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EVOLUCIÓN DEL DIMORFISMO SEXUAL EN EL GÉNERO *SCELOPORUS* (SQUAMATA: PHRYNOSOMATIDAE): INTERACCIÓN ENTRE LA SELECCIÓN NATURAL Y SEXUAL

TESIS

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Me permito informar a usted que en la reunión ordinaria del Subcomité de Ecología y Manejo Integral de Ecosistemas del Posgrado en Ciencias Biológicas, celebrada el día 26 de febrero de 2018, se aprobó el siguiente jurado para el examen de grado de DOCTOR EN CIENCIAS del alumno JIMENEZ ARCOS VICTOR HUGO, con número de cuenta 98140233, con la tesis titulada "Evolución del dimorfismo sexual en lagartijas del género Sceloporus (Squamata: Phrynosomatidae): interacción entre la selección natural y sexual", realizada bajo la dirección del DR. RAÚL CUEVA DEL CASTILLO MENDOZA:

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Sin otro particular, me es grato enviarle un cordial saludo.

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DR. ADOLFO GERARDO NAVARRO SIGÜENZA COORDINADOR DEL PROGRAMA



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Realizar estudios de posgrado, especialmente un doctorado, no es una tarea sencilla. Parte de lograr esa meta radica además de adquirir los conocimientos especializados, en resolver problemas potenciales durante el desarrollo de la investigación considerando el tiempo limitado para su ejecución. Es así que el posgrado comprende no solo la formación académica, también la adquisición de diversas herramientas y habilidades para lograr una formación integral. Considerando esto, quiero agradecer a mi tutor principal, Dr. Raúl Cueva del Castillo Mendoza por todos sus consejos y orientación a través de los años, más allá de la realización de este trabajo. Raúl es uno de los mejores profesores que he conocido en el área de biología evolutiva, y un gran investigador con una visión clara que incentiva la investigación. Agradezco todo el tiempo invertido en mi formación y su honestidad en cada una de estas etapas. Sus enseñanzas han permeado más allá del ámbito académico. Muchas gracias Raúl.

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Índice

Abstract1
Introducción general2
Capítulo I8
The interplay between natural and sexual selection in the evolution of sexual size dimorphism in <i>Sceloporus</i> lizards (Squamata: Phrynosomatidae)
Artículo de requisito para la obtención de grado
Ecology and Evolution, 7: 905-917
Capítulo II
Habitat use and sexual dimorphism in <i>Sceloporus grammicus</i> (Squamata: Phrynosomatidae)
Artículo enviado
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Resumen

El dimorfismo sexual es una característica ampliamente distribuida en animales bilaterales con reproducción sexual. La selección sexual explica la evolución de caracteres sexuales secundarios y/o mayor talla corporal en el sexo seleccionado. Por selección en fecundidad se esperan tallas corporales mayores en hembras o mayor volumen o tamaño abdominal favoreciendo la maduración de un mayor número o tamaño de huevos o crías. También la divergencia del nicho ecológico entre sexos puede generar dimorfismo sexual en cualquier rasgo asociado al uso o explotación de recursos, aunque no es posible predecir tendencias generales en talla y forma. La divergencia entre sexos puede resultar de la interacción entre la selección natural y sexual, debido a que los rasgos fenotípicos pueden estar sujetos a diferentes presiones selectivas. El estudio del impacto relativo de la selección natural y sexual proporciona un análisis completo de los mecanismos responsables de generar la divergencia adaptativa entre los sexos. Las lagartijas del género Sceloporus son un modelo ideal para evaluar la importancia relativa de la selección natural y sexual en la evolución del dimorfismo sexual. La gran variación morfológica, ecológica y conductual sugieren que ambas fuerzas evolutivas han moldeado la evolución del género. Además presentan modo reproductor ovíparo y vivíparo, y se ha sugerido que las hembras de especies vivíparas debido a la extensión en el periodo de gestación presentan mayor talla que hembras de especies ovíparas. El objetivo de esta tesis fue analizar el impacto relativo de la selección natural y sexual en la evolución del dimorfismo sexual en las lagartijas del género Sceloporus utilizando métodos comparativos filogenéticos. El dimorfismo sexual puede resultar del balance entre la selección natural y la selección sexual. Una vez que los efectos filogenéticos son controlados, nuestros resultados muestran un mayor impacto relativo de la selección sexual en la divergencia en talla en el género Sceloporus. La regla de Rensch es un patrón explicado por las ventajas selectivas de machos con mayor talla corporal y el incremento en la magnitud a medida que aumenta la talla promedio de las especies. En lagartijas la selección intrasexual es la principal causa de dimorfismo sexual en talla sesgado a machos. La historia evolutiva dentro del género sugiere un mayor rol diversificador de la selección sexual sobre la selección en fecundidad. A nivel interpoblacional (Capítulo 2), algunos rasgos están bajo diferentes fuerzas selectivas. Talla, tamaño de cabeza y extremidades pueden está bajo selección sexual en machos. En las hembras, la longitud del tronco presentó un pendiente mayor a 1 (hiperalometría) en la población generalista. Es posible que la interacción entre selección natural y sexual tenga un efecto antagónico, como en lagartijas arborícolas (sobre tamaño de extremidades y cabeza en machos) o sinérgico (mayor longitud de tronco) en función del contexto ecológico. El género Sceloporus exhibe la mayor diversidad en México y las especies son encontradas en todos los tipos de vegetación. Su gran diversidad morfológica, ecológica y conductual sugieren que la selección natural y sexual han tenido un papel central en su evolución. Es probable que Sceloporus represente un ejemplo de una radiación adaptativa. Sin embargo, elementos básicos de historia natural, ecología y reproducción son desconocidos, especialmente en especies con distribución limitada a México. Estudios futuros deben encaminarse en obtener información de historia natural como una primera aproximación. Estudios experimentales evaluando la significancia adaptativa de los rasgos fenotípicos, tanto por selección natural, sexual y variables ecológicas (i.e. bióticas y abióticas) son necesarios para determinar los mecanismos que han conducido favorecido la divergencia y diversificación del género.

Abstract

Sexual dimorphism is a widely distributed characteristic in bilateral animals with sexual reproduction. Sexual selection explains the evolution of secondary sexual characters and / or greater body size in the selected sex. By selection in fecundity, larger body sizes are expected in females or larger volume or abdominal size favoring the maturation of a greater number or size of eggs or offspring. Also the divergence of the ecological niche between the sexes can generate sexual dimorphism in any feature associated with the use or exploitation of resources, although it is not possible to predict general trends in size or shape. Divergence between sexes can result from the interaction between natural and sexual selection, because phenotypic traits can be subject to different selective pressures. The study of the relative impact of natural and sexual selection provides a complete analysis of the mechanisms responsible for generating the adaptive divergence between the sexes. The lizards of the genus Sceloporus are an ideal model to evaluate the relative importance of natural and sexual selection in the evolution of sexual dimorphism. The great morphological, ecological and behavioral variation suggests that both evolutionary forces have shaped the evolution of the genus. They also have an oviparous and viviparous reproductive mode, and it has been suggested that females of viviparous species due to the extension in the gestation period are larger than females of oviparous species. The objective of this thesis was to analyze the relative impact of natural and sexual selection on the evolution of sexual dimorphism in lizards of the genus Sceloporus using comparative methods. Sexual dimorphism can result from the balance between natural selection and sexual selection. Once the phylogenetic effects are controlled, our results show a greater relative impact of sexual selection on the divergence in body size in the genus Sceloporus. Rensch's rule is a pattern explained by the selective advantages of males with larger body size and the increase in magnitude as the average size of the species increases. In lizards, intrasexual selection is the main cause of sexual dimorphism in males biased size. The evolutionary history within the genus suggests a greater diversifying role of sexual selection over fecundity selection. At the interpopulation level (Chapter 2), some features are under different selective forces. Body Size, head and limbs size may be under sexual selection in males. In the females, the length of the trunk presented a slope greater than 1 (hyperalometry) in the generalist population. It is possible that the interaction between natural and sexual selection has an antagonistic effect, as in arboreal lizards (on limb size and head in males) or synergistic (greater trunk length) depending on the ecological context. The genus Sceloporus exhibits the greatest diversity in Mexico and the species are found in all types of vegetation. Its great morphological, ecological and behavioral diversity suggest that natural and sexual selection have played a central role in its evolution. It is likely that Sceloporus represents an example of adaptive radiation. However, basic elements of natural history, ecology and reproduction are unknown, especially in species with limited distribution to Mexico. Future studies should aim to obtain natural history information as a first approximation. Experimental studies evaluating the adaptive significance of phenotypic traits, both natural selection, sexual and ecological variables (biotic and abiotic i.e.) are necessary to determine the mechanisms that have led to the divergence and diversification of gender.

Introducción general

El dimorfismo sexual es una característica ampliamente distribuida en animales bilaterales con reproducción sexual (Fairbairn 2013). Se han planteado tres hipótesis para explicar la evolución y mantenimiento del dimorfismo sexual. Las diferencias fenotípicas entre hembras y machos pueden evolucionar como resultado de distintos óptimos reproductivos entre ambos sexos (West-Eberhard 1983; Andersson 1994; Fairbairn et al. 2007). Así, la selección sexual explica la evolución de caracteres sexuales secundarios y/o mayor talla corporal en el sexo seleccionado (usualmente machos; Darwin 1871; West-Eberhard 1983; Andersson 1994). Este tipo de dimorfismo sexual evoluciona porque los caracteres sexuales o talla corporal incrementan las oportunidades de apareamiento o probabilidades de fertilización, ya sea por elección de pareja y/o incrementando las habilidades competitivas (Andersson 1994; Andersson & Simmons 2006). La selección en fecundidad explica tallas corporales mayores en hembras o mayor volumen o tamaño abdominal. Bajo esta hipótesis es de esperarse un incremento positivo entre la talla y el número o tamaño de la progenie (Fairbairn 1997; Fairbairn et al. 2007; Cueva del Castillo & Fairbairn 2011; Pincheira-Donoso & Hunt 2015). El dimorfismo sexual también puede originarse por la divergencia del nicho ecológico entre sexos, asociado a estrategias de dispersión distintas o adaptaciones para reducir la competencia trófica (revisado en Slatkin 1984; Shine 1989). Bajo esta hipótesis es de esperarse divergencia en rasgos asociados al uso o explotación de recursos (Losos et al. 2003). Sin embargo, está sujeto a debate si la divergencia del nicho ecológico es realmente independiente de otros factores selectivos (ver Fairbairn et al. 2007).

Debido a que los rasgos fenotípicos pueden estar sujetos a diferentes presiones selectivas, la divergencia entre sexos puede resultar de la interacción entre la selección natural y sexual. El estudio del impacto relativo de la selección natural y sexual proporciona un análisis completo de los mecanismos responsables de generar la divergencia adaptativa entre los sexos (Panhuis et al. 2001; Jones & Ratterman 2009; Cornwallis & Uller 2010; Bonduriansky 2011; Kraaijeveld et al. 2011; Maan & Seehausen 2011; Scordato et al. 2014). Si la selección en fecundidad es intensa, el volumen abdominal puede ser desproporcionalmente mayor en hembras aún con tallas corporales menores a machos (Braña 1996; Cox et al. 2003; Cox et al. 2007). No obstante, aun cuando la selección en fecundidad favorezca mayor talla en hembras, la importancia relativa de la selección sexual puede ser mayor generando patrones de dimorfismo sexual sesgados a machos (Fairbairn et al. 2007; Pincheira-Donoso et al. 2008; Pincheira-Donoso & Tregenza 2011). En diversos grupos de vertebrados e invertebrados, la magnitud del dimorfismo sexual cambia, aumentando o decreciendo en función de una mayor talla corporal promedio entre especies (Fairbairn et al. 2007; Webb & Freckleton 2007). El incremento en la magnitud del dimorfísmo sexual se correlaciona con especies donde los machos son más grandes que las hembras, y es atribuido a una intensa selección sexual favoreciendo a los machos de mayor tamaño (Fairbairn et al. 2007; Cox et al. 2007; Stillwell et al. 2010). Aunque cabe señalar que en diversos grupos se ha favorecido la evolución de menor tamaño corporal en machos, favoreciendo mayor movilidad o agilidad lo que incrementa las oportunidades de fertilización (ver Serrano-Meneses & Székely 2006; Husak & Fox 2008). Aunque es menos común, el patrón donde la magnitud del dimorfismo sexual incrementa en función de una mayor talla corporal de las hembras es asociado a presiones intensas de selección en fecundidad (Foellmer & Moya-Laraño 2007; Webb & Freckleton 2007). Ambos patrones son asociados a una mayor divergencia en el tamaño corporal de los machos comparado con la talla femenina. Este patrón es conocido como la regla de Rensch (Rensch 1950; Fairbairn 1997; Blanckenhorn et al. 2007).

Las lagartijas son organismos modelo en el estudio de la divergencia fenotípica entre sexos, debido a que usualmente los sexos difieren en talla y forma (Olsson et al. 2002; Cox et al. 2007). Además hay familias, géneros y especies con modo reproductor ovíparo y vivíparo (ver Lambert & Wiens 2013; Watson et al. 2014). En algunas especies vivíparas el desarrollo embrionario sucede en una placenta (e.g. familia Mabuyidae), mientras que en otras, las hembras retienen los huevos dentro del útero hasta que el desarrollo es completado (Méndez-de la Cruz et al. 1998). Debido a la extensión en el periodo de gestación, se ha sugerido que las especies vivíparas exhiben mayor talla corporal o abdómenes más grandes que las especies ovíparas (Qualls & Shine 1995; Braña 1996; Pincheira-Donoso & Tregenza 2011; Scharf & Meiri 2013; Sun et al. 2012). En ambos modos reproductores, especies no relacionadas cercanamente exhiben dimorfismo sexual con hembras de mayor tamaño y una relación positiva entre el número o tamaño de huevos o crías (Braña 1996; Cox et al. 2003; Cox et al. 2007; Pincheira-Donoso & Hunt 2015). Inclusive en especies con machos de mayor tamaño corporal, un incremento desproporcionado en la longitud del tronco de las hembras es asociado a la maduración de más o mayor tamaño de progenie (Braña 1996; Olsson et al. 2002; Cox et al. 2003).

