. neotesselata* pattern class B moved northwest from the site of hybridization. Because *A. neotesselata* pattern class A is found further northwest behind *A. neotesselata* pattern class B, it is likely that *A. neotesselata* pattern class A resulted from a mutation in *A. neotesselata* pattern class B. We also now know that *A. neotesselata* pattern class D has moved due north from the hybridization site.

SOURCES

Taylor, Harry, James Walker, and James Cordes. 1996. Systematic implications of morphologically distinct populations of a parthenogenetic whiptail lizards: *Cnemidophorus tessellatus* Pattern Class D. *Herpetologica*, 52, (2) 254-262.

Walker, James, Harry Taylor and James Cordes. 1994. Hybrid *Cnemidophorus* (Sauria:Teiidae) in Ninemile Valley of the Purgatoire River, Colorado. *The Southwestern Naturalist* 39 (3) 235-240.

Walker, James, James Cordes, and Harry Taylor. 1997. Parthenogenetic *Cnemidophorus tessellatus* Complex (Sauria: Teiidae): A Neotype for Diploid *C. tessellatus* (Say, 1823), Redescription of the Taxon, and Description of a New Triploid Species. *Herpetologica*, 53, (2) 233-259.

ACKNOWLEDGEMENTS

- Special Thanks to:
- Dr. Chad Montgomery (Truman State University)
 - Dr. James Walker (Univ. AR Fayetteville)
 - Anthony Wilmes, Laura Garey, Jennifer Newby, Tony Kroeger (Truman State Univ.)
 - University of Wisconsin-Eau Claire
 - Truman State University