

Therya

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La portada

La zorra gris (*Urocyon cinereoargenteus*) es uno de los cánidos de más amplia distribución en Norteamérica, se encuentra en prácticamente todos los Estados Unidos de Norte América y México. Solamente existen dos especies de este género y la segunda especie está restringida a las islas frente al estado de California. Aunque las zorras son del orden de los carnívoros, su alimentación es prácticamente omnívora, siendo común que un alto porcentaje de su dieta sea plantas e insectos (foto tomada por Sergio Ticul Álvarez Castañeda).

Nuestro logo "Ozomatli"

El nombre de "Ozomatli" proviene del náhuatl se refiere al símbolo astrológico del mono en el calendario azteca, así como al dios de la danza y del fuego. Se relaciona con la alegría, la danza, el canto, las habilidades. Al signo decimoprimeros en la cosmogonía mexicana. "Ozomatli" es una representación pictórica de los mono arañas (*Ateles geoffroyi*). La especie de primate de más amplia distribución en México. " Es habitante de los bosques, sobre todo de los que están por donde sale el sol en Anáhuac. Tiene el dorso pequeño, es barrigudo y su cola, que a veces se enrosca, es larga. Sus manos y sus pies parecen de hombre; también sus uñas. Los Ozomatin gritan y silban y hacen visajes a la gente. Arrojan piedras y palos. Su cara es casi como la de una persona, pero tienen mucho pelo."

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Volumen 13, número 2

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Contenido

ARTICLES

Abundance, microhabitat and feeding of *Peromyscus yucatanicus* and *Peromyscus mexicanus* in the Mexican tropics

Elisa Paulina Zaragoza-Quintana, Nallely Verónica Rodríguez-Santiago, Silvia Filomena Hernández-Betancourt, Livia Socorro León-Paniagua, and María Cristina MacSwiney González _____ 129

Analysis of the male annual antler cycle, reproductive behavior and spotted fawn presence in the tropical white-tailed deer

Miguel Rodríguez-Ramírez, and José Manuel Mora _____ 143

Daytime diet of the lesser sac-winged bat (*Saccopteryx leptura*) in a Colombian Pacific Island

Isabela Vivas-Toro, and Julián Alexander Mendivil-Nieto _____ 153

In search of bachelorettes: Observations of male *Leptonycteris yerbabuena* with dorsal patches across its range

Theresa M. Laverty, and Kathryn E. Stoner _____ 163

Habitat use and activity patterns of ungulates in a tropical rainforest of southern México

Fredy A. Falconi-Briones, Eduardo J. Naranjo, Rafael Reyna-Hurtado, Manuel Spínola, Paula Enríquez-Rocha, and Rodrigo A. Medellín _____ 171

Effect of an urban area in the distribution pattern and diversity of Neotropical rodents

Gloria Tapia-Ramírez, Consuelo Lorenzo, Arturo Carrillo-Reyes, Darío Navarrete, and Óscar Retana _____ 183

Spatial and temporal distribution of bat mortality on a highway in southeast Brazil

Marcione Brito de Oliveira, and Cecília Bueno _____ 195

Evidence of the genetic and spatial structure of <i>Nasua narica</i> in Central America and northern South America from mitogenomic analysis	
María Fernanda Jaramillo, and Manuel Ruiz-García	<u>205</u>
Potential Distribution of the Neotropical Otter (<i>Lontra longicaudis annectens</i>) in the State of Yucatán, México	
Alicia Andrea Ortega-Padilla, Juan Pablo Gallo-Reynoso, Verónica Farías-González Javier Enrique Sosa- Escalante, Silvia Hernandez-Betancourt, Gloria Ponce-García, and Tania Elizabeth Quintana-Salvador	<u>225</u>
Effect of anthropogenic noise on the echolocation pulses of the bats <i>Molossus sinaloae</i> and <i>Mormoops megalophylla</i>	
Ana Cristel Lara-Nuñez, José Antonio Guerrero, and Areli Rizo-Aguilar	<u>235</u>
Evaluation of the distribution pattern on a Neotropical microcarvora	
Rodolfo Rodríguez-Ruiz, Alejandro Juárez-Agis, Silberio García Sánchez, Branly Oliver Salome, and Víctor Hugo Reza Galicia	<u>245</u>

fascículo 38 <http://www.revistas-conacyt.unam.mx/therya/index.php/THERYA/issue/view/42>

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Abundance, microhabitat and feeding of *Peromyscus yucatanicus* and *Peromyscus mexicanus* in the Mexican tropics

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Rodents influence the processes of succession and regeneration in tropical forests, functioning as important dispersers and predators of seeds and plants. In this study, we describe aspects of the population structure and dynamics, and characterize the microhabitat and composition of the feces of the semi-tree-dwelling rodents *Peromyscus yucatanicus* and *Peromyscus mexicanus* in tropical forests of Quintana Roo and Veracruz, in Mexico. We trapped *Peromyscus yucatanicus* with 122 Sherman traps between 2.00 to 10.00 m of height in 62 trees. *Peromyscus mexicanus* was trapped with 105 Sherman traps between 0 to 11.00 m of height on 57 trees. We characterized the microhabitat, identified the trees, and calculated the canopy openness in the sites where individuals were trapped. We collected the feces of each species from inside the traps and were analyzed to know their composition. From September 2014 to February 2015, we captured 48 individuals of *Peromyscus yucatanicus* at an average height of 2.58 m above ground level. Its population density was 26.60 ind/ha, with reproductive activity in the dry season. The average canopy openness was 7.75 %. Their feces mainly contained seeds, fruit pulp and starch. From March to September of 2015, we recorded 54 individuals of *Peromyscus mexicanus* at an average height of 1.15 m. Its population density was 20.83 ind/ha, with reproductive activity in both dry and rainy seasons. The canopy openness was 4.78 % (dry season) and 4.50 % (rainy season). Their feces mainly contained fruit pulp, starch and chitin remains in both seasons. The captured of rodents were higher on trees with small diameters and low leaf litter percentage; the rainy season favored the captures. Both species were mainly captured in sites with a covering of organic matter on the soil and in sites with higher vegetal cover and reduced canopy openness. Conservation of a diverse tropical forest is fundamental for the conservation of both semiarboreal rodents.

Los roedores influyen en los procesos de sucesión y regeneración de las selvas, siendo importantes dispersores y depredadores de semillas y plantas. En este estudio describimos aspectos sobre la estructura y dinámica poblacional, caracterización del microhábitat y composición de los excrementos de los roedores semiarborícolas *Peromyscus yucatanicus* y *Peromyscus mexicanus*, en selvas de Quintana Roo y Veracruz, México. Se realizaron capturas de *Peromyscus yucatanicus* colocando 122 trampas Sherman entre los 2.00 y 10.00 m de altura sobre 62 árboles. *Peromyscus mexicanus* se capturó disponiendo 105 trampas entre 0 y 11.00 m de altura sobre 57 árboles. Se caracterizó el microhábitat, se identificaron los árboles y se calculó la apertura de dosel de los sitios donde ocurrieron las capturas. De ambas especies se colectaron excrementos del interior de las trampas y se analizaron para conocer su composición. De septiembre 2014 a febrero de 2015, capturamos 48 individuos de *Peromyscus yucatanicus* a una altura promedio de 2.58 m. Su densidad poblacional fue de 26.60 ind/ha y actividad reproductiva en temporada de secas. La apertura de dosel fue de 7.75 %. Sus excrementos estuvieron mayormente integrados por semillas, pulpa de frutos y almidón. De marzo a septiembre de 2015 registramos 54 individuos de *Peromyscus mexicanus* a una altura promedio de 1.15 m. Su densidad poblacional fue de 20.83 ind/ha, con actividad reproductiva en ambas temporadas. La apertura de dosel fue de 4.78 % (secas) y 4.50 % (lluvias). Sus excrementos estuvieron mayormente compuestos por pulpa de frutos, almidón y restos de quitina en ambas temporadas. Las capturas de los roedores fueron mayores sobre árboles con diámetros pequeños y bajos porcentajes de hojarasca, además, la temporada de lluvia favoreció el número de capturas. Las dos especies se capturaron principalmente en sitios con una cobertura de materia orgánica en el suelo y en sitios con mayor cobertura vegetal y dosel cerrado. La conservación de las selvas tropicales y su diversidad biológica, es clave para la conservación de ambos roedores semiarborícolas.

Keywords: Density; feeding habits; microhabitat; Quintana Roo; Rodentia; Veracruz.

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Introduction

Rodents influence the processes of tropical forest regeneration and the structure and function of plant communities, since they prey on and disperse seeds (Sánchez-Cordero and Martínez-Gallardo 1998; Shiels and Drake 2011; Fleury et al. 2014), as well as consuming other plant parts (Meyer and Butaud 2009; Shiels et al. 2013). Likewise, they influence the populations of other groups through their role as predators of invertebrates and small vertebrates (Trujano-Alvarez and Álvarez-Castañeda 2010; Witmer and Pitt 2012). They use a wide range of ecological niches, and changes in their abundance and diversity reflect modifications in their habitat (Cimé-Pool et al. 2010; Whitehead et al. 2014).

In Mexico, few studies have described the biology, structure and population size of the small tropical rodents, especially those of tree-dwelling and semi-tree-dwelling habits (Schnell et al. 2010; Hernández-Betancourt et al. 2008, 2012; Panti-May et al. 2014). Equally, patterns relating to the use or selection of habitat have rarely been described in this group (Domínguez-Castellanos et al. 2007; Poindexter et al. 2013). For some rodents, this differential site selection depends on the structural and vegetal characteristics that comprise their specific microhabitat and that, in turn, affect their distribution and behavior. For example, *Heteromys irroratus* is associated with high proportions of dead plant material and most heteromids are generally recorded in certain combinations of stony sites with a cover typical of scrublands (Tapia-Ramírez et al. 2012). Likewise, microhabitat use can vary considerably according to the habitat structure, species population density and the inter-specific interactions (Bellows et al. 2001; Rojas-Martínez et al. 2012; Villanueva-Hernández et al. 2017). In this sense, it has been reported that the females of *Peromyscus leucopus*, unlike the males, present an association with different microhabitats that include the canopy, since they make greater use of the vertical space of the habitat in the search for resources, or as a response to competition for food due to high population density (Klein and Cameron 2012). Studies addressing the feeding habits of small rodents are scarce; however, these mammals play an important ecological role in the ecosystems they inhabit (Montenegro-Díaz et al. 1991; San-José et al. 2014). Some studies of small rodents have used methods of analysis of feces and stomach contents, since these techniques can provide reliable information regarding the material ingested by the species (e. g., López-Cortés et al. 2007; Peralta 2015; Panti-May et al. 2019).

The group of small rodents includes the genus *Peromyscus*, which is the most diverse in Mexico. Some of its species have been studied from an ecology perspective (Morris et al. 2011; Dallas et al. 2012; Kalkvik et al. 2012), behavior (Weber and Hoekstra 2009; Williams et al. 2013), physiology (Schmidt and Hood 2014; Sun et al. 2014), systematics and evolution (Kenney-Hunt et al. 2014; Harris et al. 2015). However, little has been reported about the biology of the species, such as the Yucatecan deer mouse *Peromyscus yucatanicus*, which is semi-tree-dwelling and endemic to the

Yucatan peninsula, with one record in each of Guatemala and Belize (MacSwiney et al. 2012). The same is true for the Mexican deer mouse *Peromyscus mexicanus*, which is also semi-tree-dwelling in habit and presents the widest geographic distribution within the genus *Peromyscus*, stretching from San Luis Potosí, Mexico to Panama, except for the Yucatan peninsula (Trujano-Alvarez and Álvarez-Castañeda 2010). Its abundance is highest in conserved remnants of tropical medium and high forest present in states such as Veracruz, Oaxaca and Chiapas, Mexico (Sánchez-Hernández et al. 2001; Cruz-Lara et al. 2004; Cruz-Lara et al. 2010).

Considering the ecological importance of the rodents and the paucity of biological information regarding these two species *P. yucatanicus* and *P. mexicanus*, this paper studies these two species to evaluate aspects of their population structure and dynamics, characterization and microhabitat and feeding preferences in sites of tropical medium forest in the states of Quintana Roo and Veracruz, Mexico, in order to obtain basic information regarding their biology that could contribute to the conservation of both the rodents and the ecosystems they inhabit.

Materials and Methods

Study areas. The study was conducted in two localities. The first site was located within a tropical medium subevergreen forest (21° 12' 35" N, -87° 12' 26" W and 21° 12' 38" N, -87° 12' 28" W) of El Edén Ecological Reserve (EEER), in the municipality of Lázaro Cárdenas in Quintana Roo, Mexico (Figure 1). The EEER covers an area of 3,077 ha and presents an elevation range of 5 to 10 masl. The vegetation types present are tropical medium subevergreen forest, wetlands with savannah, palm stands, tintales and areas of acahuales of tropical medium forest in recovery (Allen and Rincón 2003). The tropical medium subevergreen forest has an average canopy height of 10 to 12 m, with emergent trees that reach up to 15 m in height (Schultz 2003). Its most abundant species are *Metopium brownei*, *Manilkara zapota*, *Lysiloma latisiliquum*, *Thrinax radiata*, *Sabal yapa*, *Bursera simaruba*, *Brosimum alicastrum* and *Vitex gaumeri* (Schultz 2003). The climate is warm subhumid, with a dry season in winter and spring and a rainy season from June to October. Mean annual temperature is 26 °C and mean annual precipitation is 1,200 mm (Allen and Rincón 2003).

The second site was located in a tropical medium subevergreen forest (19° 50' 54" N, -96° 35' 49" W and 19° 50' 55" N, -96° 35' 46" W) of the Zona de Protección Forestal y Faúnic Santa Gertrudis (ZPSG), in the municipality of Vega de Alatorre in Veracruz, Mexico (Figure 1). This reserve covers an area of 925 ha and has an elevation range of 400 to 900 masl (Bojorges and López-Mata 2005). The climate is semi-warm, with a mean annual temperature of 22 °C and mean annual precipitation of 1,845 mm (Godínez-Ibarra and López-Mata 2002), with a rainy season from June to November (García 2004). The trees of the tropical forest in this study site reach heights exceeding 20 m and the species most prominent for their structural importance are

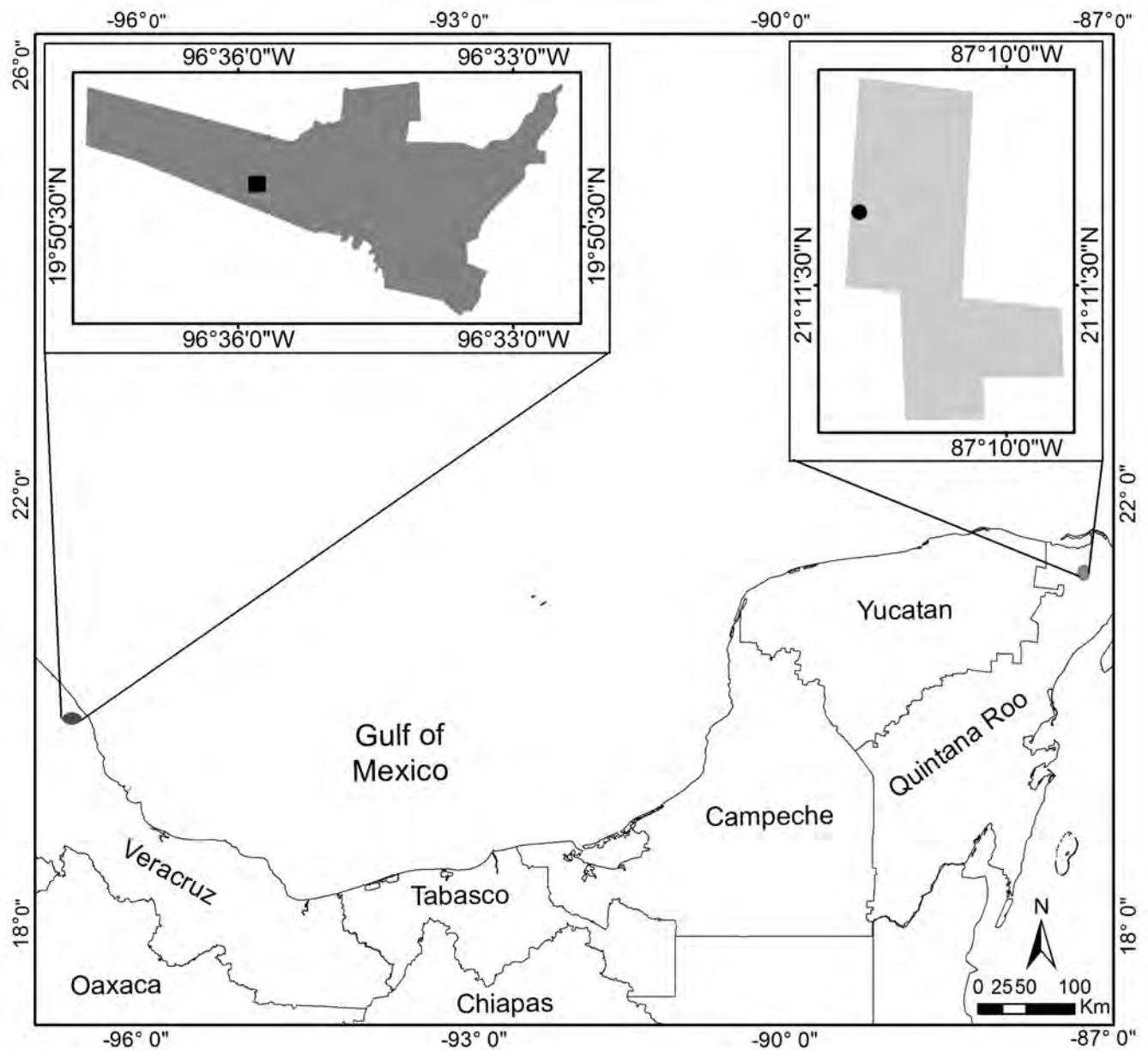


Figure 1. Geographic location of the study site (black square) in Zona de Protección Forestal y Faúnica Santa Gertrudis, Veracruz (dark gray polygon) and study site (black circle) in El Edén Ecological Reserve, Quintana Roo (light gray polygon), México.

Aphananthe monoica, *Brosimum alicastrum*, *Bursera simaruba*, *Dendropanax arboreus*, *Faramea occidentalis*, *Protium copal*, *Sapindus saponaria* and *Tabernaemontana alba* (Godínez-Ibarra and López-Mata 2002).

Data collection. To capture *P. yucatanicus* in the EEER, one field visit was conducted during the rainy season (September 2014) and two in the dry season (November 2014 and February 2015). A total of 122 Sherman traps (23 x 8 x 9 cm) were set at between 2.00 and 10.00 m above ground level, in 62 trees spaced equidistantly at 10.00 m apart, forming a grid of 11 columns by six rows. To capture *P. mexicanus* in the ZPSG, three samplings were conducted in the dry season (March, May and June 2015) and three in the rainy season (July, August and September 2015). A total of 48 trees were selected at 9.00 m apart, forming a grid of eight

columns and six rows, over which 96 traps (23 x 8 x 9 cm) were distributed at between 0 and 4.50 m in height above ground level. In addition, to record captures of *P. mexicanus* at greater height, a trap was set at between 6.60 and 11.20 m above ground level on each of nine trees selected from the interior of the grid.

In each site, the traps remained open for five consecutive nights per sampling, and used sunflower seeds and oats mixed with vanilla as bait. Then trees selected for the traps were characterized by presenting branches and lianas that interconnected them with other individuals. The traps were fixed to the trunks and branches using metal mesh wire and an elevator system with wooden platforms, nylon strings and carabiners (techniques modified from Vieira 1998 and Graipel 2003). The capture and recapture

method (Krebs 1966) was used, and the captured individuals were marked with perforations on the ears (Sikes and The American Society of Mammalogists 2016). For each captured individual, the weight, sex, age (juvenile or adult), reproductive condition (whether the males presented scrotated testicles and the females presented an open vagina, were pregnant or in lactation) and the following morphometric measurements were recorded with a digital vernier: total length (TL), tail length (TaL), right hind-foot length (HFL) and right ear length (EL). The feces of both captured species were collected from inside the traps and stored in Eppendorf tubes at -20 °C (Vázquez et al. 2004).

Analysis of the population information. The capture effort for each species was calculated from the number of traps located in each site (122 in the EEER and 105 in the ZPSG), multiplied by the number of nights of each sampling, expressed as night/traps. The percentage of sampling success was calculated with the total number of captures in each month divided by the number of night/traps in the month. The population structure of each species was obtained considering the sex and age data of the captured individuals. From the total number of reproductive individuals, it was possible to determine the variation of the reproductive activity in each site (Rojas-Martínez et al. 2012). Mann-Whitney U tests were used to determine whether differences existed in the heights of capture between sexes per sampling period. Population density was calculated using the method of Minimum Number Alive (MNA, Krebs 1966). Contingency tables and Pearson χ^2 tests were used to determine the probable dependence of the frequency of sexes, ages and reproductive condition (with the latter used only for *P. mexicanus*), with respect to the months and seasons of sampling. Given that, in both species, only the proportions of ages showed dependence, *post-hoc* Analysis of Standardized Residuals was conducted to determine which age classes were dependent. In order to evaluate whether significant differences existed in the somatic measurements between sexes, a one-way analysis of variance (ANOVA) was used for the variables with normal distribution, while the Mann-Whitney U test was used for those without normal distribution.

Characterization and preference of microhabitat. The trees in which the rodents were captured were identified taxonomically using keys (Castillo-Campos and Medina-Abreo 2005) and the help of botanical experts. Tree diameter at breast height (DBH, in cm) was recorded and the percentage of canopy openness calculated (CO, Frazer et al. 1999). Around the base of each tree, four plots of 1.00 m² were established, each oriented towards a cardinal point. These were used to characterize the microhabitat at ground level through the percentage of vegetal coverage, organic matter (composed of leaf litter and dead wood deposited on the soil), rocky and bare soil surfaces (Poindexter et al. 2013). Characterization was conducted in February 2015 for *P. yucatanicus*, and in June and September 2015 for *P. mexicanus*. For *P. mexicanus*, one-way ANOVA and Mann-

Whitney U tests were used to determine whether significant differences existed in the percentages of the variables between seasons. The variables coverage of grasses and cacti were not subjected to these statistical tests, since the data were insufficient to make the comparisons. Principal components analysis (PCA) with matrices of variance-covariance and generalized linear models (GLM) were used to define which variables of the microhabitat influenced the frequency of capture of both species (Dobson and Barnett 2008). For *P. mexicanus*, GLM were developed between seasons and sexes.

Composition of the feces. The fecal material of each species was analyzed using preparations on slides, with a 70.00 % alcohol solution and crystalline mucilage adhesive (Stafford de México, S. A. de C. V.) for mounting (Baltazar 2014). Each preparation was placed on millimetric paper under a stereoscopic microscope (Modelo CSM2-Labomed, Labomed, Inc.) and elements of vegetal (seeds, epidermis, fruit pulp and starch, fibers, roots and bark) and animal (larvae, complete insects, arthropod appendages and chitin remains) origin identified in five randomly selected fields of area 25.00 mm² (Montenegro-Díaz et al. 1991; Peña-Ramos et al. 2009; Lanzone et al. 2012). The percentages of appearance were estimated based on the number of fields occupied by each element (López-Cortés et al. 2007). Remains of animal origin were identified through consultation of specialized literature (Triplehorn and Johnson 2005; AntWeb 2017) and specialist taxonomists. The remains of some insects, apparently consumed by *P. mexicanus* and found within the traps in which the rodent was captured, were collected and identified.

Contingency tables and calculations of Pearson χ^2 were used to determine whether the frequencies of the elements were dependent on the months of sampling, in the case of *P. yucatanicus*, and between seasons for *P. mexicanus*. To determine which elements were dependent, *post-hoc* Analysis of Standardized Residuals was performed. One-way ANOVA, Kruskal-Wallis and Mann-Whitney U tests were used to determine whether differences existed in the frequencies of the elements between sexes and ages for *P. yucatanicus* and between seasons, sexes and reproductive conditions for *P. mexicanus*. Only those elements with sufficient data to make the comparisons were subjected to these statistical tests. The seeds found were assigned to different morphotypes based on their shape, color, surface texture and width (Wells et al. 2009) for which reason their lengths and widths were measured (in mm) with the software ImageJ Version 1.48 (Ferreira and Rasband 2012). The contingency tables and calculations of Pearson χ^2 were used to determine whether the frequencies of the morphotypes were dependent on the sampling periods. To determine which morphotypes were dependent, *post-hoc* Analysis of Standardized Residuals was performed. Statistical analysis was conducted using the software STATISTICA Version 7 (Stat Soft, Inc.) and the graphic options of the statistical package VCD (Meyer et al. 2006; Zeileis et al. 2007;

Meyer et al. 2015) for the software R (R Core Team 2014; RStudio, Inc.).

Results

Peromyscus yucatanicus: *Population aspects*. A total of 48 individuals of *P. yucatanicus* were captured and marked. This group comprised 26 males (54.00 %) and 22 females (46.00 %). Of these, 85 recaptures were achieved in 1,205 night/traps, with a capture success of 11.00 %. The average population density was 26.60 ind/ha (± 23.00 SD), with the highest density found in February (50.00 ind/ha). Over the entire sampling, 48 males (56.50 %) and 37 females (43.50 %) were recaptured. The greatest number of individuals of both sexes was obtained in November (21 males and 14 females, Figure 2a). The frequency of sexes was not dependent on the sampling month (contingency table of 2×3 , $\chi^2 = 0.875$, $d. f. = 2$, $P = 0.646$). Twenty-two juvenile (52.40 %) and 20 adult (47.60 %) males, and 17 juvenile (48.60 %) and 18 adult (51.40 %) females were recorded. More juveniles of both sexes were recorded in November (15 males and eight females), while the highest number of adults was obtained in February (13 males and 10 females, Figure 2b). Only the frequencies of juvenile and adult males depended on the month of February (contingency table of 4×3 , $\chi^2 = 24.39$, $d. f. = 6$, $P < 0.001$) (Supplementary material 1, Figure A1). Of the total number of individuals captured, 10 presented reproductive activity (seven males and three receptive females); these were present only in February. None of the somatic measurements of adult males and females (Table 1) presented significant differences between sexes: TL ($F_{1,26} = 0.12$, $P = 0.73$), TaL ($F_{1,26} = 1.43$, $P = 0.24$), HFL ($U = 75$, $P = 0.13$), EL ($F_{1,28} = 1.52$, $P = 0.22$).

Characterization and preference of the microhabitat. The rodents were captured on 41 trees with mean DBH of 19.10 cm (± 12.53 SD, range: 3.80 to 55.40 cm) and a CO of 7.75 % (± 3.71 SD). The identified tree species were: *Lysiloma latisiliquum*, *Brosimum alicastrum*, *Pouteria campechiana*, *Bursera simaruba*, *Ceiba pentandra*, *Chrysophyllum cainito*, *Guettarda combsii* and one further unidentified species of the family Sapotacea. The captures occurred at between 2.00 and 5.00 m in height above ground level, with an average height of 2.58 m (± 0.82 SD). Table 2 presents the mean heights per month, sex and age. In general, the population of males presented a mean capture height of 2.45 m (± 0.74 SD, height: 2.00 to 4.50 m) and the females 2.73 m (± 0.90 SD, height: 2.00 to 5.00 m), values that differed significantly ($U = 1502.5$, $P = 0.006$).

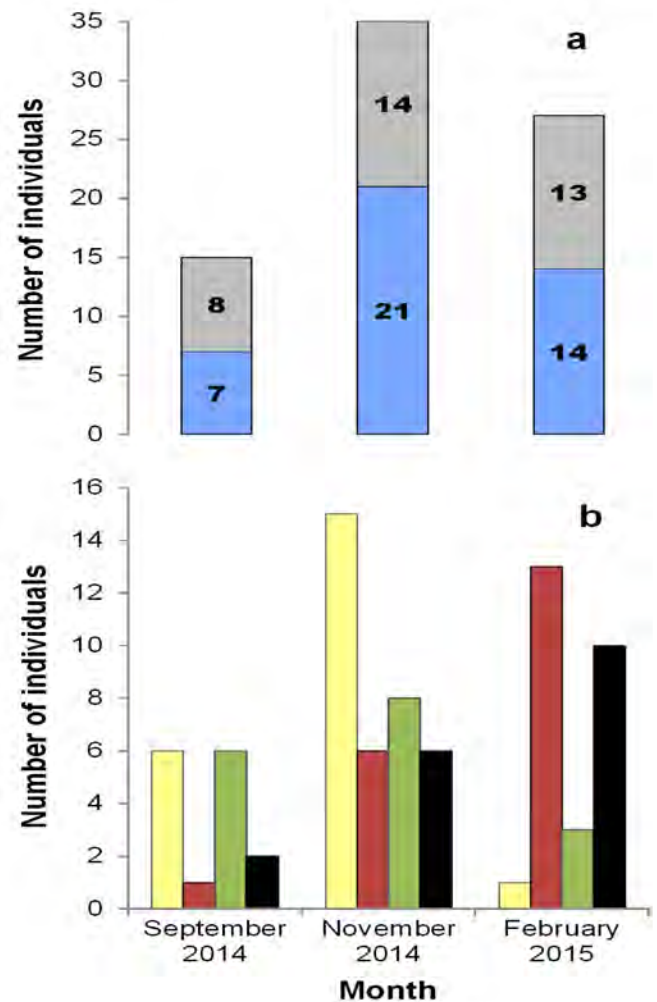


Figure 2. Structure according to: a) sex (males in blue, females in gray) and b) age (juvenile males in yellow, adult males in red, juvenile females in green, adult females in black) of the mouse *Peromyscus yucatanicus* in the El Edén Ecological Reserve in Quintana Roo, Mexico.

The dominant element of the microhabitat consisted of organic matter, with a proportion of 65.71 % (± 14.62 SD), followed by vegetal cover with 26.83 % (± 14.47 SD), which comprised climbing and herbaceous plants, as well as trees (Table 3). According to the PCA, the variables coverage of trees and leaf litter (Component 1) and DBH (Component 2) presented the greatest variations. Both components explained 86.67 % of the variation (Supplementary material 2, Table B1). The GLM conducted with the variables selected from the PCA showed that the vegetal cover of the trees positively influenced the frequency of capture ($D_{1,39} = 6.910$, $P = 0.02$) (Supplementary material 1, Figure A2). In

Table 1. Mean values of somatic measurements (in mm), \pm standard deviations, of adult individuals of *Peromyscus yucatanicus* and *Peromyscus mexicanus*.

Species	Sex	TL	TaL	HFL	EL
<i>P. yucatanicus</i>	Males ($n = 15$)	194.86 \pm 8.23	100.80 \pm 5.99	21.05 \pm 0.82	16.58 \pm 0.70
<i>P. yucatanicus</i>	Females ($n = 13$)	195.92 \pm 7.97	103.69 \pm 6.81	20.53 \pm 0.87	16.24 \pm 0.81
<i>P. mexicanus</i>	Males ($n = 17$)	215.23 \pm 28.16	124.70 \pm 21.21	23.64 \pm 0.93	18.10 \pm 1.07
<i>P. mexicanus</i>	Females ($n = 22$)	211.22 \pm 31.33	126.09 \pm 13.44	23.68 \pm 0.89	17.60 \pm 0.75

n (number of individuals), TL (total length), TaL (tail length), HFL (right hind-foot length) and EL (right ear length)

contrast, leaf litter had a negative influence on the number of rodents captured of the rodent ($D_{1,39} = 9.497, P = 0.008$) (Supplementary material 1, Figure A3).

Composition of the feces. A total of 80 fecal samples of *P. yucatanicus* were analyzed (47 males and 33 females) for a total of 800 fields of 25.00 mm². The composition of the feces was dominated by elements of vegetal origin: seeds (85.00 %), fruit pulp and starch (34.60 %), fibers (2.50 %) and different types of epidermis (0.75 %). The components of animal origin were chitin remains (0.50 %) and different types of arthropod appendages (0.10 %), including some parts of legs of the Orders Orthoptera and Coleoptera, scales of Lepidoptera and complete specimens of ants of the family Formicidae. The material that could not be identified represented 3.10 % of the total.

In both November and February, seeds were the element that presented the greatest proportion, and remains of animal origin were present only in November (Table 4). The frequencies of the elements seeds and fruit pulp and starch were dependent on the sampling month (Supplementary material 1, Figure A4). Likewise, the element of fibers was found to be dependent on the month of February (contingency table of 6 x 2, $\chi^2 = 108.887, d. f. = 5, P < 0.001$). The frequencies of the elements seeds and fruit pulp and starch, did not present significant differences between sexes (seeds: $U = 657, P = 0.24$; fruit pulp and starch: $U = 646.5, P = 0.20$) or ages (seeds: $H = 3.60, d. f. = 3, n = 80, P = 0.30$; fruit pulp and starch: $H = 2.27, d. f. = 3, n = 80, P = 0.51$). The seeds were grouped into nine morphotypes; the morphotype V was the largest in size (Length = 0.26 mm, Width = 0.26 mm), while the morphotype VIII was the smallest (Length = 0.04 mm, Width = 0.03 mm). The morphotypes I and II were mainly present in both sampling months (Supplementary material 2, Table B2). Only the frequencies of the morphotypes III, IV, V and VIII were dependent on the month of sampling (contingency table of 9 x 2, $\chi^2 = 211.010, d. f. = 8, P < 0.001$) (Supplementary material 1, Figure A5).

Peromyscus mexicanus: Population aspects. A total of 54 individuals were marked (27 males and 27 females), with 196 recaptures in 2,429 night/traps. Capture success was 10.30 %. The average population density was 20.66 ind/ha ($\pm 8.70 SD$), with a mean value of 14.30 ind/ha ($\pm 5.50 SD$) in the dry season and 27.00 ind/ha ($\pm 6.24 SD$) in the rainy season. Moreover, the highest record occurred in August with 32.00 ind/ha (Figure 3). A total of 95 recaptures of males was obtained: 27 in the dry season (28.40 %) and 68

in the rainy season (71.60 %). The females presented 101 recaptures: 32 in the dry season (32.00 %) and 69 in the rainy season (68.00 %). During the dry season, the month of March presented the highest number of individuals (12 males and 16 females), while in the rainy season, the highest numbers of both sexes were obtained in July (10 and 8, respectively, Figure 4a). The frequency of sexes was not dependent on the season (contingency table of 2 x 6, $\chi^2 = 1.0, d. f. = 1, P = 0.317$).

Eleven juvenile (33.30 %) and 17 adult (60.70 %) males were captured, while the total numbers of females were seven juveniles (23.30 %) and 23 adults (76.70 %). The highest number of juveniles was presented in the dry season (nine males and six females) and no juveniles were captured in September (Figure 4b). The frequencies of juvenile and adult males were dependent on the month of March in the dry season, while those of females of both ages were dependent on the month of July in the rainy season (contingency table of 4 x 6, $\chi^2 = 41.32, d. f. = 15, P < 0.001$) (Supplementary material 1, Figure A6).

Twenty-three reproductive individuals were obtained: 11 males (47.80 %) and 12 females (52.20 %). Pregnant females were the most abundant, with 11 records (48.00 %), and these were present in all samplings (Figure 4c). The frequencies of reproductive males and females were not dependent on the season of sampling (contingency table of 5 x 6, $\chi^2 = 3.299, d. f. = 1, P = 0.069$). The mean values of the somatic measurements are shown in Table 1. None of these measurements presented significant differences between sexes, for which reason sexual dimorphism did not exist: TL ($U = 183.50, P = 0.92$), TaL ($U = 140.50, P = 0.18$), HFL ($U = 185.50, P = 0.96$), EL ($F_{1,37} = 2.79, P = 0.10$).

Characterization and preference of the microhabitat. In the dry season, the mice were captured in 25 trees with an average DBH of 38.62 cm ($\pm 41.60 SD$, range: 8.11 to 149.60 cm) and a CO of 4.78 % ($\pm 2.20 SD$). In the rainy season, the captures occurred in 38 trees with an average DBH of 29.98 cm ($\pm 29.60 SD$, range: 6.36 to 132.73 cm) and a CO of 4.50 % ($\pm 2.37 SD$). The tree species identified were *Pimenta dioica*, *Psychotria* sp., *Pouteria* sp., *Spondias* sp., *Ficus* sp., *Bursera simaruba* and *Forchhammeria trifoliata*. The captures and recaptures occurred at between 0 and 11.00 m in height above ground level, and consisted of 173 captures on the ground (14 juvenile males, 69 adult males, 15 juvenile females and 75 adult females) and 77 in the trees (3 juvenile males and 36 adult males, 3 juvenile

Table 2. Mean height above ground level (in meters) \pm standard deviations, at which male and female individuals of different ages and of both study species were collected.

Species	Sampling/Season	Male juveniles	Male adults	Female juveniles	Female adults
<i>Peromyscus yucatanicus</i>	Sep-2014	2.12 \pm 0.21	2.10	2.44 \pm 0.33	2.0
	Nov-2014	2.35 \pm 0.12	2.80 \pm 0.24	2.89 \pm 0.25	2.95 \pm 0.28
	Feb-2015	2.20	2.57 \pm 0.18	3.40 \pm 0.36	2.48 \pm 0.18
<i>Peromyscus mexicanus</i>	Dry	-	1.18 \pm 1.55	0	1.42 \pm 1.41
	Rainy	2.92 \pm 2.77	0.97 \pm 1.36	0.89 \pm 1.35	1.28 \pm 2.28

(-) no data

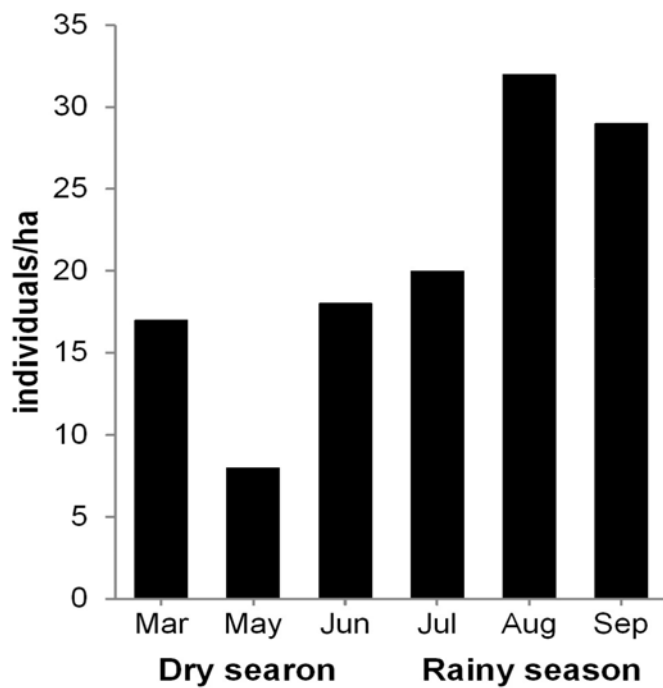


Figure 3. Population density of *Peromyscus mexicanus* in a tropical medium sub-evergreen forest of Zona de Protección Forestal y Faúnica Santa Gertrudis, in Veracruz, Mexico.

females and 35 adult females), at an average height of 1.15 m (± 1.75 SD). In the rainy season, the juvenile males presented the greatest average capture height of 2.92 m (± 2.70 SD, Table 2), while in the dry season, the adult females presented an average capture height of 1.42 m (± 1.41 SD). In general, the population of males was captured at an average height of 1.09 m (± 1.50 SD, height: 0 to 6.70 m), while that of the females was 1.21 m (± 1.98 SD, height:

0 to 11.00 m). These values did not differ significantly ($U = 5085$, $P = 0.97$). The mean heights of capture between sexes in the dry (males = 1.18 m ± 1.55 SD, height: 0 to 4.30 m; females = 1.17 m ± 1.39 SD, height: 0 to 4.50 m) and rainy (males = 1.07 m ± 1.49 SD, height: 0 to 6.70 m, females = 1.23 m ± 2.18 SD, height: 0 to 11.00 m) seasons presented no significant differences (dry: $U = 360.50$, $P = 0.97$; rainy: $U = 2713$, $P = 0.92$).

In both seasons, the organic matter (mainly leaf litter) was mainly present in the microhabitat, comprising 61.45 % (± 13.45 SD), followed by the vegetal cover at 29.25 % (± 13.33 SD), bare soil at 7.52 % (± 9.90 SD) and rocky surface at 1.76 % (± 3.37 SD; Table 3). The CO did not differ significantly between seasons ($U = 427$, $P = 0.50$). The percentage of climbing plants was significantly greater in the dry season ($U = 212$, $P < 0.001$), while the herbaceous plants and ferns did not differ between seasons (herbaceous plants: $U = 345.50$, $P = 0.06$; ferns: $U = 471$, $P = 0.95$). The percentage of shrubs was significantly greater in the dry season ($U = 316$, $P = 0.02$) and the coverage of trees was similar between the two seasons ($U = 390.50$, $P = 0.23$). The percentages of remains of wood ($U = 460$, $P = 0.83$) and leaf litter ($F_{1,61} = 0.207$, $P = 0.65$) did not differ significantly between seasons. The rocky surface was also similar between seasons ($U = 427.50$, $P = 0.50$) and the proportion of bare soil was greater in the rainy season ($U = 198.50$, $P < 0.001$; Table 3).

The three first components of the PCA of the rainy and dry seasons were selected. These explained 89.36 % of the accumulated variation. The variables DBH (Component 1), leaf litter (Component 2) and herbaceous plants (Component 3) presented the greatest variation (Supplementary material 2, Table B3). The GLM were conducted with the variables selected from the PCA, which showed that the interaction

Table 3. Mean values \pm standard deviations, of the variables used for characterization of the microhabitat of both study species.

Variable	<i>Peromyscus yucatanicus</i>		<i>Peromyscus mexicanus</i>	
	February-2015 (n = 41)	Dry season (n = 25)	Rainy season (n = 38)	General (n = 63)
DBH	19.11 \pm 12.53	38.62 \pm 41.60	29.98 \pm 29.60	33.41 \pm 34.80
CO	7.75 \pm 3.71	4.78 \pm 2.20	4.50 \pm 2.37	4.61 \pm 2.29
Plant cover (%)				
Climbing plants	3.21 \pm 3.07	1.06 \pm 0.91	0.30 \pm 0.36	0.60 \pm 0.73
Grasses	0	0.15 \pm 0.48	0	0.06 \pm 0.31
Herbaceous plants	0.30 \pm 1.49	17.10 \pm 13.65	11.48 \pm 10.94	13.70 \pm 12.30
Cacti	0	0.15 \pm 0.48	0.14 \pm 0.49	0.14 \pm 0.48
Ferns	0	5.41 \pm 7.59	4.16 \pm 4.74	4.65 \pm 6.01
Shrubs	0	2.48 \pm 4.60	0.26 \pm 0.68	1.14 \pm 3.11
Trees	23.31 \pm 13.65	9.40 \pm 15.77	8.65 \pm 5.69	8.94 \pm 10.76
Organic matter (%)				
Dead wood	5.41 \pm 3.42	4.13 \pm 2.17	4.37 \pm 2.78	4.27 \pm 2.54
Leaf litter	60.29 \pm 14.83	56.21 \pm 13.81	57.81 \pm 13.60	57.17 \pm 13.59
Rocky surface (%)	3.87 \pm 4.74	1.23 \pm 2.44	2.11 \pm 3.85	1.76 \pm 3.37
Bare soil (%)	3.58 \pm 3.55	2.70 \pm 2.17	10.70 \pm 11.63	7.52 \pm 9.90

n (number of trees), DBH (diameter at breast height in cm), CO (canopy openness: %)

Table 4. Proportion (%) of the elements found in the feces of *Peromyscus yucatanicus* during the months of sampling. The percentages of appearance were estimated based on the number of fields occupied by each element in five randomly selected fields of area 25 mm² (López-Cortés *et al.* 2007).

Month/Season	Seeds	Fruit pulp and starch	Fibers	Epidermis	Chitin remains	Arthropod appendages
<i>P. yucatanicus</i>						
November-2014	78.50	48.50	3.80	1.10	0.75	0.20
February-2015	98.0	7.40	-	-	-	-
<i>P. mexicanus</i>						
Dry	1.72	74.0	0.17	21.20	30.30	0.51
Rainy	6.48	60.70	0.13	10.13	68.20	2.70

(-) no data

with the variables DBH and leaf litter had a negative effect on the frequency of capture of the rodents ($D_{1,58} = 5.726$, $P = 0.04$) (Supplementary material 1, Figure A7). Moreover, the rainy season had a positive influence on the number of captures ($D_{1,61} = 14.907$, $P = 0.001$; Supplementary material 1, Figure A8). The three first components of the PCA of males and females were selected; these individually presented the variables DBH, leaf litter and herbaceous plants as those of greatest explanatory variation. The accumulated variation of the three components was 88.76% (Supplementary material 2, Table B4). The GLM produced with the variables selected from the PCA showed the interaction of DBH and leaf litter to be significant, negatively influencing the number of mice captured ($D_{1,88} = 9.567$, $P = 0.001$; Supplementary material 1, Figure A9).

Composition of the feces. A total of 132 fecal samples of the Mexican deer mouse (62 males and 70 females) were collected, of which 1320 fields of area 25.00 mm² were analyzed. The feces contained fruit pulp and starch (66.51 %), chitin remains (51.59 %), different types of epidermis (15.00 %), seeds (4.40 %), arthropod appendages (1.70 %) and fibers (0.15 %), and 5.70 % of the material fecal could not be identified. In both seasons, the elements fruit pulp and starch as well as chitin remains were present in greater proportion. Seeds and remains of arthropod appendages were more frequent in the rainy season, while the element epidermis was more frequent in the dry season (Table 4).

The frequencies of all of the elements of the diet were dependent on both seasons (Supplementary material 1, Figure A10), apart from fibers in both seasons and arthropod appendages in the rainy season only (contingency table of 6 x 2, $\chi^2 = 145.049$, $d. f. = 5$, $P < 0.001$). The element chitin remains presented significant differences between seasons ($U = 714.5$, $P < 0.001$) but did not differ between sexes ($U = 1981.5$, $P = 0.39$) or with the reproductive condition of the males ($F_{1,54} = 0.164$, $P = 0.68$) and females ($H = 1.11$, $d. f. = 3$, $n = 25$, $P = 0.77$). Likewise, fruit pulp and starch differed between seasons ($U = 1460$, $P = 0.001$), but not between sexes ($U = 2147$, $P = 0.91$), or male ($U = 361$, $P = 0.91$) and female ($H = 1.96$, $d. f. = 3$, $n = 25$, $P = 0.57$) reproductive conditions. The element epidermis presented similar proportions in both seasons ($U = 1846.5$, $P = 0.16$), as with between

sexes ($U = 2084$, $P = 0.69$), reproductively active and inactive males ($U = 337.5$, $P = 0.61$) and among females in a reproductive state ($H = 1.15$, $d. f. = 3$, $n = 25$, $P = 0.76$).

The seeds were assigned to 24 morphotypes; morphotype number XI was that of greatest size (length = 1.31 mm, width = 0.92 mm), while number VII was the smallest (length = 0.03 mm, width = 0.04 mm; Supplementary material 2, Table B5). Remains of seeds belonging to *Ficus* sp. were identified in the samples from the months of May and June. The frequencies of the morphotypes I, II, III, VI and XII were the only ones that depended on the dry season (contingency table of 8 x 2, $\chi^2 = 53.858$, $d. f. = 7$, $P < 0.001$; Supplementary material 1, Figure A11).

Three seedlings of less than 2.00 mm in length were found in the feces, possibly belonging to the genus *Selaginella*. Some arthropod appendages corresponded to the Orders Coleoptera and Hymenoptera (some to the family Formicidae), and unidentifiable immature individuals were observed (pupae and larvae). The remains of insects collected from within the traps belonged to four individuals of the family Blattidae (Blattodea), three beetles (Coleoptera) of the family Scarabaeidae and the head of an ant (Hymenoptera) of the genus *Pachycondyla*.

Discussion

Population structure and dynamics. The population density of a species can be affected by different factors such as climatic fluctuations, site conservation state and the availability and diversity of resources (Santos-Moreno *et al.* 2007; Briones-Salas and González 2016). In this study, the population density of *P. yucatanicus*, particularly in February (50.00 ind/ha), was similar to that observed in other localities of the Yucatan peninsula during the dry season (33 to 36 ind/ha, Címé-Pool *et al.* 2007; 23 ind/ha, Hernández-Betancourt *et al.* 2012). The abundance of species of legumes and gramineae that produce large quantities of seeds during the dry season seems to explain the greater density of *P. yucatanicus* in different habitats such as agroecosystems of pasture and of the tropical forests of Yucatan (Címé-Pool *et al.* 2007; Hernández-Betancourt *et al.* 2012). In contrast, for *P. mexicanus*, the estimated population density was lower (26.60 ind/ha) than that recorded in

a cloud forest (34 ind/ha), but greater than that reported in an abandoned pasture (11 ind/ha) in Costa Rica (Rojas and Barboza 2007). Our results show that the rainy season presents a population increase in *P. mexicanus*, similar to

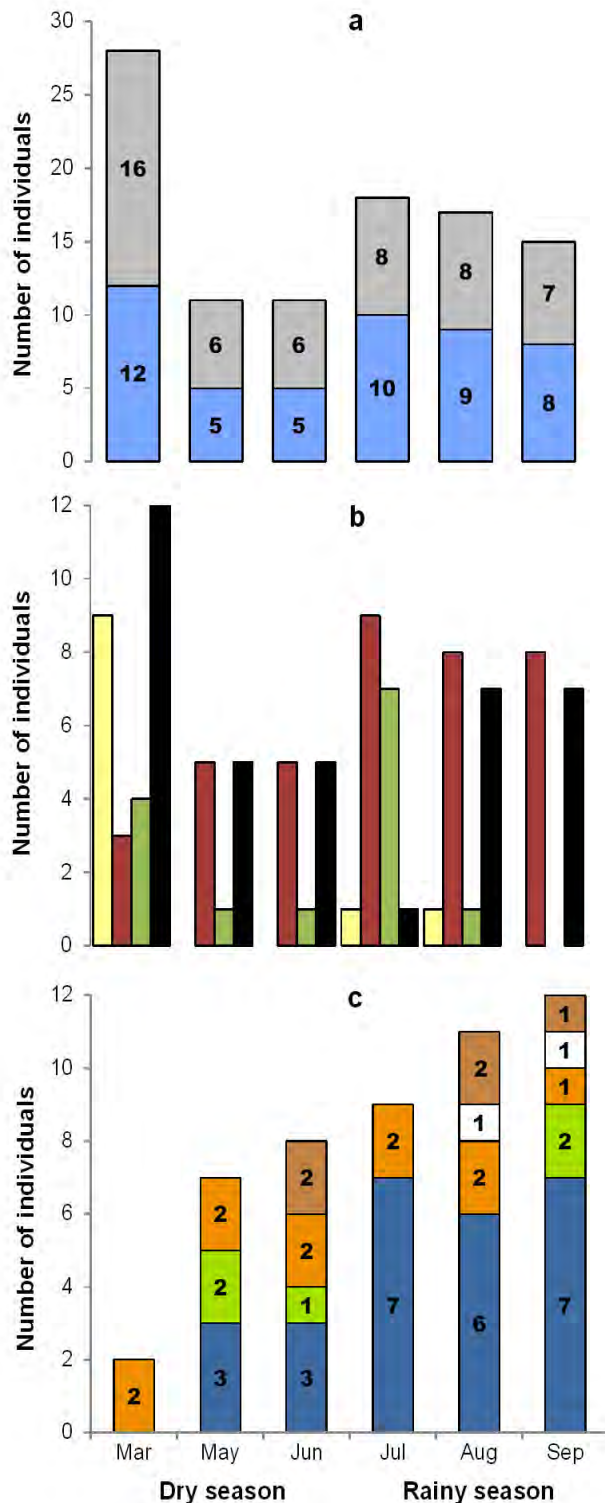


Figure 4. Structure according to: a) sex (males in blue, females in gray), b) age (juvenile males in yellow, adult males in red, juvenile females in green, adult females in black) and c) reproductive state (active males in blue, receptive females in green, pregnant females in orange, lactating female in white, postlactating females in brown) of the mouse *Peromyscus mexicanus* in Zona de Protección Forestal y Faúnic Santa Gertrudis, Veracruz, México.

that found in other studies (Cruz-Lara et al. 2004; Rojas and Barboza 2007; Rodríguez-Macedo et al. 2014).

Some environmental factors can influence the proportion of sexes in some species of small rodents, as is the case in *Peromyscus maniculatus borealis*, the proportion of which seems to be affected by precipitation causing a biased mortality among the young (Havelka and Millar 1997). For *Sigmodon hirsutus*, a greater mortality among juvenile females could be the cause of the existence of a greater quantity of adult males (Monge 2008). In other rodents, such as *Oryzomys chapmani*, it is proposed that some of their populations of tropical montane cloud forest present a greater proportion of males as a response to disturbances in their environment (Santos-Moreno et al. 2007). In this study, despite the fact that there were no significant differences in the proportion of sexes of *P. yucatanicus*, the capture of males was slightly greater, as has been reported in other environments of tropical low forest and pasture in Yucatan (Hernández-Betancourt et al. 2012). It should be noted that the presence of fires and hurricanes is common in the state of Yucatán, for which reason future studies should evaluate the effect of these phenomena on the populations and sexual proportions of *P. yucatanicus*, as have been reported for other rodent species (Santos-Moreno et al. 2007). Likewise, we identified that the frequency of sexes of *P. mexicanus* did not depend on the season, which could indicate that neither species has suffered a selective pressure that influences the proportion of the sexes in their populations.

Some species present the birth of their young in favorable periods such as the rainy season, since this is a strategy that maximizes the availability of food for the young and increases their probability of survival and maturation (Crespin and Lima 2006; Santos-Moreno et al. 2007). More juveniles of the Yucatecan deer mouse were captured in November, possibly due to the fact that most births occur at the end of the dry season and, by the rainy season, the juveniles have separated from their mothers (MacSwiney et al. 2012). We also recorded the highest capture of adults and reproductive individuals in the dry season, which coincides with another study conducted in the same area, in which receptive females were observed in the month of February (MacSwiney et al. 2012). This leads us to suggest that the reproductive activity of *P. yucatanicus* occurs with greater frequency at the end of the dry season and beginning of the rainy season (Hernández-Betancourt et al. 2012; MacSwiney et al. 2012), as is the case with *Heteromys gauderi* in the tropical forests of Yucatan, where the number of pregnant and post-lactating females is higher during the dry season (Hernández-Betancourt et al. 2003).

In general, the number of adult *P. mexicanus* was usually greater than that of the juveniles. However, in March, mainly juvenile males were caught, while a greater quantity of juvenile females was captured in July. Under experimental conditions, *P. mexicanus* can reach adulthood 35 days after birth, regardless of sex, and reach sexual maturity at 46 to 66 days (Duquette and Millar 1995; Trujano-Alvarez

and Álvarez-Castañeda 2010). This rapid maturation of the juvenile rodents could explain the difference in ages observed in our study. Moreover, the availability of vegetation with high productivity could allow the juveniles to reach adulthood in a short time (Duquette and Millar 1995; Rojas and Barboza 2007).

During the dry and rainy seasons, we observed that *P. mexicanus* maintained its reproductive activity, since we captured reproductive males in each month of sampling (except March), with a slightly greater abundance in the rainy season. Receptive females were also observed in both seasons and pregnant females were present in almost all samplings, with lactating and post-lactating females mainly present in the rainy season. This leads us to assume that *P. mexicanus*, as with other species of the same genus, is an opportunist in terms of its reproduction since in favorable years or environments, it can reproduce throughout the year (Heideman and Bronson 1993; Duquette and Millar 1995; Rojas and Barboza 2007; Ventura 2014).

Characterization and preference of microhabitat. Different species of semi-tree-dwelling rodents, such as *P. leucopus*, *P. maniculatus* and *P. perfulvus*, demonstrate the recurring use of the arboreal stratum in search of food, refuge in the high parts of the trees or for establishment of their nests (Graves et al. 1988; Sánchez-Hernández et al. 2009; Klein and Cameron 2012). In the case of *P. yucatanicus*, the present study recorded the maximum height at which it was captured at 5.00 m above ground level. It had previously been recorded at 1.65 m in a tropical medium sub-evergreen forest of Quintana Roo (MacSwiney et al. 2012). Our results indicate that the females can move to a greater height towards the canopy and both juveniles and adults make use of the arboreal stratum, a situation that contrasts with some records of other species, such as *Ototylomys phyllotis*, in which only the adults were found to use this stratum (Hernández-Betancourt et al. 2008).