No obstante en la mayoría de las especies de lagartijas los machos muestran talla corporal mayor a las hembras. También confrontaciones entre machos con movimientos acrobáticos y mordidas son comunes por defensa de territorio y acceso a apareamientos. Se ha planteado que rasgos fenotípicos como extremidades y cabezas son de mayor tamaño en machos, puesto que incrementan las habilidades competitivas y las probabilidades de ganar confrontaciones con otros machos por territorios o parejas (Lappin et al. 2006; Husak & Fox 2008). Además las conductas de despliegue de coloración sexual son frecuentes en diversas familias (Carpenter et al. 1970; Carpenter 1978; Butler & Losos 2002; Alfaro-Juantorena & Jiménez-Arcos 2017). Durante los despliegues se muestran zonas con coloración sexual y se realizan elongaciones de extremidades y movimientos de cabeza. Estas conductas sugieren que la selección sexual puede favorecer mayor tamaño corporal de cabezas, extremidades y el desarrollo de coloración sexual conspicua en machos (Anderson & Vitt 1990; Wiens et al. 1999; Stuart-Fox & Ord 2004; Cox et al. 2007).

Las lagartijas del género *Sceloporus* son un modelo ideal para evaluar la importancia relativa de la selección natural y sexual en la evolución del dimorfismo sexual. Este género comprende más de 90 especies distribuidas desde el sur de Canadá hasta el norte de Panamá, con su mayor diversidad en México (Köhler & Heimes 2002; Bell et al. 2003). Se distribuyen en prácticamente todos los ecosistemas terrestres del país desde los 0 hasta más de 4000 msnm (Smith 1939; Sites et al. 1992). Las poblaciones son abundantes, siendo el elemento más conspicuo de la herpetofauna mexicana (Sites et al. 1992). Los organismos adultos presentan una gran diversidad en tallas, que van desde los 40 mm (*S. bicanthalis*; Rodríguez-Romero et al. 2010) hasta más de 100 mm (*S. magister*; Fitch 1985) de longitud hocico-cloaca (aproximación de talla corporal en lagartijas; Losos 1990, Cox et al. 2003; Cox et al. 2007). El dicromatismo sexual es común, los machos presentan parches ventrales de color azul (o rosa; e.g. *S. variabilis* y *S. smithi*), así como diversos patrones de coloración sexual en cabeza y cuerpo (Wiens et al. 1999; Köhler & Heimes 2002). El dicromatismo sexual y conductas de despliegue sugieren que la selección sexual

ha jugado un papel central en la divergencia fenotípica entre sexos dentro del género (Carpenter 1978; Martins 1994; Wiens et al. 1999). Asimismo, hay especies ovíparas y vivíparas, y en estas últimas los periodos de gestación son mayores (Méndez–de la Cruz et al. 1998). A nivel comparativo, sin incorporar métodos comparativos filogenéticos, se han registrado dimorfismo sexual en talla sesgado a ambos sexos dentro de la familia Phrynosomatidae (Cox et al. 2007) y dentro del género *Sceloporus* (Fitch 1978). Actualmente las relaciones filogenéticas del género son relativamente bien comprendidas, y diversas filogenias congruentes entre si están disponibles (Leaché 2010; Wiens et al. 2010; Leaché et al. 2016), lo que permite su incorporación al analizar la evolución adaptativa del grupo.

Debido a la gran diversidad morfológica, conductual y ecológica es probable que la selección natural y selección sexual hayan moldeado la divergencia fenotípica del género. El objetivo de esta tesis fue analizar el impacto relativo de la selección natural y sexual en la evolución del dimorfismo sexual en las lagartijas del género *Sceloporus*. Estudios previos han registrado dimorfismo sexual en talla sesgado a ambos sexos, con una tendencia a presentar machos de mayor tamaño corporal (ver Phrynosomatidae: Cox et al. 2007; *Sceloporus*: Fitch 1978). Sin embargo, estos estudios no consideran las relaciones filogenéticas entre las especies, por lo que no es posible separar los componentes asociados a una ancestría común, de aquellos que han sido resultado de la adaptación a las condiciones particulares en las que ha evolucionado cada especie (Felsenstein 1985; Harvey & Pagel 1991; Martins & Hansen 1997). En el Capítulo 1 de este trabajo, empleando métodos comparativos filogenéticos se analizó la relación entre la talla corporal de hembras y el tamaño de camada o nidada. Además se comparó la talla entre especies con

modo reproductor vivíparo y ovíparo. También se analizaron las tendencias alométricas en la magnitud del dimorfismo sexual en talla (i.e. regla de Rensch), y la reconstrucción de estados de carácter ancestral en el género y grupos externos. Este capítulo fue publicado en la revista *Ecology and Evolution*. En el Capítulo 2 se compararon las tendencias alométricas entre poblaciones en el dimorfismo sexual en la lagartija vivípara *S. grammicus* entre poblaciones con diferente uso de hábitat. También se exploraron las diferencias en el uso del hábitat entre sexos como aproximación de la divergencia del nicho ecológico y su impacto en el dimorfismo sexual. En la última parte presento la discusión y conclusiones generales sobre los hallazgos encontrados en esta tesis.

CAPÍTULO I

The interplay between natural and sexual selection in the evolution of

sexual size dimorphism in *Sceloporus* lizards (Squamata:

Phrynosomatidae)

ORIGINAL RESEARCH

WILEY Ecology and Evolution

The interplay between natural and sexual selection in the evolution of sexual size dimorphism in Sceloporus lizards (Squamata: Phrynosomatidae)

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Abstract

Sexual size dimorphism (SSD) evolves because body size is usually related to reproductive success through different pathways in females and males. Female body size is strongly correlated with fecundity, while in males, body size is correlated with mating success. In many lizard species, males are larger than females, whereas in others, females are the larger sex, suggesting that selection on fecundity has been stronger than sexual selection on males. As placental development or egg retention requires more space within the abdominal cavity, it has been suggested that females of viviparous lizards have larger abdomens or body size than their oviparous relatives. Thus, it would be expected that females of viviparous species attain larger sizes than their oviparous relatives, generating more biased patterns of SSD. We test these predictions using lizards of the genus Sceloporus. After controlling for phylogenetic effects, our results confirm a strong relationship between female body size and fecundity, suggesting that selection for higher fecundity has had a main role in the evolution of female body size. However, oviparous and viviparous females exhibit similar sizes and allometric relationships. Even though there is a strong effect of body size on female fecundity, once phylogenetic effects are considered, we find that the slope of male on female body size is significantly larger than one, providing evidence of greater evolutionary divergence of male body size. These results suggest that the relative impact of sexual selection acting on males has been stronger than fecundity selection acting on females within Sceloporus lizards.

KEYWORDS

dimorphism, fecundity, Lizards, natural selection, Rensch's rule, Sceloporus, sexual selection

1 | INTRODUCTION

In animal species that reproduce sexually, adult males and females often differ in body size. This difference is termed sexual size dimorphism (SSD) and generally evolves because body size is commonly related to reproductive success through different pathways in females and males (Blanckenhorn, 2005; Fairbairn, Blanckenhorn, & Székely,

2007). In females, body size is strongly correlated with fecundity, whereas in males, body size is correlated with mating success. As result of these differences, the body size that conveys maximal fitness often differs between the sexes (Fairbairn et al., 2007). The impact of sexual selection on SSD has been well established in many studies of individual species as well as in many phylogenetically controlled comparisons among species (Andersson, 1994; Fairbairn, 1997; Fairbairn

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WILEY_Ecology and Evolution

et al., 2007). In addition, fecundity selection favors large female body size in species where females mature large numbers of eggs or live young within their abdomens, as in most fish, insects, and spiders (Blanckenhorn, 2005; Fairbairn, 1997; Fairbairn et al., 2007; Ruckstuhl & Neuhaus, 2005). SSD also can arise through ecological niche divergence, such as sex-specific foraging/dispersal strategies or adaptations to reduce intersexual trophic competition (reviews in Blanckenhorn, 2005; Fairbairn, 1997; Fairbairn et al., 2007; Hedrick & Temeles, 1989; Reiss, 1989; Ruckstuhl & Neuhaus, 2005; Shine, 1989). However, it is unlikely that niche divergence between males and females is truly independent of sexual divergence in reproductive roles (Butler & Losos, 2002; Butler, Schoener, & Losos, 2000; Fairbairn et al., 2007).

In many vertebrate and invertebrate taxa, the magnitude of SSD changes systematically with mean body size, either increasing or decreasing as body size increases (Fairbairn et al., 2007; Webb & Freckleton, 2007). The former pattern is common in species where males are larger than females, while the latter occurs commonly in species in which females are the larger sex. Both patterns are explained by greater evolutionary divergence in male size, compared with female size; a pattern known as Rensch's rule (Fairbairn, 1997; Rensch, 1950). This allometric trend is usually attributed to sexual selection acting on male body size (Fairbairn et al., 2007; Stillwell et al., 2010). The converse trend, where female size varies more than male size, is less common, but seems to be the result of strong fecundity selection acting on females (Fairbairn et al., 2007; Foellmer & Moya-Laraño, 2007; Webb & Freckleton, 2007). Lizards exhibit a broad range of SSD. However, in the majority of species, males are larger than females (Cox, Butler, & John-Alder, 2007; Cox, Skelly, & John-Alder, 2003), mainly because body size often determines success in agonistic encounters, and it is correlated with dominance and territoriality (Carpenter, 1995; McMann, 1993; Molina-Borja, Padron-Fumero, & Alfonso-Martin, 1998; Perry et al., 2004). Nonetheless, in some species, females are larger than males, suggesting that fecundity selection may have favored the evolution of large female body size because it may allow females to (1) accommodate more offspring (Cox et al., 2003; Stuart-Fox, 2009; Zamudio, 1998) and (2) increase the capacity for storing energy to be invested in reproduction (Calder, 1984; Pincheira-Donoso & Tregenza, 2011).

Lizards species can be oviparous or viviparous (Blanckenhorn, 2000; Méndez-de la Cruz, Villagrán-Santa Cruz, & Andrews, 1998). In some viviparous species, the embryos develop in a placenta with little or no shell forming, whereas in other species, the female retains the eggs within the uterus until development is complete. In any case, because placental gestation or extended egg retention requires more space within the abdominal cavity associated with an increased gestation period (Pincheira-Donoso & Tregenza, 2011; Qualls & Shine, 1995), it has been suggested that the females of viviparous lizards possess larger body size or greater abdomens than their oviparous relatives (Braña, 1996; Scharf & Meiri, 2013; Yan-Yan et al., 2012).

The lizard genus *Sceloporus* serves as an excellent example of SSD in lizards. This is a widely distributed genus (from southwestern Canada to northern Panama), which can be found in several environments and along broad altitudinal ranges (0 to >4,000 m; Sites et al.,

1992: Smith. 1939). There are both oviparous and viviparous species. in the genus (Méndez-de la Cruz, Villagrán-Santa Cruz & Andrews, 1998). In the majority of species, males are the larger sex and exhibit a conspicuous coloration formed by belly and gular patches. However, these characteristics are also present in the females of some species within the group (Calisi & Hews. 2007: Carpenter, 1978: Fitch, 1978: Jiménez-Cruz et al., 2005; Köhler & Heimes, 2002; Ramírez-Bautista & Pavón, 2009; Ramírez-Bautista et al., 2008; Ramírez-Bautista, Stephenson, Lozano, et al., 2012; Weiss, 2006). In addition, conspicuous coloration is also present on the dorsum, including the head, tail, and limbs (e.g., Sceloporus minor, S. aureolus, S. horridus; Köhler & Heimes, 2002; Stephenson & Ramírez-Bautista, 2012). The sexual coloration in males, principally the belly and gular patches, is related to species recognition, territory defense, agonistic interactions, and courtship (Carpenter, 1978; Martins, 1994; Sites et al., 1992; Wiens, Reeder, & Nieto Montes de Oca, 1999), which suggests that sexual selection has generated much of the divergence among males and females in Sceloporus lizards. However, in other species, females are larger than males (Fitch, 1978), suggesting that in these species, selection on female fecundity has been stronger than sexual selection on males.

In this study, we explore the relationship between female body size, fecundity and reproductive modes, and the potential impact of these relationships on body size divergence between females and males of *Sceloporus* lizards. In addition, we tested Rensch's rule in order to evaluate the relative impact of sexual selection on the evolution of SSD, and we performed an ancestral character reconstruction to infer the evolutionary trends of SSD in these lizards. We expected differences in body size between oviparous and viviparous females and that these differences affect the body size relationships between the sexes. Nonetheless, if sexual selection has been the main force driving the evolution of SSD in *Sceloporus*, we predict that the regression of male size on female size will have a slope steeper than 1, following the Rensch's rule.

