Impacto del cambio climático en la distribución geográfica de dos vectores silvestres de la enfermedad de Chagas en Chile, *Mepraia spinolai* y *Mepraia gajardoi* (Hemiptera:Reduviidae).

Tesis entregada a la Universidad de Chile en cumplimiento parcial de los requisitos para optar al grado de Magíster en Ciencias Biológicas

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FACULTAD DE CIENCIAS

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INFORME DE APROBACIÓN

TESIS DE MAGÍSTER

Se informa a la Escuela de Postgrado de la Facultad de Ciencias que la Tesis de Magíster presentada por el candidato.

RUBÉN ACORD GARRIDO BAHMONDES

Ha sido aprobada por la comisión de Evaluación de la tesis como requisito para optar al grado de Magíster en Ciencias Biológicas, en el examen de Defensa Privada de Tesis rendido el día 7 de Noviembre del 2016.

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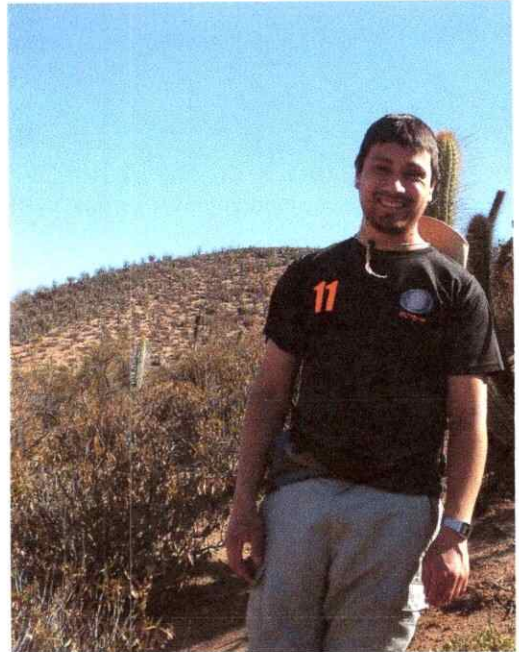Comisión de Evaluación de la Tesis

Dr. Mauricio Canals

Dr. Pablo Guerrero

.

A mis papás, por estar a mi lado brindándome su apoyo y consejos para hacer de mí una mejor persona

BIOGRAFÍA

Mi nombre es Rubén Garrido Bahamondes, nací en Constitución el día 17 de julio de 1988. El año 2002 me fui a vivir a Talca donde terminé mi educación básica y media. El año 2008 ingresé a la carrera Pedagogía en Ciencias con mención Biología en la Universidad Católica del Maule, Talca. Mientras cursaba la carrera de pedagogía, el año 2010, tuve la oportunidad de trabajar en el laboratorio del Profesor Víctor Monzón donde descubrí mi gusto por la investigación en insectos. Con el tiempo el interés en la investigación superó con creces el trabajo de aula. Ya seguro de lo que quería para mi vida profesional, el año 2014 comencé mis estudios de Magister en la Universidad de Chile, bajo la tutela de la Dra. Carezza Botto. Hoy estoy terminando este proceso, me siento muy agradecido por todo lo aprendido y por haber conocido gente maravillosa. Además, tengo en cuenta que el proceso de formación sigue y me siento más motivado que nunca para seguir en este camino.

