FACTORS INFLUENCING THE FAUNAL RECOLONIZATION OF RESTORED THORNSCRUB FOREST HABITATS

A Thesis

by

AUDREY J. HICKS

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COMMITTEE MEMBERS

Dr. Christopher Gabler
Chair of Committee

Dr. Frederic Zaidan
Committee Member

Dr. Karl Berg
Committee Member

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ABSTRACT

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Tamaulipan thornscrub forests have high ecological and economic value, yet over 90% of these forests have been lost, primarily due to agriculture and urban expansion, and they remain threatened, making them a conservation hotspot. For decades, federal, state, NGO, and corporate entities have been acquiring land and actively or passively restoring these forests, but results have been mixed and seldom monitored. This study characterized and quantified faunal communities of restored thornscrub forest habitats in south Texas and examined the relationships between restored faunal communities and key site characteristics and environmental factors. We surveyed and analyzed mammals, birds, Lepidoptera, and herptiles within 12 restored sites in the eastern Lower Rio Grande Valley. Results indicated that if actively restoring a site, efforts towards invasive plant control, fostering native plant diversity, and ensuring there is a nearby water source are likely the most practical steps that can be taken to encourage faunal recolonization.

DEDICATION

I’d like to dedicate my thesis to my son, Peregrine, who accompanied me on every field visit.

ACKNOWLEDGMENTS

I am grateful to the professional and technical support provided by Dr. Christopher Gabler. Additionally, I thank Mitch and Ernesto for their support in scouting sites and providing me with access. I thank Dr. Frederic Zaidan for sparking my interest in herpetology and teaching me identification skills. I also want to acknowledge and thank Andrea, Jerald, and William for their invaluable help with my fieldwork.

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CHAPTER I

INTRODUCTION

Habitat loss is one of the leading causes of the loss of biodiversity and ecosystem function worldwide and is occurring at an alarming rate due to human activities such as urbanization and the expansion of agriculture. Forests, which are home to about 80% of the earth's terrestrial biodiversity, have especially suffered. Since 1990, an estimated 420 million hectares of forest worldwide have been lost through conversion to other land uses (FAO and UNEP, 2020).

The Lower Rio Grande Valley, a region spanning the border of Texas (Ricketts and Imhoff 2003) and Mexico in a floodplain of the Rio Grande River, has seen high rates of deforestation and land conversion over the past century, primarily due to agriculture and expanding industrialization and urbanization (Leslie Jr. 2016). This region contains many different biological communities, but one of particular importance is Tamaulipan thornscrub forests, a plant community usually found in clay soils on gently rolling to nearly level sites, sometimes interspersed with calcareous ridges or low lying drainages and bottomlands (Elliott 2016). Tamaulipan thornscrub forests are one of the most biodiverse habitats in the U.S., boasting around 1,200 plant species, 530 bird species, and 300 butterfly species ("Rio Grande Valley" 2022), and this abundance supports an estimated $300 million per year ecotourism industry in the region (Mathis et al. 2004). These forests also sustain several endangered species of flora and fauna, including *Leopardus pardalis albescens* (northern ocelot), *Falco femoralis septentrionalis* (northern aplomado falcon), *Astrophytum asterias* (star cactus), and *Ayenia*

limitaris (Texas ayenia) (Leslie Jr. 2016). According to the U.S. Fish and Wildlife Service, only 5% of the native landscape remains on the lower river and its nearby reaches.

Ecological restoration, a process that helps the recovery of an ecosystem that has been degraded, damaged or destroyed, has become a key strategy in combatting habitat loss around the world (Gann et al. 2019). In fact, the 10-year period from 2019 has been declared the decade of ecosystem restoration (Lindenmayer 2020). Ecosystem restoration has the potential to reverse forest clearance and desertification, slow biodiversity loss, sequester carbon, improve air quality and other important services (Perring et al., 2015). It can generally be classified into two types according to the strategy used: passive restoration, which allows for unassisted natural succession and involves minimal intervention, and active restoration, where restoration activities such as planting native species or removing invasive species are implemented to accelerate the recovery of the ecosystem (Alanís-Rodríguez et al. 2021). Restoring an ecosystem is a complex task that requires careful planning, an in-depth understanding of the ecosystem at hand, and often requires a lot of time and resources.

Since the 1980s, federal, state, NGO and corporate entities have been working to reverse the loss of Tamaulipan thornscrub by acquiring properties that had been converted to farmlands or rangelands, then taking measures to return those areas to as close to the structural and functional state of reference conditions as realistically possible through either passive or active restoration. Following acquisition by USFWS or TPWD, land was sometimes simply protected, allowing for unassisted regeneration, while in other cases the land was actively planted with native seeds or seedlings. More than 16,000 acres have been seeded, planted, or managed at great cost and through a great deal of labor, and more have been set aside and protected to allow for natural generation (Dale and Wahl-Villarreal 2021). In the majority of cases, however, the focus

on maximizing acres restored has meant that there have been insufficient resources to allow for monitoring following the initial restoration efforts. This lack of monitoring has made it challenging to evaluate the success of restoration efforts of Tamaulipan thornscrub and identify which methods of restoration have been most effective. Many important questions remain unanswered. Do tracts that were actively restored have greater animal abundance or diversity than tracts that were passively restored? How does the degree of isolation or size of the restored tract influence restoration outcomes? Answers to such questions are needed to identify the most effective restoration strategies going forward.

There is not consensus, however, on the best way to assess restoration outcomes. Many different principles and conceptual frameworks have been put forth to guide such assessments (Perring et al., 2015, Suding et al., 2015, Gann et al., 2019), but a key assumption is that successful restoration will provide favorable conditions for the native biota (Block et al. 2001). The Society for Ecological Restoration has produced a list of ecosystem attributes as a guideline for measuring restoration success, emphasizing an absence of threat, physical conditions, species composition, structural diversity, ecosystem function, and external exchanges (Gann et al. 2019). The Field of Dreams hypothesis posits that "if you build it, they will come", indicating that the rehabilitation of physical habitat diversity will lead to the restoration of biological communities (Palmer et al. 1997), and advocating for a focus on restoration of plant communities. Others advocate, however, that wildlife monitoring should play a central role in any restoration program with conservation objectives to ensure restoration efforts are actually achieving their targeted goals and to allow for adaptive management when threats to restoring systems emerge (Sinclair et al. 2017).

In the Lower Rio Grande Valley, very few studies have been conducted that aimed to evaluate restoration outcomes, and they have generally focused on woody plant communities. Ewing and Best, for example, evaluated the performance of woody species in planted sites within the first decade of planting and compared those to a remnant community, resulting in a list of the canopy cover and survival rate of common woody species, intended to inform future planting efforts (Ewing and Best 2004). Another study by Perez et. al measured the regeneration of woody species in abandoned plots with varying land-use histories, including clear-cutting, agriculture, and livestock production, discovering that the area of intensive production of livestock showed the lowest values for abundance and species richness (Pérez et al. 2013). In another study, the structure and composition of woody plant communities of the Tamaulipan thornscrub was compared between assisted/unassisted ecological succession and control areas. Alanís-Rodríguez et. al (2021) found significant differences in richness and diversity between assisted and unassisted plots, with assisted plots having much higher values.

Other studies examined passive restoration of Tamaulipan thornscrub by examining plant communities after various disturbances. For example, one examined thornscrub plots after livestock have been removed and discovered that *Vachellia farnesiana* (Huisache) and *Prosopis glandulosa* (Honey Mesquite) were the dominant species after passive regeneration (Pequeño-Ledezma et al. 2012). A similar study examined passive regeneration of Tamaulipan plant communities after fires, which led to an understanding of which species held greater ecological weight in the study area and which were pioneers after that specific type of disturbance (Alanís-Rodríguez et al. 2020). Alexander et al. (2016) evaluated the growth and survival of seedlings after being planted and their ability to overcome common stressors, discovering that thornscrub seedlings grew best after a single prescribed fire and when planted in shelter tubes.

All of this research contributed to the present understanding of which species should be planted and under what conditions in order to optimize thornscrub restoration. What these studies did not investigate, however, was the faunal re-colonization of areas that were undergoing restoration once they had been restored. Animals are a key component of these ecosystems and are the rationale for the mission of many managing agencies like TPWD and USFWS. To the best of our knowledge, no multi-taxa studies have been conducted to quantify and characterize the wildlife communities present in Tamaulipan thornscrub forests after restoration efforts. Surveying multiple taxa of wildlife is important because some studies show that just surveying for indicator species results in an inaccurate picture of wildlife communities because different faunal groups may return at different rates and are selecting sites based on different factors, so might not ever show up (Nichols and Nichols 2003). One study which evaluated the efficacy of multiple-species monitoring found that the approach could "provide a robust characterization of the sum total of all vertebrate species" and highlighted that "any effort that relies solely on a small set of indicator species will be subject to skepticism given the history of misuse, overuse, and poor performance of the indicator concept" (Manley et al. 2004). Another study, which evaluated the impact of habitat modification on biodiversity, emphasized the need to survey different taxonomic groups to understand whether they respond in similar ways (Schulze et al. 2004), and we feel that such an understanding is particularly important in our study region. For these reasons, we surveyed the community composition of key animal taxa, specifically mammals, birds, Lepidoptera, and herpetofauna, and quantify the richness, abundance, and diversity of these focal taxa at 12 different thornscrub sites around the Rio Grande Valley.

Assessing restoration outcomes is important, but it is also important to understand what influenced those outcomes because that information can be used to inform restoration efforts

going forward. Examining the relationships between animal communities and environmental and geographic factors can help elucidate the effects those facts can have faunal community composition and traits. Grman et al. (2013) posit that there are four classes of drivers that affect a restored community; management decisions, site characteristics, landscape context, and historical factors. Restoration actions like planting seedlings may be overwhelmed by site attributes unrelated to the restoration effort, such as the soil conditions (Grman et al. 2013). Another study conducted in Canada's boreal forest found that the soil profile could have a profound effect on early forest establishment in reclaimed areas (Stack et al. 2020). Gabler and Siemann (2012) found that reinvasion of exotic plants, which may be driven partially by exotic propagule abundance, can strongly influence restoration outcomes. In a study that focused on the recovery of plant life, Suganuma et al.(2018) found rainfall, soil fertility and invasive grasses to be significantly influential to understory richness and density. Analyzing the relationships between environmental factors and animal communities can shed light on restoration outcomes and contribute to management decisions when restoration is undertaken.

The objectives of this study are to (1) characterize and quantify faunal communities of restored thornscrub forest habitats in south Texas, and (2) better understand the relationships between faunal communities in these restored sites and key site characteristics, such as habitat patch size, time since restoration began, restoration method (passive versus active), edge to interior ratio, degree of isolation, and characteristics of the local plant community including the diversity and richness of ground cover, understory and canopy levels in addition to factors like soil temperature and moisture. By selecting restored sites that vary in these factors, we aim to detect significant relationships and evaluate how these various factors influence the recolonization of different animals after restoration.

We know from previous studies in the LRGV and other research conducted in various habitats that site characteristics and environmental factors can impact the recolonization of wildlife. In a review of 83 terrestrial restoration studies, it was found that as restorations aged, mean biodiversity increased (Atkinson et al. 2022). This suggests that older sites would have more faunal diversity than sites that were more recently restored, but the relationship between time and diversity is unlikely to be that simple, because the time it takes for wildlife to recolonize a restored site can vary between faunal groups. For example, one study found that generalist foraging mammals recolonized rapidly while reptiles took much longer (Nichols and Nichols 2003). Another long-term study which examined the recolonization of post-mining forests found that there can be unidirectional (decreasing gradually over time) and dynamic (fluctuating over time) filters that impede wildlife recolonization and affect population persistence at different times for different taxa (Craig et al. 2018). Gabler and Stilley (2021) examined plant and Lepidoptera communities in human impacted habitats in the eastern LRGV, but this was not done in a restoration context and did not consider time since restoration began. Nevertheless, they found that patch size, edge to interior ratio, and various aspects of plant communities influenced Lepidoptera community composition, richness, abundance, and diversity. Though we expect that community composition will be impacted by the time since restoration, we expect that other site characteristics will play a role as well.

Many studies have demonstrated how lack of connectivity (what we refer to in this study as “degree of isolation”) can impact the composition and abundance of wildlife. Isolation can restrict the movement and dispersal of wildlife, creating sinks around reserves (Newmark 2008). It can also result in demographic effects or increased genetic differentiation between neighboring populations (Uezu et al., 2005, Amos et al., 2014). Insular or island biogeography is an entire

field of study itself that examines the effects of isolation of animal communities. With that said, some research has found that the degree of isolation of a patch can be a poor predictor for occupancy of most species and that the properties of the intervening matrix may be of more importance (Prugh et al. 2008).

Isolation and patch size are site characteristics that are often studied together. Whether a single large patch or several smaller patches of equal size more effectively conserves greater species diversity and richness has been debated for decades; however, the current consensus is that it simply depends on the situation and goals of the project (Tjørve 2010). It may be that the effects of isolation and patch size vary by taxa or even by species; in a study that followed the recolonization of 69 patches by a species of butterfly, Hill et. all (1996) found that larger patches were more likely to be colonized, whereas, in a study that examined bird populations in patches within logged areas, Lindenmayer et. al (2015) found that patch size had no significant effect on bird species richness. By surveying multiple taxa in our restored patches, we will be able to examine similarities and differences in the impact of patch size across taxa.

The method of restoration (active versus passive) could also affect faunal recolonization, though research varies widely on this front. Trujillo-Miranda et al. (2018) found that tree richness and diversity in both active and passively restored sites rapidly recovered (in contrast to similar studies), and they posited that this difference was likely due to the sites' proximity to propagule sources. In a study that compared wildlife responses to different treatments of dune restoration, however, Russell et al. (2009) found that diversity and abundance of wildlife was greater in the actively restored areas. A meta-analysis of over 150 studies on the effectiveness of active versus passive restoration of forests found that simply ending the land use, whether the plot was formerly mined, farmed, or logged, was sufficient for most forests to recover and that

actively restoring these plots, primarily by planting trees (as in the case of our study sites), did not result in consistently faster or more complete recovery than passively restored sites (Meli et al. 2017).

In addition to these site characteristics, it is important to explore the relationships between animal communities and environmental variables, like distance to water sources. Both permanent water sources and ephemeral water sources can impact animal communities; riparian zones frequently support disproportionately high species richness and abundance for many faunal groups (Catterall et al. 2012), and ephemeral wetlands can contribute to landscape connectivity (Allen et al. 2020) and can enhance vertebrate activity and diversity in certain landscapes (Dixneuf et al. 2021). Understanding animal community relationships with plant diversity and richness at the ground, understory, and canopy levels is also important, as all have been documented as predictors of animal community composition (Provete et al. 2014, Brunbjerg et al. 2018, Bailey et al. 2019, Coddington et al. 2023). Soil moisture and temperature will also be examined, which are intricately linked to plant cover (Clinton 2003) and can therefore impact some animal communities. Finally, relationships to exotic cover will be analyzed. A literature review of 287 publications on the subject found that the impact of invasive plant species is strongly context dependent but can affect species richness and diversity (Pyšek et al. 2012).

We hypothesize that many of the site characteristics and environmental factors discussed above will influence the community composition, abundance, and/or diversity of restored animal communities; however, it is unclear which factors will have the strongest effects, and how their effects will vary among different taxa and within different ecological contexts. To improve our understanding of animal communities in restored Tamaulipan thornscrub forests and how site

characteristics and environmental factors influence those communities, this study aimed to (1) quantify the community composition of four key animal taxa (mammals, birds, Lepidoptera, and herptiles) observable within 12 restored Tamaulipan thornforest habitat patches; and (2) examine and quantify the relationships between the community composition, richness, abundance, and diversity of each taxa (and the ensemble community) and key habitat characteristics and environmental variables, including patch size, time since restoration, interior to edge ratio, degree of isolation, and restoration method (active vs. passive). Our findings will help inform future restoration and management efforts, potentially by informing decisions about land-acquisition and the methodological approaches to restoration, as well as by producing recommendations for promoting faunal return to restored sites.

CHAPTER II

METHODS

Site Selection

This study was performed at 12 different field sites located around Cameron County, Texas. The goal when selecting sites was to represent variation in time since restoration began, restoration method, patch size, and degree of isolation. Given the ubiquity of human impacts and uncertainty regarding land use history in the LRGV, no clearly "pristine" sites were available within the focal region that could be used as traditional reference sites (Leslie Jr. 2016, Stilley and Gabler 2021). However, one site (Goat Island) is notable in that its land use history includes at least 77 years of protection from most human impacts – though it has been hunted regularly in that time – and it may have experienced minimal agricultural use prior to 1946. All other study sites are known to have been previously used heavily for agriculture but were acquired for restoration (either passive or active) between 15-70 years ago. Of the 12 sites selected, six are owned and managed by the Texas Parks and Wildlife Department (TPWD), five by the United States Fish and Wildlife Service (USFWS), and one by the University of Texas Rio Grande Valley.

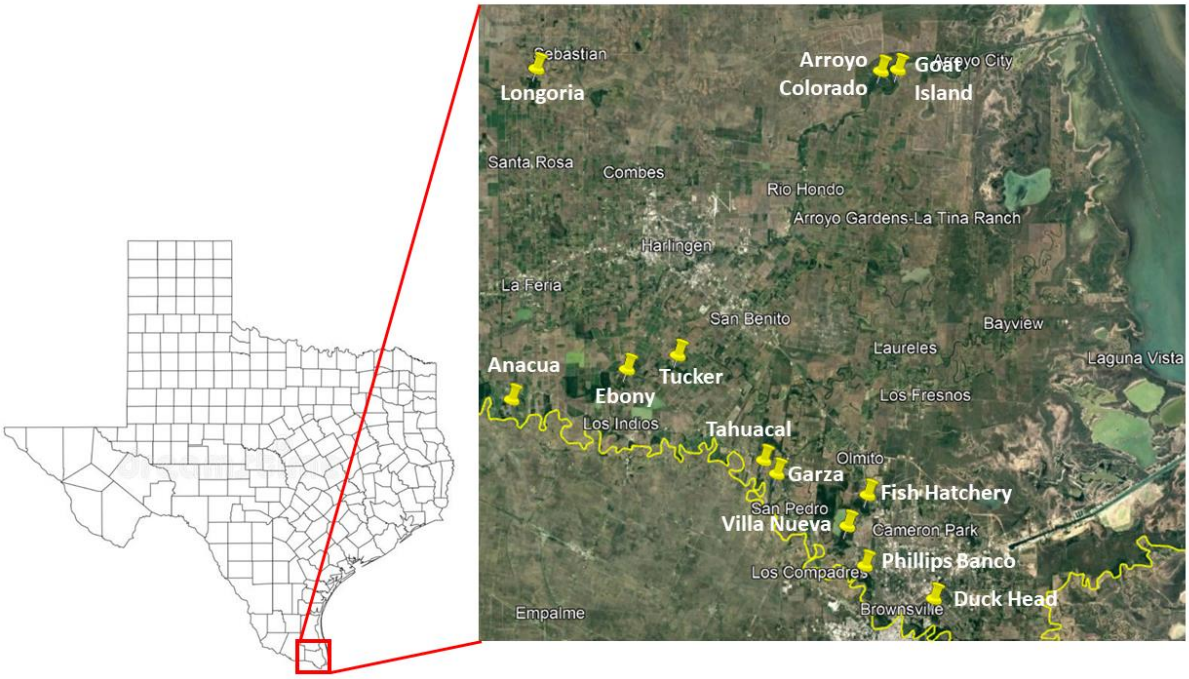

Figure 1. Locations of the 12 study sites used for this study. All are located within Cameron County, Texas, USA.

Although the exact dates of when each tract of land was acquired and/or planted were not always available, estimates to at least the decade were always provided by land managers and considered sufficiently accurate. Regarding restoration method, we were able to divide sites into two groups based on the primary method of restoration, which was not necessarily the only method of restoration. For example, two sites had very small sections planted with native tree seedlings, while the majority of the site was allowed to naturally regenerate. These sites were categorized as passively restored, since that was the primary method. To determine the degree of isolation for each habitat patch, we calculated the percentage of the surrounding area within a radius of 1 kilometer from the center of the patch that was not composed of thornscrub habitat using aerial images from Google Earth Pro version 7.3 (2022; Google LLC, Mountain View, CA, USA). The higher the percentage, the more isolated the patch.

We quantified patch size, degree of isolation, and time since restoration for each site from a larger pool of about 35 candidates within Cameron County and identified whether each site was primarily restored through planting of seeds or seedlings (actively restored) or primarily through natural regeneration (passively restored). We then strategically selected the 12 sites that maximized the spread and roughly even distribution of values across these focal metrics in order to ensure variety and a sufficiently balanced design. We did this by first finding the range in values for each focal factor among the larger pool of available sites, then dividing those range values into three arithmetically equal segments and scoring each candidate site for each factor on a scale from 1-3 based on whether its value was in the bottom third of the range of observed values, the middle third, or the upper third, respectively. Final site selection aimed to minimize correlation between these factors by including an equal number of sites (4) from each scoring group for each focal factor, and by choosing sites so that sites with the same score for one focal factor had a spread of scores for the other focal factors. However, this was not entirely possible given the choices available. For example, the largest patches of available deforested land were generally the first to be restored, and patches acquired and restored in later decades tended to be smaller and more likely to be actively restored. Thus, although we deliberately maximized the variability across our set of site characteristics, some criteria were unavoidably partially confounded due to our limited options.

Table 1. Summary of focal site characteristics for our 12 study sites. The scores represent the ranking system used to maximize spread of values and minimize correlation between factors in each category.

		Time since restoration (approx)		Isolation		Patch Size	
Site Name	Restoration Method	Years	Score	% of area within 1km that is not thornscrub	Score	Size (Ha)	Score
Goat Island	None	77+	3	53%	1	104	3
Arroyo Colorado	Mostly natural	37	2	78%	2	175	3
Longoria	Mostly natural	67	3	85%	3	122	3
Ebony	Natural	37	3	23%	1	89	2
Tucker	Natural	67	3	59%	2	72.7	2
Anacua	Natural	37	3	81%	3	56.4	2
Tahuacal Banco	Seedlings	15	1	49%	1	5.93	1
Phillips Banco	Seedlings	29	2	61%	2	28.2	1
Garza-Cavazos	Seeds	28	2	48%	1	4.51	1
Fish Hatchery	Seedlings	20	1	92%	3	18.4	1
Villa Nueva	Seedlings	18	1	72%	2	18.2	1
Duck Head	Seedlings	32	2	88%	3	26.8	1

Avian Surveys

Avian richness and abundance are typically measured by conducting either line transects, point-count surveys, or area searches. Each method has its own advantages and disadvantages, sometimes depending on the type of habitat in which the survey is conducted (Pascoe et al. 2019). Some studies found that line transects yielded greater richness and abundance (R.R. Wilson et al., 2000), whereas others found that point-counts yielded higher quality data (Cumming and Henry 2019). We elected to conduct point-count surveys during our research, primarily because attempting to walk a straight line through thick thornscrub vegetation was not always possible and would, at the least, make it challenging for the observer to be looking and listening with their full attention. Standing still while conducting point-counts also allowed a

recording device to be used so that any uncertain identification could be checked and confirmed after the survey was finished.

At each site, we established three sampling points, dispersed throughout each site, and separated by at least 200 meters from one another to ensure that sample points were independent (Huff et al. 2000). Sampling points were selected based on accessibility and distance from one another. We conducted two point-count surveys at each point, one in May and one in June of 2022. It was important to conduct at least two surveys per point, as some studies have found that conducting only one survey results in many missed birds (Dobkin and Rich 1998). We chose to survey bird populations during breeding season because (1) more birds would be vocalizing, increasing chance of detection and (2) fewer migrants would be passing through, which narrows the focus to resident birds. All surveys were conducted before 10:30 AM in order to avoid high temperatures. If it was raining or if sustained winds exceeded 30 km/h, the survey was delayed to another day in order to optimize detection. Because all 3 points at each site were surveyed on the same day, during the second survey the order in which the points were surveys was reversed to account for changes in abundance due to time or temperature.

Point-count surveys are typically conducted as either fixed-radius surveys or unlimited radius surveys, each with their own advantages. Unlimited radius methods can result in more species detected but can also hinder comparisons of relative abundance estimates among sites and habitats due to factors like weather, vegetation, saturation effects, and observer limitations (Ralph et al. 1995). Following the protocol outlined by Ralph et al. (1993, 1995a), all birds were recorded, regardless of distance, but birds detected within an estimated 50 meters of the sampling point were recorded separately from birds detected beyond an estimated 50 meters. These

distances were gauged by sight and sound and therefore were imprecise, but because the same surveyor conducted all surveys, estimates were made consistently.

The standard time intervals for conducting point-count surveys are 3-minutes, 5-minutes, 10-minutes, and 15-minutes. One study found that on average, 55 percent and 82 percent of all initial species detections occurred within the first 5 minutes and first 10 minutes, respectively, of 15-minute counts, regardless of the time of morning or the use of aural stimuli (Ralph et al. 1995). Again, following the protocol set out by Ralph et al. (1993, 1995a), the time spent at each point-count station was 10 minutes and the data was separated into those individuals first seen or heard in the intervals 0–3, 3–5, and 5–10 minutes. This method allows data to be comparable to other surveys of various intervals (Matsuoka et al. 2014). In our analysis, we used the birds counted within the 10-minute time frame.