2 | METHODS

2.1 | Data collection

Our study comprised data collected for 56 *Sceloporus* species, four *Urosaurus* species and *Petrosaurus* thalassinus for a total of 61 evolutionary units (*Urosaurus* and *P. thalassinus* were used as outgroup taxa). The *Sceloporus* species sampled included all major species groups of the genus (Leaché, 2010; Wiens et al., 2010); 41 species were oviparous and 20 were viviparous (Table 1). We performed a literature search for data on snout-vent length (SVL; a standard measure used as a proxy for lizard size; Cox et al., 2003; Losos, 1990) for both females and males and clutch/litter sizes (number of eggs or embryos) for the species studied. We collected information from the literature by executing searches on Google Scholar using the terms "snout-vent length," "clutch size," "litter size," "number of eggs/embryos," "sexual size dimorphism," or "reproductive cycle" for a list of species of the genus *Sceloporus*, reported by Wiens, Kozak, and Silva (2013). Google

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TABLE 1 Mean snout-vent length (SVL), clutch/litter size, and reproductive mode (O = oviparous and V = viviparous) for 56 *Sceloporus* species and five outgroup taxa

Species	SVL females (mm)		SVL males (mm)		Clutch size		Reproductive mode	References
Petrosaurus thalassinus	99.15 (71-110)	(44)	107.23 (80-152)	(44)	8.6 (4-18)	(10)	0	Goldberg and Beaman (2004)
Sceloporus adleri	63.11 (54-78.8)	(23)	65.28 (59-72)	(14)	6.57 (2-11)	(14)	V	Fitch (1978), Santos- Bibiano (unpublished data)
S. aeneus	51.88 (43.4-59.1)	(194)	52.98 (43.4-62.8)	(138)	7.3 (7–12)	(32)	0	Jiménez-Arcos (2013)
S. angustus	62.8 (61-66)	(5)	78.2 (65–86)	(6)	5.5 (4-7)	(5)	0	Goldberg (2014)
S. arenicolus	53.8 (49-62.2)	(339)	54.5 (49-64.9)	(507)	5 (4-6)	(?)	0	Fitzgerald et al. (2011)
S. bicanthalis	51.84 (42.4-58)	(85)	43.6 (42-53.2)	(42)	7.18 (3-9)	(68)	V	Rodríguez-Romero et al. (2010), This study ^a
S. chrysostictus	51.3	(82)	53.95	(82)	2.4 (1-4)	(16)	0	Fitch (1985), Köhler and Heimes (2002)
S. clarkii	88.08 (72-120)	(57)	103 (91–138)	(56)	10.85 (1-24)	(39)	0	Fitch (1978, 1985), Parker and Pianka (1973)
S. consobrinus	68.4 (54–77)	(58)	60.5 (50-68)	(44)	9.9	(39)	0	Vinegar (1975a)
S. couchii	50	(36)	58	(32)	4	(?)	0	García de la Peña et al. (2004), Lemos-Espinal and Smith (2007)
S. cozumelae	45.48 (41–57)	(33)	50.72 (43-60)	(57)	1.8	(12)	0	Fitch (1978)
S. cryptus	67.06 (58.5-76.6)	(8)	61.6 (58.9-68.5)	(6)	9 (6-12)	(4)	V	This study ^b
S. cyanogenys	63	(15)	66	(15)	16.45 (6-18)	(36)	V	Fitch (1985), García-de la Peña, Castañeda, and Lazcano (2005)
S. dugesii	61.5 (50-78)	(91)	65.9 (50-98)	(73)	4.4 (1-10)	(27)	V	Ramírez-Bautista and Dávila-Ulloa (2009)
S. edwardtaylori	107	(?)	107	?	8.5 (8-9)	(2)	0	Köhler and Heimes (2002)
S. for. formosus	67.46 (50-83.3)	(113)	67.98 (50-87.4)	(99)	8.63 (6-18)	(16)	V	Ramírez-Bautista and Pavón (2009), This study ^b
S. for. scitulus	66.49 (62.5-84.9)	(82)	70.88 (63.3-87.3)	(73)	6.04 (2-12)	(27)	V	Ramírez-Pinilla et al. (2009), This study ^a
S. gadoviae	54.95 (45.7-57.2)	(6)	64.9 (69.6-73.5)	(6)	3.6 (1-5)	(20)	0	Lemos-Espinal, Smith, and Ballinger (1999), This study ^a
S. graciosus	57.59 (48-69)	(197)	55.18 (48-63)	(182)	4.55 (1-10)	(381)	0	Burkholder and Tanner (1974), Fitch (1978, 1985), Tinkle (1973)
S. grammicus	56.05 (42.1-72.5)	(278)	60.06 (45-79.9)	(412)	5.35 (2-12)	(167)	V	Ramírez-Bautista, Stephenson, Hernández- Íbarra, et al. (2012), Ramírez-Bautista, Stephenson, Lozano, et al. (2012), This study ^a
S. grandaevus	58.5 (58-59)	(2)	72.1 (67-78)	(5)	6.5 (6-7)	(2)	0	Goldberg (2014)
S. horridus	82.17 (60-100)	(46)	85.49 (52-118)	(82)	14 (7-18)	(16)	0	Valdéz-González and Ramírez-Bautista (2002), This study ^a
S. hunsakeri	64.13	(19)	73.96	(20)	7.5 (5-10)	(2)	0	Galina Tessaro et al. (2015)
S. jalapae	46 (42-50)	(24)	49.3 (45-62)	(17)	5.6 (4-8)	(10)	0	Ramirez-Bautista et al. (2005)
S. jarrovii	66.21 (60-86)	(787)	69.67 (46-98)	(668)	7.35 (2-16)	(405)	V	Ballinger (1973), Gadsden and Estrada-Rodríguez (2007)

(continues)

TABLE 1 (Continued)

Species	SVL females (mm)		SVL males (mm)		Clutch size		Reproductive mode	References
S. licki	63.83	(13)	71.46	(24)	6	(?)	0	Galina Tessaro et al. (2015)
S. macdougalli	83.84 (72.5-95.4)	(29)	88.82 (81.8-92.5)	(7)	3.88 (2-5)	(9)	V	Martínez Bernal (2004)
S. magister	93.64 (80-120)	(54)	111.45 (80-140)	(53)	6.98 (2-12)	(43)	0	Fitch (1978, 1985)
S. malachiticus	75.49 (64–86)	(208)	79.12 (67–90)	(146)	6 (3-10)	(44)	V	Fitch (1978, 1985)
S. megalepidurus	44.99 (37-48)	(36)	47.28 (39-55)	(76)	2.04 (1-4)	(25)	V	Fitch (1978), Godinez-Cano (1985)
S. melanorhinus	87.9 (62-98)	(30)	84.6 (62-95)	(32)	7.7 (5–9)	(12)	0	Ramirez-Bautista et al. (2006)
S. merriami	48.13 (39-55)	(164)	52.24 (42-61)	(355)	4.33 (2-7)	(127)	0	Fitch (1978), Grant and Dunham (1990)
S. minor	65.65 (41.6-92.9)	(182)	70.32 (53.6-99.4)	(169)	6.09 (2-13)	(46)	V	Ramírez-Bautista et al. (2008, 2014)
S. mucronatus	78.89 (56.5–102)	(170)	87.02 (55.2-111.2)	(146)	5.8 (2-13)	(49)	V	Ortega-León et al. (2007), Villagrán-Santa Cruz et al. (2009), This study ^a
S. nelsoni	52.14 (48-58)	(21)	60.15 (53-65)	(26)	6.25 (4-8)	(4)	0	Fitch (1978)
S. occidentalis	74.63 (68–87)	(43)	68.35 (61-81)	(46)	8.12 (3-14)	(243)	0	Fitch (1978), Herrel, Meyers, and Vanhooydonck (2002)
S. ochoterenae	44.39 (31-67)	(110)	48.23 (44–56)	(143)	6.77 (3-7)	(35)	0	Bustos-Zagal et al. (2011), Smith and Lemos-Espinal (2003)
S. olivaceus	93 (63–107)	(107)	82.9 (60-93)	(34)	14.3 (8-30)	(14)	0	Blair (1960)
S. omiltemanus	83.08	(39)	98.11	(25)	6.23 (6-8)	(13)	V	Ramírez-Pinilla et al. (2009)
S. orcutti	92 (85–106)	(77)	102 (90–115)	(17)	11 (8-15)	(4)	0	Mayhew (1963)
S. parvus	46.85 (44.7–49)	(?)	50	(?)	3.8	(>2)	0	García-Vázquez, Trujano- Ortega, and Contreras- Arquieta (2014), Lemos-Espinal and Dixon (2013)
S. pictus	47.86 (44–52)	(7)	48.88 (47-51)	(8)	3.6 (2-6)	(5)	V	Fitch (1978)
S. poinsettii	89.45 (79-116)	(55)	96.79 (77-130)	(79)	10.5 (4-23)	(90)	V	Fitch (1978, 1985), Gadsden et al. (2005)
S. pyrocephalus	53.41 (47-62)	(88)	62.01 (50-75)	(84)	5.65 (4-9)	(24)	0	Fitch (1978), Ramírez- Bautista and Olvera Becerril (2004)
S. spi. caer- uleopunctatus	87.22 (77-96)	(18)	88.29 (82-99)	(17)	12.82 (8-19)	(23)	0	Calderón-Espinosa, Andrews, and Méndez de la Cruz (2006), Fitch (1978)
Sceloporus spi. spinosus	91.11 (65.7–110.5)	(164)	92.66 (60-112)	(164)	14.09 (6-22)	(38)	0	Méndez de la Cruz et al. (2013), Ramírez-Bautista, Stephenson, Hernández- Íbarra, et al. (2012), Ramírez-Bautista, Stephenson, Lozano, et al. (2012), Ramírez-Bautista et al. (2014), Valdéz- González and Ramírez- Bautista (2002)
S. scalaris	51.25 (40-60)	(203)	45.53 (40-55)	(45)	8.28 (4-15)	(109)	0	Carbajal-Márquez and Quintero-Díaz (2013), Fitch (1978, 1985), Vitt (1977)

(Continues)

Ecology and Evolution

JIMÉNEZ-ARCOS ET AL.

TABLE 1 (Continued)

Species	SVL females (mm)		SVL males (mm)		Clutch size		Reproductive mode	References
S. siniferus	49.88 (40-61)	(139)	52.49 (53-61)	(235)	4.94 (2-8)	(15)	0	Fitch (1978), Ramírez- Bautista et al. (2015)
S. smaragdinus	62.24 (55-77)	(17)	67.22 (60-80)	(14)	4.2 (3-6)	(10)	V	Fitch (1978)
S. subpictus	66.47 (63.1-69)	(41)	63.54	(1)	13 (12-14)	(2)	V	This study ^b
S. torquatus	94.03 (65-110)	(4)	101.51 (43.2-115.9)	(37)	7.78 (3-17)	(84)	V	Feria Ortiz, Salgado Ugarte, and Nieto-Montes de Oca (2001), Guillette and Méndez-de la Cruz (1993), This study ^a
S. tristichus	63.3 (48-67)	(57)	55.9 (53-73)	(54)	7.2	(29)	0	Vinegar (1975b)
S. undulatus	61.11 (53-72)	(118)	55.78 (45-65)	(177)	8.02 (3-15)	(376)	0	Fitch (1978, 1985), Herrel et al. (2002)
S. utiformis	63.41 (51-73)	(104)	61.25 (45-84)	(122)	6.94 (3-10)	(31)	0	Fitch (1978), Ramírez- Bautista and Gutiérrez- Mayén (2003)
S. variabilis	52.65 (44-68)	(424)	61.99 (42-74)	(457)	3.92 (1-7)	(216)	0	Benabid (1994), Cruz- Elizalde & Ramírez- Bautista (2016 and references in table 6), Fitch (1978, 1985)
S. virgatus	63.81 (51-74.2)	(54)	50.42 (48-58)	(22)	9.44 (4-16)	(228)	0	Abell (1999), Herrel et al. (2002), Vinegar (1975a)
S. woodi	57.24	(64)	51.89	(78)	4.62 (2-8)	(231)	0	Jackson and Telford (1974), Williams (2010)
Urosaurus bicarinatus	45.84 (40-53)	(249)	49.66 (38-61)	(322)	6.26 (2-11)	(50)	0	Ramírez-Bautista, Uribe-Peña, and Guillette (1995), Ramirez-Bautista and Vitt (1998)
U. graciosus	38.69 (44-66)	(60)	62.35 (42-66)	(42)	4.05 (2-10)	(25)	0	Fitch (1985), Vitt, Van Loben Sels, and Ohmart (1978)
U. nigricaudus	51.82 (44-60)	(121)	62.47 (57.2-65.4)	(42)	4.05 (2-6)	(25)	0	Romero-Schmidt, Ortega-Rubio, and Acevedo-Beltran (1999)
U. ornatus	49.98 (45–58)	(14)	50.87 (47-60)	(34)	7.25 (2-12)	(1454)	0	Fitch (1985), Martin (1973), Van Loben Sels and Vitt (1984)

Size and clutch/litter size ranges are shown in parentheses below mean values. Numbers between parentheses refer to sample sizes. The symbol (?) represents a lack of sample size data in the literature.

^aOnly SVL data obtained in this study.

^bBoth SVL and litter size data obtained in this study.

Scholar was used as the search engine instead of other engines because it cataloged full-text versions of published papers. Moreover, terms that were included in our search like "clutch size," "litter size," and "snout-vent length" were not the principal focus of the papers, and the phrases were usually referred to only briefly. Thus, we were less likely to locate the pertinent information using literature databases that contain only keywords, titles, and abstracts (see Dornhaus, Powell, & Bengston, 2012). We excluded data in which the number of vitellogenics follicles were reported as part of clutch size, because the follicular atresia may occur in any stage of the ovogenesis, including previtellogenic and vitellogenic follicles, and thus does not represent an accurate estimation of clutch/litter size (Méndez-de la Cruz et al., 2013). For species with data on more than one clutch per reproductive season, we used the average of all clutches reported in the literature.

In addition to this data set, we incorporated unpublished measurements collected by us from the individuals of ten species. Both SVL and litter size data were incorporated for *S. cryptus*, *S. formosus formosus*, and *S. subpictus* (all viviparous species). SVL data from both sexes were collected for *S. bicanthalis*, *S. formosus scitulus*, *S. gadoviae*, *S. grammicus*, *S. horridus*, *S. mucronatus*, and *S. torquatus*. Litter size was obtained from direct observations of females giving birth in captivity

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(see Bastiaans et al., 2014 for care details). Digital calipers were used to take SVL measurements to the nearest 0.1 mm (Mitutoyo CD-15DC; Mitutoyo Corp., Tokyo, Japan). All lizards captured for this study were unharmed and released at their original capture locations following data collection.

The number of eggs or embryos was used as an estimation of fecundity. Prior to further analyses, all measurements were \log_{10} -transformed to improve linear fits. In addition, we estimated a sexual size dimorphism index (SDI) on SVL following the Lovich and Gibbons (1992) criteria. This index expresses SSD as [(length of larger sex/length of smaller sex) – 1]. For convention, the SDI is arbitrarily changed to negative when males are the larger sex and positive when females are the larger sex (Cox et al., 2007).

2.2 | Phylogenetic reconstruction

We inferred the phylogenetic relationships between the 56 studied species of Sceloporus using the nucleotide sequences of eight nuclear (BDNF, ECEL, PNN, PRLR, PTPN, R35, RAG1, TRAF6) and five mitochondrial genes (12S, 16S, ND1, ND2, ND4) available on GenBank. We also retrieved the same genetic information from five outgroup taxa which included four Urosaurus species, representing the sister group of Sceloporus (Leaché, 2010; Wiens et al., 2010) and Petrosaurus thalassinus. The number of species sampled for each gene was BDNF = 48, ECEL = 25, PNN = 47, PRLR = 27, PTPN = 26, R35 = 48, TRAF6 = 46, 12S = 57, 16S = 56, ND1 = 54, ND2 = 35, and ND4 = 57. All matrices were similar to previous studies (Leaché, 2010; Wiens et al., 2010). However, we treated the two subspecies of S. formosus (i.e., S. formosus formosus and S. formosus scitulus) as putative species based on previous evidence for distinct lineages (Pérez-Ramos & Saldaña de La Riva, 2008; Wiens & Reeder, 1997). A similar situation is present in S. spinosus (with S. spinosus spinosus and S. spinosus caeruleopunctatus). Wiens et al. (2010) recognized these taxa as putative species, which was also supported by more recent evidence (Grummer et al., 2015). Our inclusion of these taxa as distinct evolutionary lineages was not an endorsement of their recognition as different species, but we did not want to ignore important previous taxonomic work on these groups (see Pérez-Ramos & Saldaña de La Riva, 2008; Wiens & Reeder, 1997; Wiens et al., 2013).