With respect to *P. mexicanus*, one third of the total number of captures and recaptures were made on the trees, reaching a maximum capture height of 11.00 m, confirming this species as semi-tree-dwelling. The Mexican deer mouse generally establishes its burrows beneath fallen tree trunks, among the tree roots or under the ground (Trujano-Alvarez and Álvarez-Castañeda 2010), which could explain why we captured them more frequently at ground level. The average heights at which we recorded this rodent indicate that the species does not present a marked response according to sex or season in terms of climbing to the arboreal stratum. This contrast with other species of *Peromyscus*, such as *P. perfulvus*, which increase their movements on the trees during the rainy season (Domínguez-Castellanos et al. 2007).

The trees on which *P. yucatanicus* was captured had an average DBH of 19.11 cm, i. e., a low value if we consider that some individuals were captured in trees of up to 55.00 cm in diameter. Prominent among the tree species on which the species was captured were *L. latisiliquum*, *B. alicastrum*

and *B. simaruba*, which are common species in the tropical medium subevergreen forest of the EEER (Schultz 2003). In contrast, *Peromyscus mexicanus* was captured on trees with a DBH of almost 150.00 cm; however, the average diameter of the trees on which it was captured was 33.41 cm. *Bursera simaruba* was a species on which *P. mexicanus* was captured at ground level, and one that is included among those of greatest importance for the vegetal structure of the tropical medium subevergreen forest of the ZPSG (Godínez-Ibarra and López-Mata 2002). Most of the trees on which both species were captured presented rough bark and were covered with climbing plants, which can facilitate the ascent of the rodents on the trunk (Lambert et al. 2006; Kilgore et al. 2010). Tree-dwelling and semi-tree-dwelling rodents prefer to move on arboreal substrates (trunks and branches) of small and medium diameters. This is due to morphological adaptations of the cranium and feet (in addition to the claws that help them climb vertical strata), their specialized locomotion and corporal posture, which allow them unlimited movement on narrow substrates (Graves et al. 1988; Hyams et al. 2012; Youlatos et al. 2015; Camargo et al. 2019).

The specific sites of capture for both species displayed a closed canopy since low percentages of canopy openness (7.75 % for *P. yucatanicus* and 4.61 % for *P. mexicanus*). Different authors state that tree-dwelling and semi-tree-dwelling rodents often prefer habitats with dense vegetation in both understory and canopy (Schnell et al. 2008; Pérez-Lustre and Santos-Moreno 2010; Briones-Salas et al. 2012), since these characteristics offer the advantage of avoiding detection by predators (Villanueva-Hernández et al. 2017).

Captures of both *P. yucatanicus* and *P. mexicanus* diminished in sites with a higher percentage of leaf litter. In this regard, some studies document that rodents of the same genus prefer to inhabit sites with less leaf litter and organic material, or at least to limit their movements in areas in which these are abundant (preferring to move along the length of fallen trunks and branches), with the aim of avoiding being more visually or aurally detectable by predators (Roche et al. 1999; Klein and Cameron 2012).

Composition of the feces. The dominant element in the feces of *P. yucatanicus* was the seeds, which comprised nine microscopic morphotypes. This indicated the likelihood that the fruits that produced these seeds are important in its diet, particularly in the middle of the dry season (February). Fruit pulp and starch was abundant at the beginning of the dry season (November), but diminished considerably by the middle of this period (February), possibly due to the lack of fruits. However, some tropical forests of the Yucatan peninsula can maintain this particular food supply throughout the year, due to succession in the production of fruits, such as those of the species *Diospyros anisandra*, *Diospyros tetrasperma* and *Diospyros acapulcensis* subsp. *verae-crucis* (Hernández-Betancourt et al. 2003; MacSwiney et al. 2012).

The elements of vegetal origin that dominated the feces of *P. mexicanus* were different types of epidermis,

as well as fruit pulp and starch. The latter element is the most recurring during the dry season. This coincides with that reported in other studies that consider this rodent to be a consumer of a great variety of fruits, stems and leaves (Trujano-Alvarez and Álvarez-Castañeda 2010). Species of the same genus, such as *P. aztecus* and *Peromyscus dif- ficilis*, also present a diet dominated by vegetal elements, with the consumption of fruits and stems prominent in these two species, respectively (Vázquez et al. 2004; Peralta 2015). Although seeds had a low abundance in the feces, 24 morphotypes were recorded, indicating the wide variety of resources available in the tropical forest, particularly in the dry season.

Studies of diet in small rodents rarely analyze the diversity and quantity of seeds that are ingested and defecated by these mammals (Montenegro-Díaz et al. 1991; Wells et al. 2009; Shiels and Drake 2011; Yang et al. 2018). These analyses could influence the knowledge regarding the ecological role of each rodent species as a predator and potential disperser of seeds (Yang et al. 2018), as well as providing information relating to the distribution of resources and mechanisms of coexistence among rodent species of similar sizes (Vieira et al. 2006; Wells et al. 2009). In this study, the types of microscopic seeds that pass through the digestive tract of the study species could not be identified; however, their sizes and frequencies of appearance were recorded. Of the total number of morphotypes, 70.00 % were smaller than those reported in other rodents of similar length and corporal weight to *P. yucatanicus* and *P. mexicanus* (Vieira et al. 2006).

In its feces, the Yucatecan deer mouse presented low proportions of elements of animal origin, and even then only in the month at the beginning of the dry season. The arthropods found in the feces included ants and acari of less than 1.00 mm² in size, which could have been the result of accidental ingestion and association with the vegetal elements consumed by the rodent (López-Cortés et al. 2007; Peña-Ramos et al. 2009). In contrast, the feces of the Mexican deer mouse presented a high proportion of chitin remains, with a higher presence in the rainy season, which could be related to the fact that some arthropods are often more abundant during this season (Zavala-León et al. 2016). In this sense, it has been determined that the presence of arthropods in the diet can indicate a dietary flexibility that is advantageous in disturbed environments, or in situations where trophic resources are scarce (Vázquez et al. 2004; Lanzone et al. 2012). These arthropods also act as protein and hydric supplements that can increase the nutritional quality of the diet (Vázquez et al. 2004; Orr et al. 2015).

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Analysis of the male annual antler cycle, reproductive behavior and spotted fawn presence in the tropical white-tailed deer

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The rutting season of the white-tailed deer (*Odocoileus virginianus*) is seasonal in North America, but in tropical latitudes it occurs year-round with peaks locally variable. Reproductive cycle of this species in Costa Rica is variable, clearly seasonal in San Lucas Island but continuous with two birth peaks in Palo Verde and Santa Rosa national parks in northwestern Costa Rica. In Hacienda y Refugio de Vida Silvestre Curú in the Nicoya Peninsula, a site south of these parks but in a different life zone, we observed males with hard antlers in 2015 but only from July to November. We therefore hypothesized that white-tailed deer have a continuous reproductive cycle during the year in Curú because the rainfall pattern is the same as in Palo Verde and Santa Rosa. We visited Curú every month and recorded the status of white-tailed deer antler growth: nubs, velvet, and hard, from January 2016 to December 2019. We also recorded other rut behaviors and the presence of spotted fawns. We recorded 1,134 observations of the status of antler growth, 13 observations on reproductive behavior and 133 observations of spotted fawns. The antler cycle was seasonal in the four years of study. Male antler casting took place from mid-November to mid-February and the growth of new antlers began in mid-December and lasted until mid-March. Velvet shedding occurred in April, May and June, and by July males had hard antlers. The rutting season lasted three months from mid-June to mid-August. Small spotted fawns were observed from the middle of the dry season to the beginning of the rainy season. All this highly contrasts with the reproduction pattern observed in Santa Rosa. Lack of seasonal variation in the photoperiod is likely an important factor that allows deer to reproduce throughout the year in these protected areas, but this variation does not exist in Curú either, where the species is seasonal. The reproductive patterns of white-tailed deer in Central and South America may have evolved in response to seasonal fluctuations in specific food availability, competition, or predation, all of which may be directly related to rainfall patterns. Greater knowledge of the link between rainfall patterns and food availability for deer would be of great help to further our understanding of factors driving the reproduction cycle of the White-tailed deer.

La temporada de reproducción o brama del venado cola blanca (*Odocoileus virginianus*) es estacional en América del Norte, pero en latitudes tropicales ocurre durante todo el año con picos variables localmente. El ciclo reproductivo de esta especie en Costa Rica es variable, claramente estacional en la isla San Lucas, pero continuo con dos picos de nacimientos en los parques nacionales Palo Verde y Santa Rosa en el noroeste de Costa Rica. En Hacienda y Refugio de Vida Silvestre Curú en la Península de Nicoya, un sitio al sur de estos parques, pero en una zona de vida diferente, observamos machos con astas duras en 2015, pero solo de julio a noviembre. Por lo tanto, planteamos la hipótesis de que el venado cola blanca tiene un ciclo reproductivo continuo durante el año en Curú porque el patrón de lluvia es igual al de Palo Verde y Santa Rosa. Visitamos Curú todos los meses y registramos el estado del crecimiento de las astas de los venados de enero de 2016 a diciembre de 2019. También registramos otros comportamientos de celo y la presencia de cervatillos manchados. Registramos 1,134 observaciones del estado del crecimiento de las astas, 13 observaciones sobre el comportamiento reproductivo y 133 observaciones de cervatillos manchados. El ciclo de las astas fue estacional en los cuatro años de estudio. Los machos botaron las astas de mediados de noviembre a mediados de febrero y el crecimiento de las nuevas astas inició a mediados de diciembre y se prolongó hasta mediados de marzo. La caída del terciopelo ocurrió en abril, mayo y junio y a partir de julio los machos tenían astas duras. La brama duró tres meses, desde mediados de junio hasta mediados de agosto. Observamos cervatillos manchados pequeños desde la mitad de la estación seca hasta el inicio de la temporada de lluvias. Todo esto contrasta con el patrón de reproducción observado en Palo Verde y Santa Rosa. La falta de variación estacional en el fotoperiodo es probablemente un factor importante que permite que los venados se reproduzcan durante todo el año en estas áreas protegidas, pero esta variación tampoco existe en Curú, donde la especie es estacional. Los patrones reproductivos del venado cola blanca en América Central y del Sur pueden haber evolucionado en respuesta a fluctuaciones estacionales en la disponibilidad de alimentos específicos, la competencia o la depredación, todo lo cual puede estar directamente relacionado con los patrones de lluvia. Un mayor conocimiento del vínculo entre los patrones de lluvia y la disponibilidad de alimentos para los venados sería de gran ayuda para comprender mejor los factores que impulsan los ciclos de reproducción del venado cola blanca.

Keywords: Antler status; dry forest; humid forest; nubs; reproduction; rut; velvet.

Introduction

White-tailed deer (*Odocoileus virginianus*) has the widest distribution and is the most abundant of all New World cervids (Teer 1994). Its distribution extends from south-eastern Alaska in North America to northern South America with up to 38 recognized subspecies (Mattioli 2011). There is controversy regarding whether there is only one species or several species (Molinari 2007). In the latter case, the species found in Central America corresponds to *Odocoileus cariacou* of wide distribution on the Neotropical region (Molinari 2007).

Endogenous recognition of photoperiod changes drives seasonal reproductive cycles (Bronson 2009). A decrease in the daylight-darkness ratio triggers the onset of the reproductive cycle. Since the photoperiod is related to latitude (Ditchkoff 2011), the rutting season of white-tailed deer progresses along a continuum from November in most of North America, to January to March in northern México (Mattioli 2011), and from January to April in central and southern México (Weber *et al.* 1994; Contreras-Moreno *et al.* 2019). The annual cycle of antlers is related to the reproductive cycle with variation in the reproductive chronology linked to environmental variables mainly associated with latitude, especially photoperiods and food availability (Goss 1983; Price *et al.* 2005a; Hanon *et al.* 2008; Contreras-Moreno *et al.* 2019).

The annual phases of primary development of the testes, the complete production of sperm, and the rest period (Robinson *et al.* 1965) are associated with the onset of antler growth, shed of velvet, and antlers fall off, respectively (Verme and Ullrey 1984). The photoperiod acts through melatonin to modulate the secretion of reproductive hormones, mainly testosterone (Goldman 2001; Hanon *et al.* 2008) and regulates antlers cycle in white-tailed deer (Price *et al.* 2005a; Price *et al.* 2005b). However, because there is only a change in photoperiod in the tropics with a weak temporal association with seasonal climatic changes, it results that this environmental factor could have a reduced influence in controlling antler development in Southern México (Contreras-Moreno *et al.* 2019).

In temperate and cold regions of North America, severe weather and food availability are the critical environmental factors that dictate the timing of the birth season (Lincoln 1992; Price *et al.* 2005b). The reproductive cycle of white-tailed deer in these regions of North America is seasonal (Verme and Ullrey 1984; Mattioli 2011). The status of the antlers is associated with the growth and secretion cycle of testosterone by the testicles (Vasanth 2016). The testosterone cycle is governed largely by photoperiod (Loudon and Curlew 1988; Tomás 1995). The decrease of daylight and the increase in testosterone cause antlers to mineralize and shed their velvet (Tomás 1995). In contrast, increased daylight and decreased testosterone cause antler casting (Vasanth 2016). On the opposite, there is little information about the reproductive aspects of white-tailed deer in the Neotropics (Contreras-Moreno

et al. 2019). The birth of fawns and the development and casting of male antlers attracted the interest of the first naturalists working in the region (Rodríguez and Solís 1994). They speculated that fawns are born throughout the year and that there is no annual cycle in the growth and shedding of antlers due to the lack of seasonality in tropical and subtropical regions (Rodríguez and Solís 1994). However, studies conducted in the 1980s concluded that there may be some degree of synchrony in the growth of antlers and the birth of fawns in some places (Klein 1982; Branán and Marchinton 1987; Rodríguez and Solís 1994). Nonetheless, even in sites located nearby, the results seem contradictory because births occur in any season and the time of the year in which males shed their antlers is a function of individual age (Webb and Nellis 1981; Brox 1984; Rodríguez 1994; Fuller *et al.* 2020).

Studies on the reproductive cycle of white-tailed deer in Costa Rica have yielded contrasting results with clearly seasonal cycles at San Lucas Island (Rodríguez and Solís 1994) and continuous cycles with two birth peaks in Palo Verde and Santa Rosa national parks (Rodríguez 1994; Fuller *et al.* 2020). In the Nicoya Peninsula in northwestern Costa Rica, a peninsular site south of these areas and a different life zone, we observed males with hard antlers in 2015 but only from July to November. As a result, we made extensive, regular field observations from 2016 to 2019 to analyze the antler cycle in a white-tailed deer population in this area. We also recorded fawn birth periods in these four years. We hypothesize that white-tailed deer have a continuous reproductive cycle during the year in Curú because the rainfall pattern in this area is the same as in Palo Verde and Santa Rosa National Parks, where this species has an almost continuous annual reproductive pattern.

Material and methods

Study site. The Hacienda y Refugio de Vida Silvestre Curú (Curú) combines private and public lands totaling 1,496 ha: 312 ha dedicated to cattle ranching and 1,184 ha dedicated to conservation and ecotourism (Schutt and Vaughan 1995). It is located on the Nicoya Peninsula in northwestern Costa Rica (9° 47' 23" N, -84° 55' 28" W; Figure 1). Curú vegetation belongs to the Tropical Humid Forest Life Zone (Holdridge 1967; Bolaños *et al.* 2005).

Although the refuge is relatively small it is part of a continuum mosaic of cattle ranching operations and forest remnants along most of the south of the peninsula. Adjacent to Curú there is a secondary forest of over 5,000 ha located at the Peninsula de Nicoya Protected Zone. Curú is known to contain a high level of biodiversity due to the presence of several habitat types and its protection status (Schutt and Vaughan 1995). Seventy-eight species of mammals, 232 species of birds, 87 species of reptiles, and at least 500 species of plants have been identified in the refuge (McKinney 2014). Annual precipitation averaged 1,957 mm for the period 1970-2005, but it was 2,177 mm during our study (MN 2020a; IMN 2020b).

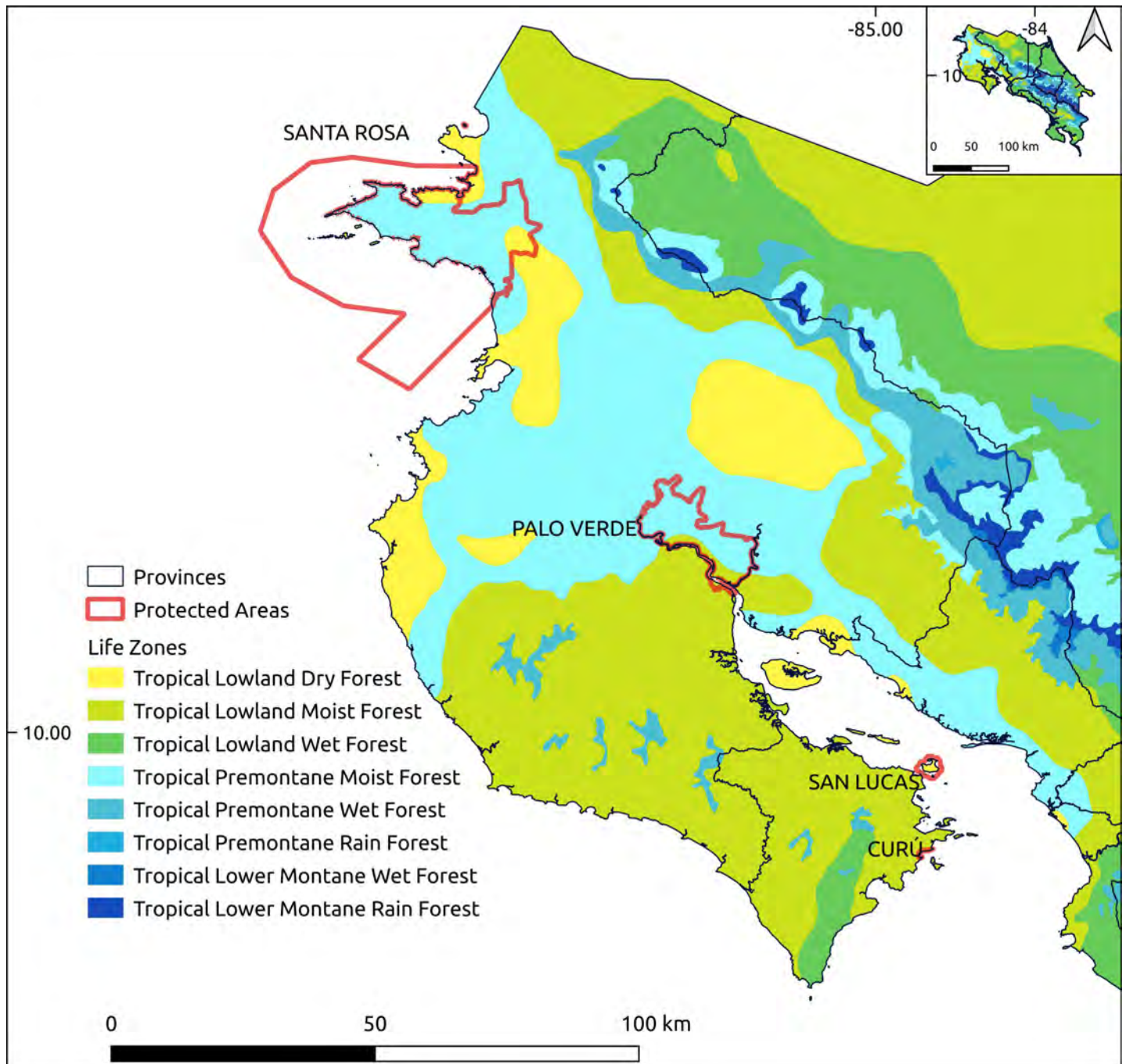


Figure 1. Life zones in Guanacaste province at Northwestern Costa Rica, and the four study sites mentioned in the text. The Hacienda y Refugio de Vida Silvestre Curú is located at the extreme southeastern portion of the Nicoya Peninsula in the Tropical Lowland Moist Forest. Map by G. Chaves (Cachi).

The dry season occurs from December to March when only 4 % of total annual rainfall accumulates. The transition to the rainy season is in April and by the third week in May, the rainy season is typically well established (IMN 2020). The first rainy period occurs between May and August when 50 % of the annual total precipitation accumulates. The first maximum of rains occurs in June as the southeastern trade winds intensify causing local storms and heavy downpours. The northeast trade winds intensify again causing a brief dry season between July and August called the “Pacific summer” or “canicula”. A second rainy season extends from September to November. The

greatest amount of rain, 46 % of the annual total, falls during September and October due to the greater influence of Caribbean cyclonic events. The transition to the dry season occurs in November (IMN 2020).

Data collection. We visited Curú once a month between January 2016 and December 2019, except in September 2016 and September 2019 when it was impossible to enter the area due to flooding and landslides on the access road. However, this did not affect our study since September is not of high significance for our purposes. We looked for deer on two transects: the main road (2,090 m) and a secondary road (1,958 m). We walked each transect in the

morning (6:00 h to 9:00h) and the afternoon (15:00h to 17:00h) every month. We recorded deer data using 10 x 50 binoculars and a digital camera.

Every time we observed a deer we recorded the sex and age group (fawn, yearling, adult) of each individual. We classified adult males by the presence of antlers and testicles, as well as by the presence of one or two fawns. Juvenile deer were classified as males or females based on body size and by the presence or absence of pedicels and testicles, respectively. Fawns were identified by the presence of spots on their fur. Both researchers have vast experience identifying and classifying deer by age.

Each time we observed an adult male we took a digital photograph for a database on the monthly growth status of deer antlers. For individual recognition of males and to avoid double-counting, we considered: 1) antlers size, 2) antler shape (number of tips, malformations) and 3) physical characteristics of each animal (presence of scars and wounds). Later we classified adult males as 1) nubs (no antlers or just one antler, pedicels in velvet), 2) velvet (growing antlers covered in velvet with rounded tine ends), and 3) hard (fully formed antlers, velvet-less; Figure 2). Additionally, we recorded rubs, odor marks, nonaggressive sparring, fights matching dominant bucks, chasing, and tending bucks, and bucks scraping the ground and leaving odor marks locally known as “rascaderos” (Rodríguez 2015). Although we also recorded the presence of adult females in the field, we made no effort to identify them individually. At each visit, we also counted spotted fawns and recorded them as small and large spotted fawns (see below).

Data interpretation and assumptions. All data were analyzed by month and year, however, for this report, the data were grouped for the whole study period: 2016 to 2019. To identify the reproductive seasonality of deer, we made the following assumptions concerning deer morphology and development based on a literature review. Antlers are shed annually (Sauer 1984). Antler’s growth lasts six months, and velvet dries and falls. Adult males keep hard antlers for about six months and then shed them (Sauer 1984). Testis’s cycle has three phases: 1) primary development, 2) full sperm production, and 3) resting period (Verme and Ullrey 1984). These phases are associated with the onset of antler growth, velvet shedding, and antler casting respectively (Verme and Ullrey 1984). Adult males are fertile only during the hard antler period. Female gestation varies among subspecies and ranges from 187 to 222 days, with a mean of 202 days (Smith 1991). Fawns spend most of their time hidden away from their mothers for three to four weeks (Marchinton and Hirth 1984), but gradually fawns spend more time with their mothers.

It is not possible to know the date of birth of the fawns in the field. Therefore, we classified spotted fawns into two groups: 1) small spotted fawns were two weeks to two months old, they do not reach the height of the mother’s

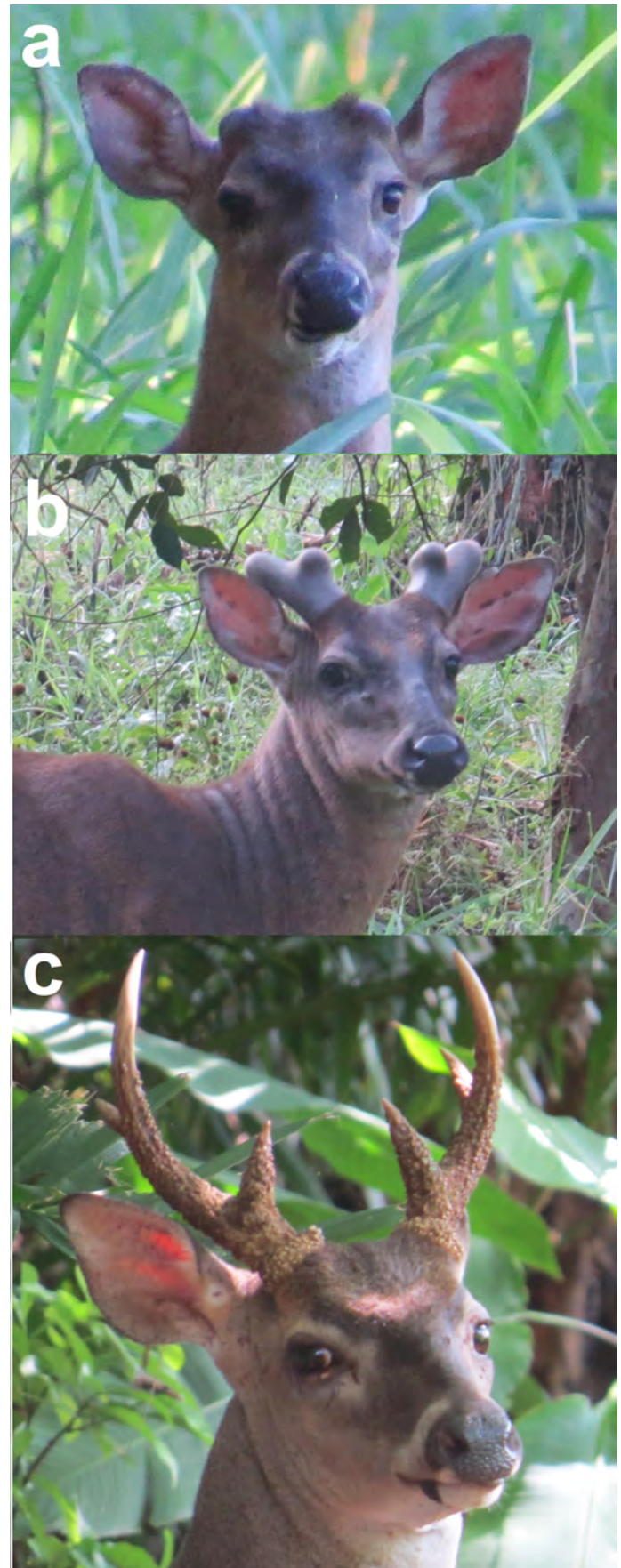


Figure 2. Antler growth stages of white-tailed deer (*Odocoileus virginianus*) at Hacienda y Refugio de Vida Silvestre Curú, Northwestern Costa Rica: a) nubs, b) velvet, c) hard.

belly, and they are generally observed alone in the forest or accompanied by the mother, and 2) large spotted fawns were three to four months old, they exceed the height of the mother's belly, and they are usually accompanied by the mother and other deer.

To test for the independence between the status of antler growth and the month of the year (which are related to the amount of rain) we analyzed the data with a Chi Square Test. We compared the absolute number of white-tailed deer (1,134) according to antler status per month. We used the adjusted residuals of the Chi Square Test as a posteriori test to evaluate in which cells of the contingency table it is observed more or less frequently than is expected at random. The critical value is the range from -1.96 to 1.96, so the values outside this range differ from the frequency expected by pure chance (Table 2).

Results

We totaled 1,134 observations of the status of antler growth of male white-tailed deer at Curú ($n = 233$ in 2016, $n = 367$ in 2017, $n = 294$ in 2018 and $n = 240$ in 2019; Table 1). The way we walked the transects and our knowledge of the area reduced the probability to count any male more than once. Additionally, we recorded 13 observations on reproductive behavior and 133 observations of spotted fawns.

Antlers. The antler cycle of the white-tailed deer at Curú was seasonal in the four years of study ($\chi^2 = 970$, d.f. = 22, $P < 0.001$). Antlers casting occurred over a three-month period that began in mid-November and ended in mid-February, during the first part of the dry season. The earliest antlerless or single-antlered deer were observed on 19 November 2017. The last single-antlered deer was observed on 5 February 2017. Antlerless or single-antlered males were not observed in any other month. Antlers grew during the dry season from mid-December to mid-March. A hundred percent of the males had velvet antlers in March in the four years of study (Figure 3a, Table 1).

Velvet shedding started in April and lasted through May and June, just at the beginning of the rainy season. In July less than 5 % of the males presented velvet antlers. We did not observe males with velvet antlers from August to October. We observed males with hard antlers from April until January or February of the following year. From July to October, 100 % of the males had hard antlers (Figure 3a, Table 1).

There was a significantly lower frequency of hard antlers than expected by chance in the first five months of the year, and significantly more frequency from June to December (Table 2). On the opposite, there was significantly higher frequency of antlers in velvet than expected from February to May and a lower frequency from July to January of the following year. Nubs were less frequent than expected in general during the year except in January and December, although differences were not significant in February, September, and November (Table 2).

Table 1. The absolute number of white-tailed deer (*Odocoileus virginianus*) according to antler status per month in the Hacienda y Refugio de Vida Silvestre Curú between January 2016 and December 2019. Nicoya Peninsula, Costa Rica.

Month	Antler status			n
	Hard	Velvet	Nubs	
Jan	33	37	47	117
Feb	4	106	9	119
Mar	0	96	0	96
Apr	7	93	0	100
May	25	78	0	103
Jun	75	42	0	117
Jul	88	2	0	90
Aug	82	0	0	82
Set	42	0	0	42
Oct	70	0	1	71
Nov	69	1	8	78
Dec	80	15	24	119
Total				1,134

$\chi^2 = 970$, d.f. = 22, $P < 0.001$.

Rutting season. The rutting season of white-tailed deer in Curú Refuge lasted three months from mid-June to mid-August. Rutting began when adult males were ready to reproduce, indicated by their hard antlers and reproductive

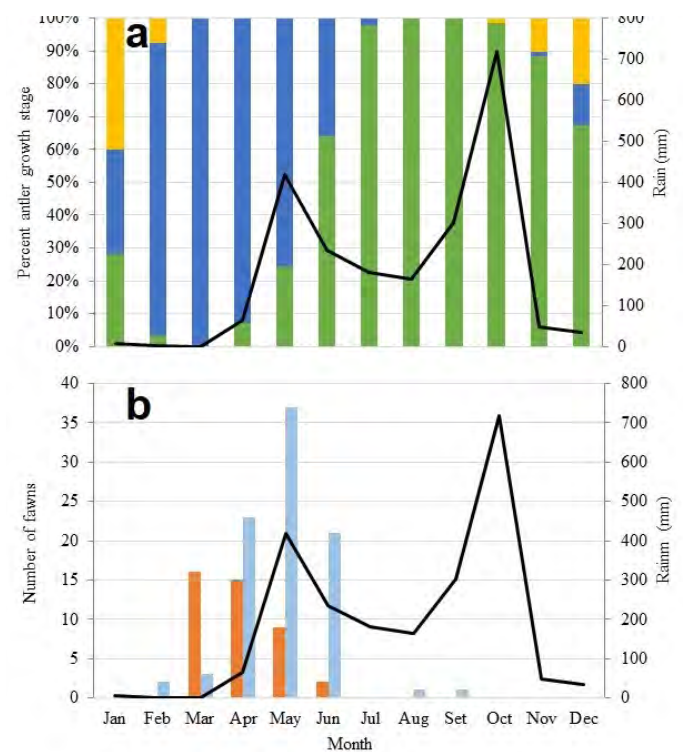


Figure 3. a) Monthly relative frequency (%) of antler status ($n = 1134$, monthly range 42-119). Hard (green), velvet (blue) and nubs (yellow). b) number of monthly observations of small spotted fawns (orange) and large spotted fawns (light blue) of white-tailed deer (*Odocoileus virginianus*) in Hacienda y Refugio de Vida Silvestre Curú between January 2016 and December 2019. Black lines indicate the average monthly precipitation (mm) in the same period at the Paquera Station: 2016 = 1,473.4 mm; 2017 = 2,475.8 mm; 2018 = 2,436.4 mm; 2019 = 2,327.8 mm (IMN 2020a), Nicoya Peninsula, Costa Rica.

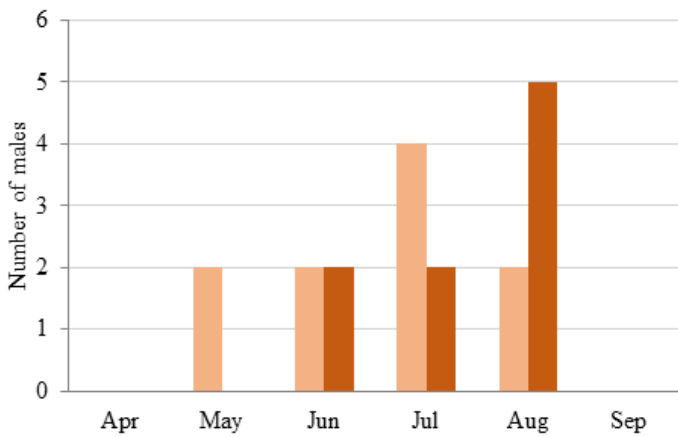


Figure 4. The number of males white-tailed deer (*Odocoileus virginianus*) per month that chased females, and the number of males per month that accompanied females, between January 2016 and December 2019 (other months have zero males engage in these activities). Hacienda y Refugio de Vida Silvestre Curú, Nicoya Peninsula, Costa Rica. Chasing deer males (pink) and tending deer males (brown).

behavior. In mid-June, males started rubbing antlers, scraping, and sparring. This behavior lasted for the first part of the rainy season. They adopted tending bond mating systems, courtship and copulating receptive does in August and September when males had hard antlers (Figures 3a, 4). The first males observed chasing does entering estrus were in August. We observed does accompanied by bucks in August and September, and by October neither chasing nor courtships were observed (Figure 4).

Fawning season. Small spotted fawns (Figure 5) were observed between March and June (Figure 3a); this is from the middle of the dry season to the beginning of the rainy season. During March most of the observations were of small spotted fawns (16 out of 19), while only three observations corresponded to large spotted fawns (Figure 3a). On the opposite, observations of large spotted fawns (Figure 5) predominated in April (23 out of 38).

A peak of spotted fawns was reached in May, although most of them were large-bodied spotted fawns (37 out of 46). Large-bodied spotted fawns (21 out of 23) also predominated in June when only two small spotted fawns were observed (Figure 3a). Fawns were five months old by July and had no spots. We did not see any spotted fawns after June, except by two large spotted fawns in August and September 2017, that were born probably by April-May given their sizes.

Discussion

Because there are comparatively few studies of white-tailed deer in the Neotropical region, a general conclusion emerged over time that white-tailed deer would be less seasonal in antler growth and casting in regions without strong seasonal changes in weather (Marchinton and Hirth 1984). The assumption was that the same would happen with other reproductive processes such as rut and fawn births. However, some studies challenge this generalization.

White-tailed deer reproduction seemed seasonal, lasting four to six months, as reported from limited observations in the Virgin Islands (Webb and Nellis 1981), Honduras (Klein 1982), Venezuela (Brox 1984), Colombia (Blouch 1987) and Surinam (Branan and Marchinton 1987). A recent study in Campeche wetlands in Southeastern México, a tropical site, showed that the antler cycle of the white-tailed deer is seasonal (Contreras-Moreno *et al.* 2019).

Studies of white-tailed deer reproduction in Costa Rica have shown considerable variation in reproductive processes among relatively nearby populations. Rodríguez (1994) found no seasonality in antlers casting and growth or in fawn births in Palo Verde National Park in the mid- 1990s and recently Fuller *et al.* (2020) obtained similar results in a study in Santa Rosa National Park. However, on San Lucas Island, situated approximately 78 km in a straight line from Santa Rosa, the white-tailed deer life cycle had a marked seasonality (Rodríguez and Solís 1994). Antler growth occurred from March to June, velvet shedding in June and July, hard antlers from July to December, and antler casting in January and February (Rodríguez and Solís 1994). Antler status pattern, as well as fawn births, were even more seasonal in Curú than in San Lucas Island, the only real dry forest in Costa Rica included in this comparison (Figure 1). These processes took three months to complete in Curú. Some minor variations in the onset of antler casting and velvet shedding appear to be responses to variations in precipitation patterns between consecutive years. The first signs of the start of the rut appeared in June in Curú when antler velvet had dried and shed, and bucks had hard antlers (Figure 2c). Antler cycle as well all other processes were significantly seasonal (Table 2). Antler cycle seasonality in Curú coincides with the antler cycle of the white-tailed deer in a tropical site in southeastern México (Contreras-Moreno *et al.* 2019). In Curú, fawns were five months old by July and

Table 2. Value of adjusted residuals of the χ^2 test for antler status of white-tailed deer (*Odocoileus virginianus*) per month in the Hacienda y Refugio de Vida Silvestre Curú Nicoya Peninsula, Costa Rica, between January 2016 and December 2019. Residuals in bold indicate significant differences. The value of the sign indicates if the frequency is higher (+) or lower (-) than expected by chance.

Month	Antler status		
	Hard	Velvet	Nubs
Jan	-5.140	-2.277	13.728
Feb	-10.919	11.148	-0.122
Mar	-10.387	12.172	-2.988
Apr	-9.155	10.959	-3.056
May	-5.628	7.407	-3.106
Jun	3.061	-1.286	-3.333
Jul	9.309	-7.872	-2.885
Aug	9.270	-7.909	-2.744
Set	6.512	-5.556	-1.927
Oct	8.336	-7.322	-2.084
Nov	6.912	-7.462	0.819
Dec	3.810	-6.750	5.282

had no spots, which means they were born in February but were not observed sooner due to their hiding behavior during the first weeks of life (Rodríguez 2015).

Rain seasonality at Santa Rosa National Park (Fuller *et al.* 2020) is similar to that of Curú. Rainfall peaks in May - June, decrease in July – August, and peaks again with greater precipitation around October. That could explain why the phenology of Curú vegetation demonstrates similar patterns to those of other sectors in Northwestern Costa Rica where many dry forest species are deciduous and recover much of their foliage at the beginning of the rainy season in May and June (Castro *et al.* 2018). However, several tree species maintain foliage throughout the dry season, as do half of the shrubs, saplings, and seedlings (Frankie *et al.* 1974; Opler *et al.* 1980), and many animal species reflect these patterns (Rockwood 1975; Janzen 1993; Orkin *et al.* 2019).

Curú is located in a more humid life zone than Santa Rosa (Figure 1), but this seems to not affect the white-tailed deer reproductive cycle. Although the rainy season determines the availability of food, which is a proximate cause of high variation of the reproductive cycle in Santa Rosa during the year (Fuller *et al.* 2020), it does not seem to have a strong influence on the deer cycle in Curú. However, there was a coincidence between the peak of precipitation occurring in May and the highest number of fawns with spots (36, Figure 3a).

Lack of seasonal variation in the photoperiod is the decisive factor that likely favor deer reproduction throughout the year in Santa Rosa (Fuller *et al.* 2020). Yet this variation is identical in Curú, where the reproduction of the species is seasonal. The peak of births in February and March ensures the survival of the fawns, which will be weaned at the beginning of the rainy season when there is plenty of food. The high amount of rain in September and October, including flooding, will not affect the fawns because they are already grown up by this time of the year (Figure 3a). However, these severe rains and flooding could be an impacting seasonal factor on the fawning season at Curú. The association of flooding with changes in the fawning season has been reported in white-tailed deer populations that occur in areas affected by severe flooding such as the Everglades in Florida (MacDonald-Beyers and Labisky 2005).

The reproduction pattern we observed in Curú is similar to the pattern on San Lucas Island, located in a dry forest at a distance less than 20 km in a straight line (Rodríguez and Solís 1984). What is different among the sites? The traditional or more commonly used system of ecosystem classification in Costa Rica is Holdridge's Life Zones (Bolaños *et al.* 2005). In this classification, Santa Rosa and Palo Verde are in the Pre-montane humid Forest Life Zone and Curú in the Tropical humid Forest zone, leaving San Lucas Island as the only one of the sites included in our comparison that is located in a tropical dry forest. This explains to some degree the highly seasonal reproductive process of the white-tailed deer in San Lucas, but it does not explain



Figure 5. a) Small spotted fawn and b) large spotted fawn of white-tailed deer (*Odocoileus virginianus*) at Hacienda y Refugio de Vida Silvestre Curú, Northwestern Costa Rica.

the seasonality pattern we found in Curú. However, Curú is even more humid than Santa Rosa and Palo Verde, even though all three of these sites as well as San Lucas have a marked dry season. Rainfall in Curú is higher than in Santa Rosa, and it may make a difference in year-round food availability, but severe rains and flooding by September and October can have a more determining impact on fawning seasonality.

The reproductive patterns of white-tailed deer in Central and South America may have evolved in response to seasonal fluctuations in specific food availability, competition, or predation, all of which may be related to rainfall patterns (Asher 2011). However, these factors do not explain why white-tailed deer reproduction is seasonal in some places, but not in others that are very close. Is there a direct relationship to weather or is some other factor that differs between the sites responsible for the differences in white-tailed deer reproduction? Are white-tailed deer more genetically related to North American forms that are more seasonal, or does another factor make them different from non-seasonal deer? It appears that white-tailed deer exhibit a very flexible and therefore variable reproductive pattern (Fuller *et al.* 2020). More research is needed to understand what factors more directly explain the observed pattern in the white-tailed deer reproduction.

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Daytime diet of the lesser sac-winged bat (*Saccopteryx leptura*) in a Colombian Pacific Island

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Insectivorous bats represent more than half of all the Chiropterans of the world. Although they are important stabilizers of insect populations within their habitat due to their feeding habits, just few studies have been focused on the diet of insular bat species. The lesser sac-winged bat, *Saccopteryx leptura*, is widely distributed in the new world tropics, but little is known about its prey selection. In this study we determined the diet composition of the population of *S. leptura* from Gorgona Island, Colombia, using stomach and intestinal content samples. We focused our research on their atypical daytime feeding behavior to evaluate differences in prey selection considering two main factors: 1) plant canopy cover and 2) bat sex. We found prey representatives of nine orders of insects, with Hymenoptera, Coleoptera and Hemiptera as the most consumed according to their abundance and volume percentage. We identified two new records at genus level in *S. leptura*'s diet, *Camponotus* (Formicidae) and *Trigona* (Apidae). In general terms, we did not find differences in the diet between canopy covers nor sexes. However, when analyzing the consumed percentage volume by order, there were significant differences in consumption of Psocoptera in both factors. Our results suggest that *S. leptura* has an opportunistic diet, as they tend to feed on prey of a wide range of sizes, usually the most abundant and available in the environment.

Los murciélagos insectívoros representan más de la mitad de la diversidad de quirópteros del mundo. Aunque son importantes estabilizadores de las poblaciones de insectos dentro de su hábitat debido a sus hábitos de alimentación, pocos estudios se han centrado en la dieta de las especies de murciélagos insulares. El murciélago de sacos pequeño, *Saccopteryx leptura*, es una especie ampliamente distribuida en el trópico del nuevo mundo, pero con poca información sobre su dieta. En este estudio se determinó la composición de la dieta de una población de *S. leptura* en la isla Gorgona, a partir de muestras de contenido estomacal e intestinal. Esta investigación se centró en su patrón atípico de alimentación diurna para evaluar las diferencias en la selección de presas considerando dos factores: (1) la cobertura de dosel y (2) el sexo. Se encontraron representantes de nueve órdenes de insectos, siendo Hymenoptera, Coleoptera y Hemiptera los más consumidos, según la abundancia y porcentaje de volumen. Se identificaron dos nuevos registros a nivel de género dentro de la dieta de *S. leptura*, *Camponotus* (Formicidae) y *Trigona* (Apidae). En términos generales, no se encontraron diferencias de la dieta entre coberturas de dosel o entre sexos. Sin embargo, al analizar el porcentaje de volumen consumido a nivel de orden, se encontraron diferencias significativas en el consumo del orden Psocoptera para ambos factores. Los resultados sugieren que *S. leptura* adopta una alimentación oportunista, ya que consume presas de una amplia gama tamaños, usualmente las más abundantes y disponibles en el medio.

Keywords: Daytime activity; diet; Gorgona island; insectivorous bat; intestinal content; stomach content.

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Introduction

Insectivorous and arthropodophagous bats represent about 70 % of the world's Chiropteran diversity, and more than half of its Neotropical diversity (Fenton and Simmons 2014). Their eating habits highlight their importance as crop pest controllers and stabilizers of arthropod populations (Boyles et al. 2011; Boyles et al. 2013). However, little is known about the feeding habits of insular arthropodophagous and insectivorous bat species, which, unlike their mainland conspecifics, have limited resources that depend on the availability and population dynamics of the island's exclusive invertebrates, as well as on the competition with sympatric species (Sedlock et al. 2014). This means that island bats must adapt to the restrictions imposed by their environment to survive (McNab 2010). Some bat trophic strategies reported on islands are: 1) opting for a general-

ist diet (Razakarivony et al. 2005; Rakotoarivelo et al. 2007; Racey et al. 2010), 2) resource partitioning to reduce competition (Zhang et al. 2005; Fukui et al. 2009; Rolfe et al. 2014), and 3) modifying their foraging periods according to the activity patterns of their prey (Bradbury and Vehrencamp 1976; Pavey et al. 2001).

The lesser sac-winged bat, *Saccopteryx leptura*, is a small insectivorous bat that is widely distributed in the new world tropics, mainly in the intertropical zone. This species can live in a wide range of habitats, from preserved tropical forests to urban areas, and there are even populations on islands (Bradbury and Emmons 1974; Cadena et al. 1990; Vivas-Toro and Murillo-García 2019). Knowledge about *S. leptura* is scarce, including that concerning its feeding habits. Bradbury and Vehrencamp (1976) made an approxima-

tion of *S. leptura*'s diet composition based on analyses of other emballonurid sympatric species, which suggested they have a diet mainly consisting of Coleoptera and Diptera, with lower consumption of Lepidoptera. However, there are two studies (albeit consisting of few individuals or samples) that propose Hymenoptera as the most consumed order (Nogueira *et al.* 2002; Cruz-Parrado *et al.* 2018). Although these studies provide valuable contributions, they still represent first data regarding the diet of *S. leptura*.

Interestingly, *S. leptura* has shown a positive response to moonlight intensity, implying higher activity at brighter nights (Appel *et al.* 2017, 2019). Furthermore, this species has also been reported foraging during the day on islands such as Trinidad (Bradbury and Emmons 1974) and Gorgona (Vivas-Toro and Murillo-García 2020), generating more questions concerning *S. leptura* feeding habits and what they eat during those time frames. Frequent daytime activity of insectivorous bats is unusual (Russo *et al.* 2011a). Except for the early forager *Pipistrellus pygmaeus* from central Italy (Russo *et al.* 2011a), to date, all species reported exhibiting this behavior reside on islands (Bradbury and Emmons 1974; Moore 1975; Russo *et al.* 2011a; Russo *et al.* 2011b; Chua and Aziz 2019; Vivas-Toro and Murillo-García 2020). Among the common patterns displayed by these bats during the day are the tendency to feed mainly in closed canopy sites with abundant insect prey, and a decreasing activity with increasing light intensity (Speakman 1995; Russo *et al.* 2011a; Russo *et al.* 2011b; Chua and Aziz 2019; Vivas-Toro and Murillo-García 2020). There is no detailed information on the selection of prey during the day in most species of bats that exhibit these habits, however, *P. pygmaeus* tends to feed on insect swarms when available, particularly nematocerans flies, and on the most abundant taxa, such as brachycerans (Russo *et al.* 2011b).

Various studies have shown that bats foraging emergence times are closely related to canopy cover and forest closure (Russo *et al.* 2007; Marques *et al.* 2015), being common the occurrence of earlier emergences in cluttered areas compared with open areas (Jones *et al.* 1995; Russo *et al.* 2007; Thomas and Jacobs 2013). This has been associated to strategies to evade the detection of predators or the risk of hyperthermia (Speakman 1995) and to maximize foraging time (Jones and Rydell 1994; Duvergé *et al.* 2000). Furthermore, the early emergence and late return of pregnant and lactating females in some species has been observed, which has been considered a strategy to feed for longer to meet energy demands during reproduction (Shiel and Fairley 1999; Duvergé *et al.* 2000; Lee and McCracken 2001).

There are currently 15 bat species reported for Gorgona Island, 9 of them are insectivorous (Murillo *et al.* 2014). Since *S. leptura* is abundant on Gorgona and exhibits an extended active period (Vivas-Toro and Murillo-García 2020), its insular population is suitable for studying diet composition and feeding habits of the species. Therefore, the aim of this study is to describe the diet composition of *S. leptura*, based

on the daytime foraging of an insular resident population. Particularly, we seek to answer to the following questions: 1) are there differences in *S. leptura* prey consumption according to the canopy cover? 2) Are there differences in prey selection between males and females? 3) Is daytime feeding a good representation of the diet of *S. leptura*?

Materials and Methods

This study was conducted in Gorgona National Natural Park (GNNP; 2° 58' 4" N, -78° 11' 3" W), a continental island of volcanic origin located 35 km from the Pacific coast of Colombia (Giraldo 2012). The island has an equatorial climate with super-humid rainforest vegetation, that is part of the Chocó biogeographic province, and is mainly constituted by secondary forest (Vásquez-Vélez 2014). We determined *S. leptura*'s diet by analyzing stomach content and fecal samples collected in roosts only occupied by *S. leptura*, or from bats captured in flight. Sampling was carried out over 10 days between July and November 2017, five days during each month, in areas with high ($\geq 70\%$) and low ($\leq 35\%$) plant canopy cover. We collected fecal samples from roosts between 8:00 and 15:00 h. We collected fresh scats which were no more than four hours old; that is, of a soft consistency; a moist, dark color; and recognizable odor. We consider the foraging territory of bats in roosts, who was recorded in a previous study (Vivas-Toro and Murillo-García 2020), to define what type of canopy cover the samples belonged to. We captured bats between 17:00 and 19:00 h using a hand net and kept them in individual cloth bags until they defecated. All individuals were released after collecting the droppings. We carried out all captures and management of bats following the protocol for obtaining data on mammals on GNNP (Murillo *et al.* 2011). We stored the samples individually in plastic vials filled with 80% alcohol. We also analyzed the stomach content of a recently dead individual (not collected), found around 11:00 h in November. Since in most cases several taxonomic groups were detected within a single scat, for a better standardization of the samples, and to avoid possible biases in the subsequent analyzes (according to Whitaker *et al.* (1996) for differences in size or volume of the samples), each scat (of approximately 6 x 2 mm) was considered as an independent unit. We identified prey at the most specific taxonomic level possible, in most cases to family, based on all recognizable fragments such as legs, wings, antennae, heads, tegument, scales, and/or structures with diagnostic characteristics (Whitaker *et al.* 2009). We estimated prey size by reconstructing them by grouping structures and fragments found using a Nikon SMZ745 stereomicroscope. All the material was identified, size estimated and quantified according to the taxonomic criteria and knowledge of an expert taxonomist.

We calculated the frequency of occurrence (FO) as the number of scats including the taxa divided by the total number of scats; the percentage composition (C) as the number of individuals of each taxon divided by the total

number of individuals from all taxa, multiplied by 100 (Deagle *et al.* 2018; Vallejo *et al.* 2019); and the percentage volume (V) as the total volume of each taxon in the fecal-stomach samples divided by the total volume of all samples, multiplied by 100 for each taxon within the samples. We used the spheroid volume formula to approximate the volume value for each prey (Toshiaki 2004). We performed an arcsine transformation of all percentage data to correct non-normality before the analyses (Zar 1984). We used V to determine whether there were significant differences in diet between canopy covers and sexes through independent non parametrical ANOVAs, since the data was not normally distributed. Additionally, we tested differences in prey consumption by order relating the percentage volume of each order with each independent variable (canopy cover and sex) trough simple lineal regressions (Moosman *et al.* 2012) or fitted for quasi-Poisson distributions according to prior examination of the distribution and dispersion of each data set. All the analyses were conducted in R v.4.0.2 (R Development Core Team 2021).

Results

Intestinal content. We collected 63 fecal samples, 24 pellets from 7 bats captured in flight and 39 pellets from roosts; 29 pellets in low canopy cover and 34 in high canopy cover; 29 pellets were from males, 13 from females, and 21 mixed

samples from a roost occupied by 2 males and 2 females. We identified 493 prey items belonging to 9 orders and 23 families of insects (Table 1). We also found mites (Arachnida), which are not intentionally ingested, but are present due to their phoretic relationship with the consumed insects; thus, they were not considered in the analyses.

The average size of prey eaten by *S. leptura* on Gorgona island was 5.1 ± 2.1 mm, ranging from 2 to 13 mm. The most abundant orders found were Hymenoptera (C = 32.25 %), Coleoptera (C = 30.83 %) and Hemiptera (C = 20.08 %; Figure 1), with Formicidae as the most consumed family (C = 18.46 %), followed by Chrysomelidae (C = 7.91 %) and Miridae (C = 7.71 %). The order Hymenoptera also comprised the highest percent volume (V = 36.25 %), followed by Hemiptera (V = 32.08 %) and Coleoptera (V = 21.18 %; Figure 1); with Formicidae as the most consumed family (V = 26.65 %), followed by Miridae (V = 15.46 %) and Chrysomelidae (V = 13.62 %) respectively. We identified the genus *Trigona* (stingless bees) and *Camponotus* (carpenter ants, two winged-morphospecies; Hymenoptera), representing new records in the diet of these bats. We also found two cephalic capsules of lepidopteran larvae.

We found no significant differences in the diet of *S. leptura* between between plant canopy covers ($X^2 = 0.004$, $df = 1$, $P > 0.05$) or between sexes ($X^2 = 0.370$, $df = 1$, $P > 0.05$). When analyzing by order, we only found significant differ-

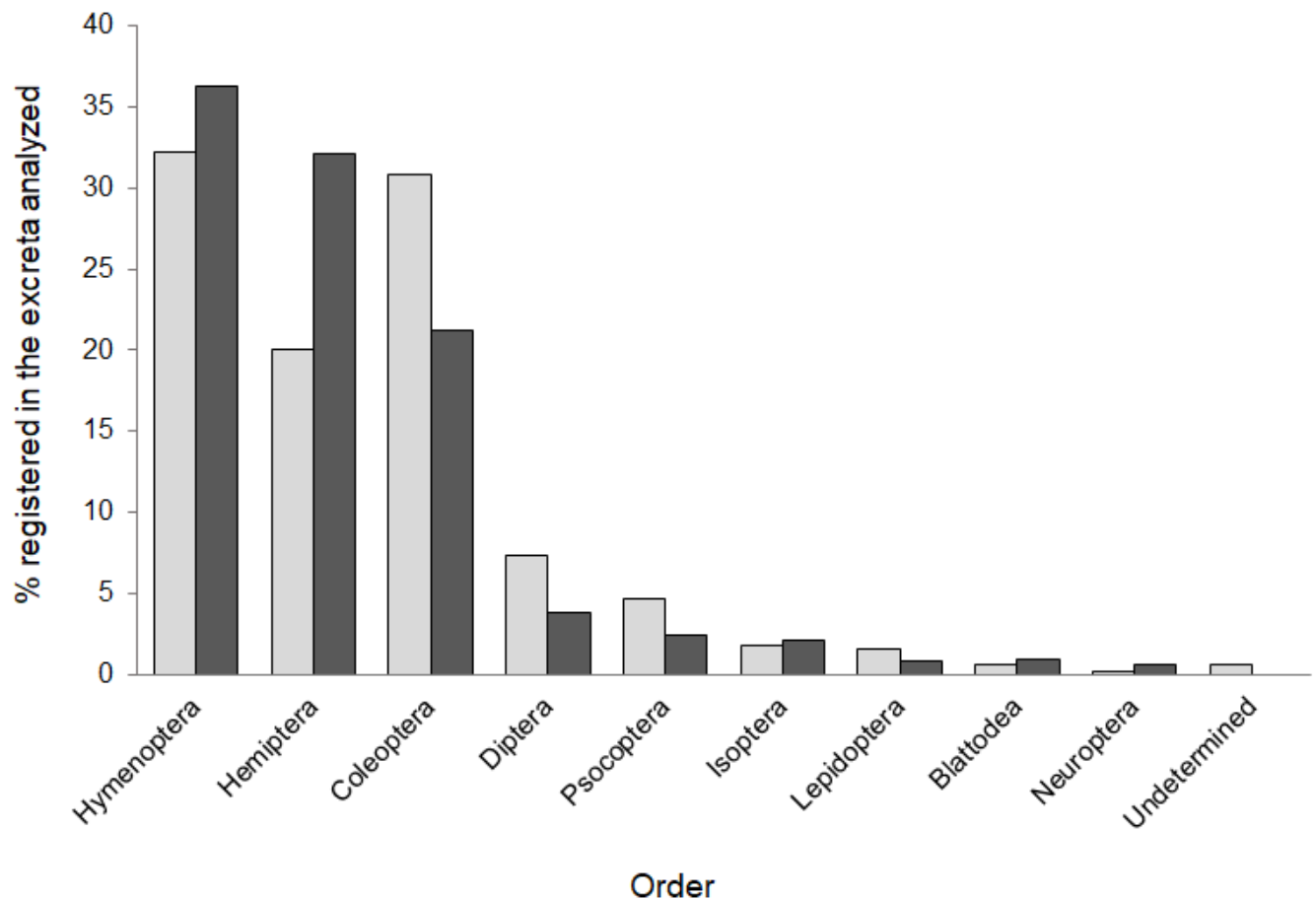


Figure 1. Percentage composition (light gray) and percentage volume (dark gray) of insect orders consumed by *Saccopteryx leptura* on Gorgona Island.

ences for Psocoptera, which were consumed more often in low canopy cover ($F_{1,61} = 9.38, P < 0.01$; Figure 2a) and by males ($F_{1,40} = 6.62, P < 0.05$; Figure 2b). That is, a volume of 74.40 % in low canopy cover vs. 25.60 % in high cover, and 90.27 % in males vs. 9.73 % in females from the total volume of Psocoptera consumed.

