

# Tamarisk Beetle Colonization of the Rio Grande in New Mexico

A long-term, multi-faceted study of the spread, impacts, and hybridization of tamarisk beetles along the Rio Grande in central and southern N.M.

Levi Jamison<sup>1</sup>, Amanda Stahlke<sup>2</sup>, Zeynep Özsoy<sup>3</sup>, Matt Johnson<sup>1,4</sup>

<sup>1</sup> EcoPlateau Research, <sup>2</sup> University of Idaho, <sup>3</sup> Colorado Mesa University, <sup>4</sup> Northern Arizona University

## Introduction:

Tamarisk beetles (*Diorhabda* spp.) are a biocontrol agent used to control non-native tamarisk (*Tamarix* spp.), a small invasive riparian tree. Tamarisk beetles were first introduced in the USA in 2001. Since, four species of tamarisk beetles have been released across different portions of the West. Our study is the first to combine genetic analysis and on-the-ground field surveys to track the colonization of a large region by multiple species of these beetles, while also studying long-term (8 years) population dynamics and impacts to the target weed.

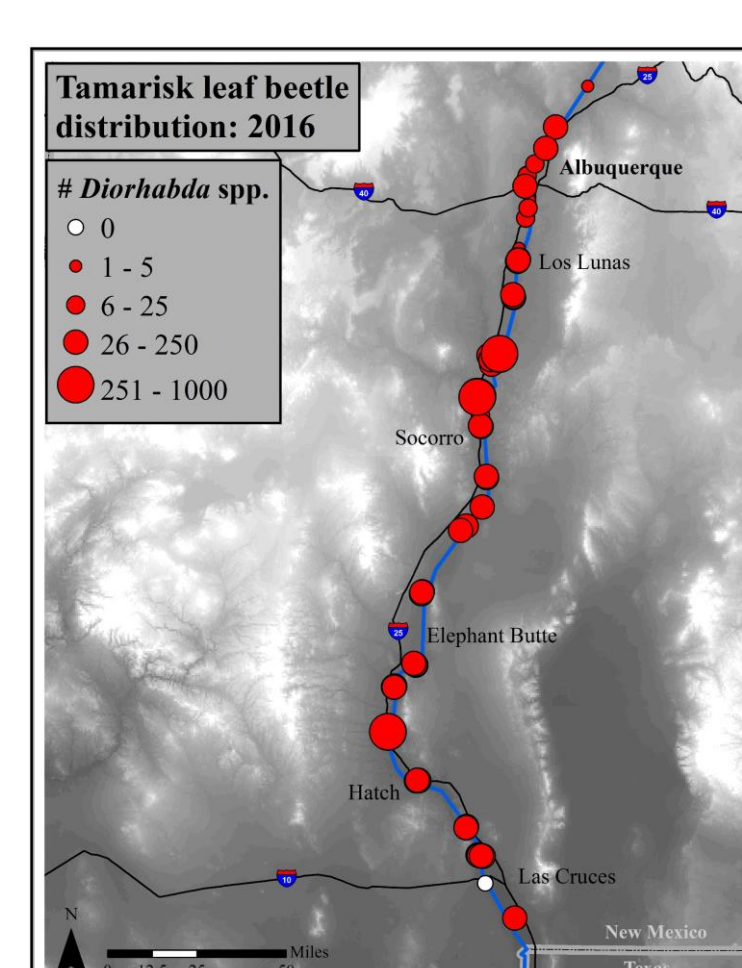
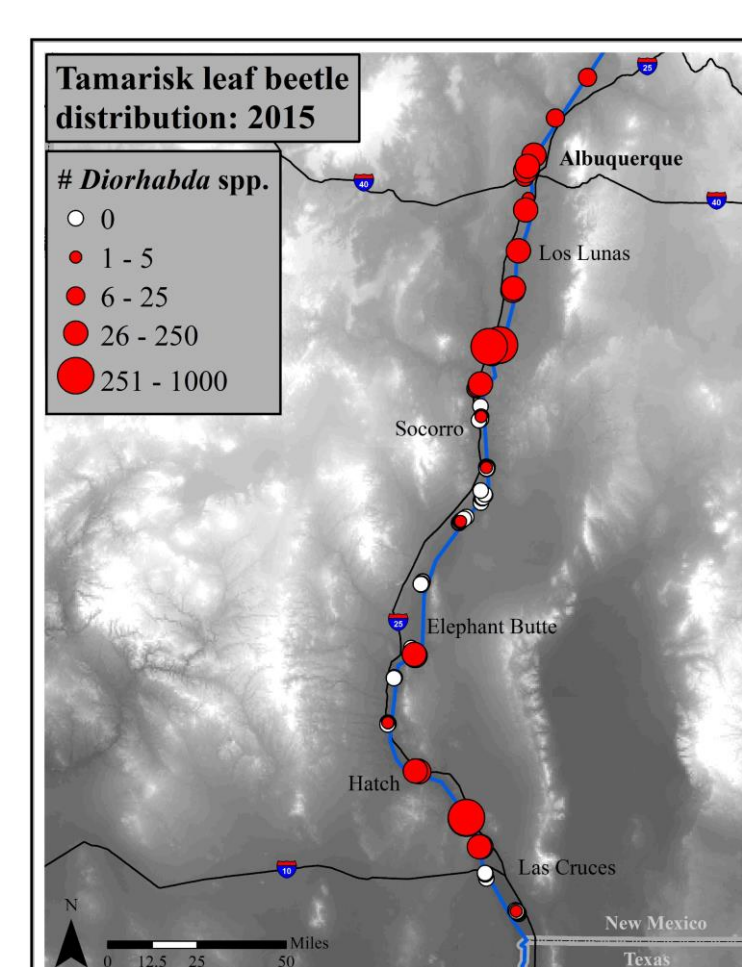
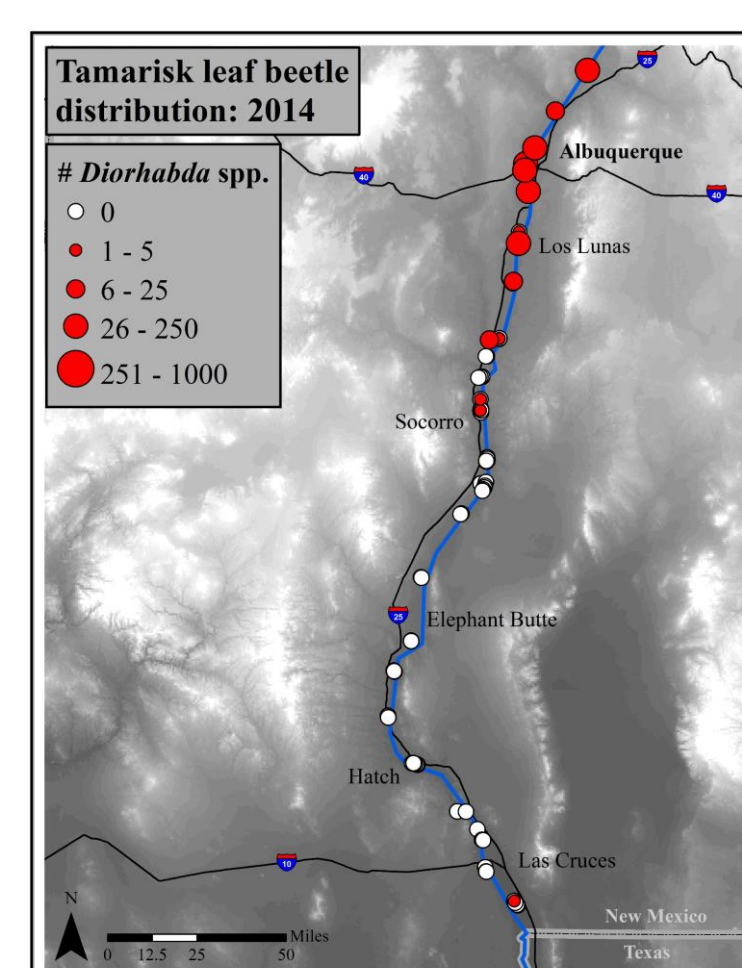
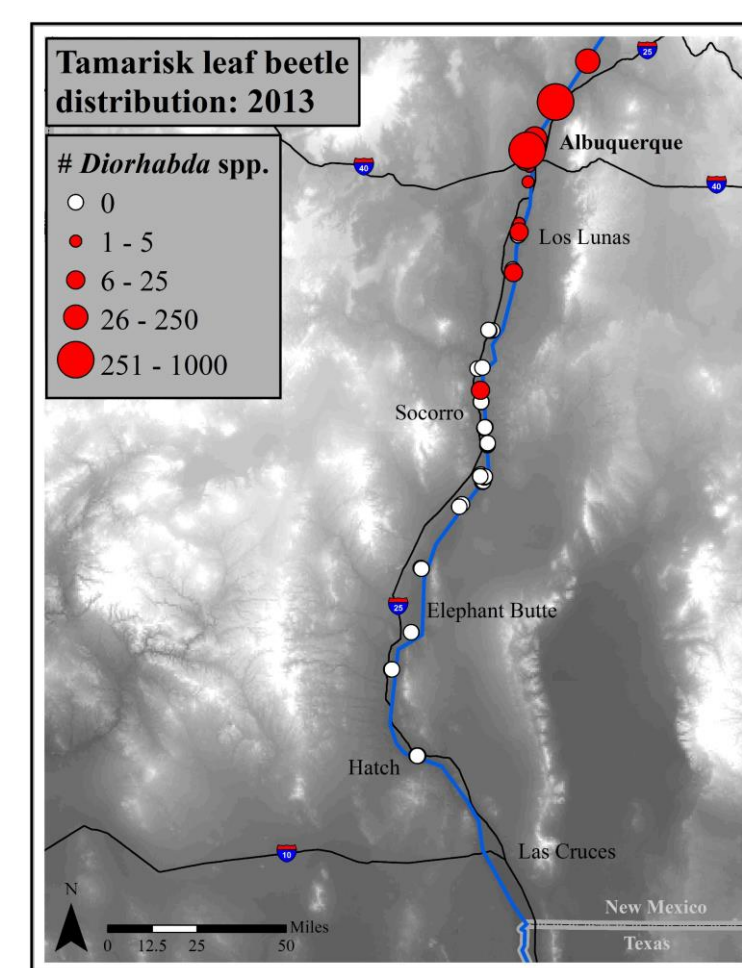
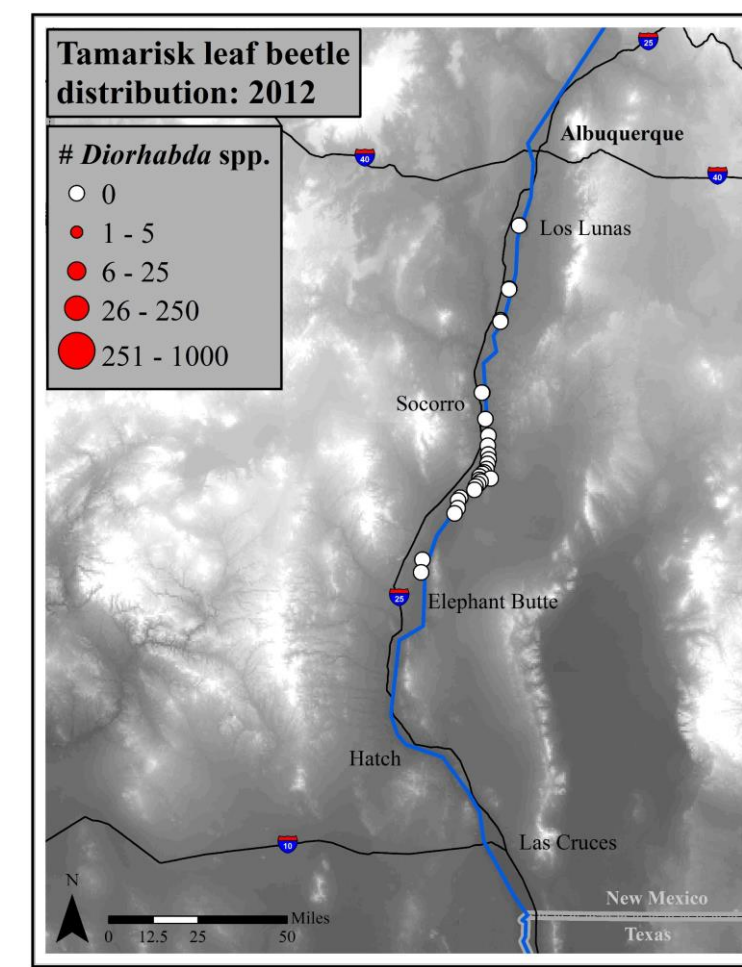
## Methods:

### Field Surveys

We surveyed the spread of tamarisk beetles from 2012–2019 using standardized sweep net sample protocols. In addition to sweep net sampling, we began studying tamarisk phenology in 2016, using visual estimations of canopy defoliation, mortality, and flowering.

### Genetic Analysis

In 2016 we began collecting tamarisk beetles for genetic analysis to track species movement and potential hybridization. Genetic research consisted of looking at both the mitochondrial DNA and DNA markers from the whole genome. Mitochondrial DNA was analyzed using CO1 (Cytochrome C Oxidase Subunit 1) sequencing to indicate the maternal lineage of the individual and RADseq (Restriction site associated DNA sequencing) was used on the whole genome to look for hybridization among species.



**Figure 1.** The spread of tamarisk beetles (*Diorhabda* spp.) along the Rio Grande in central and southern New Mexico. A population of Northern tamarisk beetles (*D. carinulata*) started moving into the study reach from the north in 2013. While a second population consisting primarily of Sub-tropical tamarisk beetles (*D. sublineata*) began moving northward from the Texas border in 2014. By 2016 these two populations began to overlap.

## Main Findings:

### Field Surveys

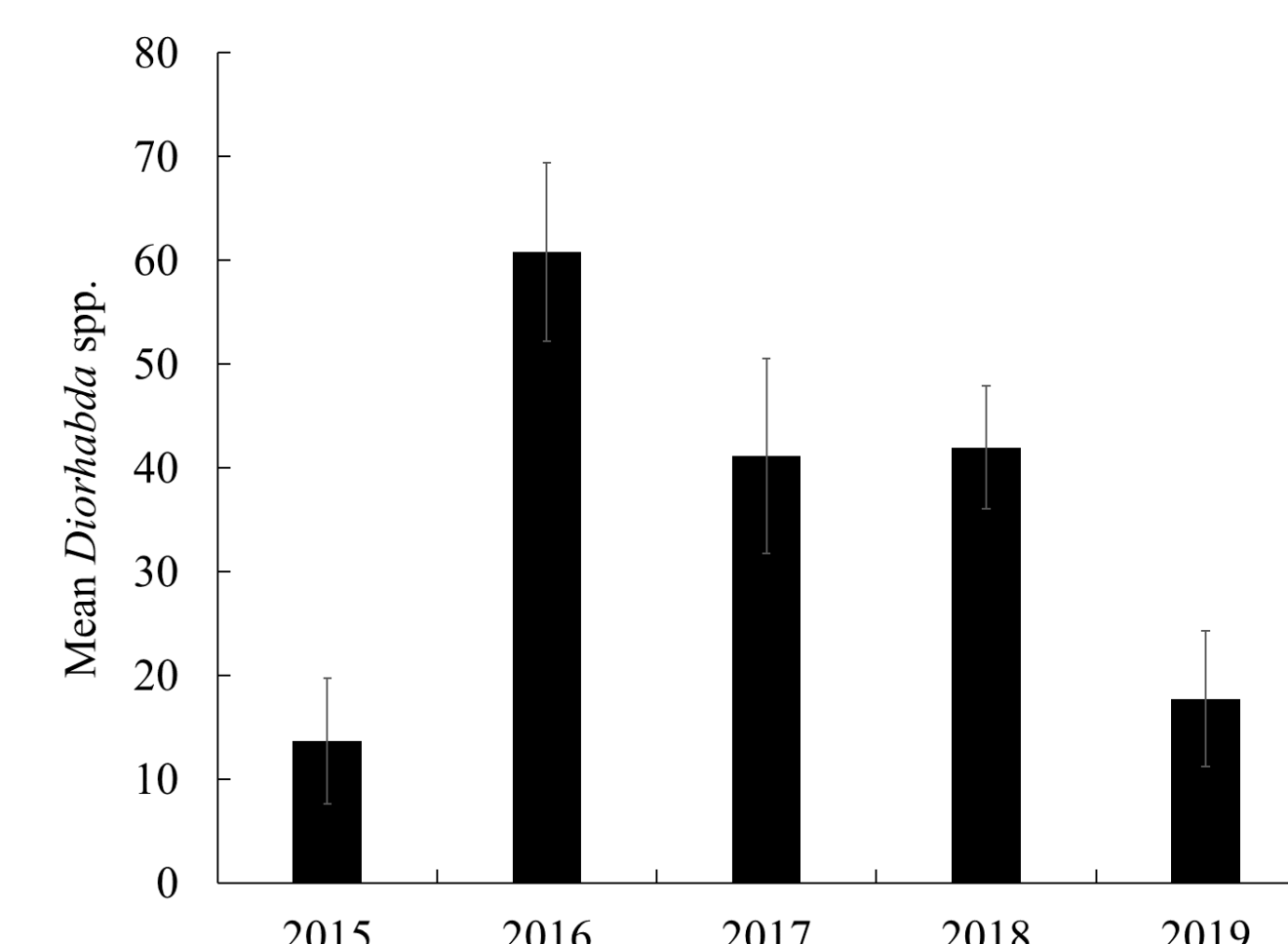
Two tamarisk beetle (*Diorhabda* spp.) populations (one moving north and one moving south) spread rapidly across the study reach from 2013–2016 (Figure 1). These populations began to overlap in 2016. As beetle populations increased tamarisk defoliation increased, leading to modest increases in canopy mortality in the long term (Figure 2) and major decreases in tamarisk flowering in the short term (Figure 3). Tamarisk beetle abundance decreased from 2017–2019, reducing the extent of defoliation events, and characterized a boom and bust dynamic.