We used MUSCLE algorithm (Edgar, 2004) to align each gene data set using the default parameters in the software MEGA (version 7; Kumar, Stecher, & Tamura, 2016). We then used the software MESQUITE (Maddison & Maddison, 2015) to combine the sequences of each gene, and to make the final concatenated matrix for all genes (see below). We provide the GenBank accession numbers of the sequences used in Appendix S1. Our concatenated alignment consisted of genetic information from 61 terminals (56 *Sceloporus* species, five outgroups taxa) and 11,113 characters. We estimated the best partition scheme and nucleotide substitution models for the data using the greedy algorithm of PARTITIONFINDER (version 1.1.1; Lanfear et al., 2014). We conducted a concatenated Bayesian inference (BI) analysis in MRBAYES (version 3.2.6; Ronquist et al., 2012) by applying the specific substitution model estimated for each partition. The BI

analysis consisted of four independent runs, each with 10,000,000 generations and four chains, sampling every 1,000 generations. We used default priors for other parameters in the analysis. We assessed parameter convergence and proper mixing of independent runs using TRACER (version 1.6; Rambaut & Drummond, 2013). All parameter values sampled during the MCMC of the analysis resulted in ESS values greater than 200. We discarded 25% of the samples obtained prior to stability as burn-in to obtain a final consensus tree (See Appendix S1 for details).

Our analysis only considered the phylogeny that resulted from a concatenated matrix of both mitochondrial and nuclear loci, utilizing a total evidence approach for *Sceloporus* species and outgroup taxa. Although this approach may be controversial because nuclear and mitochondrial genes may have incongruent histories due to incomplete lineage sorting and exhibit different substitutions rates (see Maddison, 1997), concatenated matrices have improved the resolution of the phylogenetic relationships of phrynosomatid lizards (Wiens et al., 2010). Moreover, our phylogenetic results were largely congruent with a recent phylogenetic study on *Sceloporus* that involved a wider taxonomic and genetic sampling, as well as different methodological approaches (concatenation and coalescent-based methods) to infer phylogenetic relationships (Leaché et al., 2016).

2.3 | Comparative analyses

We converted the molecular branch lengths from the Bayesian analysis to units of time using a penalized likelihood method (Sanderson, 2002). For branch length conversion, we used the R (version 3.1.3; R Core Team 2015) package "ape" (Paradis, Claude, & Strimmer, 2004) and performed all the comparative analysis on the resulting ultrametric phylogeny. For more details, see Appendix S1.

2.4 | Reproductive modes, female body size, fecundity, and SDI

We used the phylogenetic generalized least squares (PGLS) model to test for an association between fecundity, body size, and reproductive mode. The PGLS approach incorporates phylogenetic information into linear models to account for the statistical nonindependence of residuals using a variance-covariance matrix (see Martins & Hansen, 1997) specified by the phylogeny. For all models, the maximum likelihood value of the weighting parameter λ was estimated simultaneously with the models (Gonzalez-Voyer & Kolm, 2010; Revell, 2010). The λ parameter indicates whether trait evolution is independent of the phylogeny ($\lambda = 0$) or evolving according to Brownian motion $(\lambda = 1)$. Intermediate values of λ suggest a process in which the effect of the given phylogeny is weaker than expected by Brownian motion evolution (Pagel, 1999). The models were fitted as implemented in the R package "caper" (Orme et al., 2012). The first model included fecundity (dependent variable), log₁₀ SVL female (independent variable), and reproductive mode (categorical independent variable) as well as the interaction between SVL and reproductive mode. In order to evaluate the impact of fecundity on SDI, we first saved the residuals

of the previous model and then constructed a model with SDI as the dependent variable, reproductive mode as a categorical independent variable, and the fecundity residuals as a covariate. We used the residuals to eliminate potential confounding effects associated with female body size.

2.5 | Rensch's rule and ancestral reconstruction of SDI

Rensch's rule predicts that the slope of a regression of male body size on female body size will be steeper than 1. To test this prediction in the studied species, we used the phylogenetic independent contrasts method (PIC method; Felsenstein, 1985), as implemented by the R package "caper" (Orme et al., 2012) to control for the phylogenetic nonindependence of species (Harvey & Pagel, 1991). We examined the studentized residuals for outliers $> |\pm 3|$, but found none in our data set. Also, in order to verify whether the standardized contrasts are independent from their estimated nodal values (see Felsenstein, 1985), we plotted the standardized contrasts against their estimated nodal values using the "plot" function provided by "caper". Ultimately, we tested the allometric relationship between independent contrasts of log₁₀ SVL male (dependent variable) and log₁₀ SVL female (independent variable) by fitting major axis regression using the R package "smatr" (Warton et al., 2012). Major axis regression offers an accurate approach to test the null hypothesis of isometry (h_0 : $\beta = 1$), because both variables were measured on the same scale and residual variance is minimized in both x and y dimensions, rather than the y dimension only (Cox et al., 2007; Pincheira-Donoso & Tregenza, 2011; Warton et al., 2006). Given that the mean value of contrasts is expected to be zero (Sanabria-Urbán et al., 2015), we forced the major axis regression through the origin. We used the Wald statistic (r_w) and confidence intervals (95%) of the slope to test the null hypothesis (see Warton et al., 2006). In addition, in order to explore the evolutionary trends in body size and SDI, we performed an ancestral character reconstruction following Revell (2013). This method estimates the maximum likelihood value for internal nodes and then interpolates the states along the branches of the tree (see Revell, 2013, 2014 for details). For the reconstruction and visualization of ancestral state reconstruction of SDI (see Figure 3), we used the R package "phytools" (Revell, 2012).

3 | RESULTS

3.1 | Reproductive modes, body size, and fecundity

After controlling for phylogenetic nonindependence among of the species studied, the results of the PGLS analysis were highly significant ($r^2 = 0.3$, $F_{3,57} = 8.025$, p = .0001). We found a strong and significantly positive relationship between body size and fecundity ($\beta = 0.98 \pm 0.26$, t = 3.801, p = .0003; Figure 1). Nonetheless, there were no differences in fecundity between reproductive modes ($\beta = -0.15 \pm 0.85$, t = -0.174, p = .86). The interaction between



FIGURE 1 The relationship between the SVL of females and fecundity. Note this graph is shown only for illustrative purposes and was created with ordinary least squares linear model

reproductive modes and body size was not significant ($\beta = 0.04 \pm 0.47$, t = 0.086, p = .93), indicating a similar fecundity response to an increase in the body size of both oviparous and viviparous species. The model showed intermediate λ values ($\lambda = 0.54$), indicating a relatively weak phylogenetic effect on the relationships between body size and fecundity.

3.2 | Reproductive modes, fecundity, and SDI

The results of PGLS analysis were not significant ($r^2 = .003$, $F_{3,57} = 0.071$, p = .98). There were no significant differences in the SDI of oviparous and viviparous lizards ($\beta = 0.01 \pm 0.05$, t = 0.433, p = .67). Similarly, there were no significant effects of fecundity residuals on SDI ($\beta = -0.005 \pm 0.08$, t = -0.063, p = .95). The model showed a high λ value ($\lambda = 0.95$), indicating a strong phylogenetic effect on the relationships between fecundity residuals and SSD.

3.3 | Rensch's rule and ancestral reconstruction of SDI

The results of the major axis regression of independent contrasts indicated strong coevolution between females and males (r = .80; df = 58, p = .0001, Figure 2). The regression showed a slope significantly steeper than 1.0 ($\beta = 1.17$, $r_w = .29$, p = .02; Figure 2). Most of the taxa (46 species, 75%) showed male-biased SSD, and 14 species (23%) showed some degree of female-biased SSD. The males and females of only one species showed similar body sizes (*S. edwardtaylori*). The SDI reconstruction showed six independent origins of the female-biased SSD. In a clade with male-biased SSD (*formosus* group), the branch of *S. cryptus* and *S. subpictus* showed a female-biased SSD. Other independent origin of female-biased SSD was found in the *scalaris* (*S. bicanthalis* and *S. scalaris*) group. Another origin for *undulatus* group (*S. olivaceus*, *S. occidentalis*, *S. virgatus*, *S. woodi*, *S. undulatus*, *S. consobrinus*, and *S. tristichus*). Finally, three additional species independently evolved female-biased SSD: *S. utiformis* (*utiformis*)



FIGURE 2 Independent contrasts of SVL of males as a function of SVL of females. The solid line indicates isometry ($\beta = 1$), while the dashed line denotes the allometric relationship between both variables as fitted by major axis regression. Values in parentheses indicate the upper and lower confidence interval (95%) for the slope and *p* value the probability for a $\beta > 1$

group), S. graciosus (gracious group), and S. melanorhinus (clarkii group; Figure 3).

4 | DISCUSSION

Once we control for phylogenetic effects, our results confirm a strong relationship between female body size and fecundity, suggesting that in Sceloporus lizards selection on fecundity has had a main role on the evolution of female body size. However, regardless of the reproductive mode (oviparous or viviparous), the size of females of Sceloporus is similar and has evolved in a similar fashion. We must point out that the similar response in the relationship of body size with increase in the clutch/litter size between both reproductive modes does not imply that the overall reproductive output (i.e., reproductive fitness of the female's life) is similar. The potential impact of fecundity selection on the different reproductive modes may be underestimated (Niewiarowski et al., 2004; Pincheira-Donoso & Hunt, 2015; Shine, 2005). Oviparous species like S. gadoviae, S. siniferus, S. undulatus, and S. variabilis may have multiple clutches in a reproductive season (i.e., per year; Cruz-Elizalde & Ramírez-Bautista, 2016; Ramirez-Bautista et al., 2005; Ramírez-Bautista et al., 2015; Vinegar, 1975b), whereas other species like S. magister, S. melanorhinus, and S. spinosus have just one clutch per year, but they may have more than one reproductive event in their life (Méndez-de la Cruz et al., 2013; Parker & Pianka, 1973; Ramirez-Bautista et al., 2006; Valdéz-González & Ramírez-Bautista, 2002). On the other hand, all viviparous species have one litter per year, but in the majority of species, females can have several reproductive events (Méndez-de la Cruz et al., 1998; Ramírez-Bautista et al., 2014; Villagrán-Santa Cruz, Hernández-Gallegos, & Méndez-de La Cruz, 2009).

The differences in the gestation period between reproductive modes do not have any impact on the evolution of SSD, but according to the Renchs' rule, the slope of the regression of males on females is significantly steeper, providing evidence of greater evolutionary divergence in male size than in female size. Fitch (1978) noted that the high variation of SSD in Sceloporus lizards, and the implications of sexual and natural selection in order to explain the differences in body size between females and males. For lizard species in which body size often determines male mating success, males are typically larger than females (Cox et al., 2007). Body size often determines success in agonistic encounters, and it is correlated with dominance and territoriality (Carpenter, 1995; Martins, 1994; McMann, 1993; Molina-Borja et al., 1998; Perry et al., 2004). However, in other species, females are larger than males, suggesting that fecundity selection may have favored the evolution of larger-than-average female body size (Cox et al., 2003; Zamudio, 1998). Furthermore, as Sceloporus lizards follow Rensch's rule, it can be argued that this allometric trend is the result of sexual selection favoring large male body size and that the relative impact of sexual selection on males has been stronger than fecundity selection on female body size (Fairbairn, 1997; Fairbairn et al., 2007; Pincheira-Donoso & Tregenza, 2011).

The reconstruction of the evolution of SSD in Sceloporus lizards suggests that the ancestor and most of the extant species show a pattern of male-biased SSD. This could indicate that directional sexual selection acting on males has been greater than the selection acting on female fecundity. Territoriality and aggressive behaviors are common in Sceloporus: These are mainly associated with defense of mates in males (Martins, 1994), and resources (e.g., food, water, perches) in both sexes (Cooper & Wilson, 2007; Martins, 1994; Vinegar, 1975c; Woodley & Moore, 1999). In general, larger individuals have an advantage when defending territories in agonistic encounters (Martins, 1994; Swierk, 2014). However, female-biased SSD has evolved independently at least six times (Figure 3). Perhaps in these taxa, selection on fecundity has been stronger than sexual selection. Nonetheless, it is possible that in these species, sexual selection has also favored small male body size (see Cox et al., 2007; Olsson et al., 2002), albeit there is no clear pattern as to the ecological factors associated with the evolution of female-biased SSD. These species, like other Sceloporus species that show male-biased SSD, live in different environments, including tropical deciduous forest, grasslands, scrubland, woodlands, and open coniferous forests, and can be found from sea level up to elevations >4,000 m. Moreover, species showing female-biased SSD are oviparous and viviparous (e.g., undulatus group versus S. bicanthalis, respectively), and with single or multiples clutches per reproductive season (e.g., S. melanorhinus versus S. consobrinus, respectively). The diversity of ecological and social factors provides opportunities for changes in the direction and magnitude of natural and sexual selection between and within species. However, the information available for female preference and agonistic interactions between males are, in the majority of species, severely scarce or absent (see Martins, 1994; Swierk, 2014).