Throughout the surveys, two different tools were used to detect species presence. First, the surveys were recorded with a Zoom H1n Portable Recorder (Zoom H1n, Zoom, New York), allowing us to later review for species not detected during the survey. Secondly, the application BirdNET was activated throughout the entirety of each survey so that identifications could be double-checked in real time in the case of uncertainty (Kahl et al. 2022).

Medium to Large Mammal Surveys

Estimating population sizes of large- and medium-sized mammals can be difficult due the nocturnal habits of many species and general tendency to avoid human presence (Gonthier and Castañeda 2013). Camera traps are a common non-invasive tool that has been used to collect data on mammal occurrence, abundance, density, and habitat use (Assou et al. 2021). In our study, three camera sampling points were centered on the same sampling point locations used for

bird surveys, each along or near a visible game trail or clearing in order to enhance visibility, when possible. To ensure that the camera events were independent, photographs of the same species captured within 60 minutes of each other by the same camera will be treated as a single event, unless the number of individuals in the picture increased (Assou et al., 2021). For each camera event, the date, time of day, species, and habitat type were recorded. Cameras were checked and SD cards replaced every 2-4 weeks for a period of 3-4 months (April-August).

Cameras were placed approximately 1.0 meter off the ground and at least 200 meters apart from one another. The height and positioning of our camera traps may bias data towards medium- to large-mammals, but this is acceptable for our study, as our objective is not to exhaustively inventory all mammals present, but rather to compare mammal communities across sites.

To analyze mammal photographs, we used a collection of programs called CameraSweet (2022; Small Wild Cat Conservation Foundation, Corrales, NM, USA). We first manually sorted our photographs into those that had mammals in them and those that did not. Then we sorted the mammal photos by species, and finally by the number of a given species in each photograph. We then used the ReNamer program version 6.8 to label the photos with their date and time. We then utilized the DataOrganizer program version 4.5 to produce a file showing camera trapping days per camera, the number of independent captures per species, activity patterns, and much more. An independent capture meant that if the same species was captured within a 60-minute period, it was not counted. The number of trapping days per point ranged from 28-118 days, so we normalized our mammal abundance values based on sampling effort by dividing the number of independent captures by the number of trapping days to produce an average daily capture rate

and multiplying that value by 30 to produce values that represented the average number of independent captures at each point per 30-day period of sampling.

Herpetofauna Surveys

To survey reptiles and amphibians, we used artificial cover objects (ACOs), which are objects like plywood or tin which are laid out to serve as cover for target species. This method can be as accurate at detecting activity and abundance of some species as pitfall drift fences (Sutton et al., 1999), in which animals are funneled towards a pit trap that they fall into and where they usually remain until a surveyor removes them, but ACOs do not restrain the animals that use them. Mortality is therefore less likely when using ACOs, compared to some other techniques (Hampton 2007). Studies in various parts of the world have found that different species have different preferences for ACOs, likely influenced by factors such as the type of ACO, ACO age, how often ACOs are surveyed, vegetation, habitat, weather, predators, and more (Lemm and Tobler 2021). The size of the ACO may impact the use of artificial cover by some species while other species may use cover boards regardless of size (Lemm and Tobler 2021). However, the purpose of this study was not to be exhaustive in cataloguing every reptile and amphibian present, but rather to make an equal comparison across sites, so it was more important that ACOs were installed in the same way and in the same types of places across sites.

For our survey, we installed 3 ACOs at each of the 3 points in each site (9 ACOs per site). The ACOs were cover boards made of untreated and unpainted plywood that was 9.5 mm thick. At each point, two boards were 60 × 60 cm and one was 120 × 60 cm. We used two different size boards in case the size of the ACO mattered for different species. We elected to use plywood instead of metal, like in some other studies, because it is an insulating material that

prevents heat transfer; temperatures commonly reach thermal extremes during May-June in Cameron County, and the aim was for boards to serve as a refuge from the heat. The installation of the cover boards involved placing pieces of plywood horizontally under various degrees of canopy coverage within 10 meters of the sampling point. Canopy cover can influence the effectiveness of ACOs as it filters some solar radiation and can help maintain a more stable ambient temperature (Hampton 2007). One study found that the odds of detecting herpetofauna were the best in open canopy sites compared to those with high amounts of canopy cover, because larger-bodied snakes could thermoregulate more quickly under cover objects in open canopy sites with warmer temperatures (Hampton, 2007). In our study, we selected sites to capture variation in the amount of canopy cover above each board in order to increase the likelihood of species detected.

Because reptiles and amphibians tend not to immediately utilize newly installed cover objects, a certain period of time must pass before they can be accurately compared. We installed the cover boards and the left them undisturbed for at least 3 weeks before data collection began (Hampton 2007). ACOs were checked every 2-4 weeks between April and August of 2022. To check underneath each cover board, it was slowly lifted, and a photograph was taken of each species present. Afterwards the cover board was slowly set back down to avoid harming any animals.

After two months of checking cover boards, however, we had very few observations of herpetofauna underneath. For that reason, we added an additional herpetofauna survey approach in order to supplement the data. We elected to perform two time-constrained area searches at each of the three established sampling points at each study site, one in July and one in August. A time-constrained area search entails actively searching for animals in a given area for a pre-

defined amount of time (Eekhout 2010). We chose this method of surveying instead of line-transects due to the difficulty in walking a straight line in thick thornscrub and to make more comparable to bird surveys. One of the main limitations of this method is that the results of area searches are highly influenced by environmental factors such as time of the day, season, and weather (Eekhout 2010). For that reason, we tried to conduct these surveys within a specific timeframe at each site and under similar weather conditions within a one-month period. It was important that equal effort was expended in each area searched, and we measured this by tracking the time each researcher spent searching (Corn and Bury 1990). For all taxa, we tried to minimize seasonal variability by performing all surveys in the late spring and summer, but some important ecological and environmental factors (e.g., migratory activity and climate) naturally and inevitably varied among sampling periods and thus sampling of different taxa. However, because we varied the order in which we visited sites for each round of sampling and pooled our data from different surveys for each sampling point or site, the importance of these temporal differences for our spatial (point- and site-based) comparisons is minimal, especially for a given taxonomic group.

To conduct the area searches, two surveyors searched an area within a radius of approximately 50 meters of each point for 15 minutes. Any debris or rocks that could provide cover for herpetofauna were briefly removed, leaf litter was searched, and trees were scanned for arboreal or climbing species. If a specimen was seen, it was recorded (not captured) and identified immediately. These searches were performed twice at each point, for a total of one hour of searching per point.

Lepidoptera Surveys

There are two different common methods for surveying Lepidoptera; walking transects and setting bait traps. In one study that compared the two methods, they observed far fewer specimens but observed more species, genera, and families using "zigzag walks" (meaning zigzagging along a transect as opposed to walking straight) than bait traps, (Jakubikova and Kadlec 2015). For our survey, we decided to use bait traps because, although they will be biased towards certain families of Lepidoptera, it is a more conductive method for identification of species. Walking transects depend on the observer's knowledge of Lepidoptera species by sight or on their proficiency at capturing Lepidoptera by net, which can be difficult in thick thornscrub, whereas bait traps allow the observer to examine and photograph each specimen, increasing the likelihood of correct identification. These surveys therefore primarily compared abundance and diversity of Lepidoptera that are attracted to fruit.

In our study, we conducted butterfly surveys twice at each site, once in May and once in July. We set up the bait traps in the morning and left them up for 24 hours before returning to inventory the individuals captures. Each individual was carefully removed from the trap, photographed, and then released within one minute of being extracted. For our first round of surveys, we used homemade bait traps composed of thin, durable netting with a bowl suspended by a 4 cm rope below the opening (Austin and Riley 1995). The bowl was filled with bait (rotting bananas). The traps were hung from a tree at 1-1.5 meters in height, depending on trees available near the point. Studies show that certain Lepidoptera will be attracted by the fruit to enter the trap by landing on it and then walking in, then when leaving they habitually take flight and are caught in the trap, as opposed to walking back out the way they came (Rydon 1964, Austin and Riley 1995). The trap is set up for only 24 hours and is equipped with food, water,

and shade. If the weather was predicted to be rainy, traps were not set to lessen the likelihood of false zero detections.

The capture rates of the homemade traps were below expectations, so for the second round of surveys we opted to purchase traps that were a similar design, but also included an inverted funnel above the bait bowl and within the netting that was more effective in preventing Lepidoptera from escaping during the 24-hour period. These traps resulted in about 10 times more captures than the first design.

Vegetation Surveys

At each sampling point (3 per site), vegetation was systematically surveyed in two sampling areas using different sampling approaches tailored to different forest layers that together quantified forest structure and plant community composition. These methods allowed us to quantify large canopy layer trees; understory tree, shrub, and climbing epiphytes; and all ground layer vegetation, including low-statured grasses and forbs. Information on soil temperature and moisture was also collected.

These surveys were performed as part of a separate thesis research project led by Jerald Garrett conducted in parallel to this one, so the sampling and analytical methods utilized are not described in detail here. However, we do use some of the data and results from the plant community surveys in this study as part of our analyses and to inform our findings.

Analysis

We normalized any response variables that differed in sampling effort based on the actual effort exerted (e.g., operational days for trail cameras) to ensure values were comparable across sites or groups.

It is well established that environmental factors can influence animal communities, and environmental conditions clearly varied among our sampling points. To allow us to examine the impacts of environmental variables on animal communities and explain variance in our observations not attributable to our focal site characteristics, we used various environmental and geographic metrics measured either *in-situ* at our sampling points or using publicly available GIS data for each sampling point or site by (Garrett 2023) However, not only are there many potentially important environmental metrics, but many of these factors are also often correlated, especially if they are mathematically related (e.g., patch size and edge to interior ratio, or invasive grass cover and the ratio of native to exotic plant cover). Therefore, we conducted a principal component analysis (PCA) using the PCA() function from the 'FactoMineR' package in R to reduce the number of variables to two axes and to help us understand and visualize how different environmental factors were related to one another and how they varied across our study sites and sampling points.

To characterize the observed faunal communities and explore the relationships among species and environmental variables, we first performed separate multivariate analyses for the observed mammal, bird, Lepidoptera, herpetofauna, and ensemble (all groups combined) communities. To do so, we used the metaMDS() function in the 'vegan' package in R (R Foundation for Statistical Computing, Vienna, Austria) to fit nonmetric multidimensional scaling (NMDS) ordinations using Bray–Curtis dissimilarity values. Where necessary, we used relative

abundance values to reduce the stress of the ordination fit to acceptable levels (below 0.2). Except for birds, the observational units for each ordination were the sampling points (n = 36), with abundance values from different individual surveys summed for each sampling point. If a sampling point had no observations for a given taxa (row sum equaled zero), that sampling point was excluded from the ordination so a fit could be achieved. For mammals, two points were excluded (Anacua 2 and Duck Head1). For birds and herptiles, we had to combine the three sampling points for each site and perform the ordination using sites as the observational unit (n = 12) in order to reduce the NMS fit stress to acceptable levels. We did not count birds, so we used the number of surveys during which the species was detected (out of the 6 conducted at each site) as a proxy for abundance for our multivariate analysis. We excluded one site for herptiles (Goat Island) because it had only one observation, and that observation was unique to that site. For Lepidoptera, we had to combine any taxa observed only once with their closest taxonomic relative to reduce fit stress to acceptable levels, but we did so minimally and preserved distinct taxa wherever possible to minimize information loss. No points were excluded for Lepidoptera.

We then used the envfit() function from the 'vegan' package in R to fit relevant environmental variables to our NMS ordinations, including the method of restoration (categorical) and continuous variables for patch size, time since restoration, degree of isolation, interior to edge ratio, canopy cover, soil moisture, soil temperature, distance to permanent water, distance to temporary water, invasive grass cover, understory total cover, canopy density, total plant richness, total plant diversity, ground cover plant richness, ground cover plant diversity, understory richness, understory diversity, canopy richness, canopy diversity, the natural log of the ratio of native to exotic cover, feral hog disturbance and combined exotic cover. For a full list of values and additional details regarding these environmental factors beyond the focal site

characteristics, see Garrett (2023). Hog disturbance was plotted to illustrate key patterns and trends in the observed animal communities but was not included in subsequent PerMANCOVAs (see below), whereas the rest were hypothesized to have influenced or at least been associated with animal community composition and were included in subsequent PerMANCOVAs.

To visualize the results of these ordinations and environmental fits, we used the ggplot2() graphing function in R to plot the values generated by metaMDS() and envfit(). Due to the high number of observed species and environmental predictor variables, we plotted vectors only for those species that most strongly influenced the spread of sites and only for those environmental factors most strongly associated with the spread of sites defined by metaMDS(). We also used ggplot2() to calculate and display 95% confidence ellipses around the centroids (hypothetical average community composition) for the groups of sites defined by our categorical variable for method of restoration (active vs. passive).

To examine the effects of our categorical and continuous environmental variables on community composition, we used the adonis2() function from the 'vegan' package in R to perform a permutational multiple analysis of covariance (PerMANCOVA) for each community. Given the abundance of environmental factors under consideration, careful model selection was necessary. First, we reduced any sets of correlated environmental variables to a single variable by omitting the variables in a correlated set that explained the least variance. We then used the ordistep() function in the 'vegan' package to prune our complex models based on the Akaike Information Criterion (AIC) values of alternative models and thereby remove model terms that explained the least variance and increase the statistical power of our final models. In doing so, we used both forward and backward model selection, starting at the null or full models, respectively, and iteratively adding or removing one term at a time that best improved the model

AIC value until no further additions or removals improved the model. We then used human oversight to rectify differences between the forward- and backward-selected models and determine the final model for each response variable. The PerMANCOVAs performed using our final models utilized a bootstrapping procedure to generate 10,000 randomized datasets by sampling with replacement from the pool of observed values and then compared the F statistics generated using the randomized dataset to the F statistics generated using the actual observed values to calculate p-values for each model term.

Guided by the results of our multivariate analyses and to better understand how site characteristics relate to restoration outcomes, we next performed a series of univariate analyses for the same five taxonomic groups. For each group, we fit linear or permutational linear models using the lm() or lmp() functions in R and performed ANCOVAs or multiple regressions using marginal (Type III) sums of squares to examine the effects of our focal environmental variables on three key community-level response variables: richness, abundance, and diversity. Our full models included all the site and environmental variables considered in our PerMANCOVAs, but some of these terms were correlated. So, as before, we first purged the least explanatory of any correlated environmental variables and then used the step() function in R with forward and backward model selection based on AIC values (as described above) to prune our relatively complex models by removing model terms that explained the least variance and increase the statistical power of our final models. To confirm that these models and our PerMANCOVAs met all relevant model assumptions, we performed Shapiro–Wilk tests of normality on model residuals and Breusch-Pagan tests of homoscedasticity for all linear models, and we calculated the variance inflation factor of all model terms for all models to quantify multicollinearity using

the vif() function in R. A p-value of 0.05 was used to determine significance and test model assumptions.

CHAPTER III

RESULTS

Principal Component Analysis of Environmental Factors

The first principal component explained 35.5% of environmental variance and was defined primarily by total diversity (10.75%), total richness (9.25%), ground cover diversity (9.2%), and invasive grass cover (9%) (Figure 2, Panel B). The second principal component explained 14.5% and was defined primarily by patch size (20.5%), interior to edge ratio (19%) and time since restoration (17.5%) (Figure 2, Panel C). The third principal component explained 10.1% of environmental variance and was defined primarily canopy cover (22.5%) and canopy density (13%) (Figure 2, Panel D). Figure 3 summarizes the contributions of all environmental factors to the principal components by plotting them as vectors in two dimensions using the first two principal components. This allows us to visually identify clusters of closely related environmental factors. We can see, for example, that patch size and time since restoration are closely correlated, which aligns with what we know about our sites (our larger sites were typically older). Invasive grass cover and combined total exotic plant cover are also correlated because invasive grass accounted for a very large percentage of the overall exotic cover. Figure 4 (a) expands on this plot to show where each site falls on the plot and how they differ based on the method of restoration, while (b) shows the previous two figures combined, allowing us to see how sites and environmental factors cluster and correlate along the principal component axes.

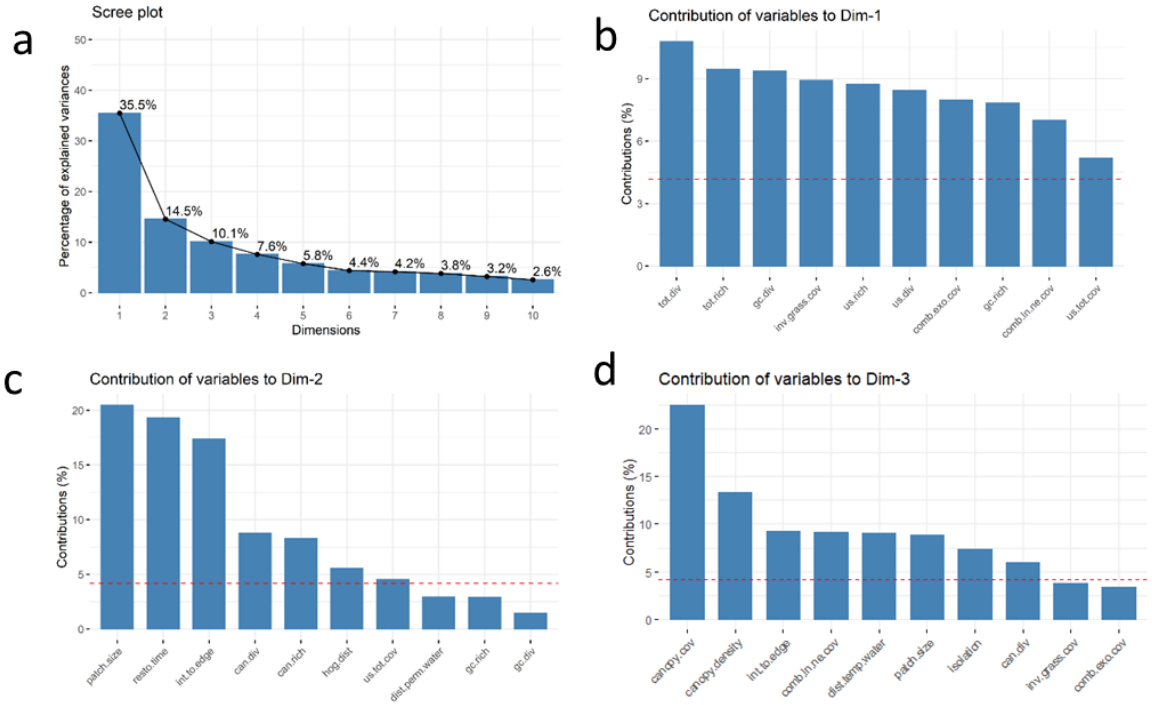

Figure 2. Principal component analysis results showing (a) a scree plot displaying the percentage of explained variance per dimension, (b) contributions of variables to dimension 1, (c) contribution of variables to dimension 2 and (d) contribution of variables to dimension 3.

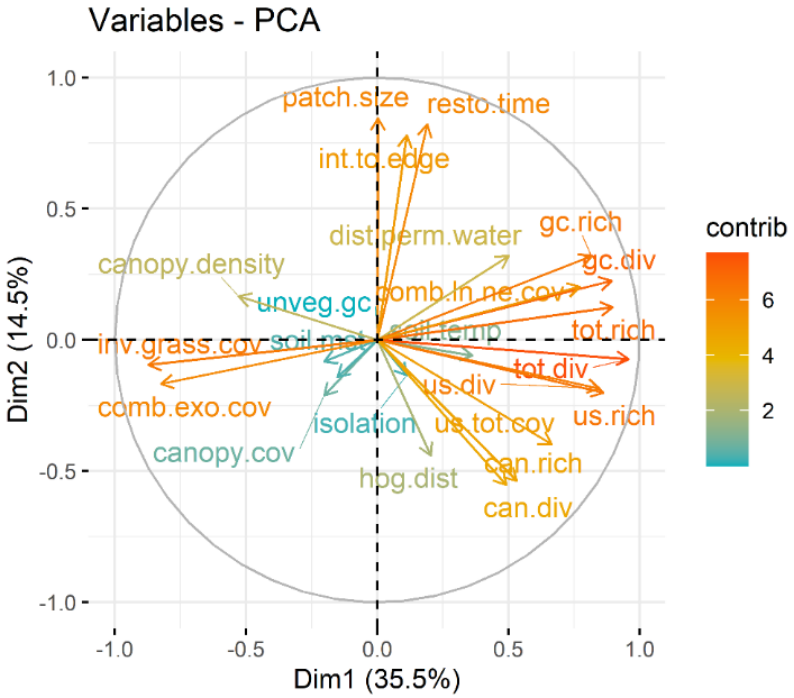

Figure 3. Environmental variables plotted in two dimensions using the first two principal components as axes. Longer vectors represent larger contributions to variability.

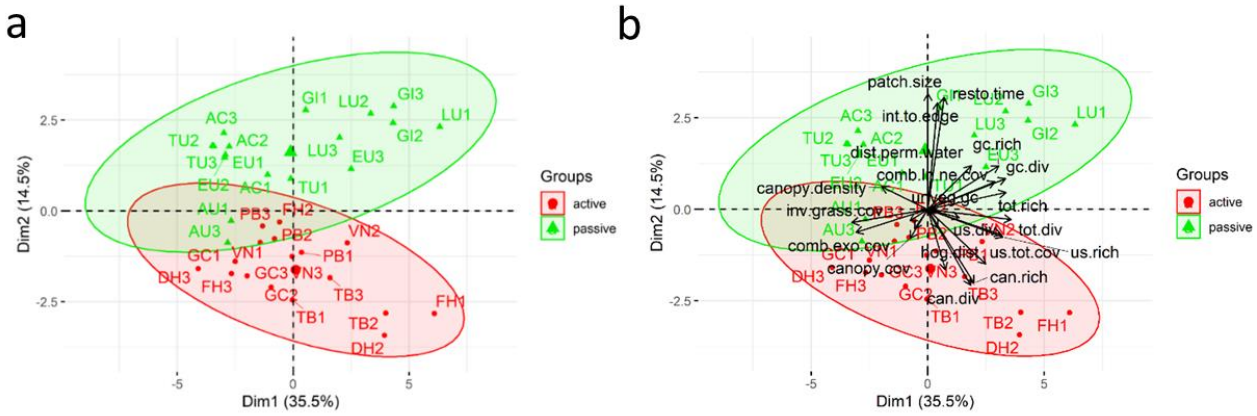

Figure 4. Plots showing (a) how sites map against the two principal component axes and (b) how sites and environmental variables map against the principal components. Both plots also show ellipses that represent method of restoration.

Mammals

Multivariate Analysis of Mammal Communities

In total, we observed 18 different mammal species across sites over the course of the data collection period. Three of those were domestic species (cow, dog, and cat), and one of the species encountered was humans. The five most commonly encountered species out of our total observations were *Procyon lotor* (Raccoon) (92.59 independent observations per 30-day period), *Odocoileus virginianus* (White-tailed Deer) (62.19), *Dasypus novemcinctus* (Nine-banded Armadillo) (56.1), *Dicotyles tajacu* (Collared Peccary, also commonly referred to as Javelina)(36.48), and *Lynx Rufus* (Bobcat) (23.31). Of all the species observed, cats and cows were encountered at only one of the 36 points, while *Leopardus pardalis* (ocelot), *Mephitis mephitis* (skunk) and Chiroptera (unknown bat species) were each only encountered at two different points. Duck Head 2 had the most overall independent observations per 30-day period

(82.19), followed by Garza-Cavazos 1 (41.72), then Arroyo Colorado 3 (39.22). Anacua 2 and Duck Head 1 had zero observations. At Goat Island, 9 species were observed, none of which were domestic or invasive species, and it was the only site at which ocelots were observed.

Appendix 1 shows the number of independent observations at each of our 36 points per species, scaled to the number of pictures per 30 days due to differing sampling efforts between points. At the point level, the most diverse mammal species were observed at Duck Head 2 (10), Longoria 2 (9) and Fish Hatchery 2 (9). At two points (Anacua 2 and Duck Head 1), zero mammal pictures were captured. At the site level, Duck Head, Fish Hatchery, and Longoria Unit each had the most species observed (10 each), while the Anacua Unit had the least with only two.