### Genetic Analysis

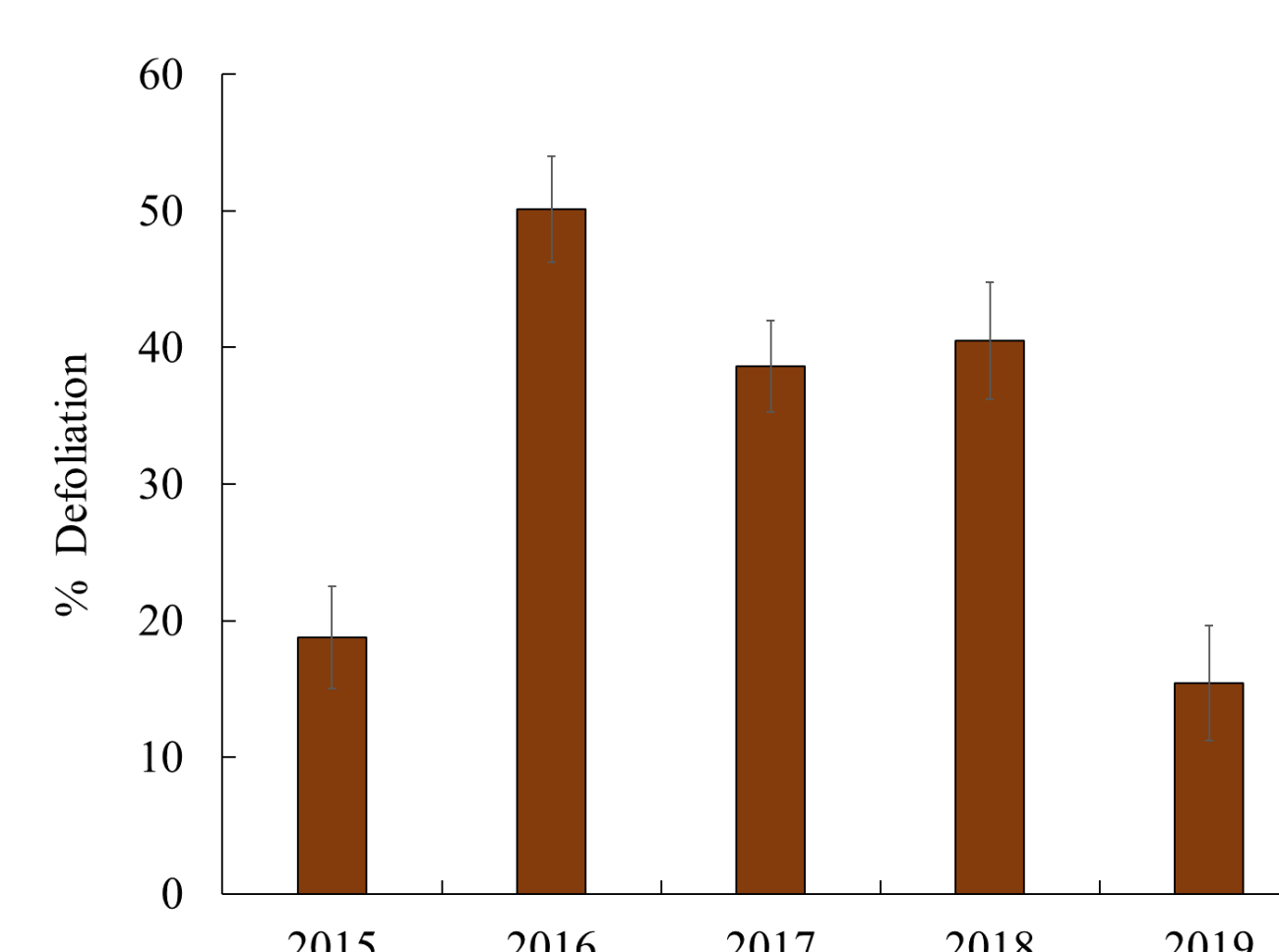
We found the two populations of tamarisk beetles spreading across the study reach to be composed of different species (*D. carinulata* moving south and *D. sublineata* moving north). Within the *D. sublineata* population we found genetic evidence of two other species of tamarisk beetles that have been released in the U.S.A. (*D. carinata* and *D. elongata*), suggesting these three species are hybridizing in the field. Alternatively, when the populations of *D. carinulata* and *D. sublineata* overlapped in our study reach in 2016 we found no evidence of hybridization. Our findings support other's findings (see Bean et al. 2013) that *D. carinulata* may be out-competed in parts of the U.S.A. where these other three species of tamarisk beetles succeed.