Stomach content. The stomach content of the *S. leptura* male we found dead during the study consisted of insects almost entirely of the order Hymenoptera ($C = 94.40\%$), with remains from the families Braconidae and Formicidae, and the subfamilies Myrmicinae and Formicinae (*Camponotus* sp.1 and *Camponotus* sp.2; Table 2); and a bupres-

Table 1. Diet of *Saccopteryx leptura* in Gorgona Island. Frequency of occurrence (FO), percentage composition (C) and percentage volume (V) of prey found in *S. leptura* feces. N = number of individuals.

Order	Suborder/Family	Minimum taxa level	N	FO	C	V
Blattodea			3	0.05	0.61	0.88
	Ectobiidae		1	0.02	0.20	0.72
	Undetermined		2	0.03	0.41	0.15
Isoptera	Termitidae		9	0.14	1.83	2.05
Hemiptera			99	0.76	20.08	32.08
	Delphacidae		3	0.06	0.61	0.97
	Cicadellidae		24	0.29	4.87	4.66
	Reduviidae		2	0.03	0.41	1.16
	Cixiidae		1	0.02	0.20	0.18
	Rhyparochromidae		3	0.05	0.61	0.37
	Miridae		38	0.38	7.71	15.46
	Auchenorrhyncha		6	0.11	1.22	1.27
	Fulgoromorpha		6	0.08	1.22	2.25
	Undetermined		16	0.25	3.25	6.18
Psocoptera			23	0.35	4.67	2.40
	Psocidae		6	0.10	1.22	0.77
	Epipsocidae		3	0.05	0.61	0.64
	Undetermined		14	0.21	2.84	0.98
Coleoptera			151	0.86	30.83	21.18
	Chrysomelidae		39	0.54	7.91	13.62
	Curculionidae		30	0.37	6.09	4.47
		Scolytinae	28	0.35	5.68	4.35
		Platypodinae	2	0.03	0.41	0.12
	Endomychidae		1	0.02	0.20	0.35
	Staphylinidae		6	0.11	1.22	1.23
	Undetermined		76	0.59	15.42	1.64
Neuroptera	Undetermined		1	0.02	0.20	0.55
Hymenoptera			159	0.79	32.25	36.25
	Formicidae		91	0.70	18.46	26.65
		Myrmicinae	18	0.21	3.65	0.87
		Formicinae	20	0.19	4.06	5.49
		<i>Camponotus</i> sp. 1	28	0.30	4.46	13.08
		<i>Camponotus</i> sp. 2	14	0.19	2.84	5.47
		Undetermined	17	0.19	3.41	1.75
	Apocrita (parasitica)		1	0.02	0.20	0.01
	Braconidae		16	0.17	3.25	1.26
	Ichneumonidae		2	0.03	0.41	0.32
	Halictidae		30	0.38	6.09	4.66
	Apoidea		1	0.03	0.20	0.26
	Apidae		15	0.17	3.04	2.49
		<i>Trigona</i>	10	0.11	2.03	1.04
		Undetermined	5	0.08	1.01	1.45
	Vespoidea		2	0.02	0.41	0.34

Table 1. Continuation...

Lepidoptera		8	0.08	1.62	0.80
	Noctuidae	4	0.03	0.81	0.37
	Undetermined ¹	2	0.02	0.41	0.06
	Undetermined	2	0.03	0.41	0.25
Diptera		36	0.44	7.30	3.81
	Muscomorpha	2	0.03	0.41	0.30
	Nematocera	3	0.05	0.61	0.21
	Ulidiidae	1	0.02	0.20	0.12
	Dolichopodidae	1	0.02	0.20	0.62
	Sciaridae	1	0.02	0.20	0.02
	Phoridae	1	0.02	0.20	0.06
	Undetermined	27	0.37	5.48	2.47
Undetermined		3	0.03	0.61	-

¹ Undetermined Lepidoptera family represented by larvae cephalic capsules.

tid beetle (C = 5.60 %). The largest prey found was a 13 mm *Camponotus* sp.2 ant; while the smallest was a 3 mm braconid wasp.

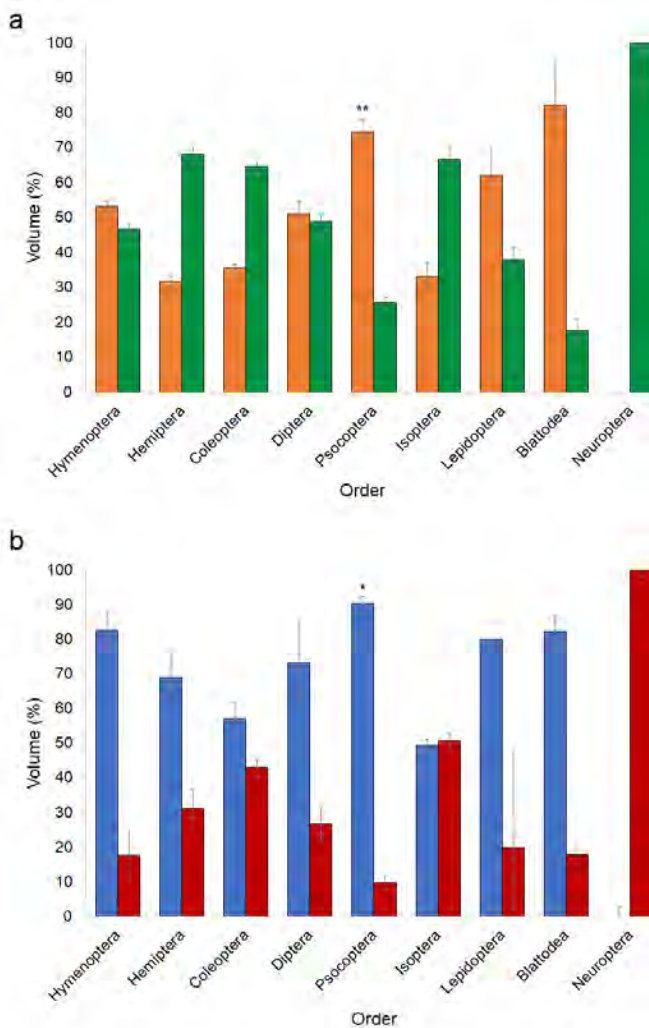


Figure 2. Variation in the diet of *Saccopteryx leptura* in Gorgona island in relation to (A) canopy cover and (B) sex. Percent volume and standard error are illustrated for each insect order. Asterisks represent significant differences in the diet of *S. leptura* according to individual regression tests for each order (* = $P < 0.05$; ** = $P < 0.01$). Colors code: orange, low canopy cover; green, high canopy cover; blue, males; red, females.

Discussion

Insectivorous bats tend to be selective with their food, their preferences may depend on features such as hunting methods and echolocation, prey characteristics such as size and texture (Barclay and Brigham 1994; Jung et al. 2007; Sedlock et al. 2014), the bat's cranial morphology, among others (Freeman 1979; Van Cakenberghe et al. 2002). Also, several studies have demonstrated that they can be flexible in terms of food selectivity according to the availability and seasonality of their prey (Whitaker 1994; Whitaker et al. 1996; Agosta et al. 2003), by inter or intraspecific competition (Whitaker 2004; Novella-Fernandez et al. 2020) and even due to their reproductive and/or developmental states (Verts et al. 1999; Agosta and Morton 2003). According to the stomach and fecal samples content found in this study, the insular population of *S. leptura* on Gorgona had a considerable variety of prey in its diet compared with what was previously reported in continental populations (Nogueira et al. 2002; Cruz-Parrado et al. 2018), and the approximations for *S. leptura* populations in Trinidad Island (Bradbury and Vehrencamp 1976). In general, we found that *Saccopteryx leptura* feeds on a wide variety of prey, from soft insects such as Psocoptera, Diptera and Lepidoptera; to harder insects such as Coleoptera and Hemiptera. For example, the relative consumption of Hymenoptera, in terms of composition and volume, was mainly determined by the FO of winged formicids in the samples (70 %). The latter can be explained by the abundance of these insects in the island since they are social insects whose populations and colonies are very numerous (Universidad del Valle 2014). Additionally, the caste of reproductive (winged) individuals within their colonies perform daytime nuptial flights consisting of hundreds of individuals, (Quirán and Corró 1998; Lara-Juárez et al. 2015). The consumption of winged ants has been previously reported in *S. leptura*'s diet, representing one of its most frequent prey (Nogueira et al. 2002; Cruz-Parrado et al. 2018). Many tropical bats feed on seasonal nuptial swarms of termites or ants, since they involve an important food resource, clustered in one single

Table 2. Percentage composition (C) and percentage volume (V) of prey found in the stomach content of a dead male specimen of *Saccopteryx leptura* found in Gorgona island. N = number of individuals.

Order	Family	Subfamily	Minimum taxa level	N	C	V
Coleoptera				1	5.60	0.40
	Buprestidae			1	5.60	0.40
Hymenoptera				17	94.4	99.6
	Formicidae	Myrmicinae		7	38.9	3.80
		Formicinae	<i>Camponotus</i> sp. 1	4	22.2	49.60
			<i>Camponotus</i> sp. 2	5	27.8	45.10
	Braconidae			1	5.60	1.20

area (Kunz *et al.* 1995; Pavey *et al.* 2001). There are even species such as *Rhinopoma microphyllum* that can feed almost exclusively on *Camponotus* alates during their summer massive nuptial flights (Levin *et al.* 2009). Therefore, since *S. leptura* also feeds during the day, it makes perfect sense that it takes advantage of the activity patterns of these formicidae swarms (mainly *Camponotus*) as an abundant food resource to complement its diet. It is worth noting that, as far as we know, the only prey identified at genus level in *S. leptura*'s diet is *Pheidole* (big-headed winged ant; Nogueira *et al.* 2002), therefore, both *Camponotus* and *Trigona* (Apiidae) represent new records within the diet of these bats.

Similarly, the high consumption of beetles may be because Coleoptera is a very abundant order of flying insects on the island (Universidad del Valle 2014), and very accessible to the bats even during the daytime, which is demonstrated by the highest FO (86 %) among the insect orders in the samples. This coincides with the study conducted by Bradbury and Vehrencamp (1976), which demonstrated that the foraging cycles of *S. leptura* are spatially and temporally correlated with patterns of insect abundance in riparian forests in Costa Rica and Trinidad Island. On the latter, daytime flight was also reported for the species under the canopy. The average size of prey eaten by these bats in Gorgona (5.1 ± 2.1 mm) was almost twice the expected size of 2.6 mm suggested for bats of similar sizes (Bradbury and Vehrencamp 1976). Also, the smallest prey captured (2 mm) was 1.3 times smaller than the expected average suggested by Bradbury and Vehrencamp (1976), and the largest (13 mm), was 2.6 times larger than that reported by Nogueira *et al.* (2002). Therefore, our results demonstrate the plasticity of *S. leptura* prey selection, compared with many insectivorous species that are very strict with their prey selection (Burles *et al.* 2008; Kolkert *et al.* 2019). This could be considered a strategy of the species to take advantage of as many resources as possible on the island through opportunism. Opportunistic feeding behavior has been recorded in many bats under a variety of environmental and competitive pressures (Brigham *et al.* 1992; Heim *et al.* 2017), showing a tendency to consume locally abundant taxa (Whitaker 2004; Krauel *et al.* 2018). Note that the representativity of other soft insects, such as Diptera, which is a very abundant group on Gorgona,

and which have sizes within the range of prey consumed by *S. leptura*, could be underestimated, since they are easily destroyed during digestion. It is also worth noting the presence of two cephalic capsules of lepidoptera larvae within the food remains as an atypical finding, since, from what is known, *S. leptura* only hunt airborne prey; gleaning or trawling behaviors have not been reported to date (Kalko 1995; Jakobsen *et al.* 2015). However, this could be explained by the fact that there are larvae of Noctuidae and Geometridae (both present in the island) that, in their first development stages, hang on silk threads to evade parasitoids and predators (Hagstrum and Subramanyam 2010), thus, facilitating its detection and predation by *S. leptura*.

The significant differences in prey consumption, which were only found in order Psocoptera, can be attributed to the distribution of these insects in different microhabitats of Gorgona, since they are more abundant in low canopy coverage areas (Sarria *et al.* 2014), and because in tropical moist forests they are usually found in the middle to upper part of the vertical strata, which just overlaps with the daytime feeding territory of these bats. *Saccopteryx leptura* usually chooses specific feeding territories that they defend constantly (even for generations), below the canopy during the day, and in open areas above the canopy at night (Bradbury and Emmons 1974; Bradbury and Vehrencamp 1976; Kalko 1995). Something similar could be happening between males and females, since we observed that it is common for individuals that roost together to share their feeding territories both simultaneously and asynchronously. If we consider the assumption that *S. leptura* feeds on the insects available in its territory, then the chances of differentiation in prey consumed between the sexes would decrease considerably. Thus, it is possible that the heterogeneity in the diet of this species is mostly determined by the richness, composition, and abundance of prey in its hunting areas as well as its ability to locate and capture them, rather than some type of prey preference or specialization.

Although we only limited our sampling to *S. leptura* daytime activity, we consider our data to be a valid approach to trophic habits of the species. However, considering the type of food consumed and the activity of some insects found in our samples, we can infer that their diet composition during the day and during the night is not completely homog-

enous. For example, the presence of bees such as *Trigona* sp., winged ants and diurnal chrysomelid beetles in the samples analyzed are irrefutable proof that there is some diet differentiation with respect to their conspecifics and other nocturnal insectivorous bats species residing on the island. Although there is no previous research in insectivorous bats with diurnal habits that explore the differences between the diurnal and nocturnal diet, differentiation has been previously suggested (Russo *et al.* 2011a). However, when comparing the results of diet surveys for *Pipistrellus pygmaeus* during the night (Bartonička *et al.* 2008) and the day (Russo *et al.* 2011b) to provide an example, we did not observe noticeable differences in the main food resources, but in insects whose frequency of occurrence seems to be related to the bats' foraging activity and the characteristics of the foraging sites. Thus, more detailed studies focused on this topic are required for a better understanding of the general diet of these species. In the same way, more studies providing a better understanding of the night-time prey selection *S. leptura* are still required.

Our data is sufficient to suggest that the population of *S. leptura* in GNNP has a heterogenous and opportunistic diet, without an apparent preference for a particular type of insect, presumably to take advantage of the most abundant and available seasonal resources. It is important to increase the research on the prey selection of this species on the mainland in order to determine whether the diet composition of *S. leptura* on the island is locally exclusive or is generalized for the species. Studying insular species allows us to inquire about the strategies and adjustments that their populations use to survive, given the resources that the environment provides. Thus, studying the diet of other resident species would increase our understanding of the similarities and differences between them, and would allow us to determine how these species contribute to the balance of the ecosystem on the island.

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In search of bachelorettes: Observations of male *Leptonycteris yerbabuena* with dorsal patches across its range

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The lesser long-nosed bat (*Leptonycteris yerbabuena*) is a partially migratory, nectarivorous species that exhibits reproductive asynchrony across its range. Both migratory and resident populations of sexually active males of *L. yerbabuena* may form an odoriferous dorsal patch during their mating season. This is created by smearing saliva, urogenital fluids, and anal secretions over the interscapular dorsal region with their feet. Dorsal patches are believed to influence female mate choice. We synthesized the sightings of male dorsal patches across the species' range, including gathering new observations of male *L. yerbabuena* with dorsal patches captured at the northern extent of their range and citing previously unreported observations that we obtained by contacting other researchers. We also conducted a literature review to include all previously documented records of male *L. yerbabuena* presenting dorsal patches. We document the first observations of male *L. yerbabuena* with dorsal patches in the southwestern United States. In the Big Hatchet Mountains in New Mexico, we captured 1 male with a developed dorsal patch (*i. e.*, bare dorsal skin with sticky fur) on 25 July 2019 and two others on the night of 13 August 2019. New observations of males with developed dorsal patches were obtained from Hilltop Mine in Arizona (June 2006 or 2007) and at a hummingbird feeder at a residence near the Hilltop Mine (July 2013). A male with a recovering dorsal patch (*i. e.*, bare dorsal skin with regenerating fur) was also captured in a roost near Patagonia, Arizona, in late August 2008 and at a hummingbird feeder at a residence near Silver City, New Mexico (September 2021). All previously published records of males with dorsal patches occurred in roosts in Mexico during known mating seasons. These new observations suggest that *L. yerbabuena* may breed in New Mexico and Arizona between June and August, but follow-up studies are needed to confirm this behavior. Much of the reproductive biology of this important pollinator remains unknown. Therefore, identifying regions where males present dorsal patches may not only assist in locating and protecting mating roosts, but would also further our understanding of the population ecology of this migratory species.

El murciélago magueyero menor (*Leptonycteris yerbabuena*) es una especie nectarívora parcialmente migratoria que exhibe asincronía reproductiva en toda su área de distribución. Tanto las poblaciones migratorias como las residentes de machos sexualmente activos de *L. yerbabuena* pueden formar un parche dorsal odorífero durante la temporada de apareamiento. Esto se crea por el comportamiento de frotar la saliva con sus patas, los fluidos urogenitales y las secreciones anales en la región dorsal interescapular. Se cree que los parches dorsales influyen en la elección de pareja. Sintetizamos los avistamientos de parches dorsales masculinos en el área de distribución de la especie, e incluimos la recopilación de nuevas observaciones de machos de *L. yerbabuena* capturados con parches dorsales en el norte de su distribución, citando observaciones no reportadas previamente que obtuvimos al contactar a otros investigadores. También realizamos una revisión de la literatura para incluir todos los registros previamente documentados de machos de *L. yerbabuena* que presentan parches dorsales. Documentamos las primeras observaciones de machos de *L. yerbabuena* con parches dorsales en el suroeste de los Estados Unidos. En las montañas Big Hatchet en Nuevo México, capturamos un macho con un parche dorsal desarrollado (*i. e.*, piel dorsal desnuda con pelaje pegajoso) el 25 de julio de 2019 y otros dos en la noche del 13 de agosto de 2019. Se obtuvieron nuevas observaciones de machos con parches dorsales desarrollados de la mina Hilltop en Arizona (junio de 2006 o 2007) y en un comedero para colibríes en una residencia cerca de la mina Hilltop (julio de 2013). También fue capturado un macho con un parche dorsal en recuperación (*i. e.*, piel dorsal desnuda con pelaje en regeneración) cerca de Patagonia, Arizona, a finales de agosto de 2008 y en un comedero para colibríes en una residencia cerca de Silver City, Nuevo México (septiembre de 2021). Todos los registros anteriores de machos con parches dorsales, provienen hasta ahora de refugios de murciélagos en México durante las temporadas de reproducción conocidas. Estas nuevas observaciones sugieren que *L. yerbabuena* puede reproducirse en Nuevo México y Arizona entre junio y agosto, pero se necesitan más estudios para confirmar este comportamiento. Gran parte de la biología reproductiva de esta importante especie de murciélago polinizador aún es desconocida. Por lo tanto, identificar las regiones donde los machos presentan parches dorsales, no solo puede ayudar a localizar y proteger los refugios de apareamiento, sino que también mejoraría nuestra comprensión de la ecología de la población de esta especie migratoria.

Keywords: Dorsal patch; Glossophaginae; lesser long-nosed bat; México; migratory; reproductive status; southwestern United States.

Introduction

Migration, an important life history trait for many species, allows individuals to spatially and temporally exploit changing environments, including ephemeral food sources. Long-range movements are exhibited by several mammals, including some ungulates, pinnipeds, cetaceans, and bats (Dingle 2014). With over 1,400 extant species (Simmons and Cirranello 2020), bats are one of the most diverse groups of mammals in the world. Despite their recognized importance in community ecology as seed dispersers, pollinators, and suppressors of insect populations, many aspects of their basic biology remain unknown due to the difficulties of studying nocturnal, flying organisms (Frick et al. 2020). Adding to their complexity, reproductive cycles of bats can vary within the same family and even within the same genus at similar latitudes making generalizations difficult (Racey 1982). To assist with bat conservation strategies and planning, studies should aim to increase our understanding of bat reproductive ecology (Racey and Entwistle 2000), including the effect of mating opportunities on the distributions of migratory bats.

Among North American bats, migratory species include temperate bats (many vespertilionids) that move seasonally between hibernation roosts and breeding habitats, temperate species (mostly tree-roosting bats) that migrate south for the winter, and tropical bats that move north to follow food resources and/or give birth (McNab 1982). Long-nosed bats, *Leptonycteris* spp. (Chiroptera: Phyllostomidae: Glossophaginae), are tropical migrants that rely on the availability of flowering plants. Their migration follows nectar corridors of flowering columnar cacti and paniculate *Agave* spp. between seasonal roosts (Fleming et al. 1993; Burke et al. 2019), and *Leptonycteris* spp. are among the most important nocturnal pollinators for many of these species (Valiente-Banuet et al. 1996; Peñalba et al. 2006; Rocha et al. 2006). Observations of low *Leptonycteris* densities may be caused by population declines due to habitat destruction or natural variation in flowering plant density (Moreno-Valdez et al. 2000), thus requiring a spatial and temporal understanding of bat and plant populations across their range.

Due to current technology limitations, most long-nosed bat movements are inferred from direct observations, passive integrated transponder (PIT) tag detections (Frick et al. 2018), and genetic studies (Wilkinson and Fleming 1996; Menchaca et al. 2020), which led to the discovery that only some populations of the lesser long-nosed bat (*Leptonycteris yerbabuena*) migrate. Of the populations dwelling in Mexico, some females are resident to central and southern Mexico, where they form maternity roosts in the winter. Other females migrate between winter roosts in central Mexico and summer maternity roosts in northern Mexico and the southwestern United States (Nassar et al. 2016). For both migratory and resident populations, sexually active males of *L. yerbabuena* may form an odoriferous dorsal patch during the mating season, created

by a smearing behavior in which saliva, urogenital fluids, and anal secretions are spread over the interscapular dorsal region, similar to the behavior displayed by reproductive males of the Curaçaoan long-nosed bat (*Leptonycteris curasoae*) in Venezuela (Muñoz-Romo et al. 2011a). Indeed, one observation of a *L. yerbabuena* male displaying a similar behavior supports this hypothesis (Lavery and Stoner 2022). Males with developed dorsal patches (*i. e.*, bare dorsal skin with sticky fur; Frick et al. 2018) have larger testes (Rincón-Vargas et al. 2013), and may have lower ectoparasite loads as noted by studies of *L. curasoae* (Muñoz-Romo and Kunz 2009; Muñoz-Romo et al. 2011b). Together, this suggests that dorsal patches may influence female mate choice; however, other potential explanations have not yet been evaluated.

Due to the differences in migratory behavior among *L. yerbabuena* populations combined with reproductive asynchrony, we asked how does the phenology of male reproductive status, specifically the presence of dorsal patches, vary temporally across the species' range? By identifying where and when mating may occur based on distributions of males with dorsal patches, this study furthers our understanding of the reproductive ecology of *L. yerbabuena* and highlights potential mating roosts or regions. We also document the first observations of dorsal patches at the northern extent of *L. yerbabuena*'s migratory range and discuss the conservation implications of these findings.

Materials and methods

Study species. The pattern of reproduction of *Leptonycteris yerbabuena* has been described as either bimodal polyestrous and monoestrous, but individuals are thought to mate only once per year (Ceballos et al. 1997; Rojas-Martínez et al. 1999; Stoner et al. 2003; Cole and Wilson 2006). The timing of reproduction varies across the species' range such that females either give birth in the winter or in the spring (Rojas-Martínez et al. 1999; Menchaca et al. 2020). Those that give birth in the winter are residents of central and southern Mexico, and may remain in a single roost year-round (Galindo et al. 2004), or move between roosts seasonally (*e. g.*, altitudinal movements due to food availability; Ceballos et al. 1997; Herrera 1997; Stoner et al. 2003). Females that give birth in the spring are believed to mate in the fall or winter in central Mexico, and migrate in the spring along the Pacific Coast to maternity roosts in northern Mexico and southern Arizona to give birth (Cockrum 1991; Ceballos et al. 1997; Rojas-Martínez et al. 1999; Stoner et al. 2003). Those arriving in the southwestern United States later in the summer fly along the foothills of the Sierra Madre Mountains and may travel from as far south as Jalisco (Wilkinson and Fleming 1996). Occupancy of *L. yerbabuena* in southeastern Arizona and southwestern New Mexico generally peaks from mid-August to mid-September and then dwindles by early October when most individuals are thought to have returned south to Mexico

(Cockrum 1991; Bogan *et al.* 2017). Occasionally, small groups of *L. yerbabuena* are found beyond October in Arizona (US Fish and Wildlife Service 2016; Menchaca *et al.* 2020), but it is not known if these individuals survive the winter (S. Wolf, pers. comm.).

While *L. yerbabuena* was originally classified as endangered at the northern extent of its range in the late 1980s (Cole and Wilson 2006), the species was removed from the Endangered Species List in the United States in 2018, following its removal from threatened status in México in 2013 (Frick *et al.* 2018). It is one of three species of nectar-feeding bats—along with the Mexican long-nosed bat (*Leptonycteris nivalis*) and the Mexican long-tongued bat (*Choeronycteris mexicana*)—that migrate seasonally from Mexico to the southwestern United States along corridors of ephemeral flowers of cacti and *Agave* spp. (Bogan *et al.* 2017; Burke *et al.* 2019). These bat species are thought to benefit the tequila and mezcal industries by enhancing the genetic diversity of *Agave* spp. through cross-pollination (Trejo-Salazar *et al.* 2016).

Study site. Our fieldwork focuses on the migratory populations of *L. yerbabuena* at the northern extent of its range. We specifically study those bats inhabiting a cave in the Big Hatchet Mountains in New Mexico, which harbors the easternmost distribution of *L. yerbabuena* in the United States (Bogan *et al.* 2017). *Leptonycteris nivalis* and *L. yerbabuena* in this region are believed to mostly feed on nectar and pollen in the Animas Mountains, requiring bats in the Big Hatchet Mountains roost to commute >20 km in each direction across the Playas Valley to reach this foraging area (Bogan *et al.* 2017). While the diet of *L. yerbabuena* includes flowering cacti in Arizona, the main food source in southwestern New Mexico appears to be limited to *Agave* spp. (mostly *Agave palmeri*; Ober and Steidl 2004; Scott 2004). This region is comprised of semidesert grasslands interspersed at higher elevations with patches of Madrean evergreen woodland (alligator bark juniper, piñon, Chihuahuah pine, and species of oak), lower interior chaparral (manzanita, mountain mahogany), and interior southwest riparian deciduous forest (sycamore, cottonwood, and rabbitbrush–Apache plume; Brown 1994).

Bat sampling. We captured individuals of *L. yerbabuena* in the Big Hatchet Mountains during their seasonal occupancy in 2019, for a total of six nights of sampling between 13 July and 12 September 2019. To capture bats, we placed a 12 m long by 2.6 m high mist net (38-mm mesh; Avinet Inc., Dryden, NY) just downhill of the main entrance of the cave opening. Mist nets were opened at sunset (*i. e.*, at 2030 h in July or as early as 1940 h in September), but the amount of time the net remained open each night was dependent on bat activity and varied across our sampling period (median = 3.84 h/night, range = 3.28 – 6.47 h/night, total = 26.62 h). We scanned for bats in the net every five min, untangling captured individuals that were then temporarily stored in cotton bags until they could be processed. For each individual, we recorded age, sex, reproductive condition,

forearm length, and body mass. We determined the age of individuals (*i. e.*, juveniles or adults) based on the relative ossification of the metacarpal-phalangeal joint in the wings (Brunet-Rossinni and Wilkinson 2009). Females were classified as non-pregnant, pregnant, lactating, or post-lactating by abdominal palpation and nipple examination (Racey 2009). Reproductive condition of adult males was determined by examining if the testes were swollen and distended, and if an individual's interscapular dorsal region presented a dorsal patch (Figure 1). For those individuals without a dorsal patch or wing damage, we inserted a PIT tag subcutaneously between the shoulder blades as part of an on-going migration study. All bats were released at the capture location within 30 min of capture. Field protocols were approved prior to implementation by Colorado State University's Institutional Animal Care and Use Committee (Protocol #19-8891A), the New Mexico Department of Game & Fish (Permit #3611), and the U.S. Fish & Wildlife Service (Permit #TE63195B-0).

Literature review. In addition to our field study, we searched for peer-reviewed publications that included information on the dorsal patch of male *Leptonycteris* spp. On 27 August 2020, we used Google Scholar to search for articles published through August 2020 including the keywords “*Leptonycteris*” and “male” that also included the term “dorsal patch” or “sebaceous patch.” We similarly conducted a search on Web of Science on 27 August 2020 using the topic search TS = *Leptonycteris* AND male AND (“dorsal patch” OR “sebaceous patch”).

To supplement data at the northern extent of *L. yerbabuena*'s range, we also searched through grey literature materials and contacted various researchers in New Mexico and Arizona for observations of reproductive males with dorsal patches.

Results

New observations of dorsal patches in New Mexico and Arizona. Between July and September 2019, we captured a total of 55 *L. yerbabuena*, which were comprised of 33 adults (9 males and 24 females) and 22 juveniles (5 males and 17 females) in the Big Hatchet Mountains. Three (33 %) of the adult males were identified as reproductively active due to the presence of swollen testes and developed dorsal patches (*i. e.*, bare dorsal skin with sticky fur; Figure 1 and Table 1). A reproductively active male with a forearm length of 55.4 mm and a weight of 29.0 g was captured at 2158 h on 25 July 2019 and a wing punch was taken. Two different males were captured at 2339 h on 13 August 2019 and 0042 h on 14 August 2019. While no marking techniques were used on these latter individuals, they differed in forearm length (54.8 and 56.0 mm), weight (23.5 and 27.5 g), and the appearance of the dorsal patch (*i. e.*, one individual had more bare skin exposed). Since neither of these individuals presented a scar on their wings where the wing punch was taken from the first male and they all differed in forearm lengths and body mass, we could confidently assume these were 3 different adult males (Figure 2).

Three separate studies on *L. yerbabuena* in Arizona and one recent study in New Mexico also reported observations of dorsal patches (Figure 2 and Table 1), and three of those observations were confirmed through photographs (Figure 1). Males with developed dorsal patches were captured at the Hilltop Mine (June 2006 or 2007; D. Dalton, pers. comm.) and at a hummingbird feeder located at a residence near the mine (July 2013; J. Danielson and K. Ekholm, pers. comm.). In late August 2008, a male with a recovering dorsal patch (*i. e.*, bare dorsal skin with regenerating fur) was captured at a roost near Patagonia, Arizona (D. Buecher and J. Ramirez, pers. comm.). More recently, another male with a recovering dorsal patch was captured in mid-September 2021 at a hummingbird feeder near Silver City, New Mexico (M. Davies and R. Burke, pers. comm.).

Published observations of dorsal patches from other roosts. Our literature review using Google Scholar resulted in 29 publications: 20 peer-reviewed articles, 3 book chapters, 2 independent study reports, 1 Ph.D. dissertation, 1 M.Sc. thesis, and 1 preprint. We found 9 peer-reviewed articles using Web of Science, all of which were also identified by Google Scholar. Of the 29 publications, only 14 were primary lit-

erature studies that sampled *Leptonycteris* spp. in the field. Reproductive males of *L. nivalis* do not develop dorsal patches as documented by a study that included observations from several mating seasons at the only known mating roost for the species, Cueva del Diablo near Tepoztlan, Morelos, central Mexico (Nassar *et al.* 2016). Dorsal patches do occur, however, in both *L. curasoae* and *L. yerbabuena* and were first described for both species by Nassar *et al.* (2008). For *L. curasoae*, males with dorsal patches have been observed during November and December in Guano Cave and Piedra Honda Cave, Paraguaná Peninsula, Falcón State, Venezuela (Nassar *et al.* 2008; Muñoz-Romo and Kunz 2009; Muñoz-Romo *et al.* 2011b; Muñoz-Romo *et al.* 2011a; Muñoz-Romo *et al.* 2012). The 8 remaining publications in addition to Nassar *et al.* (2008) described dorsal patches of male *L. yerbabuena* in Mexican roosts (Table 1), where the phenology of dorsal patches—like mating seasons—appears to be asynchronous (Figure 2). Dorsal patches were documented between May and September at southern roosts, between September and January in Chamela, Jalisco, and between September and October at roosts on the southern Baja peninsula.

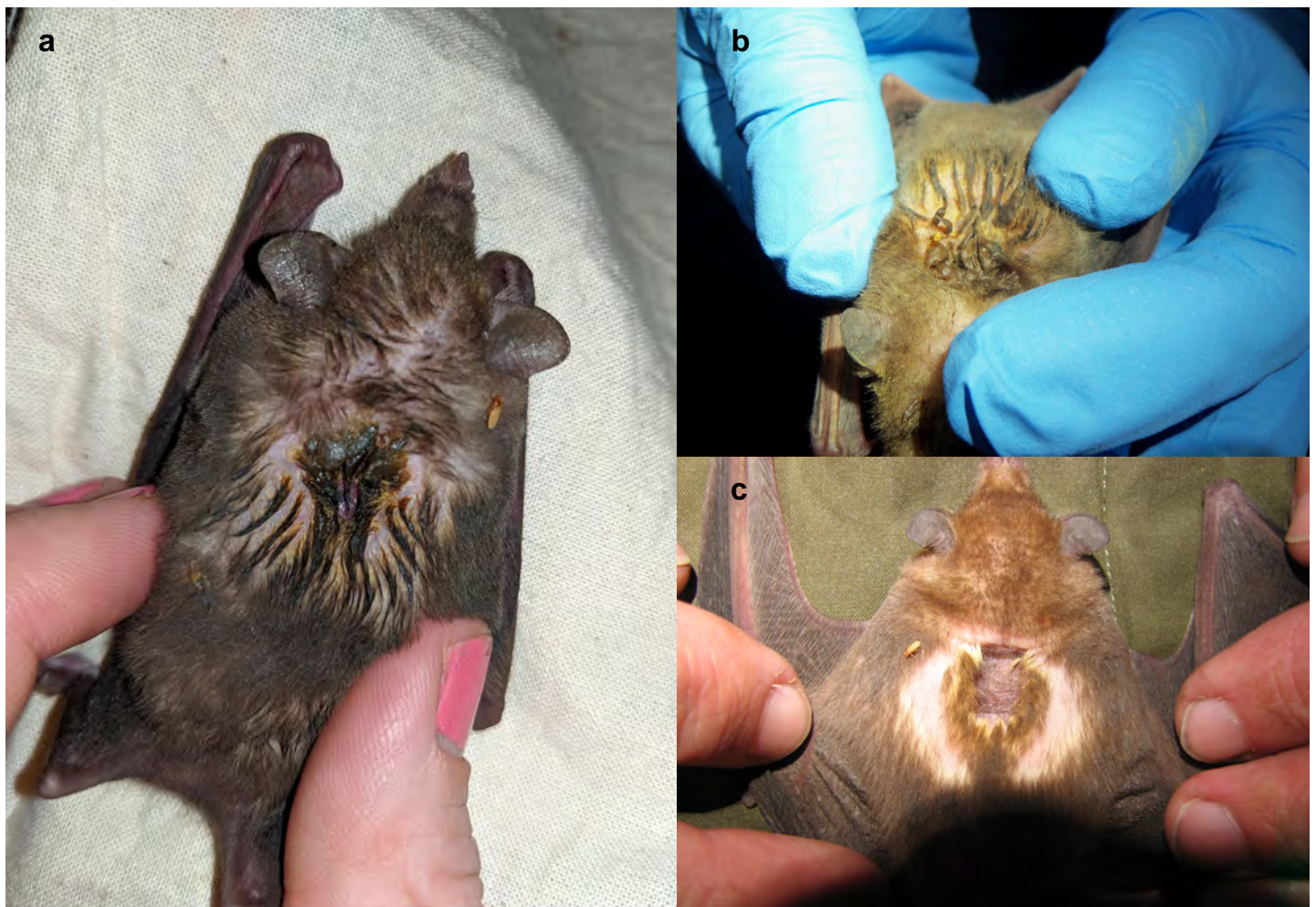


Figure 1. Photographs of new observations of male *Leptonycteris yerbabuena* individuals with dorsal patches in the southwestern United States. Images include (a) a male with a developed dorsal patch at the Big Hatchet Mountains roost, New Mexico in July 2019, (b) a male with a developed dorsal patch at a hummingbird feeder near Hilltop Mine, Arizona in July 2013, and (c) a male with a recovering dorsal patch at the Patagonia bat cave, Arizona in August 2008. Photographs by (a) Theresa Laverty, (b) Joseph Danielson, and (c) Debbie Buecher.

Table 1. The location, timing, and prevalence of male dorsal patches in *Leptonycteris yerbabuena*.

Location	Timing of dorsal patch	Percentage of males with dorsal patch	Reference
Big Hatchet Mountains, New Mexico, USA	July – August 2019	33.3 % ($n = 3/9$)	This study
Hummingbird feeder near Silver City, New Mexico, USA	mid-September 2021	20.0 % ($n = 1/5$) with a recovering dorsal patch ^a	M. L. Davies & R.A. Burke, pers. comm.
Hilltop Mine, Arizona, USA	June 2006 or 2007	20 to 30 males, most with dorsal patches ^b	D. C. Dalton, pers. comm.
Hummingbird feeder near Hilltop Mine, Arizona, USA	July 2013	1 male with dorsal patch ^c	J. R. Danielson & K. L. Ekholm, pers. comm.
Patagonia, Arizona, USA	late August 2008	1 male with recovering dorsal patch ^d	J. Ramirez & D. C. Buecher, pers. comm.
Chivato, southern Baja California península, México	September 2017	61.1 % ($n = 11/18$)	(Frick <i>et al.</i> 2018)
Las Cuevas, southern Baja California península, México	early October 2013	90.0 % ($n = 9/10$)	(Frick <i>et al.</i> 2018)
Chamela Bay, Jalisco, Mexico	November 2002	24.2 % ($n = 16/66$)	(Nassar <i>et al.</i> 2008)
	December 2002	35.1 % ($n = 27/77$)	(Nassar <i>et al.</i> 2008)
	September 2003	35.5 % ($n = 22/62$)	(Nassar <i>et al.</i> 2008)
	October 2003	50.0 % ($n = 24/48$)	(Nassar <i>et al.</i> 2008)
	October 2008 –January 2009	22.2 % ($n = 26/117$)	(Rincón-Vargas <i>et al.</i> 2013)
Tlilapan, Veracruz, México	January 2019	20 of 33 males were reproductive ^e	(Zamora-Mejías <i>et al.</i> 2020)
	June – September 2011 and 2012	38.9 % ($n = 7/18$)	(Ramírez Hernández and Herrera 2016)
El Salitre, Morelos, México	June 2019	15 of 28 males were reproductive with incipient patches ^e	(Zamora-Mejías <i>et al.</i> 2020)
Colotlipa, Guerrero, México	July 2017	18 of 25 males were reproductive ^e	(Zamora-Mejías <i>et al.</i> 2020)
San Juan Noxchitlán, Oaxaca, México	June 2015	17 males captured, but only 11 used for DNA extraction ^f	(Gaona <i>et al.</i> 2016; Gaona <i>et al.</i> 2019a; Gaona <i>et al.</i> 2019b)
		61.9 % ($n = 13/21$) in May diminished to 11.7 % ($n = 2/17$) in August	(Martínez-Coronel <i>et al.</i> 2017)

^a Correspondence including photographs with researchers Mallory L. Davies and Rachel A. Burke confirmed that a male was captured with a recovering dorsal patch (*i. e.*, new hair growth present) at a hummingbird feeder at a private residence in mid-September 2021. There was a suspected second male with a recovering dorsal patch, but unfortunately no photograph was taken.

^b Correspondence with researcher David C. Dalton indicated that all of the 20-30 individuals captured were adult males. Most, if not all, had a dorsal patch. In some cases, the dorsal patches were mostly healed and were partially re-furred. In other cases, the dorsal patches were still open wounds that looked very fresh.

^c Correspondence including photographs with researchers Joseph R. Danielson and Kelsey L. Ekholm confirmed that a male was captured with a dorsal patch at a hummingbird feeder at a private residence in July 2013.

^d Correspondence including photographs with researchers Judith Ramirez and Debbie C. Buecher confirmed that a male was captured with a recovering dorsal patch (*i. e.*, new hair growth was present) in late August 2008.

^e Authors did not state in the publication how many reproductively active males had a dorsal patch. Correspondence with Daniel Zamora-Mejías indicated the presence of males with dorsal patches as well as observed copulations during these time periods with the exception of El Salitre (*i. e.*, where incipient dorsal patches were observed, and it was assumed mating would begin in the upcoming weeks).

^f Authors did not state in these publications how many males they captured without a dorsal patch. Correspondence with Osiris Gaona indicated that at least 50 % of the males captures in the Obispos cave presented a dorsal patch.

Discussion

Much of what is already known about the reproductive ecology of *L. yerbabuena* is derived from research in Mexico. Reproductive males with dorsal patches have been documented at several mating roosts in Mexico since first being documented in the literature by Nassar *et al.* (2008). Due to the individual variation in the timing of dorsal patches throughout the species' range, more longitudinal studies are needed to identify periods in which dorsal patches are present and when mating occurs (*e. g.*, Rincón-Vargas *et al.* 2013; Frick *et al.* 2018). Thus far, these odoriferous patches have only been found in males of *L. curasoae* and *L. yerbabuena* during their mating seasons. Although dorsal patches do not form in *L. nivalis* (Nassar *et al.* 2016), they likely play an important role in female mate choice for *L. curasoae* (Muñoz-Romo and Kunz 2009; Muñoz-Romo *et al.* 2011a). Dorsal patches could have a similar function in *L. yerbabuena* since copulations observed in western cen-

tral Mexico (Chamela, Jalisco) have only included male individuals with developed dorsal patches (*i. e.*, bare dorsal skin with sticky fur; Lavery and Stoner 2022).

Given the important functions that mating and maternity roosts play in bat population ecology, these roosts are often the focus of conservation efforts. Prior to this study, roosts of *L. yerbabuena* in the southwestern United States were thought to function as maternity roosts and transient roosts (*i. e.*, where females and volant young feed before migrating south; Bogan *et al.* 2017). Through our fieldwork and communication with other researchers in New Mexico and Arizona, we report occasional sightings of developed or recovering dorsal patches (*i. e.*, bare dorsal skin with sticky or regenerating fur, respectively) at the northern extent of *L. yerbabuena*'s range, suggesting that males may be seeking out mating opportunities in the southwestern United States between June and September. If so, one or more transient roosts may also function as mating roosts

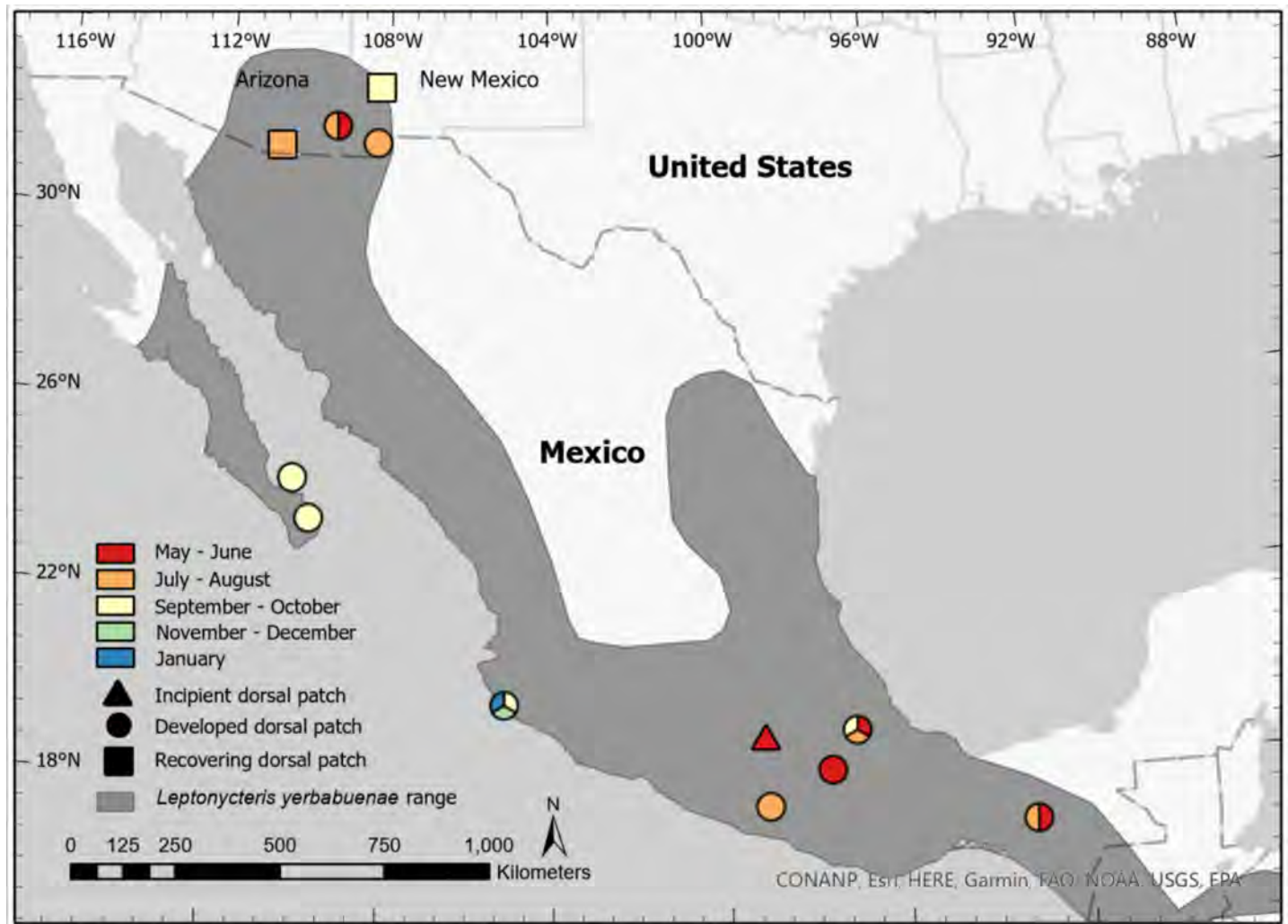


Figure 2. Map displaying locations and timing of observations of male *Leptonycteris yerbabuena* with incipient (triangle), developed (circle), and recovering (square) dorsal patches. Sites with observations spanning multiple months are represented by multiple colors. Polygon data obtained from <http://www.iucnredlist.org/>

and harbor additional conservation value. Future studies should confirm if *L. yerbabuena* breeds in the southwestern United States. Ideally, this would involve researchers briefly visiting roosts during their periods of occupancy to scan for copulating *L. yerbabuena*. While netting bats, reproductive males have historically been identified by observing swollen and distended testes, but we recommend that all future studies of *L. yerbabuena* measure the external testes with calipers to confirm they meet a minimum size corresponding to complete spermatogenesis (e. g., 48.2 mm² for *L. yerbabuena* in Chamela; [Rincón-Vargas et al. 2013](#)) to relate dorsal patch presence with reproductive activity. Prior to the discovery of dorsal patches, [Cockrum and Ordway \(1959\)](#) reported gravid female *L. yerbabuena* and males with enlarged testes in mid-August 1955 at a mine near Paradise, Arizona, which suggests that reproductively active males may not be a new occurrence in the United States. While further research is needed exploring the functional role of dorsal patches, all known mating roosts of *L. yerbabuena* contain males presenting dorsal patches (e. g., [Rincón-Vargas et al. 2013](#); [Frick et al. 2018](#); [Laverty and Stoner 2022](#)). Therefore, our study highlights how the

reproductive status and presence of dorsal patches in male *L. yerbabuena* may inform research priorities and aid in the identification of mating roosts.

The role of migration in determining the reproductive status of *L. yerbabuena* remains largely unknown. Research in Chamela, Jalisco, found spermatogenesis (i. e., the process of sperm cell development) and the presence of dorsal patches in *L. yerbabuena* to occur during peak food availability and the return of migratory females to the region ([Rincón-Vargas et al. 2013](#)). However, males can be captured year-round at this study site ([Stoner et al. 2003](#)). Roosts in the southwestern United States, on the other hand, are largely unoccupied and food is not available for nectarivorous bats from roughly November to May ([Cockrum 1991](#); [Bogan et al. 2017](#)). Given the presumed energetic costs of developing a dorsal patch and mating ([Muñoz-Romo and Kunz 2009](#); [Rincón-Vargas et al. 2013](#)), particularly after migrating from and before migrating to unknown roosts in Mexico, we did not expect to find males with dorsal patches that could potentially be seeking out mating opportunities in the southwestern United States. Therefore, our research echoes other studies cit-

ing the need for more information on the movements of male *L. yerbabuena* (Cockrum 1991; Menchaca et al. 2020). While we do not encourage PIT tagging males with dorsal patches, we recommend future studies mark these males (e. g., with a wing punch or banding) to ensure accurate counts of individuals with dorsal patches at a roost. Males without dorsal patches should continue to be PIT tagged. Until more information is known on the movements of males and until roosts are thoroughly searched for copulatory behaviors, we cannot confirm the presence of a mating roost in the southwestern United States, but the presence of dorsal patches at transient roosts at the northern extent of the species' range demands further investigation into this matter.

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Habitat use and activity patterns of ungulates in a tropical rainforest of southern México

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Baird's tapir (*Tapirella bairdii*), white-lipped peccary (*Tayassu pecari*), and collared peccary (*Dicotyles tajacu*) sympatrically occur in the Lacandon Forest of Chiapas, México. These species contribute to maintain ecosystem dynamics through herbivory, seed dispersal, and seed predation, constituting important prey for large carnivores and hunters. We analyzed activity patterns and habitat use of the three focal species to assess the degree of temporal and spatial habitat segregation among them in Montes Azules Biosphere Reserve (REBIMA) and surrounding communities. Between February and October 2015 we deployed camera-traps during 8,463 camera-trap days to estimate the presence and activity of tapirs and peccaries in two habitat types: "conserved" (REBIMA), and "transformed" (community forests; AFC). Habitat use and activity patterns of tapirs and peccaries were assessed through logistic regression models. We found that Baird's tapir was almost exclusively nocturnal with a trend towards crepuscular activity, while both peccary species were diurnal, therefore showing a high daily temporal segregation from the tapir. Both peccary species were similarly active in the two study sites, while tapirs were more active in continuous forest within the protected area. The occurrence of tapirs and white-lipped peccaries depended on the presence and proximity of water sources and roads. Our results suggest that spatial segregation of the habitat allows coexistence of both peccary species in the study area. AFC have potential for maintaining populations of tapirs and peccaries in the Lacandon Forest. Conserving these forests by local communities is essential to ensure the persistence of these mammals.

El tapir centroamericano (*Tapirella bairdii*), el pecarí de labios blancos (*Tayassu pecari*) y el pecarí de collar (*Dicotyles tajacu*) habitan en la Selva Lacandona, Chiapas, México, los cuales contribuyen a mantener la dinámica de los ecosistemas a través de la herbivoría, la dispersión y la depredación de semillas, además de constituir presas importantes para grandes carnívoros y cazadores locales. Analizamos el uso de hábitat y los patrones de actividad de las tres especies para evaluar su grado de segregación espacio-temporal en un paisaje con selva continua y en un paisaje modificado en el área de estudio. Entre febrero y octubre de 2015 utilizamos cámaras-trampa durante 8,463 días- cámara para estimar la presencia y actividad de las especies focales analizando dos tipos de hábitat: "conservado" (Reserva de la Biosfera Montes Azules; REBIMA), y "transformado" (bosques comunitarios; AFC). Evaluamos el uso de hábitat de las especies mediante modelos de regresión logística. Encontramos que el tapir fue casi exclusivamente nocturno con una tendencia hacia la actividad crepuscular, mientras que ambas especies de pecaríes fueron diurnas, mostrando una alta segregación temporal diaria, respecto al tapir. Ambas especies de pecaríes tuvieron una actividad similar en los dos sitios de estudio, mientras que los tapires fueron más activos en el bosque continuo dentro del área protegida. La presencia del tapir y el pecarí de labios blancos dependió de la presencia y cercanía del agua, caminos y carreteras. Nuestros resultados sugieren que la segregación espacial del hábitat permite la coexistencia de ambas especies de pecaríes en el área de estudio. AFC tiene potencial para mantener poblaciones de estas especies; su conservación por las comunidades locales es esencial para asegurar la persistencia de estos mamíferos.

Keywords: Coexistence; habitat use; Maya forest; resource partitioning; ungulates.

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Introduction

The Lacandon Forest of Chiapas hosts one of the largest remnants of humid tropical forest in Mexico, inhabited by numerous species of wild flora and fauna ([Carabias et al. 2015](#); [Carrara et al. 2015](#)), many of which are also natural resources for the inhabitants of rural communities ([Naranjo et al. 2010](#)). However, it has been shown that habitat deterioration, fragmentation, and loss in these tropical forests have resulted in the local and regional disappearance and

isolation of populations of white-lipped peccary (*Tayassu pecari*) and tapir (*Tapirella bairdii*; [Tejeda-Cruz et al. 2009](#); [Schank et al. 2017](#); [Meyer et al. 2019](#); [Thornton et al. 2020](#)). These two species, along with the collared peccary (*Dicotyles tajacu*), live in sympatry in southern Mexico ([Naranjo et al. 2015](#)). Tapir and white-lipped peccary are threatened of extinction in Mexico ([SEMARNAT 2010](#)). Both species currently face reductions in their population sizes and distribution ranges in southern Mexico, Central America, and

South America, as a consequence of changes in plant cover and land use, poaching, and disease transmissions (Naranjo *et al.* 2015; Moreira-Ramírez *et al.* 2019).

Tapir and peccary populations (orders Perissodactyla and Cetartiodactyla, respectively; hereafter referred to as ungulates) play important ecological roles (Eisenberg 1989; Bodmer 1991; Reyna-Hurtado *et al.* 2014; Naranjo 2018). As primary consumers, they contribute to the dynamics and structuring of the ecosystems where they thrive through herbivory, seed dispersal or seed predation, and are also important prey of large Neotropical carnivores (Naranjo 2009; Reyna-Hurtado *et al.* 2014; Malhi *et al.* 2016). Conservation actions for these threatened species require reliable information on the ecology and spatio-temporal dynamics of their populations. For this reason, the need to accurately estimate variables related to habitat use and the relationships between these large herbivores is now greater than ever. Considering the current effects of various environmental stressors such as climate change and habitat loss (Frey *et al.* 2017) and the pressures from human activities (Naranjo 2009), it is important to understand the relationships between the local fauna and its habitat, how they use the habitat (Pianka 1983; Dirzo *et al.* 2014), and their responses to these emerging effects (*e.g.*, loss of biodiversity and changes in abundance and distribution; Schaefer *et al.* 2008).

Closely related sympatric species tend to differ ecologically to coexist, so that they become segregated in some niche dimensions (Gause 1934; Schoener 1974). The tapir and peccary species inhabiting the Lacandon region live in sympatry and, although differing in how they use the local habitat (Tejeda-Cruz *et al.* 2009), they consume similar food resources such as fruits, stems, and leaves (Reyna-Hurtado *et al.* 2014; Naranjo 2019). This leads to assuming that there is clear segregation in terms of hours of activity and sites used most frequently.