A nonmetric multidimensional scaling (NMDS) ordination of the mammal community data is shown in Figures 5 and 6. Figure 5 shows an NMDS ordination representing mammal community composition and similarities among observed communities, which are represented as the position and spatial proximity of labels, respectively. In the NMDS ordination in Figure 6, points represent observed communities and correspond to individual sampling points (n = 36, 3 per study site). The color and size of points denote method of restoration and patch size. Black vector arrows denote influential species that most strongly drove separation among communities in the directions specified; points located farther in a given direction can be interpreted as having higher abundances of species whose vectors point in that direction relative to other sites. Red vector arrows denote continuous environmental factors that were most strongly associated with the separation among communities in the directions specified. Colored ellipses represent the 95% confidence intervals around the theoretical average communities (centroids) for the groups defined by the method of restoration. In one direction the distance to permanent water was

associated with separation between communities and correlated closely with presence of peccaries and bobcats. Invasive grass cover and combined exotic plant cover were strongly correlated (because invasive grasses were the predominant type of exotic species observed) and were associated with separation of communities in the same direction as observations of humans. In another cluster total diversity, total richness, and ground cover diversity all drive separation of mammal communities and are associated with rabbit and hog presence. There was also a correlation between nilgai abundance and the environmental factor of isolation.

Table 2 shows PerMANCOVA results examining the effects of key environmental variables on the observed mammal communities in the NMDS ordination. These results indicate that restoration and patch size had a significant effect on mammal communities. Time since restoration, distance to permanent water, and distance to temporary water were also significantly associated with differences in mammal community composition.

Here and in our other models, it is important to note that we can interpret factors that were pruned (removed) to increase model power as having non-significant relationships with the response variable; however, the same is not true for the factors that were removed because they were correlated with at least one other model term. In these cases, strongly correlated factors are confounded and we cannot rule out the possibility that the factors excluded from our models to meet model assumptions about multicollinearity actually had significant relationships with the response variable. For example, ground layer plant diversity was strongly correlated with other plant diversity metrics (total plant diversity and total plant richness) and the natural log of the ratio of native to exotic plant cover. Although ground plant diversity explained more of the variance in observed mammal communities than these other correlated factors, it does not necessarily mean that those other factors were unimportant, or that ground plant diversity was

the mechanism driving variation in mammal community composition. Our PCA results are important here; they quantify and illustrate which groups of factors are correlated in this fashion and should be considered when interpreting the results of our PerMANCOVAs, ANCOVAs, and multiple regressions.

Table 2. PerMANCOVA results examining the effects of patch size, method of restoration, time since restoration, distance to permanent water, ground cover plant diversity and distance to permanent water on mammal community composition. More complex models with additional terms and interactions between terms were considered prior to model pruning. Environmental factors not included in this model were removed either to avoid multicollinearity or because they explained an insignificant amount of variance. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	d.f.	$F_{6,27}$	*p*	
Patch size	1	3.54	0.0001	***
Method of restoration	1	3.15	0.0001	***
Time since restoration	1	2.4	0.0700	**
Distance to permanent water	1	2.31	0.0110	**
Ground cover plant diversity	1	1.60	0.0769	.
Distance to temporary water	1	1.80	0.0400	*

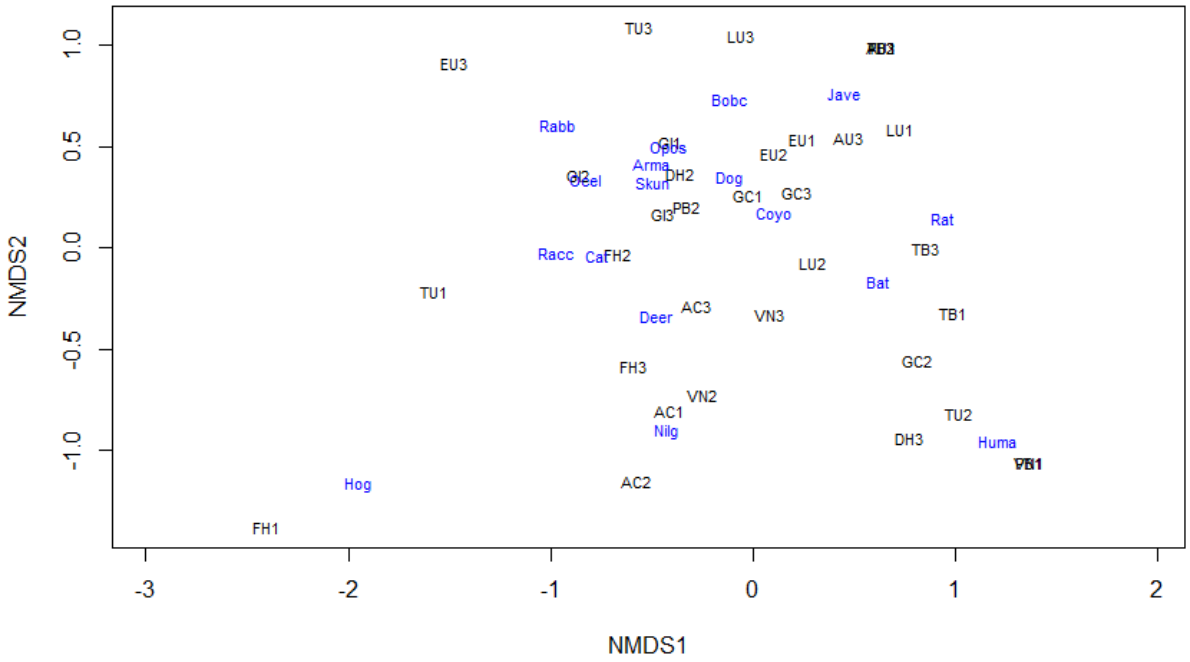

Figure 5. NMDS ordination representing mammal community composition and similarities among observed communities, which are represented as the position and spatial proximity of labels, respectively. Labels in black are abbreviations for observed communities and correspond to individual sampling points. Labels in blue are abbreviations of the common names of observed mammal species.

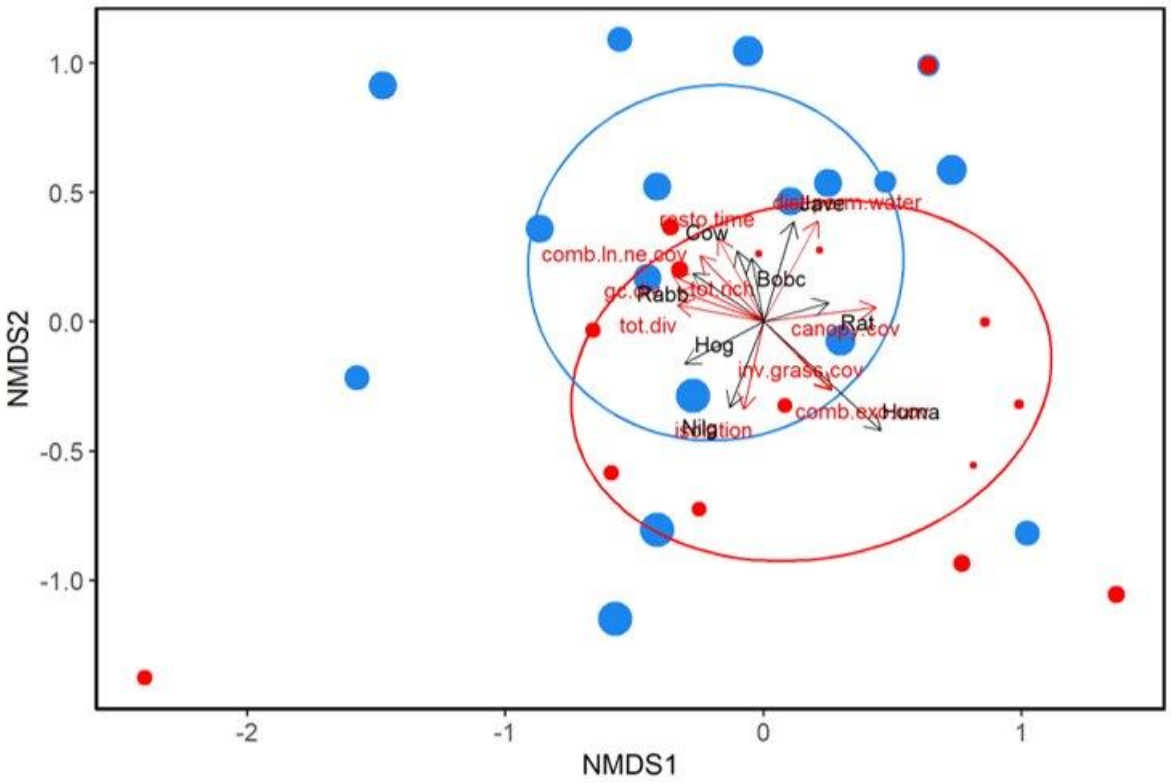

Figure 6. NMDS ordination representing mammal community composition and similarities among observed communities, which are represented as the position and spatial proximity of points, respectively. Points represent observed communities and correspond to individual sampling points (n = 36, 3 per study site). The color and size of points denote method of restoration and patch size. Black vector arrows denote influential species that most strongly drove separation among communities in the directions specified; points located farther in a given direction can be interpreted as having higher abundances of species whose vectors point in that direction relative to other sites. Red vector arrows denote continuous environmental factors that were most strongly associated with the separation among communities in the directions specified. Colored ellipses represent the 95% confidence intervals around the theoretical average communities (centroids) for the groups defined by the method of restoration.

Mammal Community Univariate Analyses

Mammal richness averaged 3.82 ± 2.49 across sampling points and was influenced by understory richness, ground layer vegetation richness, soil temperature, understory diversity, and extent of isolation (Table 3). Relationships to ground layer vegetation richness, soil temperature, isolation, understory richness and understory diversity are shown in figures 7, 8, 9, 10 and 11, respectively. Ground layer vegetation richness, soil temperature, isolation, and understory diversity had a positive linear relationship with richness, whereas understory richness had a

negative relationship. Mammal richness was the same in passively and actively restored sites (3.82).

Table 3. Results from a multiple regression using marginal (Type III) sums of squares examining the effects of ground cover richness, soil temperature, isolation, understory richness and understory diversity on mammal richness. Legend: ***, p < 0.001; **, 0.001 ≤ p < 0.01; *, 0.01 ≤ p < 0.05; ., 0.05 ≤ p < 0.1.

Factor	Effect size	d.f.	$F_{5,28}$	p	
Ground layer vegetation richness	0.37178	1	12.27	0.0016	**
Soil temperature	0.44156	1	7.32	0.0115	*
Isolation	0.04384	1	5.54	0.0258	*
Understory richness	-1.80909	1	16.81	0.0003	***
Understory diversity	4.07437	1	6.60	0.0158	*
Model		5	5.65	0.0010	

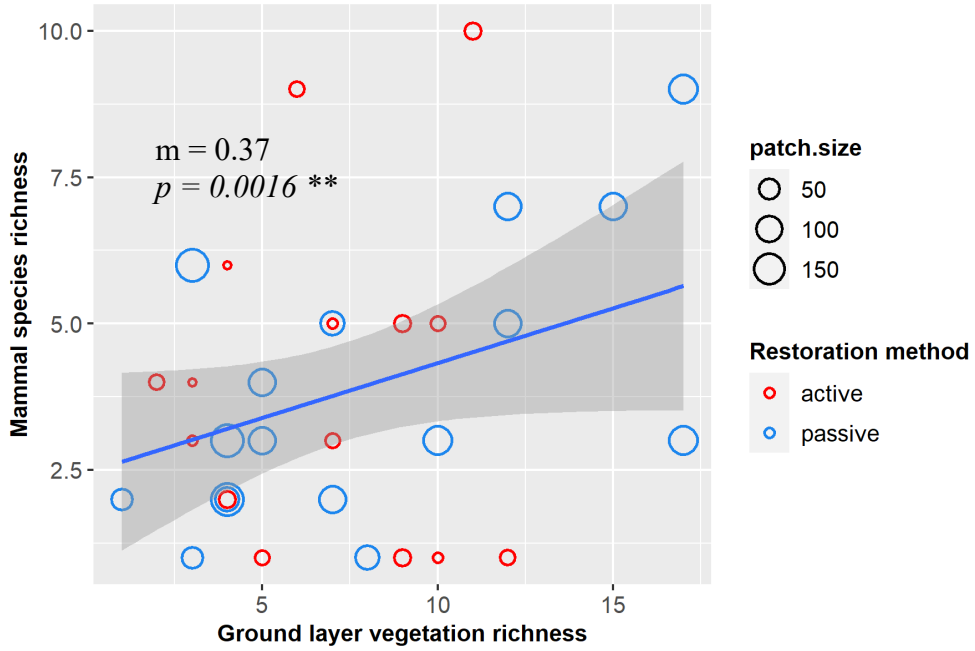

Figure 7. Linear relationships between mammal species richness and ground layer vegetation richness. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

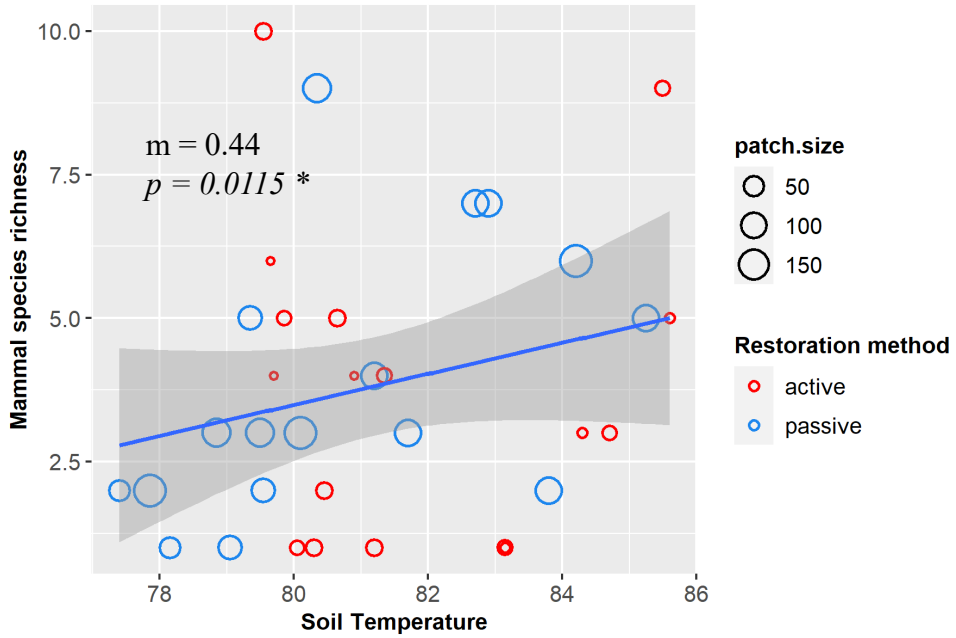

Figure 8. Linear relationships between mammal species richness and soil temperature. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

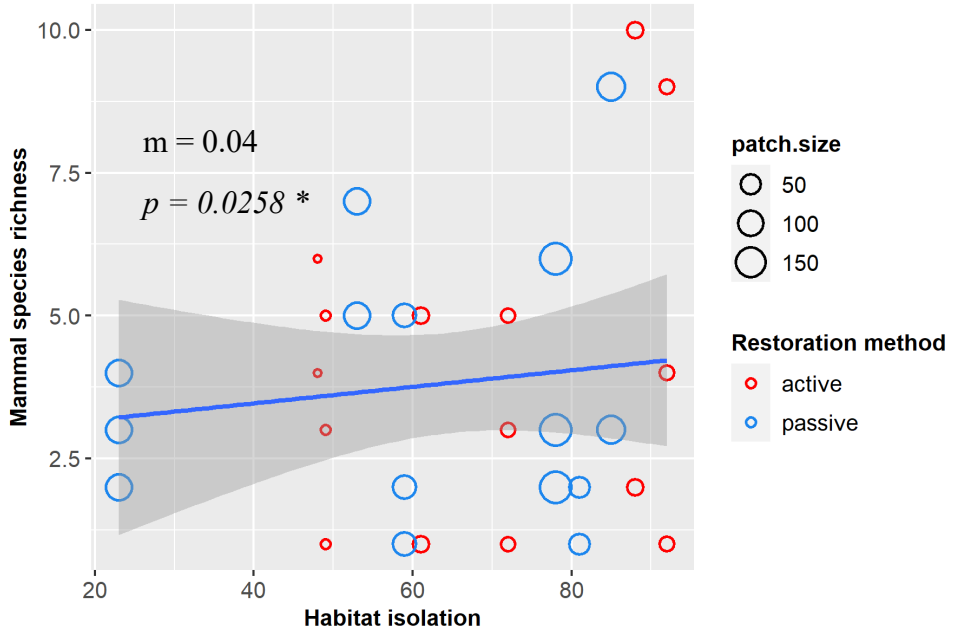

Figure 9. Linear relationships between mammal species richness and habitat isolation. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

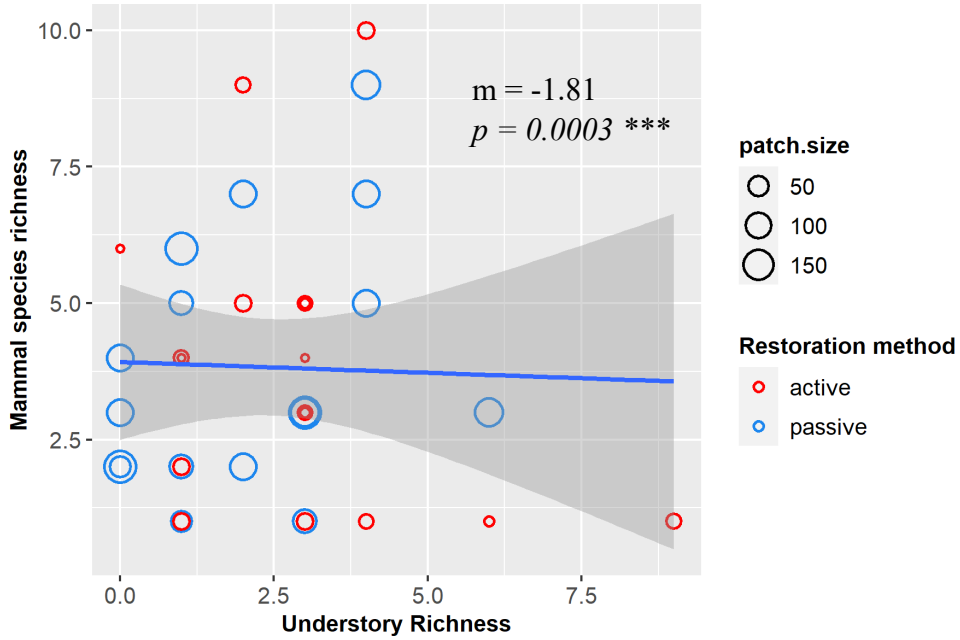

Figure 10. Linear relationships between observed mammal species richness and understory plant species richness. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

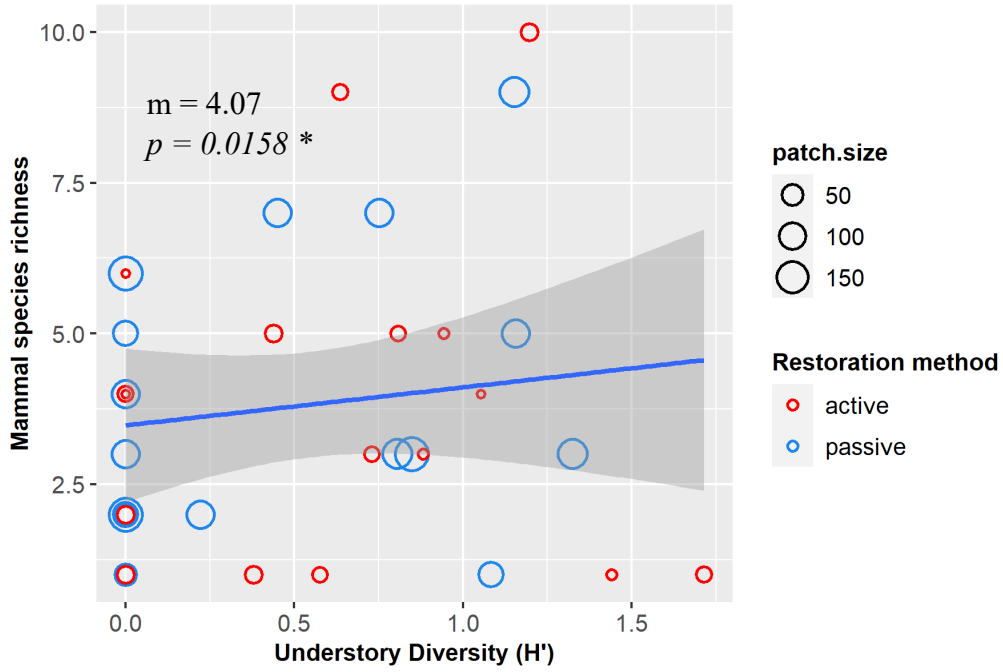

Figure 11. Linear relationships between observed mammal species richness and understory plant species diversity. Open circles denote values from one study site; they are colored based on method of restoration and sized according

to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Mammal diversity averaged 0.91 ± 0.59 across sampling points and was influenced by understory total cover and ground cover richness (Table 4). Our focal variables of time since restoration, method of restoration, isolation and patch size were considered but were not significant. Relationships to understory total cover and ground cover vegetation richness are shown in Figures 12 and 13. Understory total cover had a negative linear relationship with mammal diversity whereas ground cover vegetation richness had a positive relationship. Diversity was higher on average in passively restored sites (0.91 ± 0.55) than in actively restored sites (0.89 ± 0.64).

Table 4. ANCOVA Type III results examining the effects of understory total cover, ground cover vegetation richness, and soil temperature on mammal diversity. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{3,30}$	p	
Understory total cover	-0.013571	1	7.18	0.0118	*
Ground cover vegetation richness	0.052059	1	4.58	0.0406	*
Soil temperature	0.068606	1	2.88	0.1003	
Model		30	3.73	0.0217	

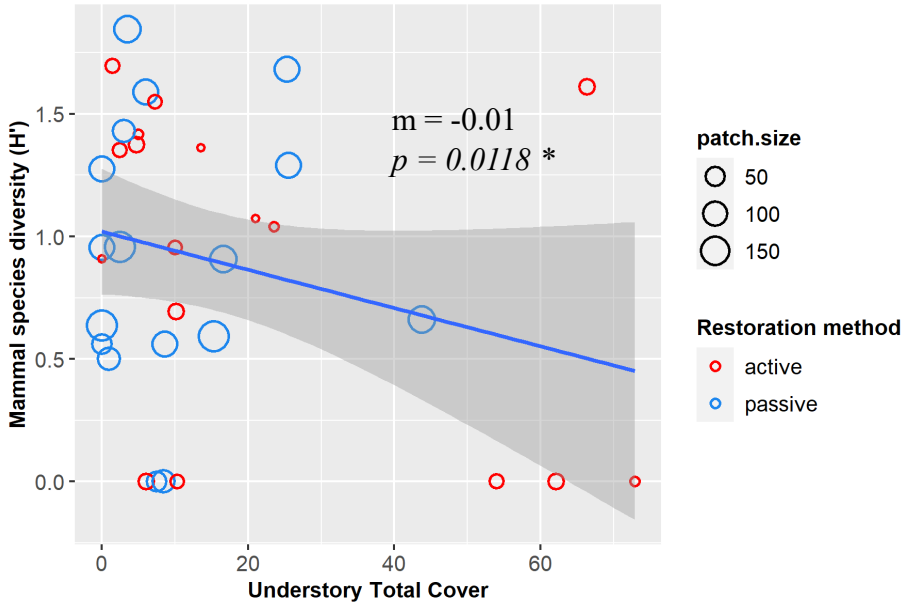

Figure 12. Linear relationships between mammal species diversity and understory total cover. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

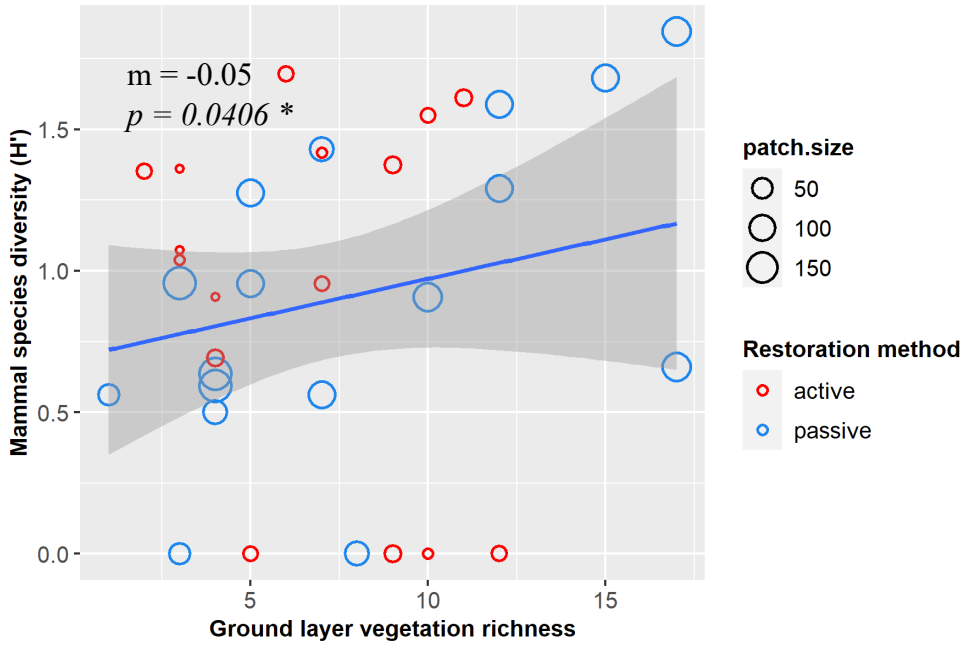

Figure 13. Linear relationships between mammal species diversity and ground layer vegetation richness. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Mammal abundance averaged 10.40 ± 16.92 across sampling points. The model for mammal abundance explains little variance (Table 5). Ground cover diversity appears to be significant, but the model itself is not significant. The relationship to ground cover plant diversity is shown in Figure 14. Mammal abundance was higher in actively restored sites (10.95 ± 21.71) than in passively restored sites (9.85 ± 10.90).