### Literature Cited:

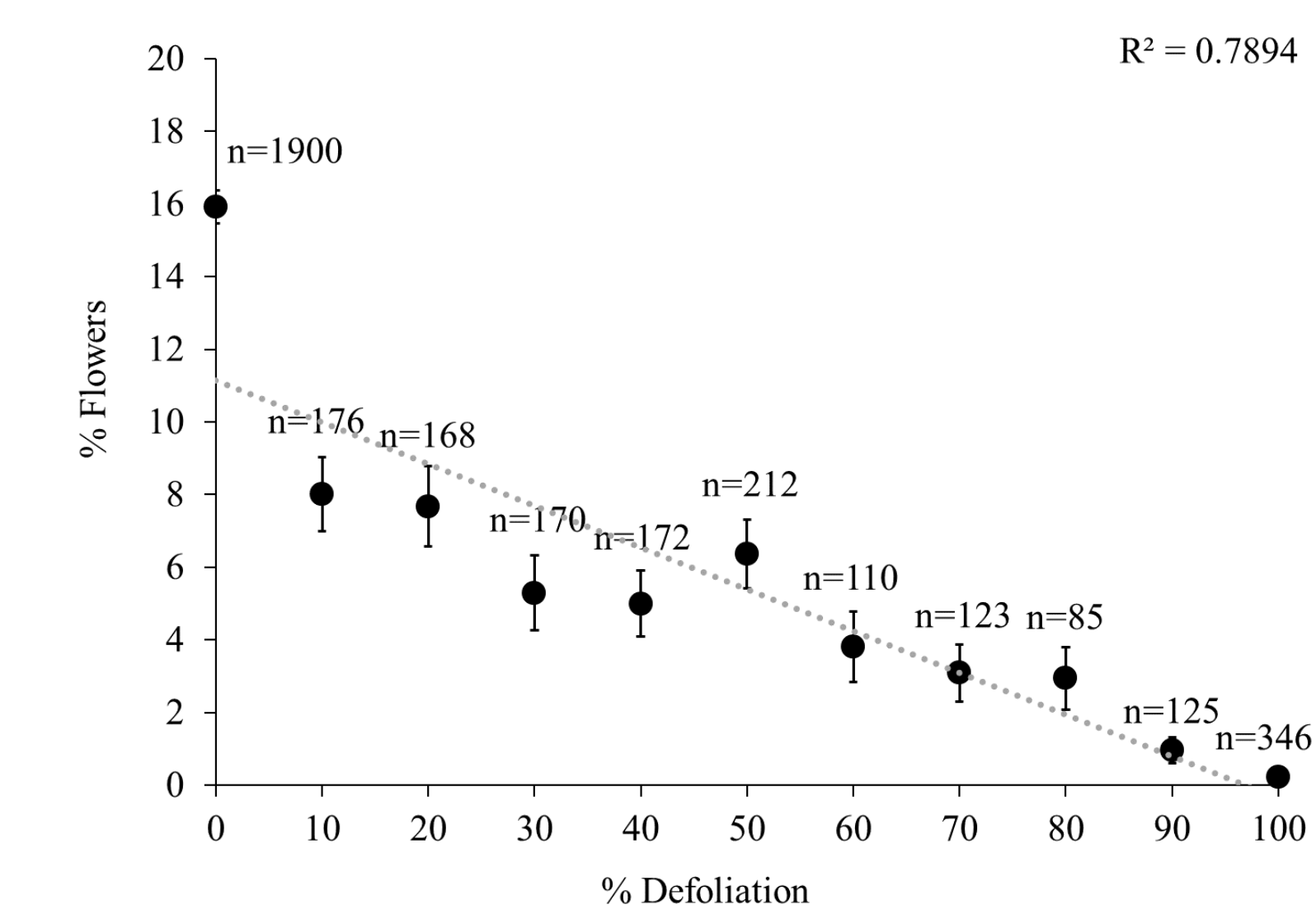
Bean, D. W., D. J. Kazmer, K. Gardner, D. C. Thompson, B. (Petersen) Reynolds, J. C. Keller, and J. F. Gaskin. 2013. Molecular Genetic and Hybridization Studies of *Diorhabda* spp. Released for Biological Control of *Tamarix*. *Invasive Plant Science and Management* 6:1–15.



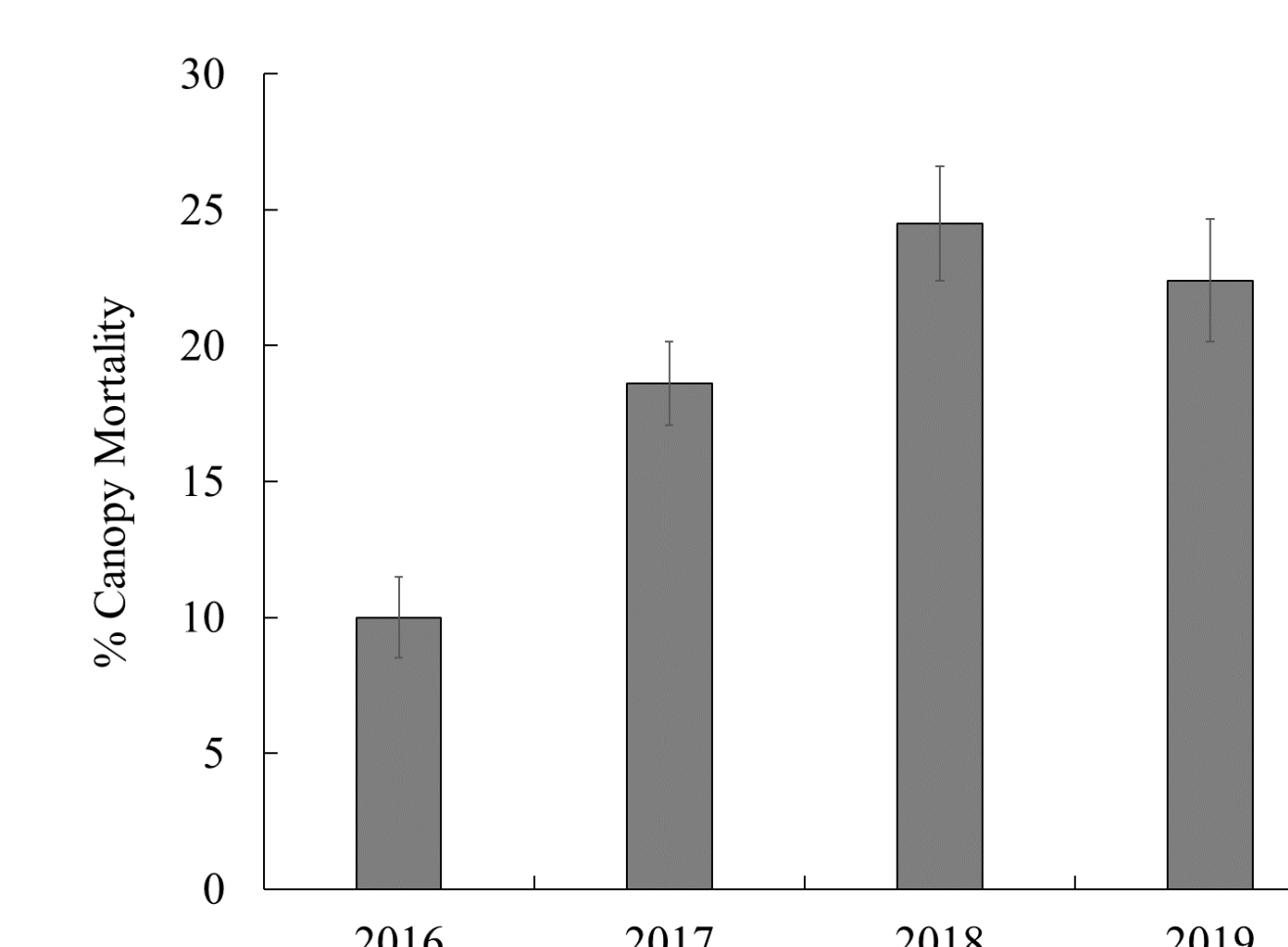
**Figure 2a.** The rapid increase and gradual decrease of tamarisk beetle (*Diorhabda* spp.) abundance across our study reach from 2015–2019.