Previous studies in Phrynosomatidae do not support Rensch's rule (Cox et al., 2007). However, these results could be obscured by



FIGURE 3 Maximum likelihood ancestral reconstruction of SDI for 56 species of *Sceloporus* and five outgroup taxa performed in R package "phytools" (Revell, 2012). For the analysis, we used the ultrametric phylogeny and the values of SDI estimated for each species. The values in the color ramp represent the range of SDI registered for the study species. Negative values indicate male-biased SSD (blue to paleyellow) and positive values female-biased SSD (palepurple to red). Open and filled circles indicate, respectively, oviparous and viviparous lizard species

the large diversity in morphology, behavior, ecology, and life-history traits between different lizards genera (Cox et al., 2003). In addition, these studies do not consider the phylogenetic relationship between the species (see Cox et al., 2007). Conversely, our results are similar to previous studies in the genus *Liolaemus* (Liolaemidae). The clutch/litter size increases as a function of female body size. Nonetheless, fecundity is not correlated with SSD, but *Lioalemus* species appear to follow Rensch's rule (Pincheira-Donoso & Tregenza, 2011). Both *Sceloporus* and *Liolaemus* species occupy a great diversity of environments, along wide latitudinal and altitudinal ranges and showing great variation in morphological, ecological, behavior, and life-history traits (Pincheira-Donoso, Scolaro, & Sura, 2008; Sites et al., 1992). The similarity between our results and those reported in *Liolaemus* suggests that fecundity selection may have driven the divergence in female body size

but that the diversifying effects of sexual selection may often exceed fecundity selection on females in both genera.

The genus *Sceloporus* includes more than 90 species and has been proposed as a group with an accelerated diversification rate (Bell, Smith, & Chiszar, 2003; Leaché, 2010; Wiens et al., 2010). *Sceloporus* lizards have colonized diverse niches throughout its distribution range, from northern Panama to southwestern Canada, and show one of the widest altitudinal ranges for reptiles. Due to the broad spread of niches, it is likely that the relative impact of natural and sexual selection has changed along novel environmental conditions, generating divergence from the optimum body size of females and males. In any case, the causal mechanisms associated with changes in the direction of SSD bias toward females in this group remain an open question that demand further investigation.

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CONFLICT OF INTEREST

None declared.

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SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

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- 1 Appendix 1.
- 2 The Table S1 and S2 showed the GenBank accession numbers for the 61 species used in the phylogenetic analyses.
- 3 Nuclear and mitochondrial genes are listed alphabetically.
- 4

Table S1. GenBank accession numbers of the eight nuclear genes used for the present study

	BDNF	ECEL	PNN	PRLR	PTPN	R35	RAG1	TRAF6
P_thalassinus		GQ895767.1	KP820518.1	GQ896079.1	GQ896211.1	KP820536.1	GQ896006.1	GQ895940.1
S_adleri								
S_aeneus						KF437157.1		
S_angustus				GQ896082.1	GQ896214.1			GQ895944.1
S_arenicolus	GQ464421.1		KC853996.1			GQ464645.1	GQ464701.1	
S_bicanthalis	GQ464435.1	KR360374.1	GQ464603.1	KR359866.1	KR359920.1	GQ464659.1	GQ464715.1	KR360099.1
S_chrysostictus								
S_clarkii	GQ464412.1	GQ895769.1	GQ464580.1	GQ896083.1	GQ896215.1	GQ464636.1	GQ464692.1	GQ895945.1
S_couchi	GQ464461.1	GQ895770.1	GQ464629.1	GQ896084.1	GQ896216.1	GQ464685.1	GQ464741.1	GQ895946.1
S_cozumelae								
S_cryptus	GQ464415.1		GQ464583.1			GQ464639.1	GQ464695.1	
S_cyanogenys								
S_dugesii	GQ464439.1		GQ464607.1			GQ464663.1	GQ464719.1	
S_edwardtaylori	GQ464414.1		GQ464582.1			GQ464638.1	GQ464694.1	
S_f_formosus		GQ895771.1		GQ896085.1	GQ896217.1			GQ895947.1
S_f_scitulus	GQ464416.1		GQ464584.1			GQ464640.1	GQ464696.1	
S_gadoviae	GQ464453.1	GQ895772.1	GQ464621.1	GQ896086.1	GQ896218.1	GQ464677.1	GQ464733.1	GQ895948.1
S_graciosus	GQ464422.1	GQ895773.1	GQ464590.1	GQ896087.1	GQ896219.1	GQ464646.1	GQ464702.1	GQ895949.1
S_grammicus	GQ464424.1	GQ895774.1	GQ464592.1	GQ896088.1	GQ896220.1	GQ464648.1	GQ464704.1	GQ895950.1
S_grandaevus	GQ464452.1		GQ464620.1			GQ464676.1	GQ464732.1	

S_horridus	GQ464437.1		GQ464605.1			GQ464661.1	GQ464717.1	
S_hunsakeri	GQ464427.1		GQ464595.1			GQ464651.1	GQ464707.1	
S_jarrovii	GQ464440.1		GQ464608.1			GQ464664.1	GQ464720.1	
S_jalapae	GQ464456.1	GQ895775.1	GQ464624.1	GQ896089.1	GQ896221.1	GQ464680.1	GQ464736.1	GQ895951.1
S_licki	GQ464428.1		GQ464596.1			GQ464652.1	GQ464708.1	
S_melanorhinus	GQ464413.1		GQ464581.1			GQ464637.1	GQ464693.1	
S_mucronatus	GQ464443.1		GQ464611.1			GQ464667.1	GQ464723.1	
S_omiltemanus								
S_macdougalli	GQ464442.1		GQ464610.1			GQ464666.1	GQ464722.1	
S_magister	GQ464429.1	GQ895777.1	GQ464597.1	GQ896091.1		GQ464653.1	GQ464709.1	GQ895953.1
S_malachiticus	GQ464417.1		GQ464585.1			GQ464641.1	GQ464697.1	
S_megalepidurus	GQ464432.1	GQ895778.1	GQ464600.1	GQ896092.1	GQ896222.1	GQ464656.1	GQ464712.1	GQ895954.1
S_merriami	GQ464459.1	GQ895779.1	GQ464627.1	GQ896093.1	GQ896223.1	GQ464683.1	GQ464739.1	GQ895955.1
S_minor								
S_nelsoni								
S_occidentalis	GQ464448.1		GQ464616.1	KP820502.1		GQ464672.1	GQ464728.1	
S_ochoterenae	GQ464457.1		GQ464625.1			GQ464681.1	GQ464737.1	
S_olivaceus	GQ464434.1	GQ895780.1	GQ464602.1	GQ896094.1	GQ896224.1	GQ464658.1	GQ464714.1	GQ895956.1
S_orcutti	GQ464430.1		GQ464598.1			GQ464654.1	GQ464710.1	
S_parvus	GQ464462.1	GQ895781.1	GQ464630.1	GQ896095.1	GQ896225.1	GQ464686.1	GQ464742.1	GQ895957.1
S_pictus			GQ464601.1			GQ464657.1	GQ464713.1	
S_poinsettii	GQ464445.1	GQ895782.1	GQ464613.1	GQ896096.1	GQ896226.1	GQ464669.1	GQ464725.1	GQ895958.1
S_pyrocephalus	GQ464454.1	GQ895783.1	GQ464622.1	GQ896097.1	GQ896227.1	GQ464678.1	GQ464734.1	GQ895959.1
S_s_caeruleo.		GQ895785.1			GQ896230.1			GQ895962.1
S_s_spinosus	GQ464438.1		GQ464606.1			GQ464662.1	GQ464718.1	
S_scalaris	GQ464436.1	GQ895784.1	GQ464604.1	GQ896098.1	GQ896228.1	GQ464660.1	GQ464716.1	GQ895960.1
S_siniferus	GQ464460.1		GQ464628.1	GQ896099.1	GQ896229.1	GQ464684.1	GQ464740.1	GQ895961.1
S_smaragdinus	EU085927.1						EU085721.1	
S_subpictus	GQ464419.1		GQ464587.1			GQ464643.1	GQ464699.1	
S_torquatus	GQ464446.1	GQ895786.1	GQ464614.1	GQ896100.1	GQ896231.1	GQ464670.1	GQ464726.1	GQ895963.1

S_consobrinus	GQ494864.1		GQ494849.1			GQ494834.1	GQ494819.1	
S_tristichus	GQ494860.1		GQ494845.1			GQ494830.1	GQ494815.1	
S_undulatus	GQ464449.1	GQ895787.1	GQ464617.1	GQ896101.1	GQ896232.1	GQ464673.1	GQ464729.1	GQ895964.1
S_utiformis	GQ464455.1		GQ464623.1		GQ896233.1	GQ464679.1	GQ464735.1	GQ895965.1
S_variabilis	GQ464464.1	GQ895788.1	GQ464632.1	GQ896102.1	GQ896234.1	GQ464688.1	GQ464744.1	GQ895966.1
S_virgatus	GQ464450.1		GQ464618.1			GQ464674.1	GQ464730.1	
S_woodi	GQ464451.1		GQ464619.1			GQ464675.1	GQ464731.1	
U_bicarinatus	JN648384.1	GQ895790.1		GQ896104.1	GQ896236.1		GQ896030.1	GQ895968.1
U_graciosus	JN648393.1	GQ895791.1		GQ896105.1			JN648493.1	GQ895969.1
U_nigricaudus	GQ464465.1	GQ895792.1	GQ464633.1	GQ896106.1	GQ896237.1	GQ464689.1	GQ464745.1	GQ895970.1
U_ornatus	KP820848.1	GQ895793.1	KP820515.1	GQ896107.1	GQ896238.1	KP820533.1	GQ896033.1	GQ895971.1

Table S2. GenBank accession numbers of the five mitochondrial genes used for the present study

	12S	16S	ND1	ND2	ND4
P_thalassinus	L40445.1	L41451.1	KP899454.1	KP899454.1	KP899454.1
S_adleri	AF000799.1	AF000839.1	AY297519.1	AY297519.1	GQ895850.1
S_aeneus					JN985666.1
S_angustus	L40450.1	L41457.1	AF049859.1	AF049859.1	AF210360.1
S_arenicolus	GQ464524.1	AF000863.1	GQ464468.1		GQ464748.1
S_bicanthalis	GQ464525.1	AF000840.1	GQ464469.1		GQ464749.1
S_chrysostictus	L40451.1	L41458.1			AF210367.1
S_clarkii	GQ464527.1	L41459.1	GQ464471.1	AY297511.1	GQ464751.1
S_couchi	GQ464528.1	AF000829.1	GQ464472.1		GQ464752.1
S_cozumelae	AF000790.1	AF000830.1			
S_cryptus	GQ464529.1	AF000842.1	GQ464473.1		GQ464753.1
S_cyanogenys	DQ525893.1	L41460.1	AY297524.1	AY297524.1	DQ525868.1
S_dugesii	GQ464530.1	L41461.1	GQ464474.1		GQ464754.1

S_edwardtaylori	GQ464531.1		GQ464475.1		GQ464755.1
S_f_formosus	L40455.1	L41462.1	AY297498.1	AY297498.1	
S_f_scitulus	GQ464532.1		GQ464476.1		GQ464756.1
S_gadoviae	GQ464533.1	AF000836.1	GQ464477.1		GQ464757.1
S_graciosus	GQ464534.1	L41463.1	GQ464478.1	AF049860.1	GQ464758.1
S_grammicus	GQ464535.1	L41464.1	GQ464479.1	AY297509.1	GQ464759.1
S_grandaevus	GQ464536.1		GQ464480.1		GQ464760.1
S_horridus	GQ464538.1	AF000844.1	GQ464482.1		GQ464762.1
S_hunsakeri	GQ464539.1	AF000845.1	GQ464483.1	AY297506.1	GQ464763.1
S_jarrovii	GQ464541.1	L41465.1	GQ464485.1	AY297512.1	GQ464765.1
S_jalapae	GQ464540.1	AF000837.1	GQ464484.1	AY297504.1	GQ464764.1
S_licki	GQ464542.1	AF000848.1	GQ464486.1		GQ464766.1
S_melanorhinus	GQ464549.1	AF000852.1	GQ464493.1		GQ464773.1
S_mucronatus	GQ464551.1	DQ525902.1	GQ464495.1	AY297497.1	GQ464775.1
S_omiltemanus		AF000888.1			AF154233.1
S_macdougalli	GQ464544.1	AF000849.1	GQ464488.1		GQ464768.1
S_magister	GQ464546.1	L41466.1	GQ464490.1	AF528741.1	GQ464770.1
S_malachiticus	GQ464547.1	L41467.1	GQ464491.1	AY297518.1	GQ464771.1
S_megalepidurus	GQ464548.1	AF000862.1	GQ464492.1		GQ464772.1
S_merriami	GQ464550.1	L41468.1	GQ464494.1	AY297520.1	GQ464774.1
S_minor	DQ525891.1	AF000866.1			DQ525872.1
S_nelsoni					AF210351.1
S_occidentalis	GQ464552.1	AB079242.1	GQ464496.1	AY297515.1	GQ464776.1
S_ochoterenae	GQ464553.1	AF000853.1	GQ464497.1	AF528743.1	GQ464777.1
S_olivaceus	GQ464554.1	L41471.1	GQ464498.1	AY297521.1	GQ464778.1
S_orcutti	GQ464555.1	L41472.1	GQ464499.1	AY297508.1	GQ464779.1
S_parvus	GQ464558.1	AF000832.1	GQ464502.1		GQ464782.1
S_pictus	GQ464559.1	AF000831.1	GQ464503.1	AY297500.1	GQ464783.1
S_poinsettii	GQ464560.1	L41473.1	GQ464504.1	AY297510.1	GQ464784.1
S_pyrocephalus	GQ464561.1	AF000833.1	GQ464505.1	AY297502.1	GQ464785.1

S_s_caeruleo.	EF025755.1	AF000864.1			EF025748.1
S_s_spinosus	EF025756.1	L41475.1	GQ464509.1	AY297525.1	EF025749.1
S_scalaris	GQ464562.1	L41474.1	GQ464506.1	AF528742.1	GQ464786.1
S_siniferus	GQ464563.1	AF000834.1	GQ464507.1	AY297494.1	GQ464787.1
S_smaragdinus	EU086043.1	AF000855.1	AY297517.1	AY297517.1	EU085838.1
S_subpictus	GQ464565.1	AF000857.1	GQ464511.1		GQ464791.1
S_torquatus	DQ525888.1	DQ525905.1	GQ464513.1		GQ464793.1
S_consobrinus	AF000820.1	AF000860.1	AF440079.1		
S_tristichus	AF440068.1	AF440024.1	EF031910.1		
S_undulatus	GQ464570.1	AF000886.1	GQ464514.1	AY297514.1	GQ464794.1
S_utiformis	GQ464571.1	HM012692.1	GQ464515.1	AF528740.1	GQ464795.1
S_variabilis	GQ464573.1	L41479.1	GQ464517.1	AY297507.1	GQ464797.1
S_virgatus	GQ464574.1	L41480.1	GQ464518.1	AY297516.1	GQ464798.1
S_woodi	GQ464575.1	AF000858.1	GQ464519.1	AY297513.1	GQ464799.1
U_bicarinatus		HM012694.1	JN648463.1	JN648424.1	AF210338.1
U_graciosus	L41433.1	L41484.1	AF049862.1	JN648433.1	GQ895841.1
U_nigricaudus	GQ464577.1	KP091282.1	GQ464521.1	JN648426.1	GQ464801.1
U_ornatus	AF194247.1	L41487.1	JN648470.1	AY297493.1	AY141065.1