Table 5. ANCOVA Type III results examining the effects of ground cover plant diversity and total richness on mammal abundance. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{2,31}$	p	
Ground cover plant diversity	17.42	1	4.79	0.0363	*
Total richness	-1.63	1	2.00	0.1169	
Model		31	2.653	0.0864	

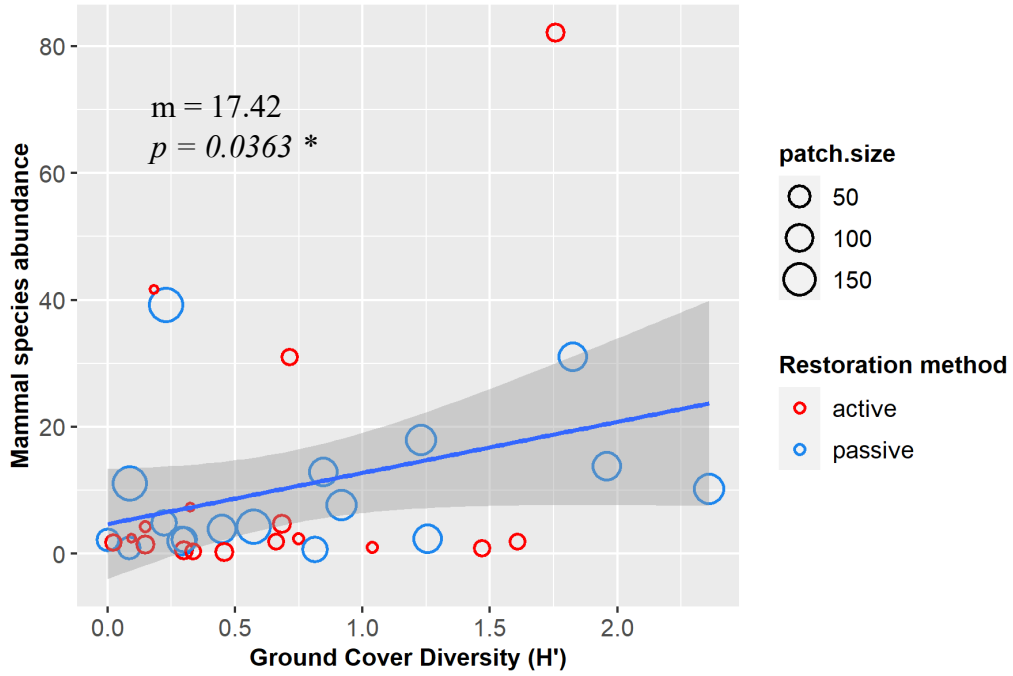

Figure 14. Linear relationships between mammal species abundance and ground cover diversity. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Birds

Multivariate Analyses of Bird Communities

We observed a total of 53 bird species over the course of two surveys at each sampling point (Appendix 2). At the site level, Anacua Unit, Arroyo Colorado, and Villa Nueva had the most species (25 each) while Longoria and Duck Head had the fewest (17 and 18 respectively). Goat Island had 24 species. The five most commonly encountered species were *Zenaida macroura* (Mourning Dove), *Arremonops rufivirgatus* (Olive Sparrow), *Melanerpes aurifrons* (Golden-fronted Woodpecker), *Tyrannus couchii* (Couch's Kingbird), and *Toxostoma longirostre* (Long-billed Thrasher). Sixteen of the 53 species (30.2%) were encountered during only one survey. Fifty-eight and a half percent of species were encountered on less than 10 surveys, while 15.1% were encountered during more than 20 of the 72 surveys conducted. Table 6 shows a list of species observed and the number of surveys during which they were encountered.

A nonmetric multidimensional scaling (NMDS) ordination of the bird community data is shown in Figure 15. A large group of species which drove separation amongst communities in the same direction as two of the older, larger, passively restored sites, included *Myiarchus cinerascens* (Ash-throated Flycatcher), *Spiza americana* (Dickcissel), *Tyrannus melancholicus* (Tropical Kingbird), and *Lanius ludovicianus* (Loggerhead Shrike), amongst others. Another set of influential species, including *Thryomaes bewickii* (Bewick's Wren), *Leucophaeus atricilla* (Laughing Gull), *Cathartes aura* (Turkey Vulture) and *Toxostoma longirostre* (Long-billed Thrasher), drove separation amongst communities in the opposite direction in association with a few other larger, older, passively restored sites. Actively restored sites clustered in the middle, spreading from the top right to the bottom left based on *Zenaida macroura* (Mourning Dove) and

Cardinalis cardinalis (Northern Cardinal) presence in association with distance to temporary water, soil moisture and hog disturbance.

The PerMANCOVA results in Table 6 show that distance to temporary water and canopy density were significantly associated with bird community composition.

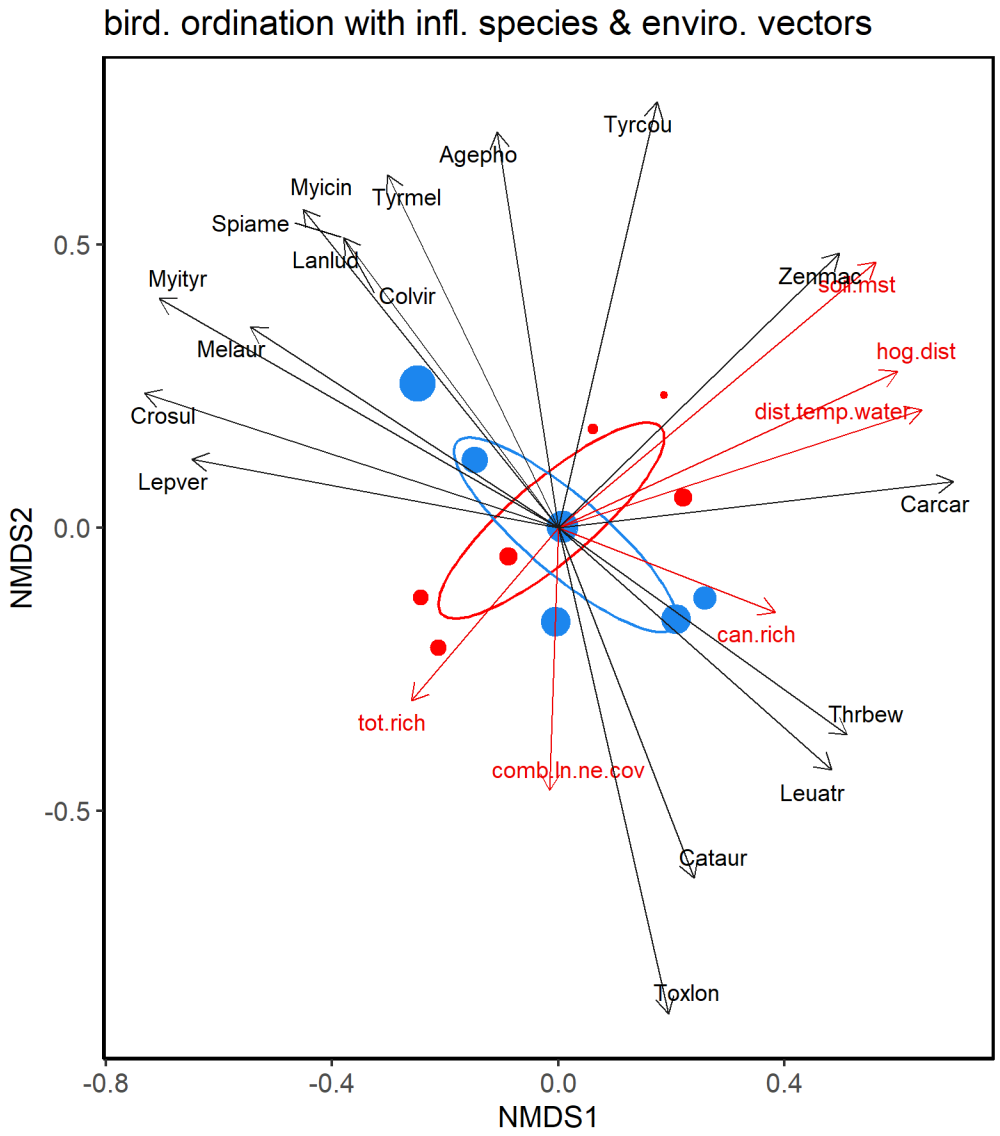

Figure 15. NMDS ordination representing bird community composition and similarities among observed communities, which are represented as the position and spatial proximity of points, respectively. Points represent observed communities and correspond to individual sampling points (n = 36, 3 per study site). The color and size of points denote method of restoration and patch size. Black vector arrows denote influential species that most strongly drove separation among communities in the directions specified; points located farther in a given direction can be interpreted as having higher abundances of species whose vectors point in that direction relative to other sites. Red vector arrows denote continuous environmental factors that were most strongly associated with the separation among communities in the directions specified. Colored ellipses represent the 95% confidence intervals around the theoretical average communities (centroids) for the groups defined by the method of restoration.

Table 6. PerMANCOVA results examining the effects of distance to permanent water and canopy density on bird community composition. More complex models with additional terms and interactions between terms were consider ed prior to model pruning. Environmental factors not included in this model were removed either to avoid multicoll-inearity or because they explained an insignificant amount of variance.: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, 0.0 $1 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	d.f.	$F_{2,9}$	*p*	
Distance to temporary water	1	2.05	0.0010	**
Canopy density	1	1.65	0.0450	*

Bird Community Univariate Analyses

We did not count the actual number of birds observed during surveys, therefore we could not analyze bird diversity or abundance. Bird richness averaged 13.56 ± 2.26 across study sites and was influenced by method of restoration, canopy diversity and invasive grass cover (Table 7). Relationships to canopy plant diversity, method of restoration, and invasive grass cover are shown in figures 16, 17, and 18. Canopy plant diversity and invasive grass cover had a positive linear relationship with bird richness. The difference in effect between passive and active sites was 1.14. Passively restored sites averaged a higher abundance (13.06 ± 2.56) than actively restored sites (14.06 ± 1.86).

Table 7. ANCOVA Type III results examining the effects of canopy diversity, method of restoration, invasive grass cover, and understory richness on bird richness. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{4,31}$	p	
Canopy plant diversity	2.46525	1	7.15	0.0119	*
Method of restoration	-1.13579	1	9.42	0.0044	**
Invasive grass cover	0.04104	1	6.16	0.0187	*
Understory plant richness	0.39877	1	3.64	0.0657	.
Model		31			

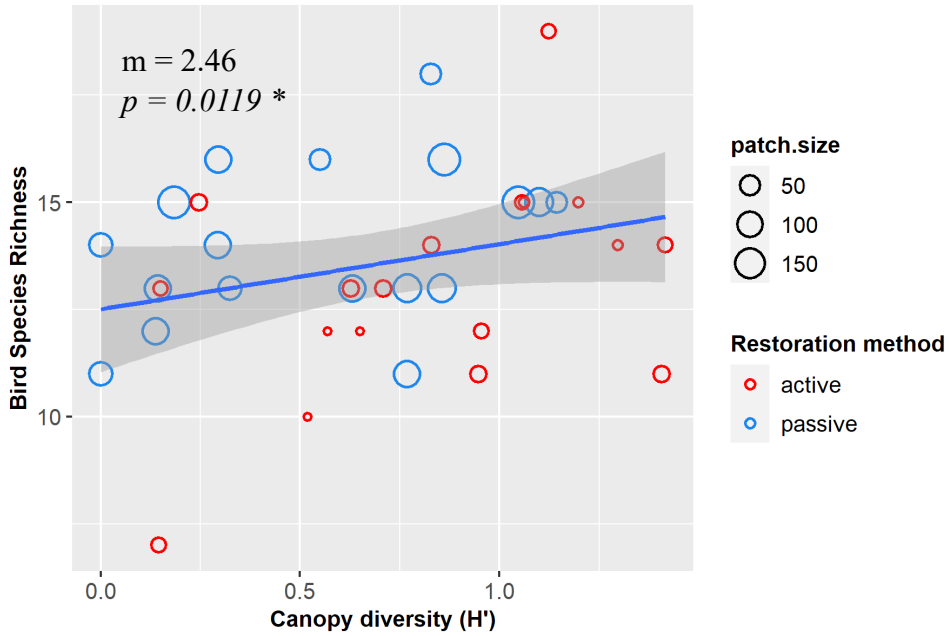

Figure 16. Linear relationships between bird species richness and canopy diversity. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Figure 17. Observed values with means (black dots) and 95% confidence intervals (error bars) of bird species richness broken down by method of restoration. Open circles denote values from one sampling point; color denotes method (red = active, blue = passive) and size denotes patch size.

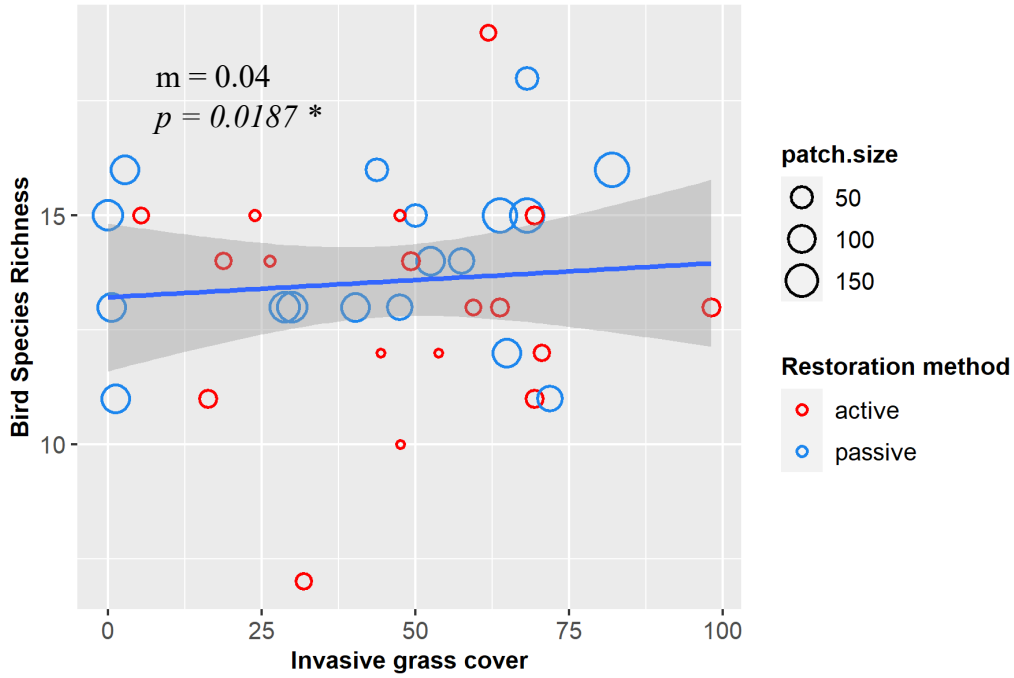

Figure 18. Linear relationships between bird species richness and invasive grass cover. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Lepidoptera

Multivariate Analyses of Lepidoptera Communities

We identified over 1600 Lepidoptera and observed 77 different species over the course of 2 trap surveys at each of our 36 points. Eight of the 77 species were butterflies, whereas the rest were moths. At the site level, Phillips Banco and Tucker Unit had the highest abundance of Lepidoptera (265 and 234), while Fish Hatchery and Goat Island had the most species (53 and 50). Anacua Unit had both the lowest abundance and richness with only 37 Lepidoptera collected and 17 different species. The number of each Lepidoptera species observed at each sampling point can be found in Appendix 3.

A nonmetric multidimensional scaling (NMDS) ordination of the Lepidoptera community data is shown in Figure 19 and 20. *Helia agna*, *Focillidea texana* (Southern Focillidea Moth), and a morphospecies of Erebidae strongly drove separation between communities and were strongly associated with older, larger, passively restored sites. Moths in the subfamily Sterrhinae, *Elaphria chalcedonia* (Chalcedony midget), and an unidentified species in the genus *Agonopterix* all drove separation strongly amongst communities in the same direction associated with isolation and canopy cover. *Bleptina caradrinalis* (Bent-winged Owlet), an unidentified *Renia* species, and *Plusiodonta compressipalpis* (Moonseed Moth) all drove separation amongst communities and were associated with younger, smaller, passively restored sites. A cluster of influential species consisting of *Melipotis agrotoides* (Indomitable Graphic), *Metria bilineata*, *Numia bicoloraria* (Bicolored Chloraspilates), *Prochoerodes lineola* (Large Maple Spanworm), *Libytheana carinenta* (American snout), a morphospecies of Herminiinae morphospecies, and a morphospecies of Erebidae morphospecies all drove separation in the same direction as ground layer plant richness and were associated with both methods of restoration.

Table 8 shows PerMANCOVA results examining the effects of key environmental variables on the observed Lepidoptera communities. Isolation, canopy cover, soil moisture, method of restoration, the natural log of the ratio of native to exotic plant species, time since restoration, ground layer plant diversity, and invasive grass cover all had significant effects.

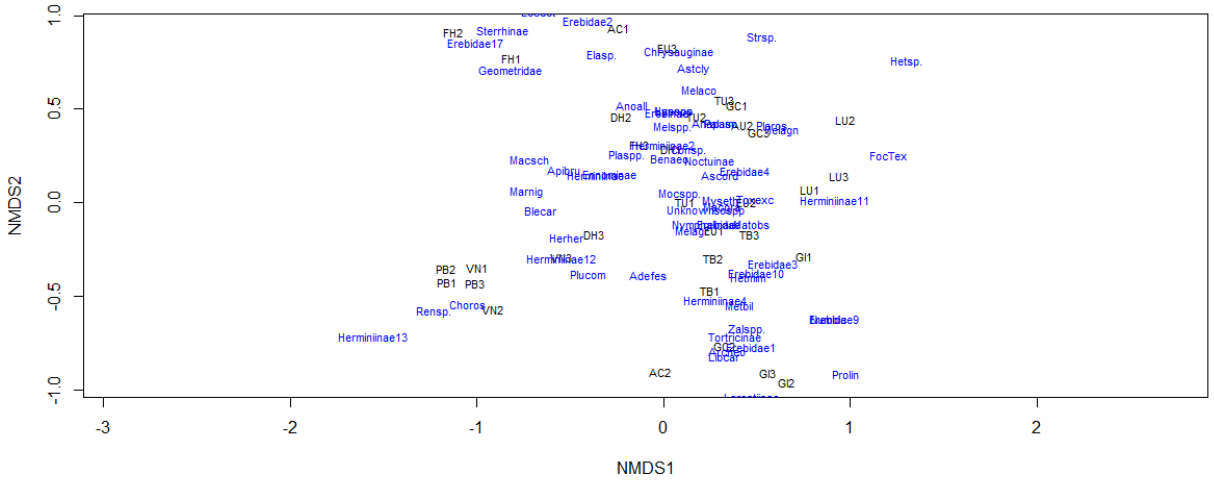

Figure 19. NMDS ordination representing Lepidoptera community composition and similarities among observed communities, which are represented as the position and spatial proximity of points, respectively. Labels in black are abbreviations for observed communities and correspond to individual sampling points. Labels in blue are abbreviations of observed Lepidoptera species, or in cases where species was unidentified, either the genus, subfamily, family, or morphospecies of a family if multiple species in a family were unidentified.

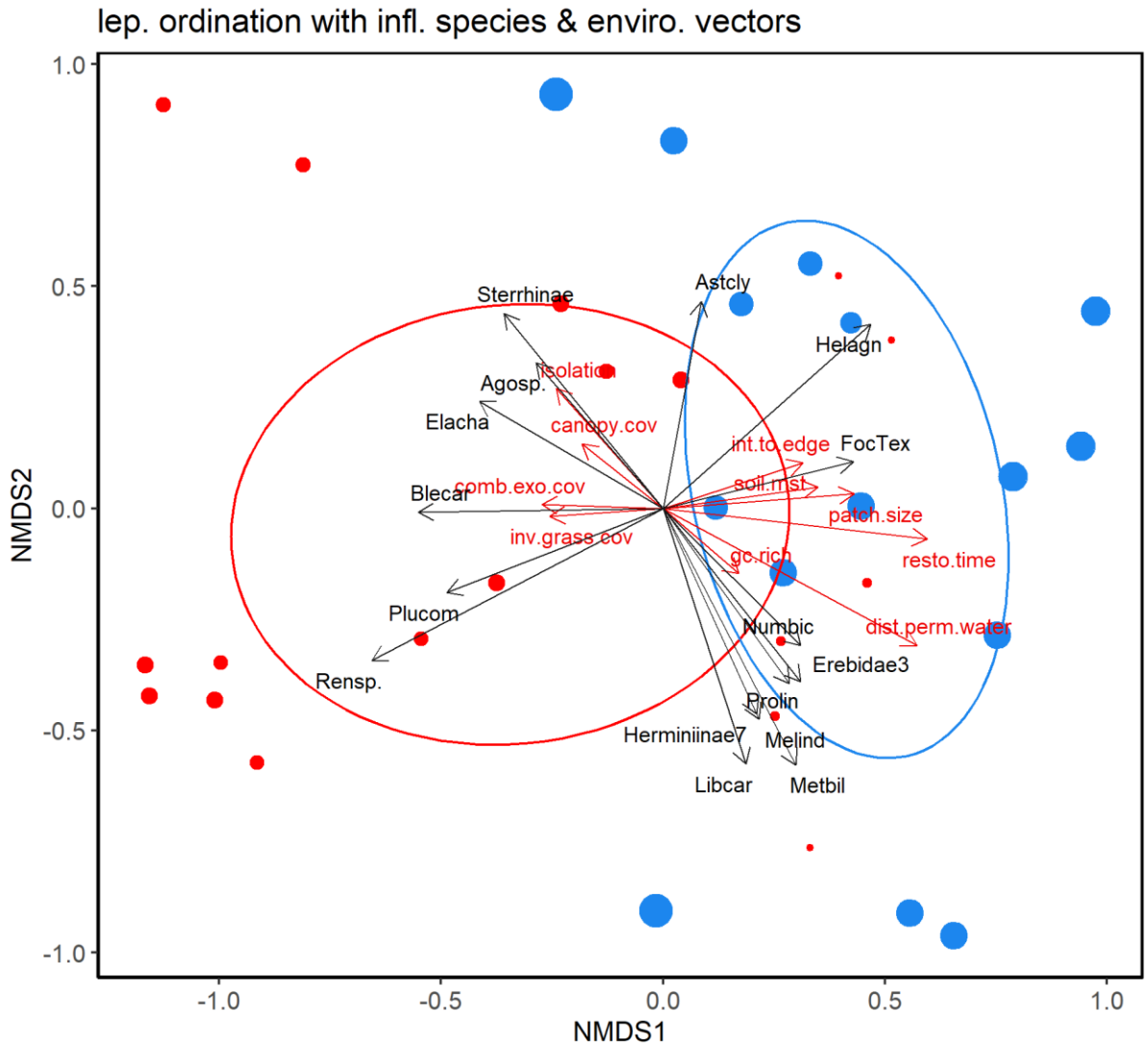

Figure 20. NMDS ordination representing Lepidoptera community composition and similarities among observed communities, which are represented as the position and spatial proximity of points, respectively. Points represent observed communities and correspond to individual sampling points (n = 36, 3 per study site). The color and size of points denote method of restoration and patch size. Black vector arrows denote influential species that most strongly drove separation among communities in the directions specified; points located farther in a given direction can be interpreted as having higher abundances of species whose vectors point in that direction relative to other sites. Red vector arrows denote continuous environmental factors that were most strongly associated with the separation among communities in the directions specified. Colored ellipses represent the 95% confidence intervals around the theoretical average communities (centroids) for the groups defined by the method of restoration.

Table 8. PerMANCOVA results examining the effects of canopy cover, soil moisture, method of restoration, invasive grass cover, the ratio of native to exotic cover, isolation, time since restoration, distance to temporary water, and ground cover plant diversity on Lepidoptera community composition. More complex models with additional terms and interactions between terms were considered prior to model pruning. Environmental factors not included in this model were removed either to avoid multicollinearity or because they explained an insignificant amount of variance. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	d.f.	$F_{9,32}$	*p*	
Canopy cover	1	3.01	0.0020	**
Soil moisture	1	2.25	0.0050	**
Method of restoration	1	2.47	0.0060	**
Invasive grass cover	1	2.04	0.0220	*
ln(ratio native:exotic cover)	1	2.07	0.0100	**
Isolation	1	2.64	0.0100	***
Time since restoration	1	2.47	0.0050	**
Distance to temporary water	1	1.56	0.0920	.
Ground cover plant diversity	1	2.20	0.0079	**

Lepidoptera Community Univariate Analyses

Lepidoptera richness averaged 13.97 ± 4.44 across sampling points and was influenced by the natural log of the ratio of native to exotic plant cover and canopy layer plant richness (Table 9). Relationships to the natural log of the ratio of native to exotic cover and to canopy richness are shown in figures 21 and 22. The natural log of the ratio of native to exotic cover had a positive linear relationship with Lepidoptera richness whereas canopy richness had a negative relationship. Lepidoptera richness was higher on average in actively restored sites (14.67 ± 4.31) than in passively restored sites (13.13 ± 4.60).