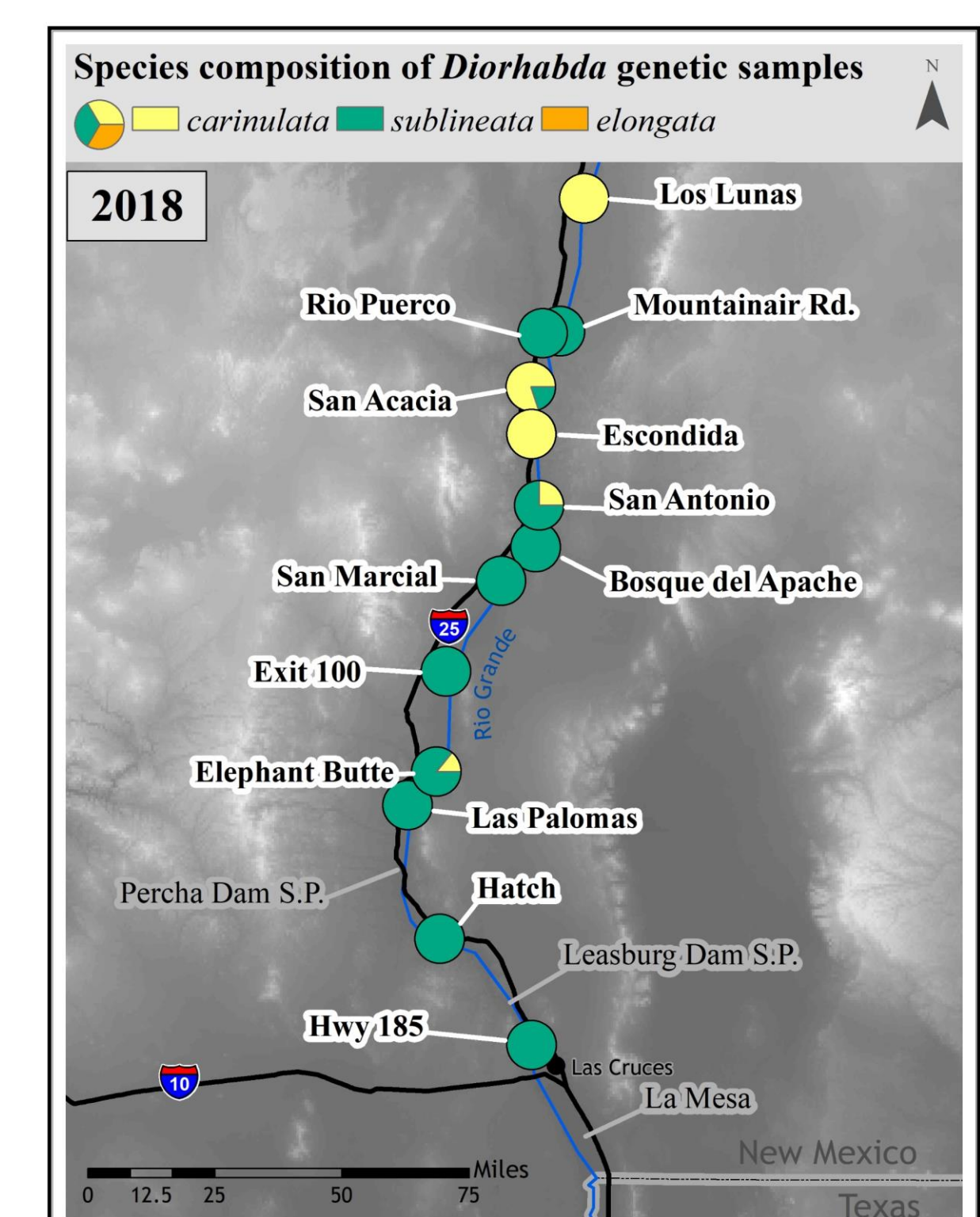
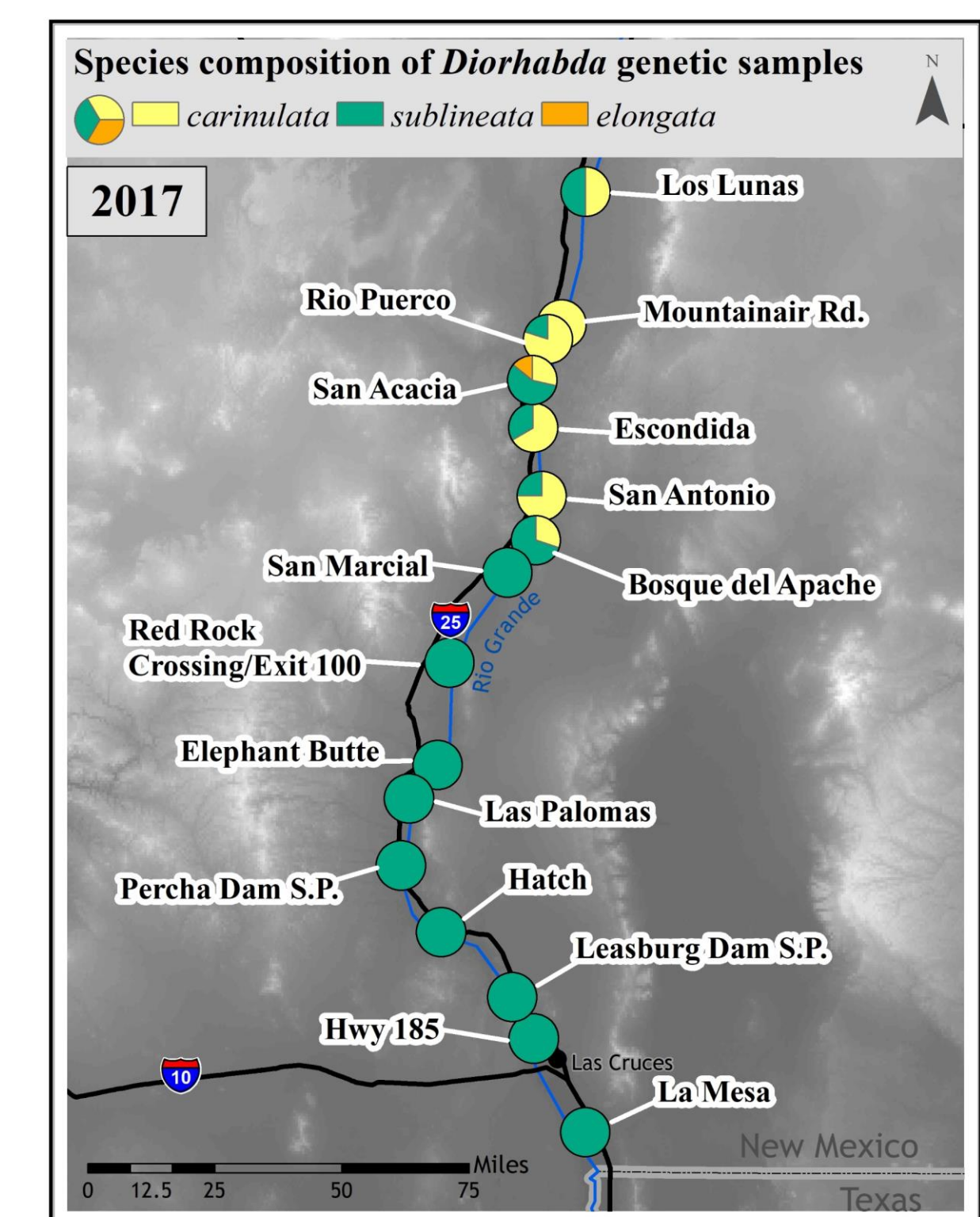
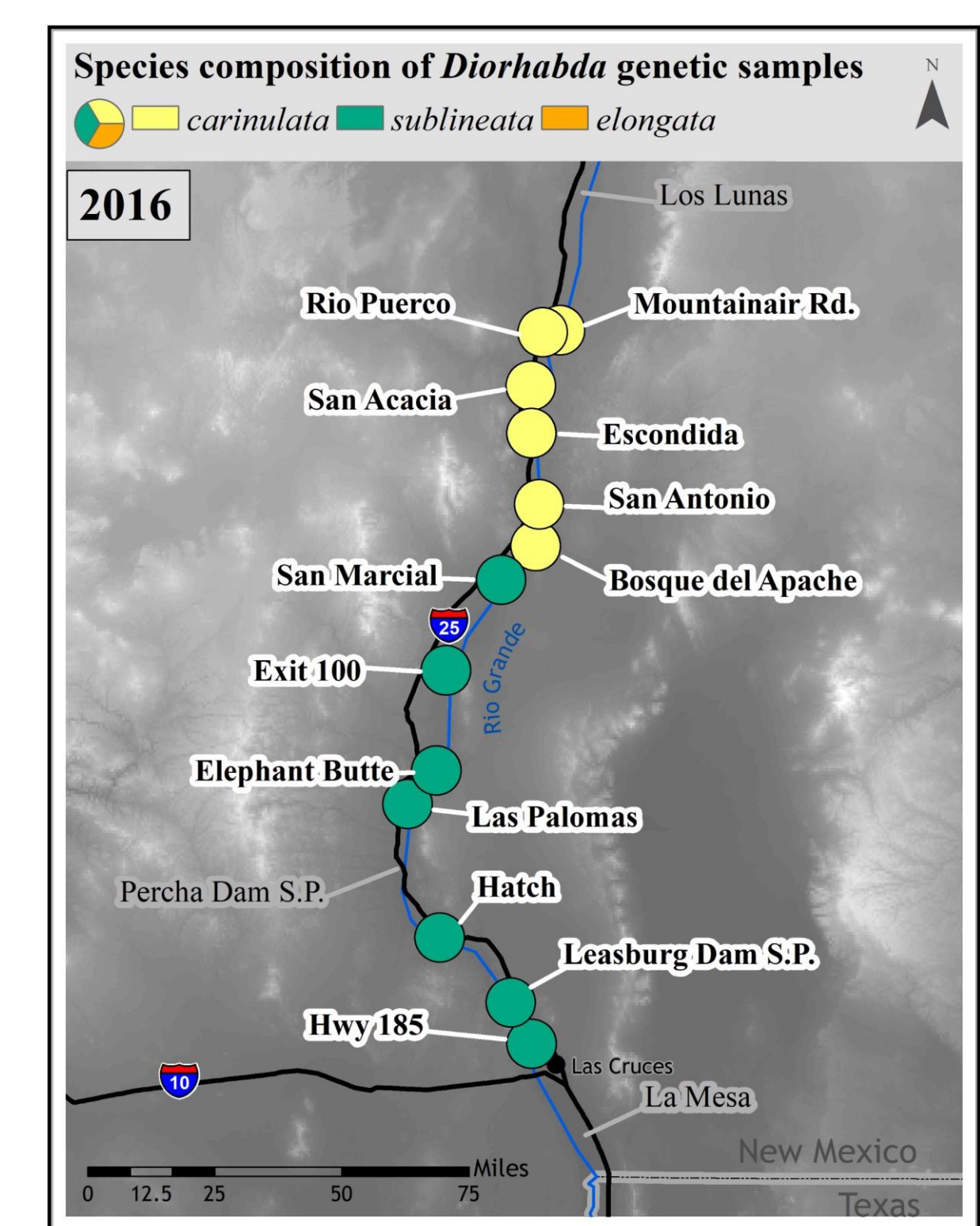
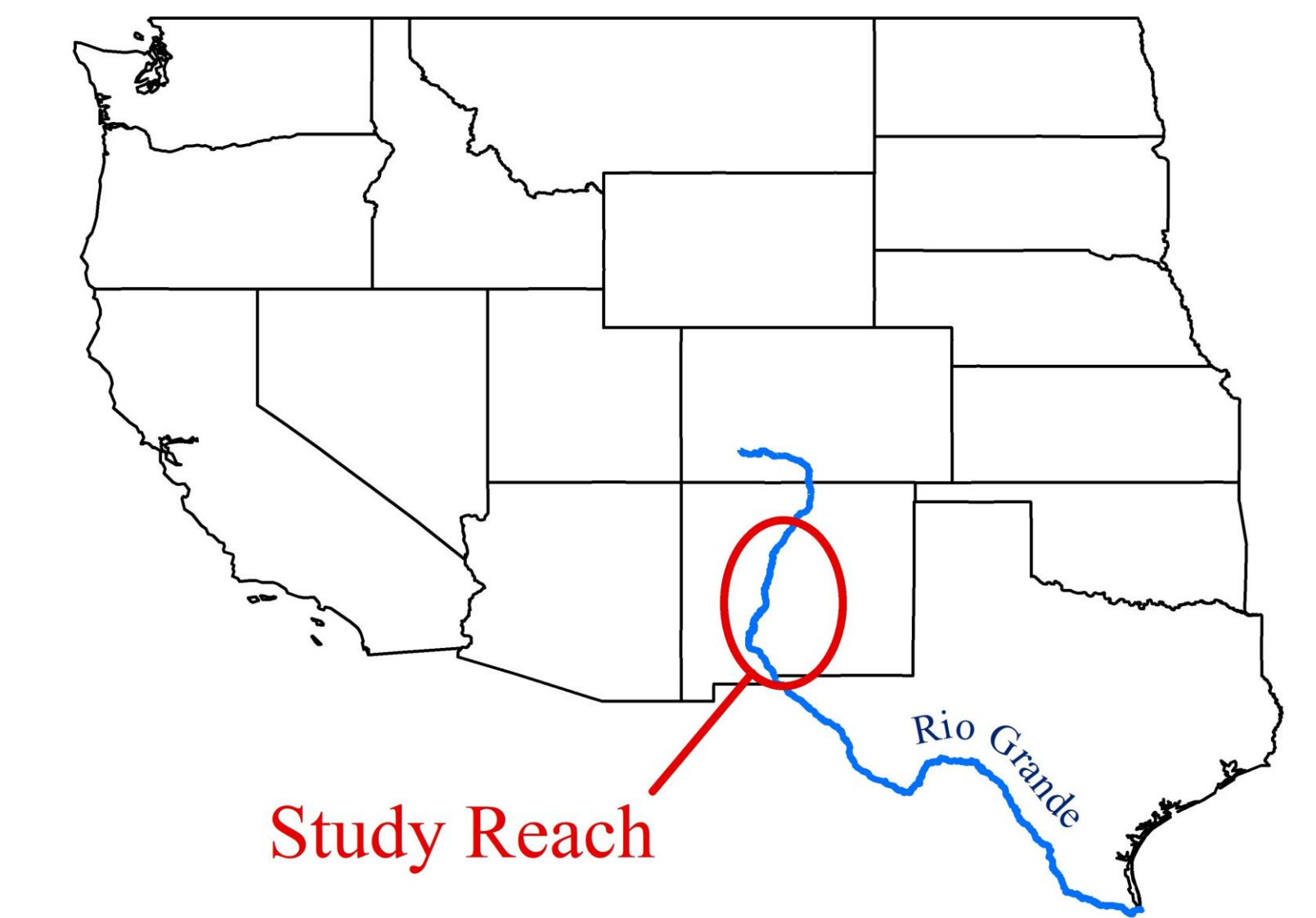
**Figure 2b.** The rapid increase and gradual decrease of tamarisk (*Tamarix* spp.) defoliation across our study reach. Defoliation trends matched the changes in tamarisk beetle (*Diorhabda* spp.) abundance.



**Figure 3.** The negative linear correlation between the percentage of a tamarisk's (*Tamarix* spp.) canopy flowering and the percentage of its canopy that is defoliated, found on tamarisk across our study. When tamarisk are defoliated by even 10% the amount of flowers produced drops by half.



**Figure 2c.** The gradual increase in tamarisk (*Tamarix* spp.) canopy mortality following increased defoliation beginning in 2016.



**Figure 4.** Genetic results of tamarisk beetles (*Diorhabda* spp.) collected along our study reach from 2016–2018. Based on mitochondrial CO1 gene the most common two species are *D. carinulata* and *D. sublineata*. RADseq data (not shown) suggested the presence of DNA markers of all four species in some hybrids in di-specific or tri-specific combinations.