8 Phylogeny Estimation and divergence times

9 The phylogeny was estimated based on a concatenate data matrix of 11,113 characters.

- 10 The best nucleotide substitution models for the nuclear genes are showed in Table S1.
- *Table S1. Nucleotide substitutions models selected for eight nuclear genes*

Nuclear gene data	Nucleotide substitution
partitions	model
BDNF	K80 +I
ECEL	K80 + Γ
PNN	$GTR + \Gamma$
PRLR	$ m K80+\Gamma$
PTPN	$HKY + \Gamma$
R35	$K80 + I + \Gamma$
RAG1	$HKY + \Gamma$
TRAF6	$ m K80+\Gamma$

- 14 For the mitochondrial genes, the best scheme and nucleotide substitution models are
- 15 showed in Table S2.
- *Table S1. Nucleotide substitutions models selected for eight nuclear genes*

Nuclear gene data	Nucleotide substitution
partitions	model
128	$GTR + I + \Gamma$
16S	$GTR + \Gamma$
ND1	
1st position	$GTR + I + \Gamma$
2nd position	$HKY + I + \Gamma$
ND2	
1st position	$GTR + I + \Gamma$
2nd position	$HKY + I + \Gamma$
ND4	
1st position	$GTR + I + \Gamma$
2nd position	$GTR + \Gamma$

For converted the molecular branch lengths from the Bayesian analysis to units of time we 20 used a penalized likelihood method with the chronopl() function in R package 'ape' 21 22 (Sanderson 2002). The penalized likelihood is a semiparametric approach that allows differential rates of evolution across the phylogenetic tree. The method used a trade-off 23 24 between a parametric formulation where each branch has its own rate, and a nonparametric 25 term where changes in rates are minimized between contiguous branches. A smoothing parameter (lambda) controls this trade-off. If lambda = 0, then the parametric component 26 27 dominates and rates vary as much as possible among branches, whereas for increasing 28 values of lambda, the variation are smoother to tend to a clock-like model (same rate for all branches). We used a lambda value of 0.5 for our analysis which maintained an 29 intermediated value in the substitution rates. 30

- 31 Figure 1S. Phylogeny of 56 Sceloporus species based on a combined, and partitioned analysis of eight nuclear genes and five
- 32 mitochondrial genes. The maximum likelihood values are show in the nodes.



33
CAPÍTULO II

Habitat use and sexual dimorphism in *Sceloporus grammicus* (Squamata:

Phrynosomatidae)



Habitat use and sexual dimorphism in Sceloporus grammicus (Squamata: Phrynosomatidae).

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Keywords:	sexual dimorphism, allometry, natural selection, sexual selection, lizards



Allometry refers to the relationships observed between body size and other
organismal traits (Pélabon et al., 2014). Scaling traits of individuals of the same
developmental stage are called static allometry (Bonduriansky & Day, 2003; Pélabon et al.,
2014; Stillwell et al., 2016). Allometric slopes can evolve adaptively if natural selection
persistently favors the scaling relationships that are observed between traits and size
(Petrie, 1988, 1992; Eberhard et al., 1998; Frankino, Emlen, & Shingleton, 2009). The
allometric equation of log-log transformed measurements allows linear comparison of
slopes; when trait size scales with body size. The relationship is called isometric when the
slope has a value of $ 1 $, which can be positive or negative. When the traits scales
disproportionality with body size it is classified as hyperallometry (slope > 1 ; < -1) or
hypoallometry (slope between 0 and 1;-1; Bonduriansky & Day, 2003; Mirth, Frankino, &
Shingleton, 2016; Stillwell <i>et al.</i> , 2016).
Natural and sexual selection are recognized to cause allometric scaling of
morphological traits, showing positive scaling with body size (Bonduriansky & Day, 2003;
Voje, 2016). However, it is poorly known how different types of selection affect the
allometric slope (see Pélabon et al., 2014). One mechanism to determine whether a certain
trait is under natural or sexual selection might be to compare scaling relationships between
the sexes. If the same selective pressures operate on the same trait in both males and
females, there is little reason to expect differences in the allometric slopes between the
sexes (Voje 2016), although other sources of divergence (e.g. ontogenetic constraints)
should be considered.

Page 1

Differences between females and males in size and shape (sexual dimorphism; SD) may result from natural selection on female fecundity. The fecundity selection hypothesis explains the positive relationship between female body size and the quantity or quality of progeny in species where females are larger than males (Fairbairn, 1997; Blanckenhorn, 2005; Ruckstuhl & Neuhaus, 2005; Cox, Butler, & John-Alder, 2007; Fairbairn, Blanckenhorn, & Székely, 2007). Even if males are larger than females, fecundity selection can favor the evolution of relatively larger trunks and abdominal volume in females (Braña, 1996; Cox, Skelly, John-Alder, 2003; Fairbairn et al., 2007; Pincheira-Donoso & Hunt, 2015). In addition, it is well established that sexual selection explains the evolution of secondary sexual characters and an increase in male body size (Darwin, 1871; West-Eberhard, 1983: Andersson, 1994). Because larger traits are favored by strong directional selection due to sexual competition and female choice, selection favors the evolution of positive allometric traits (but see Bonduriansky & Day, 2003; Bonduriansky, 2007). Classical examples of this

37 deviation include peacock's tails, enlarge chelae of fiddler crabs, and the lager body size of

38 pinipeds, in which males can be up to ten times the size of the females (Andersson 1994;

Fairbairn *et al.*, 2007). The SD also can be result of the divergence of ecological niche

40 between females and males, where differences are expected in size and shape of any

41 phenotypic trait directly related to the acquisition and exploitation of resources (Selander,

42 1966; Slatkin, 1984; Shine, 1989; Butler, Schoener, & Losos, 2000; Losos, Butler, &

43 Schoener, 2003). Nonetheless, the direction of SD under the niche divergence hypothesis is

44 not predictable, and it cannot be established if the ecological niche partition is the cause or

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45	consequence of other selective pressures (e.g. sexual selection; Shine, 1989; Fairbairn et
46	al., 2007).
47	Because individual traits can be under different selective pressures, the phenotypic
48	divergences between populations could be result for the interplay between natural and
49	sexual selection (Serrano-Meneses & Székely, 2006; Cornwallis & Uller, 2010; Maan &
50	Seehausen, 2011; Scales & Butler, 2016). The study of the relative impact of natural and
51	sexual selection provides a complete analysis of the mechanisms responsible for generating
52	adaptive divergence (Panhuis et al., 2001; Jones & Ratterman, 2009; Cornwallis & Uller,

53 2010; Bonduriansky, 2011; Kraaijeveld, Kraaijeveld-Smit, & Maan, 2011; Maan &

54 Seehausen, 2011; Network, 2012; Safran *et al.*, 2013; Scordato *et al.*, 2014).

55 Lizards are ideal models to investigate the mechanisms of phenotypic divergence 56 associated with the interplay between natural and sexual selection. Under fecundity selection, distantly related lizard species show female-biased size dimorphism and a 57 positive relationship between body size and number or size of the offspring (Cox et al., 58 59 2003; Cox et al., 2007; Jiménez-Arcos, Sanabria-Urbán, & Cueva del Castillo, 2017). Even in species in which males are larger than females, the allometric relationship between size 60 and the trunk length are larger in females (Braña, 1996; Cox et al., 2003, Cox et al., 2007; 61 62 Pincheira-Donoso & Hunt, 2015). Nevertheless, in most species traits that are involved in sexual displays ("push-up" behavior) and agonistic encounters are larger in males than in 63 females (Carpenter 1978; Martins 1994; Butler et al., 2000; Butler & Losos 2002; Butler 64 2007; Kaliontzopoulou et al. 2015; Baeckens et al., 2017). The "push-up" behavior is 65 associated with territorial defense and mate acquisition, and it can be found among diverse 66

Page 3

67 lizard species with distinct degrees of territoriality and habitat use requirements (Carpenter,
68 1978; Anderson & Vitt, 1990; Butler *et al.*, 2000).

The habitat impacts the evolution of lizard size and shape (Losos 1990a, 2009; Perry et al., 2004; Melville & Swain 2000; Herrel et al., 2002; Kaliontzopoulou et al., 2015). In climbing species that inhabit rocks or canyons-walls it would be expected that heads and bodies will be flat and the length of both pairs of limbs are expected to be short and similar. These features allow maintenance of the center of gravity closer to substrate, which reduces the risk of fall during climbing (Garland & Losos, 1994; Zaaf & Van Damme, 2001; Olberding et al., 2016). Conversely, tree-dwelling lizards are expected to possess shorter limbs and longer and narrower bodies associated with enhanced maneuverability for displacement on reduced perches (Losos, 1990b; Sinervo & Losos, 1991; Herrel, Meyers, & Vanhooydonck, 2001; Herrel et al., 2002). Interestingly, limbs and heads are involved in sexual behaviors and agonistic confrontations in males, which can be associated with mate acquisition, suggesting that these attributes are also targets of sexual selection in diverse lizards species (Carpenter, Badham, & Kimble, 1970; Carpenter, 1978; Hover, 1985; Butler & Losos, 2002).

The mesquite lizard (*Sceloporus grammicus*) represents an excellent model to study
the relative impact of natural and sexual selection on interpopulation phenotypic
divergence. *Sceloporus grammicus* inhabits a diverse array of microhabitats including wallrocks, stumps, trunks and arboreal-cacti of the genus *Opuntia* spp., within a wide range of
macrohabitats ranging from desert scrub to high elevation forest, from Texas to Oaxaca,
Mexico (Jiménez-Cruz *et al.*, 2005; Ramírez-Bautista *et al.*, 2012; Bastiaans *et al.*, 2014).
In addition, *S. grammicus* performs push-ups with elongation of the limbs and dorso-lateral

Biological Journal of the Linnean Society

flattening to demonstrate belly and gular sexual color patches—behaviors generally associated with antagonistic male interactions (Carpenter, 1978; Bastiaans, 2013). In this study we compare the SD patterns among three populations of S. grammicus that differ in habitat use. We selected three populations that comprise the principal habitat of S. grammicus along its distribution. The arboreal population utilizes branches of the cacti like-trees of the genus Opuntia, which represents narrower perches. The saxicolous population occupies higher and wider perches in wall rocks in abandoned human buildings. The third population can be classified as a "generalist-climbing" population. Lizards in these populations are found on trunks, branches of conifers, stumps and wall rocks simultaneously. Because lizards in these populations exhibit differential habitat use, the direction and intensity of natural and sexual selection pressures are expected to be different. In this study we test if the allometric relationship between females and males results in changes in the magnitude of SD in body, head and appendicular characters. Tree-dwelling lizard species have relatively short limbs, flat heads, and elongated bodies (Losos, 1990b; Sinervo & Losos, 1991; Herrel et al., 2001, 2002). However, because of sexual selection we predict that males of the arboreal population will exhibit larger limbs and

106 heads (Losos, 1990a; Herrel *et al.*, 2001, 2002), resulting in different allometric slopes

between sexes. Furthermore, in arboreal populations elongated bodies (i.e. distance

between limbs) are also favored by fecundity selection. Thus, we expect that the allometricslope between females and males are similar, in contrast to the other two populations where

- the allometric slope will be different between females and males. For saxicolous and
- 111 generalist-climbing populations, because of sexual selection we predict that the allometric

Page 5

slope between limbs and heads regressed on body size will be steeper in males thanfemales.

114 Material and Methods

115 Habitat use and morphometry

We collected females and males lizards from three populations that show qualitative differences in the structural habitat. We collected 38 females and 28 males from an arboreal population in Los Manantiales, Mexicaltzingo, Mexico, Mexico (20° 02'. 46.12" N; 99° 32' 18.90" W; elevation 2500 m), which corresponded to an ecotone between xerophytic scrub and oak forest. Most individuals were recorded on branches of cacti like-trees (85% in branches and 15% on rocks). Sceloporus mucronatus and S. torquatus also inhabit the area. These species occupy rocky outcrops and are larger than S. grammicus. For the saxicolous population we collected 50 females and 41 males in San Cristobal, Ixtenco, Tlaxcala, Mexico (19° 14' 43.27" N; 97° 55' 33.87" W; elevation 2700 m) within habitat consisting of crops and some remnants of oak forest. Lizards in this population inhabit rock walls of human abandoned buildings ranging from approximately one to five meters in height where the majority of lizards were collected (93%). The remaining lizards were captured on trunks (4%), branches (1%), and the ground (1%). Sceloporus aeneus and S. spinosus were also present in this area, with the former restricted to the ground and the latter usually found climbing branches of *Opuntia*, trees, and rocks. In the generalist-climbing population we collected 50 females and 33 males on rock walls (43%), stumps (33%), stacks of fallen branches (12%), and trunks (12%) within the vicinity of Estación Científica La Malinche, Ixtenco, Tlaxcala, Mexico (19° 14' 27.85" N; 97° 58' 38.32" W; elevation 3000 m). In this

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population only *S. aeneus* was sympatric, but was mainly associated with the ground (i.e.
non-climber). All the lizards were marked with ink to maintain identity and were released
at the collection site once the measurements had been completed.

Although the structural habitat of three populations showed qualitative differences, we compared the perch height and perch diameter for the sites where females and males were collected. With a commercial measuring tape (Milwaukee 1 mm precision), the height of the perch was measured from the perch site to the ground. Because of habitat differences in perch diameter between lizard populations (saxicolous lizards use rock walls over five meters wide, whereas arboreal populations use narrower perches); measurements of the perch diameter were reduced. For each individual we estimated a perch index by adding up the measurements of SVL, fore limb, and hind limb lengths, and the sum was multiplied by 10. This index indicates that values close to 10 do not represent limitations for vertical and horizontal displacement, which is associated with wider perches (Losos & Sinervo, 1989; Sinervo & Losos, 1991).