Table 9. ANCOVA Type III results examining the effects of the natural log of the ratio of native to exotic species cover, distance to permanent water, canopy richness, understory total cover, and patch size on Lepidoptera richness. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{5,27}$	p	
Ln(ratio native:exotic cover)	1.320132	1	6.54	0.0165	*
Distance to permanent water	-0.003973	1	3.18	0.0860	.
Canopy richness	-1.310606	1	5.33	0.0288	*
Understory total cover	0.053662	1	1.86	0.1838	
Patch size	-0.023370	1	2.77	0.1074	
Model		27	3.695	0.0112	

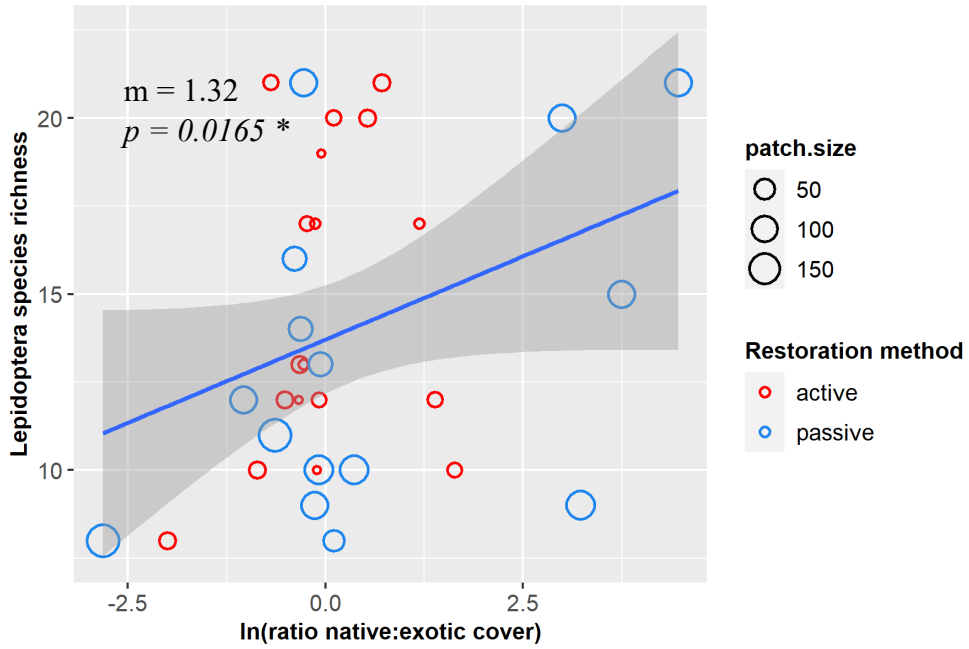

Figure 21. Linear relationships between Lepidoptera species richness and the natural log of the ratio of native to exotic plant cover. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

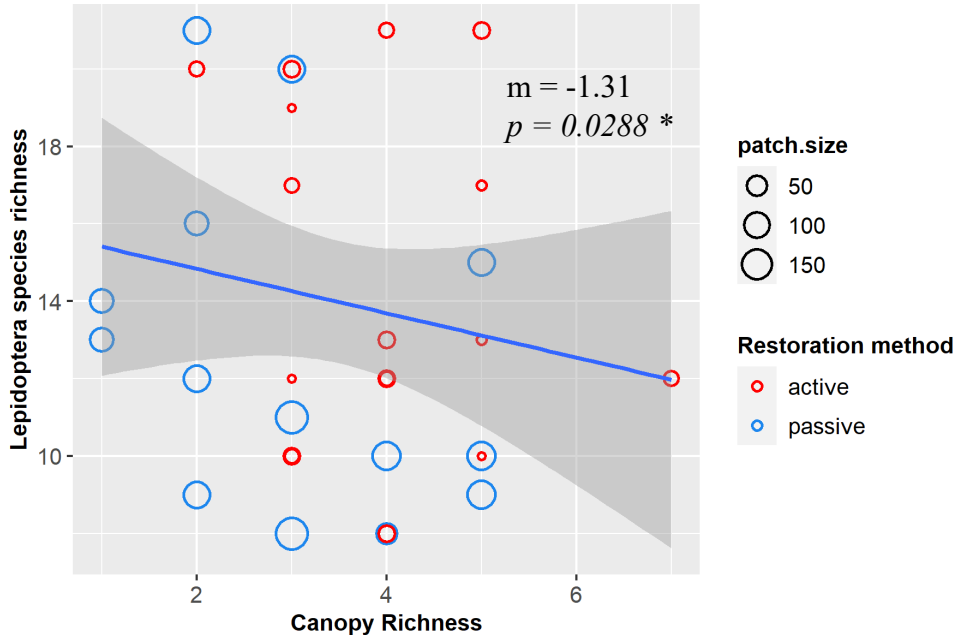

Figure 22. Linear relationships between Lepidoptera species richness and canopy richness. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple

predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Lepidoptera diversity averaged 1.95 ± 0.42 across sampling points and was influenced by soil moisture (Table 10). The relationship to soil moisture is shown in Figure 23. Soil moisture had a positive linear relationship with Lepidoptera diversity. Passively restored sites were on average more diverse (1.97 ± 0.33) than actively restored sites (1.95 ± 0.49).

Table 10. ANCOVA Type III results examining the effects of soil moisture, distance to permanent water, and invasive grass cover on Lepidoptera diversity. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{3,29}$	p	
Soil moisture	0.0190127	1	15.19	0.0005	***
Distance to permanent water	-0.0003774	1	3.29	0.0800	.
Invasive grass cover	-0.0043479	1	2.46	0.1276	
Model		29	6.05	0.0025	

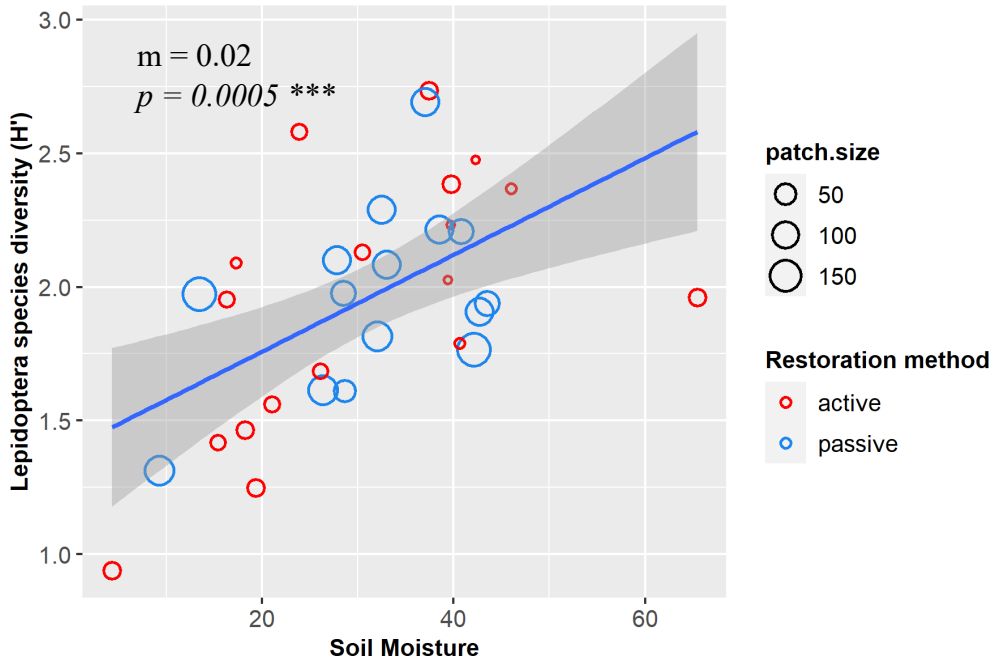

Figure 23. Linear relationships between Lepidoptera species diversity and soil moisture. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Lepidoptera abundance averaged 50.64 ± 29.16 across sampling points and was influenced by soil moisture, time since restoration began, method of restoration, ground cover plant diversity, and the natural log of the ratio of native to exotic cover (Table 11). Relationships to soil moisture, time since restoration began, method of restoration, ground cover plant diversity, and the natural log of the ratio of native to exotic cover are shown in figures 24, 25, 26, 27, and 28. Time since restoration, and the natural log of native to exotic cover had positive linear relationships to Lepidoptera abundance whereas soil moisture and ground cover plant diversity had negative relationships. The estimated difference in effect between passive and active sites was 19.14. Actively restored sites averaged a higher abundance (53.28 ± 30.76) than passively restored sites (47.47 ± 27.83).

Table 11. ANCOVA Type III results examining the effects of soil moisture, time since restoration, method of restoration, ground cover plant diversity and the natural log of the ratio of native to exotic cover on Lepidoptera abundance. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{5,27}$	p	
Soil moisture	-1.0883	1	10.66	0.0030	**
Time since restoration	1.0860	1	9.38	0.0049	**
Method of restoration	19.1387	1	7.91	0.0091	**
Ground cover plant diversity	-44.8182	1	17.82	0.0002	***
Ln(ratio native:exotic cover)	15.2299	1	14.07	0.0008	***
Model		27	5.46	0.0013	

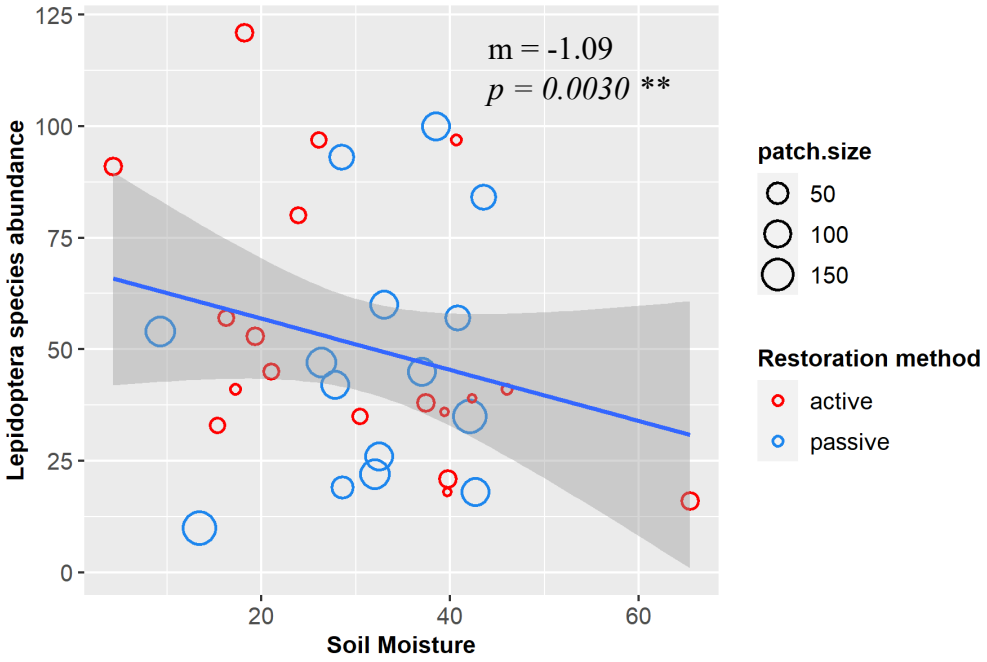

Figure 24. Linear relationships between Lepidoptera species abundance and soil moisture. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

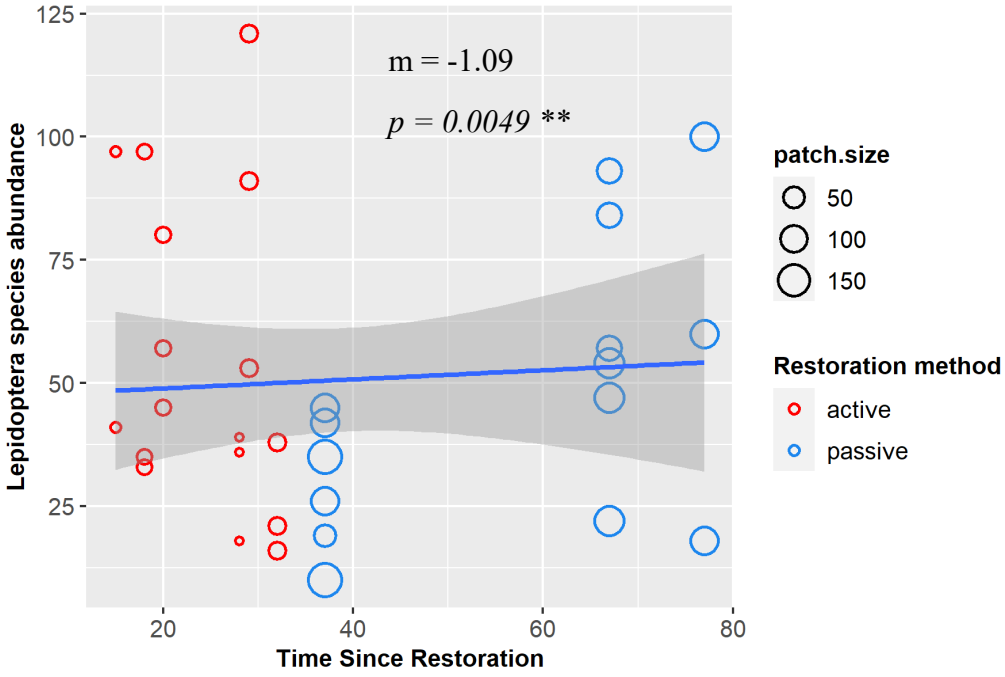

Figure 25. Linear relationships between Lepidoptera species abundance and time since restoration. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in

the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Figure 26. Observed values with means (black dots) and 95% confidence intervals (error bars) of Lepidoptera species abundance broken down by method of restoration. Open circles denote values from one sampling point; color denotes method (red = active, blue = passive) and size denotes patch size.

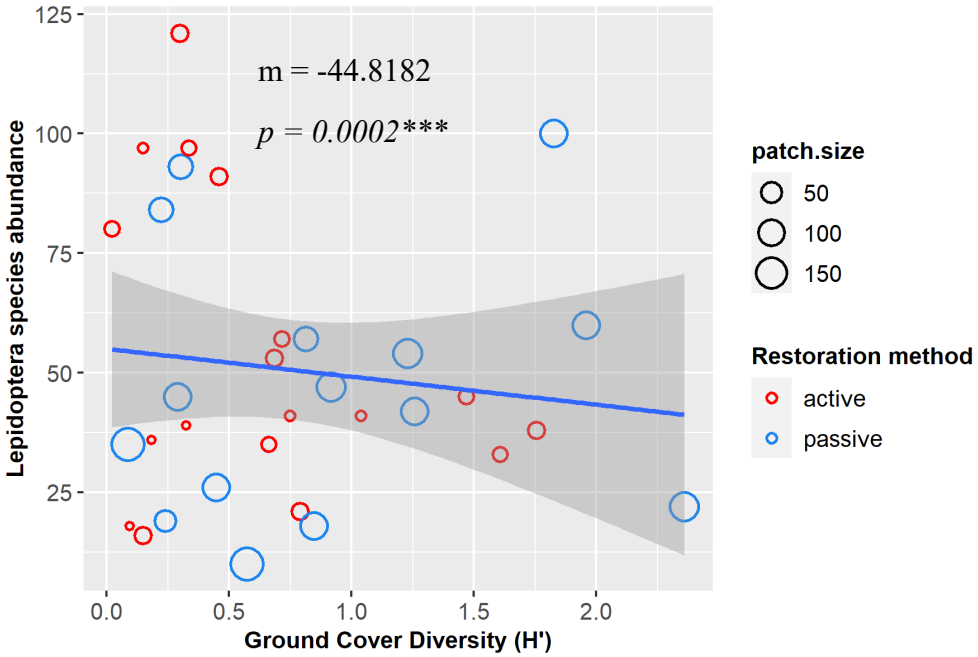

Figure 27. Linear relationships between Lepidoptera species abundance and ground cover diversity. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

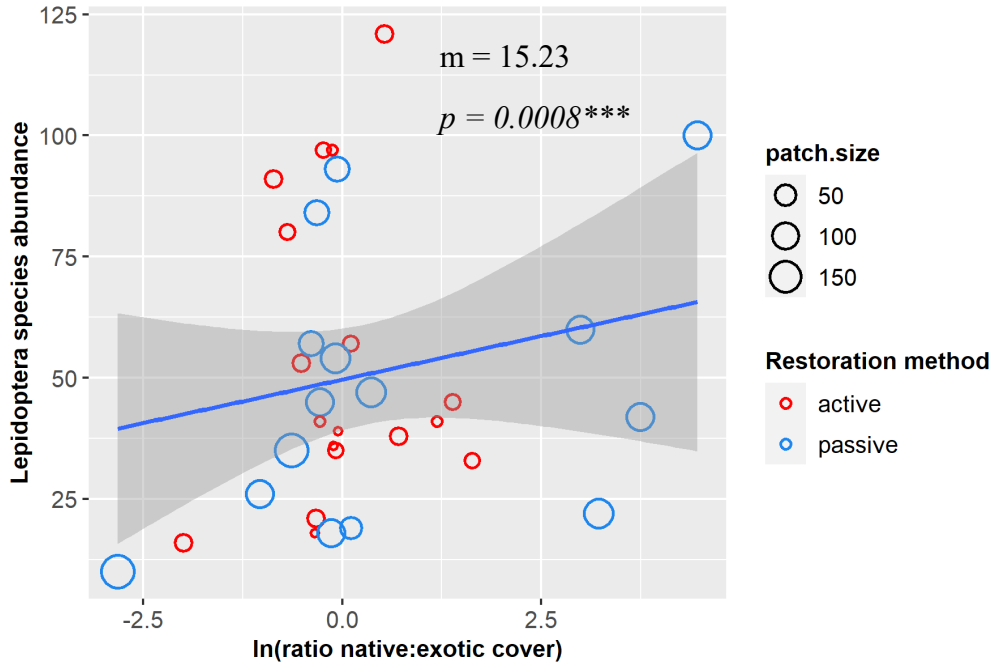

Figure 28. Linear relationships between Lepidoptera species abundance and the natural log of the ratio of native to exotic cover. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Herpetofauna

Multivariate Analyses of Herpetofauna Communities

Over the course of our surveys (both area searches and cover boards), we observed 83 herptiles and a total of 10 different species consisting of 4 lizard species, 3 frog species, 2 skink species and 1 snake species (Appendix 4). A full list of species observed at each sampling point can be found in Table 15. 70 herptiles were discovered via area search while only 14 were observed under cover boards throughout the study. *Anolis sagrei* was by far the most abundant

(37), accounting for 44% of our observations, while *Plestiodon tetragrammus* was second-most abundant (17). Four species were only observed once. At the site level, Fish Hatchery had the highest abundance of herps (21) while Garza-Cavazos and Duck Head had the highest richness (6 each). We observed zero herps at 13 of our 36 points, which we had to exclude from our multivariate analysis. The snake species was both only observed at Goat Island and was the only herp observed at Goat Island, so Goat Island also had to be excluded from the multivariate analysis because its calculated distances from all other sampling points were so high that it rendered all other distance measures essentially meaningless in the ordination.

A nonmetric multidimensional scaling (NMDS) ordination of the Herp community data is shown in Figure 29. *Anolis sagrei* (Brown anole, an invasive species), *Incilius nebulifer* (Gulf Coast Toad), *Hypopachus variolosus* (Northern Sheep Frog), and *Plestiodon tetragrammus* (Four-lined Skink) most strongly drove separation amongst communities in the same direction as distance to temporary water and canopy richness, and high abundances of these species were also closely associated with smaller, younger, actively restored sites. *Aspidoscelis laredoensis* (Laredo Striped Whiptail) was closely associated with ground cover diversity while *Scincella lateralis* (Little Brown Skink), *Aspidoscelis gularis* (Common Spotted Whiptail) and *Anolis carolinensis* (Green Anole) most strongly drove spread in directions closely associated with older, larger, passively restored sites.

Table 12 shows PerMANCOVA results examining the effects of key environmental variables on the observed Herp communities in the NMDS ordination shown in Figure 1a. These results indicate that isolation, distance to temporary water and method of restoration were significantly associated with reptile and amphibian community composition.

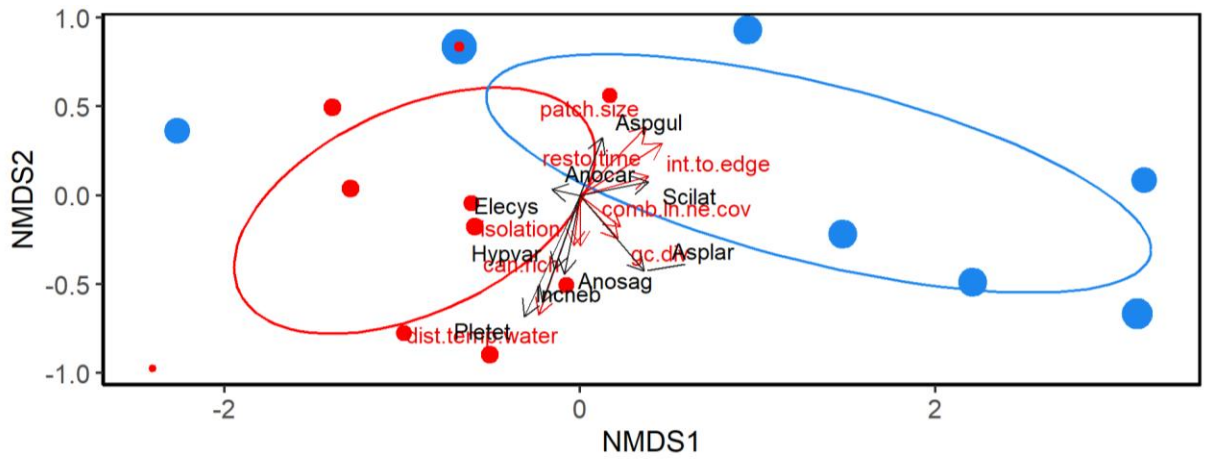

Figure 29. NMDS ordination representing Herptile community composition and similarities among observed communities, which are represented as the position and spatial proximity of points, respectively. Points represent observed communities and correspond to individual sampling points (n = 36, 3 per study site). The color and size of points denote method of restoration and patch size. Black vector arrows denote influential species that most strongly drove separation among communities in the directions specified; points located farther in a given direction can be interpreted as having higher abundances of species whose vectors point in that direction relative to other sites. Red vector arrows denote continuous environmental factors that were most strongly associated with the separation among communities in the directions specified. Colored ellipses represent the 95% confidence intervals around the theoretical average communities (centroids) for the groups defined by the method of restoration.

Table 12. PerMANCOVA results examining the effects of isolation, distance to temporary water and method of restoration on herpetofauna community composition. More complex models with additional terms and interactions between terms were considered prior to model pruning. Environmental factors not included in this model were removed either to avoid multicollinearity or because they explained an insignificant amount of variance. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	d.f.	$F_{3,21}$	*p*	
Isolation	1	3.13	0.0100	**
Distance to temporary water	1	3.63	0.0070	**
Method of restoration	1	3.45	0.0030	**

Herpetofauna Community Univariate Analyses

Herptile richness averaged 0.39 ± 0.44 across all study sites and were influenced by time since restoration, ground cover plant diversity, distance to permanent water, and understory richness (Table 13). Relationships to time since restoration, ground cover plant diversity and distance to permanent water are shown in Figures 30, 31, 32, and 33. Ground cover plant diversity had a positive linear relationship with herptile richness whereas time since restoration,

distance to permanent water, and understory richness had negative relationships. Actively restored sites averaged higher richness (0.85 ± 0.69) than passively restored sites (0.30 ± 0.67).