A broad variety of methods have been used for analyzing how wild animals use the resources available in the local habitat (Johnson 1980; Burnham and Anderson 2004). The present study considered the use of the habitat and the analysis of activity patterns of tapir and peccaries as a proxy to assess the existence of spatio-temporal segregation in the areas inhabited by these species at the landscape scale in the Lacandon Forest. We sought to understand the relationships of the tapir and peccaries with their environment, especially to assess the influence of the landscape on the probability of habitat use of the species studied. To this end, we considered the effects of anthropic influence (*i.e.*, expansion of the farming frontier) as *a priori* variables (*i.e.*, occurrence of wildlife in relation to towns, water bodies, roads, and vegetation types; MacKenzie and Royle 2005; Kéry and Royle 2016).

This work addressed the following research questions: 1) Is there segregation in the activity patterns of the tapir the two peccary species that inhabit the Lacandon Forest? 2) Which of the *a priori* variables considered in this study are

drivers of habitat use by each species in the study area? Our overall objective was to assess the habitat use and activity patterns of the ungulates under study in the Montes Azules Biosphere Reserve and adjacent areas. In particular: 1) we compared the occurrence, distribution, and patterns of activity of these species at sites with and without frequent human presence in the study area; 2) we analyzed habitat use for the three species studied.

Materials and methods

Study area. This work was conducted from February to October 2015, in the southern portion of the Lacandon Forest (16°08'56"-16°11'58.3" N and 90°53'57"-91°18'45" W), Chiapas, Mexico. The sampling was carried out in an effective sampling area (ESA) of 150 km² within the southern sector of the Montes Azules Biosphere Reserve (REBIMA, 3,312 km²) and in community forest areas (ACF; ESA = 162.5 km²) of *ejidos* (communal land) adjacent to the REBIMA in the municipality of Marques de Comillas (Figure 1). The altitude of the study area ranges from 150 to 250 meters a.s.l. (Naranjo 2008), with approximately 50 % of the natural forest cover still present (Tejeda-Cruz *et al.* 2009; Garmendia *et al.* 2013, Muench and Martínez-Ramos 2016).

The prevailing climate in the region is warm humid with abundant summer rainfall (Am (i') gw"; García 2004). The mean annual precipitation oscillates between 2,500 and 3,500 mm, with 80 % of rains between June and November (García-Alaniz *et al.* 2010; Arce-Peña *et al.* 2019). Currently, the Lacandon region, except for the REBIMA, is dominated by heterogeneous landscapes composed of fragments of evergreen tropical forest of different sizes and successional states (Rzedowski 1978; Challenger and Soberón 2008) within a matrix of crop fields (mainly maize and oil palm), livestock ranches, and scattered human settlements (Carrara *et al.* 2015; Muench and Martínez-Ramos 2016; De La Torre and Rivero 2019).

We analyzed two types of habitats, namely "conserved areas" (the REBIMA) and a transformed landscape ("community forest areas"; ACF) as this anthropic condition is one of the key drivers of the abundance and distribution of the tapir and peccaries (Naranjo 2019). Fieldwork took place over 250 days between February and October 2015, comprising the rainy season (which peaked in September) and the dry season of the year (*i.e.*, March), as well as the maximum mean temperature (28°C) recorded in May (García and Lugo 1992). The sampling effort was 8,463 camera trap-days. Cuddeback® Black Flash E3 digital cameras were installed in 64 sampling points (hereafter camera trap stations) with a detection zone of 134 m² per camera trap, approximately. Of these, 32 camera trap stations were located in the southern REBIMA sector and 32 in ACFs. These traps were used for recording data on occurrence and frequency, sex (tapir only), and hours of activity of the ungulates of interest in the study area. Using a geographic information system (GIS), the study area was spatially delimited and the proportion of different types of coverage (for-

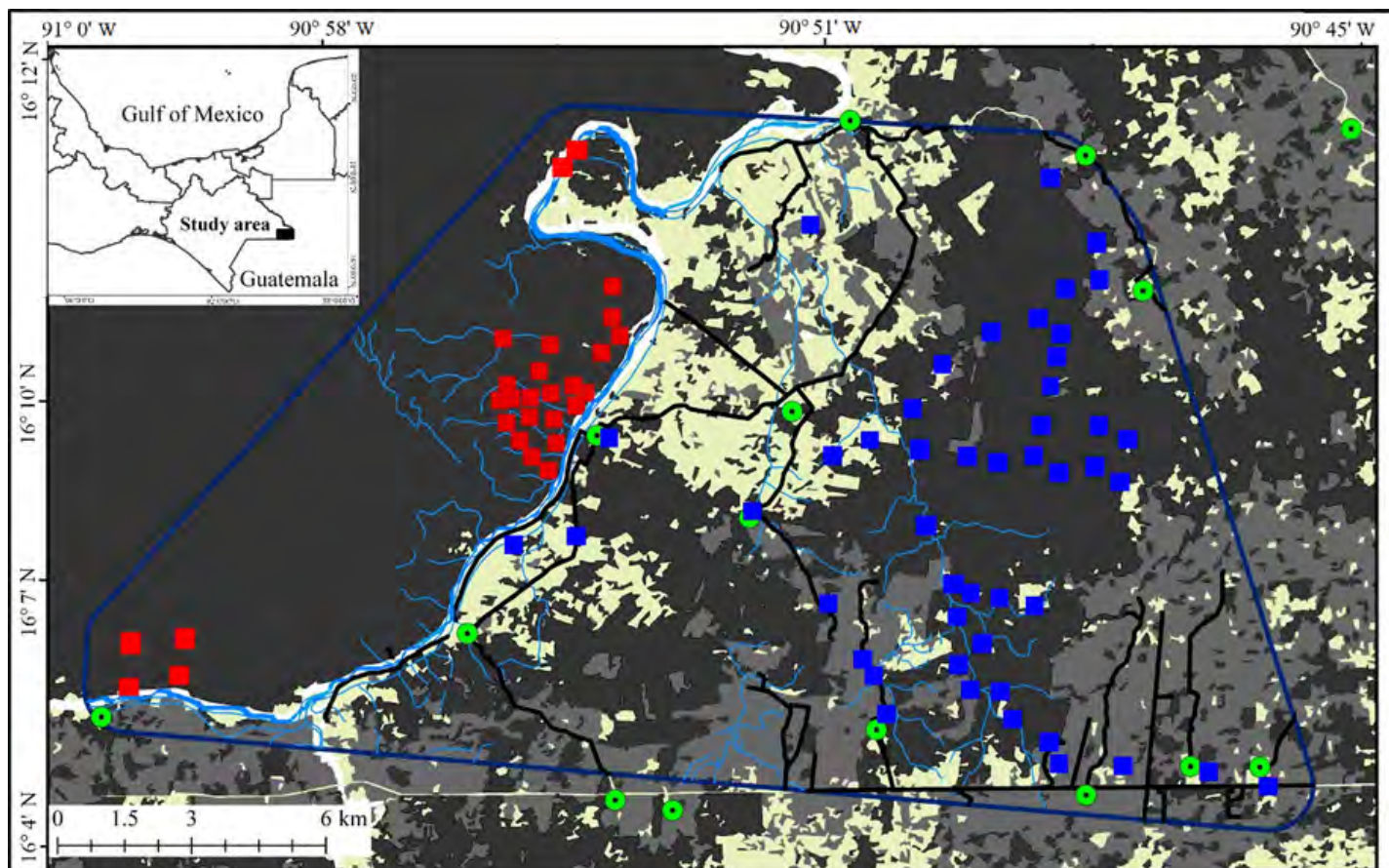


Figure 1. Study Area. Location of sampling sites, which include a portion of the southern sector of the Montes Azules Biosphere Reserve (REBIMA, red squares), and community forest areas (ACF, blue squares). Lacandon Forest, Chiapas, Mexico (February–October 2015).

est cover, land uses, and water bodies) and the proximity to anthropic elements (e.g., roads and towns) in the study area were estimated.

The spatial distribution of camera trap stations followed a grid layout in each of the study sites (REBIMA and ACF), with a minimum separation of 1 km between them to ensure the independence of records, considering the monitoring protocols applied to the study of other big mammals (modified from Silver 2004 and Chávez et al. 2013; Figure 1). Trap cameras were set to operate 24 hours a day and capture sequences of three photos per minute in case of motion detection. For each capture, the date, time, and geographic location of each camera trap station (sampling unit) were verified, as well as the number of individuals recorded. To consider a record as an independent capture and thus minimize any potential autocorrelation (Moreira-Ramírez et al. 2019), only photographs captured with a separation of more than 24 h between them were considered for each species.

Sampling was carried out on areas of dense evergreen tropical forest of various successional stages, as well as patches of riparian vegetation, which were randomly selected to record tapir and peccary individuals and their traces, and for use as sites for installing camera traps. Although pastures and meadows were excluded because they have not been mentioned in the literature as suitable

for tapir or white-lipped peccary in Mexico (March and Naranjo 2005; Carrillo-Reyna et al. 2015; Reyna-Hurtado et al. 2009), some camera-trap stations were placed in areas adjacent (~10 to 100 m) to these types of land use, considering that the collared peccary is listed as a generalist species (Sowls 1997; Reyna-Hurtado et al. 2014). Photographic records were used to construct binomial matrices (“1” to “0”, where 1 = presence and 0 = absence) for each camera-trap station. The matrix for each species was processed with the *Tidyverse* (Wickham 2017) and *SjPlot* (Lüdecke 2018) libraries in R v.4.0.2 (R Core Team 2019).

Habitat use. The use of the habitat by each species was analyzed using logistic regression models with the *Glmulti* package (Calcagno 2019); these models are suggested for their suitability to work with binomial variables (Manly et al. 2002). In addition, covariates were used to identify some of the environmental conditions (Table 1, Supplementary material) that influenced habitat use by ungulates in the study area (Manly et al. 2002; Gaillard et al. 2010). To this end, a high-resolution multi-spectral satellite image for the year 2014 (Landsat 8 Oli Tars) was used, along with the classification of plant cover and land uses previously generated in the Geographic Information Analysis Laboratory (LAIGE, in Spanish) at Colegio de la Frontera Sur (ECOSUR). This monitored classification was modified in the ArcMap program to produce a map of the study area with four lay-

ers of different types of classification of the landscape elements studied: 1) water bodies, 2) human settlements, 3) roads, and 4) vegetation and land use (evergreen tropical forest, secondary tropical forest, crops, pastures and meadows, water bodies, and roads). The logistic regression models were compared using the Akaike information criterion corrected for small sample size (AICc) and weight of each variable, to determine the relative evidence in favor of each model (Burnham and Anderson 2004; Fletcher and Fortin 2018) and the influence of each covariate on the probability of occurrence (interpreted as the probability that a given species is present or absent, and thus, that sites with certain characteristics are used). The models with the best support were selected considering those that yielded the minimum AIC score and $\Delta\text{AICc} \leq 2$ as proposed by Burnham and Anderson (2004), in addition to the weight (W_i). The models with $\Delta\text{AICc} \leq 2$ were selected and averaged to evaluate the relative importance of the variables and the significance of their values (Barton 2019).

Spatio-temporal comparisons of occurrence records for each species were performed using parametric (Student's t) and non-parametric (Mann-Whitney U) tests to evaluate the differences between frequencies of photographic records, occurrences, and relative abundances of species within and between types of conditions across sites in the study area (Sokal and Rohlf 1995).

Activity patterns. We consider the total number of photographs captured and pooled the number of capture events into one-hour intervals for the 24 hours of the day to search for patterns in the actual hours of activity of each focal species (Tobler et al. 2008). We used the "Overlap" package in R by Meredith and Ridout (2017), which allowed plotting the hours of activity of each species using the kernel density estimation, in addition to estimating the overlap coefficient (Dhat) between the patterns of one or two species in different sites.

Results

Frequency of records. Of the 64 camera-trap stations, 24 recorded tapir individuals (11 in REBIMA and 13 in ACF). Collared peccaries were recorded in 11 REBIMA and 16 ACF stations, respectively, while white-lipped peccaries were recorded in 18 stations (6 in REBIMA and 12 in ACF). According to independent photographic records, the tapir was captured more frequently in the protected area (REBIMA; $n = 59$) than in community forest areas (ACF, $n = 28$; $U = 89.5$, $P = 0.01$). The collared peccary was most frequently recorded at the ACF site, attaining statistical significance ($n = 47$; $U = 386.5$, $P = 0.04$). However, this trend was not observed for the white-lipped peccary; although it had more records in the ACF site (48 records) than in REBIMA (33), this difference between sites was non-significant ($U = 127$; $P = 0.60$). In the case of the tapir, a higher proportion of males was recorded in REBIMA versus ACF ($U = 30$; $P = 0.01$), while females showed a similar proportion between sites ($U = 66.5$, $P = 0.78$; Table 2, Supplementary material). The sex of peccary

individuals captured could not be determined based on the photographs recorded.

Habitat-use models. For each of the models generated for the species, the number of variables included, AICc, difference between each model and the model with the lowest delta AICc (Δ), and Akaike weight (W_i) are reported (Tables 2-4, Supplementary material). According to the AICc, the best models to explain the occurrence of the tapir in the study area (Table 2a, Supplementary material) included the variables *distance to permanent water bodies* and *roads* (e.g., dirt roads and roads; with weight [$W_i = 0.63$]) and the vegetation types *evergreen tropical forest* (BTP) and *secondary tropical forest* (BTS; Table 2b, Supplementary material). The best model indicated that the probability of site use by the tapir increases as the distance to water bodies decreases, especially when considering the tropical forest (BTP and BTS; Tables 2a, 2b, Supplementary material; Figure 2).

In the case of the collared peccary, the probability of habitat use increased with the presence and proximity of roads and human settlements, and with the distance from water bodies ($W_i = 0.20$; Table 3a, Supplementary material; Figure 2). However, the presence of different types of vegetation in the study landscape was relatively unimportant (Table 3b, Supplementary material). On the other hand, the probability of habitat use by the white-lipped peccary increased in sites with little anthropic intervention. The response in the probability of use was directly related to the distance to variables associated with anthropic disturbance, such as human settlements, roads and dirt roads, and inversely related to the distance to water bodies ($W_i = 0.42$; Tables 4 and 5, Supplementary material; Figure 2).

Activity patterns. A total of 235 independent photographic records were captured for the ungulates under study (tapir: $n = 87$; white-lipped peccary: 81; collared peccary: 67), including date and time. For the tapir, the photographic evidence revealed a clear preference for nighttime activity (mostly between 2:00 h and 5:00 h; Figure 3). In contrast, photographic records of collared peccary and white-lipped peccary suggested that both species are mostly diurnal, with a slight tendency to be active in the afternoon (after 16:00 h), and with virtually no activity at night (Figure 3).

The overlap coefficients allowed distinguishing the high degree of segregation between the ungulates in the study area across the time dimension. The two peccary species showed an overlap of more than 80 % (Dhat = 0.82; Figure 3). Each of these two species showed a high temporal segregation relative to the tapir. The indicators of temporal overlap between each of the peccary species and the tapir showed little overlap in their hours of activity (i.e., white-lipped peccary vs. tapir: Dhat = 0.34; collared peccary vs. tapir: Dhat = 0.42; Figure 3).

Discussion

Our results show trends in habitat use for the three ungulates studied and high levels of temporal segregation between the peccaries and the tapir in the study area. Considering

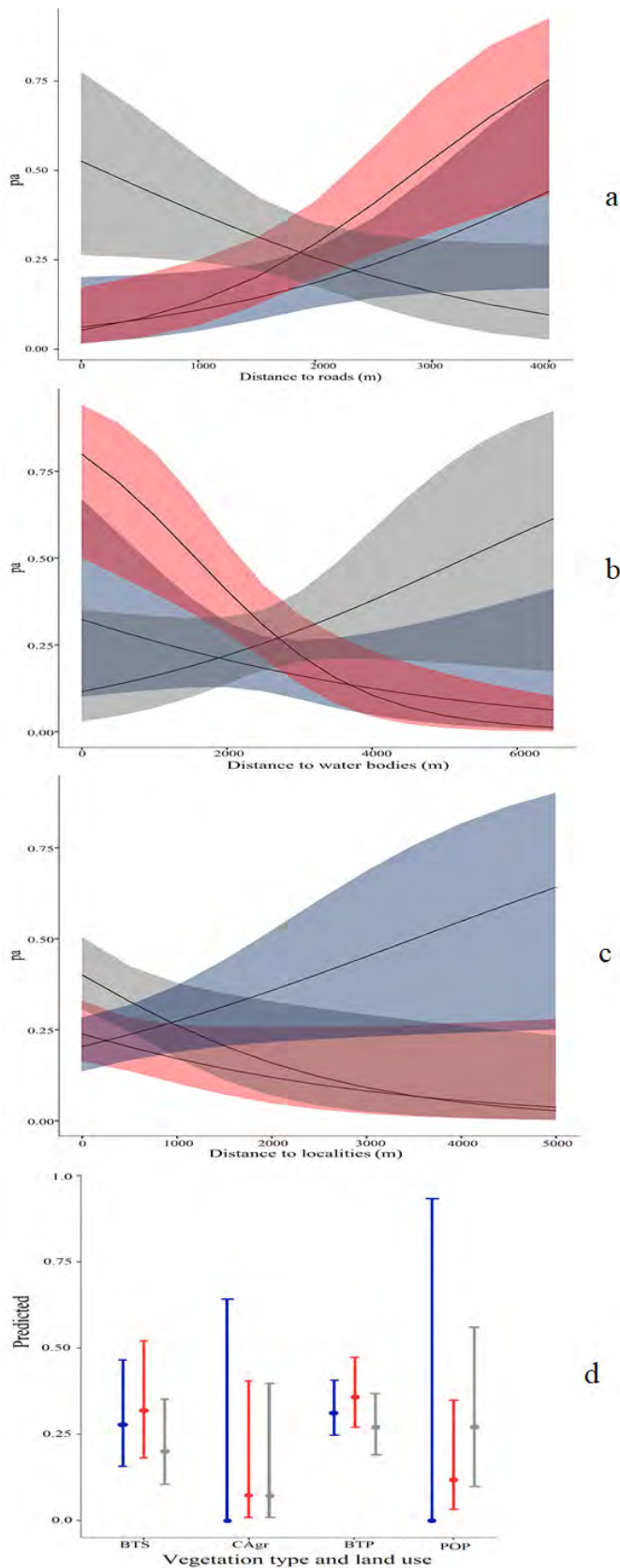


Figure 2. Logistic regression graphs considering variables predictive of habitat use by *Tapirella bairdii* (red), *Dicotyles tajacu* (gray), and *Tayassu pecari* (blue) with respect to distance to roads (a), distance to water bodies (b), distance to human settlements (c), and types of vegetation and land use (d) in community forest areas (ACF) and the protected area (Montes Azules Biosphere Reserve; REBIMA) in the Lacandon Forest, Mexico. pa: Presence-absence predictive values Aca: Mature secondary forest, BTP: Evergreen tropical forest, BTS: Secondary tropical forest, CAgr: Agricultural crops, POP: Pastures and meadows.

time as a resource (*i.e.*, something that is 'consumed', similar other resources; [Kronfeld-Schor and Dayan 2003](#); [Frey et al. 2017](#)), the tapir and peccaries have partitioned niches. It is important to highlight the difference between the habitat use by the two peccary species, as they exhibit opposite response patterns to anthropic variables, such as the presence of roads and proximity to human settlements, and to resources such as water (Figure 2). The habitat variables considered *a priori* in this study were limited; however, their assessment could be key for continuing the study of the interactions between the spatial and temporal dimensions of the ecological niches of these species ([Frey et al. 2017](#)).

Habitat use. Given the frequencies and occurrences observed in collared peccary records at both sites, our null hypothesis was validated since this species indiscriminately used both habitat types. This result has been reported in other studies conducted in America for this species, which have documented the presence of collared peccary in a wide range of habitats and environmental conditions, as well as its high tolerance to anthropic pressures ([Kiltie 1982](#); [Reyna et al. 2014](#); [Briceño-Méndez et al. 2016](#)). The similar use intensity of both habitat types by the white-lipped peccary despite the anthropic disturbance factors in the ACF is probably because the ecological conditions meet the resource requirements (*i.e.*, water, food, and shelter, among others) of this species in this site. [Muench and Martínez-Ramos \(2016\)](#) reported that the ACF preserved all species of medium- and large-sized mammals in the region. Thus, in spite of the anthropic pressures, this area still functions as a suitable habitat for peccary populations ([Fryxell et al. 2014](#); [Krausman and Morrison 2016](#)). This area also contains numerous water bodies (Figure 1), a key factor for the movement of white-lipped peccaries ([Reyna-Hurtado et al. 2009](#)). However, to determine the viability of the local populations of these ungulates in ACF, studies on age structure and population movement ecology are required, which may indicate that the species is reproducing in the area and that there is structural and functional connectivity ([Morrison et al. 2006](#); [Garrido-Garduño and Vázquez-Domínguez 2013](#)).

The fact that a higher number of tapir records were recorded in REBIMA ($n = 59$) than in ACF ($n = 28$), *i.e.*, a higher relative abundance of tapir in the former (20.9 ind/1000 camera trap-days in REBIMA vs 10.8 ind/1000 camera trap-days in ACF; Tables 3 to 5, Supplementary material) may be due to the greater surface area covered by mature forest in the protected site. Besides, the tapir tends to move away or become more elusive in areas with human presence and hunting ([Naranjo and Cruz 1998](#); [Zapata-Ríos and Branch 2015](#)). It has also been documented that the presence of domestic or feral canids can lead to changes in the habitat use of native species, thus affecting their movement and hours of activity ([Vanak and Gompper 2009](#); [Silva-Rodríguez et al. 2010](#)).

The ACF contains a large fragment of tropical forest (~5800 ha) in different successional stages that maintains some connectivity with other adjacent forest patches (Fig-

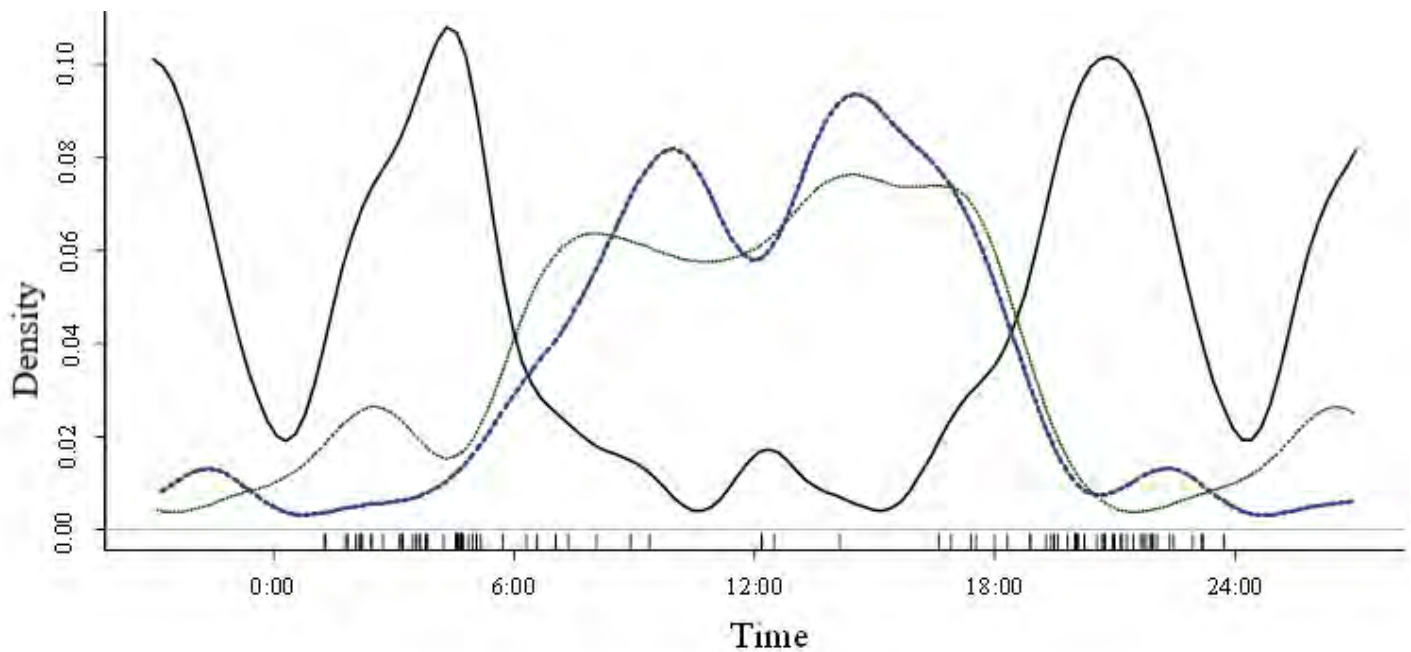


Figure 3. Overlap of activity between ungulate species in community forest areas (ACF) and the protected area (Montes Azules Biosphere Reserve; REBIMA) in the Lacandon Forest, Mexico. Black line: *Tapirella bairdii*; blue line: *Tayassu pecari*; green line: *Dicotyles tajacu* (overlap coefficient), values of the confidence interval. *D. tajacu*-*T. bairdii*-*T. pecari* = 0.34 (0.17–0.37); *T. pecari*-*D. tajacu* = 0.82 (0.84–1.03), and *D. tajacu*-*T. bairdii* = 0.42 (0.22–0.44).

ure 1; [Gil-Fernández et al. 2017](#)). The white-lipped peccary was recorded more frequently in ACF than in REBIMA (Table 5, Supplementary material), likely due to migratory or episodic movements that favor their presence even in non-protected areas ([Mendes-Pontes and Chivers 2007](#); [Reyna-Hurtado et al. 2009](#)).

Habitat use models. The models constructed to evaluate habitat use by the species confirm previous reports, which describe low tolerance to anthropic effects (*i.e.*, presence of roads and infrastructure) and preference for areas with connectivity to water bodies by the tapir and white-lipped peccary ([O’Farrill et al. 2014](#); [Naranjo 2019](#); [Reyna-Hurtado et al. 2014](#); [Moreira-Ramírez et al. 2019](#)). In contrast, our results show that the collared peccary uses both types of sites (protected area and community forest areas) in a similar way. Consistent results have been reported for this species in similar Neotropical environments where food is not a limiting factor ([Terborgh 1986](#); [Peres 19946](#); [Galetti et al. 1999](#)). This helps to explain the occasional records of this species crossing roads and in agricultural areas in the present study. To note, the use of agricultural systems by *T. pecari* has been documented in dry savannas of Venezuela, the dry Chaco in Paraguay ([Mayer and Wetzel 1987](#); [Redford and Eisenberg 1992](#)), and grasslands of central and central-western Brazil, where they are even considered a pest for the damage and losses caused to farmers ([Jacomio et al. 2013](#); [Lima et al. 2019](#)). This is not the case in southeastern Mexico, since the populations of *T. pecari* rarely cause damages to agricultural systems, to the best of our knowledge ([Naranjo 2002](#); [Romero-Balderas et al. 2006](#)). This discrepancy may be related to the regional context of the areas where this

species thrives, since the great Chaco and the Amazon are characterized by large extensions of habitat (> 1.5 million km²; [Cartes et al. 2015](#); [Camino et al. 2017](#)) and low human densities, contrary to our study area, which shows smaller areas of suitable habitat and high human density and disturbance ([Naranjo 2019](#)).

Activity patterns. For the tapir, previous studies in Mexico and elsewhere report activity patterns within a specific time span (nocturnal or diurnal; [Eisenberg 1989](#); [Sanderson and Trolle 2005](#)), or with hours of activity split into two periods of the day (typically daytime and nighttime; [Matola et al. 1997](#); [Foerster and Vaughan 2002](#)). Besides, these ungulates tend to move away or become more elusive in areas with human presence and hunting ([Naranjo and Cruz 1998](#); [Zapata-Ríos and Branch 2015](#)). It has also been documented that the presence of domestic or feral canids can lead to changes in the habitat use of native mammals, affecting their movement and hours of activity ([Vanak and Gompper 2009](#); [Silva-Rodríguez et al. 2010](#)). In the study area, intrusion events of domestic dogs and hunters were recorded in the ACF; however, the current hunting rate or frequency has not been documented (Figures 2 and 4).

This study found that the tapir displays activity patterns with two marked peaks of nighttime activity (20:00 to 23:00 h and 2:00 to 5:00 h; Figure 3). This finding is consistent with reports for other tapir populations in Mexico, such as those inhabiting Los Chimalapas, Oaxaca ([Lira-Torres et al. 2014](#)) and the Calakmul Biosphere Reserve, Campeche (unimodal period of activity: 20:00 to 3:00 h; [Sánchez-Pinzón et al. 2020](#)). The bimodal pattern reported in this study has also been observed for *T. pinchaque* in the central Andes of Colombia ([Lizcano and Cavelier 2000](#)).

and *T. terrestris* in the Ecuadorian Amazon (Espinosa and Salvador 2017). In contrast, the unimodal pattern of activity of the tapir in Calakmul may be the result of monitoring associated with water bodies (open canopy areas), a vegetation structure allowing greater moonlight permeability (i.e., subdeciduous tropical forest; Lizcano and Cavalier 2000), and anthropic pressures such as hunting (Oliveira-Santos et al. 2010; Sánchez-Pinzón et al. 2020). In addition, environmental heterogeneity in different habitats can influence wildlife activity patterns (Liu et al. 2017). The evergreen tropical forest of the Lacandon Forest is more exuberant and rich in food resources and moisture than other vegetation types (Rzedowski 1978; Hubbel 2001; Pennington and Sarukhan 2005), which may influence the activity pattern of this species.

The activity patterns recorded for both peccary species show that they were mainly diurnal, with peaks of activity between 14:00 and 18:00 h and sporadic activity in the evenings or nights. Our results are consistent with Briceño-Méndez et al. (2016), who reported for these peccary species diurnal patterns with peak activity between 08:00 h and 14:00 h in sites with persistent hunting in Calakmul, Mexico. However, they differ slightly from the findings in a similar ecosystem in Brazil (Galetti et al. 2015), where peaks of activity were recorded between 5:00 and 10:00 h



Figure 4. Evidence of firearm hunting and presence of domestic canids within the ACF, Lacandon Forest, Chiapas, Mexico (2015).

for the white-lipped peccary and from 17:00 to 22:00 h for the collared peccary. Other studies have shown activity patterns different from those exhibited by both peccary species in the present study, showing that they can be active throughout the day (Mayer and Wetzel 1987; Arroyo-Arce et al. 2017). Our results differ from those of Keuroghlian et al. (2004), who did not observe a temporal overlap between these species in a landscape of southeast Brazil. The differences in the hours of activity just mentioned may be due to factors associated with particular habitat characteristics, community structure, and local (hunting) or regional disturbance variables that influence the activity patterns of species (Frey et al. 2017). The hours of activity of peccaries recorded in this study suggest a mechanism to avoid predation since these are opposite to the activity peaks of their main predator in the study area, the jaguar *Panthera onca* (De la Torre and Medellín 2011), as well as to avoid hunting (Briceño-Méndez et al. 2016).

This suggests that habitat segregation (spatial dimension) rather than temporal segregation, may be one of the main mechanisms allowing the sympatric coexistence of both species of peccaries in the Lacandon Forest. Niche partitioning between these two tayassuids in the study area could be based on: 1) the differential use of food resources, with minor variations in the diet, as reported in several studies throughout its distribution range (Reyna-Hurtado et al. 2014); and 2) differences in the movement ecology of the white-lipped peccary, which, given the amplitude of its displacement, allows gaining an advantage over collared peccaries (Reyna-Hurtado and Tanner 2005; Reyna-Hurtado et al. 2009). This means that while *T. pecari* is able of traveling long distances of up to 120 km in preserved forests in search of food, forced by its metabolism, the collared peccary can meet its metabolic and ecological requirements even in disturbed areas (Reyna-Hurtado et al. 2014) and in smaller areas of suitable habitat, according to the home range of 7.3 km² reported by Naranjo (2002) in the Lacandon Forest.

The similarities and differences in the parameters evaluated in this study versus other studies were due to different causes, considering that animals can modify their spatio-temporal activity behavior, either to reduce the risk of natural predation (Oliveira-Santos et al. 2010; Lone et al. 2017) or as an effect of anthropic alterations such as habitat fragmentation and hunting (Tejeda-Cruz et al. 2009; Carreira et al. 2020). This has cascading effects on the rest of the community (Carreira et al. 2020), a potential situation that should be monitored by managers of protected and non-protected areas under the current laws and regulations seeking to preserve the viability of populations through management plans and conservation actions (Robinson et al. 2016; Dellinger et al. 2019).

Although the low tolerance of the white-lipped peccary to the effects of human activities has been documented (Reyna-Hurtado and Tanner 2007; Altrichter et al. 2012; Keuroghlian et al. 2013; Mandujano and Reyna-Hurtado

2019), the fitness of logistic regression models showed an unexpected positive projection for the use of the ACF forest area, similar to that of areas within the REBIMA (see Figure 2). The fact that white-lipped peccaries have been observed in areas with human settlements is encouraging for their conservation. We hope these results will contribute to convince decision-makers and the inhabitants of the Lacandon Forest that the coexistence between human and wildlife populations in the region is feasible.

Our results indicate that: 1) both peccary species display different habitat preferences in the study area, while tapir preferred using the protected area, as significant evidence of niche partitioning; and 2) the ACF site is an important relict of tropical forest with the potential to maintain populations of these species; therefore, the conservation of these forests by local communities is essential to ensure the persistence of these ungulates. The conservation of these populations and other natural resources in the Lacandon Forest has become urgent given the unsustainable production practices that promote deforestation (*i.e.*, extensive livestock ranching and commercial agriculture) in areas adjacent to federal and community protected natural areas. In our view, more environmentally friendly productive activity schemes such as agroforestry systems should be implemented in the region to mitigate unsustainable practices and their effects. Also, the protection and management of the remaining habitat in managed areas (ACF) are relevant and necessary, as well as the protection of wildlife from poaching.

We suggest addressing this information gap in future studies by assessing the movements of wild ungulates to better know their habitat occupation, distribution, and potential metapopulation dynamics, which may explain their presence in fragments of habitat surrounding the REBIMA (Naranjo and Bodmer 2007). Another aspect worth investigating is the influence of structural and functional connectivity, as well as habitat suitability for these species at the landscape level in the study area.

It is both convenient and relevant to generate information with spatially explicit variables that ensure greater fidelity and independence of captures of the movements of ungulates across the study area, such as the estimation of their home ranges (Frey *et al.* 2017; Mandujano and Reyna-Hurtado 2019) and approximations with occupation models, habitat preferences, and other resource selection models (*e.g.*, resource selection functions; Manly *et al.* 2002; Lele *et al.* 2013). Future research should contribute to reversing these processes, for instance, by supporting the generation of conservation strategies and strengthening management plans for the populations of wild ungulates and their habitats in the Lacandon Forest. One approach to this end would be through Wildlife Conservation Management Units with species that tolerate the sustainable use of their populations, such as the collared peccary and the lowland paca (*Cuniculus paca*).

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Effect of an urban area in the distribution pattern and diversity of Neotropical rodents

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Urbanization implies the loss of biodiversity and promotes the extirpation of local flora and fauna. It favors habitat fragmentation and the establishment and increase of non-native species and, eventually, the homogenization of the landscape. This study aims to evaluate the urbanization process in a medium-sized city in the Mexican southeast, San Cristóbal de Las Casas (SCLC) in the Neotropics, and the response of the rodent community to such process. The study area was categorized according to its structural characteristics into four coverage classes: urban, forest, agricultural and mountain wetlands. Rodents were sampled over urbanization gradients. In each gradient, nine sampling sites were established. The responses of rodent alpha and beta diversities to landscape structure (landscape metrics) were evaluated. The larger diversity of rodents was found in the mosaic and transition landscape categories and the least diverse were the conserved and urban ones. In SCLC, rodent richness responds to the number of fragments and the diversity of the landscape. *Mus musculus* and *Rattus rattus* were more abundant in landscapes with a high percentage of urban cover, while *Peromyscus mexicanus* and *P. beatae*, in landscapes with higher forest cover. San Cristóbal de Las Casas is a city that grows over areas with native vegetation, forests and mountain wetlands; of which fragments remain embedded in the urban matrix. Mosaic and transition landscapes favor areas with high diversity and richness of rodent species (intermediate disturbance hypothesis). This study suggests that both native and non-native rodent species are abundant in areas with natural vegetation and also in urban sites. Sanitary measures are granted, since reservoir species of pathogens with zoonotic potential can be found in the area.

La urbanización representa la pérdida de biodiversidad y promueve la extirpación de la flora y fauna locales. Favorece la fragmentación y el establecimiento e incremento de especies no nativas, y eventualmente, la homogenización del paisaje. Este estudio tiene como objetivo evaluar el proceso de urbanización en una ciudad mediana del sureste mexicano, San Cristóbal de Las Casas (SCLC) en el Neotrópico, y la respuesta de la comunidad de roedores a ésta. Se caracterizó el área de estudio en 4 clases de cobertura: urbana, boscosa, agropecuaria y humedal de montaña. Se muestrearon roedores en gradientes de urbanización. En cada gradiente se establecieron 9 sitios de muestreo. El área de estudio se categorizó según sus características estructurales. Se evaluó la diversidad alfa y beta, y la respuesta de la diversidad de roedores a la estructura del paisaje (métricas de paisaje). La mayor diversidad de roedores, se encontró en las categorías de paisaje tipo mosaico y de transición y las menos diversas fueron las conservadas y urbanas. En SCLC la riqueza de roedores responde al número de fragmentos y a la diversidad del paisaje. *Mus musculus* y *Rattus rattus* fueron más abundantes en paisajes con alto porcentaje de cobertura urbana y *Peromyscus mexicanus* y *P. beatae*, en paisajes con mayor cobertura de bosque. San Cristóbal de Las Casas es una ciudad que avanza sobre las áreas con vegetación nativa, bosques y humedales de montaña, de las cuales, quedan fragmentos embebidos en la matriz urbana. Los paisajes de mosaico y transición propician áreas con altas diversidades y riqueza de especies de roedores (hipótesis del disturbio intermedio). Este estudio sugiere que las especies de roedores nativos y no nativos son abundantes en áreas con vegetación natural y también en sitios urbanos. Es importante considerar algunas medidas sanitarias, pues existen especies reservorios de patógenos con potencial zoonótico.

Keywords: Cities; Cricetidae; fragmentation; landscape; Muridae.

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Introduction

Nearly fifty-six percent of the global human population lives in medium-sized cities harboring between 100,000 to 500,000 inhabitants. It has been predicted that, by the year 2035, 62.5 % of the human population will live in a city (UN-HABITAT 2020). Such an increase in the world's urban population implies: 1) The establishment of new cities or the growth of those already established to the detriment of natural landscapes; since, this entails the extirpation of native

flora and fauna at rates even higher than those produced by agriculture or forestry (Marzluff and Ewing 2001; McKinney 2006). 2) The establishment and increase of non-native wildlife species adapted to urban conditions and, eventually, the homogenization of the landscape (McKinney 2006).

The expansion of the urban territory onto the natural landscape alters its structure in terms of composition (cover classes) and configuration (spatial arrangement of cover classes; Liu et al. 2016), reconfiguring the landscape.

Additionally, fragmented and disorderly growth (coupled with the lack of associated regulations) favors urban configurations where limits (or peripheries) are unclear. Since poorly urbanized neighborhoods are constantly added to the peripheries, they represent points of growth blurring the limits of cities (Terradas *et al.* 2011). This gives rise to cities with a broad variety of landscapes, with a varying degree of disturbance, sometimes mixed with fragments of conserved vegetation (Doygun 2009).

The reconfiguration of urban space alters the communities of native flora and fauna, in terms of species composition, abundance, richness and equitability (Aronson *et al.* 2014; Lättman *et al.* 2014). Wildlife has been reported to present different types of response to urbanization, according to the taxonomic group in question (Magle *et al.* 2019); for example, large predatory mammals are poorly adapted to survive in large cities (Ordiz *et al.* 2013). In contrast, other medium and large mammals, such as raccoons (*Procyon lotor*) or capybaras (*Hydrochoeris hydrochaeris*), are well adapted to urban conditions in some regions of the continent (Dybas 2017; Serra-Medeiros *et al.* 2021).

In the case of small mammals such as rodents, there are species that respond positively to urbanization, increasing their abundances (Santini *et al.* 2019); the so-called “urban dwellers”, which live permanently in the urban environment. The abundance increase of these species represents serious economic and public health problems for humans, similar those generated from the non-native rodent species like *Mus musculus* and *Rattus* species in the World (Meerburg *et al.* 2009; McFarlane *et al.* 2012). Other species exist that make occasional visits: “urban visitors” (Baker *et al.* 2003). Finally, some species respond negatively, reducing their abundances (Lopucki and Kitowski 2017), and are known as “urban avoiders” (McKinney 2006).

Previous studies have shown that urbanization influences the diversity of native rodent species, regardless of city size, reducing native species richness while increasing richness of non-native species. At the same time, these studies recognize the importance of preserving fragments of the landscape with natural coverage, in order to maintain high diversity of native rodents in urban areas (Rizkalla and Swihart 2009; Fernández and Simonetti 2013; Johnson and Karels 2016; Lopucki and Kitowski 2017). It is also important to control stray dogs and cats, common in many cities throughout the continent, which can be predators of native species and endanger their survival (Coronel-Arellano *et al.* 2021; Mella-Méndez *et al.* 2022).

The main objective of this work was to evaluate the response of the rodent community to the urbanization process in San Cristóbal de Las Casas, Chiapas, México (SCLC). For this purpose: 1) The alpha and beta diversity of the rodent community were recorded and compared against urbanization gradients; 2) the relationships between landscape metrics (in terms of configuration and composition) with rodent species richness and abundance were evaluated; and 3) based on the landscape-site approach, the

study area was categorized into different categories of landscapes. We explain the rodent species distribution and suggest areas for conservation based on landscape categories and rodent diversity.

Materials and Methods

Study area. The city of San Cristóbal de Las Casas, Chiapas (SCLC; 16° 44' 12" N, -92° 38' 18" W) is in the region of The Highlands of Chiapas. The main ecosystem types in the city are: mountain wetlands (Ramsar sites; [The Ramsar Convention Secretariat 2013](#)), coniferous forests (pine, oak and pine-oak), and cloud forests (Trucíos-Caciano *et al.* 2013). The original layout of SCLC was made up of 18 blocks and 12 streets (Aubry 2008; Appendix 1). The city continued to expand towards the mountains, and towards the south of the valley, where the wetlands are located (Cantú Luna and Fenner Sánchez 2020). Today, it is a medium-sized city of 202,459 inhabitants (INEGI 2021). The urban area has increased by 12.5 % between 2001 and 2018 (Camacho-Valdez *et al.* 2019). Natural areas embedded in the city have reduced their size, and the current fragments have been designated for conservation in private, federal, and municipal reserves: Huitepec Ecological Reserve, Moxviquil Ecological Reserve, El Encuentro Ecological Park, Montetik Natural Park, La Kisst Wetland, and María Eugenia Wetland (Supplementary material 1).

Delimiting and characterizing the study area. The study area was delimited by 6 km radius circumference (Figure 1a). The characterization was conducted through a supervised classification of a Sentinel 2 image, of 10 m resolution. The image, from 2020, was analyzed using QGIS 3.16 (QGIS Development Team 2021) and the SCP (Semiautomatic Classification Plugin) plug-in 6.4 (Congedo 2020). The classification was performed with the method Maximum Similarity Algorithm. The accuracy of the classification was established by the Kappa coefficient at 80 % confidence value per land cover class. The area, was classified into four land cover classes, served for the subsequent categorization of the sampling sites: urban (soil covered by concrete, devoid of vegetation, houses, roads), forests (altered coniferous forest, oak forest, pine-oak forest), agriculture (agricultural plots, sown agricultural, agricultural in preparation, pastures), and wetlands (grasslands, areas covered by water).

Rodent species sampling. Seven bimonthly rodent samplings were performed, three in 2019 (June, August and October), one in 2020 (January) and three in 2021 (March, May and July), along seven urbanization gradients, established through the study area in straight line, and directed to the cardinal points (see Figure 1a). Along each of the seven urbanization gradients, nine sampling sites were established for each one: at 0 (1), 1.5 (2), 3.5 (3) and 6 km (3; Figure 1a). The minimum distance between sampling sites was 500 m. At each sampling site, 20 Sherman traps were placed simultaneously, for a total of 180 traps per gradient, per sampling month. The sampling sites had the following characteristics: at 0 km, the urban sites included houses,

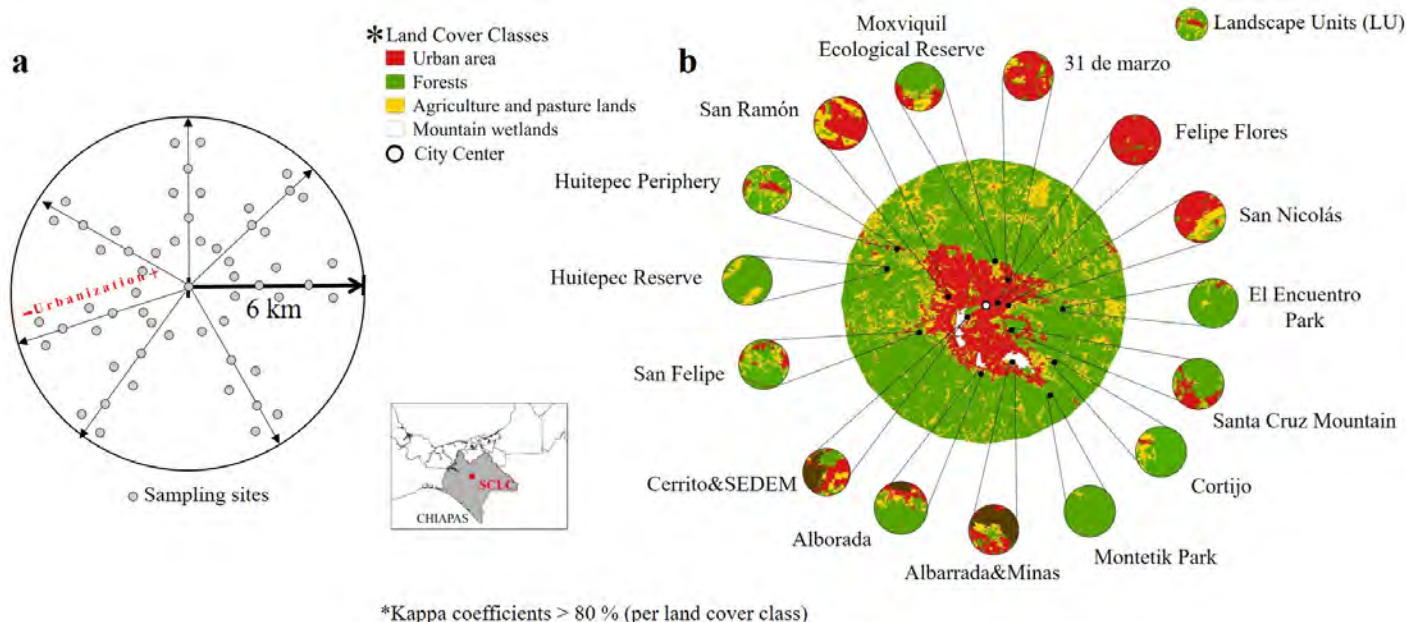


Figure 1. a) Sampling design for rodents in San Cristóbal de Las Casas, Chiapas, México. Arrows = representing urbanization gradients performed in this study; b) classified land use classes and landscape units (LU) in San Cristóbal de Las Casas, Chiapas, México.

parking lots, hotels or hostels. Then, at 1.5 km, two contrasting sites were chosen, forests and wetlands or agricultural plots or urban areas. At 3.5 km, three contrasting sites were chosen, forests and wetlands and agricultural plots or pastures or urban areas. Finally, at 6 km, the selection of three contrasting sites was repeated.

In each sampling site, the traps were placed in two lines of 10 traps each one, with a separation of 10 meters between each trap and 10 meters between lines. However, in the case of traps placed in houses, five traps were located per house (totaling four houses). Traps were placed inside rooms, kitchens, grain storage warehouses, corrals, or patios. All traps were baited with a mixture of oats, peanut butter, and sunflower seeds. The traps were checked every morning at 7:00 hrs. Each specimen sampled was identified to species level with specialized guides and taxonomic keys (Álvarez-Castañeda et al. 2017); sex, reproductive condition and weight were recorded, in addition to conventional somatic measurements.

Rodents were marked with ear notches (Sántiz-Vázquez 2018) and released *in situ*. Each ear sample was stored in 70 % alcohol, for future genetic analysis. Two specimens of each native species by location were collected and deposited in the Mammal Collection of El Colegio de la Frontera Sur (ECOSUR). All non-native rodents were sacrificed and conserved in 70 % alcohol. The scientific collection license FAUT-0143 provided to CL from SEMARNAT was used. Rodents were handled according to the guidelines of the American Society of Mammalogists (Sikes and The Animal Care and Use Committee 2016).

Categorizing the study area. To categorize the study area into different landscape categories, we used a site-landscape approach (Fahrig 2013). This approach consisted of

establishing a buffer of 500 m ratio in each effective sampling site, considering landscape units (LU; Figure 1b). The buffer was set to the home range of the rodent species previously collected in the region (San-José et al. 2014; Rodríguez Macedo 2016; Arce-Peña et al. 2019).

Each LU was characterized in terms of its composition and configuration, using eight landscape metrics obtained with FRAGSTATS 4.2.1 software (McGarigal and Ene 2015). We chose two metrics for composition: PLAND (percentage of landscape / land cover class), and Shannon’s diversity index (SHDI). The land cover classes considered were: urban (URB), forest (FOR), agricultural (AGRO), and wetland coverage (WET). Other six metrics for configuration were, number of patches (NP), contagion index (CONTAG), percentage of like adjacencies index (PLADJ), division index (DIVISION), patch richness (PR), and aggregation index (AI). The definition of each landscape metric is in Supplementary material 2.

Through a Principal Component Analysis (PCA), the spatial relationship between the LUs, the landscape metrics, and the relative abundance were explored via correlations. With the resultant ordination, landscape categories were assigned according to the structural characteristics with the highest loadings. The threshold to recognize those components best explaining variation was the asymptote of the distribution of the variance. This analysis was performed using the FactoMineR package (Le et al. 2020) in the R 4.10 programming language (R Core Team 2018).

Data Analysis. Alpha diversity was calculated using Hill numbers ⁰D (species richness), ¹D (exponential of the Shannon diversity index), and ²D (inverse Simpson index; Moreno et al. 2011). Diversity analyzes were performed using the Vegan 1.8 package (Oksanen et al. 2007). Range-abundance graphs were built to simultaneously visualize

abundance and diversity in the categories of LU (Magurran 1988). Differences in abundance and richness were estimated with a Hutcheson t-test (Zar 2010) between landscape categories. Additionally, beta diversity (*i. e.*, species turnover) was calculated using the multiplicative-partition-of-diversity method. Furthermore, the Sorensen dissimilarity index was used to determine the dissimilarity between the LUs categories, as well as the partition of beta diversity into its components $\beta_{SOR} = \beta_{SIM} + \beta_{SNE}$; for which we used the betapart 1.5.4 package (Baselga and Orme 2012). Finally, the hypothesis of a relationship between rodent diversity and landscape metrics was tested, using a series of generalized linear models with the Glmulti 1.0.8 package (Calcagno and de Mazancourt 2010).

Results

Characterization of the study area. The study area covered 15,143 ha; forests of oak, pine, pine-oak or oak-pine forests, in some state of conservation covered the 66 % of the area, urban 14 %, agricultural crops and pastures 18 %, and conserved mountain wetlands less than 2 % (Figure 1b).

Categorization of the study area. Rodents were captured only in 15 out of 63 sampling sites, such sites were established as landscape units (LUs; Figure 1b). Landscape metrics are presented in Table 1. The study area was categorized into four categories of landscape: urban, of transition, of mosaic and conserved. This categorization was conducted using principal component analysis (PCA). The first principal component (PC1) explained 53.1 % of the variation and was interpreted as a proxy for habitat heterogeneity (Figure 2), since it showed higher weights for the number of patches (NP), landscape division index (DIVISION), contagion index (CONTAG), and percentage of like adjacencies

(PLADJ; Table 2). Consequentially, the LUs positively related to PC1 were units diverse in composition, with a mixture in land cover classes, subdivided into fragments, mainly with urban and forest coverage. Principal component two (PC2), explained 22 % of the variation and was interpreted as a proxy for conservation (Figure 2). This component represents the urban gradient, due to the weight presented by the percentage of forest and urban coverage (Table 2).

Describing the landscape categories. The urban category was represented only by one unit (FFL; Figure 2). This category had the highest urban coverage and the highest aggregation index. The unit is located at the center of SCLC. In turn, the transition category was represented by heterogeneous units, with the highest richness of fragments (types of land cover). This category grouped units in process of urban transformation, with urban coverage between 28 % and 65 %; even though they retained proportions of other land cover classes; units are located between 1.5 and 3.5 km (Figure 2). The mosaic category gathered the units with the highest number of fragments; separated one from another, describing more than a continuum, a mosaic of forest, houses, agricultural plots and wetlands (Figure 2). Mosaic units were placed between 3.5 and 6 km from the city center. Conserved category was formed by units with the highest percentages of forest cover, and the lowest coverage of urban, and all are located at 6 km from the city center (Figure 2). A more detailed description of each category is presented in Supplementary material 3.

Rodent diversity, richness, and abundance. A sampling effort of 3,780 trap nights was carried out, during which 10 rodent species and 147 individuals were recorded (Supplementary material 4). Seven of these species, *Oligoryzomys fulvescens*, *Peromyscus beatae*, *P. mexicanus*, *Reithrodonto-*

Table 1. Landscape metrics per landscape units (LU) in San Cristóbal de Las Casas, Chiapas, México.

LU name	ID	Landscape metrics of composition						Landscape metrics of configuration					Distance (m)	
		%URB	%FOR	%AGRO	%WET	SHDI	PR	NP	DIVISION	AI	CONTAG	PLADJ	DIS	
Felipe Flores	FFL	95.44	3.72	0.84	0.00	0.21	3.00	16.00	0.09	96.80	85.01	95.49	0	
C.31 de marzo	C31	78.84	9.77	11.39	0.00	0.66	3.00	27.00	0.37	92.12	56.04	90.59	1500	
San Nicolas	SNI	60.01	13.67	28.91	0.00	0.93	3.00	17.00	0.60	90.84	41.93	89.17	1500	
Santa Cruz	SCR	26.60	67.00	6.39	0.00	0.80	3.00	31.00	0.57	91.00	48.06	89.41	3500	
Cerrito SEDEM	CSE	32.50	22.91	13.46	31.13	1.34	4.00	34.00	0.80	89.88	35.60	87.89	3500	
Reserva Moxviquil	MOX	20.58	63.17	16.25	0.00	0.91	3.00	16.00	0.60	93.26	45.36	91.54	3500	
San Ramón	SRA	65.26	5.83	28.91	0.00	0.80	3.00	18.00	0.55	92.35	49.63	90.73	3500	
San Felipe	SFE	14.03	65.86	20.12	0.00	0.87	3.00	29.00	0.57	84.43	37.37	82.90	3500	
Albarrada Minas	ALM	28.75	12.94	11.54	46.77	1.23	4.00	28.00	0.71	89.84	40.81	87.93	3500	
Alborada	ALB	14.65	65.55	11.96	7.84	1.01	4.00	21.00	0.56	91.46	51.51	89.61	3500	
Parque Encuentro	ENC	2.37	91.24	6.39	0.00	0.35	3.00	15.00	0.17	95.55	76.40	94.14	6000	
Cortijo	COR	2.26	83.12	14.61	0.00	0.52	3.00	17.00	0.32	95.33	67.36	93.81	6000	
Parque Montetik	MON	0.00	98.57	1.43	0.00	0.08	2.00	2.00	0.03	99.06	91.85	97.84	6000	
Periferia Huitepec	PHU	12.69	63.75	23.56	0.00	0.89	3.00	41.00	0.59	83.44	36.38	81.91	6000	
Reserva Huitepec	RHU	0.00	84.32	15.68	0.00	0.43	2.00	3.00	0.28	95.94	57.02	94.53	6000	

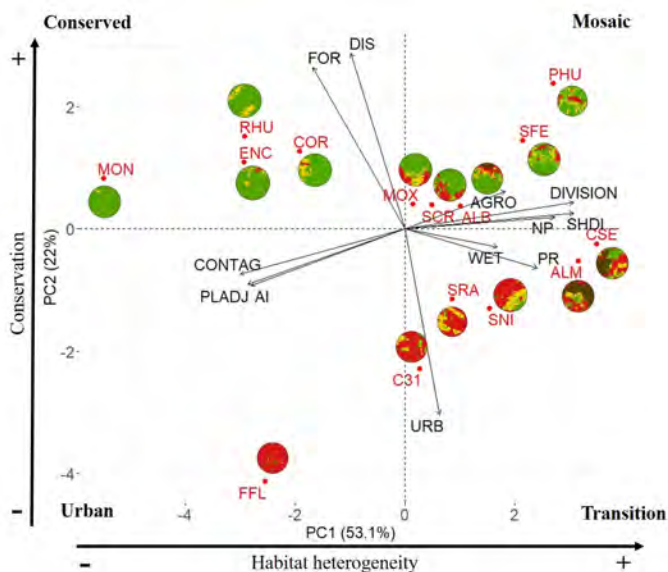


Figure 2. Plot loadings of PCA model, for landscape units by landscape metrics. Arrows = loadings per landscape metrics. Color polygons = landscape units.