For each lizard we measured the snout-vent length (SVL; a standard measure used as a proxy for lizard size; Losos 1990a; Cox *et al.* 2003), head width (HW), head height (HH), head length (HL), relative trunk-length (TL; distance between limbs), fore limb length (FLL; sum of all fore limb segments) and hind limb length (HLL; sum of all hind limb segments). The measures were taken to the nearest 0.01 mm using digital calipers (Mitutoyo CD-15DC; Mitutoyo Corp., Tokyo, Japan).

156 Statistical Analysis

157 Comparison of height and diameter of perch

Because the morphological differences between females and males can results from distinct habitat use (i.e. ecological niche divergence; Shine 1989), we compared whether females and males differ in perch height and diameter within each population, using both variables as a proxy of habitat use. Prior to comparison, we corroborated whether perch height and diameter satisfied the parametric tests assumptions. Because normality and homoscedasticity of variances were not met, we used non-parametric Mann-Whitney test (two tailed test for all analysis) for comparisons.

165 Sexual size dimorphism and allometric relationships

Prior to analysis all trait values were log_{10} transformed. Differences in body size were tested using a two way ANOVA. Population, sex, and their interaction were used as categorical variables, and SVL (our proxy of body size) as the response variable. To test if the occupation of different habitat it is associated with changes in the magnitude of SD, we performed (for females and males separately) major axis (MA) regression with the six phenotypic variables versus SVL. We used the Wald test and the T-student statistic to determine if allometric slopes were heterogeneous between females and males (for details see Warton et al. 2006). Although other methods, like analysis of covariance (ANCOVA) have been used for such purposes (Smith & Lemos-Espinal, 2003; Ramírez-Bautista et al., 2016), we selected MA regression because this method is appropriate when the purpose of line-fitting is not to predict Y from X, but to summarize the relationship between two variables, describing how size variables are related through linear relationships on

logarithmic scales (Warton *et al.* 2006). The main advantage of this regression is that it estimates and infers the lines (slopes) considering the residual values of X and Y, which provides a more accurate estimate of allometric slope (Warton *et al.*, 2006). Additionally, we compared if the allometric slope differed from isometry ($\beta = 1$) using an *F* statistic for the phenotypic traits that diverged in slopes between females and males (for details of calculation see Warton *et al.* 2006).

For variables where the allometric slopes were comparable (i.e. slopes were equal and a common slope could be estimated), we determined changes among common axis and changes in elevation, this latter test is analogous to ANCOVA. We used the Wald test with chi-square (χ^2) for comparison analyses (for details see Warton *et al.* 2006). For all MA analyses we used the program SMATR ver 2.0. In Appendix I we present the statistic values for common axis and elevation comparisons.

Results

Habitat use. There was no divergence in female and male habitat use in the three populations. The height and diameter perch for females and males did not differ in arboreal (height: $U_{(l, 0.05)} = 483$, P = 0.53; diameter: $U_{(l, 0.05)} = 901.5$, P = 0.64), saxicolous (height: $U_{(l, 0.05)} = 950$, P = 0.55; diameter: $U_{(l, 0.05)} = 1918$, P = 0.56), and generalist-climbing (height: $U_{(l, 0.05)} = 800$, P = 0.82; diameter: $U_{(l, 0.05)} = 814.5$, P = 0.90) populations.

Sexual size dimorphism. Males were significantly larger than females ($F_{(1, 234)} = 60.32$,

P < 0.0001). Moreover, there were significant differences in body size among the three

199 populations ($F_{(2,234)} = 26.54$, P<0.0001). Post-hoc comparisons using the Tukey HSD test

indicated that the saxicolous population contained the largest individuals (adjusted mean ± SE; 1.80 ± 0.008), followed by generalist (1.78 ± 0.008) and arboreal populations (1.75 ± 0.009). However, there were no interpopulation differences in the magnitude of body size differences between females and males (Interaction Sex * Population: $F_{(2, 234)} = 1.24$, P =0.29, Fig. 1).

205 Allometric relationships

In the arboreal population four of the six traits showed a heterogeneous slope (Table 1 and Fig. 2). Males had steeper allometric slopes than females for HW, HL, FLL and HLL (Fig. 2A to D), whereas males and females showed homogeneous slopes in TL and HH. Females and males diverged along a common slope in both TL and HH (Table 2). The TL elevation was greater in females, which indicate that females have larger TL with respect the body size. There were no significant differences between sexes in elevation on HH (Table 3). In contrast, females and males from the saxicolous population showed homogeneous slopes in the six phenotypic traits (Table 1). In all traits we found significant changes among common axes (Table 2). This indicated that even when males were larger than females in overall size, the allometric relationship between phenotypic traits and SVL remains similar for both sexes. We also found that four of six traits showed changes in elevation. Females had greater TL values, whereas HL, FLM, and HLM showed higher values in males (Table 3). The generalist-climbing population showed a heterogeneous slope in TL (Fig. 2E), and homogeneous slopes for the other five phenotypic traits (Table 1). For changes in common slope, as well as in elevation, males were larger than females in the five phenotypic traits (Table 2 and Table 3).

Page 10

222 Discussion

Our results indicate that within the three populations of S. grammicus there are no differences in habitat use between females and males. However, the saxicolous and arboreal populations contain the largest and smallest lizards, respectively. Moreover, males are larger than females, even though there are no interpopulation differences in the magnitude of sexual size dimorphism between them. Perhaps the differences in body size between populations could be explained by distinct habitat uses. Both females and males from saxicolous populations may have lower mobility constraints than generalist or arboreal lizards. These last two populations have similar allometric trends between them, suggesting that, at some level, the selective pressures remains similar (see Table 1). However, because habitat use of females and males do not differ, our results may suggest that selection on fecundity and sexual selection rather than differences in ecological niche may be shaping the morphological divergence between females and males.

The interplay between fecundity selection, sexual selection and habitat use pressures could explain the allometric relationships we find in the arboreal population. In females, fecundity selection (number or size of the offspring) can favor the evolution of elongated bodies (Braña, 1996; Cox et al., 2003; Jiménez-Arcos et al., 2016), and the short limbs may compensate for the climbing instability due to the extra weight of the offspring. Moreover, in narrow substrates, elongated and flattened bodies and heads results in a low center of gravity closer to substrate in both sexes (Losos, 1990b; Herrel et al., 2001, 2002; Leyte-Manrique et al., 2017), reducing the risk of falling. Conversely, sexual selection may explain why the allometric relationships on limbs and width and length of the head are

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steeper in males than females. The head and limbs are involved in sexual display behavior,principally for male-male combat for defense of mates and territory (Carpenter, 1978).

246 The selective pressures can operate in similar directions in the arboreal and 247 generalist-climbing populations, even though in the latter the habitat may impose less locomotor constraints than in the arboreal environment. Thus, only generalist climbing 248 249 females show a hyper allometric relationship between SVL and the trunk length, suggesting 250 that selection on fecundity may favor a faster increase in the females' trunk length. Conversely, in females from the saxicolous population where there are presumably no 251 252 climbing constraints on movement, fecundity selection perhaps has favored a general 253 increase in size. Although it is likely that ecological niche constraints are shaping inter 254 population differentiation, the generalist climbing and arboreal males show similar, but steeper allometric trends than females, suggesting that these traits can be under sexual 255 selection. Larger trait size confers benefits due to sexual competition and/or female mate 256 257 choice (Bonduriansky & Day, 2003; Bonduriansky, 2007; Eberhard, Rodriguez & Polihronakis, 2009). However, we stress that none of the allometric slopes in males are 258 steeper than one so perhaps the evolutionary response to sexual selection is constrained by 259 260 the niche (see Bonduriansky & Day, 2003; Bonduriansky, 2007), and that the allometric relationships can be explained by other sources, including ontogenetic and phylogenetic 261 constraints (Butler, Sawyer, & Losos, 2007; Kaliontzopoulou et al., 2015). Thus, 262 experimental studies are needed in order to test the relative impact of natural and sexual 263 264 selection on the evolution of S. grammicus.

265 The correlative evidence in our study suggests an interplay of fecundity and sexual266 selection generating the divergence in body size between females and males. These results

Biological Journal of the Linnean Society

are similar to those conducted in a comparative study on phrynosomatids, where males and females show a differential correlative response associated to habitat use (Herrel *et al.*, 2002). Males possess larger limbs than females, which are associated with territoriality. In the 20 species analyzed, all males perform sexual display behavior (push-ups), which suggests that perhaps limbs are targets of sexual selection (Carpenter, 1978; Martins, 1994; Herrel et al., 2001, 2002). In Anolis lizards the magnitude of SD in size and shape changes among ecomorphs (Butler et al., 2000, 2007; Butler & Losos, 2002). Males usually show fewer lamellae, smaller relative mass and relative body length than females (Butler *et al.*, 2007). Larger relative body length in females can be explained by fecundity selection. Even when clutch size in *Anolis* is fixed to one egg, large differences in clutch number per reproductive season can be associated with fecundity selection pressures. Large sizes in male SVL and head and limb length may be associated with sexual selection pressures, as sexual display behavior associated with territory defense is common among *Anolis* species (Butler & Losos, 2002; Butler et al., 2007). The evidence suggests that interplay between fecundity and sexual selection is the main force explaining the phenotypic divergence between females and males, and differences in habitat use are responsible for interpopulation phenotypic diversification among both sexes.

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450 Figure Legends

Figure 1. Comparison of body size (SVL) in three populations of *S. grammicus:* A) Males
were larger than females considering all the data of the three populations together. B)
Interpopulation size comparison with females and males together. Saxicolous (SAX) was
the largest population, followed by generalist (GEN) and arboreal (ARB) populations. C)
Interaction of sex*population. Males were larger than females in the three populations,
without changes in the magnitude of sexual size dimorphism in body size among three

457 populations.

Figure 2. Allometric relationships for the five traits where the slopes of females and males are significantly heterogeneous in the arboreal population (A to D), and for one trait (E) in the generalist population. The dashed and solid lines represent allometric relationship for females and males respectively. Open and filled symbols represent values of females and males respectively. Abbreviation: t_w = Wald test using *T*-student statistic. Only phenotypic traits that showed significantly heterogeneous slopes are depicted.

(1.23-1.60) (0.84-1.06)

P = 0.001 **

climbing

(0.60-0.81) (0.69-1.00)

P = 0.14

466	Tables						
467	Table 1. Allo	metric slope value	s for six phenotypic t	raits versus snout-ve	nt length (SVL) amo	ong three population	s of <i>Sceloporus</i>
468	grammicus. V	alues in parenthe	ses indicate 95% conf	fidence intervals of the	ne slope. * = Signific	cantly different from	isometry ($\beta = 1$). **
469	= Significant	slope heterogenei	ty between females an	nd males. TL: trunk	ength, HW: head wi	dth, HL: head lengt	n, HH: head height,
470	FLM: fore lin	nb length, and HL	M: hind limb length.				
	Population	TL	HW	НН	HL	FLM	HLM
		¥ 3'	<u>ұ</u> д	<u> </u>	Ŷ 3	₽ ð	<u> </u>
	Arboreal	1.08 1.06 (1.00-1.18) (0.94-1.19	0.77* 1.05 (0.64-0.90) (0.89-1.26)	0.82 0.82* (0.60-1.09) (0.67-0.99)	0.65* 0.80* (0.58-0.72) (0.72-0.89)	0.61* 0.89 (0.52-0.72) (0.77-1.02)	0.60* 0.87* (0.50-0.71) (0.76-0.99)
		P = 0.77	P = 0.004 **	<i>P</i> = 0.99	P = 0.01 **	P = 0.001 **	P = 0.001 **
	Saxicolous	1.1 0.89 (0.96-1.26) (0.70-1.08	1.09 1.11) (0.71-1.71) (0.90-1.36)	0.83* 01.01 (0.69-0.99) (0.69-1.48)	0.72* 0.82* (0.65-0.80) (0.71-0.95)	0.70* 0.77 (0.56-0.85) (0.58-1.01)	0.66* 0.90 (0.52-0.82) (0.67-1.19)
		P = 0.91	<i>P</i> = 0.95	P = 0.31	P = 0.15	<i>P</i> = 0.53	<i>P</i> = 0.09
	Generalist	1.40* 0.95	0.70^{*} 0.76	0.74^{*} 0.64^{*}	0.68* 0.80*	0.60* 0.79 (0.44-0.79) (0.60-1.02)	0.63* 0.75*

(0.61-0.89) (0.47-0.84)

P = 0.36

(0.61-0.92) (0.70-0.92)

P = 0.05

(0.50-0.77) (0.62-0.90)

P = 0.19

(0.44-0.79) (0.60-1.02)

P = 0.15

Table 2. Mean values for fitted axis scores (F). The empty cells correspond to heterogeneous slopes where no comparison can be

476 made. * = significant changes among common slope. Data are mean of F ± 1 SE. TL: trunk length, HW: head width, HL: head length,
477 HH: head height, FLM: fore limb length, and HLM: hind limb length.

Denulation	TL	1	Н	W	Н	Н	Н	L	F	LM	Н	LM
Population	Ŷ	2	Ŷ	3	9	8	4	3	9	3	9	3
	3 38	3 44			2.36	2.44						
Arboreal	±0.02	±0.02		_ (± 0.01	±0.02						
	P = 0	.04			P < 0	0.001						
	3.48	3.60	2.96	3.11	2.48	2.60	2.64	2.75	2.81	2.93	2.97	3.08
Saxicolous	±0.01	±0.01	±0.01	± 0.01	±0.01	± 0.008	±0.01	± 0.008	±0.01	± 0.007	± 0.01	± 0.008
	<i>P</i> < 0.001		<i>P</i> < 0.001		<i>P</i> < 0.001		P < 0	0.001	P <	0.001	$P \leq$	0.001
Conoralist			2.57	2.67	2.34	2.42	2.58	2.67	2.76	2.84	2.89	2.98
climbing			±0.01	± 0.08	± 0.01	± 0.01	±0.07	±0.01	± 0.01	±0.01	± 0.07	± 0.08
climbing			P <	0.001	<i>P</i> < 0.001							

⊿0 Table 3. Mean values for residual axis scores (R). Changes in elevation are analogous to analysis of covariance (Warton *et al.* 2006).

484 The cells with dashes correspond to heterogeneous slopes where no comparison can be made. * = significant changes in elevation

based on common slope. Data are mean of $R \pm 1$ SE. TL: trunk length, HW: head width, HL: head length, HH: head height, FLM: fore

486 limb length and HLM: hind limb length.