Table 13. ANCOVA Type III results examining the effects of time since restoration, ground cover plant diversity, distance to permanent water, and understory richness on herpetofauna richness. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{4,18}$	p	
Time since restoration	-0.0248600	1	16.42	0.0007	***
Ground cover plant diversity	0.8989293	1	16.85	0.0007	***
Distance to permanent water	-0.0011489	1	8.45	0.0094	**
Understory richness	-0.1699974	1	7.35	0.0142	*
Model		18	7.33	0.0011	

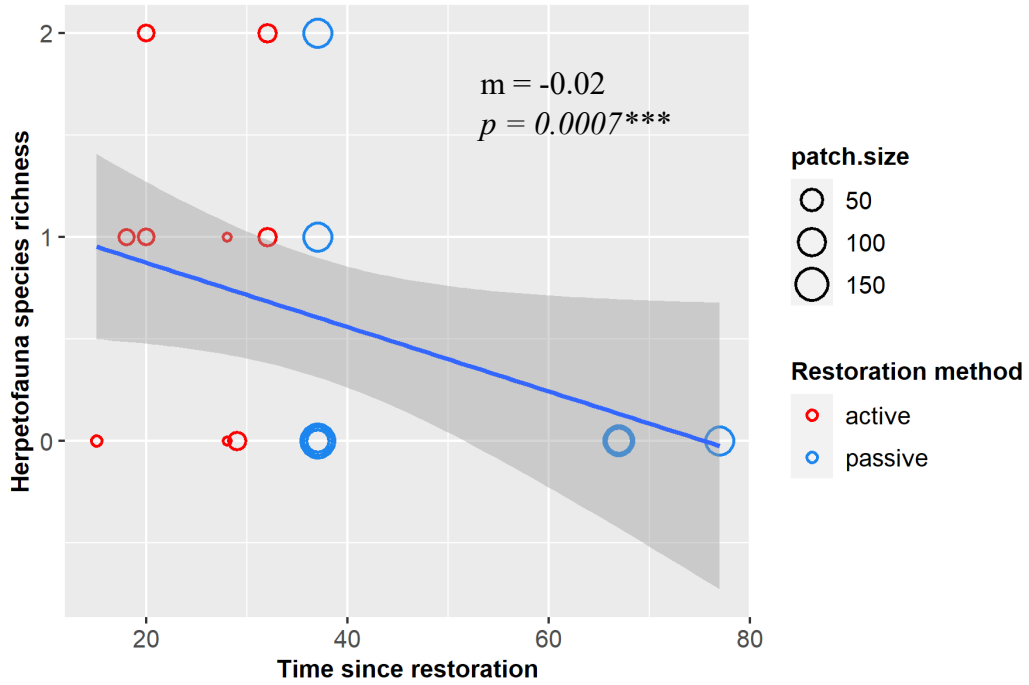

Figure 30. Linear relationships between Herpetofauna speci es richness and time since restoration. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

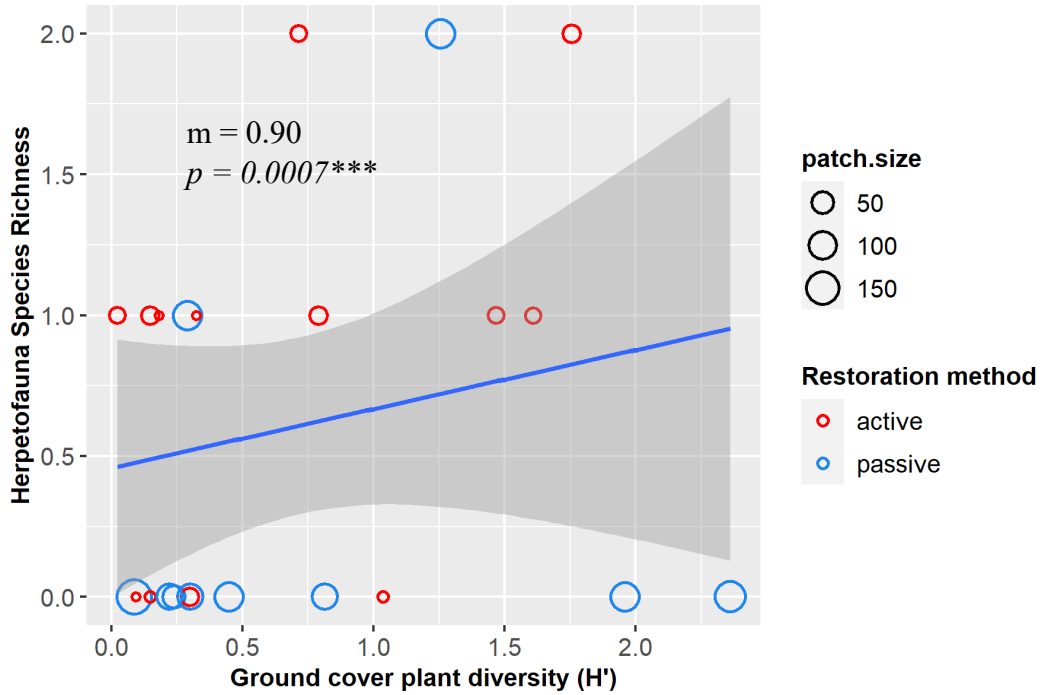

Figure 31. Linear relationships between Herpetofauna species richness and ground cover plant diversity. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

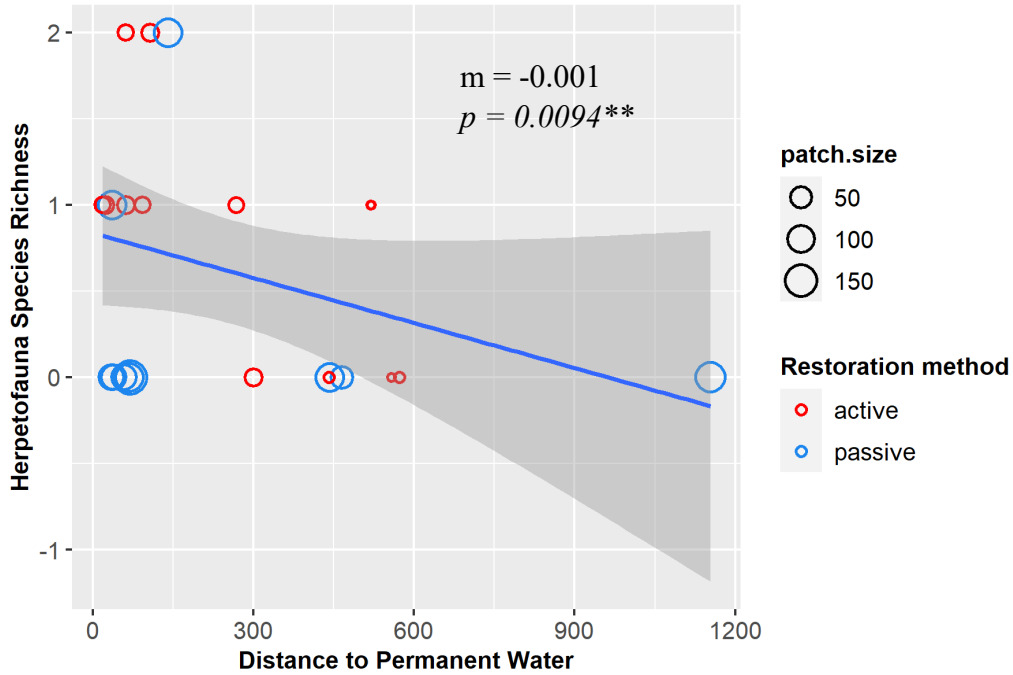

Figure 32. Linear relationships between Herptile species richness and distance to permanent water. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in

the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

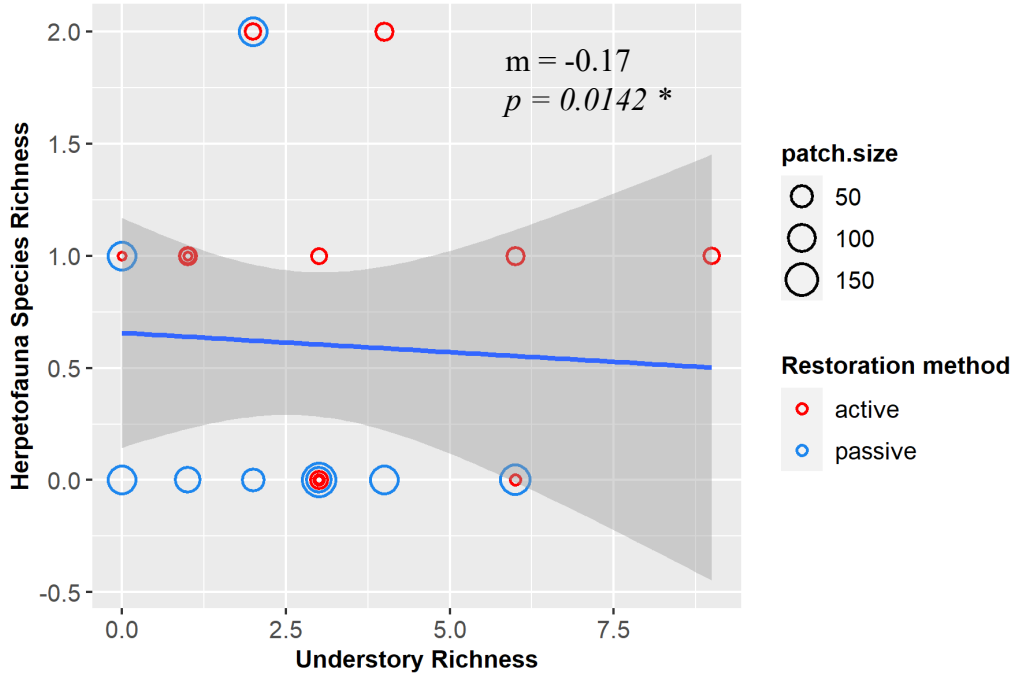

Figure 33. Linear relationships between Herptile species richness and understory richness. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

Herptile diversity averaged 0.39 ± 0.44 across study sites and was independent of all the environmental factors tested. Distance to permanent water explained the most variance, but its effect on herptile diversity was not significant, both when tested alone and in models with the next most explanatory variables. Actively restored sites averaged higher diversity (0.52 ± 0.45) than passively restored sites (0.22 ± 0.38).

Herptile abundance averaged (0.30 ± 0.67) across study sites and was influenced by method of restoration and distance to permanent water (Table 14). Relationships to distance to permanent water and method of restoration are shown in figures 34 and 35. Distance to permanent water had a negative linear relationship with herptile abundance. The estimated

difference in effect size between actively and passively restored sites was 1.52. Actively restored sites averaged a higher abundance of herptiles (4.77 ± 3.22) than passively restored sites (2.10 ± 2.28).

Table 14. ANCOVA Type III results examining the effects of method of restoration, distance to permanent water, soil moisture, and invasive grass cover on herpetofauna abundance. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{4,18}$	p	
Method of restoration	1.518099	1	7.26	0.0148	*
Distance to permanent water	-0.005838	1	7.26	0.0245	*
Soil moisture	0.067431	1	1.21	0.2858	
Invasive grass cover	-0.054546	1	3.34	0.0843	.
Model		18	3.03	0.0449	

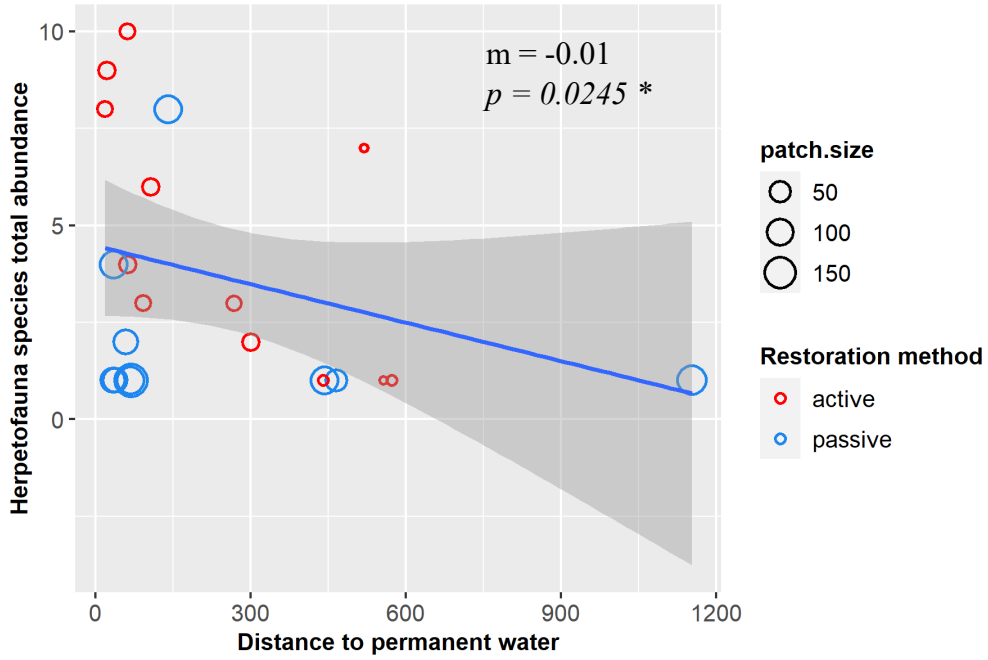

Figure 34. Linear relationships between Herpetofauna species abundance and distance to permanent water. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

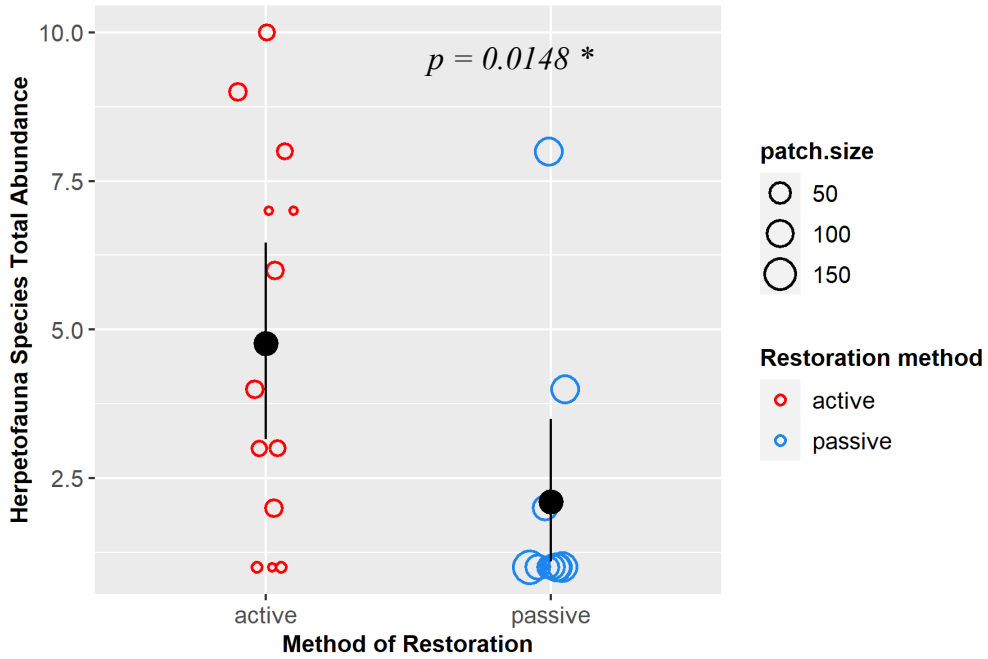

Figure 35. Observed values with means (black dots) and 95% confidence intervals (error bars) of Herpatofauna species total abundance broken down by method of restoration. Open circles denote values from one sampling point; color denotes method (red = active, blue = passive) and size denotes patch size.

Ensemble (Combined) Animal Communities

Multivariate Analyses of Ensemble Animal Communities

In total, we observed 158 animal species consisting of 77 lepidoptera, 53 birds, 18 mammals, and 10 herps. Each species was given equal weight in this analysis; we did not make adjustments to give each group equal influence. This means that Lepidoptera, which accounted for 49% of species, will have more relative influence on results than other groups and herptiles, which accounted for only 6% of species, will have the least relative influence.

A nonmetric multidimensional scaling (NMDS) ordination of the combined animal community data is shown in Figures 36 and 37. A number of influential species, but most strongly *Mephitis mephitis* (Striped Skunk), *Anolis sagrei* (Brown Anole), and *Lesmone detrahens* (Detracted Owlet), drove separation among communities and were associated with

younger, smaller, actively restored sites, as well as with higher levels of understory total cover and hog disturbance. *Asterocampa clyton* (Tawny Emperor), *Dryobates scalaris* (Ladder-backed Woodpecker), and *Dicotyles tajacu* (Collared Peccary/Javelina) drove separation in the directions associated with higher values for patch size, interior to edge ratio, restoration time, and distance to permanent water. *Melanerpes aurifrons* (Golden-fronted Woodpecker) and *Myiarchus tyrannulus* (Brown-crested Flycatcher) drove separation in the same direction as isolation and were most abundant at more isolated sites.

Table 15 shows PerMANCOVA results examining the effects of key environmental variables on combined animal communities in the NMDS ordinations. Time since restoration, soil temperature, distance to permanent water, total richness and combined exotic cover had significant effects on ensemble animal community composition.

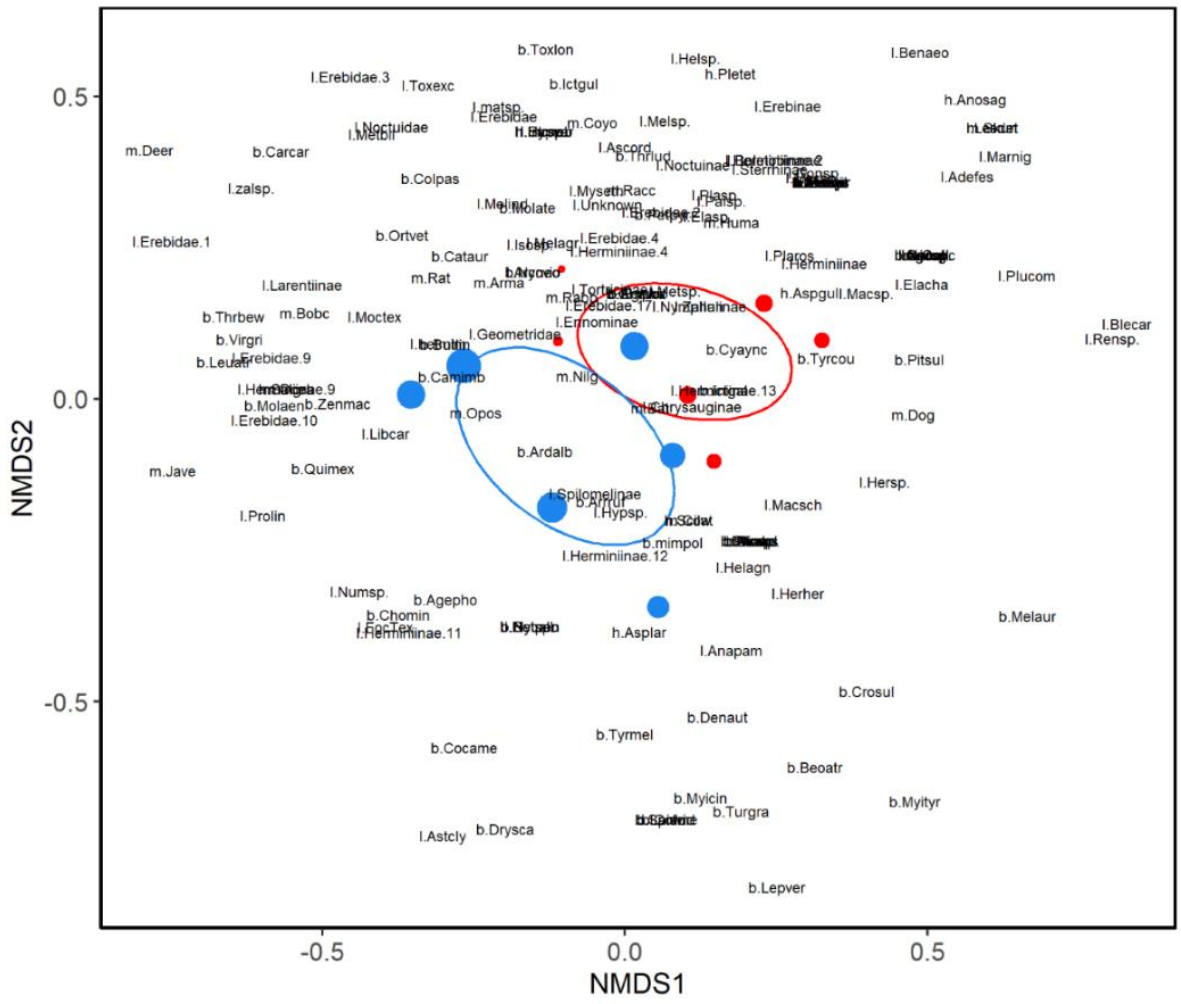

Figure 36. NMDS ordination representing combined animal community composition and similarities among observed communities, which are represented as the position and spatial proximity of points, respectively. Points represent observed communities and correspond to individual study sites. The color and size of points denote method of restoration and patch size. Colored ellipses represent the 95% confidence intervals around the theoretical average communities based on method of restoration.

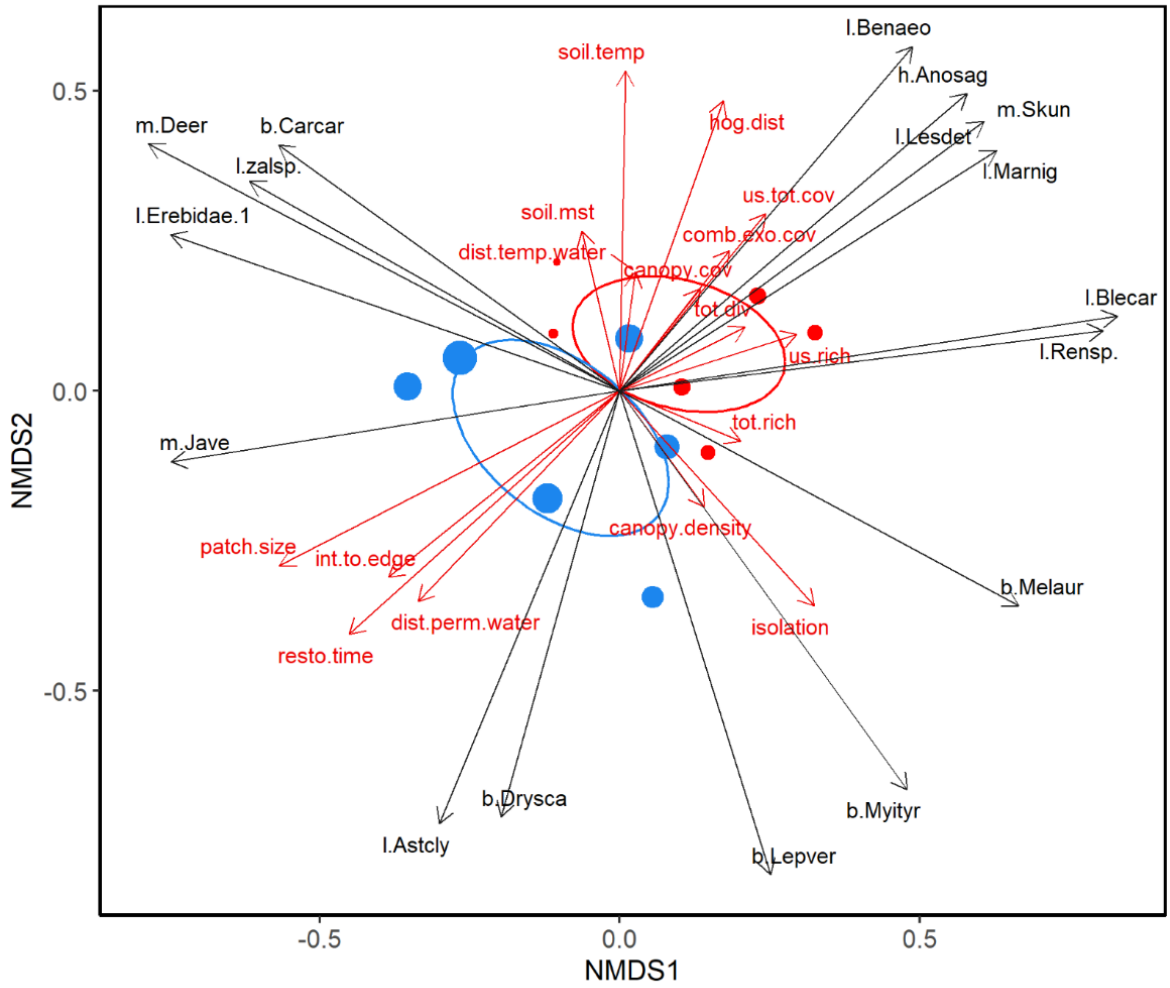

Figure 37. NMDS ordination representing ensemble community composition and similarities among observed communities, which are represented as the position and spatial proximity of points, respectively. Points represent observed communities and correspond to individual sampling points (n = 36, 3 per study site). The color and size of points denote method of restoration and patch size. Black vector arrows denote influential species that most strongly drove separation among communities in the directions specified; points located farther in a given direction can be interpreted as having higher abundances of species whose vectors point in that direction relative to other sites. Red vector arrows denote continuous environmental factors that were most strongly associated with the separation among communities in the directions specified. Colored ellipses represent the 95% confidence intervals around the theoretical average communities (centroids) for the groups defined by the method of restoration.