Table 2. Scores of Principal Component Analysis (PCA) of landscape metrics and abundance of rodents in Landscapes Units (LU) in San Cristóbal de Las Casas, Chiapas, México.

PCA Landscapes Unites (LU)		PCA Landscapes Unites (LU) and Rodent species			
Loadings	PC1	PC2	Loadings	PC1	PC2
URB	0.193	-0.935	URB	0.275	-0.918
FOR	-0.518	0.812	FOR	-0.591	0.759
AGRO	0.562	0.191	AGRO	0.563	0.102
WET	0.516	-0.090	WET	0.519	0.056
PR	0.738	-0.195	SHDI	0.915	0.184
NP	0.835	0.061	PR	0.719	-0.033
DIVISION	0.943	0.128	NP	0.833	0.182
AI	-0.862	-0.287	DIVISION	0.915	0.202
CONTAG	-0.924	-0.229	AI	-0.846	-0.325
PLADJ	-0.881	-0.280	CONTAG	-0.895	-0.270
Eigenvalue	6.379	2.639	Eigenvalue	7.713	3.782
% of variance	53.161	21.991	% of variance	35.060	17.191
Cumulative % of variance	53.161	75.152	Cumulative % of variance	35.060	52.251

mys fulvescens, *R. microdon*, *R. sumichrasti*, and *Sigmodon toltecus*, belonged to the Cricetidae family and were considered native species; the remaining three species belong to the Muridae family and were considered non-native: *Mus musculus*, *Rattus rattus* and *R. norvegicus*. Regarding landscape categories, the most abundant species in the transition was *S. toltecus* and *M. musculus* was the most abundant in the mosaic (Figure 3). *Rattus rattus* was present through-

out the study area, except in conserved units. In the conserved units, the most abundant species was *P. mexicanus*, which was also abundant in the mosaic units (Figure 3). The results of alpha diversity for each of the 15 LUs and for category of landscape are in Supplementary material 5.

According to the diversity of order 1 (¹D), the units in the transition category have a diversity of 4.56 abundant species. In contrast to the 5.77 of the mosaic units

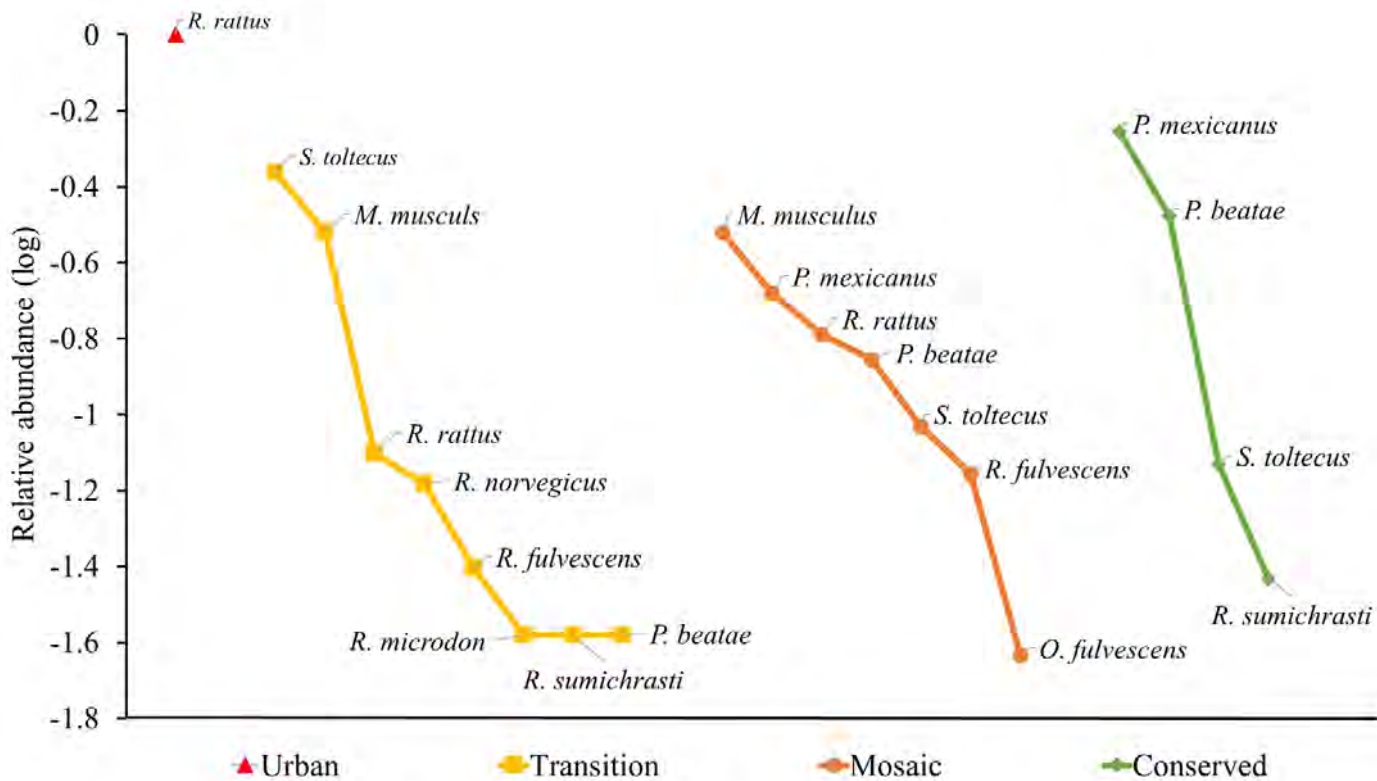


Figure 3. Range-abundance graphs by landscape categories in San Cristóbal de Las Casas, Chiapas, México.

(Supplementary material 5). This means that, among mosaic units, there are 1.21-fold more abundant species, in comparison to transition units, and 3-fold more than among conserved units (2.73). On the other hand, the highest-richness landscape categories were the transition (8 species) and the mosaic (7 species) units, while the lowest were the urban units (1 species; Figure 3). There are significant differences in richness between urban and transition categories ($t = 4.2, P = 0.0005$), and between urban and mosaic units ($t = 3.28, P = 0.0041$). Regarding abundance, coincidentally, the most abundant categories are the transition ones ($n = 76$) and the mosaic ($n = 43$), and the lowest was the urban ($n = 2$). There are significant differences between abundance of urban and transition categories ($t = 2.12, P = 0.0478$), and between urban and mosaic ($t = 2.99, P = 0.0077$; Supplementary material 5).

The relationships between rodent species, landscape units, and the landscape metrics were also examined with an exploratory ordering analysis, via a PCA. The components 1 and 2 explained 35.1 % and 17.2 % of the variation, respectively (Figure 4). The presence of rodent species in SCLC is a function of two components: 1) habitat heterogeneity, defined by the landscape metrics: landscape division index (DIVISION), Shannon's Diversity index (SHDI), contagion index (CONTAG), and aggregation index (AI; Table 2; Figure 4); and 2) urbanization, defined by the landscape metrics: forests cover (FOR), DIVISION, urban cover (URB), and aggregation index (AI; Table 2; Figure 4). There is a species' grouping pattern that corresponds to the grouping pattern of landscape units (Figure 4). The units of mosaic category are associated to the presence of *S. toltecus*, *R. fulvescens*, and *Oligoryzomys fulvescens*. Urban units are characterized by the presence of *Rattus rattus*. Transition units group together due to sharing *R. microdon*, *R. sumichrasti*, *R. norvegicus*, and *M. musculus*. Finally, conserved units group due to *P. beatae* and *P. mexicanus*, although not exclusively (Figure 4).

Regarding beta diversity, the Sorensen index (β_{SOR}) was 0.62; 52 % of this dissimilarity was due to species turnover (β_{SIM}) and the remaining 48 %, due to the component resulting from nesting (β_{SNE}). The landscape categories sharing the most species between them were the mosaic and transition units, with five species (*P. beatae*, *R. fulvescens*, *S. toltecus*, *R. rattus*, and *Mus musculus*). Conversely (according to the Sorensen dissimilarity index), the conserved LUs were the most dissimilar. Finally, six models explained the relation between metrics and rodent diversity. The landscape-composition variable that best explained species richness was the percentage of wetland coverage (AIC 55.9; Table 3). Abundance was better explained by the urban and forest cover variables (AIC 120.3) and Shannon's Diversity Index (SHDI, AIC 105.7; Table 3). In the case of landscape configuration metrics, DIVISION and CONTAG explained better the abundance of the species (AIC 98.094), and richness was better explained only by DIVISION (AIC 60.28).

Discussion

In the middle-sized city of SCLC, the greatest diversity in terms of rodent species richness and abundance, was found in the categories of landscape mosaic and transition. In contrast, the lowest richness was in the urban and conserved categories. According to our results, there are more rodent species in the most heterogeneous landscapes, *i. e.*, transition and mosaic landscape categories, where there is more than one type of land coverage and fragmentation occurs. The combination of urban, agricultural and wetland coverages contributed to the highest abundance and richness of rodent species in SCLC. This showed the importance of conserving those areas with wetland coverages and other natural vegetation coverages. Also, the majority of rodent species were distributed throughout the entire study area, regardless of the type of landscape, still some of them were more abundant in some landscape units.

Table 3. Estimated parameters for the best models of Generalized Linear Models for the effects of composition and configuration landscape on abundance and richness rodent in an urbanization gradient in San Cristóbal de Las Casas, Chiapas, México. SE = Standard error. AIC = Akaike criterion. P values < 0.05, are significant.

Landscape composition	Parameters	Estimate	SE	AIC	Z-value	P-value
Abundance~URB+FOR	Intercept	4.81	0.36	120.3	13.36	< 0.00
	URB	-0.03	0.00		-5.96	0.00
	FOR	-0.03	0.00		-6.91	0.00
Abundance~SHDI	Intercept	0.64	0.27	105.7	2.37	0.01
	SHDI	1.94	0.27		7.08	0.00
q0 ~ WET	Intercept	0.90	0.17	55.2	5.09	0.00
	WET	0.01	0.00		1.85	0.06
q0 ~ SHDI	Intercept	0.09	0.44	51.9	0.20	0.83
	SHDI	1.16	0.47		2.43	0.01
Landscape configuration						
Abundance ~ DIVISION + CONTAG	Intercept	-4.82	1.65	98.0	-2.91	0.00
	DIVISION	7.37	1.33		5.54	0.00
	CONTAG	0.06	0.01		3.39	0.00
q0~DIVISION	Intercept	0.06	0.45	60.2	0.13	0.89
	DIVISION	1.94	0.80		2.41	0.01

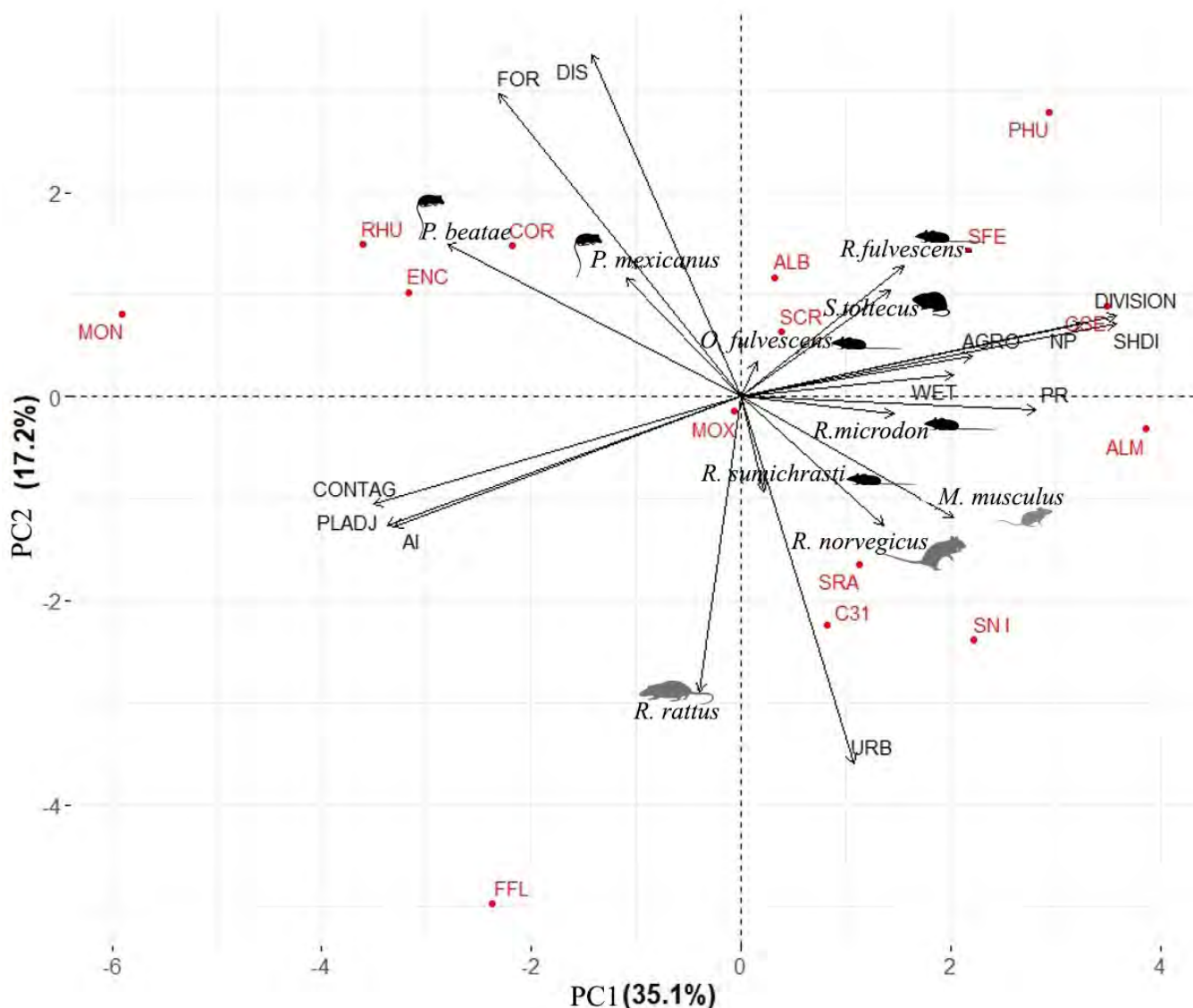


Figure 4. Plot loadings of PCA model. Arrows = loadings per landscape metrics and abundance of rodents. Points = landscape units. Black figures = native rodents. Gray figures = non native rodents.

The urbanization process in SCLC generates more than one landscape category, non-sequentially distributed, rather as spots in the study area and where the rodents are disseminated. The non-native rodents, *M. musculus* and *R. rattus*, were abundant in landscape categories with the highest proportions of urban coverage and were considered here as “urban dwellers”. This data matches reports in other cities, although of different sizes, in Argentina, United States and the Netherlands (Castillo et al. 2003; Gomez et al. 2009; Johnson et al. 2016; Maas et al. 2020). In Argentina, the community of non-native rodents was accompanied by native species, in smaller proportions (Castillo et al. 2003; Gomez et al. 2009). This structure of the rodent community was attributed to the urbanization processes of Latin American cities; which grow disorderly and settle in areas with natural vegetation. This drives native and non-native species to cohabit (Castillo et al. 2003), just like happens in San Cristóbal de Las Casas.

Some scholars attributed this community structure to the configuration of cities. For example, old cities (more than 100 years) that conserve riparian areas, small parks, or even large trees possess greater structural diversity, favoring a greater diversity of mammals (Parsons et al. 2018). Contrary to areas with less structural diversity or more homogeneous (e. g., monospecific forest areas) where there is less diversity of mammals. This reflects the patterns found in the city of SCLC, an old city preserving fragments with natural vegetation, agricultural plots and urban areas, generating a structurally complex landscapes, where native and non-native rodents cohabit.

Contrary to what was expected, the greatest richness and abundance of rodent species were concentrated in the mosaic and transition categories, and not in the conserved. This result coincides with that reported by García-Méndez et al. (2014) in SCLC. However, other studies carried out previously in the SCLC conserved units reported greater

species richness. For example, [Cruz Lara \(2000\)](#), found five and three species of rodents in the Huitepec and Moxviquil reserves, respectively (versus one and two species reported in this study for the same reserves, respectively). [Naranjo and Espinoza Medinilla \(2001\)](#) reported a total of 11 species of the Cricetidae family and two of the Muridae, for the Huitepec Reserve. Finally, in 2018, [Sántiz-Vázquez \(2018\)](#) reported six species of cricetids in the Huitepec Reserve, two of which were also reported in this work. It is worth mentioning that these previous reports correspond to collections carried out systematically, monthly, during periods of six months or one year, which makes it likely that their numbers of species were greater than those reported in this study. Additionally, we believe that dogs, cats, chickens and other poultry (observed chasing mice) are contributing to the decrease in the number of rodents present in the reserve and park of SCLC.

Despite not being the richest sites, the conserved units harbored the greatest abundance of *P. mexicanus* and *P. beatae*, and no individuals of the non-native species *M. musculus* or *Rattus* species were found; although they had already been reported in the Huitepec Reserve ([Naranjo and Espinoza Medinilla 2001](#)). Even though the Mexican rodent, *P. mexicanus*, was present in two landscape categories in SCLC, these were the categories with the greatest forest coverage and with agricultural plots. This rodent species is widely distributed in the Mexican southeast and is considered a habitat generalist ([Trujano-Ávarez and Álvarez-Castañeda 2010](#)).

Our study indicates that habitat heterogeneity generates a landscape with intermediate disturbance, favoring an increase in species richness, as previously reported in other countries ([Pardini et al. 2010](#)). It is suggested that a structurally complex matrix in composition (*i. e.*, heterogeneous landscapes) can increase rodent species richness within such landscapes. This argument was also suggested by [San José et al. \(2014\)](#); who reported that species richness may benefit from the matrix that generates fragmentation of the tropical forest as a source of food and shelter. Similarly, [Medellín and Equihua \(1998\)](#) showed that rodents “residing in the forest” may be able to use the corridors that form the matrix and benefit from the resources of places such as pastures or crops.

Given this study shows that rodent species (native and non-native) are abundant in human settlements, it is important to consider some sanitary measures; since *R. norvegicus*, *R. rattus*, and *M. musculus* are reservoirs of pathogens with zoonotic potential ([Panti-May et al. 2012, 2018](#)). However, native species such as *P. mexicanus*, *S. toltecus*, *R. sumichrasti*, and *R. fulvescens* are also reservoirs of zoonotic viruses potentially transmissible to humans and possible causes of hemorrhagic fever outbreaks ([Inizan et al. 2010; Milholland et al. 2018](#)). This is particularly important if we consider that *S. toltecus* and *R. fulvescens* are considered here as “urban visitors” and were found in houses, *i. e.*, the contact with people is frequent.

This study highlights the necessity for more long-term studies focused on understanding landscape changes of the city of SCLC, as well as structural changes of the rodent community and their interactions with human populations. We suggest carrying out future monitoring activities that include virological analyses of the collected rodent specimens, to know the prevalence of zoonotic pathogens and establish the possible health risks of disorderly urban growth in SCLC.

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Spatial and temporal distribution of bat mortality on a highway in southeast Brazil

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Roads and highways can work as barriers to the movement of many species, thereby preventing the individuals from accessing feeding and reproduction sites and the immediate risk of colliding wild species with vehicles. Identifying the impacts of roads on wildlife can contribute to the establishment of actions that promote conservation. In Brazil, data on collisions between bats and vehicles are scarce and underestimated in the literature. We described bat roadkill from 2008 to 2019 on a stretch of the BR-040 highway, which crosses an area of Atlantic Forest. Roadkill species were identified and the sites with high collision frequencies were characterized. A total of 923 individuals of 57 species and five families of chiropterans were identified. Frugivore bats showed the largest number of affected individuals, with *Artibeus lituratus*, a common species in the study region, with the highest number of roadkills. The diet and foraging behaviour were the most likely factors explaining most of the bats killed on the highway. The highest roadkill rate was documented in the fall, and the critical points located nearby the APA Petrópolis and REBIO of Tinguá, environmental protection areas. We reinforce the need to mitigate these roadkills, ensuring that road systems, which constitute municipal, state and federal highways, are built to prevent major disturbance of habitat and displacement routes of these species. We believe in the need for mitigations, and considering the various species involved, we suggest speed bumps construction reducing the speed limit, installing bridges, and signaling the presence of wildlife, before the stretches identified as hotspots.

Los caminos y carreteras pueden funcionar como barreras para el movimiento de muchas especies, impidiendo así el acceso de los individuos a los sitios de alimentación y reproducción y el riesgo inmediato de colisión de especies silvestres con vehículos. Identificar los impactos de los caminos sobre la vida silvestre puede contribuir al establecimiento de acciones que promuevan la conservación. En Brasil, los datos sobre colisiones entre murciélagos y vehículos son escasos y subestimados en la literatura. Describimos murciélagos atropellados entre 2008 y 2019 en un tramo de la carretera BR-040, que atraviesa un área de Mata Atlántica. Se identificaron las especies de animales atropellados y se caracterizaron los sitios con alta frecuencia de colisión. Se identificaron un total de 923 individuos de 57 especies y cinco familias de quirópteros. Los murciélagos frugívoros mostraron el mayor número de individuos afectados, con *Artibeus lituratus*, una especie común en la región de estudio, con el mayor número de atropellamientos. La dieta y el comportamiento de búsqueda de alimento fueron los factores más probables que explicaron la mayoría de los murciélagos muertos en la carretera. La mayor tasa de atropellamientos se registró en otoño, y los puntos críticos se ubicaron en las cercanías de APA Petrópolis y REBIO de Tinguá, áreas de protección ambiental. Reforzamos la necesidad de mitigar estos atropellamientos, asegurando que los sistemas viales, que constituyen las carreteras municipales, estatales y federales, se construyan para evitar que se alteren el hábitat y las rutas de desplazamiento de estas especies. Creemos en la necesidad de mitigaciones y considerando las diversas especies involucradas. Sugerimos la construcción de topes para reducir el límite de velocidad, instalar puentes y señalizando la presencia de fauna, antes de los tramos identificados como hotspots.

Keywords: Chiroptera; collisions; mitigation; road ecology; southeast Brazil.

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Introduction

The human population in recent decades has caused several changes in the environment, including road and highway construction that is currently a significant concern for biodiversity conservation ([do Prado et al. 2006](#); [Gumier-Costa and Sperber 2009](#); [Bueno et al. 2015](#)). Road impacts on wildlife include deaths from vehicle collisions, habitat destruction and fragmentation, barrier effect, edge effects and disturbances caused by light, noise and chemical pollution ([Forman and Alexander 1998](#); [Gibbs and Shriver 2002](#); [Row et al. 2007](#); [Kerth and Melber 2009](#); [Stone et al. 2009](#); [Zurcher et al. 2010](#); [Berthinussen and Altringham 2012](#); [Bueno et al. 2013](#); [Esperandio et al. 2019](#)). For several vertebrate species,

some of the ecological consequences include a reduction in the gene flow between populations and a decrease in both migration rates and genetic diversity ([Corlatti et al. 2009](#); [Esperandio et al. 2019](#)).

The order Chiroptera is the second largest among mammals, with more than 1,400 living species ([Simmons and Cirranello 2020](#)). In Brazil, this order is represented by 68 genera and 181 species subdivided into nine families ([Garbino et al. 2020](#)). The chiropterans play a fundamental role in maintaining the ecological processes of different vegetation domains, being excellent objects of study for characterizing habitats and their quality since they are also sensitive to changes ([Fenton et al. 1992](#); [Medellín et al. 2000](#);

[Gorresen et al. 2005](#)). However, most data on bat deaths on the roads comes from Europe, where several studies have been developed ([Bafaluy 2000](#); [Lesiński 2007](#); [Gaisler et al. 2009](#); [Kerth and Melber 2009](#); [Berthinussen and Altringham 2012](#); [Medinas et al. 2013](#); [Ramalho and Aguiar 2020](#)), while in Brazil, data on bat collisions are scarce ([Pracucci et al. 2012](#); [Pinheiro and Turci 2013](#); [Almeida and Cardoso Junior 2014](#); [Ceron et al. 2017](#); [Valadão et al. 2018](#); [Damásio et al. 2021](#); [de Figueiredo Ramalho et al. 2021](#)). The bat's low body mass, flight speed and nocturnal behavior make it difficult to find bat carcasses, resulting in the subsampling of the group in studies of road ecology ([Bafaluy 2000](#); [Lesiński et al. 2011](#); [Berthinussen and Altringham 2012](#)).

The bats forage using echolocation ([Kalko et al. 1996](#); [Siemers and Schnitzler 2000](#); [Schaub et al. 2008](#)) and hearing the sound of prey such as amphibians and insects ([Marimuthu and Neuweiler 1987](#); [Faure and Barclay 1992](#); [Altringham and Kerth 2016](#)). According to [Schaub et al. \(2008\)](#), the 'passive listening' strategy is adopted by bat species specialized in hunting arthropods in vegetation or on the ground, where other sounds of the environment mask the noises emitted by prey; thus, the sounds produced by cars can compromise the echolocation of bats nearby, reducing their feeding effectiveness. Therefore, roads act as barriers, reducing the bats' ability to access suitable places to forage or shelter, thus being a concerning factor, especially regarding migratory species ([Zurcher et al. 2010](#); [Lesiński et al. 2011](#); [Ceron et al. 2017](#); [Claireau et al. 2019](#)).

Although some studies show that bats recognize vehicles as a threat ([Baxter et al. 2006](#); [Zurcher et al. 2010](#); [Altringham and Kerth 2016](#)), many others show that bats are killed on the roads by vehicle collisions ([Bafaluy 2000](#); [Gaisler et al. 2009](#); [Ceron et al. 2017](#)). Moreover, some studies recent provide only a list of affected species ([Ceron et al. 2017](#); [Novaes et al. 2018](#)). Important variables that affect the collision rates between bats and vehicles, such as the diversity and abundance of specific plants in the landscape, the presence of flight corridors, habitat fragmentation and foraging routes ([Gaisler et al. 2009](#); [Medinas et al. 2013](#)), are poorly documented in Brazil. Despite these factors, bat species moving on the road may vary from region to region, indicating other differences in the structure of the local landscape ([Lesiński 2007](#); [Kerth and Melber 2009](#)).

Due to the lack of studies on collisions between vehicles and bats on the roads, the need to obtain data on mortality from being run over in different regions and landscapes is evident since the impact on natural populations can be severe and may cause a decline due to the cumulative effect of roadkills ([Lesiński et al. 2011](#); [Berthinussen and Altringham 2012](#); [de Figueiredo Ramalho et al. 2021](#)). In that regard, monitoring of the occurrence of collisions between vehicles and bats was carried out on a long stretch on the BR-040 highway in the period from 2008 to 2019, identifying the affected species and the points with the highest collision frequencies.

Materials and Methods

Study area. Data was collected on the BR-040 highway, which covers nine municipalities, from Rio de Janeiro to Juiz de Fora (Figure 1), accounting for 180.4 km. In the State of Rio de Janeiro, it goes from 0 km to 125.2 km, and in the State of Minas Gerais from 773.5 km to 828.7 km. Six municipalities are located in the state of Rio de Janeiro: Rio de Janeiro, Duque de Caxias, Petrópolis, Areal, Três Rios, Comendador Levy Gasparian, and three in the state of Minas Gerais: Simão Pereira, Matias Barbosa and Juiz de Fora. Along the studied stretch, the BR-040 highway crosses three Conservation Units of Atlantic Forest: Petrópolis Environmental Protection Area (APA Petrópolis), the Tinguá Biological Reserve (REBIO for Tinguá), and the Serra da Estrela Wildlife Refuge. The climate along the monitored highway is humid subtropical with a hot temperate summer and a dry winter, according to the Köppen classification, with precipitation concentrated in the summer, in an annual total that varies in the region between 1,300 and 2,200 mm ([Alvares et al. 2013](#)). We plot a final map with the critical areas of fatalities identified from analysis in Siriema software in the ArcGIS Desktop ([Ormsby et al. 2010](#)).

Monitoring and data collection. The data were compiled in the period from 2008 to 2019, and the stretches were travelled weekly at 40 km/h by two observers, in



Figure 1. BR-040, stretch from the municipality of Rio de Janeiro to Juiz de Fora.

addition to highway traffic inspectors monitoring 24 hours a day, seven days a week. The bats found dead were collected; when possible, they were identified at the lowest taxonomic level, stored in individual plastic bags, and frozen at the four User Service Centers. Subsequently, the specimens were sent to the Wild Animal Studies Center located at the Veiga de Almeida University, where they were prepared for deposition in the mammalogy section of the National Museum of Rio de Janeiro, a reference collection. Roadkill locations were georeferenced, and bats were photographed, sexed, measured, and identified more accurately in the laboratory. In this study, we included all individuals that could be identified within the order Chiroptera. Bats were identified with the help of identification keys provided by [Gardner \(2007\)](#), and [Reis et al. \(2017\)](#), and whenever necessary, identification was checked in the laboratory with available literature ([Gregorin and Taddei 2002](#); [Dias and Peracchi 2008](#); [Velazco et al. 2010](#); [Moratelli et al. 2013](#); [Cirranello et al. 2016](#)).

The collections of roadkill specimens were made under SISBIO License, Number: 30727-12. The use of these animals in this study complies with and is under the Operating License, Number: 1187/2013 and Authorization for Capture, Collection, and Transport of Biological Material - Abio (Renewal) No. 514/2014.

Data analysis. Siriema 2.0 software was used ([Coelho et al. 2014](#)) to identify the main stretches of significant groupings within a highway, the hotspots, and the analyses were 2D HotSpots and Ripley 2D K statistics. Ripley's K statistic describes the dispersion of data across a range of spatial scales ([Ripley 1981](#); [Levine 2004](#)). To define the different scales evaluated, we used an initial radius of 100 m and an increment of 400 m for each step. To assess the meaning of possible aggregations, we subtracted the observed K values from the average obtained in 1,000 simulations of random roadkill distributions for each step. The values above the 95% confidence limits obtained in the simulations indicate scales with significant aggregations ([Levine 2004](#); [Teixeira et al. 2013](#); [Coelho et al. 2014](#)). To find the critical hit-and-run points, we performed a two-dimensional analysis of the identification of the hotspots. Using an average of 1,000 simulations with a 95% confidence interval, we divided the highway into segments of 200 meters each ([Teixeira et al. 2013](#); [Coelho et al. 2014](#)).

Data on the number of individuals run over in each of the four years and comparing the seasons were tested for normality of residues, using the Shapiro-Wilk test and homoscedasticity of residues, using the Bartlett test. Having the data sets in which the assumptions of normality and homoscedasticity of the residuals were accepted, ANOVA (one way) was performed, and a BoxPlot was plotted to verify differences between the results obtained in the present study. The significance level used in the tests was 0.05%, and the R software was used to perform all the statistical tests ([R Core Team 2021](#)).

Results

A total of 923 roadkilled individuals of 57 species of bats were recorded. Five families (Table 1) were observed; amongst them, the Phyllostomidae ($n = 652$; 71%) and Vespertilionidae ($n = 204$; 22 %) were the most common roadkilled. The species with the highest collision frequency were *Artibeus lituratus* ($n = 216$; 23.4 %), *Glossophaga soricina* ($n = 61$; 6.61 %), *Carollia perspicillata* ($n = 55$; 5.96 %), *Platyrrhinus recifinus* ($n = 46$; 4.98 %), *Sturnira lilium* ($n = 41$; 4.44 %), *Platyrrhinus lineatus* ($n = 40$; 4.33 %), *Phyllostomus hastatus* ($n = 38$; 4.12 %), *Nyctinomops laticaudatus* ($n = 33$; 3.58 %), *Artibeus fimbriatus* and *Anoura caudifer* ($n = 31$; 3.36 %); other species had less than 20 records each, and 151 individuals (16.36 %) could only be identified to the order level.

Frugivores represented the most roadkills, represented by 19 species and 52.87 % of the total number of individuals; however, the greatest recorded richness was that of insectivores, represented by 24 species and 14 % of individuals roadkills. The nectarivores were represented by five species and 10.83 % of the total roadkill. The other trophic guilds were hematophagous, with two species, and carnivore, omnivore and piscivore, represented by one species each. These represent a total of 5.9 % of roadkill recorded in the study. In most of the specimens, it was not possible to identify sex and age; however, in those where it was possible, the male/female rate was similar, and most of them were adults (Table 1). Differences were observed in the frequency of bat collisions between the seasons. The highest mortality was documented in the fall with 330 (35.75 %) individuals killed in collisions, followed by 251 (27.19 %) in the summer, 217 (23.51 %) in the winter and 125 (13.54 %) in the spring. Considering the number of individuals run over in relation to the seasons and each monitoring year (2014, 2015, 2016, 2017, and 2018). According to the Shapiro-Wilk test, the data are normally distributed ($W = 0.98471$, $\alpha = 2$, $P = 0.8891$) and are homoscedastic according to the Bartlett test (2.1022 , $\alpha = 3$, $P = 0.5515$). Therefore, the data were submitted to the parametric ANOVA (One Way) test, where significant differences were observed between the data set of individuals hit by cars in relation to the seasons of the year in each monitored year ($F = 1.337$, $\alpha = 3$, $P = 0.297$). The BoxPlot showed a difference, in terms of the number of individuals run over, between the spring season and the other seasons of the year (Figure 2).

In the analyses to determine the scales in which road deaths were significantly aggregated in space, we found different aggregation points for bats. The stretch in the city of Rio de Janeiro, that cover less than 1 km, was the only one that had no record of bat's roadkills. The spatial distribution of roadkill along the BR-040 highway was not random, indicating that the records concentrated on some specific points along the highway. Many stretches had significant aggregations, with the most probable and most significant extension being located between the Duque de Caxias and Petrópolis kilometers. This most critical stretch begins at the ascent of the sierra of Petrópolis. Other peaks of signifi-

Table 1. Species of bats roadkill during the study and the number of collisions according to their age and sexual classification. Undefined sex = SexInd; Undefined age category = AgeInd. Conservation status for species at global level follows IUCN (2020). Data Deficiente (DD); Least Concern (LC); Near Threatened (NT); No identification (S/ID).

Family / Species	Female	Male	SexInd	Adult	Young	AgeInd	IUCN
Emballonuridae							
<i>Saccopteryx leptura</i>	0	0	1	1	0	0	LC
Phyllostomidae							
<i>Anoura caudifer</i>	6	6	19	16	0	15	LC
<i>Anoura geoffroyi</i>	1	1	1	1	0	2	LC
<i>Anoura</i> sp.	0	0	1	0	0	1	
<i>Artibeus cinereus</i>	1	0	2	1	0	2	LC
<i>Artibeus fimbriatus</i>	5	9	17	16	0	15	LC
<i>Artibeus lituratus</i>	43	50	123	105	4	107	LC
<i>Artibeus obscurus</i>	0	0	1	0	0	1	LC
<i>Artibeus planirostris</i>	0	1	0	1	0	0	LC
<i>Artibeus</i> sp.	0	0	17	8	0	9	
<i>Carollia perspicillata</i>	17	11	27	24	2	29	LC
<i>Chiroderma doriae</i>	3	1	2	3	0	3	LC
<i>Chiroderma</i> sp.	0	0	1	1	0	0	
<i>Chiroderma villosum</i>	1	2	1	2	0	2	LC
<i>Choeroniscus minor</i>	1	0	0	1	0	0	LC
<i>Chrotopterus auritus</i>	0	0	4	0	0	4	LC
<i>Desmodus rotundus</i>	2	2	5	6	0	3	LC
<i>Diphylla ecaudata</i>	0	1	1	1	0	1	LC
<i>Glossophaga soricina</i>	18	13	30	35	1	25	LC
<i>Lonchophylla peracchii</i>	0	1	2	1	0	2	LC
<i>Macrophyllum macrophyllum</i>	0	0	1	0	0	1	LC
<i>Micronycteris hirsuta</i>	0	0	1	1	0	0	LC
<i>Micronycteris megalotis</i>	1	1	0	2	0	0	LC
<i>Micronycteris microtis</i>	0	0	1	0	0	1	LC
<i>Micronycteris minuta</i>	1	0	0	1	0	0	LC
<i>Mimon bennettii</i>	2	2	1	4	0	1	LC
<i>Phyllostomus hastatus</i>	5	7	26	24	1	13	LC
<i>Platyrrhinus</i> sp.	0	0	1	0	0	1	
<i>Platyrrhinus lineatus</i>	12	4	24	17	0	23	LC
<i>Platyrrhinus recifinus</i>	10	8	28	20	1	25	LC
<i>Pygoderma bilabiatum</i>	1	2	10	3	0	10	LC
<i>Sturnira lilium</i>	9	8	24	16	3	22	LC
<i>Sturnira tildae</i>	0	0	3	0	0	3	LC
<i>Uroderma</i> sp.	0	0	1	0	0	1	
<i>Vampyressa pusilla</i>	5	1	1	5	0	2	DD
<i>Vampyrodes caraccioli</i>	1	0	0	1	0	0	LC
Noctilionidae							
<i>Noctilio leporinus</i>	1	0	0	1	0	0	LC
Molossidae							
<i>Eumops</i> sp.	0	0	1	0	0	1	
<i>Molossops neglectus</i>	1	0	0	0	0	1	DD
<i>Molossus molossus</i>	1	3	11	5	0	10	LC
<i>Molossus rufus</i>	1	0	5	1	0	5	LC
<i>Nyctinomops aurispinosus</i>	0	0	1	0	0	1	LC
<i>Nyctinomops laticaudatus</i>	1	4	28	18	0	15	LC
<i>Nyctinomops</i> sp.	0	0	5	2	0	3	
<i>Tadarida brasiliensis</i>	0	0	1	0	0	1	LC
Molossidae (unidentified)	0	0	2	2	0	0	

Table 1. Continuation...

Family / Species	Female	Male	SexInd	Adult	Young	AgeInd	IUCN
Vespertilionidae							
<i>Eptesicus brasiliensis</i>	1	1	3	3	0	2	LC
<i>Eptesicus diminutus</i>	1	0	0	1	0	0	LC
<i>Eptesicus</i> sp.	1	0	2	2	0	1	
<i>Histiotus velatus</i>	1	0	0	1	0	0	DD
<i>Dasypterus ega</i>	1	1	4	2	0	4	LC
<i>Myotis albescens</i>	0	0	1	1	0	0	LC
<i>Myotis izecksohni</i>	1	1	1	2	0	1	DD
<i>Myotis nigricans</i>	1	3	5	3	0	6	LC
<i>Myotis riparius</i>	2	0	2	1	0	3	LC
<i>Myotis ruber</i>	0	1	0	1	0	0	NT
<i>Myotis</i> sp.	0	0	16	4	0	12	
Vespertilionidae (unidentified)	0	0	3	0	0	3	
S/ID	0	1	150	27	1	123	
Total	159	146	618	394	13	516	

cant aggregations were observed between the kilometers of Três Rios and Comendador Levy Gasparian (Figure 3). The most critical points on the road, according to the analyses, were in the Atlantic Forest Biodiversity Corridor, which includes the Tinguá Biological Reserve, the Serra da Estrela State Wildlife Refuge and the APA Petrópolis (Figure 4).

Discussion

Bats are valuable indicators of biodiversity and ecosystem health, as a result of his sensitivity to fragmentation, that can decrease the richness and abundance of the order in altered areas (Reis *et al.* 2003; Alurralde and Díaz 2021). Thus, habitat fragmentation could be an aggravating factor in the seed dispersal process carried out by Chiroptera species. Despite the relative richness and abundance observed during the monitoring of the current study, these values can be related to the time and

size of the sample. However, still can be underestimated for the region due to the limitation of the study that only recorded species found dead by collisions. Species richness during this monitoring was similar to other studies in southeastern Brazil (Dias and Peracchi 2008; Esbérard and Bergallo 2008; Tavares *et al.* 2010; Perini *et al.* 2014), yet, we observed a high variation between the richness and diversity of these studies, which is probably due to differences in capture techniques, such as the use of mist nets or active search for shelters in areas with landscape mosaic varying from conserved to degraded environments (Dias and Peracchi 2008; Esbérard and Bergallo 2008; Tavares *et al.* 2010; Perini *et al.* 2014; Alurralde and Díaz 2021), and differences in collision probabilities by bat species in the present study.

Frugivore bats are usually the most frequent group in collisions with vehicles on the roads, according to our data and other studies on South America (Pinheiro and Turci 2013; Ceron *et al.* 2017; Valadão *et al.* 2018; de Figueiredo Ramalho *et al.* 2021), where frugivores are more representative (Fenton *et al.* 1992; Martins *et al.* 2014). Species as *Artibeus lituratus*, *Carollia perspicillata*, and *Sturnira lilium* are not inhibited by fragmentation and are more abundant in disturbed areas than other bat species (Medellín *et al.* 2000; Reis *et al.* 2003; Alurralde and Díaz 2021). However, these species have been most affected by collisions with vehicles on the roads (Pinheiro and Turci 2013; Ceron *et al.* 2017; Valadão *et al.* 2018; de Figueiredo Ramalho *et al.* 2021). These species have been considered abundant in the study region (Dias and Peracchi 2008; Tavares *et al.* 2010; Luz *et al.* 2011), and have characteristics that make them good indicators of damaged areas, providing advantages for plants whose fruits are consumed by them, is a key factor for dispersion and genetic flow of plants in regions affected by fragmentation (Muller and dos Reis 1992; Reis *et al.* 2003; Bianconi *et al.* 2006).

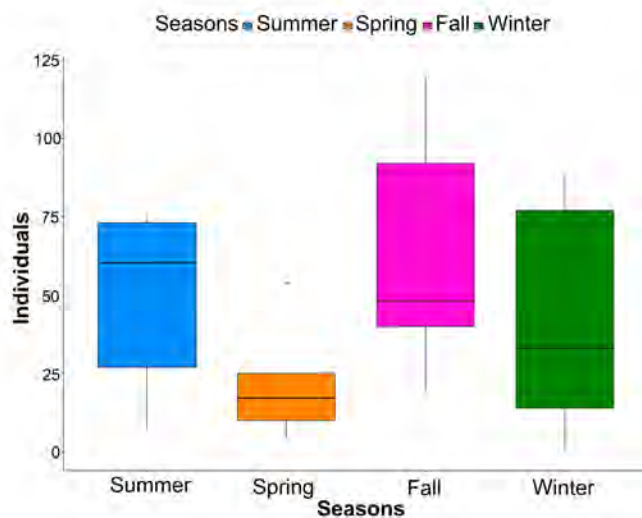


Figure 2. Boxplot (median with upper and lower quartiles) of the number of individuals of bats killed in collisions by season of the year on highway BR-040.

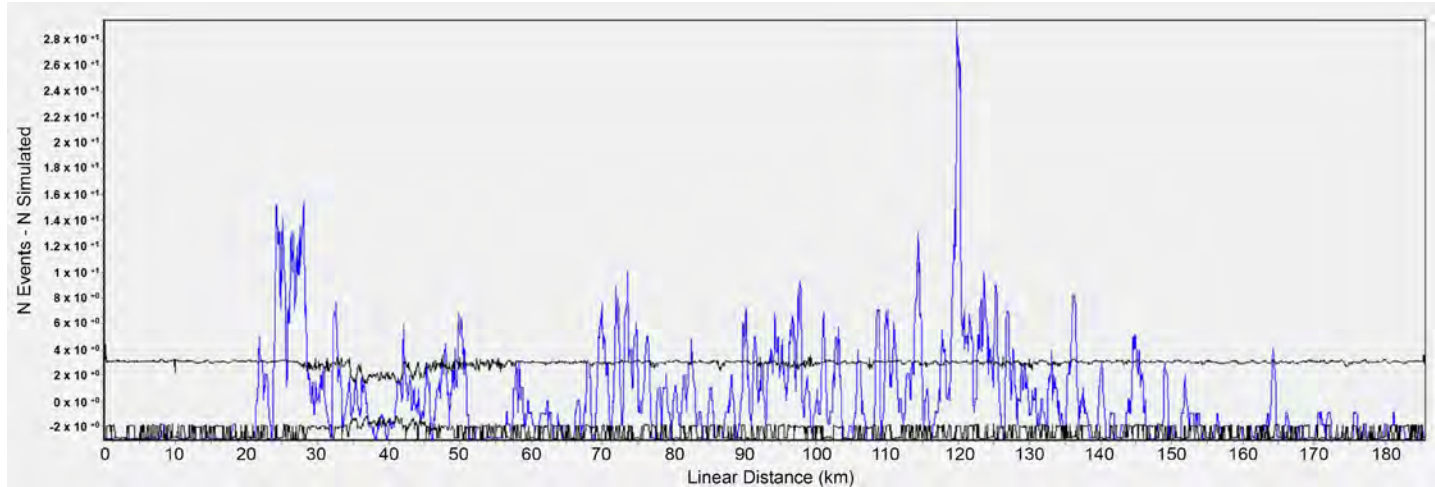


Figure 3. Bat roadkill aggregation intensity (blue line) and 95% confidence limits (black line) along 180.4 km of BR-040.

This higher rate of collisions with frugivores bats is probably due to some associated factors, such as flight height, displacement patterns in foraging, the temporal and spatial distribution of the fruits and the plants, as well as the landscape structure (Bernard and Fenton 2003; Clevenger *et al.* 2003; Bianconi *et al.* 2006; Gumier-Costa and Sperber 2009; Pracucci *et al.* 2012; Gomes *et al.* 2020). An essential factor is that many of these frugivorous species are consumers of pioneer plants, which are usually found in large densities in degraded areas, such as the vicinity and edges of roads (Muller and dos Reis 1992; Reis *et al.* 2003). The species most impacted by the collisions on BR-040, *Artibeus lituratus*, was also the most abundant in studies in the south-eastern region (Esbérard and Bergallo 2008; Tavares *et al.* 2010; Luz *et al.* 2011; Perini *et al.* 2014). Although roadkills did not show marked seasonal trends, fewer bat collisions were documented during the spring. Moreover, there is evidence of the difference in the number of collisions by bats in the seasons (Lesiński *et al.* 2011), but little is known about the factors that can influence the number of roadkills by these species, needing further investigations.

Different species of bats can be impacted differently by the fragmentation of habitats resulting from a road network. Some factors may be contributing to this difference in the amount of roadkill by bat species, such as foraging strategies, diet, or resilience of species in degraded areas (Kalko *et al.* 1996; Stone *et al.* 2009; Bhardwaj *et al.* 2017; Claireau *et al.* 2019), and need be investigated. Rare species can potentially be affected even by small mortality rates (Fensome and Mathews 2016; Damásio *et al.* 2021). In the present study, many insectivores considered rare were found roadkilled. The study by Bhardwaj *et al.* (2021) pointed out that the activity of seven of ten insectivorous bats species decreased significantly within the proximity of a highway due to changes created in the surrounding environment by traffic, such as pollution, light, noise, and vibrations. The authors called the surrounding environment a “road effect zone,” and in this area, the habitat is degraded or entirely unsuitable for wildlife, which leads to an indirect loss of habitat (Bhardwaj *et al.* 2021).

One of the stretches identified in this study as a highly significant hotspot is in an area of Atlantic Forest in the municipality of Petrópolis, a region inserted in the APA Petrópolis, the Serra da Estrela State Wildlife Refuge, and close to the Biological Reserve (REBIO) of Tinguá. Twenty-eight species of bats have been registered in REBIO so far, the most abundant being *C. perspicillata*, *S. liliium*, and *A. lituratus* (Dias and Peracchi 2008), also the most frequently recorded in the present study. We highlight the species *Myotis ruber*, which had a run-over record close to the REBIO area, and which is listed as almost threatened with extinction in the IUCN Red List (IUCN 2020). The most critical points were on the stretch that crosses Tinguá Biological Reserve, highlighting the need for more urgent conservation measures in this region. However, the simple counting of carcasses found on the roads is an underestimation of the actual rate of bats killed by being run over. Even in regular monitoring, some factors may influence this count. Bat carcasses can be completely destroyed by continuous vehicle traffic, some can be thrown off the road and lost in the vegetation, and some individuals could be removed by other animals for consumption (Pracucci *et al.* 2012; Cunha *et al.* 2015; Ramalho and Aguiar 2020).

The roads that cross parks and forest reserves can have an extremely negative impact, a barrier to the natural movement of the species, and establishing a population decline, as well as decreasing the genetic flow for the wildlife of these regions (Samson *et al.* 2016). Critically, bat collisions with vehicles have been observed mainly in these areas where endangered and endemic bat species occur (Lesiński 2007). Moreover, these regions also harbor other wild species, thus making roadkills more critical for the conservation of species (IUCN 2020). Efforts to mitigate these accidents in the region are carried out with wildlife warning signs, yet these had not shown been proved effective. Roads are already proven to be harmful to many wild animals (Trombulak and Frissell 2000; Fahrig and Rytwinski 2009; Gumier-Costa and Sperber 2009), and there are several approaches that can be used to reduce the effects of

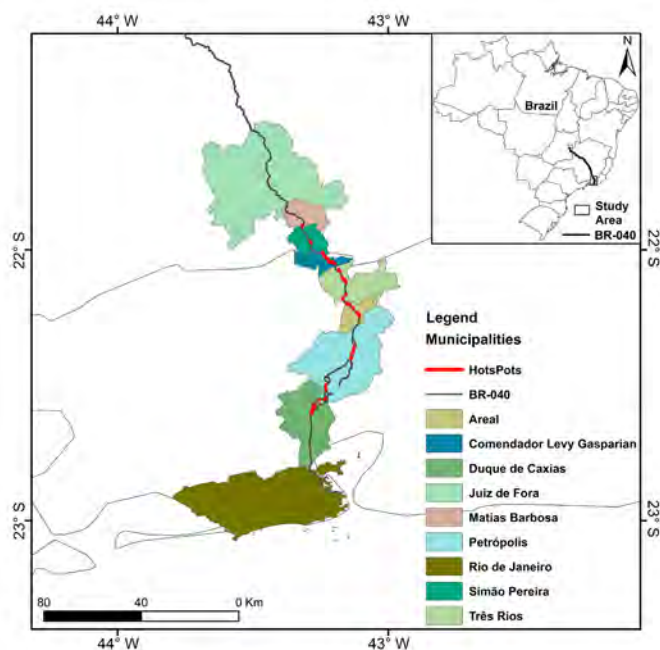


Figure 4. The sections marked in red indicate the critical areas of fatalities (HotSpots) identified from monitoring of run over bat fauna, analysis in Siriema software.

roads and mortality in wild animal populations (Jackson 2000; Glista *et al.* 2009). The use of underpasses and ecological bridges for wild fauna probably varies from species to species, depending on their behavior in terms of movement (Berthiusen and Altringham 2012; Bhardwaj *et al.* 2017). However, a combination of monitoring and ecological bridges has shown great effectiveness in decreasing roadkill rates (Bhardwaj *et al.* 2017).

Our results suggest that bats are particularly vulnerable to the impact of roads. Consequently, they may take a long time to recover from disturbances due to their low fertility, longevity, and foraging activity in large areas of the landscape (Findley 1993). Roads can affect the amount of area available to wildlife habitat, particularly through the fragmentation, and also affect the quality of this area by traffic of vehicles that cause collisions and deaths of wild animals (Bafaluy 2000; Bueno *et al.* 2015; de Figueiredo Ramalho *et al.* 2021). Other factors that influence this mortality are the lack of proper signs and awareness of drivers who travel on these highways. Hybrid mitigation is applied to reduce the adverse effects of roads on wildlife and comply with environmental legislation. These mitigations should account for several species, considering the broad diversification of habits showed by bats (Bernard and Fenton 2003; Bianconi *et al.* 2006; Gomes *et al.* 2020), and their sensitivity to increased lighting, which can change their activity pattern (Stone *et al.* 2009; Appel *et al.* 2017; Gomes *et al.* 2020). We suggest speed bumps construction to reduce the speed limit, install bridges, and signaling the presence of wildlife on the stretches identified as hotspots in our analyses, that is, with a higher risk of collision for these species of bats.

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Evidence of the genetic and spatial structure of *Nasua narica* in Central America and northern South America from mitogenomic analysis

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Carnivores are extremely important in ecosystem dynamics. Coatis (Procyonidae) are a group of Neotropical species with highly developed social behavior. One coati species is the Central American or white-nosed coati (*Nasua narica*). This work describes the analysis of two sets of mitochondrial data for a sample of *N. narica* covering most of the geographic distribution range of the species. The first data set analyzed 74 specimens for three mitochondrial loci; the second, 59 specimens for complete mitochondrial genomes. Our phylogenetic analyses revealed six distinct genetic groups of *N. narica* in southern México, Central America, and South America, which, together with three additional groups found in northern México and southern USA in a previous study, resulted in a total of nine genetically distinct groups of *N. narica*. The first genetic group (G1), which began to differentiate 4.1 to 3.2 million years ago, was located on the Pacific coast of Ecuador and northern Colombia. A second genetic group (G6) was detected in northern Colombia, Panama, and southern Costa Rica, being introgressed by mitochondrial DNA from the mountain coati (*Nasuella olivacea*). The third genetic group (G3) was located in Costa Rica, Nicaragua, El Salvador, Honduras, and southern Guatemala. The fourth genetic group (G4) was located in north-central Guatemala and Belize. The fifth genetic group (G5) was distributed in southern México (Chiapas, Tabasco, Campeche, Quintana Roo, and Yucatán) and northern Guatemala. Finally, the sixth genetic group (G2) was found only in Mérida (Yucatán, México). Groups G2 to G5 became mitochondrially diversified over 1.9 to 1.1 million years. All groups showed high mitochondrial genetic diversity, although the South American genetic group (G1) had the highest diversity. The northern genetic groups (G4, G5) had lower genetic diversity, except for the Merida group, which is likely composed of other undetected subgroups. The existence of six (nine, considering another study) well-developed groups in *N. narica* is related to female philopatry and climatic changes during the Pleistocene. A spatial autocorrelation analysis showed a very high structure, well in line with the south-to-north colonization of the American continent by *N. narica*.

Los carnívoros son extremadamente importantes en la dinámica de los ecosistemas. Los coatíes (Procyonidae) son un grupo de especies neotropicales con un comportamiento social muy desarrollado. Una especie de coatí es el coatí centroamericano o de nariz blanca (*Nasua narica*). Este trabajo describe el análisis de dos conjuntos de datos mitocondriales para una muestra de *N. narica* que cubre la mayor parte del rango de distribución geográfica de la especie. El primer conjunto de datos analizó 74 especímenes para tres loci mitocondriales; el segundo, 59 especímenes para genomas mitocondriales completos. Nuestros análisis filogenéticos revelaron seis grupos genéticos distintos de *N. narica* en el sur de México, América Central y América del Sur, que, junto con tres grupos adicionales encontrados en el norte de México y el sur de EE. UU. en un estudio anterior, dieron como resultado un total de nueve genéticamente distintas grupos de *N. narica*. El primer grupo genético (G1), que comenzó a diferenciarse hace 4,1 a 3,2 millones de años, se ubicó en la costa del Pacífico de Ecuador y el norte de Colombia. Un segundo grupo genético (G6) fue detectado en el norte de Colombia, Panamá y el sur de Costa Rica, siendo introgresado por ADN mitocondrial del coatí de montaña (*Nasuella olivacea*). El tercer grupo genético (G3) se ubicó en Costa Rica, Nicaragua, El Salvador, Honduras y el sur de Guatemala. El cuarto grupo genético (G4) se ubicó en el centro-norte de Guatemala y Belice. El quinto grupo genético (G5) se distribuyó en el sur de México (Chiapas, Tabasco, Campeche, Quintana Roo y Yucatán) y norte de Guatemala. Finalmente, el sexto grupo genético (G2) se encontró únicamente en Mérida (Yucatán, México). Los grupos G2 a G5 se diversificaron mitocondrialmente durante 1,9 a 1,1 millones de años. Todos los grupos mostraron una alta diversidad genética mitocondrial, aunque el grupo genético sudamericano (G1) presentó la mayor diversidad. Los grupos genéticos del norte (G4, G5) tuvieron menor diversidad genética, excepto el grupo Mérida, que probablemente esté compuesto por otros subgrupos no detectados. La existencia de seis (nueve, considerando otro estudio) grupos bien desarrollados en *N. narica* está relacionada con la filopatría femenina y los cambios climáticos durante el Pleistoceno. Un análisis de autocorrelación espacial mostró una estructura muy alta, en línea con la colonización de sur a norte del continente americano por *N. narica*.