D	TL	L	Н	W	H	H	I	IL	F	LM	Н	LM
Population	4	2	Ŷ	8	<u> </u>	3	9	8	9	8	Ŷ	2
Arboreal	-0.32 ±0.002	-0.35 ±0.003	_		-0.63 ±0.005	-0.62 ±0.02			-		-	
	P < 0.0	001*			P = 0.053							
Saxicolous	-0.37 ±0.003	-0.39 ±0.003	-0.87 ±0.007	-0.86 ±0.003	-0.70 ±0.003	-0.69 ±0.02	-0.19 ±0.002	-0.17 ±0.002	0.15 ±0.003	0.18 ±0.003	0.31 ±0.003	0.33 ±0.00
	P = 0.003*		P = 0.35		P = 0.22		<i>P</i> < 0.001*		<i>P</i> < 0.001*		<i>P</i> < 0.001*	
Generalist			-0.25 ±0.003	-0.21 ±0.003	-0.44 ±0.003	-0.41 ±0.004	-0.13 ±0.002	-0.11 ±0.003	0.21 ±0.004	0.24 ±0.004	0.38 ±0.003	0.42 ±0.00
chinoing			P < 0	0.001*	P < 0	.001*	P < 0.001*		P < 0.001*		P <	0.001*





Figure 1. Comparison of body size (SVL) in three populations of S. grammicus: A) Males were larger than females considering all the data of the three populations together. B) Interpopulation size comparison with females and males together. Saxicolous (SAX) was the largest population, followed by generalist (GEN) and arboreal (ARB) populations. C) Interaction of sex*population. Males were larger than females in the three populations, without changes in the magnitude of sexual size dimorphism in body size among three populations.

297x420mm (300 x 300 DPI)





Figure 2. Allometric relationships for the five traits where the slopes of females and males are significantly heterogeneous in the arboreal population (A to D), and for one trait (E) in the generalist population. The dashed and solid lines represent allometric relationship for females and males respectively. Open and filled symbols represent values of females and males respectively. Abbreviation: tw = Wald test using T-student statistic. Only phenotypic traits that showed significantly heterogeneous slopes are depicted.

297x420mm (300 x 300 DPI)

1 Appendix 1

Table A1. Wald test values using an *F* statistic for comparing if slope differs from isometry (H_0 : $\beta = 1$) for females and males using

major axis regression. d.f. = degrees of freedom. HW: head width, HL: head length, HH: head height, FLM: fore limb length and

HLM: hind limb length. * = Significantly different from isometry.

Trait /	1.6	T	TL	Н	W	H	IH]	HL	F	LM	H	ILM
Population	d.1.	F	Р	F	Р	F	Р	F	Р	F	Р	F	Р
Anhonool	♀ (1, 36)	3.72	0.06	10.93	0.002*	2.03	0.16	63.55	<0.001*	39.497	< 0.001*	39.96	< 0.001*
Arboreal	J (1, 26)	1.04	0.32	0.40	0.53	4.73	0.04*	19.33	<0.001*	3.057	0.09	5.19	0.03*
Sariaslana	$\stackrel{\bigcirc}{+}$ (1, 48)	1.88	0.18	0.18	0.67	4.71	0.03*	38.15	<0.001*	13.597	<0.001*	14.24	<0.001*
Saxicolous	ond (1, 39)	0.55	0.46	1.01	0.32	0.005	0.94	7.54	0.009*	3.809	0.06	0.60	0.44
Generalist	$\stackrel{\bigcirc}{+}$ (1, 48)	27.97	< 0.001*	22.68	< 0.001*	10.52	0.002*	61.42	<0.001*	14.276	<0.001*	20.66	<0.001*
climbing	ð (1, 31)	0.98	0.33	4.05	0.053	11.28	0.002*	11.35	0.002*	3.467	0.07	10.41	0.003*

			8						• • • • • • •	(espoi
to significa	antly h	eterog	eneous	slope.]	HW: he	ad wid	lth, HL:	head l	ength,	HH: hea	id heig	ght, FLN	A: fore	limb l	ength	and HL	M: hi	nd lir
length.																		
Population		TL			HW	<u>.</u>		HH			HL			FLL			HLL	
	β_{comm}	<i>t</i> _w	Р	β_{comm}	t _w	Р	β _{comm}	t _w	Р	β_{comm}	t_w	Р	β_{comm}	t_w	Р	β_{comm}	t_w	P
Arboreal	1.08	0.1	0.78				0.82	0.001	0.99									
Saxicolous	1.09	0.01	0.91	1.1	0.003	0.95	0.86	1.02	0.31	0.75	1.97	0.15	0.72	0.4	0.53	0.74	2.91	0.09
Generalist climbing				0.75	2.12	0.14	0.71	0.77	0.36	0.72	3.93	0.054	0.69	2.12	0.15	0.7	1.67	0.1

	TI	_	I	IW	НН		HL		FLM		HLM	
Population	χ^2	Р	χ^2	Р								
Arboreal	4.11	0.04*			13.33	< 0.001	-					
Saxicolous	42.70	< 0.001	64.63	< 0.001	61.23	< 0.001	45.22	< 0.001	73.81	< 0.001	72.29	< 0.00
Generalist climbing			28.15	< 0.001	23.47	< 0.001	21.95	< 0.001	22.18	< 0.001	25.59	< 0.00

Biological Journal of the Linnean Society

Table A4. Statistic values for Wald test using chi-square (χ^2) to evaluate changes in elevation based on a common slope for the six phenotypic traits. The degrees of freedom were the same (d.f. = 1) for all the variables. * = Significantly changes in elevation. The cells with dashes correspond to significantly heterogeneous slope. HW: head width, HL: head length, HH: head height, FLM: fore limb length and HLM: hind limb length. $\frac{TL}{Population} = \frac{TL}{2} = \frac{HW}{2} = \frac{HH}{2} = \frac{HH}{2} = \frac{HL}{2} = \frac{FLM}{2} = \frac{HLM}{2}$

Donulation	T	L	F	IW		HH	ł	HL	F	LM	ŀ	ILM
Population	χ^2	Р	χ^2	Р	χ^2	Р	χ^2	Р	χ^2	Р	χ^2	Р
Arboreal	51.11	< 0.001*			3.74	0.053						
Saxicolous	8.67	0.003	0.87	0.35	1.50	0.22	74.15	< 0.001*	20.51	< 0.001*	15.77	< 0.001*
Generalist climbing			72.56	< 0.001*	21.23	< 0.001*	57.82	< 0.001*	16.18	< 0.001*	49.14	< 0.001*
							<i>e</i> ₁	0				

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Discusión y conclusiones generales

El dimorfismo sexual puede resultar del balance entre la selección natural y la selección sexual. Una vez que los efectos filogenéticos son controlados, nuestros resultados muestran un mayor impacto relativo de la selección sexual en la divergencia en talla en el género Sceloporus (Capitulo 1). La regla de Rensch se refiere al incremento en la magnitud del dimorfismo sexual a medida que aumenta la talla corporal promedio. Cuando la talla corporal es mayor en machos, la magnitud del dimorfismo sexual se incrementa. Cuando el dimorfismo en talla es sesgado a hembras, asociado a presiones de selección en fecundidad, se esperaría que la selección sexual reduzca la magnitud del dimorfismo sexual (Rensch 1950; Fairbairn 1997). En el caso de las lagartijas, se ha reportado que la selección intrasexual es la principal causa de dimorfismo sexual en talla sesgado a machos (Ord et al. 2001; Cox et al. 2003; Cox et al. 2007). Las peleas entre machos son comunes y ligadas a defensa de territorio y/o recursos, donde mayor tamaño puede incrementar la probabilidad de apareamiento (Lopez et al. 2002). En Sceloporus, la dominancia y comportamiento territorial son comunes en diversas especies del género, y la conducta de despliegue es ligada principalmente a enfrentamientos entre machos (Carpenter 1978; Martins 1993; Martins 1994). Aunque en lagartijas, y reptiles en general, los estudios en los que se analizan las preferencias femeninas son limitados (Ptacek 2000), la talla también puede ser sujeta a elección de pareja (Lappin et al. 2006), por lo que la selección intersexual puede estar involucrada en favorecer machos de mayor tamaño (Censky 1997). En cualquier caso, la historia evolutiva dentro del género Sceloporus sugiere un mayor rol diversificador de la selección sexual sobre la selección en fecundidad. Es importante recalcar que en este trabajo se exploró el patrón de dimorfismo sexual resultante de presiones de selección natural (i.e. fecundidad) y sexual. Son necesarios estudios de experimentales y de selección que midan el impacto de ambas fuerzas sobre los rasgos fenotípicos analizados.

La selección en fecundidad favorece un incremento en cantidad y/o calidad de la nidada o camada en función de un aumento en el tamaño corporal de hembras (Darwin 1871; Cox et al. 2007; Pincheira-Donoso & Hunt 2015). Aun cuando el efecto de la selección en fecundidad sobre la evolución del dimorfismo en talla en Sceloporus es menor, puede explicar la evolución de la talla corporal femenina, tanto en especies ovíparas como vivíparas (Jiménez-Arcos et al. 2017). El que las especies con diferente modo reproductor dentro del género Sceloporus presenten tallas similares puede asociarse a la transición de la oviparidad a la viviparidad. Durante la transición de modo reproductor se ha sugerido que un prolongado periodo de retención uterino de los huevos es un paso inicial y transicional a la viviparidad (Shine 1985; Demarco 1993). Ambientes templados y áridos se han correlacionado con la capacidad de retención uterina en lagartijas (Méndez-de la Cruz et al. 1998; Calderón-Espinosa et al. 2006), especialmente en phrynosomatidos (Lambert & Wiens 2013). El género Sceloporus alcanza su mayor diversidad en las zonas áridas de México y Estados Unidos, así como las zonas templadas en el trópico de México (sistemas montañosos de México; Smith 1939; Sites et al. 1992; Wiens et al. 2013). Es probable que estos ambientes hayan favorecido la retención de huevos y un incremento global en la talla de las hembras de especies ovíparas. Esto podría potencialmente reducir las diferencias en talla en las hembras con diferente modo reproductor, independientemente del tiempo de gestación.

Actualmente tenemos un entendimiento profundo de como la selección natural y sexual moldean los atributos fenotípicos (Kraaijeveld et al. 2011; Maan & Seehausen 2011;

Safran et al. 2013; Scordato et al. 2014; Gomes et al. 2018). La divergencia entre sexos puede dar un indicio de diferencias en las fuerzas selectivas actuando sobre atributos fenotípicos (Bonduriansky & Day 2003; Bonduriansky 2007). No obstante, la interacción, balance e importancia relativa de ambas fuerzas genera interacciones complejas difíciles de explorar (Jones & Ratterman 2009; van Doorn et al. 2009; Network 2012; Gomes et al. 2018). *Sceloporus grammicus* (Capítulo 2) es un ejemplo de esta interacción, los resultados muestran como la magnitud del dimorfismo sexual puede cambiar en función del contexto ecológico, en rasgos sujetos a selección natural o sexual.

La diferencia en las pendientes alométricas de machos y hembras de la población arborícola de S. grammicus sugiere que la restricción de movimiento puede tener un impacto en la magnitud del dimorfismo sexual en extremidades, con machos presentando extremidades más largas que las hembras, lo cual puede ser resultado de selección sexual (Herrel et al. 2001; Herrel et al. 2002; Losos 2009). En las otras poblaciones, quizá perchas de mayor diámetro reducen las restricciones en movimiento y favorecen extremidades más largas en ambos sexos, patrón ecomorfológico documentado en diversas lagartijas (Losos 1990; Melville & Swain 2000; Herrel et al. 2001; Herrel et al. 2002; Stuart-Fox & Moussalli 2007; Da Silva & Tolley 2013). Solamente la longitud del tronco de hembras en la población generalista presento una pendiente significativamente diferente de 1 (hiperalometría), lo que sugiere que quizá ocupar diferentes perchas y una menor restricción de movimiento a menor altura favorece un incremento general en la talla. La evidencia correlativa sugiere que algunos rasgos están bajo diferentes fuerzas selectivas con un efecto antagónico, como en lagartijas arborícolas (sobre tamaño de extremidades y cabeza en machos) o sinérgico (mayor longitud de tronco) en función del contexto ecológico. Estudios experimentales y de selección son necesarios para determinar la contribución relativa de ambas fuerzas selectivas en la divergencia fenotípica.

Considerando los resultados de este trabajo en conjunto, la evolución del dimorfismo sexual a nivel de especies puede asociarse a la interacción entre la selección natural y sexual. A nivel interpoblacional, la divergencia fenotípica puede ser asociada a las condiciones ecológicas particulares de cada población, concordando con la teoría ecológica (Schluter 2001; Schoener 2011), pero la divergencia entre machos y hembras (i.e. dimorfismo sexual) es asociada a la interacción de la selección en fecundidad y sexual. Además, la reconstrucción de estados de carácter ancestral sugiere que a lo largo del tiempo evolutivo el patrón de dimorfismo sexual se origina desde el ancestro de *Sceloporus*.

El género *Sceloporus* exhibe la mayor riqueza de especies en México y es actualmente el género de vertebrados terrestres más diverso en nuestro país. Prácticamente es encontrado en todos los tipos de vegetación. Su gran diversidad morfológica, ecológica y conductual sugieren que la selección natural y sexual han tenido un papel central en la divergencia fenotípica. Patrones similares de diversidad fenotípica han sido reportados para los géneros *Anolis* (Losos 2009) y *Liolaemus* (Pincheira-Donoso et al. 2015), ambos grupos de lagartijas considerados como ejemplos de radiación adaptativa. Es probable que *Sceloporus* represente también un ejemplo de una radiación adaptativa (Sites et al. 1992; Wiens et al. 2010; Leache et al. 2016). Sin embargo, aún resta información por ser obtenida. Durante el desarrollo de esta tesis, notamos que elementos básicos de historia natural, ecología y reproducción son desconocidos, especialmente en especies con distribución limitada a México. Estudios futuros deben encaminarse en obtener información de historia natural, fuente de cualquier hipótesis en evolución y ecología (Endler 2015).

72

Estudios experimentales evaluando la significancia adaptativa de los rasgos fenotípicos, tanto por selección natural, sexual y diferentes condiciones ecológicas son necesarios para determinar los mecanismos que han conducido la divergencia y diversificación del género de vertebrados terrestres más diverso de México.

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