Table 15. PerMANCOVA results examining the effects of time since restoration, soil temperature, total plant richne ss, distance to permanent water, combined exotic cover, and understory total cover on combined animal community composition. More complex models with additional terms and interactions between terms were considered prior to model pruning. Environmental factors not included in this model were removed either to avoid multicollinearity or because they explained an insignificant amount of variance. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	d.f.	$F_{5,11}$	*p*	
Time since restoration	1	1.95	0.001	**
Soil temperature	1	2.13	9.999e-05	***
Total richness	1	1.55	0.0380	*
Distance to permanent water	1	1.99	0.0011	**
Combined exotic cover	1	1.53	0.0338	*
Understory total cover	1	1.40	0.0807	.

Ensemble Communities Univariate Analyses

Ensemble community richness averaged (31.44 ± 6.01) and was influenced by invasive grass cover, method of restoration, and canopy plant species richness (Table 16). Relationships to invasive grass cover, method of restoration and canopy richness are shown in figures 38, 39, and 40. Invasive grass cover and canopy richness had negative linear relationships with ensemble richness. The estimated difference in effect size between passively and actively restored sites was 2.69. Actively restored sites averaged a higher richness (32.72 ± 6.17) than passively restored sites (30.17 ± 5.73).

Table 16. ANOVA Type III results examining the effects of invasive grass cover, method of restoration, and canopy richness on ensemble species richness. Legend: ***, $p < 0.001$; **, $0.001 \leq p < 0.01$; *, $0.01 \leq p < 0.05$; ., $0.05 \leq p < 0.1$.

Factor	Effect size	d.f.	$F_{3,32}$	p	
Invasive grass cover	-0.14231	1	14.94	0.0005	***
Method of restoration	2.68873	1	8.22	0.0073	**
Canopy richness	-2.04467	1	7.48	0.0101	*
Model		32	6.33	0.0017	

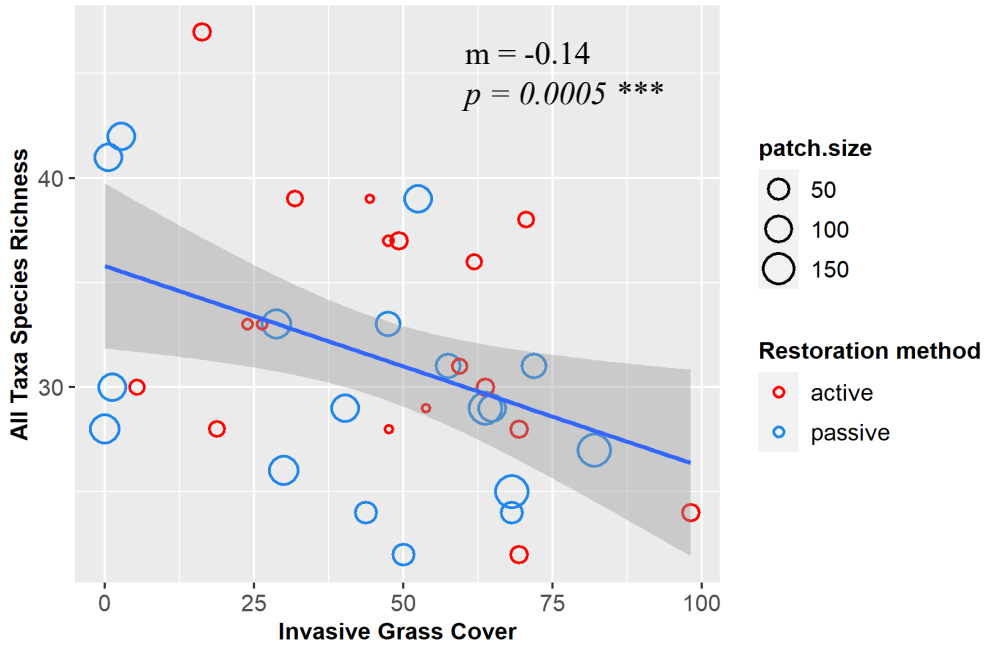

Figure 38. Linear relationships between ensemble species richness and invasive grass cover. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

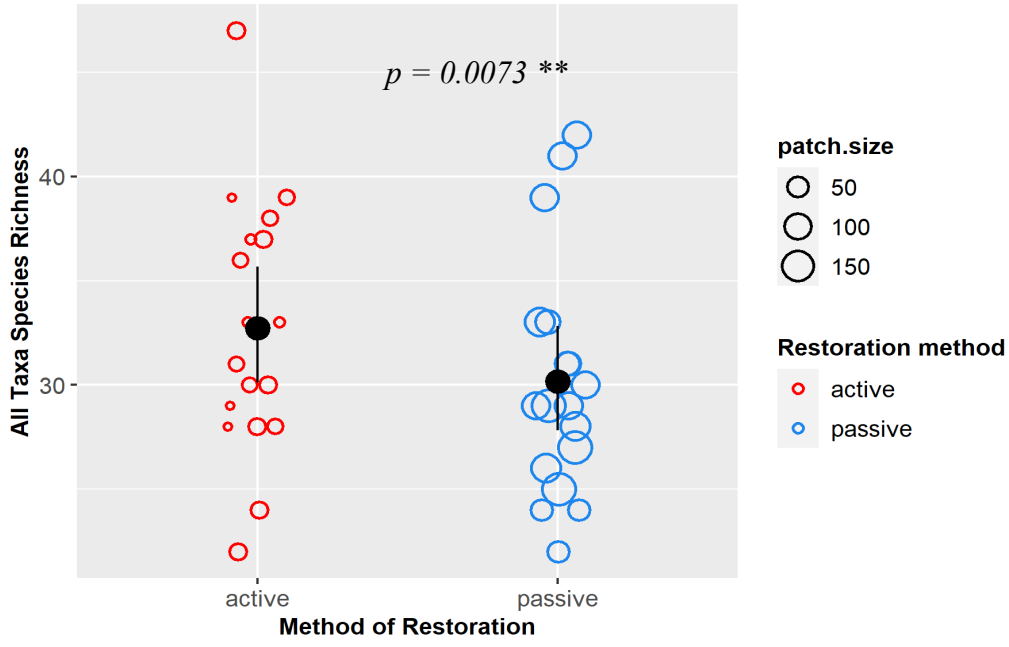

Figure 39. Observed values with means (black dots) and 95% confidence intervals (error bars) of ensemble animal community species richness broken down by method of restoration. Open circles denote values from one sampling point; color denotes method (red = active, blue = passive) and size denotes patch size.

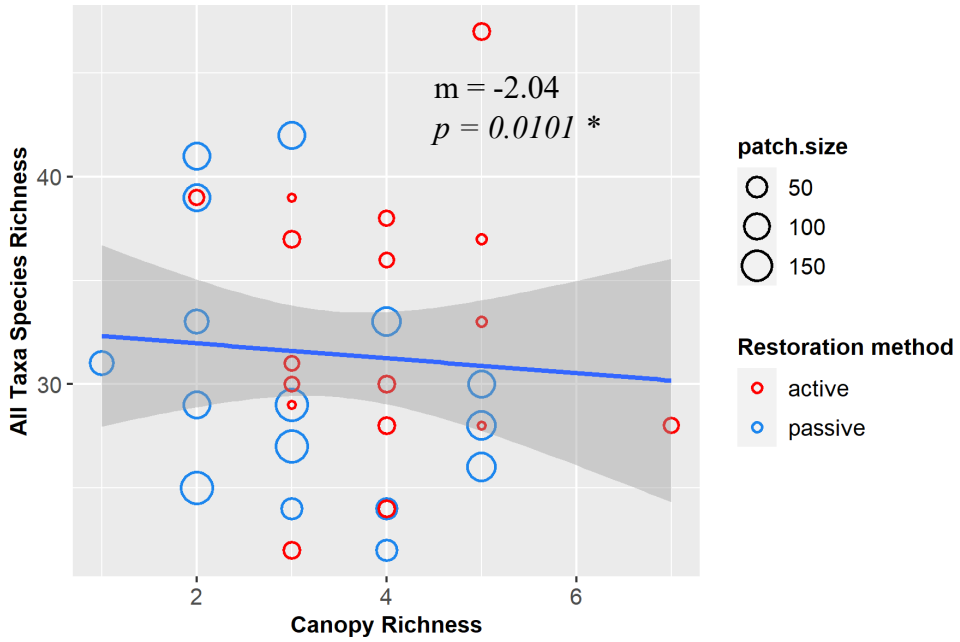

Figure 40. Linear relationships between ensemble species richness and canopy richness. Open circles denote values from one study site; they are colored based on method of restoration and sized according to patch size. The blue trendline denotes the ordinary least squares regression line calculated using only the variables depicted in the plot (hence its slope does not necessarily reflect the effect size in our results table, which considers multiple predictor variables simultaneously); the curved gray band illustrates the standard error of the slope and y-intercept of the regression line.

CHAPTER IV

DISCUSSION

Discussion of Influential Factors

In this study, we documented and characterized the animal communities within four taxa (mammals, birds, herptiles, and Lepidoptera) within 12 restored Tamaulipan thornscrub forest habitats in the eastern Lower Rio Grande Valley of southernmost Texas. We hypothesized that site and environmental characteristics influenced the composition of animal communities and other community-level response variables (richness, diversity, and abundance), and that the nature and strength of these environmental factors would vary based on the animal taxa and ecological context. We found that each of our focal site characteristics (restoration time, restoration method, patch size, and degree of isolation) significantly influenced at least one aspect of the surveyed animal communities, but they were not always as widely influential as we expected. Other environmental factors, such as ground layer plant diversity, distance to permanent or temporary water, and soil temperature (which reflects shading and thus overall vegetation density) influenced many community-level responses and often explained a larger proportion of the observed variance than our focal site characteristics, but this was not true for all animal communities or community response variables. Out of our focal site characteristics, time since restoration and method of restoration were most often significant, followed by the degree of isolation and then patch size. However, as discussed above and elaborated below, some of

these factors were unavoidably confounded, so we must be careful not to discount the importance of factors like patch size.

One challenge that we faced with our analysis was that the method of restoration, time since restoration, and patch size were all somewhat confounded because the older sites in the study region also tended to be larger and passively restored, whereas more recently restored sites were typically smaller and actively restored. This makes historical sense, in that it was logical for the largest patches of former thornscrub forests (and possibly those deemed not to require active restoration) to be the first sites to become protected, and this occurred before active restoration became both better understood and more commonplace. This historical pattern often made it difficult to disentangle the specific effects of these factors.

Method of Restoration

Method of restoration significantly influenced mammal, Lepidoptera and herptile community composition, as well as bird richness, Lepidoptera abundance, herptile abundance, and ensemble community richness. The average overall animal richness was slightly but significantly higher among sampling points in actively versus passively restored sites (31.1 vs. 30.2 species observed), and our final model examining ensemble richness had a predicted effect size of 2.68 more species in actively restored areas. In the case of birds, there were significantly more species at sampling points in passively restored sites (14.05) than in actively restored sites (13.05). Passive restoration has been found to be an effective method in supporting bird richness in some cases (da Silva et al. 2019) but other studies that compared active and passive restoration found active restoration to be more effective in restoring bird communities (Rey-Benayas et al. 2010), while still others saw little difference between the two methods (Barros et al. 2022).

Method of restoration was significant in the case of Lepidoptera abundance, but in the opposite direction, with more individuals found at each point in actively restored sites (53.2) than in passively restored sites (41.2). Actively restored sites also resulted in higher herptile abundance, with an average of 2.3 individuals per point in comparison to 1.2 individuals per point at passively restored sites.

At least one aspect of each of our taxa was significantly influenced by method of restoration. Our results reflect findings in literature; method of restoration is important, but the impact of the method varies by taxa. Most often, the actively restored sites had richer or more diverse communities, but sometimes the passively restored sites did. These results substantially increase our understanding of the efficacy and outcomes of active restoration in the LRGV region on animal communities, but important questions remain, especially related to birds and restored plant communities, which are not regularly monitored and for which results of active restoration are known to be mixed.

Time Since Restoration

Time since restoration drove separation in community composition in the case of mammals, Lepidoptera, and all taxa combined (Table 17). It also significantly influenced herptile richness and Lepidoptera abundance. It seems very logical that time since restoration would impact animal communities, as there are both early and late successional species and differences in dispersal ability, as with plants, and because some animal species depend on early or late successional plants or other animal species for food or other resources. However, the mechanisms underlying why time since restoration significantly community composition of Lepidoptera and mammals, but not birds and herptiles, are not clear. In the case of birds, this could be because flight conveys greater dispersal capabilities than other taxa, allowing birds to

recolonize new patches much more rapidly than other animals. The lack of impact on herptile community composition, on the other hand, is more challenging to understand. It may be related to the species our survey methods were likely to detect; perhaps we were detecting better dispersers or cosmopolitan species, and those dependent on specific plant species or environmental conditions were less likely to be detected. It may also just be that plant metrics are better predictors of herptile communities than time; in our results, herptiles responded to ground and understory vegetation. Time since restoration did, however, significantly influence herptile richness; the longer it had been since the restoration began, the greater the richness. Because herptile richness increased with time, but its community composition did not vary with time, it is possible that we had detection issues and that our sample did not represent the true status of the herptile community. Calculating species-accumulation curves for the restored sites would be an informative next step to help us better understand and interpret our results.

Lepidoptera abundance was also greater in older sites. Although increases in diversity are a typical expectation as communities assembly over time, this is not the case for abundance. Abundance patterns associated with successional stages are usually specific to particular groups. We expected to generally see diversity increase with time, but our results did not show this.

Degree of Isolation

The degree of isolation influenced mammal richness as well as the community composition of Lepidoptera and herptiles (Table 17). The effect on mammal richness was small but statistically significant; for every unit of increase in isolation (percent of the area in a 1 km radius that was not thornscrub forest), mammal richness increased by 0.04 species. This result was unexpected and the mechanism underlying this pattern is unknown. One possible explanation is that isolated patches have fewer predators, allowing a variety of prey species to

proliferate. This would be testable using our data by separately considering predator and prey species. Alternatively, isolation could have a concentrating effect, with thornforest-dependent species in an area having fewer options for where to forage or den. A closer examination of the effect of isolation on individual species could tell us more.

The degree of isolation was also significantly associated with differences in Lepidoptera and herptile community composition, but again the mechanism is unclear, as is the reason why mammals and birds were unaffected by isolation. The answer is likely related to dispersal ability. Herptiles have a more difficult time getting from one patch to another than birds or larger mammals. One study conducted in Australia found that common reptile species were not impacted by isolation, while rarer species were significantly impacted; Shutz and Driscoll (2008) speculated that a larger abundance of a herptile species increases its likelihood of being able to disperse (Schutz and Driscoll 2008). One would think that Lepidoptera, on the other hand, could overcome dispersal challenges related to isolation. The literature supports this supposition. A study on *Acrobasis betulella* (Birch Tube-maker) found that isolation had no impact on their ability to disperse to other suitable habitats (Cappuccino and Martin 1997). A study of *Coenonympha tullia* found that habitat quality was more important than patch size and isolation combined (Dennis and Eales 1997). It is interesting, therefore, that our results show otherwise. Perhaps isolation is more influential on frugivorous Lepidoptera, which our survey method attracted. Perhaps the size of the Lepidoptera affects their ability to disperse; many of the Lepidoptera we caught were very small. While our results make sense for herptiles, they are harder to explain for Lepidoptera.

Patch size

Patch size significantly influenced mammal community composition but did not affect the composition of any other animal taxa studied (Table 17). It is possible that patch size was important to more taxa but was overshadowed by the strong effects of time since restoration, which correlated with patch size. Patch size was often removed from models to avoid multicollinearity, which means that other factors explained more variance but does not rule out patch size as important. It is also possible that this pattern is real, and that patch size is relatively unimportant for birds and Lepidoptera because flight allows them to utilize multiple patches more easily, or for herptiles because they typically have smaller home ranges than medium and large mammals. The negative effects of habitat fragmentation and reduced patch size on medium to large mammals are well documented by other studies (Garmendia et al. 2013, Schnetler et al. 2021).

The literature surrounding birds, however, is less consistent on the importance of patch size. Studies investigating the importance of patch size to bird communities are mixed, for example; some found that patch size was important to functional diversity (Maseko et al. 2020) or abundance (Smallwood et al. 2009), whereas others found that patch size was not important in comparison to the trees present (Mellink et al. 2017), and it is unclear if these patterns vary among major climate zones. Our results align more the Mellink et al. study in that canopy density significantly influenced bird richness, while patch size had no significant effect on any aspect of bird communities. It may be that it depends on the species; Smallwood et al. were studying American Kestrels, which require larger territories than songbirds, for example. Mellink et al. found that patch size didn't matter for 54 out of 55 species present, but it did matter for one

particularly sensitive species of sparrow. For future work, we would like to analyze the impacts of habitat and environmental factors on individual bird species to see how our findings compare.

In the case of Lepidoptera, another study conducted in South Texas also found that patch size did not have a significant impact on community composition; factors like plant diversity, wind speed and habitat class were of more importance (Stilley and Gabler 2021). Our study found many other factors to be more influential on community composition than patch size, including time since restoration, extent of isolation, method of restoration, soil moisture, canopy cover, invasive grass cover, and ground cover plant diversity. When it comes to herptiles, our results contrast with much of the literature when it comes to the importance of patch size to reptiles and amphibians. While patch size was insignificant in our analyses, many other studies found that larger patches resulted in higher herptile richness, diversity, or abundance, or otherwise influenced community composition (Garden et al. 2010, Cabrera-Guzmán and Reynoso 2012, Russildi et al. 2016).

From our results and from other studies we can conclude that the effects of patch size on animal communities may depend on several factors. It could depend on the needs of the species, the size of the species, and the mobility of the species. The scale of sizes considered may also have limited our capacity to detect the effects of patch size; our study sites ranged in size from 4.5 to 174.5 ha (11 to 431 acres), which is below the range that many studies consider to be large patch sizes. Lastly, patch size may have been important, but, even if it was, it was not as good of a predictor as time since restoration or method of restoration. Further analysis should be conducted to understand its effects in more detail.

Other important environmental factors

Other environmental variables also frequently had significant impacts on our surveyed animal communities. Both metrics of distance to water sources were significantly influential in multiple cases. Distance to permanent water significantly influenced mammal community composition and the community composition of all taxa combined. For every kilometer that the distance to permanent water increased, the herptile richness decreased by 1.15 species and ensemble richness decreased by 5.84 species. Distance to temporary water significantly influenced the community composition of mammals, birds, and herptiles. It is interesting that distance to temporary water drove separation amongst bird and herptile community composition, whereas distance to permanent water did not. In the case of birds, this could be because ephemeral shallow wetlands would attract different species than deeper, more permanent water sources, or because birds have an easier time travelling farther to a permanent source if the temporary source is not available.

The influence of factors related to invasive species prevalence, which were overwhelmingly driven by introduced forage grasses, was also often significant. Ensemble richness had a significant negative relationship with invasive grass cover (richness decreased as grass cover increased) and combined exotic cover (total cover by all exotic species across all forest layers) significantly influenced the ensemble animal community composition. There are many different studies that demonstrate the negative impact that invasive plants can have on faunal communities (Abom et al. 2015, Drake et al. 2016, Schlesinger et al. 2020), and our results are yet another example. Ground cover plant diversity had a negative relationship with exotic plant cover (Fig. 3) and was also often significant, influencing Lepidoptera community

composition and positively influencing mammal abundance, mammal richness, mammal diversity, and herptile richness.

Soil moisture was particularly important in the case of Lepidoptera, for example, significantly impacting community composition, diversity, and abundance. With that said, we only measured soil moisture once, so we cannot distinguish whether this was due to a long-term effect resulting from different moisture regimes amongst sites, or due to a short-term effect of recent rain, perhaps resulting in higher abundances of blooming plants. Studies do show, however, that soil moisture can be very important to Lepidoptera. Some studies discuss how low moisture conditions during larval pupation can adversely affect certain species (Wang et al. 2018), or adversely affect larval escape (Ma et al. 2017). One recent study points out that Lepidoptera typically spend more of their lives in the chrysalis and caterpillar stages, and these two stages are often directly related to litter and soil (about 25% of lepidopteran species have obligatory interaction with soil) (Legal 2023).

Table 17. Displays all environmental variables used in analysis and their level of significance to community composition, richness, diversity and abundance for each taxa where possible. Legend: '***' p < 0.001; '**' p < 0.01; '*' p< 0.05; '.' p<0.1

	Mammals				Birds		Lepidoptera				Herpetofauna				All Taxa	
	Comm	Rich	Div	Abun	Comm	Rich	Comm	Rich	Div	Abun	Comm	Rich	Div	Abun	Comm	Rich
Time since restoration	**						**			**		***			**	
Patch size	***															
Extent of isolation		*					***				**					
Method of restoration	***					**	**			**	**			*		**
Interior to edge ratio																
Canopy cover							**									
Soil moisture							**		***	**						
Soil temperature		*													***	
Distance to permanent water	**							.	.			**		*	**	
Distance to temporary water	*				**		.				**					
Invasive grass cover						*	*							.		***
Understory total cover			*												.	
Canopy density					*											
Total plant richness															*	
Total plant diversity																
Ground cover plant richness		**	*													
Ground cover plant diversity	.			*			**			***		***				
Understory richness		***				.						*				
Understory diversity		*														
Canopy richness								*								*
Canopy diversity						*										
ln(ratio of native:exotic cover)							**	*		***						
Combined exotic cover															*	

Conclusions

The sites that we surveyed varied in time since restoration, method of restoration, patch size, degree of isolation, and a variety of other environmental variables. For all but one of our response variables, one or more of the focal factors resulted in significant differences between animal communities. Method of restoration and time since restoration were the two focal factors that most frequently had a significant effect across the 16 different community-level analyses conducted in this study. Overall, restoration time and restoration method had more frequent and/or stronger effects on animal communities than patch size or extent of isolation, though the relative important of patch size is complicated by the fact it was confounded with time since restoration and restoration method. Other factors that frequently significantly influenced animal communities were ground layer plant diversity, distance to permanent water, and soil moisture. When all taxa were considered together, animal community composition was impacted by time since restoration, soil temperature, distance to permanent water, total plant richness, and overall exotic plant cover (across all forest layers). Ensemble community richness was impacted by invasive grass cover, method of restoration, and canopy richness.

From this study, we can draw several conclusions. Our research reinforces the well-established notions that animal communities will change as the time since restoration efforts began increases and as plant communities develop and progress through succession. It reinforces the commonly observed pattern that invasive grasses and other exotic plants negatively impact the richness of animal communities as they attempt to recolonize and can cause significant differences in ensemble animal communities. Our findings suggest that the method of restoration is important, as it was associated with significant differences difference between the community composition of both Lepidoptera and herptiles, but our results do not suggest that one method is

necessarily superior to another in the case of faunal recolonization of restored Tamaulipan thornscrub forests. If actively restoring a site, efforts towards invasive plant control, fostering native plant diversity, and ensuring there is a nearby water source are likely the most practical steps that can be taken to encourage faunal recolonization. At larger scales, promoting variation in vegetation structure will likely increase overall animal diversity.

Future Directions

Many further analyses are merited that could be performed using this data set. Investigation of how individual species were affected by different environmental variables, particularly conservation foci like bobcats and ocelots, would be particularly valuable to land managers. It would also be informative to separate our data by method of restoration and analyze community richness, abundance, diversity, and composition separately for actively and passively restored sites. This would further disentangle restoration time, patch size, and restoration method and help us better understand the relative contributions of these focal factors, and would allow us to determine whether these and other environmental variables had different impacts depending on the method of restoration. Additionally, analyses that separately consider exotic versus native species and their patterns and prevalence across sites are merited and would be valuable to land managers. Finally, several particularly timely and important analyses could be done with this data to investigate the effects of proximity to the U.S.-Mexico border wall and/or the landscape-scale position of a habitat patch along the broader border wall system. Some of our sites are very near the border wall while others are not, so this is feasible with the current dataset. Furthermore, some study sites represent narrow gaps in the border wall (bottlenecks); so it may even be

possible to compare patches near the wall, patches far from the wall, and patches that are present within a wall ‘gap’ or habitat bottleneck.

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APPENDIX A

APPENDIX

Appendix 1. Lists of all mammal species observed over the course of the study period at each sampling point. Survey effort varied among points, so abundance was normalized to the number of independent observations per 30-day period.