Keywords: Coati; mitochondrial genes; *Nasua* sp.; phylogeography; Pleistocene; population genetics; spatial patterns.

Introduction

Regardless of the time when North and South America became connected in geological times and the physical substrate that was established in Central America (islands, isthmus of Panama, etc.) for the Great American Biotic Exchange (GABI), the orographic, biotic, biogeographical, and climatological complexity of the zone (southern North America, Central America, and northern South America) is of such diversity and magnitude that evolutionary processes in this area, including diversification and speciation, have occurred at a high speed (Marshall 2007; Hardy et al. 2013). Therefore, the evolutionary study of the species with a broad distribution range in this geographic area can reveal essential information for understanding the colonization, adaptation, diversification, and speciation processes of migrant organisms between previously separate continents (Webb 2006; Morgan 2008).

A species that meets these characteristics is the white-nosed coati (*Nasua narica* Linnaeus 1766, Order Carnivora, Family Procyonidae) since it has a wide distribution from North America to northern South America (González-Maya et al. 2011). The evolutionary and biogeographical history of procyonids is controversial from the molecular and paleontological perspectives (Soibelzon and Prevosti 2013; Nigenda-Morales et al. 2019; Ruiz-García et al. 2019b, 2020a). In fact, procyonids are one of the taxonomic groups that can provide surprising insights into how and when GIBA occurred (Koepfli et al. 2007; Forasiepi et al. 2014).

Nasua narica is distributed from Arizona and New Mexico (USA) through Central America, including the Pacific coast of Colombia, Ecuador, and northern Peru (Emmons 1990; Emmons and Feer 1997; Tirira 2007, 2011). However, Gompper (1995) excluded the Ecuadorian and Peruvian Pacific areas because this author considered that *Nasua nasua* lives there. Although Gompper (1995) excluded *N. narica* from the South American mammal fauna, other authors, such as those previously mentioned, and the results of the present study postulate the existence of *N. narica* in northwestern South America, which is why we used South American specimens of this species.

Nasua narica is a strongly gregarious species that forms social groups including up to 30 females and juveniles per group, while males tend to be solitary and are the only ones to disperse after reaching sexual maturity (Gompper 1997; Gompper et al. 1997, 1998). On the other hand, females are strongly philopatric and frequently do not disperse outside the area where they were born (Valenzuela and Ceballos 2000). This species potentially participates in controlling small-sized pests such as rodents and arthropods, besides being a seed disperser and a potential prey for large cats such as jaguar (*Panthera onca*) and puma (*Puma concolor*) (Gompper 1995, 1997).

Four subspecies have been recognized according to body size, differences in coat color, and cranial characteristics (Hershkovitz 1951; Hall 1981; Decker 1991; Gompper

1995). These differences may be related to geographic barriers and ecological differences (Hershkovitz 1951). The four subspecies are: 1) *N. n. molaris* (Merriam 1902; Type locality: Manzanillo, Colima, México), distributed from the north of the Trans-Mexican Volcanic Belt to Arizona and New Mexico USA; 2) *N. n. narica* (Linnaeus 1766; Type locality: "America", restricted to Achotal, Isthmus of Tehuantepec, Veracruz, México), distributed south of the Trans-Mexican Volcanic Belt to south Panama; 3) *N. n. nelsoni* (Merriam 1901; Type locality: Cozumel Island, Quintana Roo, México), distributed exclusively in the type locality; and 4) *N. n. yucatanica* (Allen 1904; Type locality: Chichen Itzá, Yucatán, México), confined to the Yucatán Peninsula. McFadden et al. (2008) designated the insular subspecies as a different species (*N. nelsoni*) based on a morphometric analysis.

To date, only two works have analyzed the genetic structure of *N. narica*. The first, by Silva-Caballero et al. (2017), used a fragment of 800 base pairs (bp) of the mitochondrial gene (mt) *Cyt-b* and 12 nuclear microsatellites in 60 specimens from five different populations in México (Nayarit, Jalisco, Morelos, Tabasco, and Quintana Roo). Moderate and high levels of genetic diversity were found for both types of molecular markers (mitochondrial: haplotypic diversity, $H_d = 0.968$; microsatellites: expected heterozygosity, $H_e = 0.774$). A total of 22 haplotypes were detected in the five areas analyzed, and each of the populations with unique haplotypes, except for three haplotypes shared between the two geographically closest populations (Puerto Morelos, Quintana Roo, and La Venta, Tabasco). Both genetic markers clearly separated the five populations studied and identified a strong genetic structure between them, suggesting isolation by distance.

The second study was conducted by Nigenda-Morales et al. (2019) with sequences of three mt genes (*Cyt-b*, *NAD5*, and *16S rRNA*) and 11 nuclear microsatellites in 85 specimens from Arizona and New Mexico (USA), México (Jalisco, Morelos, Yucatán, and Cozumel Island), Belize, Guatemala, Costa Rica, and Panama. They found a strong genetic structure with five distinct Evolutionary Units (EU). The southernmost (Panama) was the most differentiated EU, with genetic distances between 9.9 % and 10.8 % from the other four EU, and which appeared 3.8 million years ago (Ma). A second EU consisted of specimens from Costa Rica, Guatemala, Belize, Cozumel Island, and Yucatán (México). A third EU included specimens from Morelos (central México), while the fourth EU included specimens from Jalisco (western México); finally, the fifth EU comprised specimens from southwest USA. The diversification of this group was calculated to have occurred 1.2 Ma. The genetic flow took place from south to north and from east to west.

The present study used two sets of mitochondrial genes (three loci: *ND5*, *Cyt-b*, and *D-loop*; and complete mitogenomes) analyzed in 74 and 59 specimens, respectively, of *N. narica* sampled in México, Belize, Guatemala, Honduras, El Salvador, Nicaragua, Costa Rica, Panama, Colombia, and Ecuador. We focused on mtDNA to expand the scope

of previous results with a larger number of data (mitogenomes) and samples of specimens from South America that clearly belong to this species because of their external morphology (phenotype). It is also possible to compare our results with those of [Nigenda-Morales et al. \(2019\)](#) since the present study included Colombia and Ecuador, whereas the study referred to was limited to northern Mesoamerica.

Mitochondrial DNA genes allow reconstructing phylogenetic relationships to determine recent intra- or inter-specific genetic divergence processes, while nuclear genes reveal deeper relationships ([Collins and Dubach 2000, 2001](#); [Cortés-Ortiz et al. 2003](#); [Ruiz-García et al. 2016](#)). In fact, mtDNA has been extremely effective for detecting new groups or taxa that had been left out with other techniques ([Krause et al. 2010](#); [Derenko et al. 2012](#); [Sawyer et al. 2015](#)). Mitochondrial genes have high mutation accumulation rates, short coalescence times, absence of introns and recombination, and haploid inheritance ([Avise et al. 1987](#)). In addition, although they represent a single linked locus, the selection pressure and evolutionary rates are heterogeneous, depending on the genes considered ([Nabholz et al. 2012](#)). An additional advantage is that the number of mtDNA copies per cell is high, thus making it easier to obtain sequences and mitogenomes from low-quality samples (teeth, hair, skin, etc.; [Guschanski et al. 2013](#)). However, caution should be exercised with mtDNA because gene trees do not always match species trees ([Freeman and Heron 1998](#)). Also, mtDNA only shows the evolution of female lineages, so hybridization events produced by males as vectors of gene flow go unnoticed ([Burrell et al. 2009](#)).

Therefore, considering that this work covers the broadest distribution range analyzed to date for *N. narica* and that, for the first time, complete mitogenomes are analyzed for this species, the objectives are to 1) determine the number of lineages in *N. narica* throughout its geographic range, and whether the putative morphological subspecies described for *N. narica* match the molecular groups detected; 2) estimate genetic heterogeneity among these groups and the ancestor-descendant relationship between them; 3) determine the relationship of historical geographic, geological, and climatological events to the divergence times found in the genetic groups of *N. narica*; 4) estimate the levels of genetic diversity within them; and 5) determine significant patterns of spatial structure throughout the area analyzed.

Materials and Methods

Sample collection. We analyzed 74 specimens of *N. narica* from México ($n = 25$), Guatemala ($n = 21$), Belize ($n = 3$), Honduras ($n = 7$), El Salvador ($n = 3$), Nicaragua ($n = 1$), Costa Rica ($n = 3$), Panama ($n = 1$), Colombia ($n = 4$), Ecuador ($n = 5$), and Robinson Crusoe Island (Chile; $n = 1$, Figure 1 and Supplementary Table 1). Eight specimens of *Nasuella olivacea* from Colombia were used as an external group, as well as 29 specimens of *Nasua nasua* from Colombia ($n = 4$), Ecuador ($n = 5$), Perú ($n = 11$), Bolivia ($n = 3$), and Brazil ($n = 6$). For mitogenomes, there were 59 specimens from

México ($n = 21$), Guatemala ($n = 14$), Belize ($n = 3$), Honduras ($n = 7$), El Salvador ($n = 3$), Nicaragua ($n = 1$), Costa Rica ($n = 3$), Panama ($n = 1$), Colombia ($n = 2$), Ecuador ($n = 3$), and Robinson Crusoe Island (Chile) ($n = 1$). Samples of six specimens of *N. olivacea* from Colombia were used as an external group, as well as 23 specimens of *N. nasua* from Colombia ($n = 4$), Ecuador ($n = 2$), Peru ($n = 10$), Bolivia ($n = 3$), and Brazil ($n = 4$).

The samples come from specimens hunted by indigenous communities and road-killed animals in southern México, and Central and South America (fragments of skin, teeth, and hairs with bulbs). Permission to collect biological materials was requested from the authorities of the communities (in addition to the corresponding ministries). During the sampling process, hunters from the local communities were interviewed to determine the exact source of the samples; these were usually collected within 5 to 15 kilometers of the interview site. Samples were gathered over 22 years (1996–2018).

DNA extraction, amplification, and sequencing. DNA extraction from skin and muscle samples was performed using the phenol-chloroform procedure ([Sambrook et al. 1989](#)). DNA from follicle hairs and teeth was extracted with Chelex 100 resin (Bio-Rad, Hercules, California, USA) using the protocol of [Walsh et al. \(1991\)](#), while the DNA from bones was extracted with the DNeasy Blood and Tissue Kit (Qiagen, Hilden, Germany). These procedures were used for all three mitochondrial loci. Three mt loci were amplified: 1) 407 bp of the *Cyt-b* gene ([Irwin et al. 1991](#)), 2) 1,800 bp of gene *ND5* ([Trigo et al. 2008](#)), and 3) 306 bp from the *D-loop* region ([Hoelzel et al. 1994](#)). The total sequenced length was 2,513 bp.

We used the PCR (Polymerase Chain Reaction) in a final volume of 25 μL : 2 μL of 1 mM MgCl_2 (CorpoGen), 1 μL of 0.2 mM dNTPs (BioLabs), 1 μL of 0.1 mM of each primer, one Taq Polymerase Unit (CorpoGen), 100–200 ng of DNA template (in 2–4 μL of DNA), 2 μL of 10X Buffer, and 14–16 μL of double-distilled H_2O . The PCR temperatures for gene amplification were 95 $^\circ\text{C}$ for 5 minutes, followed by 40 cycles at 94 $^\circ\text{C}$ for one minute: 52 $^\circ\text{C}$ (*Cyt-b*), 55 $^\circ\text{C}$ (*ND5*), and 56 $^\circ\text{C}$ (*D-loop*) for one minute, 72 $^\circ\text{C}$ for one minute, and a final extension at 72 $^\circ\text{C}$ for ten minutes. The amplification products, including positive and negative controls, were run on a 2 % agarose gel stained with ethidium bromide and visualized with ultraviolet light on a transilluminator. Both directions were sequenced using BigDye Terminator v3.1 (Applied Biosystems, Inc., Foster City, California, USA), whose products were analyzed on an ABI 3730 sequencer (Applied Biosystems, Inc., Foster City, California, USA). The sequences were assembled and edited with Sequencher 4.7 (Gene Codes, Corp., Ann Arbor, Michigan, USA).

Nucleotide sequences of the mt*ND5* and *Cyt-b* genes were translated into amino acid sequences to exclude the possibility of nuclear mitochondrial DNA segments (Numts; [Lopez et al. 1994](#)). All amino acid translations performed showed correct start and stop codons, and a total absence

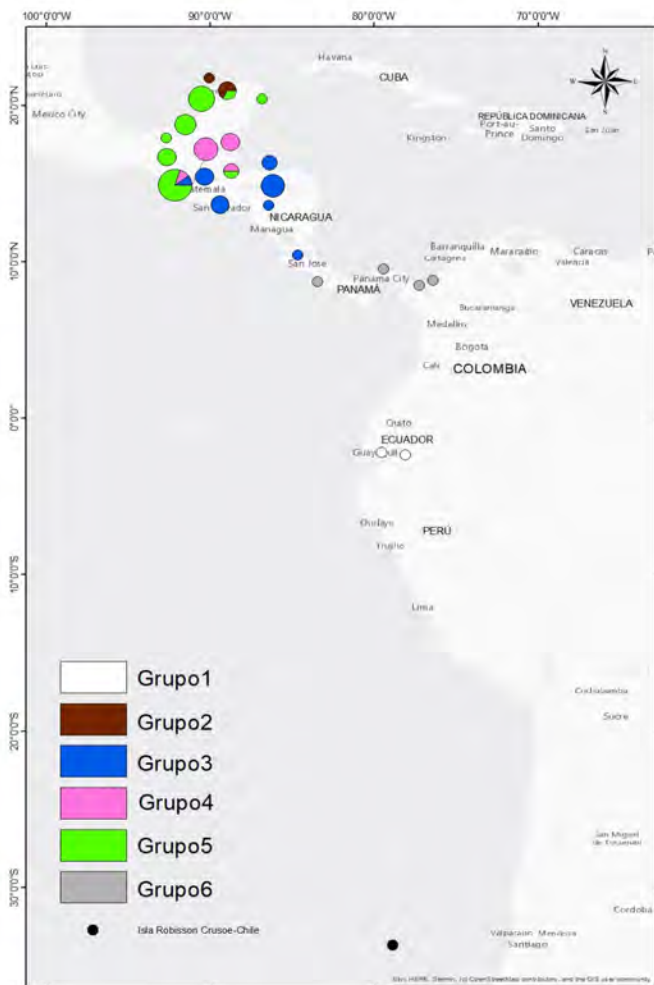


Figure 1. Map of Central America and northern South America where 74 specimens of white-nosed coati (*Nasua narica*) were sampled for three mitochondrial genes (*ND5*, *Cyt-b*, and *D-loop*), 59 of which also sampled for the complete mitogenomes. Circles are proportional to the sample size. The colors of circles mark the different molecular groups detected and are the same colors shown in phylogenetic trees and the haplotype network.

of termination codons. All the mutations observed were synonymous, which is well-related to the absence of Numts in the two mt genes mentioned.

For the mitogenomic analysis, DNA was extracted and isolated from the tissues mentioned above using the QIAamp DNA Micro Kit (Qiagen, Inc. Hilden, Germany) according to the manufacturer's protocol. Mitogenomes were sequenced by "long-template PCR", which minimizes Numts amplification (Thalmann *et al.* 2004; Raaum *et al.* 2005). The PCRs to obtain mitogenomes were performed with the LongRange PCR Kit (Qiagen, Inc. Hilden, Germany), with a reaction volume of 25 μ L. The components of each reaction were 2.5 μ L of 10x LongRange PCR Buffer, 500 mM of each dNTP, 0.6 mM of each primer, 1 unit of LongRange PCR Enzyme, and 100–250 ng of DNA template. The temperature conditions of the PCRs were 94 $^{\circ}$ C for 5 min, followed by 45 cycles of 94 $^{\circ}$ C for 30 s, with an annealing temperature of 50–57 $^{\circ}$ C (depending on the primer set) for 30 s and an extension of 72 $^{\circ}$ C for 8 min. Afterward, there were 30 denaturation cycles at 93 $^{\circ}$ C for 30 s, with annealing temperatures of 45–52 $^{\circ}$ C (depending on the primer set) for

30 s, and an extension of 72 $^{\circ}$ C for 5 min, with a final extension of 72 $^{\circ}$ C for 8 min. Four sets of primers were used to generate overlapping amplicons: PROCYONID1F (ATGAG-TAATCAGCCCTTGAT) and PROCYONID1R (ATGCATCCAC-GTCAATCAT), approximately 5,000 bp; PROCYONID2F (AAGTAATATGTCTGACATAA) and PROCYONID2R (TCATCT-GCATCTATTCTGA), approximately 4,000 bp, PROCYONID3F (CATTTAGAAGCTAATTAAGC) and PROCYONID3R (GTG-CAACTCGAAATAAATGT), approximately 4,000 bp; PROCYONID4F (TAATTGTAATAAAGCTATTT) and PROCYONID4R (TGGCACATCTCGATGGAGTA), approximately 3,200 bp. These allowed observing the circularity of the mitochondrial genome (Bensasson *et al.* 2001; Thalmann *et al.* 2004). Both DNA strands were sequenced directly using BigDye Terminator v3.1 (Applied Biosystems, Inc., Foster City, California, USA). The sequencing products were analyzed in an ABI 3730 DNA Analyzer system (Applied Biosystems, Inc., Foster City, California, USA). The sequences were assembled and edited with the Sequencher 4.7 program (Gene Codes, Corp., Ann Arbor, Michigan, USA). The overlapping regions were examined for possible irregularities, such as termination codons. The absence of such irregularities is a valid indication of the absence of Numts. Genes were concatenated (about 16,200 bp) after removing any problematic region with the Gblocks 0.91 program (Talavera and Castresana 2007) under a relaxed approach. Individual alignments were concatenated with SequenceMatrix v1.7.6 (Vaidya *et al.* 2011) to create the final alignment.

The sequences were deposited in the NCBI GenBank under access numbers MT587713-MT587788, MW410859-MW410914, and MW419814-MW419853.

Phylogenetic analyses. The sequences were concatenated for phylogenetic analyses of the three mt loci studied because they showed the same phylogenetic signal. To this end, we used the ILD test ("Incongruence-length difference test"; Farris *et al.* 1995) in the mILD program (Planet and Sarkar 2005). The programs jModeltest v2.0 (Darriba *et al.* 2012) and MEGA 6.05 (Tamura *et al.* 2013) were applied to determine the best nucleotide substitution model, using the Akaike information criterion (AIC; Akaike 1974) and the Bayesian information criterion (BIC; Schwarz 1978).

A Maximum Likelihood (ML) analysis was performed as phylogenetic inference using the RAxML v.7.2.6 program (Stamatakis 2006) with the partition scheme selected by the PartitionFinder 2.0 program (Lanfear *et al.* 2012). This program was used to simultaneously determine the optimal model for nucleotide substitution (which coincided with that of jModeltest v2.0) and sequence partition scheme. For partitions, codons 1 + 2, and codon 3 were combined for each gene (for both *Cyt-b* and *ND5* in the case of the data set with three loci and for each of the coding genes in the mitogenomic case. Additionally, RNA genes were included in the mitogenomic analysis and the control region for both data sets). The best-fit models were selected using BIC under a 'greedy' search scheme with a subset of models specific to RAxML. The GTR + G + I model

(Tavaré 1986) was used for the ML tree search, as discussed in the *Results* section. The support for nodes was estimated using the “rapid-bootstrapping” algorithm with 1,000 non-parametric bootstrap replicates (Stamatakis *et al.* 2008). Clades were considered to have good nodal support when bootstrap values were greater than 70 % (loose limit; Hillis and Bull 1993).

The relationships between the haplotypes found were determined using the Median Joining Network algorithm (MJN; Bandelt *et al.* 1999) of the Network 4.6 program (Fluxus Technology Ltd). One advantage of MJN over phylogenetic trees is that it explicitly allows the coexistence of ancestral and descendant haplotypes, while phylogenetic trees treat all sequences as terminal taxa (Posada and Crandall 2001). This allows identifying which haplotypes were the first to originate and which are the most recently derived haplotypes (Freeland *et al.* 2011). Divergence times were calculated with the p statistic (Morral *et al.* 1994) and its standard deviation (Saillard *et al.* 2000) since this statistic can be transformed into years. This statistic is unbiased and highly independent of past demographic events. This approach is called a “borrowed molecular clock” and directly uses the nucleotide substitution rates estimated in other taxa (Pennington and Dick 2010). For the set of three mt genes, we used an evolutionary rate of 1.75 % per million years, representing one mutation every 22,742 years. For all mitogenomic data, the evolutionary rate used was 2.34 % per million years, equivalent to one mutation every 2,638 years. These evolutionary rates were reported for the family Canidae (Wayne *et al.* 1997). In the present work, this methodology was used to estimate divergence times as previous studies (Ruiz-García *et al.* 2020a, 2021a, b) have used Bayesian inference methods to investigate the divergence between the species of *Nasua*, *Nasuella*, and *Bassaricyon*. However, the use of the MJN is preferable because the present study preferably analyzed the divergence times within *N. narica*, and there is a scarce fossil record for coatis. In fact, there are no fossil remains attributable to either *N. narica* or *Nasuella*, and those attributable to *N. nasua* do not exceed 0.125 MYA (Woodburne 2010), which significantly underestimates all studies of divergence times within procyonids (Koepfli *et al.* 2007; Nigenda-Morales *et al.* 2019; Ruiz-García *et al.* 2019b, 2020a, 2021a, b).

Genetic heterogeneity and diversity. The statistics H_{ST} , K_{ST} , K_{ST}^* , γ_{ST} , N_{ST} and F_{ST} (Hudson *et al.* 1992) were calculated to determine the global genetic heterogeneity among the six genetic groups of *N. narica* detected with the phylogenetic methods used for both the set of three mt loci and the mitogenomic set. Indirect estimates of the genetic flow between the six genetic groups were obtained assuming an infinite island model (Wright 1965). Statistical significance was estimated using a permutational test with 10,000 replicates. Additionally, genetic heterogeneity and genetic flow statistics were estimated in pairs for the six groups detected. To this end, the F_{ST} statistic was used with

Markov chains with 10,000 dememorization parameters, 20 batches, and 5,000 iterations per batch. All analyses were carried out using the DNAsp 5.1 (Librado and Rozas 2009) and Arlequin 3.5.1.2 (Excoffier and Lischer 2010) programs.

We estimated the number of haplotypes (NH), haplotypic diversity (H_d), nucleotide diversity (π), and the statistic \emptyset per sequence in the DNAsp 5.1 program (Librado and Rozas 2009) for the total sample and for each of the six genetic groups detected by the phylogenetic analyses.

Spatial autocorrelation analysis. A total of four spatial analyses were applied to the set of three mt loci and three to the set of mitogenomes. The first analysis was a Spatial Analysis of Molecular Variance (SAMOVA) with the SAMOVA 1.0 program (Dupanloup *et al.* 2002) to assess the spatial structure in a geographic context. This program seeks to define geographically homogeneous groups of populations and maximize differentiation with other geographic groups. This would potentially facilitate the identification of genetic barriers between population groups. The method is based on a simulated annealing procedure that helps maximize the proportion of total genetic variance due to differences between population groups. We analyzed the number of different populations (k ; from two to six), and the statistical significance was estimated with 1,000 permutations.

The second analysis was isolation by distance with the Mantel test (Mantel 1967) performed in the Alleles In Space 1.0 (AIS) program (Miller 2005). The matrix of genetic distances of the Kimura two-parameter model (Kimura 1980) between the different individuals of *N. narica* sequenced was compared with the matrix of Euclidean geographic distances between them. Statistical significance was estimated with 10,000 permutations.

The third procedure was a spatial autocorrelation analysis using the A_y statistic with AIS 1.0 (Miller 2005). This can be interpreted as the average genetic distance between pairs of individuals falling within a particular distance class (DC). A_y takes a value of 0 when all individuals within a DC are genetically identical and a value of 1 when all individuals within a DC are completely different. The probability for each DC was obtained using 10,000 permutations. To carry out this analysis, we defined 10 DCs constructed using DCs of identical size (in km) with unequal sample size per DC for the set of three mt loci (DC 1: 0–183 km; DC 2: 183–366 km; DC 3: 366–549 km; DC 4: 549–732 km; DC 5: 732–915 km; DC 6: 915–1,098 km; DC 7: 1,098–1,281 km; DC 8: 1,281–1,464 km; DC 9: 1,464–1,647 km; DC 10: 1,647–1,831 km), and 10 DCs constructed with unequal CDs but with approximately the same sample sizes per DC for mitogenomic data (DC 1: 0–26 km; DC 2: 26–83 km; DC 3: 83–183 km; DC 4: 183–270 km; DC 5: 270–337 km; DC 6: 337–381 km; DC 7: 381–547 km; DC 8: 547–730 km; DC 9: 730–1,089 km; DC 10: 1,089–2,298 km). The specimens were connected to the Gabriel and Sokal network (Gabriel and Sokal 1969) and other types of networks (Ruiz-García 1993, 1994, 1997, 1999; Ruiz-García and Álvarez 2000).

The fourth analysis was the Monmonier algorithm (Monmonier 1973; MMDA) with the AIS 1.0 program (Miller 2005). This geographic regionalization method was used to detect putative geographic barriers to gene flow by iterative identification of contiguous sets of high genetic distances across connectivity networks (Doupanloup et al. 2002; Manel et al. 2003; Manni et al. 2004). The Delaunay triangulation was used (Watson 1992; Brouns et al. 2003) to generate the connectivity network between sampling points. A graphic representation of the putative geographic barriers inferred by the algorithm was overlaid on the connectivity network to facilitate the detection of likely geographic obstacles reflected in the sequence data. In this case, the procedure was used to identify the five most important possible putative geographic barriers for the set of three mt loci.

Results

Phylogenetic analysis for three mitochondrial loci and for complete mitogenomes. The optimal nucleotide substitution models for the set of three mt loci were TN93 + G for CIA (-Ln = 11,861.36) and GTR + G + I for CIB (-Ln = 17,332.27); for the mitogenomic set, the optimal nucleotide substitution model was GTR + G + I for CIA (-Ln = 55,535.88) and TN93 + G for CIB (-Ln = 63,912.52). For the phylogenetic analyses, we used the GTR + G + I model since it was one of the two optimal models in all cases and is a model implemented in the programs used.

In the ML tree (Figure 2) with three mt loci, the *N. nasua* clade had good nodal support and was the sister group of the other clades (Bootstrap Support, BS = 100). An interesting finding is the inclusion in this clade of three specimens that *a priori* would correspond to *N. narica* based on their phenotype and geographic origin. The first is a specimen from Robinson Crusoe Island (Chile). The other two specimens were collected in northern Colombia. In both cases, the analysis with three mt genes showed that they were highly related (BS = 95). The remaining clades found in *N. nasua* were already analyzed in detail by Ruiz-García et al. (2021a).

The clade of *N. olivacea* also had high nodal support (BS = 95) and was the sister group of *N. narica*; this may be considered evidence that the genus *Nasuella* could be included in the genus *Nasua* (Ruiz-García et al. 2021b). On the other hand, a group of five specimens of *N. narica* distributed in southern Costa Rica, Panama, and northern Colombia (Antioquia and Choco) — the typical distribution of *N. narica* — with an undoubted morphotype of this species, nested within the *N. olivacea* clade. This group (BS = 72), which we named G6, has a mitochondrial DNA clearly introgressed by *N. olivacea*.

The *N. narica* group was monophyletic (BS = 74) and was composed of five distinct genetic groups. The first (G1; BS = 79) comprised two specimens from the trans-Andean (Pacific) part of Ecuador (Guayas province). The second group (G2; BS = 97) is composed of two specimens sam-

pled in Yucatán (México). The third genetic group (G3; BS = 81) is formed by specimens sampled in northern Costa Rica, Nicaragua, El Salvador, Honduras, and southern Guatemala. It should be noted that an Ecuadorian Amazonian specimen with the phenotype of *N. narica* (Macas, province of Morona-Santiago) was included in this clade. The fourth group (G4; BS = 91) consisted of specimens distributed in the northwestern part of Guatemala and Belize; however, two specimens from the Pacific coast of Ecuador (Guayas province) were also included in this group. Finally, the fifth genetic group (G5; BS = 90) comprised specimens from northwestern Guatemala and southern México, with specimens from Quintana Roo (including Cozumel Island), Campeche, Chiapas, Tabasco, and Yucatán.

The ML tree (Figure 3) with mitogenomic data was similar to the previous one, with minor differences. *Nasua nasua* was the sister clade of all others (BS = 87). The specimen from Robinson Crusoe Island (Chile) was included in this taxon. Contrary to the ML tree calculated with three mt loci, one specimen of *N. narica* from central-northern

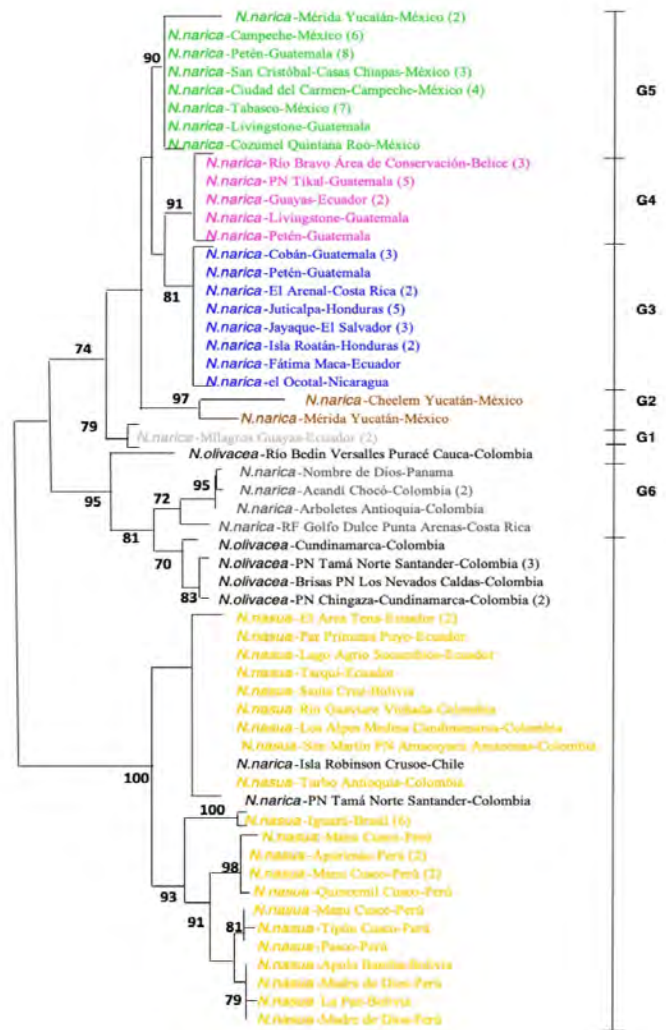


Figure 2. Maximum Likelihood Tree showing the phylogenetic relationships of 74 specimens of white-nosed coati (*Nasua narica*) for three mitochondrial genes (*ND5*, *Cyt-b*, and *D-loop*). The mountain or Andean coati, *Nasuella olivacea*, and the South American coati, *Nasua nasua*, were used as external groups. Numbers on nodes are bootstrap percentages greater than 70%. The number of specimens sampled in a given locality is shown in parenthesis.

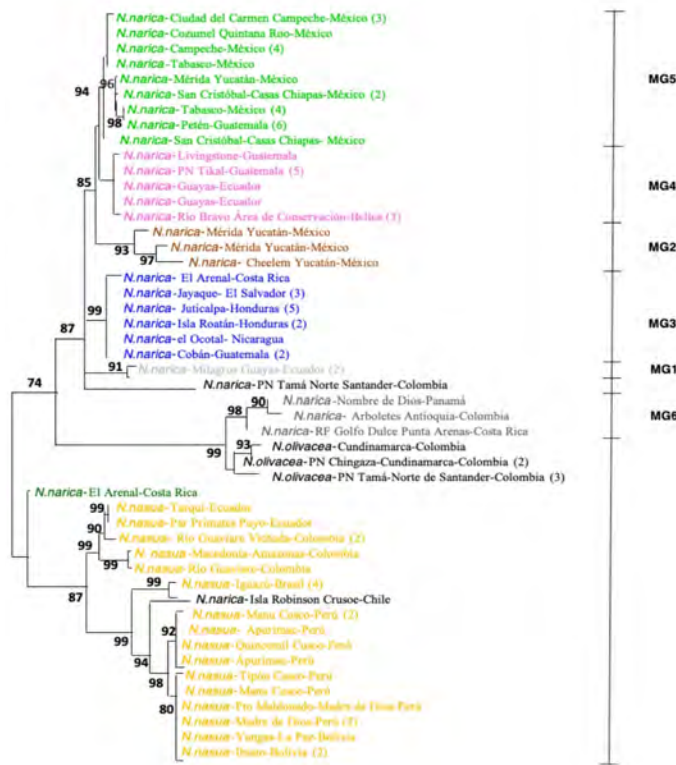


Figure 3. Maximum Likelihood Tree constructed with the complete mitogenomes of 59 specimens of white-nosed coati (*Nasua narica*). The mountain or Andean coati (*Nasuella olivacea*) and the South American coati (*Nasua nasua*) were used as external groups. Numbers on nodes are bootstrap percentages greater than 70%. The number of specimens sampled in a given locality is shown in parenthesis.

Costa Rica was shown to be the most divergent within the *N. narica* clade. The *N. olivacea* clade (BS = 99) was the sister group of *N. narica* (BS = 87); it included the genetic group (MG6) of *N. narica* (BS = 98), with which the complete mitogenomes confirmed the genetic introgression of one group of *N. olivacea* in the distribution range of *N. narica* in southern Central America and northern Colombia. In the present tree, the specimen from PN Tamá (North of Santander, Colombia) forms a polytomy with the genetic groups MG1 (BS = 91) and MG3 (BS = 99). This was followed by the subsequent divergence of groups MG2 (BS = 93; in this case, a third specimen from the Yucatán Peninsula was added, which had been included in G5 in the previous tree), MG4 (BS = 85), and MG5 (BS = 94).

The haplotype network (Figure 4) for the set of three mt loci showed that the earliest ancestral *N. narica* haplotypes would have derived from *N. nasua* haplotypes; these specimens already displayed the distinctive phenotype of *N. narica* and with haplotypes very close to one of the external groups. These were found in the trans-Andean and Pacific zones of Ecuador (H2 and H4), along with the haplotype of the specimen from the Ecuadorian cis-Andean (Amazon) zone (H3) that had been included in G3 in the phylogenetic trees for the three mt loci. In other words, the first *N. narica* (with explicit phenotypes of this species) with haplotypes already differentiated from those of *N. nasua* and closer to the Central American *N. narica* are found in Ecuador, in the

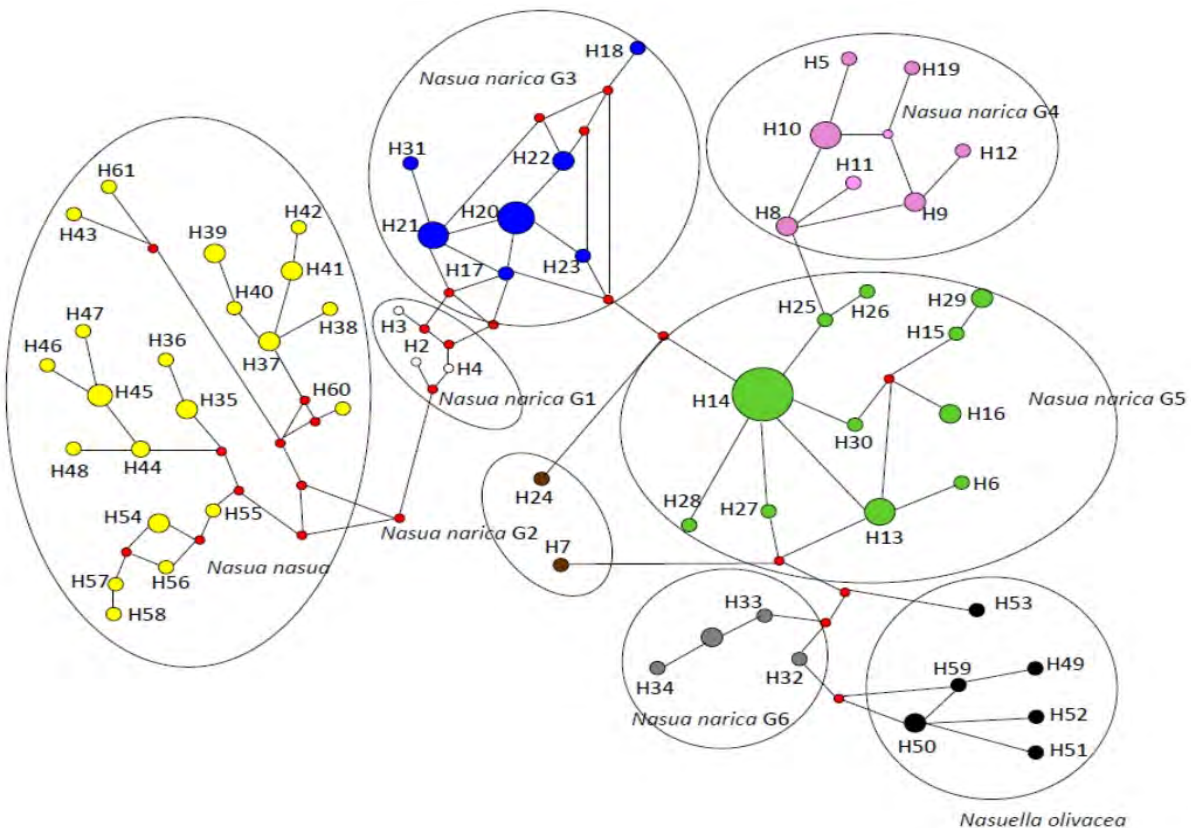


Figure 4. Median Joining Network procedure applied to the haplotypes found in 74 specimens of white-nosed coati (*Nasua narica*) for three mitochondrial genes (*NDS*, *Cyt-b*, and *D-loop*). The haplotypes of eight mountain or Andean coatis (*Nasuella olivacea*) and 29 South American coatis (*Nasua nasua*) were used as external groups. White = haplotypes of G1 specimens; brown = haplotypes of G2 specimens; blue = haplotypes of G3 specimens; pink = haplotypes of G4 specimens; light green = haplotypes of G5 specimens; gray = haplotypes of G6 specimens; black = haplotypes of *N. olivacea* specimens; yellow = haplotypes of *N. nasua* specimens; small red circles indicate intermediate haplotypes that were not found.

trans-Andean and cis-Andean areas (G1). From this group (haplotypes that were gradually differentiated from the external group), G3 would have emerged, distributed in the south-central zone of Central America, with H20 occupying the central position in the analysis (El Salvador, Honduras, and southern Guatemala). G5 would have later derived from G3, with H14 at the central position in the analysis (northern Guatemala and México, including Chiapas, Tabasco, Campeche, and part of Yucatán). G4 derived from G5 (northwestern Guatemala and Belize, although these groups also included haplotypes from the trans-Andean zone of Ecuador). Finally, G6 clearly showed that it was introgressed by *N. olivacea*, as reflected by phylogenetic trees. In this network of haplotypes, G2, clearly visible in the trees mentioned above, does not form a well-consolidated group. One haplotype (H24) appears as derived from a non-sampled haplotype between G3 and G5, and another haplotype (H7) appears as derived from G5.

Divergence times within and between N. narica groups. For the matrix of three mt loci, using the MJN, the time elapsed for the G1 haplotype to give rise to all the Central American haplotypes derived from it was 4.06 ± 0.93 million years ago (Mya). On the other hand, for the mitogenomic data set, the divergence between the intermediate haplotype of the *N. narica* specimen from central-northern Costa Rica and all other Central American haplotypes detected occurred 3.16 ± 0.34 Mya. The time elapsed since G1 gave rise to the first G3 haplotype was estimated at 2.20 ± 0.27 Ma for the set of three mt loci and 1.21 ± 0.02 Mya between the intermediate Costa Rican haplotype and the first MG3 haplotype, respectively. The time of divergence since the G3 generated all the other northernmost haplogroups in Central America was 1.93 ± 0.54 Mya and the time between the G3 haplotype and the emergence of G5 from it was 1.07 ± 0.30 Mya. The same divergence times with mitogenomic data were 0.82 ± 0.15 Mya and 0.36 ± 0.01 Mya, respectively. The time elapsed since G5 gave rise to the first G4 haplotype was estimated at 0.12 ± 0.27 Mya for the set of three mt loci and 0.09 ± 0.02 Mya for the mitogenomic set, respectively. Additionally, the time of divergence between the nearest *N. narica* haplotypes and the *N. narica* haplotypes introgressed by *N. olivacea* was 4.4 ± 0.15 Mya for the set of three mt loci and 2.34 ± 0.08 Mya for the mitogenomic set, respectively. Finally, the temporal separation between the present *N. olivacea* haplotypes and those of G6 (MG6) (*N. narica* introgressed by the latter species) was 2.32 ± 0.34 Mya for the set of three mt loci and 0.73 ± 0.08 Mya for the mitogenomic data. In general, for most estimates, the divergence times estimated with mitogenomic data are shorter than those estimated with the set of three mt loci. Additional divergence times are shown in Table 1.

Genetic heterogeneity and diversity within and among Nasua narica groups. The analysis of genetic heterogeneity for the six genetic groups of *N. narica* detected from phylogenetic analyses for the matrix of three mt loci showed a significant global genetic differentiation ($\gamma_{ST} = 0.734$, $p <$

0.0001 ; $F_{ST} = 0.658$, $p < 0.0001$; Table 2). The global genetic flow estimates showed low values among these groups, taken globally ($Nm_{\gamma_{ST}} = 0.18$; $Nm_{F_{ST}} = 0.26$). The same analysis including only the four Central American groups (excluding G1 and G6) also showed high and significant values ($\gamma_{ST} = 0.599$, $p < 0.0001$; $F_{ST} = 0.496$, $p < 0.0001$; Table 2), and genetic flow estimates were also low ($Nm_{\gamma_{ST}} = 0.33$; $Nm_{F_{ST}} = 0.51$). These results are consistent with the mitogenomic data ($\gamma_{ST} = 0.755$, $p < 0.00001$; $F_{ST} = 0.775$, $p < 0.00001$; Table 2), with low genetic flow values ($Nm_{\gamma_{ST}} = 0.16$; $Nm_{F_{ST}} = 0.14$).

The analysis of paired genetic heterogeneity of genetic groups with data from three mt loci showed that all comparison pairs were significant (Table 3), except for the pair G1 vs. G2 ($p = 0.331$). The highest genetic flow was estimated between G1 and G2 ($Nm = 0.504$) and the lowest between G3 and G6 ($Nm = 0.038$; Table 4). The mitogenomic data showed similar results. The only pair of groups with a nonsignificant difference was between MG1 and MG2 ($p = 0.103$; Table 3). The highest estimate of genetic flow was between the pair of groups MG1 and MG2 ($Nm = 0.578$) and the lowest between G5 and G6 ($Nm = 0.021$; Table 4). Therefore, there is very high genetic heterogeneity among the six groups detected with phylogenetic methods.

The levels of global genetic diversity for both three-loci-based data and mitogenomic data (Supplementary Table 2) are high. By group, G1 (MG1), G2 (MG2), and G6 (MG6) showed the highest levels of genetic diversity for both the three-loci mt matrix and the mitogenomic matrix. The groups that showed the lowest levels of genetic diversity were G3 and G5 for both the data with three mt loci and mitogenomic data.

Spatial structure in N. narica. With the three mt loci, the maximum differentiation was observed between four groups ($F_{CT} = 0.702$, $p < 0.0001$), i. e., G6, G1, G2, and the set of G3, G4, and G5. With mitogenomes, the maximum differentiation occurred between two groups ($F_{CT} = 0.817$, $p < 0.0001$), namely, between MG6 and all the other groups of *N. narica*, regardless of their geographic location (Supplementary Table 3).

Table 1. Divergence times within the different groups of white-nosed coati (*Nasua narica*) detected through its geographic distribution range in Central America and northern South America. A) Based on three mitochondrial genes (*ND5*, *Cyt-b*, and *D-loop*); B) based on complete mitogenomes. SD = Standard Deviation. Time in millions of years.

Groups of <i>Nasua narica</i>	Divergence Times \pm SD
A	
Within G1	2.99 ± 0.69
Within G3	0.25 ± 0.11
Within G4	0.49 ± 0.18
Within G5	0.60 ± 0.13
Within G6	2.47 ± 0.77
B	
Within MG1	1.34 ± 0.16
Within MG3	0.15 ± 0.04
Within MG4	0.41 ± 0.09
Within MG5	0.12 ± 0.03
Within MG6	0.37 ± 0.09

Table 2. Statistics of genetic heterogeneity and gene flow comparing simultaneously the different groups of white-nosed coati (*Nasua narica*) detected in Central America and northern South America. A) Based on three mitochondrial genes (*ND5*, *Cyt-b*, and *D-loop*) for six different groups (four in Central America and two in northern South America); B) based on three mitochondrial genes (*ND5*, *Cyt-b*, and *D-loop*) for four groups in Central America; C) based on mitogenomes for all groups detected. ** $p < 0.01$, df = degrees of freedom. Nm = Gene Flow statistic. Nm^1 = Gene flow obtained with the γ_{ST} statistic; Nm^2 = gene flow obtained with the N_{ST} statistic; Nm^3 = gene flow obtained with the F_{ST} statistic.

Genetic Heterogeneity and gene flow statistics	Values	Probabilities
A		
χ^2	360.000 $df=165$	0.00001**
H_{ST}	0.1732	0.00001**
K_{ST}	0.6718	0.00001**
K_{ST}^*	0.5162	0.00001**
Z_S	492.11	0.00001**
Z_S^*	5.8609	0.00001**
S_{nn}	0.9563	0.00001**
γ_{ST}	0.7344	0.00001**
N_{ST}	0.6689	0.00001**
F_{ST}	0.6578	0.00001**
Nm^1	0.18	
Nm^2	0.25	
Nm^3	0.26	
B		
χ^2	195.000 $df=81$	0.00001**
H_{ST}	0.1651	0.00001**
K_{ST}	0.5269	0.00001**
K_{ST}^*	0.4456	0.00001**
Z_S	465.6	0.00001**
Z_S^*	5.8262	0.00001**
S_{nn}	0.967	0.00001**
γ_{ST}	0.5995	0.00001**
N_{ST}	0.4963	0.00001**
F_{ST}	0.4956	0.00001**
Nm^1	0.33	
Nm^2	0.51	
Nm^3	0.51	
C		
χ^2	996.000 $df=240$	0.00001**
H_{ST}	0.0112	0.00069**
K_{ST}	0.7068	0.00001**
K_{ST}^*	0.3718	0.00001**
Z_S	2262.6	0.00001**
Z_S^*	5.211	0.00001**
S_{nn}	0.9464	0.00001**
γ_{ST}	0.755	0.00001**
N_{ST}	0.7862	0.00001**
F_{ST}	0.7755	0.00001**
Nm^1	0.16	
Nm^2	0.14	
Nm^3	0.14	

The results of the Mantel test were significant for the matrices of three mt loci and mitogenomes. In the first case, geographic distance significantly explained 30.59 % of the genetic distances between the specimens analyzed ($r =$

0.553, $p = 0.00009$); in the second, geographic distance significantly explained 23.81 % of genetic distances ($r = 0.488$, $p = 0.0014$). In general, evidence of isolation by distance was detected in the geographic distribution of *N. narica*.

The spatial autocorrelation analysis showed evidence of spatial structure. For the matrix with three mt loci, the global correlogram was statistically significant ($V = 0.0361$, $p < 0.000001$). The first two distant classes (DCs) showed a significant positive spatial autocorrelation (DC 1: $p = 0.000001$; DC 2: $p = 0.000001$). This indicates that in areas around 360 km in diameter there are specimens more genetically similar to each other than expected at random. From DC 6, all spatial autocorrelation values were significantly negative (DC 6: $p = 0.0021$; DC 7: $p = 0.0026$; DC 8: $p = 0.0001$; DC 9: $p = 0.0003$; DC 10: $p = 0.0002$). That is, from 1,098 km to 1,831 km, genetic differentiation progressively increased. Similar results were obtained with mitogenomic data. The overall correlogram was statistically significant ($V = 0.0146$, $p < 0.0008$), with the first six DCs showing a significant positive spatial autocorrelation (DC 1: $p = 0.00001$; DC 2: $p = 0.026$; DC 3: $p = 0.0175$; DC 4: $p = 0.0338$; DC 5: $p = 0.000001$; DC 6: $p = 0.0365$). This indicated a strong genetic similarity between specimens geographically separated by a distance of about 380 km between them. This value is very similar to the one reported above for the first spatial autocorrelation analysis. DCs 9 and 10 yielded a significant negative spatial autocorrelation (DC 9: $p = 0.0071$; DC 10: $p = 0.0023$). That is, genetic differentiation increased from 729 km to 2,297 km. Therefore, both analyses show a clear monotonic cline in northern South America and Central America.

The analysis with the Monmonier algorithm (Figure 5) was performed for only three mt loci. The first barrier detected differentiated the geographic area corresponding to G6 specimens introgressed by *N. olivacea*. The second barrier demarcated a geographic area correlated with the area where part of the G4 specimens are interspersed (Belize) with part of the G5 specimens (Cozumel Island and part of Yucatán). The third barrier bordered the geographic area corresponding to G2 specimens (Yucatán). The fourth barrier delimited the geographic area that included G1 specimens (Ecuadorian Pacific). The fifth barrier marked the geographic area that was aligned with the trans- and cis-Andean zones of Ecuador but with specimens more genetically related to the Central American group G3. The geographic structure of *N. narica* in Central America and northern South America is very pronounced.

Discussion

Systematics of N. narica. This article reports the population phylogeographic and genetic analysis encompassing the broadest geographic extension of the distribution range of *N. narica* to date and uses complete mitogenomes for this species for the first time. From a strictly systematic standpoint, this analysis provides new evidence for the re-interpretation of the systematics of this species.

The genetic distances between the different *N. narica* groups found are smaller than those observed in *N. nasua* (Ruiz-García *et al.* 2020a, 2021a). The values ranged from 1.6 % to 4.5 %, typical of well-differentiated populations or subspecies (Kartavtsev 2011). This is consistent with the fact that the ancestor of the present *N. narica* is considerably more recent than the ancestor of the present *N. nasua*, which, in turn, shows that the mitochondrial evolution of coatis occurred in South America in the first place and then in Central America. This conclusion contrasts with the traditional paleontological view that the current coatis migrated from North to South America in the early Pleistocene. The arrival of the first procionids in South America produced endemic forms (Argentina) such as *Cyonasua* and *Chapalmalania* (Soibelzon and Prevosti 2013) around 7.3 Mya. However, paleontologists consider that these procionids became extinct and did not give rise to the present *Nasua*. They are considered to have arrived in South America in a second migratory wave of procionids during GABI 4 (Woodburne 2010), which occurred during the Lujanense (126,000–8,500 before present, BP) and Platense (8,500–1,500 BP) ages. However, *N. nasua* haplotypes started to differentiate *in situ* in northwestern South America some 13–10 Mya (Ruiz-García *et al.* 2020a, 2021a, b), preceding the diversification of *N. narica* haplotypes (also in northwest South America) 4.1–3.2 Mya. These findings indicate a south-to-north migration of the current coatis, opposite to the direction suggested by paleontologists.

Four morphological subspecies of *N. narica* have been considered in recent decades (Gompper 1995): *N. n. molaris*, *N. n. nasua*, *N. n. nelsoni*, and *N. n. yucatanica*. In particular, *N. n. nelsoni* has been considered a full species (*N. nelsoni*). However, the present study showed at least six genetically distinct groups.

The first group (G1, MG1) is distributed in northwestern South America. We have detected haplotypes of this group in the Ecuadorian Pacific and, in the mitogenomic study, also in one specimen from northern Colombia (PN Tamá, North of Santander). Traditionally, the coatis of the trans-Andean and Pacific Colombian and Ecuadorian areas have been classified as *N. narica* (Emmons 1990; Emmons and Feer 1997; Tirira 2007, 2011); however, some authors (Gompper 1995; Nowak 1999) suggest that the coati living in the Pacific area of Colombia and Ecuador is *N. nasua* based on its morphological traits.

Our research showed that some of those specimens might be intermediate forms between *N. nasua* and *N. narica*. The specimens in this group from the Ecuadorian Pacific had external phenotypes (coloration and fur pattern) typical of *N. narica*. However, Ruiz-García *et al.* (2021a) observed that most specimens with the *N. narica* phenotype in the trans-Andean and Pacific areas of Ecuador had the mitochondrial haplotypes typical of *N. nasua*. The study also detected specimens in the Ecuadorian Pacific with intermediate morphotypes between *N. nasua* and *N. narica*. That study also showed that the *N. narica* haplotypes of the Ecuadorian Pacific and North Santander (Colombia) had originated from an *N. nasua* haplotype distributed in the Colombian and Ecuadorian Amazon. One specimen from the Colombian Pacific (not included in this study; Buenaventura, Valle del Cauca) with an intermediate phenotype between *N. narica* and *N. nasua* showed inconclusive results according to different molecular analyses performed (Ruiz-García *et al.* 2021a). In fact, in the present study, we detected one specimen of PN Tamá (located in an area where *N. nasua* and *N. narica* allegedly converge), which, despite having the distinct *N. narica* morphotype, resembled *N. nasua* in the analysis with three mt genes (not so in the mitogenomic analysis). The analysis with three mt genes also included one specimen (Turbo, Antioquía, Colombia; border area between Colombia and Panama) with a morphotype closer to *N. nasua* but within a distribution area typical of *N. narica*. The analysis based on three mt loci associated this specimen with the previous specimen within the *N. nasua* clade. Unfortunately, that specimen could not be sequenced for its complete mitogenome because of the poor quality of its DNA. However, there is evidence on the Pacific coast of Ecuador and Colombia, and in northern Colombia, of specimens with a full *N. narica* morphotype and with mitochondrial haplotypes intermediate between *N. nasua* and Central American *N. narica*, albeit closer to the latter. Ruiz-García *et al.* (2020a, 2021ab) showed that the haplotypes of *N. nasua* and *N. olivacea* diverged in South America before those of *N. narica*. The

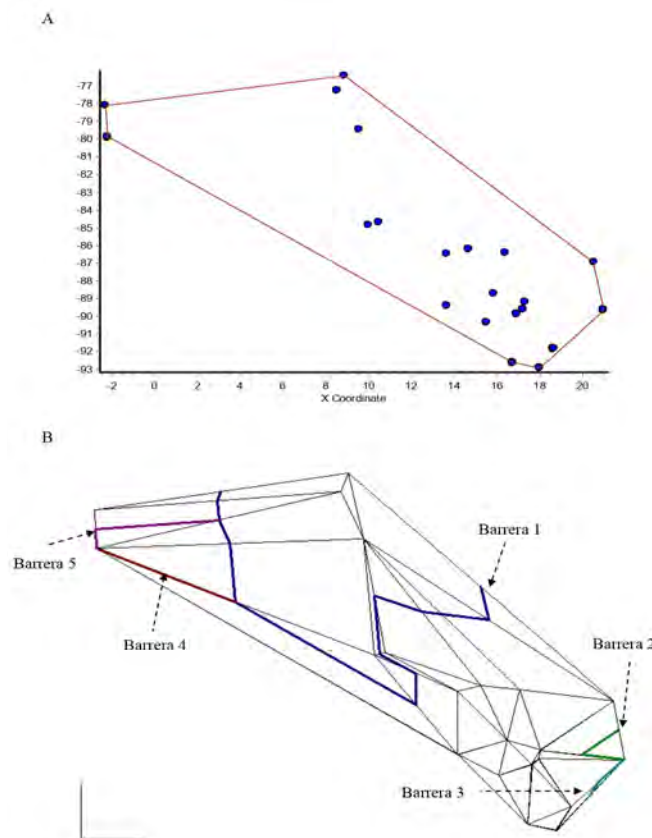


Figure 5. Analysis of the Monmonier algorithm to detect the five most important geographic barriers in the geographic distribution range of the samples of white-nosed coati (*Nasua narica*) analyzed from Central America and northern South America. A) Geographic area analyzed; B) Geographic barriers for 74 specimens of *N. narica* sequenced for three mitochondrial genes (*ND5*, *Cyt-b*, and *D-loop*).

Table 3. F_{ST} statistic for paired groups of white-nosed coati (*Nasua narica*) analyzed in Central America and northern South America. Below the diagonal, based on three mitochondrial genes (*ND5*, *Cyt-b*, and *D-loop*) (G); above the diagonal, based on mitogenomes for all groups detected (MG). * $p < 0.05$; ** $p < 0.01$.

Groups of <i>Nasua narica</i>	G1 (MG1)	G2 (MG2)	G3 (MG3)	G4 (MG4)	G5 (MG5)	G6 (MG6)
G1 (MG1)		0.463	0.786**	0.564*	0.803**	0.910
G2 (MG2)	0.498		0.734**	0.629**	0.723**	0.823
G3 (MG3)	0.822**	0.833**		0.697**	0.723**	0.952**
G4 (MG4)	0.771**	0.788*	0.764**		0.578**	0.928**
G5 (MG5)	0.817**	0.834**	0.652**	0.615**		0.960**
G6 (MG6)	0.849*	0.810*	0.928**	0.912*	0.735*	

existence of intermediate haplotypes between *N. nasua* and *N. narica* are particularly well-detected in the haplotype networks of the Ecuadorian Pacific and northern Colombia.

The case of the assumed *N. narica* from Robinson Crusoe Island in the Chilean Pacific might represent a hybridization event. In the 1950s, a couple of Germans introduced coatis to fight rodent pests on the island. The morphology of these island animals matches *N. narica*. However, this study, together with that of [Ruiz-García et al. \(2021a\)](#), showed that the mtDNA of that specimen behaved like *N. nasua*. The coatis introduced to those islands likely came from the Ecuadorian Pacific with the typical phenotype of *N. narica* but with the mtDNA of *N. nasua* that characterizes part of the coatis inhabiting the Pacific slope of Ecuador.

The problem with *N. narica* from Ecuador and Colombia is that they have not been assigned a sub-specific denomination because it has recently been considered that this species is not present in the Pacific zone of these two countries. It would be very important to perform morphological and molecular analyses of the *N. nasua* holotypes or paratypes described for the trans-Andean and Pacific areas of Ecuador. The holotype described for this Ecuadorian area was first named *N. nasua manium* ([Thomas 1912](#)), but a more recent paratype was also described for the same area, *N. nasua gualeae* ([Lönnberg 1921](#); Type locality: Guala, province of Pichincha, Ecuador). If either of these two taxa could be analyzed at molecular level and had *N. narica* mtDNA, then the G1 (MG1) specimens could be assigned to *N. narica manium* or *N. narica gualeae*, with preference for the first name.

Therefore, our results drastically change the traditional view of the existence of only *N. narica* on the Colombian and Ecuadorian Pacific coast and challenge the idea of the absence of this species in that geographic area, as claimed by other authors ([Gompper 1995](#); [Nowak 1999](#)). Indeed, most coatis living in the Pacific trans-Andean zone of Colombia and Ecuador belong to *N. nasua*. However, a small proportion of individuals in this geographic area show the oldest *N. narica* haplotypes found to date with a morphotype very similar to the Central American populations (present study and [Ruiz-García et al. 2021a](#)). Additionally, in the Ecuadorian Pacific, we detected two specimens (for the set of three mt loci, only one for mitogenomes) with the *N. narica* phenotype and the typical Central American G4 (MG4) haplotypes. Furthermore, an Ecuadorian cis-Andean animal (Macas, Morona-Santiago province, Ecu-

dorian Amazon) showed the typical Central American G3 haplotype. This would indicate that an *N. narica* haplotype would have crossed the Andes mountain range; however, we currently ignore whether this crossing was natural or resulted from humans transporting animals through the Ecuadorian Andean Cordillera. The fact that the Macas specimen showed a haplotype with some nucleotide differentiation relative to the G1 haplotypes leads us to think that the crossing of the Cordillera was not recent, likely a natural process.

Therefore, nuclear genes should be analyzed to determine the degree of hybridization or introgression (if any) between the small proportion of coatis with *N. aff. narica* phenotype and mtDNA (defined in this study as *N. narica*) and the largest proportion of specimens, many of them also with phenotypes with *N. narica* traces but with mtDNA belonging to different *N. aff. nasua* haplogroups (defined herein as *N. nasua*), especially in the Ecuadorian area considered. Nuclear DNA sequencing could contribute to defining the coati systematics. Additionally, our results indicate that in the Pacific area and northern Colombia there is another group of *N. narica* (G6, MG6) introgressed with mtDNA of *N. olivacea*. These new findings are relevant to the conservation policies of coatis in Colombia and Ecuador.

In Central America, the situation would be as follows: 1) *N. n. molaris*, from the north-central and Pacific areas of México to southern USA, was not represented in our samples. However, [Silva-Caballero et al. \(2017\)](#) showed with the mt *Cyt-b* gene, on the one hand, a clade including the haplotypes of the Mexican Pacific coast (Punta Raza and Chamela-Cuixmala, Nayarit and Jalisco, respectively) and, on the other hand, a clade comprising the haplotypes of central México (El Tepozteco; Morelos) and southeast México (La Venta and Puerto Morelos, Tabasco and Quintana-Roo, respectively). In fact, the highest F_{ST} statistic was between one of the Pacific populations (Chamela-Cuixmala) and the central population (El Tepozteco; $F_{ST} = 0.125$, $p < 0.05$). The same trend was observed with nuclear microsatellites. With the R_{ST} statistic (0.995; $p < 0.05$), the most differentiated populations were those of Chamela-Cuixmala (Mexican Pacific) and Puerto Morelos in the Yucatán Peninsula; with the F_{ST} statistic 0.258; $p < 0.05$), the most differentiated populations were Punta Raza (Mexican Pacific) and El Tepozteco (Central México). Likewise, [Nigenda-Morales et al. \(2019\)](#) detected five distinct groups in the sample of *N. narica* studied with both mitochondrial sequences

and nuclear microsatellites. Three of these groups were detected in the geographic area attributed *a priori* to *N. n. molaris*. These three groups were distributed in the Mexican Pacific, Central México, and southwestern United States. The *N. n. molaris* holotype comes from Colima in the Mexican Pacific. Therefore, the Mexican Pacific group can be related to *N. n. molaris*. In contrast, the other two groups found by [Nigenda-Morales et al. \(2019\)](#) in central-northern México and southwestern USA may correspond to *pallida* ([Allen 1904](#)), *tamaulipensis* ([Goldman 1942](#)), *vulpecula* ([Erxleben 1777](#)), or *solitaria* var. *mexicana* ([Weinland 1860](#)); the respective holotypes should be analyzed to confirm those denominations. 2) *N. n. narica*, whose holotype comes from the State of Veracruz corresponds well with our fifth genetic group (G5, MG5). It also corresponds to one of the groups detected by [Nigenda-Morales et al. \(2019\)](#) in the Yucatán Peninsula and Guatemala. 3) *N. n. yucatanica*, whose holotype comes from “Merida in the Yucatán Peninsula”, may be represented by our second genetic group (G2, MG2). However, this group, which comprises a few specimens, shows a high internal genetic heterogeneity and a variable relationship with other groups according to the analyses used. An extensive molecular study is needed in the Yucatán and north Quintana Roo since this area appears to have a highly marked genetic structure at the micro-geographic level. We have detected specimens in the area of Mérida separated by a few kilometers, belonging to groups G2 and G5, suggesting the possibility of areas with hybrid specimens of these two groups in that Mexican state. 4) *N. n. nelsoni* or *N. nelsoni* is typical of Cozumel Island. We only studied one specimen from this area, which was included in G5. Likewise, [Nigenda-Morales et al. \(2019\)](#) analyzed nine specimens from this island and found no obvious differentiation between these specimens and those from the Yucatán and north Guatemala discussed above. Therefore, molecular evidence seems to reject the validity of *N. n. nelsoni* (*N. nelsoni*). The only possibility for this taxon to be valid is that the specimen studied by us, and the nine specimens analyzed by [Nigenda-Morales et al. \(2019\)](#) had been recently introduced by human activities from southern México to Cozumel, and that an original population persists in the island, which had not been sampled in either of the two works. Otherwise, this taxon would have no systematic validity since it could have been introduced to the island in relatively recent historical times. The smaller body size of the coati of Cozumel Island may have been generated over a few generations through natural selection as an

adaptation to a small island with few food resources. We agree with [Glatston \(1994\)](#) that this coati was introduced to Cozumel by the Mayans, although we do not agree that *N. nelsoni* is a full species. Similarly, the coati sampled on Roatán Island (Honduras) had the same haplotype as the others found in G3 (MG3), suggesting that it was recently introduced in that locality by human action.

However, three of the genetic groups detected here (and one of those found by [Nigenda-Morales et al. 2019](#), which corresponds to our G6-MG6) do not match any putative morphological subspecies of *N. narica*. Two of these groups, G3 and G4, were not observed by [Nigenda-Morales et al. \(2019\)](#) because these authors did not collect samples in Honduras, southern Guatemala, El Salvador, Nicaragua, and Costa Rica (only a single specimen was analyzed). Thus, the subspecific name for these two groups remains to be established. A more complex matter is the likely subspecies designation of G6 (MG6). This group, distributed across southern Costa Rica, Panama, and the border area between northern Colombia and Panama, is introgressed with mt DNA of *N. olivacea*. We propose an ancient introgression with mtDNA from *N. olivacea* to the genetic stock of *N. narica* in the border zone between South America and the south of Central America. In the first place, this hypothesis is supported, by the MJN analysis showing a temporal separation between G6 (MG6) haplotypes and *N. olivacea* haplotypes, both located in the same clade at 2.3 Mya for the set of three mt loci and 0.8 Mya for the mitogenomic set. Secondly, the introgressed specimens lack an intermediate morphotype between *N. narica* and *N. olivacea*, but showed the typical morphotype of *N. narica*. Third, the five specimens studied in southern Costa Rica, Panama, and the area bordering Colombia, and the 13 specimens analyzed by [Nigenda-Morales et al. \(2019\)](#), showed *N. olivacea* mtDNA in all cases. If a recent hybridization event had caused this phenomenon, we would expect the *N. olivacea* mtDNA in one specimen, but not in all specimens sampled in that area. A possible subspecific denomination could be *N. narica panamensis* ([Allen 1904](#)). However, only molecular analysis of the respective holotype may solve this issue because an alternative possibility is that this subspecific denomination may correspond to G3.

In summary, considering [Nigenda-Morales et al. \(2019\)](#) and the present study, at least nine genetically differentiated *N. narica* groups are detectable across its geographic range. Three of the morphological subspecies described

Table 4. Estimated gene flow between six groups of white-nosed coati (*Nasua narica*) analyzed in Central America and northern South America. Below the diagonal, based on three mitochondrial genes (*ND5*, *Cyt-b*, and *D-loop*) (G); above the diagonal, based on mitogenomes for all groups detected (MG).

Groups of <i>Nasua narica</i>	G1 (MG1)	G2 (MG2)	G3 (MG3)	G4 (MG4)	G5 (MG5)	G6 (MG6)
G1 (MG1)		0.578	0.136	0.387	0.122	0.049
G2 (MG2)	0.504		0.182	0.295	0.182	0.107
G3 (MG3)	0.108	0.100		0.218	0.191	0.025
G4 (MG4)	0.148	0.134	0.155		0.365	0.039
G5 (MG5)	0.118	0.099	0.267	0.312		0.021
G6 (MG6)	0.088	0.117	0.038	0.048	0.041	

would match three of the genetic groups mentioned, one morphological subspecies described should be invalid, and six new subspecific names should be proposed. The large number of groups found in the present study may respond to different geographic, geological, and ecological causes. In the case of coatis, their behavior is also relevant since they have high levels of phylopatry and a limited dispersal capacity (Frantz *et al.* 2010). They form groups with a small territorial range of 0.5 to 4 km² (Valenzuela and Ceballos 2000; Hirsch and Gompper 2017). Being barely dispersed from the birth site, the groups, mainly formed by females, are strongly bonded. Occasionally, males that moved up to 20 km away from their birth sites have been detected (Lanning 1976). However, estimates of gene flow between populations in México (Silva-Caballero *et al.* 2017) or Central and South America (Nigenda-Morales *et al.* 2019 and the present study) show that the coati groups are virtually genetically isolated.

Colonization dynamics and evolutionary times of the different N. narica groups found. The results obtained are useful for reconstructing the evolutionary history of *N. narica*; to this end, different hypotheses are proposed regarding the origin of each of the *N. narica* groups detected. The analysis of three mt loci suggests the following colonization schemes: 1) The first group to emerge was the Ecuadorian (G1) (→ = gave rise), which gave rise to two separate colonization events in Central America. The oldest was of G1 → Yucatán Peninsula (G2) and, on the other hand, G1 → south-central Central America (G3) (northern Costa Rica, Nicaragua, El Salvador, Honduras, and part of Guatemala). G3 → G4 (southern Guatemala and Belize) → G5 (northern Guatemala and southern México). In this hypothesis, some differential nuances can be considered to explain the existence of two Ecuadorian trans-Andean specimens in G4 and one Ecuadorian cis-Andean specimen in G3. There are two alternatives. The first is that the oldest haplotypes of G3 and G4 were generated *in situ* in South America, followed by subsequent colonization events to Central America. Some of the original haplotypes that expanded through Central America would still “survive” in the Ecuadorian trans-Andean area. The second is that these haplotypes of G3 and G4 emerged *in situ* in Central America from G1, but there was a subsequent migration of individuals with haplotypes originating in Central America, again, to South America. Besides, in northern South America, an *N. narica* group was introgressed with mt DNA of *N. olivacea* and another colonization event took place from northern South America to southern Central America. This hypothesis is consistent with three mitochondrial colonization events from northern South America to Central America, with the G5 haplotypes (southern México and northern Guatemala) being the most recent ones and the G1 haplotypes (Pacific coast of Ecuador) as the original ones. 2) Based on the MJN analysis, only two colonizing events from northern South America to Central America would be considered. In this case, G1 → G3 → G5 → G4, and G2, and the addi-

tional colonization with the introgression of *N. olivacea*. All other details would be identical to the previous hypothesis. Other species of Neotropical mammals have also shown at least two colonization events from South America to Central America. An example is the case of the howler monkey (*Alouatta*; Ruiz-García *et al.* 2017), armadillo (*Dasypos novemcinctus*; Arteaga *et al.* 2012), or anteater (*Tamandua* sp.; Ruiz-García *et al.* 2021c). Using mitogenomic data, an alternative hypothesis can be proposed: 3) An *N. nasua* haplogroup in northern South America (Ruiz-García *et al.* 2021a) gave rise to intermediate haplotypes between the current *N. nasua* haplotypes and the current *N. narica* haplotypes, some of which could still be detectable in southern Central America (southern Costa Rica). However, the haplotypes from the Central American *N. narica* would have originated in the north of present-day Colombia, as evidenced by the specimen of the PN Tama (North of Santander), which → MG1 (trans-Andean Ecuador) → MG3 → MG2, MG4, and MG5. In addition, the colonization of specimens introgressed with the mtDNA of *N. olivacea* (MG6) would have occurred. Therefore, this hypothesis proposes two colonizing events from South America to Central America, adding the possibility of a small colonizing event of intermediate haplotypes and even of haplotypes closer to *N. nasua* that occurred before the two major colonization events.

Ruiz-García *et al.* (2021a) proposed the beginning of mitochondrial evolution of the genus *Nasua* (including *Nasuella*) in the Andean zone of northwest South America 13–10 Ma (Miocene). This is consistent with the start of an intense uplifting in the central and northern Andes estimated to have occurred between 13 and 11 Mya (Antonelli *et al.* 2009; Hoorn *et al.* 2010) and with the completion of the Pebas system, which was characterized by the complete, or almost complete, flooding of the western Amazon during the Middle Miocene (Hoorn *et al.* 2010). From 11 to 7 Mya, another rapid uplifting of the Andean zone took place (Quechua II and III phases; Noble *et al.* 1990; Antonelli *et al.* 2009), and the Pebas System was replaced by the Acre fluvial system (Hoorn *et al.* 2010). These geomorphological and hydrological changes may have contributed to the emergence of different genetic clusters within *N. nasua* and the genesis of *N. olivacea*. However, this means that the ancestors of the current coatis had already reached South America during the Middle Miocene, supporting the hypothesis that the closure of the Central American Seaway occurred 15–13 Mya (Farris *et al.* 2011; Montes *et al.* 2012a,b, 2015; Carrillo *et al.* 2015; Ruiz-García *et al.* 2018a).

According to the results reported here, the oldest *N. narica* haplotypes in South America seem to have emerged 4.5–3.2 Mya (Pliocene), with the Andes having played a major role. During the Pliocene, the eastern Andes mountain range in Colombia did not reach 40 % of their current elevation (Hoorn *et al.* 2010). The uplifting of the Andes continued until 2.7 Mya (Andriessen *et al.* 1994; Gregory-Wodzicki 2000). Therefore, the Andes mountain range itself may have been a physical and climatic barrier for multiple

species that previously would have been widely distributed in northwestern South America (Miller *et al.* 2008; Rull 2011). This period was characterized by glaciations in Argentina (3.5 Mya; Mercer 1984), Bolivia (3.27 Mya; Clapperton 1981), Chile (3–2 Mya; Caviedes and Paskoff 1975). According to the standard GABI model, the Isthmus of Panama emerged completely around 3.5–3.0 Mya (Middle Pliocene) with the definitive closure of the Central American Seaway (Coates and Stallard 2013; O’Dea *et al.* 2016), which could enable some colonizing events by *N. narica* from South America to Central America. Therefore, the case of coatis is contrary to the hypothesis supported by the fossil record, which suggests the predominance of a north-to-south colonization process that occurred 2.8–2.4 Mya (Simpson 1980; Webb 2006; Woodburne 2010). However, the Central American Seaway closure model during the Middle Miocene (15–13 Mya) seems more likely as it predicts active colonization from South America to North America over the past 6 Mya (Bacon *et al.* 2015; Marko *et al.* 2015), as observed for the coati in the present study.

The formation of the truly Central American haplotypes (excluding those of G6-MG6) took place between 1.9–1.1 Mya (Pleistocene), but the time of the introgression of *N. olivacea* into an *N. narica* group also occurred in this period (2.3–0.8 Mya). Nigenda-Morales *et al.* (2019) placed the divergence of the Central American groups at around 1.3 Mya, within the time range established in the present study. During this period, particularly in the range of 1.3–0.8 Mya, called Pre-Pastonian (maximum glacial peak of the great Gunz glaciacion), the Central American groups of *N. narica* started to emerge. This period was extremely dry, which significantly reduced the extent of forests and boosted much of the genetic structure in different species of Neotropical mammals (*Lagothrix* sp., Ruiz-García *et al.* 2014, 2019a, 2020b; *Puma yagouroundi*, Ruiz-García *et al.* 2018b; *Lycalopex* sp., Ruiz-García *et al.* 2013).

The genetic structuring of *N. narica* in Central America during the Pleistocene is consistent with the refuge hypothesis (RH; Haffer 1969, 1997, 2008; Vanzolini 1970; Vanzolini and Williams 1970) of alternating humid-dry periods as a result of the Milankovitch cycles. This led to periods of forest contraction where much of the fauna was relegated. During dry periods, forests became shelter patches isolated by shrub zones, savannas, or arid steppes. This fostered the divergence between populations of the same species that became isolated in different refuges and the emergence of new lineages within them. Conversely, forests expanded in the humid periods, and the different lineages coexisted again in sympatric territories. At that time (1.30–1.10 Mya), sixth and seventh North American glaciations occurred (1.1–0.9 Mya) that affected southern México and northern Guatemala (Barendregt and Duk-Rodkin 2011; Rutter *et al.* 2012) and could have led to the differentiation of the G3 haplotypes from G4 and G5. Subsequently, the Reid glaciacion (0.3–0.13 Mya; Barendregt and Duk-Rodkin 2011; Rutter *et al.* 2012), with severe dry peaks in North and Central

America (Dansgaard *et al.* 1993; Hodell *et al.* 2008), also significantly reduced the extension of forests in Central and North America where *N. narica* lived, leading to the diversification within groups G3 and G5.

In Central America, more recent divergence processes have already occurred. For instance, the MJN showed that G5 (MG5) may have produced G4 (MG4) about 0.12–0.09 Mya. Although Hooghiemstra (1984) defined up to 27 potential climate changes with a periodicity of 100,000 years in the Colombian Andes (which also may have been reflected in Central America), there is only definitive evidence of the start of a great glaciacion 116,000 years ago (Van der Hammen and González 1963; Van der Hammen *et al.* 1981; Helmens 1988; Florez 1992).

Genetic diversity and spatial structure. The levels of mitochondrial genetic diversity of *N. narica* were high but lower than those estimated for *N. nasua*, *N. olivacea*, or *P. flavus* (Ruiz-García *et al.* 2019b, 2020a, 2021a). This is correlated with the more recent origin of the ancestor of *N. narica*. In general, the populations that emerged more recently and peripheral to their geographic range have lower genetic diversity levels. The populations of other mammal species distributed in South America and which later colonized Central America and the south of the USA have lower genetic diversity levels than South American populations (long-nosed armadillo, *Dasypus novemcinctus*, Huchon *et al.* 1999; Arteaga *et al.* 2012; puma, *Puma concolor*, Culver *et al.* 2000; jaguarundi, *Puma yagouroundi*, Holbrook *et al.* 2013; Ruiz-García *et al.* 2018b).

In addition, a geographic pattern is observed in the distribution of genetic diversity. The groups living in northwestern South America (G1), and the southernmost part of Central America, introgressed by *N. olivacea* (G6), have the highest genetic diversities, whereas the northernmost groups of Central America have lower genetic diversity values. The group of Yucatán (México; G2) is an exception.

The spatial structure of *N. narica* was conspicuous and widespread throughout its range (Silva-Caballero *et al.* 2017, Nigenda-Morales *et al.* 2019), which appears to be common in the procionids studied from a population genetics standpoint (*e. g.*, *N. nasua*, *N. olivacea*, or *P. flavus*; Ruiz-García *et al.* 2019b, 2020a, 2021a). In addition to the philopatric behavior of coati females and the climatic and ecological changes already described, geographic barriers may also have been drivers of the high spatial structure found in *N. narica*. Three physical barriers would help understand the spatial structure found in this study. The area between the Sierra Madre Oriental and the Isthmus of Tehuantepec south to the Nicaraguan depression is home to the groups G5, G2, G4, and part of the specimens of G3. In the area between the Nicaraguan depression and the Talamanca Mountain range (southern Costa Rica and northern Panama, whose emergence is dated at 5–3 Mya; MacMillan *et al.* 2006; Mann *et al.* 2007), we found another part of the specimens of G3 and one specimen of G6. In the area between the Talamanca Mountain range and the Darien

region, we found the introgressed specimens of G6. Some of these barriers emerged at times consistent with the estimated divergence times between the *N. narica* groups and have been effective geographic barriers for different taxa. The Talamanca Mountain range has been a geographic barrier for reptiles (Daza *et al.* 2010) and mammals (Bradley *et al.* 2008; Harding and Dragoo 2012; Hardy *et al.* 2013). The same is true for the Nicaraguan depression, characterized by marine transgressions during the Pliocene and Pleistocene (Bagley and Johnson 2014), which have been effective in isolating rodent species (Gutiérrez-García and Vázquez-Domínguez 2012). The territory delimited between the Motagua-Polochic-Jocotan fault (southern Guatemala) and the Isthmus of Tehuantepec (México) has been considered an area of endemic fauna delimited by these geographic barriers (Daza *et al.* 2010; Gutiérrez-García and Vázquez-Domínguez 2013), although this area originated 6–3 Mya, that is, before the arrival of *N. narica* to that area of Central America.

However, these physical barriers only partially explain the groups found in this study. Within the first area delimited by the physical barriers just mentioned (Sierra Madre Oriental and the Isthmus of Tehuantepec south to the Nicaraguan depression), we defined three groups that, in principle, are not separated by physical barriers, and we even found specimens of G3, *i. e.*, the only group found in the second geographic area delimited by the geographic barriers mentioned above (between the Nicaraguan depression and the Talamanca mountain range). The G6 specimens were found basically in the third geographic area mentioned (between the Talamanca mountain range and the Darien region); however, one specimen was found on the other slope of the Talamanca mountain range, whereas the Colombian specimens of the same group were found on the other side of the Darien region. Therefore, we consider that the behavior of the species and climatic changes were more relevant for defining the spatial structuring of *N. narica* than orographic barriers.

Our findings based on mtDNA can be interpreted as a first step toward solving the issue regarding the systematics of *N. narica*. This study provides the most comprehensive mitochondrial analysis and includes the widest geographic range covered to date for the species. However, the study of nuclear markers is essential to determine the hybridization and gene flow levels between the different mitochondrial groups of *N. narica* and achieve a complete evolutionary understanding of this species. Similarly, sampling efforts should be expanded to better understand the origin of this species.

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Potential Distribution of the Neotropical Otter (*Lontra longicaudis annectens*) in the State of Yucatán, México

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En el Estado de Yucatán los registros de nutria neotropical (*Lontra longicaudis annectens*) son insuficientes para determinar si existen diferentes tipos de hábitat para la especie, su estatus de conservación y los riesgos potenciales que enfrenta. Nuestros objetivos son el generar un modelo de distribución potencial de la nutria neotropical para el Estado de Yucatán, y el verificar la presencia de la nutria neotropical en sitios predichos por el modelo. Se generó un modelo de distribución potencial de la nutria neotropical con MaxEnt con registros de presencia de la especie y variables ambientales de EarthEnv a 1 km² de resolución. Se verificó la presencia de la nutria en siete sitios predichos por el modelo mediante visitas en el mes de octubre de los años 2017 al 2019 y 2021. Se caracterizó el hábitat y se colectaron muestras biológicas, así como evidencia video-fotográfica de las señales de presencia de las nutrias y de su hábitat. La distribución potencial de la nutria cubrió 3,487 km², el 8 % de la superficie del Estado de Yucatán, en ríos, lagunas y ecosistemas generalmente costeros, sin embargo, el modelo permitió identificar la idoneidad ambiental del hábitat para la nutria en áreas al interior de la península, y la validación en campo de los sitios predichos produjo los primeros registros de la especie en cenotes y lagunas epicontinentales. Los sitios presentaron disponibilidad de presas, vegetación riparia para refugio y madrigueras, y conectividad acuático-terrestre con manantiales de agua dulce. Se obtuvieron observaciones directas de nutrias en dos de los sitios visitados, así como señales indirectas de su presencia en los siete sitios, las cuales consistieron en heces, letrinas, geles, huellas, rastros, residuos de alimento, madrigueras de descanso y veredas hacia el cuerpo de agua. Los resultados señalan la necesidad de continuar con el monitoreo minucioso en las áreas potenciales predichas por el modelo para poder sugerir medidas de conservación para la nutria neotropical y su hábitat en el estado de Yucatán.

Records of Neotropical otters (*Lontra longicaudis annectens*) are insufficient in the state of Yucatán, México, to determine the different habitat types where otters live, the conservation status of the species and the potential threats. Therefore, our objectives were to generate a map of the potential distribution of the Neotropical otter in Yucatán and verify the otter's presence in sites predicted by the model. A potential distribution species model of the Neotropical otter was generated with MaxEnt using species' records and EarthEnv environmental variables with 1 km² resolution. Otter's presence was verified in seven sites predicted by the model by field surveys conducted during October months of 2017 to 2019 and 2021. The habitat was characterized, and biological samples and video-photographic evidence of otter's presence and its habitat were collected. Potential distribution of the Neotropical otter covered 3,487 km², 8 % of Yucatán State's surface area, in rivers, lagoons, and coastal ecosystems with mangrove forest and wetlands; nevertheless, sites with suitable habitat and potential areas for the presence of otters were observed in epicontinental lagoons in the interior of the State. The potential distribution model allowed to identify the environmental suitability for otter's habitat in the interior of the peninsula, whereas field surveys made to validate the sites predicted by the model led us to report the first records of the neotropical otter in cenotes (sinkholes) and epicontinental lagoons. The sites presented availability of prey species, high density of riparian vegetation for shelter and dens, and terrestrial-aquatic interconnectivity between freshwater springs. Direct observations of otters were obtained in two of the visited sites, as well as indirect signals in seven of them, which consisted of feces latrines, annal jellies, footprints, tracks, food residues, active resting dens, and shore trails. Our results point out the need to continue thorough monitoring in potential areas predicted by the model to be able to suggest conservation measures for the Neotropical otter and its habitat in Yucatán State.

Keywords: Algorithm; potential distribution; monitoring; epicontinental; coastal lagoons.

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Introduction

The Neotropical otter (*Lontra longicaudis annectens*) has a wide distribution range in México; it can be found in the Pacific slope and coast including the mainland coasts of the central and southern Gulf of California, in the Gulf of México slope and coast, and in the Caribbean slope; the species inhabits in many and diverse habitat types along creeks, rivers, lakes, lagoons, wetlands, and reservoirs (Gallo-Reynoso 1997; Briones-Salas *et al.* 2008; Hernández-Romero 2016; Gallo-Reynoso and Meiners 2018). The species' altitudinal range spans from sea level to 2,500 masl and inhabits river basins across zones covered by different vegetation types including coastal marshes, mangrove forest, thorny scrubland, tropical deciduous forest, tropical evergreen forest, mountain cloud forest, and oak-pine forest (Gallo-Reynoso and Meiners 2018; Hernández-Romero *et al.* 2018).

The Neotropical otter is listed as endangered species in México (NOM-059-SEMARNAT-2010; SEMARNAT 2019) and is included in the Agreement for Priority Species and Population Conservation in México (SEMARNAT 2014). It is listed under subsection I of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES 2017) and in the red list of the International Union for Conservation of Nature (IUCN 2019).

In Yucatán, due to the karstic nature of the soil, surface water bodies are relatively shallow and streams flow underground with water outcrops and wells locally called *cenotes* (sinkholes). *Cenotes* may be of various types: the most typical are cavern-type *cenotes* with stalactites and stalagmites, but some are open *cenotes*, similar to small lagoons (Cervantes-Martínez 2007). This particular freshwater system in Yucatán favors suitable habitats for the Neotropical otter and may foster the habitat connectivity required for the species to establish viable populations, since otters have been recorded in Campeche, Quintana Roo, and Yucatán (Gallo-Reynoso 1997; Sánchez and Gallo-Reynoso 2007; Calmé and Sanvicente 2009; Santiago-Plata *et al.* 2013; Sosa-Escalante *et al.* 2013; Gallo-Reynoso and Meiners 2018; Vazquez-Maldonado *et al.* 2021).

It is worth to mention that time gaps between records in the same localities in the State of Yucatán may indicate preferential habitat types (Sosa-Escalante and Martínez-Meyer 2014). For example, the first recorded occurrence of Neotropical otter in Yucatán was reported by Leopold (1965) at Ría Celestún, 64 km W Mérida. The presence of specimens at Ría Celestún Biosphere Reserve was confirmed in 2000 (Sánchez and Gallo-Reynoso 2007). Thus, the species was recorded on two different occasions separated by circa 35 years (1965, 2000) in the same natural protected area. Although the Neotropical otter is mentioned as present in the Management Program of Ría Celestún Biosphere Reserve, there are no reports available of the species conservation status (CONANP 2000). From the above, it follows the need to investigate if the previous records of Neotropical otter at Ría Celestún, and the record of 2000 at San Crisanto in Yucatán (Leopold 1965; Sánchez and Gallo-

Reynoso 2007) may correspond to marginal (*i. e.*, isolated) populations, and/or if the species might be facing serious conservation issues in Yucatán. Thereby, it is important to identify the potential distributional range and potential suitable habitat for the Neotropical otter in Yucatán, to confirm its current distribution. The objectives of this study were to generate a model of the potential distribution of the Neotropical otter in the State of Yucatán and verify the otter's presence in sites predicted by the model.

Materials and Methods

Study Area. The Yucatán peninsula is located in southeastern México and separates the Gulf of México to the north and west from the Caribbean Sea and the northern part of Central America to the east; Yucatán is on the northern part of the peninsula, between Campeche and Quintana Roo. Climate is subhumid with summer rains, mean annual precipitation of 1,600 mm and mean annual temperature of 26°C; the dry season spans from March to May and the rainy season from June to October (García 2004; Estrada and Cobos 2014). Dominant winds from the north prevail from November to February, with a tropical cyclone season (tropical storms and hurricanes) from August to November (Herrera-Silveira 2006; INEGI 2008). Extensive areas in the Yucatán peninsula are covered by deciduous and evergreen tropical forests; nevertheless, Yucatán also have various vegetation communities that include coastal dune vegetation, mangrove forest, floodplain forest, savannah, wetland vegetation known locally as *petén*, *popal*, *tular*, and secondary vegetation (Flores-Guido *et al.* 2010; Pérez-Sarabia 2017; Zavala-Cruz *et al.* 2016).

A calcareous platform made up of a series of plains and plateaus of karstic origin with underground drainage constitute the State. The northern part has low elevations, less than 250 m, except for the Sierra de Ticul with an elevation of 350 masl (Herrera-Silveira 2006; Pérez-Sarabia 2017). In the southern part of the Yucatán and the area bordering with Campeche and Quintana Roo, the relief consists of plateaus and karstic valleys of recent formation (Herrera-Silveira 2006; Pérez-Sarabia 2017). The underground system connects areas of water recharge within deciduous and medium tropical forests with coastal areas with mangrove forests where *cenotes* are also located (Estrada-Medina *et al.* 2014). The areas where karstic rock has dissolved by water filtration through geologic time gave place to large cavern-type *cenotes* (Estrada-Medina *et al.* 2014). Some *cenotes* are deep, closed caverns; other cavern-type *cenotes* are partially open where portions of the cavern roof have collapsed; and *cenotes* with roofs that collapsed completely in the past are now fully open and exposing the underground water (Estrada-Medina *et al.* 2014).

Rainwater permeates underground due to the carbonate rocks of the peninsula platform, as well as through abundant fractures in the karstic rock which hamper the formation of surface currents like creeks or rivers. As such, a few rivers are formed in the borders between Yucatán,

Campeche, and Quintana Roo, increasing in quantity in southern Campeche towards Tabasco, the same is presented in southern Quintana Roo towards Belize, and connecting with many coastal lagoons and deltaic systems (Zavala-Cruz et al. 2016; Pérez-Sarabia 2017).

Some freshwater springs arise inside mangrove forests and petenes, as well as surface water reservoirs called "aguadas", which are topographic depressions that allow rain to be accumulated due to a fine layer of compacted clay sediment that prevents the filtration of rain to underground waters. Another type of spring water is called "sartenejas", which are reservoirs of underground water, some of which have been used by the local Maya inhabitants to excavate and build cisterns with wide fringes to delimit water sources and channels to conduct rainwater (Herrera-Silveira 2006).

Potential distribution map. We gathered georeferenced observations from international data sources GBIF (Global Biodiversity Information Facility 2016) and VertNet (Constable et al. 2010), from national collections on biodiversity (e. g., the online catalogue of the Colección Nacional de Mamíferos (CNMA) of the Instituto de Biología, Universidad Nacional Autónoma de México and from scientific literature such as articles and reports (Martínez-Meyer and Sánchez-Cordero 2006; Sánchez and Gallo-Reynoso 2007; Guzmán-Soriano et al. 2013).

The potential distribution of the Neotropical otter was modeled considering the georeferenced otter records and environmental variables that favor its presence in Yucatán. Spatial autocorrelation was eliminated from the record database with the geographic information system ArcMap 10.2 (produced by ESRI 2014) and the tool "Spatially Rarefy Occurrence Data for SDMToolbox" (Brown 2014) to prevent over-adjustment in areas subjected to more intensive sampling (Veloz 2009; Boria et al. 2014; ESRI 2014b). The refined database was split into two subsets: 1) correspond to species records within its geographic range, excluding Yucatán (hereafter 'calibration base') and 2) that considered the records only for the Yucatán peninsula Biotic Province or YBPB (hereafter 'evaluation base'). The two subsets were defined to have independent records of the species to evaluate the estimated environmental suitability and the potential distribution area. As predictors of the potential distribution modeling, several environmental variables from EarthEnv (Domisch et al. 2015) were used, which contain suitable information on freshwater organisms at ~1 km² resolution (Table in Appendix 1). All variables were delimited accordingly with the area of the two scenarios mentioned above. A MaxEnt algorithm (Maximum Entropy; Phillips et al. 2006) were used to generate the model because it requires presence data only and allows the use of categorical variables and flexible parameterization (Elith et al. 2011).

The calibration area of the model was delimited from the shapefile of Terrestrial Ecoregions of the World (Olson et al. 2001); from it, a polygon was drafted representing

the hypothesis of historic accessibility for Neotropical otter populations, constituted by the ecoregions that contained records of *L. longicaudis annectens* within the Neotropical region ('M' area in the BAM diagram; Soberón and Peterson 2005). M was partitioned in two polygons according to the data subsets previously split into two stages: 'stage one', which included the complete distribution range of the species, excluding Yucatán, which corresponded to the 'calibration base'; and 'stage two', which included the Yucatán peninsula, corresponding to the 'evaluation base'.

The model was calibrated with the information from stage one using the observations from the calibration base as inputs. Then, the model was transferred to stage two (Yucatán) to represent the environmental suitability for Neotropical otter in Yucatán based on environmental characteristics of its distribution range for the whole country. The effectiveness of the model was corroborated by using the projection of the evaluation base in the resulting model for stage two; and to validate the models, an analysis of the partial ROC curve was performed, which was configured to perform 1000 "bootstrap" tests using the iPartialROC function (Barve 2008) from the ENMGadgets package in R (R Development Core 2017). To estimate the potential distribution of the species, we reclassified the data from the MaxEnt model and generated binary probability models (absence/presence), using ArcMap 10.2.

Otter's presence verification in the field. In October of years 2017, 2018, 2019 and 2021, we visited a total of seven sites which included coastal ecosystems of marshes and mangrove forests, cenotes, and epicontinental lagoons (Table 1). The sites were selected accordingly to the presence of suitable habitat predicted by the potential distribution map previously generated (Figure 1).

Otter vocalizations sessions were held in locations where the presence of otters was predicted by the model. Previously, we recorded otter vocalizations consisting of barks and high-pitched barks of an individual otter from the Miguel Álvarez del Toro Zoo, in Tuxtla Gutierrez, México. These vocalizations were played every 10 minutes, for one minute, during the surveys, until there was a response or after 30 minutes with no response.

In every visit, we recorded geographic data with a GPS (Garmin GPSmap 78s) to obtain locations, distances, routes, altitude, and survey effort. The perimeter of cenotes, coastal lagoons, continental lagoons, marshes, and wetlands was surveyed on foot and/or navigating on a canoe or a kayak, searching for direct sightings and indirect signs of Neotropical otter's presence. At the seven sites surveyed, habitat characteristics were described, and the habitat requirements of Neotropical otters were verified including freshwater presence, a stable water level, water transparency, subaquatic vegetation, presence of suitable prey types inside and outside of the water body, tree coverage, and suitable areas to establish breeding and resting dens like rocky areas and holes excavated in banks of cenotes or lagoons, or among dense vegetation.

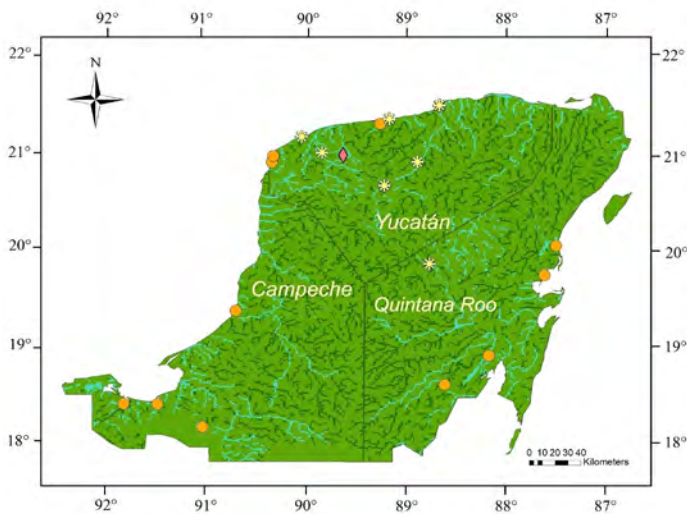


Figure 1. Potential distribution of the Neotropical otter habitat in Yucatán (Dark green), with historical records of this species (orange circles); from Sánchez and Gallo-Reynoso (2007) and Gallo-Reynoso and Meiners (2018). Favorable environmental sites in blue. Surveyed sites are indicated (yellow stars) for seven localities: San Crisanto, Cenote Tunkás, Yalahau Lagoons State Park (Parque Estatal Lagunas de Yalahau), Chichankanab Lagoon, Sisal, San Antonio Chel, and El Isote (Dzilam de Bravo). Binary map. Coordinate System WGS84. Environmental layers from Earth Env. Domisch *et al.* 2015.

The information on tracks, footprints, latrines, and dens was recorded in a database. We collected biological samples and specimens (spraints, anal jellies, food residues, and plant specimens), and recorded photographic and video material that showed the characteristics of the studied areas. With a GoPro Hero2 video camera, we recorded underwater video to understand the underwater habitat characteristics such as presence of underwater vegetation, species of fish present and features of each site such as the depth of water, as well as otter vocalizations. Collected materials were deposited at the Laboratorio de Biología de la Conservación at the Parque Científico y Tecnológico de Yucatán. Also, in the surveyed areas, we searched for connection between water bodies (*i. e.*, several lagoons that were separated by 500 to 1,000 m) that would facilitate the movement of Neotropical otters.

Results

Otter's potential distribution. The potential distribution of the Neotropical otter in Yucatán covered an estimated area of approximately 3,487 km², equivalent to 8 % of the area of Yucatán and 2.6 % of the Yucatán peninsula. The potential distribution modeling allowed us to identify suitable habitat for the Neotropical otter in inland areas of the Yucatán peninsula; although most known records were located near the coast in mangrove forest and wetland vegetation known as *petén*, *popal*, and *tular*. Seven sites predicted with potential habitat for otter in Yucatán were visited to confirm the presence of otters.

Otter's presence verification in the field. San Crisanto (site 1). With a total survey effort of 5 km, the paths between the artisanal salt evaporation plots were checked on foot, the mangrove area was not visited because it was flooded

by the high tide. The vegetation consisted of mangroves (*Rizophora mangle*, *Laguncularia racemosa*), and coastal dune vegetation (shrubs and grasses) in the salt evaporation plots, particularly a pioneer vegetation zone (*Soriana maritima*, *Sesuvium portulacastrum*, *Sporobolus virginicus*, *Distichlis spicata*).

Feeding sites were found with presence of bones, feathers, and wings mostly of Blue-winged Teal (*Spatula discors*); one site presented remains of an American flamingo juvenile (*Phoenicopterus ruber*). We found a series of footprints and tracks of Neotropical otter in one of the clay shores of the marsh and a spraint on the vegetation (Figure 2).

Cenote Tunkás (site 2). With a total effort of 2.3 km, we surveyed the perimeter of an open cenote with a slope of approximately 7 m from the upper edge to the water body. The vegetation in Cenote Tunkás was tropical deciduous forest with *petén* along the shore and aquatic vegetation with dense riparian vegetation in a gallery forest composed by *Metopium brownei*, *Bursera simaruba*, *Phitcelobium albicans*, *Thrinax radiata*, and *Nymphaea ampla*, to mention some of the species that provided shade to the cenote.

In the bank, paths leading from the cenote to an otter's burrow were found devoid of vegetation and the path edge vegetation flattened at ground level, which indicates constant use by otters. Two burrows were found near the water's edge, outside one of them tracks were found; an anal gland jelly mark was found on top of a rock in the middle of the slope near one of the burrows (Figure 2). During the survey the high-pitched bark of an otter was heard, and the recording was reproduced to entice the otter to answer the calls, which the otter did.

Yalahau Lagoons State Park (site 3). This site was visited during the month of October for four years (2017 to 2019 and 2021). The survey conducted in 2017 included a lagoon's bank section, with a total effort of 2.1 km. The following years the area surveyed was increased to include the total perimeter of the lagoon of 8 km. The vegetation at Yalahau Lagoon was composed by *popal* and tropical deciduous forest subjected to annual floods, with species such as *Haematoxylum campechianum*, *Dalbergia glabra*, and *Mimosa bahamensis*. As evidence, an otter spraint was collected from a rocky outcrop among grasses in the lagoon's bank, even though the water level was overflowed due to the extra seasonal rains.

During the 2018 survey, an otter latrine was found on a rock, in the northern portion of the lagoon (Figure 2). The islands of hydrophilic vegetation that are near the northern portion of the body of water were also visited, during this activity we heard an otter's bark, thus we reproduced the zoo's vocalization recording to incite the otter to answer the call to confirm the presence of the species; then, the individual came close enough to obtain a visual record. For the 2019 survey, the latrine was abandoned probably due to the overflow of the lagoon's water level, as many areas of riparian vegetation.

Table 1. Characteristics of the seven sites visited to verify the Neotropical otter's (*Lontra longicaudis annectens*) presence in areas with predicted suitable environmental conditions in the State of Yucatán, southeastern México.

Site name, geographic coordinates, and location	Site description
1. San Crisanto. 21° 20.914 N, -89° 10.281 W. 51 km E of the city of Progreso, north Yucatán.	Coastal locality with marshes, wetlands, mangrove forests, cenotes, estuaries, and coastal areas, as well as evaporation parcels for obtaining artisanal salt within a mangrove preservation zone. San Crisanto Mangroves Management Unit for Wildlife Preservation (Unidad de Manejo para la Conservación de Vida Silvestre [UMA] Manglares de San Crisanto [SEMARNAT-UMA-EX0196-YUC-11; 21.34735 N, -89.18113 W]).
2. Cenote Tunkás. 20° 54.558 N, -88° 52.013 W. 30 km W of Cenotillo.	Open cenote with an approximate diameter of 75 m. This water body is located within a complex of 20 cenotes, lagoons, and aguadas located in the northeastern portion of the Yucatán State where large-scale tourism is not yet developed.
3. Yalahau Lagoon. 20° 39.435 N, -89° 13.034 W. Yalahau Lagoons State Park, 60 km SE of the city of Mérida.	Yalahau Lagoon in the main lagoon of Yalahau Lagoons State Park, a Yucatán State Natural Protected Area encompassing three epicontinental lagoons, cenotes and aguadas located in the central part of the State of Yucatán (DOF 2004).
4. Chichankanab Lagoon. 19° 52.113 N, -88° 45.886 W. 150 km SW of the city of Mérida.	Chichankanab Lagoon is located at the central-west portion of the State of Quintana Roo, limiting with the State of Yucatán, and is approximately 30 km long stretching from La Presumida to Kantemó. Chichankanab is the largest epicontinental lagoon system of the Yucatán peninsula.
5. Sisal. 21° 09.554 N, -90° 02.930 W. 53 km NW of the city of Mérida.	Sisal is near Punta Piedra in a tide-flooded area with gravel bottom, several kilometers away from the "Paraíso Sisal" residential complex. A portion of the wetland is part of the "El Palmar" State Ecological Reserve.
6. San Antonio Chel. 20° 59.903 N, -89° 50.659 W. 7.6 km east of Hunucmá.	Abandoned quarry flooded with water from a cenote and surrounded by native vegetation.
7. El Islote. 21° 28.656 N, -88° 39.975 W. 25 km NE of Dzilam de Bravo State Reserve.	El Islote is located between the coastal lagoon and the eastern coast of the Dzilam de Bravo State Reserve, close to a place called "Las Bocas", characterized by extensive sandy areas devoid of vegetation and with mangrove trees bordering the lagoon.

In 2020, due to the COVID 19 pandemic, no surveys were carried out because the lagoon's state park was closed during the contingency. Activities resumed in October 2021, when indirect records of the species were found in the northern portion of the water body, a site close to where we observed an otter in 2018. In 2021 we also surveyed other two smaller lagoons close to the main one and in all of them we found indirect evidence of otter's presence consisting in tracks and feeding sites.

Chichankanab Lagoon (site 4). We covered 4.8 km on canoe and 1.7 km on foot. The vegetation at the western bank was tropical deciduous forest with *popal*. The tropical forest species at the eastern bank were *Lonchocarpus castilloi*, *Alseis yucatanensis*, *Brosimum alicastrum*, *M. zapota*, *Ceiba pentandra*, and *H. campechianum*, and banks were surrounded by red mangrove (*R. mangle*; Merediz-Alonso 2004). Three places with abundant otter signs consisting of feces on the roots and branches of mangrove trees were found on the banks of the lagoon. However, many of these were washed away after the rain that occurred that same day.

Sisal (site 5). We surveyed 10 km of coastal lagoons and mangrove forest at coastal areas in the El Palmar State Ecological Reserve. The vegetation was dominated by coastal dune bushes and mangrove, with *Suaeda linearis*, *Lycium carolinianum*, *Tribulus cistoides*, *Canavalia rosea*, *Euphorbia mesembrianthemifolia*, *Ernodea littoralis*, *Ipomea pes caprae*, *Coccoloba uvifera*, *R. mangle*, and *T. radiata*. Neotropical

otter footprints were found over a sand-gravel substrate near Cocodrilo Lagoon at low tide.

San Antonio Chel (site 6). The survey consisted of 1.5 km on an abandoned limestone quarry with an excavated pit filled with water. The surrounding area included a flat section of fine gravel of about 3,000 m² with vegetation corresponding to floodplain forest with *H. campechianum*, *Cameraria latifolia*, *M. brownei*, *M. zapota*, *B. simaruba*, *C. aesculifolia*, *Cochlospermum vitifolium*, button mangrove (*Conocarpus erecta*), *D. glabra*, Neotropical otter footprints and tracks were found over a sand and gravel substrate near the pit.

El Islote (site 7). In October 2019, 10 km were surveyed in mangrove and beach sandbars areas near the coast of Dzilam de Bravo State Reserve. The area was mostly devoid of vegetation; however, it covered part of the mangrove forest in the swamp. The vegetation included red mangrove, button mangrove, and black mangrove (*Avicennia germinans*), some dune vegetation with sea grape or uvero de playa (*C. uvifera*) and grasses. We found indirect signs of otters consisting of footprints on a humid sandy substrate between the coastal lagoon's shore and coastal dunes. In October 2021, a combined boat and foot survey was done in the same area, on this occasion the tide was high, and the cenotes inside the mangrove forest were also overflowed due to extra-seasonal rains, therefore we found no evidence of otters on the mangrove branches and roots.



Figure 2. Records of *Lontra longicaudis* in Yucatán. A) Tracks at San Crisanto. B) and C) Den and otter trail from the water to the den at Cenote Tunkás. D) Latrine at Yalahau Lagoons State Park (Parque Estatal Lagunas de Yalahau). E) A spraint dispersed by recent rain on a trunk at Chichankanab Lagoon, Quintana Roo (border with Yucatán). Note the presence of fish scales and fresh remains of water crab. F) Footprint at Cocodrilo Lagoon near Sisal. G) Footprint at San Antonio Chel. H) Footprint at El Islote near Dzilam de Bravo.

Discussion

According to the potential distribution model, the available habitat for the otter were generally located in the coastal lagoons in the western and northern coasts of Yucatán, and in a geological structure named "Ring of Cenotes" which are the remnants of the meteorite that impacted the area of northern Yucatán at Chicxulub *ca* 66 Myr and produced thousands of cenotes and other geological features (Connors *et al.* 1996). The "Ring of Cenotes" probably connects suitable habitat with many cenotes of several types including open cenotes which are nearby, and land depressions subject to flood during rainy season which form temporal lagoons (Aguilar *et al.* 2016).

Direct and indirect evidence of otter's presence was found in seven verified sites predicted with habitat suitability by the potential distribution model. These sites showed availability of prey species, including crustaceans, fish, reptiles, and birds, which are the main food sources for otters, as well as adequate vegetation cover, density and interconnectivity between land, water, and freshwater sources; these two aspects are essential for the survival of otters.

Since otter's presence was confirmed in mangrove forests, epicontinental lagoons and cenotes, our results were consistent with previous studies on Neotropical otter ecology performed in other regions of Mexico (Macías-Sánchez 2003; Mayagoitia-González *et al.* 2012; Hernández-Romero 2016).

We report the first records of Neotropical otter in different inland areas of the Yucatán peninsula and noteworthy direct observations and the second record of Neotropical otter in the coastal locality of San Crisanto after a 20-year span (Sánchez and Gallo-Reynoso 2007). Otter's presence was corroborated in Ría Celestún after an 18-year span, and new coastal records were found at Sisal, Dzilam de Bravo (El Islote), as well as new records at Chichankanab epicontinental lagoon.

The Chichankanab Lagoon is probably connected to the hydrological basin of the State of Quintana Roo; this basin includes several lagoon systems connected to Laguna de Bacalar, where a Neotropical otter was filmed in April 2020 (Hernandez 2020), and Laguna de los Milagros where otters have been previously recorded (Gallo-Reynoso 1997; Gallo-Reynoso and Meiners 2018).

Outstandingly, at San Crisanto marshes, the cenote is located among salt-extraction parcels, which neutralize the high concentration of dissolved salts in the area and made it suitable for otters since they can tolerate salinity levels of 2 to 3 ppm; the same condition was recorded at Celestún, Sisal, and Dzilam de Bravo (El Islote).

The marking activity of the Neotropical otter is known to decrease during the rainy season, due to the flooding of latrine areas (Gallo-Reynoso *et al.* 2016). We visited Yalahau Lagoons State Park when supposedly the rainy season

would be over by October, but we found high-water level resulting from heavy rains of an extended rainy season during 2017 to 2019 and 2021 surveys; nevertheless, we found an active latrine in 2018. These rains overflowed the rocks, branches, roots and fallen trunks, thus washing away any spraint residues on latrine-suitable areas.

Our results pointed out that the Neotropical otter is associated with large freshwater bodies such as open cenotes, aguadas, epicontinental lagoons, coastal lagoons, and marshes in Yucatán which are major geological features of the state (Connors et al. 1996; Aguilar et al. 2016). It is important to continue searching for otters in the central areas of the Yucatan peninsula to unravel possible mobility between sites occupied by otters. The potential distribution model suggested habitat availability at many nearby locations, even though the lack of runoff waters and rivers hinders otter's mobility. Therefore, it remains unclear if otter populations might be marginal (*i. e.*, isolated) because the connectivity between these available habitats for otters is unknown, although we found otters distributed across the Ring of Cenotes and in other areas of Yucatán which points out to the presence of a certain connectivity due to geological features (Aguilar et al. 2016), that should be thoroughly investigated.

The distribution of the Neotropical otter in Yucatán is poorly known in the System of Natural Protected Areas of Yucatán (SANPY) and currently lacks a management plan or a specific conservation strategy for the species (Gallo-Reynoso 2013; Sosa-Escalante et al. 2013). The results of our research can be used to support the prioritization of sites for the conservation of the Neotropical otter, such as the Yalahau Lagoons State Park and the Ring of Cenotes and Chichankanab lagoon.

Conservation implications. The current growth and expansion of human populations and related urbanization generates a high demand for subsurface freshwater, along with groundwater pollution due to organic and solid wastes, agricultural and urban wastewater; all of which drain to surface and subsurface waters and pose a major threat for the Neotropical otter and its preys in the studied area (Arcega-Cabrera et al. 2014; Polanco-Rodríguez et al. 2015).

In areas of environmental suitability for Neotropical otter's presence, we suggest organizing workshops to raise awareness on the biological importance and environmental services provided by this species in the different ecosystems, which might be translated into community strategies for habitat and water quality conservation (Hernández-Romero 2016). Otter populations have successfully recovered in several parts of the world thanks to legal protection programs and strict legislation addressing pollution of water bodies (Carone et al. 2014; Rheingantz et al. 2021), according to international instruments acknowledged by Mexico (Agenda 21, Río 1992).

It is recommended that the natural protected areas of Yucatán (Sisal, Yalahau Epicontinental Lagoons and Dzilam among others), and Federal protected areas such as Ria

Celestún Biosphere reserve, where we found Neotropical otter presence, be acknowledged as refuge areas for their protection based on the Mexican General Law for Wildlife (Ley General de Vida Silvestre), and the Biosphere Reserve Ria Lagartos should be examined for Neotropical otter's presence.