Common Name	Scientific Name	AC1	AC2	AC3	AU1	AU3	DH2	DH3	EU1	EU2	EU3	FH1	FH2
Nine-banded armadillo	*Dasypus novemcinctus*	0.00	0.00	0.00	0.00	0.00	27.53	0.00	0.00	0.00	0.60	0.00	9.46
Bat sp.	*Chiroptera sp.*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bobcat	*Lynx rufus*	0.00	0.00	2.02	0.00	0.00	4.11	0.00	0.29	0.57	0.00	0.00	0.00
Cat	*Felis catus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.33
Cow	*Bos taurus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Coyote	*Canis latrans*	0.00	0.00	2.88	0.00	0.56	0.82	0.00	0.57	1.13	0.00	0.00	4.57
Dog	*Canis lupus familiaris*	0.00	0.00	0.00	0.00	0.00	0.41	0.00	0.00	0.00	0.00	0.00	0.33
Feral hog	*Sus scrofa*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.88	2.61
Human	*Homo sapiens*	0.00	0.00	0.00	0.00	0.00	0.41	0.73	0.00	0.00	0.00	0.00	0.00
Collared peccary	*Dicotyles tajacu*	0.33	0.00	1.15	0.94	1.67	4.52	0.00	1.14	1.70	0.00	0.00	0.33
Nilgai	*Boselaphus tragocamelus*	1.96	1.43	3.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern ocelot	*Leopardus pardalis*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Virginia opossum	*Didelphis virginiana*	0.00	0.00	0.00	0.00	0.00	7.81	0.00	0.00	0.00	0.00	0.00	0.00
Cottontail rabbit	*Sylvilagus floridanus*	0.00	0.00	0.00	0.00	0.00	3.29	0.00	0.00	0.00	1.80	0.00	3.91
Common raccoon	*Procyon lotor*	0.00	0.00	0.87	0.00	0.00	30.41	0.73	0.00	0.57	0.00	0.00	8.80
Rat sp.	*Rattus sp.*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Striped skunk	*Mephitis mephitis*	0.00	0.00	0.00	0.00	0.00	2.88	0.00	0.00	0.00	0.00	0.00	0.65
White-tailed deer	*Odocoileus virginianus*	8.80	2.86	29.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Totals	*11.09*	*4.29*	*39.22*	*0.94*	*2.23*	*82.19*	*1.46*	*2.00*	*3.97*	*2.40*	*0.88*	*30.99*

Common Name	Scientific Name	FH3	GC1	GC2	GC3	GI1	GI2	GI3	LU1	LU2	LU3	PB1	PB2
Nine-banded armadillo	*Dasypus novemcinctus*	0.00	2.11	0.00	0.00	2.06	0.00	10.71	0.00	0.88	1.40	0.00	1.35
Bat sp.	*Chiroptera sp.*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bobcat	*Lynx rufus*	0.00	1.17	0.00	0.00	0.59	0.92	0.00	0.00	6.76	4.88	0.00	0.00
Cat	*Felis catus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Cow	*Bos taurus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Coyote	*Canis latrans*	0.51	4.22	0.31	1.97	0.00	0.00	1.07	0.29	1.18	0.00	0.00	0.34
Dog	*Canis lupus familiaris*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18	0.00	0.00	0.00
Feral hog	*Sus scrofa*	0.51	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Human	*Homo sapiens*	0.00	0.00	1.55	0.00	0.00	0.00	0.00	0.00	0.88	0.00	0.54	0.00
Collared peccary	*Dicotyles tajacu*	0.00	2.34	0.31	2.46	1.47	0.46	2.14	7.57	2.65	1.40	0.00	0.34
Nilgai	*Boselaphus tragocamelus*	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern ocelot	*Leopardus pardalis*	0.00	0.00	0.00	0.00	0.00	1.85	2.14	0.00	0.00	0.00	0.00	0.00
Virginia opossum	*Didelphis virginiana*	0.00	0.00	0.00	0.00	1.18	0.00	0.00	0.00	0.29	0.00	0.00	0.00
Cottontail rabbit	*Sylvilagus floridanus*	0.00	0.00	0.00	0.00	1.47	0.00	2.14	0.00	1.18	0.00	0.00	0.67
Common raccoon	*Procyon lotor*	0.51	31.41	0.00	1.48	0.29	4.62	5.36	0.00	2.94	0.00	0.00	2.02
Rat sp.	*Rattus sp.*	0.00	0.47	0.00	0.00	0.00	0.00	0.00	2.33	0.00	0.00	0.00	0.00
Striped skunk	*Mephitis mephitis*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
White-tailed deer	*Odocoileus virginianus*	0.00	0.00	0.31	1.48	5.88	6.00	7.50	0.00	0.00	0.00	0.00	0.00
	Totals	*1.78*	*41.72*	*2.48*	*7.39*	*12.94*	*13.85*	*31.06*	*10.19*	*17.94*	*7.68*	*0.54*	*4.72*

Common Name	**Scientific Name**	**PB3**	**TB1**	**TB2**	**TB3**	**TU1**	**TU2**	**TU3**	**VN1**	**VN2**	**VN3**	**Totals**
Nine-banded armadillo	*Dasypus novemcinctus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*56.10*
Bat sp.	*Chiroptera sp.*	0.00	0.00	0.00	0.70	0.00	0.00	0.00	0.00	0.00	0.27	*0.97*
Bobcat	*Lynx rufus*	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.00	0.00	*23.31*
Cat	*Felis catus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*0.33*
Cow	*Bos taurus*	0.00	0.00	0.00	0.00	0.00	0.00	0.86	0.00	0.00	0.00	*0.86*
Coyote	*Canis latrans*	0.00	1.07	0.00	0.23	0.00	0.45	0.00	0.00	0.00	0.27	*22.44*
Dog	*Canis lupus familiaris*	0.00	0.00	0.00	0.00	0.00	0.00	0.29	0.00	0.00	0.00	*2.21*
Feral hog	*Sus scrofa*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*4.00*
Human	*Homo sapiens*	0.00	1.07	0.00	0.23	0.00	1.79	0.00	0.34	0.00	0.00	*7.54*
Collared peccary	*Dicotyles tajacu*	0.25	0.00	0.98	0.94	0.00	0.00	0.57	0.00	0.27	0.55	*36.48*
Nilgai	*Boselaphus tragocamelus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.08	0.55	*8.44*
Northern ocelot	*Leopardus pardalis*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*3.99*
Virginia opossum	*Didelphis virginiana*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*9.28*
Cottontail rabbit	*Sylvilagus floridanus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*14.46*

Common raccoon	*Procyon lotor*	0.00	0.00	0.00	0.00	0.63	0.00	1.14	0.00	0.54	0.27	*92.59*
Rat sp.	*Rattus sp.*	0.00	2.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*4.94*
Striped skunk	*Mephitis mephitis*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*3.53*
White-tailed deer	*Odocoileus virginianus*	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.00	0.00	0.00	*62.19*
	Totals	*0.25*	*4.28*	*0.98*	*2.33*	*0.63*	*2.24*	*4.86*	*0.34*	*1.89*	*1.91*	*353.66*

Appendix 2. List of observed bird species and the number of surveys in which each species was observed at each site. Six surveys were conducted per site.

Common Name	***Scientific Name***	**AU**	**AC**	**DH**	**EU**	**FH**	**GC**	**GI**	**LU**	**PB**	**TB**	**TU**	**VN**	***Totals***
Red-winged Blackbird	*Agelaius phoeniceus*	4	1	0	0	0	1	1	0	0	4	2	0	*13*
Red-crowned Parrot	*Amazona viridigenalis*	0	0	4	0	0	0	0	0	0	0	0	0	*4*
Black-throated Sparrow	*Amphispiza bilineata*	0	0	0	1	0	0	0	0	0	0	0	0	*1*
Hummingbird sp.	*Archilochus sp.*	0	0	0	0	0	0	0	0	0	0	0	1	*1*
Great Egret	*Ardea alba*	0	1	0	0	0	0	0	0	0	0	0	1	*2*
Olive Sparrow	*Arremonops rufivirgatus*	6	5	5	5	5	3	6	5	4	6	6	3	*59*
Black-crested Titmouse	*Beolophus atricristatus*	3	0	0	0	1	0	2	0	4	0	3	3	*16*
Red-Shouldered Hawk	*Buteo lineatus*	0	1	0	0	0	0	0	0	0	1	1	0	*3*
Northern Cardinal	*Cardinalis cardinalis*	1	5	3	1	1	3	3	4	1	5	0	2	*29*
Turkey Vulture	*Cathartes aura*	0	1	0	0	1	0	1	0	0	0	0	0	*3*
Killdeer	*Charadrius vociferus*	0	0	0	1	0	0	0	0	0	0	0	0	*1*
Common Nighthawk	*Chordeiles minor*	1	0	0	0	0	0	1	0	0	1	0	0	*3*
Yellow-billed Cuckoo	*Coccyzus americanus*	3	4	0	5	0	3	2	6	4	1	3	4	*35*
Common Ground Dove	*Columbina passerina*	1	2	0	3	1	1	1	0	0	5	0	0	*14*
Northern Bobwhite	*Colinus virginianus*	1	0	0	0	0	0	0	0	0	0	0	0	*1*
Groove-billed Ani	*Crotophaga sulcirostris*	4	0	0	1	3	1	0	0	0	1	1	2	*13*
Green Jay	*Cyanocorax yncas*	0	2	1	0	3	1	0	3	2	2	1	4	*19*
Black-Bellied Whistling Duck	*Dendrocygna autumnalis*	1	0	2	1	1	0	2	2	0	0	2	1	*12*
Ladder-backed Woodpecker	*Dryobates scalaris*	2	3	0	0	1	0	2	4	3	2	2	3	*22*
Snowy Egret	*Egretta thula*	0	0	0	1	0	0	0	0	0	0	0	0	*1*
Empidonax sp.	*Empidonax sp.*	1	1	0	0	0	1	0	0	1	1	0	0	*5*
Common Yellowthroat	*Geothylpis trichas*	0	0	1	0	0	0	0	0	0	0	0	0	*1*
Baltimore Oriole	*Icterus galbula*	0	0	0	0	0	0	0	0	1	0	0	0	*1*
Altamira Oriole	*Icterus gularis*	0	1	0	0	1	2	0	0	0	0	0	0	*4*
Loggerhead Shrike	*Lanius ludovicianus*	1	0	0	0	0	0	0	0	0	0	0	0	*1*
White-tipped Dove	*Leptotila verreauxi*	6	0	0	2	2	0	2	4	2	0	2	2	*22*

Laughing Gull	*Leucophaeus atricilla*	0	4	0	0	0	0	5	0	1	0	1	0	*11*
Golden-Fronted Woodpecker	*Melanerpes aurifrons*	6	2	6	4	5	2	2	6	4	6	6	5	*54*
Northern Mockingbird	*Mimus polyglottos*	5	0	1	2	0	1	0	0	0	1	0	0	*10*
Bronzed Cowbird	*Molothrus aeneus*	0	1	0	0	0	0	3	0	1	0	1	0	*6*
Brown-headed Cowbird	*Molothrus ater*	0	1	0	1	0	1	0	0	0	0	0	1	*4*
Ash-throated Flycatcher	*Myiarchus cinerascens*	1	0	0	0	0	0	0	0	0	0	1	0	*2*
Brown-crested Flycatcher	*Myiarchus tyrannulus*	4	0	2	0	2	1	1	2	3	1	4	3	*23*
Common Pauraque	*Nyctidromus albicollis*	0	0	0	0	0	0	0	1	0	0	0	0	*1*
Black-crowned Night Heron	*Nycticorax nycticorax*	0	0	0	0	1	0	0	0	0	0	0	0	*1*
Yellow-crowned Night Heron	*Nyctanassa violacea*	0	0	0	0	0	0	0	0	0	1	0	0	*1*
Plain Chachalaca	*Ortalis vetula*	0	4	3	0	0	0	3	0	0	4	2	1	*17*
Cliff Swallow	*Petrochelidon pyrrhonota*	0	0	2	0	0	0	1	0	0	0	0	0	*3*
Cormorant sp.	*Phalacrocorax sp.*	0	0	0	0	0	0	0	0	0	0	0	1	*1*
Great Kiskadee	*Pitangus sulphuratus*	2	1	2	3	3	3	0	4	2	3	4	6	*33*
Green Parakeet	*Psittacara holochlorus*	0	0	1	0	0	0	0	0	0	0	0	0	*1*
Great-tailed Grackle	*Quiscalus mexicanus*	2	4	5	1	1	2	3	6	1	1	3	1	*30*
Chestnut-sided Warbler	*Setophaga pensylvanica*	0	0	0	0	0	0	0	1	0	0	0	0	*1*
Dickcissel	*Spiza americana*	1	0	0	0	0	0	0	0	0	0	0	0	*1*
European Starling	*Sturnus vulgaris*	0	0	0	0	0	0	0	0	0	0	0	1	*1*
Bewick's Wren	*Thryomanes bewickii*	0	3	0	0	0	0	1	0	0	0	0	0	*4*
Carolina Wren	*Thryothorus ludovicianus*	0	2	3	1	0	6	2	0	3	0	5	1	*23*
Long-billed Thrasher	*Toxostoma longirostre*	0	5	4	5	5	2	5	4	4	3	0	6	*43*
Clay-colored Thrush	*Turdus grayi*	2	0	0	0	0	0	0	0	0	0	0	2	*4*
Couch's Kingbird	*Tyrannus couchii*	6	3	5	4	3	6	3	6	4	6	3	2	*51*
Tropical Kingbird	*Tyrannus melancholicus*	2	0	0	0	0	0	0	0	0	1	0	0	*3*
White-eyed Vireo	*Vireo griseus*	0	1	0	1	0	0	2	1	2	1	0	1	*9*
Mourning Dove	*Zenaida macroura*	6	5	6	5	2	5	6	6	4	6	4	4	*59*
	Totals	*72*	*63*	*56*	*48*	*42*	*45*	*60*	*65*	*51*	*63*	*57*	*61*	

Appendix 3. List of observed Lepidoptera species and their abundance at each sampling point. When the genus could be identified but not the species, it was denoted by the first 3 letters of the genus then 'sp.'.

Scientific Name	AC1	AC2	AU2	DH1	DH2	DH3	EU1	EU2	EU3	FH1	FH2	FH3	GC1	GC2	GC3	GI1	GI2
Adelpha fessonia	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Agonopterix sp.	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Anavitrinella pampinaria	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Anomis allita	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Apilocrocis brumalis	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0
Archirhoe neomexicana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascalapha ordorata	0	0	1	2	1	1	0	3	2	0	1	4	5	0	3	2	1
Asterocampa clyton	16	0	4	0	2	0	2	0	12	0	0	0	6	2	0	0	1
Bendisodes aeolia	7	1	1	4	3	2	2	4	13	7	1	9	5	0	4	0	1
Bleptina caradrinalis	0	0	0	0	1	2	1	0	0	1	2	4	0	0	0	0	0
Boletobinnae	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0
Cecharismena sp.	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Choristoneura rosaceana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chrysauginae	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Condica sp.	0	0	0	1	0	0	2	1	1	0	0	2	0	0	0	0	0
Condylorrhiza vestigialis	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Elaphria chalcedonia	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Elaphria sp.	2	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0
Ennominae	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	1
Erebidae (morphospecies 1)	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	2
Erebidae (morphospecies 2)	0	1	0	0	0	0	2	0	0	0	0	0	0	1	0	1	0
Erebidae (morphospecies 3)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
Erebidae (morphospecies 4)	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Erebidae (morphospecies 5)	1	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
Erebidae (morphospecies 6)	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	1
Erebidae (morphospecies 7)	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
Erebidae (morphospecies 8)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
Erebinae	0	0	0	0	0	0	1	0	1	0	2	1	0	0	2	0	0

Focillidea Texana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Geometridae	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Helia agna	0	0	9	4	5	1	6	5	0	0	0	14	9	0	13	4	0
Hermeuptychia hermybius	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Herminiinae (morphospecies 1)	0	0	0	0	1	0	1	0	0	1	1	3	0	0	0	0	1
Herminiinae (morphospecies 2)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminiinae (morphospecies 3)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminiinae (morphospecies 4)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Herminiinae (morphospecies 5)	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
Herminiinae (morphospecies 6)	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
Herminiinae (morphospecies 7)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Heteranassa mima	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Heteranassa sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypsopygia nostralis	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Isogona spp.	0	0	0	0	0	0	3	2	2	0	0	0	0	0	0	0	1
Larentiinae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lascoria spp.	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Lesmone detrahens	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
Libytheana carinenta	0	1	1	0	1	0	0	1	0	0	0	0	0	3	0	0	2
Macaria graphidaria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Macristis schausi	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0
Marimatha nigrofrimbia	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
Matigramma obscurior	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Melipotis acontioides	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Melipotis agrotoides	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Melipotis indomita	0	1	0	0	0	0	0	1	0	1	0	1	0	0	0	0	12
Melipotis spp.	0	0	0	0	3	0	0	0	0	1	0	0	0	0	0	1	0
Metria bilineata	1	1	1	1	0	3	11	4	1	2	0	4	1	4	1	6	26
Mocis spp.	1	3	1	1	7	0	2	0	2	0	1	5	1	1	2	0	0
Myscelia ethusa	0	0	0	0	0	0	0	0	0	0	0	0	5	1	2	0	0
Noctuidae	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0

Noctuinae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Numia bicoloraria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Nymphalinae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Palthis asopialis	0	0	0	0	1	0	0	2	1	0	0	0	0	0	0	0	0
Platynota rostrana	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0
Platynota spp.	0	0	0	0	0	0	0	0	0	0	0	3	1	0	1	0	0
Plusiodonta compressipalpis	0	1	0	1	1	0	1	0	1	0	1	1	0	1	1	0	0
Prochoerodes lineaola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Renia spp.	1	0	1	1	1	4	1	0	0	1	2	1	0	0	0	0	0
Sterrhinae	3	0	0	1	0	2	0	0	0	26	32	14	0	1	0	1	0
Strymon sp.	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
Tortricinae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Toxonprucha excavata	0	0	0	0	1	0	2	0	2	0	0	0	0	0	1	1	0
Zale spp.	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0
Totals	35	10	19	20	38	16	45	26	42	45	56	73	36	18	38	18	59

Scientific Name	**GI3**	**LU1**	**LU2**	**LU3**	**PB1**	**PB2**	**PB3**	**TB1**	**TB2**	**TB3**	**TU1**	**TU2**	**TU3**	**VN1**	**VN2**	**VN3**	**Totals**
Adelpha fessonia	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	6
Agonopterix sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Anavitrinella pampinaria	0	1	0	2	0	0	0	0	0	0	1	0	0	1	0	0	7
Anomis allita	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Apilocrocis brumalis	2	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	8
Archirhoe neomexicana	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Ascalapha ordorata	4	0	1	0	0	0	0	4	2	0	1	1	0	0	1	1	41
Asterocampa clyton	2	1	2	2	1	0	1	0	2	1	3	18	20	4	1	1	104
Bendisodes aeolia	0	1	0	1	4	3	7	47	6	4	18	15	16	3	0	3	192
Bleptina caradrinalis	0	0	0	0	6	1	0	0	0	0	3	3	0	3	1	3	31
Boletobinnae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Cecharismena sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Choristoneura rosaceana	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	4
Chrysauginae	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2

Condica sp.	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	8
Condylorrhiza vestigialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Elaphria chalcedonia	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	3
Elaphria sp.	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	6
Ennominae	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	5
Erebidae (morphospecies 1)	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	11
Erebidae (morphospecies 2)	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	8
Erebidae (morphospecies 3)	2	1	1	0	0	0	0	1	1	0	0	0	0	0	1	0	9
Erebidae (morphospecies 4)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Erebidae (morphospecies 5)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Erebidae (morphospecies 6)	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	4
Erebidae (morphospecies 7)	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
Erebidae (morphospecies 8)	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	5
Erebinae	0	0	1	0	0	0	1	1	0	1	0	0	0	1	0	0	12
Focillidea Texana	0	2	5	8	0	0	0	0	0	0	0	0	0	0	0	0	16
Geometridae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2
Helia agna	1	9	36	23	1	2	3	1	2	8	7	23	25	2	0	1	214
Hermeuptychia hermybius	0	0	0	0	0	1	1	0	0	0	5	5	0	3	1	5	22
Herminiinae (morphospecies 1)	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	11
Herminiinae (morphospecies 2)	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	3
Herminiinae (morphospecies 3)	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	3
Herminiinae (morphospecies 4)	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2
Herminiinae (morphospecies 5)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Herminiinae (morphospecies 6)	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10
Herminiinae (morphospecies 7)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Heteranassa mima	0	0	1	0	1	0	0	3	4	2	0	0	1	0	0	0	14
Heteranassa sp.	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Hypsopygia nostralis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Isogona spp.	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	13
Larentiinae	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	3
Lascoria spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2

Lesmone detrahens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Libytheana carinenta	3	0	0	0	1	0	0	1	1	1	0	0	1	1	0	0	18
Macaria graphidaria	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	3
Macristis schausi	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	6
Marimatha nigrofrimbia	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	3
Matigramma obscurior	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	3
Melipotis acontioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Melipotis agrotoides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Melipotis indomita	14	0	0	0	0	0	0	2	1	0	0	1	0	0	0	0	34
Melipotis spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
Metria bilineata	41	4	3	7	3	1	4	22	13	14	10	3	2	4	3	4	205
Mocis spp.	0	0	0	0	1	0	0	2	1	2	2	18	8	0	0	1	62
Myscelia ethusa	0	0	0	0	0	0	1	2	0	3	0	0	0	1	1	0	16
Noctuidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Noctuinae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
Numia bicoloraria	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	4
Nymphalinae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
Palthis asopialis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Platynota rostrana	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
Platynota spp.	0	0	0	0	3	1	1	1	0	0	0	0	3	0	0	0	14
Plusiodonta compressipalpis	0	0	2	0	6	1	0	0	0	0	0	0	1	7	2	3	31
Prochoerodes lineaola	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	4
Renia spp.	0	0	0	0	83	38	71	0	0	0	0	1	0	57	21	11	295
Sterrhinae	3	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	86
Strymon sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Tortricinae	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	3
Toxonprucha excavata	3	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	12
Zale spp.	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	6
Totals	**94**	**22**	**54**	**47**	**119**	**53**	**91**	**93**	**40**	**41**	**56**	**91**	**81**	**97**	**33**	**35**	**1641**

Appendix 4. List of observed herptile species and the abundance observed at each sampling point. Abundance values include data from two different survey methods (cover boards and area searches).

Common Name	Scientific Name	AU2	AC1	DH1	DH2	DH3	EU1	EU2	EU3	FH1	FH2	FH3	GC1
Green Anole	*Anolis carolinensis*	0	0	0	1	0	0	0	0	0	0	0	0
Brown Anole	*Anolis sagrei*	1	0	4	2	9	0	0	0	7	8	3	0
Common Spotted Whiptail	*Aspidoscelis gularis*	0	0	0	0	0	0	1	3	1	0	0	0
Laredo Striped Whiptail	*Aspidoscelis laredoensis*	0	1	0	0	0	4	0	5	0	0	0	0
Rio Grande Chirping Frog	*Eleutherodactylus cystignathoides*	0	0	0	2	0	0	0	0	0	0	0	0
Sheep Frog	*Hypopachus variolosus*	0	0	0	0	0	0	0	0	0	0	0	0
Gulf Coast Toad	*Incilius nebulifer*	0	0	0	0	0	0	0	0	0	0	0	1
Four-lined Skink	*Plestiodon tetragrammus*	0	0	0	1	0	0	0	0	0	2	0	6
Texas Patchnose Snake	*Salvadora grahamiae*	0	0	0	0	0	0	0	0	0	0	0	0
Little Brown Skink	*Scincella lateralis*	0	0	0	0	0	0	0	0	0	0	0	0
	Totals	**1**	**1**	**4**	**6**	**9**	**4**	**1**	**8**	**8**	**10**	**3**	**7**

Common Name	Scientific Name	GC2	GC3	GI2	LU1	PB1	TB1	TB2	TU1	TU2	TU3	VN2	*Totals*
Green Anole	*Anolis carolinensis*	0	0	0	0	0	0	0	0	0	0	0	*1*
Brown Anole	*Anolis sagrei*	0	0	0	0	1	0	1	0	0	0	1	*37*
Common Spotted Whiptail	*Aspidoscelis gularis*	0	0	0	0	0	1	0	0	0	1	2	*9*
Laredo Striped Whiptail	*Aspidoscelis laredoensis*	0	0	0	1	0	0	0	1	0	0	0	*12*
Rio Grande Chirping Frog	*Eleutherodactylus cystignathoides*	0	0	0	0	0	0	0	0	0	0	0	*2*
Sheep Frog	*Hypopachus variolosus*	0	1	0	0	0	0	0	0	0	0	0	*1*
Gulf Coast Toad	*Incilius nebulifer*	0	1	0	0	0	0	0	0	0	0	0	*2*
Four-lined Skink	*Plestiodon tetragrammus*	1	5	0	0	1	0	0	0	1	0	0	*17*
Texas Patchnose Snake	*Salvadora grahamiae*	0	0	1	0	0	0	0	0	0	0	0	*1*
Little Brown Skink	*Scincella lateralis*	0	0	0	0	0	0	0	1	0	0	0	*1*
	Totals	**1**	**7**	**1**	**1**	**2**	**1**	**1**	**2**	**1**	**1**	**3**	***83***

BIOGRAPHICAL SKETCH

Audrey J. Hicks graduated with degrees in Graphic Design and Marketing from Oklahoma Christian University in 2011. She joined the Peace Corps in 2014 and lived in Tanzania for 6 years, where she developed an interest in conservation. Upon returning to the United States, she pursued an M.S. in Agricultural, Environmental and Sustainability Sciences from the University of Texas, Rio Grande Valley, and graduated in 2023. She is passionate about wildlife conservation and is an avid birder. Her permanent address is 33 Avalon Drive. Brownsville TX 78520 and personal email address is audreyjhicks@gmail.com.