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Appendix 1

Variables used to make the potential distribution model for the Neotropical otter (*Lontra longicaudis annectens*) in the State of Yucatán, southeastern México.

No.	Variable	Name
1	Climate	Monthly minimum temperature (average)
2	Climate	Monthly maximum temperature (average)
3	Climate	Monthly upstream precipitation (sum)
4	Climate	Monthly minimum temperature (distance-weighted average)
5	Climate	Monthly maximum temperature (distance-weighted average)
6	Climate	Monthly upstream precipitation (distance-weighted sum)
7	Climate	Hydroclimatic variables (average and sum)
8	Climate	Hydroclimatic variables (distance-weighted average and sum)
9	Topography	Upstream elevation (min, max, range, avg)
10	Topography	Upstream slope (min, max, range, avg)
11	Topography	Stream length and flow accumulation
12	Land cover	Upstream landcover coverage (minimum)
13	Land cover	Upstream landcover coverage (maximum)
14	Land cover	Upstream landcover coverage (range)
15	Land cover	Upstream landcover coverage (average)
16	Soil	Upstream landcover coverage (distance-weighted average)
17	Soil	Upstream soil (minimum)
18	Soil	Upstream soil (maximum)
19	Soil	Upstream soil (range)
20	Soil	Upstream soil (average)
21	Soil	Upstream soil (distance-weighted average)

Effect of anthropogenic noise on the echolocation pulses of the bats *Molossus sinaloae* and *Mormoops megalophylla*

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Anthropogenic noise interferes with the acoustic signals of various wildlife species. For bats that use echolocation, noise can mask the information received in the echo. The effect of anthropogenic noise on the time and frequency components of echolocation pulses emitted by the aerial insectivorous bats *Molossus sinaloae* and *Mormoops megalophylla* in urban and natural habitats were evaluated. We hypothesized that the frequency components of pulses would increase in response to masking, while time components would not change significantly. To this end, acoustic recordings of both species were made in the two types of habitats using ultrasonic detectors; simultaneously, the intensity of the ambient noise was measured. Frequency (kHz) and time (ms) were analyzed for each echolocation pulse using the BatSound 4.2 software. Consistent with our hypothesis, the results showed that under background noise of 75 dB in an urban environment, *M. sinaloae* increased the low and high frequencies of its echolocation pulses by 5.8 kHz on average. For *M. megalophylla*, no increase in pulse frequencies was observed. Contrary to our expectation, the time components of pulses for *M. sinaloae* were modified, being of shorter duration in urban sites. Increasing the maximum amplitude-frequency by *M. sinaloae* may be a response to the Lombard effect, *i. e.*, the increase in vocal amplitude in response to increased background noise. It is important to carry out studies focused on understanding the modification of echolocation pulses, mainly for species living in urban environments.

El ruido antropogénico interfiere con las señales acústicas de diversas especies de fauna silvestre. Para los murciélagos que usan la ecolocalización, el ruido puede enmascarar la información recibida en el eco. Se evaluó el efecto del ruido antropogénico en los componentes de tiempo y frecuencia de los pulsos de ecolocalización de los murciélagos insectívoros aéreos *Molossus sinaloae* y *Mormoops megalophylla* dentro de un hábitat urbano y uno natural. Hipotetizamos que los componentes de frecuencia de los pulsos incrementarían como respuesta al enmascaramiento mientras que los componentes de tiempo no variarían significativamente. Para ello se realizaron grabaciones acústicas de ambas especies en los dos tipos de hábitat usando detectores de ultrasonidos, simultáneamente se midió la intensidad del ruido ambiental. Se analizaron para cada pulso de ecolocalización parámetros de frecuencia (kHz) y tiempo (ms) en el software BatSound 4.2. De acuerdo con nuestra hipótesis los resultados mostraron que, bajo el ruido de fondo a una intensidad de 75 dB en el ambiente urbano, *M. sinaloae* incrementó las frecuencias de sus pulsos de ecolocalización, tanto bajos como altos, en 5.8 kHz en promedio. Para *M. megalophylla*, no se observaron incrementos en las frecuencias de sus pulsos. Contrario a lo esperado, los componentes de tiempo para los pulsos de *M. sinaloae* sí se vieron modificados, siendo de menor duración para los sitios urbanos. El incremento de la frecuencia de máxima amplitud para *M. sinaloae*, podría ser una respuesta al efecto Lombard, que es el incremento en la amplitud vocal en respuesta al aumento del ruido de fondo. Es de importancia la realización de estudios enfocados a entender la modificación de los pulsos de ecolocalización, principalmente para las especies que viven en ambientes urbanos.

Keywords: Acoustic masking; Lombard effect; noise pollution; pulses variation.

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Introduction

Several studies have shown that chronic exposure to noise can have adverse effects on wildlife ([Kight and Swaddle 2011](#)), which occur at the physiological level or affect communication, behavior patterns, and the structure of communities ([Barber et al. 2010](#); [Brumm 2010](#); [Kight and Swaddle 2011](#); [Siemers and Schaub 2011](#); [Francis and Barber 2013](#); [Shannon et al. 2015](#)). In communication, noise interferes with the tone, intensity, and structure of signal emissions, so that its reception lacks information, thus producing an acoustic masking effect ([Barber et al. 2010](#); [Naguib 2013](#)). To compensate for this effect, different species of animals have made vocal adjustments in the acoustic signals emitted

([Nemeth et al. 2013](#); [Rios-Chelén et al. 2015](#); [Shen and Xu 2016](#); [Brumm and Zollinger 2017](#)). For instance, birds can increase the frequency and amplitude of the song and reduce the number of syllables ([Slabbekoorn and Peet 2003](#); [Brumm 2004](#); [Nemeth et al. 2013](#); [Rios-Chelén et al. 2015](#)). It has also been observed that some species of lizards may increase the duration of syllables or use a higher number of syllables containing more intense tones ([Brumm and Zollinger 2017](#)).

Similar to other vertebrates, bats have adapted to life in urban areas, so it is possible to find bat shelters and hunting sites within or in the periphery of cities ([Kunz and Reynolds 2003](#); [Russo and Ancillotto 2015](#)). The emission of high-fre-

quency sounds allows bats to perceive shapes and textures of the surrounding environment, thus creating an acoustic image that provides them with information for spatial orientation and the detection, identification, and location of food (Neuweiler 2000; Schnitzler and Kalko 2001). For some bat species, noise represents an aversive stimulus. It has been observed that some species avoid foraging in areas exposed to high noise levels, and that foraging becomes less efficient due to increased search effort (Schaub *et al.* 2011; Bunkley and Barber 2015; Luo *et al.* 2015a). Echolocation pulses are susceptible to different acoustic stimuli that may potentially interfere with echo reception (Gillam and Montero 2016), so that noise can mask this information in low-frequency echolocation pulses. In response, bats can adjust the components of their echolocation pulses by increasing the duration, bandwidth (Bunkley *et al.* 2015), and amplitude (Hage and Metzner 2013a; Hage *et al.* 2013b; Luo *et al.* 2015b). However, other factors such as flight height, social interactions, reproductive age, geographic isolation, foraging habitat, postnatal development, and environmental temperature and humidity influence the variation of echolocation pulses (Chaverri and Quirós 2017; Grillo *et al.* 2014; Guillam *et al.* 2009; Jiang *et al.* 2015; Kraker-Castañeda *et al.* 2019; Varela-Boydo *et al.* 2019; Voigt-Heukce *et al.* 2010).

The bats *Molossus sinaloae* (family Molossidae) and *Mormoops megalophylla* (family Mormoopidae) have been reported as urban exploiters *sensu* McKinney (2002), as they take advantage of resources available in cities for shelter and food (Rodríguez-Aguilar *et al.* 2017). Individuals inhabiting urban areas are constantly subjected to high anthropogenic noise levels, mainly from vehicular traffic (> 50 dB, Luo *et al.* 2015a). *M. sinaloae* is a fast-flight forager in open spaces that emits low-frequency, narrow-bandwidth and long-duration echolocation pulses characterized by the alternation of frequencies, visualized as steps in the spectrogram, and displays high plasticity in pulse emission (Jung *et al.* 2014). *M. megalophylla* is a forager in vegetation clearings and edges (Schnitzler and Kalko 2001). Its pulses are easily recognizable, consisting of a main component of constant frequency that ends with a downward curve of modulated frequency showing harmonics in which the first (fundamental signal) is of low intensity while the second and third are usually of high intensity (Rydell *et al.* 2002).

Lara-Núñez (2015, unpublished data), in a work carried out in Cuernavaca, Morelos, México, found that the frequencies of the echolocation pulses of *M. sinaloae* and *M. megalophylla* were higher than those described for individuals of these species recorded in a natural habitat (Orozco-Lugo *et al.* 2013). Considering the above, this study evaluated whether anthropogenic noise produces an acoustic masking effect on the time and frequency components of the echolocation pulses of *M. sinaloae* and *M. megalophylla*, by comparing the pulses of each species recorded in two sites with contrasting conditions of anthropogenic noise levels, an urban area and a natural area, located in the state

of Morelos, México. Our hypothesis is that the frequency and time components of the pulses of both species would increase in response to masking.

Materials and methods

Study areas and sites. To compare the levels of ambient noise and their effect on the components of echolocation pulses, two study areas were selected: an urban area (with anthropogenic noise) and a natural area (without anthropogenic noise; Supplementary material 1). The urban area selected was the city of Cuernavaca, which extends across an area of 151 km² and is home to 366,320 inhabitants (INEGI 2015). It covers an altitudinal range from 1,100 masl in the southern zone to 1,800 masl in the northern zone (INEGI 2009); the dominant climate is warm subhumid with a mean annual temperature of 21.1° C (IMTA 2014). The city is characterized by the transition between its main types of vegetation, from low deciduous tropical forest or deciduous tropical forest in the southern zone to pine-oak forest in the north (Dorado *et al.* 2012). The natural area selected was Sierra de Huautla (SH), located in the south of the state of Morelos. Its altitudinal range extends from 700 to 2,000 masl, characterized by a warm subhumid climate with summer rains. The main type of vegetation is low deciduous tropical forest; however, there are also areas with medium subdeciduous forest, oak forest, and a small area of pine forest (Dorado *et al.* 2005). The distance separating the two study areas is 53 km.

In Cuernavaca, four sampling sites were set for the recordings: Acapantzingo, Centro, Palmas, and Galerías Cuernavaca shopping mall. In each, a sound meter was used to record preliminary measurements of environmental noise under different conditions of vehicular traffic and environmental noise. The selected sites include housing and commercial infrastructure and government offices with an open layout; the avenues and roads that cross them are open spaces between buildings, which are mostly less than 10 m in height. In SH, three sites were selected for the recordings, one located on the road to the village of El Limón, one on the stream that runs through the town of Quilamula, and the third located in El Limón Biological Station. These are open sites surrounded by low deciduous tropical forest where trees reach heights of 4 to 10 m.

Acoustic sampling of bats. Ultrasound recordings of bats were made in May, June, October, November, and December 2016. Fixed points were set at each sampling site, where recordings were made continuously over one and a half hours from the sunset hour indicated by a GPS device (Garmin eTrex). The recording period was established by prioritizing personal safety when staying during such hours of the day in urban sites. Recordings were made in real time with the Echo Meter 3+ (Wildlife Acoustics) ultrasonic detector, at a sampling rate of 256 kHz and a 16-bit resolution, using an SDHC memory card with 4 GB storage capacity, and positioning the detector at 45 degrees at the elbow level. Recordings were made once a month at each sample site, following a random order.

Analysis of recordings. Search sequences were selected based on the emission of more than five consecutive pulses because pulses were more uniform in structure during the search phase, unlike the approach-and-capture phase. The pulses in the spectrogram were considered high-quality when the display of each pulse was complete from start to end, making sure that no more than one conspecific or heterospecific individual interfered. The recordings were analyzed with the software BatSound 4.2 (Pettersson Elektronik) following the protocol outlined below.

Spectrograms were displayed at a 16-bit resolution, with a sampling rate of 44,100 kHz/s, at a time expansion of 10x, Fast Fourier Transforms (FFT) with 512 samples, in a 95% overlapping Hanning window. Five frequency (kHz) and two time (ms) parameters were measured. The initial frequency (IF; frequency at the start of the pulse) was measured by placing the frequency cursor in the center of the start of the pulse. The final frequency (FF; frequency at the end of the pulse) was measured by placing the frequency cursor in the center at the end of the pulse. To measure the mid-pulse frequency (MPF; frequency at the middle of the pulse length), the pulse duration was divided by two, placing the frequency cursor at that point and recording the value at the intersection with time. The maximum amplitude frequency (MAF; frequency emitted at the point of highest pulse energy) was measured as the value of the highest peak recorded over the entire pulse length, as shown in the cumulative power spectrum. Also recorded were the bandwidth (BW; difference between the initial and final frequencies) and the pulse interval (PI; time elapsed from the start of one pulse to the start of the next pulse), the latter measured by placing the cursors at the start of each pulse. The pulse duration (PD; the time from pulse start to end) was measured by placing the cursors at the start and end of each pulse. For *M. megalophylla*, the second harmonic was measured according to [Rydell et al. \(2002\)](#) because this harmonic attained the highest intensity while the fundamental one was very weak and, in most echolocation sequences, it was imperceptible in the spectrogram; in the case of *M. sinaloae*, no harmonics were observed, but only the fundamental frequency.

Noise measurement. Ambient noise was measured in parallel with the ultrasound recordings at 10-minute intervals, from the time when each recording started, using a sonometer (BENETECH, GM 1351), an instrument that measures sound intensity in decibels (dB, unit of measure). These measurements were recorded at all sites in both natural and urban areas, to obtain a measure of the level of environmental noise experimented by the bat species in the study sites.

Statistical analysis. For statistical analyses, the data for each parameter obtained from the echolocation sequences of the search phase were averaged. Given that *M. sinaloae* shows alternation of pulses during commuting and search for prey, low pulses and high pulses were compared separately in the statistical analyses and the difference in initial

frequency between both pulses was evaluated as a measure of pulse alternation.

We analyzed the differences in noise levels between urban and natural sites, as well as between sampling periods, to determine whether the effect of noise is homogeneous over the spatial and temporal scales studied. To this end, we first evaluated the data normality and homoscedasticity assumptions using the MASS package ([Venables and Ripley 2002](#)) in R 4.01 ([R Core Team 2021](#)). These analyses showed that the variables considered have a normal distribution, but their variance is heterogeneous. Hence, we used the robust Welch's Analysis of Variance, which is designed to treat heteroscedastic data ([Wilcox 2012](#)), followed by a multiple comparison test of trimmed means. These analyses were implemented in the package WRS2 ([Mair and Wilcox 2020](#)).

Since the noise analyses showed no significant differences either between sites or between sampling periods (see *Results*), the analysis of each component of the echolocation pulses was carried out by sorting sites into two levels: urban (the four sites sampled in the city of Cuernavaca) and natural (SH sites). We evaluated the data normality and homoscedasticity following the same procedure described for noise levels, finding that the pulse variables have normal distribution and heterogeneous variances. Thus, univariate comparisons between urban and natural levels were made using the robust ANOVA model. A value of $\alpha = 0.05$ was used for all the analyses. In addition, a multivariate analysis of variance was used to assess the differences between the urban and natural categories, after the data were transformed into natural logarithms to homogenize the variances, followed by a discriminant analysis to illustrate the differences and test the *a priori* classification of the groups by type of habitat. This analysis allows classifying independent variables with mutually exclusive characteristics in a group established *a priori* from a dependent variable. These multivariate analyses were run using the program PAST 4.02 ([Hammar et al. 2001](#)).

Results

Seventy-five noise measurements were recorded over eight nights in urban sites, and 58 over six nights in natural sites. The average environmental noise measured was 75 (± 4.2) dB in the urban area and 45 (± 1.4) dB in the natural area. Robust analyses of variance and multiple comparison tests showed significant differences between urban and natural sites ($F = 180.08$, $P < 0.001$), but comparisons of noise levels within urban sites and within natural sites, as well as between sampling periods, showed that these differences were not significant (urban $F = 4.91$, $P > 0.05$; natural $F = 3.2$, $P > 0.05$; Figure 1).

A total of 795 sequences for both species were identified in 1530 minutes of recording during the sampling months, of which we analyzed 33 for *M. sinaloae* and 27 for *M. megalophylla*. From these sequences, a total of 545 echolocation pulses were measured for the two species, 332 for the

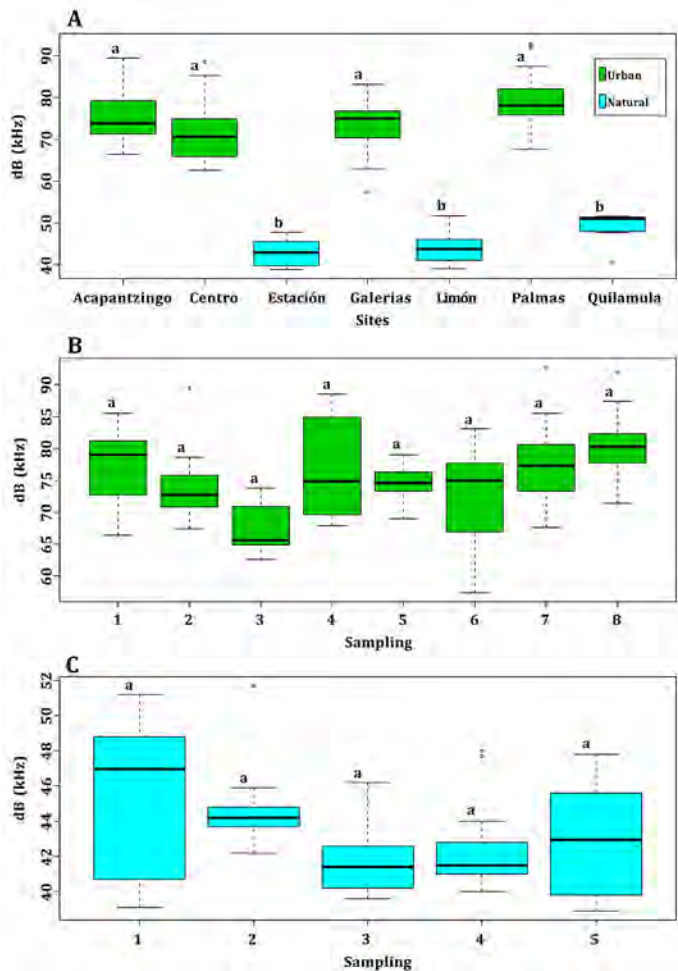


Figure 1. Box plots showing noise levels according to sampling sites in the natural and urban environments (A), and to sampling periods in the urban (B) and the natural (C) environments. The black line represents the median; boxes represent the ranges between quartiles, and whiskers represent minimum and maximum values.

urban area and 213 for the natural area. The parameters of each echolocation pulse were stored in a database, sorted by species and type of area where recordings were made. An average per recording was obtained for each parameter per sampling site in Cuernavaca and SH.

For *M. sinaloae*, 266 pulses, 93 for the natural area and 173 for the urban area, were analyzed in 33 sequences. In the urban area, the frequency and time parameters showed higher values than those obtained in the natural area (Table 1). The variables measured in the high echolocation pulses of *M. sinaloae* were contrasted between the two different types of habitats and noise intensity (urban 75 dB vs. natural 45 dB). The analyses of variance showed significant differences between the five frequency components: initial rate ($F = 114.38, P < 0.05$), final frequency ($F = 115.30, P < 0.05$), bandwidth ($F = 23.25, P < 0.05$), mid-pulse frequency ($F = 106.70, P < 0.05$), and maximum amplitude frequency ($F = 85.63, P < 0.05$). In all cases, higher frequencies were observed in the urban area (Figure 2 A-E). For the time parameters, pulse duration was significantly shorter in the urban area ($F = 17.15, P < 0.001$; Figure 2 F), while no significant differences were observed in the time elapsed between the emission of consecutive pulses ($F = 4.02, P > 0.05$). Similar results were found for low pulses, where

robust analyses of variance showed that the five frequency components were significantly higher in the urban area: initial frequency ($F = 77.93; P < 0.05$), final frequency ($F = 67.91; P < 0.05$), bandwidth ($F = 43.55, P < 0.05$), mid-pulse frequency ($F = 73.86; P < 0.05$), and maximum amplitude frequency ($F = 64.59; P < 0.05$) (Figure 3 A-E). On the other hand, pulse duration and interval of low pulses were significantly shorter in the urban area ($F = 67.24, P < 0.05$; $F = 17.15, P < 0.05$; Figure 3 F and G).

The difference in the initial frequency between the low and high echolocation pulses of *M. sinaloae* also showed significant differences ($F = 13.81, P < 0.05$). In the urban area, the difference between the low and high pulses was 7.2 kHz on average, while for the natural area, the difference between the two pulses was 5.7 kHz on average (Figure 3 H).

The discriminant analysis of the low pulses of *M. sinaloae* showed a significant difference between groups (Wilks $\lambda = 0.45; P = 0.0028$). Of the low pulses corresponding to the urban area, 84 % were correctly assigned, while of the pulses emitted in the natural area, 100 % were correctly assigned (Supplementary material 2). Differentiation was also significant for the high pulses (Wilks $\lambda = 0.32; P < 0.05$); 92 % of the high pulses emitted in the urban area and 86 % in the natural area were correctly assigned (Supplementary material 3).

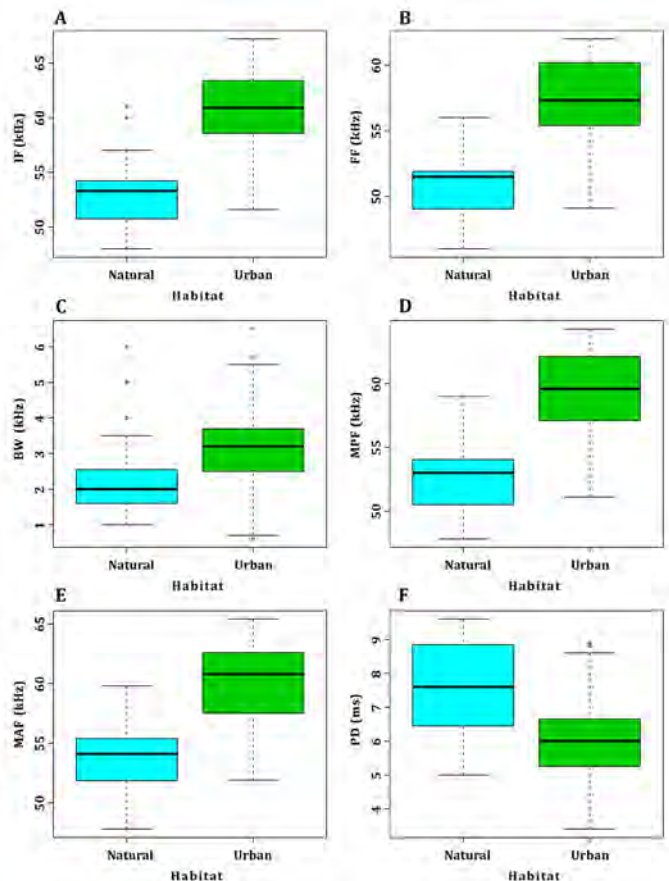


Figure 2. Box plots of the frequency and time components of the echolocation high pulses of *M. sinaloae* contrasted in the two environments studied: natural and urban. (A) Initial frequency, (B) final frequency, (C) bandwidth, (D) mid-pulse frequency, (E) maximum amplitude frequency, and (F) pulse duration. Four frequency components had higher values in the urban area. The black line represents the median; boxes represent the ranges between quartiles, and whiskers represent minimum and maximum values.

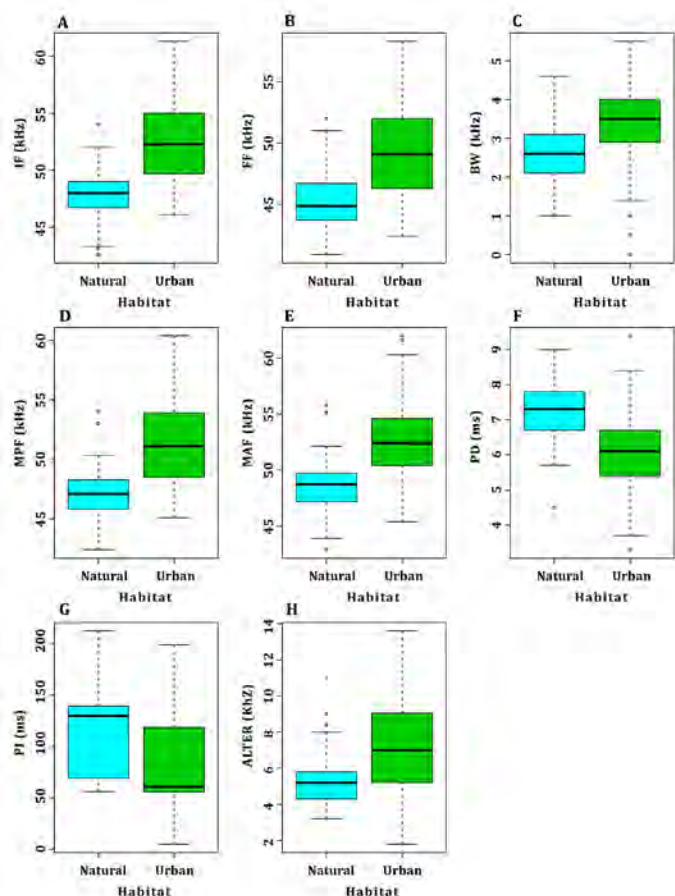


Figure 3. Box plots of the frequency and time components of the echolocation low pulses of *M. sinaloae* contrasted in the two environments studied: natural and urban. (A) Initial frequency, (B) final frequency, (C) bandwidth, (D) mid-pulse frequency, (E) maximum amplitude frequency, (F) pulse duration, (G) interval between pulses, and (H) alternation between high and low pulses. The black line represents the median; boxes represent the ranges between quartiles, and whiskers represent minimum and maximum values.

For *M. megalophylla*, 279 pulses, 120 for the natural area and 159 for the urban area, were analyzed in 27 sequences. The time and frequency components of the pulses showed similar values between the urban and natural areas (Table 2). The robust ANOVA between pulse components and urban and natural areas showed significant differences only in initial frequency ($F = 148.35$; $P < 0.05$), final frequency ($F = 95.46$; $P < 0.05$), and mid-pulse frequency ($F = 101.24$; $P < 0.05$); these were higher in the Cuernavaca urban area (Figure 4 A-D). Bandwidth ($F = 2.78$; $P = 0.74$), and the time compo-

nents pulse duration ($F = 0.48$; $P = 0.57$) and interval ($F = 0.86$; $P = 0.35$) showed non-significant differences between the two areas. The discriminant analysis of the pulses of *M. megalophylla* showed a non-significant difference between groups (Wilks $\lambda = 0.53$; $P = 0.104$; Supplementary material Figure 7). For this species, 81 % of the total data corresponding to the urban area and 87 % of those corresponding to the natural area were correctly assigned.

Discussion

The results showed that, under background noise at an average intensity of 75 dB in the urban environment, *M. sinaloae* increased the frequencies of its echolocation pulses, both low and high, by 5.8 kHz on average. This suggests that, according to the hypothesis of the present study, when facing higher background noise levels, *M. sinaloae* emits echolocation pulses of higher frequencies since anthropogenic noise masks echolocation signals, significantly affecting the components of the pulses emitted by *M. sinaloae*, while the interval duration and pulse duration decreased.

Although it has been documented that bats exhibit variations in the design of the time and frequency components of their echolocation pulses due to factors associated with geographic isolation, flight height, and foraging habitat (Gillam et al. 2009; Jiang et al. 2015; Kraker-Castañeda et al. 2019; Russo et al. 2018), particularly in species of the family Molossidae, there are changes in the frequency and alternation of navigation pulses associated with the variations in geographic location and flight altitude (Gillam et al. 2009; Jung et al. 2014). However, in none of the cases documented to date, the initial, final, and maximum amplitude frequency exceed 5 kHz between locations separated by more than 100 km or at altitudes from 30 m to 800 m. In this study, recordings were made in open spaces in both natural and urban habitats, so that the changes in frequency and time parameters are not determined by habitat structure (Kraker-Castañeda et al. 2019). Although environmental conditions such as temperature and humidity can influence the variation of echolocation pulses, the difference in kHz and ms is unclear (Chaverri and Quirós 2017). In view of these results, we consider that the increase in the frequency components of the pulses of *M. sinaloae* — mainly the maximum amplitude frequency, which is where the maximum energy of the pulse is concentrated — may be a response to the

Table 1. Mean and standard deviation of each component measured in the echolocation pulses of *M. sinaloae* in the sampling areas.

Environment	Type of Pulses	IF (kHz)	FF (kHz)	BW (kHz)	MPF (kHz)	MAF (kHz)	PD (ms)	PI (ms)
Urban	Low	52.8 ± 3.7	49.4 ± 3.5	3.3 ± 0.7	51.7 ± 3.5	52.6 ± 4.2	5.8 ± 0.9	84.2 ± 38.1
	High	60.1 ± 3.6	57 ± 3.2	3 ± 1	59 ± 3.4	59.8 ± 3.4	5.9 ± 0.9	87.9 ± 23.2
Natural	Low	47.7 ± 2	44.9 ± 2	2.7 ± 0.6	47.1 ± 2.1	48.4 ± 2.2	7.2 ± 0.4	111.4 ± 30.1
	High	53 ± 3	50.5 ± 2.3	2.5 ± 0.9	52.2 ± 2.6	53.2 ± 2.8	7.4 ± 1.1	117.4 ± 29.5

Table 2. Mean and standard deviation of each component measured in the echolocation pulses of *M. megalophylla* in the two sampling areas.

Environment	IF (kHz)	FF (kHz)	BW (kHz)	MPF (kHz)	MAF (kHz)	PD (ms)	PI (ms)
Urban	69.5 ± 1.9	65 ± 2.8	4.4 ± 2.7	68.8 ± 1.8	69 ± 2.5	6.1 ± 0.7	81 ± 20
Natural	67.4 ± 0.8	62.7 ± 0.9	4.7 ± 0.3	67 ± 0.8	67.7 ± 0.8	6.4 ± 0.5	70.4 ± 12.3

Lombard effect, defined as the increase in vocal amplitude when facing background noise (Zollinger and Brumm 2011; Luo et al. 2017). This type of response has been observed in male concave-eared torrent frogs (*Onorrana tormota*) as increased fundamental frequencies and amplitude of vocalizations when noise intensity increased by 10 dB (Shen and Xu 2016). In birds, the great tit (*Parus major*) increased the minimum frequency of its sound associated with higher background noise levels (Slabbekoorn and Peet 2003).

In the case of the bat *M. megalophylla*, statistically significant changes were observed only in the initial, final, and mid-pulse frequencies. A potential factor also influencing the difference observed in the response to noise between both bat species is the type of foraging, since *M. megalophylla* forages near or between the vegetation, i. e., it flies in areas with dense vegetation structure. As open-space foragers, molossid emit pulses of low frequency, long duration, narrow band, and with long time lapses between pulses (Schnitzler and Kalko 2001). For *M. sinaloae*, background noise is equivalent to flying in an enclosed space, so it should be able to distinguish the echo of its prey from the echo of traffic noise. Thus, by emitting pulses of high frequency, broadband, and short duration, it retrieves more accurate information about the location and characterization of the environment in which it flies, facilitating the detection of background objects, preys, and avoiding collisions (Schnitzler and Kalko 2001). This increase in pulse frequencies was also observed for *Tadarida brasiliensis*, a species for which the amplitude, duration, and bandwidth of echolocation pulses increased when individuals were exposed to digitally generated noise at 85 dB (Tressler and Smotherman 2009).

However, noise limits signal detection, thus reducing the echolocation range (Tyack and Janik 2013); also, the distance for prey detection becomes shorter in areas with background noise, so the increased frequencies and shorter pulses respond to prey detection at a shorter range.

The results also showed that, in the urban environment, there is a greater difference in the frequency between high and low pulses. Different hypotheses have been put forward about the use of pulse alternation in different bat species (Kingston et al. 2003), the most plausible being that emitting pulses at different frequencies maximizes the detection distance, allowing a precise discrimination of the echoes of calls (Jung et al. 2006). For this study, the sequences with the highest number of high pulses were those corresponding to the urban environment, so that alternating pulse fre-

quencies would improve the classification of traffic noise echoes; however, the difference between pulses is greater as pulse frequencies increase, representing a higher energy expenditure for the bat, likely related to the additional work by the muscles of the abdominal wall involved in the production of echolocation pulses (Currie et al. 2020).

Our results do not associate the increased frequencies in the pulses of *M. megalophylla* with noise. The values recorded in Cuernavaca are similar to those recorded in Sierra de Huautla in this study, where anthropogenic noise is lower. The duration of the pulses (6.4 ± 0.5 ms) recorded in the Reserve is similar to the duration (6.9 ms) reported in a previous study in the same area (Orozco-Lugo et al. 2013) and to the 5.55 ± 2.19 ms reported for a location in the state of Oaxaca (Briones-Salas et al. 2013). The variation in frequency is likely associated with harmonics, integer

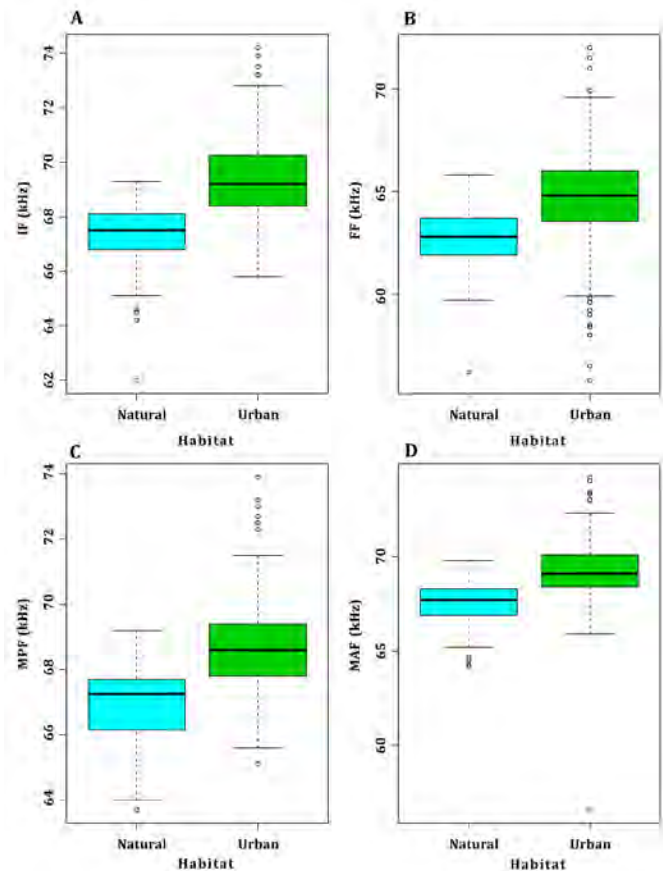


Figure 4. Box plots of the frequency and time components of the echolocation pulses of *M. megalophylla* contrasted in the natural and urban areas. (A) Initial frequency, (B) final frequency, (C) mid-pulse frequency, and (D) maximum amplitude frequency. The black line represents the median; boxes represent the ranges between quartiles, and whiskers represent the minimum and maximum values.

multiples of the lowest harmonic, or the fundamental signal (Jones and Teeling 2006). Commonly, in the echolocation pulses of the family Mormoopidae, a fundamental harmonic is emitted with frequencies around 30 kHz followed by three harmonics ranging from 60 to 120 kHz (Griffiths 1978). Specialized structures in the larynx of Mormoopids amplify the second harmonic and can suppress the fundamental signal (Griffiths 1978). The incidence of harmonic emission depends on the foraging environment and the positioning of the ultrasonic microphone toward the bat (Fenton et al. 2011). In open spaces, some species can emit narrow-band multi-harmonic signals dominated by non-fundamental harmonics (Jones and Teeling 2006). *Eptesicus fuscus* emits three harmonics above the fundamental one when flying in enclosed spaces, and one harmonic above the fundamental signal in open spaces (Fenton et al. 2011). When *M. megalophylla* flies in an open space, only the second harmonic is recorded. Research on bats addressing the effect of anthropogenic noise is still scarce. For this reason, it is important to carry out further studies to determine and understand the changes in echolocation frequencies and duration of their pulses because, depending on these modifications, bats will be able to thrive in an environment increasingly transformed by anthropogenic activities.

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Evaluation of the distribution pattern on a Neotropical microcarvívora

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The Pacific region, one of the most disturbed areas in México, is home to the pygmy spotted skunk (*Spilogale pygmaea*), a local endemic species and one of the smallest carnivores in the world. This small carnivore is currently listed as a species subjected to special protection in México and the International Union for Conservation of Nature. The objective of this work was to model environmental suitability and estimate the potential distribution of *S. pygmaea* in México. Predictive models were created using climatic, anthropic, and topographic variables with the Maxent tool. Models were assessed through partial Receiver Operating Characteristic (ROC) performance by omission rate and AUC. Finally, land use within the predicted potential area (potential distribution) was analyzed using the 2015 land cover layer of México issued by CONABIO. According to the model, *S. pygmaea* has a potential distribution from southern Sinaloa to Chiapas, comprising Michoacán and Guerrero towards the Balsas River basin in relation to dry forests. The predicted area was $95,600 \pm 0.02 \text{ km}^2$, representing a restricted distribution in México. Many localities have low environmental suitability (<0.4) and ecosystem modification and fragmentation, mainly influenced by livestock density. *Spilogale pygmaea* may be considered rare due to the lack of sampling, which jeopardizes the conservation of this group given its fragmented habitat. Additionally, *S. pygmaea* is attracted to areas with human settlements, potentially leading to human-animal conflicts. Natural areas, along with information sharing on the presence and importance of the species in nearby communities, may be an effective strategy to benefit this small carnivore.

La región del Pacífico es una de las zonas más perturbadas de México y área de distribución del zorrillo pigmeo (*Spilogale pygmaea*) una especie endémica de esta región y uno de los carnívoros de menor tamaño del mundo. Actualmente, este pequeño carnívoro se encuentra en un estatus de protección especial en México y por la International Union for Conservation of Nature. El objetivo de este trabajo fue modelar la idoneidad ambiental y estimar la distribución potencial de *S. pygmaea* en México. Se generaron modelos predictivos utilizando variables climáticas, antrópicas y topográficas desde la herramienta Maxent. Los modelos se evaluaron según la ROC parcial, el rendimiento midiendo la tasa de omisión y el AUC. Por último, se realizó un análisis de uso de suelo dentro del área potencial predicha (distribución potencial), para esto, se utilizó la capa de cobertura de suelo de México para el 2015 de CONABIO. De acuerdo al modelo de distribución potencial, *S. pygmaea* se puede distribuir desde el sur de Sinaloa hasta Chiapas y entrar por Michoacán y Guerrero hacia la Cuenca del Balsas en torno a las selvas secas en el país, con un área predicha de $95,600 \pm 0.02 \text{ km}^2$, presentando una distribución restringida en el país. Muchas localidades presentan una baja idoneidad ambiental (< 0.4) y algunas zonas presentan alteración y fragmentación de los ecosistemas, lo cual es principalmente influenciado por la densidad de ganado. *Spilogale pygmaea* se ha considerado como poco común en su distribución, sin embargo, esto pudiera estar influenciado por la falta de muestreos, lo cual puede representar un problema para la conservación de esta especie, ya que su hábitat se encuentra fragmentado. Por otro lado, *S. pygmaea* se ve influenciado positivamente hacia las zonas pobladas, lo cual puede generar conflicto humano-animal. Las áreas naturales en conjunto con la divulgación sobre la presencia e importancia de la especie en las comunidades cercanas pueden ser una estrategia que beneficie a este pequeño carnívoro.

Keywords: Conservation; carnivores, endemic; potential distribution; Mephitidae; *Spilogale pygmaea*.

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Introduction

The pygmy spotted skunk, *Spilogale pygmaea*, is one of the smallest carnivores in the family Mephitidae and the genus *Spilogale* (Medellín *et al.* 1998; Wilson and Reeder 2005). This species is endemic to México, and its distribution has been reported from southern Sinaloa to the Pacific coast of the state of Oaxaca (Medellín *et al.* 1998), from sea level to 1,630 masl (Ceballos and Miranda 2000), mainly in deciduous forests (Cantú-Salazar *et al.* 2009; Domínguez-Castellanos and González 2011). It is considered a rare species throughout its distribution range (Medellín *et al.* 1998).

This small skunk belongs to the carnivore guild (Dragoo *et al.* 1993; Wilson and Reeder 2005), but also consumes a great diversity of insects and fruits, depending on food availability (Cantú-Salazar *et al.* 2005). Thus, it plays a key role within its environment, acting as a pest controller and an efficient seed disperser (Medellín *et al.* 1998).

In México, habitat fragmentation and loss (Sarukhan 2008) threaten this small carnivore. The main disturbances affecting the distribution of this species include urbanization, agriculture, livestock, and forest fires, all of which are common in the Pacific Coast (Trejo 2005; Ceballos *et*

al. 2010; Botello et al. 2015; Mas et al. 2017). These issues can fragment natural populations and reduce connectivity between them (Tlapaya and Gallina 2010; Capdevila-Argüelles et al. 2013), which may lead to the loss of *S. pygmaea* populations in some localities.

S. pygmaea is currently listed as a species subject to special protection in NOM-059-SEMARNAT 2010 and as vulnerable by the International Union for Conservation of Nature (Helgen et al. 2016). Given the anthropic modifications in its environment, it is important to know the potential distribution and the impact of anthropic pressures on an endemic species such as *S. pygmaea*. However, for rare species, understanding the distribution and drivers of these patterns is challenging and resource-intensive (Perkins-Taylor and Frey 2020).

Environmental suitability and potential distribution models support inferences about the distribution of species (Austin 2002; Pérez-Irribe et al. 2019) from biological and environmental information (Guisan and Zimmermann 2000; Franklin 2010). These techniques are based on modeling the niche of a species in an n -dimensional space (Elith et al. 2006; Soberón et al. 2017), identifying the environmental requirements of the species (Soberón and Nakamura 2009) and visualizing them on maps to identify potential regions where these species may be distributed (Lindenmayer et al. 1991). The hypotheses derived from these models usually estimate the potential distribution in a predicted area or environmental suitability ranges (Soberón and Peterson 2005). These results can be an important support for species conservation strategies (Mercado and Wallace 2010; Cuervo-Robayo and Monroy-Vilchis 2012; Carrillo-Reyna et al. 2015).

Assessing the potential distribution of species in the Anthropocene is essential considering the current loss of biodiversity and habitats. This information may support the development of conservation strategies at local and national levels. The objective of this work was to model environmental suitability and estimate the potential distribution of *S. pygmaea* in México based on presence records and scenopoetic and interactive variables.

Materials and methods

To build environmental suitability models, a region of interest was delineated based on the area accessible to the species (Soberón and Peterson 2005; Peterson et al. 2011), using the classification of Biogeographic Regions of México issued by CONABIO (1997). The Pacific Coast, Balsas Depression, and Sierra Madre del Sur were considered as these are the layers that match the known distribution of the species (González and Arroyo-Cabrales 2012).

The model was built using data collected based on georeferenced records from publications, theses, and museum data (Cortés-Marcial and Briones-Salas 2014; Buenrostro-Silva et al. 2015; Urra-Galeano et al. 2016; Juárez-Agís et al. 2020; Briseño-Hernández and Naranjo 2021). We also con-

sulted presence records collected by Ballesteros-Barrera et al. (2016) and Lavariega and Briones-Salas (2019; available at: www.conabio.gob.mx/informacion/gis/). Private presence data were gathered from users of the NaturaLista platform. The data not provided were considered for model assessment only because they are shown as a random point within an area of ± 20 km² for species at risk.

The records were refined by removing spatially correlated and duplicate records. The SDMToolbox space tool was used in ArcMap[®] 10.3 (Brown 2014). Records were discarded at a minimum distance of 1.2 km (approximately equivalent to the size of a pixel), resulting in 76 presence records.

Variables were selected according to their importance and influence on the species (Buenrostro-Silva et al. 2015). The climatic layers by Cuervo-Robayo et al. (2013) were considered environmental variables. Only the distance to water bodies was included as a topographic variable. Vegetation attributes included distance to deciduous forest or grassland (secondary and natural) and percentage of tree cover; the anthropogenic attributes considered were distance to urban and agricultural areas and livestock density (Appendix 1).

The distance variables were estimated using the National Forest Inventory, Series VI (INEGI 2016). Polygons were divided according to the attribute, and the Euclidean distance was calculated for each polygon. Once all the geodata were obtained, the resolution of variables was adjusted based on climatic variables, resulting in an approximate size of 800 m².

The importance of the variables to the model was assessed by a jackknife analysis in Maxent and by Pearson's correlation between variables through the Ntbox package (Osorio-Olvera et al. 2020) in Rstudio; those with a ratio > 0.7 were discarded, identifying the variable with the highest percent contribution to the model and then removing the variable correlated with it (Warren et al. 2014; Perkins-Taylor and Frey 2020). The result was a set of seven climatic variables, three vegetation and anthropic variables, and one topographic variable (Appendix 1).

Models were built using the MaxEnt algorithm (Phillips et al. 2017), which has shown a good performance in predicting the potential distribution of species from presence records and environmental variables (Elith et al. 2006; Phillips et al. 2006). In addition, MaxEnt is an effective tool when limited data are available (Byeon et al. 2018), as in the case of *S. pygmaea*.

Potential models were built using 70 % ($n = 53$) and assessed using 30 % ($n = 23$) of records. We tested 29 possible combinations of entity classes including linear, quadratic, product, threshold, and hinge, which allow adjusting simple interactions (Elith et al. 2011). Models were evaluated according to their statistical significance. The area under the curve (AUC) was obtained directly from the model assessment through the "Receiver Operating Characteristic" (ROC) curve, which measures sensitivity and

specificity; values closest to 1 indicate perfect discrimination (Byeon et al. 2018). The Partial ROC (Peterson et al. 2008) was determined by resampling 1,000 bootstrap interactions using 50 % of the independent data from presence records, and setting a 5 % omission error with the Ntbox platform (Osorio-Olvera et al. 2020).

The simplest model was selected, considering as reliable AUC values above 0.75 (Elith et al. 2011) and Partial ROC >1 (Peterson et al. 2008). The model selected was exported with a logistic output, which offers an interpretation associated with environmental suitability (Mateo et al. 2011).

A cutoff threshold was applied to estimate the potential distribution, evaluate the predicted area, and exclude false positives, using 70 % of the records used to build the model. The minimum value was selected as cutoff level (Pearson et al. 2007; Espinoza-García et al. 2014).

A land-use analysis was performed within the predicted potential area using the 2015 land-cover layer of México (CONABIO 2020). First, the land-use layer was trimmed based on the potential distribution. Subsequently, land-use attributes were sorted into three categories: conserved vegetation (deciduous forest, mixed forest, temperate forest), agricultural areas, and urban zones. Finally, the area occupied by each category was calculated.

The results were interpreted and discussed by overlapping the final maps on the layer of México (INEGI 2019), to facilitate the state conservation policy.

Results

The states with the largest number of records were Jalisco ($n = 17$) and Guerrero ($n = 28$), both with 57.8 % of the data (Figure 1). The records were obtained mainly from scientific collections in museums ($n = 54$) and the rest from the NaturaLista platform ($n = 16$) and paper reports ($n = 6$). New localities were reported in Michoacán (Urrea-Galeano et al. 2016) and the most southern record in Juchitán, Oaxaca (Cortés-Marcial and Briones-Salas 2014).



Figure 1. Potential distribution of *S. pygmaea* and presence records used in the model.

The optimal model selected was created from three class types (hinge, linear, and quadratic). Its evaluation showed optimal AUC (0.89) and partial ROC (1.59 ± 0.14) values; random AUC and partial AUC values were statistically different ($P < 0.0001$).

The variables with the greatest contribution to the model were distance to water bodies (31.3 %), maximum temperature of the warmest month (14.0 %), and precipitation of the driest month (12.8 %), which together explain 58.1 % of the model. The influence observed showed a positive relationship with water bodies and a negative relationship with temperatures of the warmest month >35 °C and with areas with precipitation of the driest month >5 mm (Table 1).

In the case of anthropic variables, a positive influence was observed with agricultural areas and the periphery of urban zones (Table 1). However, livestock density responded negatively, affecting the presence of the species.

The data analysis revealed that *S. pygmaea* prefers areas adjacent to rivers and lagoons, limiting its distribution to livestock areas. It is associated with subhumid

Table 1. Percent contribution of the variables in the environmental suitability model for *S. pygmaea*.

Variable	Percent contribution (%)	Importance of permutation (%)
Distance to water bodies	31.3	26.3
Maximum temperature of the warmest month	14.0	20.9
Precipitation of the driest month	12.8	15.0
Precipitation of the wettest month	9.0	17.7
Livestock density	8.4	2.7
Average day range	6.9	0
Distance to deciduous forests	6.3	0.6
Percentage of tree cover	3.1	4.5
Minimum temperature of the coldest month	2.0	0.9
Distance to grasslands	1.9	1.0
Distance to urban areas	1.5	0.5
Annual mean precipitation	1.3	6.8
Isothermality	0.7	2.2
Distance to agricultural land	0.7	0.8

warm climates with the temperature of the warmest month between 19 °C and 32 °C, and avoids areas with high precipitation. The environmental suitability map indicated that the areas of greatest suitability (>0.4) are located around the *Huatulco* and *Lagunas de Chachahua* National Parks, Oaxaca; in areas surrounding Acapulco de Juárez, Guerrero; adjacent to the Balsas basin between Michoacán and Guerrero, where it penetrates inland to the mid Balsas, Guerrero, restrained by extreme temperatures (>35 °C). In Colima, its potential distribution ranges from the Malaque tropical forest along the coast of Jalisco to the deciduous tropical forest surrounding Puerto Vallarta, the tropical forests in Nayarit, and the *Meseta de Cacaxtla* Natural Protected Area in Sinaloa (Figure 2).

The optimal threshold for this model was 0.2, with a potential distribution of approximately 95,600 ± 0.02 km², comprising 4.9 % of the mainland area of México (INEGI 2018). The states with the largest potential distribution area are Michoacán (45,300 ± 0.05 km²), Guerrero (30,000 ± 0.1 km²), and Jalisco (26,500 ± 0.1 km²).

However, regarding the conserved habitat alone (*i. e.*, forests and tropical forests within the potential distribution range) comprises 60,900 ± 0.03 km², representing a loss of 34,700 ± 0.02 km² (agricultural area = 34,500 ± 0.2 km²; urban area = 260 ± 2.3 km²) as a result of anthropic fragmentation.

Discussion

Historically, *Spilogale pygmaea* has been considered an uncommon species across its distribution range (Medellín *et al.* 1998). This perception might be due to the lack of sampling since reports are scarce. It is worth highlighting that the reports found are new localities for Michoacán (Charre-Medellín 2012; Urrea-Galeano *et al.* 2016), Oaxaca (Cortés-Marcial and Briones-Salas 2014), and Guerrero (Briseño-Hernández and Naranjo 2021); however, the interest and focus of these studies was on larger mammals. Based on our results, *S. pygmaea* may be distributed up to Chiapas in the south and through the Balsas River basin up to Morelos and Puebla.

The records obtained on the citizen science platforms provide a useful tool when there is insufficient information on the species to conduct an analysis like the one reported herein. However, these data should be used with caution (in model assessment) as there may be uncertainty in localities or species identification. Therefore, data should be refined based on specialized literature. Historical bases of museums or in the literature are considered reliable sources, keeping in mind that environmental and land-use changes may be unsuitable for some species, thus affecting the development of conservation strategies (Plissock and Fuentes-Castillo 2011; Espinoza-García *et al.* 2014).

According to our results, much of the area predicted as potentially suitable provides an unfavorable scenario for *S. pygmaea* (Balvanera *et al.* 2000; Crooks 2002; Botello *et*

al. 2015) since it involves fragmented zones, which could hamper the conservation of the species (Cantú-Salazar *et al.* 2005). Land-use change and livestock raising have a negative impact on colonization between patches (Lira-Torres and Briones-Salas 2011). Although the distribution of this small carnivore is influenced by its affinity to disturbed areas, this does not indicate that the species thrives or remains in these areas since habitat modifications or reduction have adverse effects on its permanence and distribution patterns. In the case of species with a restricted range, distribution patterns may be influenced by anthropogenic effects (McDonald *et al.* 2018; Perkins-Taylor and Frey 2020). An aspect not addressed in this study but that is also a consequence of anthropic activities is the pollution of water bodies. Today, this issue is on the rise (Rodríguez *et al.* 2013), and although the water requirement of the pygmy spotted skunk may be lower relative to other mammals, this resource is vital (Charre-Medellín 2012) and may affect its populations.

Spilogale pygmaea has a varied diet (Cantú-Salazar *et al.* 2005), nocturnal habits (Sánchez-Cordero and Martínez-Meyer 2000), and the ability to move across patches (Nupp and Swihart 2000; Gehring and Swihart 2004). These habits could reduce the risk of conflicts with humans in semi-urban and agricultural areas, increasing its chances of survival. However, although *S. pygmaea* may potentially be found in areas of low environmental suitability, ignorance about this species might lead to interactions and problems with humans, as observed with other species (Alvarado-Barboza and Gutiérrez-Espeleta 2013).

The assessment of climatic variables shows that water bodies, marked seasonality, precipitation of the driest month of 5 mm, and warm climates favor the presence of this species; these characteristics are typical of dry forests where *S. pygmaea* is abundant (Buenrostro-Silva *et al.* 2015; Lira-Torres *et al.* 2012; Cantú-Salazar *et al.* 2009; Domínguez-Castellanos and González 2011; Cortés-Marcial *et al.* 2014; Charre-Medellín 2012; Bradie and Leung 2017).

Within the potential distribution range of this species, the *Lagunas de Chachahua* National Park, Chamela-Cuix-



Figure 2. Environmental suitability of *S. pygmaea* in México.

mala Biosphere Reserve, Zicuirán-Infiernillo Biosphere Reserve, *Meseta de Cacaxtla* Protected Natural Area, *Marismas Nacionales Nayarit* Biosphere Reserve, Huatulco and *El Veladero* National Parks and the Sierra de Manantlán Biosphere Reserve are important areas for conservation that provide shelter from habitat loss (Gallina et al. 2007; Jiménez et al. 2015). The presence of *S. pygmaea* in the first five areas is worth highlighting (Cantú-Salazar et al. 2009; Buenrostro-Silva et al. 2015; Urrea-Galeano et al. 2016; CONANP 2016; Guzmán-Pacheco 2019). Therefore, based on our results, we recommend the monitoring of non-confirmed areas to implement actions aiming to conserve this and other species.

Currently, most conservation efforts target larger mammals (>15 kg) because many are considered umbrella species due to their wide distribution (Thornton et al. 2016). Smaller mammals that are not necessarily covered by the protection of these large umbrellas, either because of their reduced range or, as in the case of *S. pygmaea*, because of their fragmented distribution, are left outside of government conservation initiatives (Thornton et al. 2016).

There is little information available about the distribution range of *S. pygmaea*. The potential distribution is well represented on the Pacific coast; however, few areas have high environmental suitability. The distance to water bodies positively influences environmental suitability, while high livestock density has the opposite effect. Although *S. pygmaea* is associated with semi-urban areas, this does not mean that its permanence is guaranteed. Semi-urbanized areas should be monitored to understand better the distribution of this species and the influence of these areas on it. It is important to focus on small species, allocate areas for conservation and maintain the connectivity between their populations (Mills and Allendorf 1996). Also, outreach and education strategies should be implemented in nearby human communities to inform the local inhabitants about the importance of this species.

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Appendix 1

Variables used in the environmental suitability model and potential distribution of the pygmy spotted skunk (*Spilogale pygmaea*).

Variable	Unit of measure	Source
Average day range		
Isothermality	°C (degrees Celsius)	
Maximum temperature of the warmest month		
Minimum temperature of the coldest month		Cuervo-Robayo <i>et al.</i> (2013)
Annual Mean precipitation		
Precipitation of the wettest month	mm ³	
Precipitation of the driest month		
Distance to deciduous forests		
Distance to grasslands		
Distance to water bodies	Distance (decimal degrees)	National Forest Inventory, Series VI (INEGI 2016)
Distance to urban areas		
Distance to livestock areas		
Percentage of tree cover	Percentage	(Defries <i>et al.</i> 2000)
Livestock density	Density (individuals/km ²)	Robinson <i>et al.</i> (2014)