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RESUMEN

Mepraia gajardoi y *Mepraia spinolai* son especies endémicas
del centro-norte de Chile y vectores de la enfermedad de
Chagas, que habitan zonas áridas y semiáridas,
respectivamente. *Mepraia gajardoi* se distribuye entre los 18°
y 25°S, y *M. spinolai* entre los 26° y 34°S. Ambas especies
difieren en hábitat, prevalencia con *Trypanosoma cruzi*,
morfología y aspectos genéticos. Este estudio tiene los
siguientes objetivos: (1) describir el nicho climático de *M.
spinolai* y *M. gajardoi,* (2) proyectar el nicho de ambas
especies a condiciones climáticas del presente y (3)
proyectar el nicho de ambas especies a escenarios de cambio
climático. Se modela el nicho ecológico de *M. spinolai* y *M.
gajardoi* usando el algoritmo de Maxent. La distriducción
potencial de ambas especies está acotada a sus rangos de
distribución conocidos. Para *M. spinolai*, las proyecciones de
cambio climático en los escenarios RCP 4.5 y RCP 8.5 muestran
pérdida de áreas adecuadas, aun cuando expandiría su rango
hacia el norte y sur de Chile. Estos datos sugieren que las
condiciones climáticas futuras ampliarían el rango de
distribución de *M. spinolai*, abriendo nuevos desafíos para el
siglo XXI en términos de control vectorial. Es necesario

estudiar la ecología, desarrollo y tolerancia térmica para *M. gajardoi.*

Palabras claves: Triatominae, Vectores silvestres, Modelación de nicho ecológico, Cambio climático, MaxEnt, Modelos de distribuciones de species.

ABSTRACT

Mepraia gajardoi and *Mepraia spinolai* are endemic vector species of Chagas disease in Chile, inhabiting arid and semiarid areas, respectively. *Mepraia gajardoi* is distributed between 18° and 25°S, and *M. spinolai* between 26° and 34°S. Both species differ in habitat, *Trypanosoma cruzi* prevalence, morphology and genetics. This study has the following objetives: (1) to describe the climatic niche of *M. spinolai* and *M. gajardoi*, (2) to project the niche of both species to climatic conditions at present, and (3) to project the niche of both species to climate change scenarios. It is modeled the ecological niche of *M. spinolai* and *M. gajardoi* using the Maxent algorithm. The potential distribution of both species was bounded to the range of their known distributions. For *M. spinolai*, climate change projections in the Representative Concentration Pathways RCP 4.5 and RCP 8.5 scenarios showed loss of suitability areas, although appears new areas expanding its northern and southern range in Chile. These data suggest that future climatic conditions would broaden the range of *M. spinolai* distribution, opening new challenges for the 21st century in terms of vector control. More studies on the ecology, development and termic tolerance are

necessary for *M. gajardoi*.

INTRODUCCIÓN

La enfermedad de Chagas o Tripanosomiasis americana es una enfermedad endémica y considerada una zoonosis, actualmente afecta cerca de 7 a 8 millones de personas en el mundo (Organización Mundial de la Salud, WHO 2013), con una incidencia anual entre 28.000 a 41.000 en la región de las Américas (García & Hernández 2014). El agente causante de esta enfermedad es *Typanosoma cruzi*, un protozoo que es transmitido por insectos triatominos (trasmisión vectorial) hacia mamíferos y viceversa (Panzera et al. 2004).

En Chile, en promedio se ha reportado una tasa de nuevos casos entre 2.65 y 11.4 por cada cien mil habitantes (García & Hernández 2014), y no está exenta de transmisión vectorial (Díaz et al. 2002). Los vectores de *T. cruzi* son *Triatoma infestans, Mepraia spinolai, M. gajardoi* y *M. parapatrica* (Frías-Lasserre 2010). Estos triatominos pueden estar en zonas rurales y suburbanas abarcando los climas desierto costero, árido y semiárido, entre las latitudes 18'30°S y 34'36°S (Bacigalupo et al. 2010). *Triatoma infestans* es considerado vector doméstico de la enfermedad de Chagas, pero en 1999 Chile se declara libre de infección domiciliaria (Moncayo 2003), mientras que los vectores silvestres no han

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sido controlados, siendo un problema en zonas rurales. Por ejemplo, *M. spinolai* es abundante en afloramientos rocosos en zonas periurbanas (Cattan et al. 2002) y se han registrado constantes denuncias de avistamientos domiciliarios (información solicitada a través del portal de transparencia www.portaltransparencia.cl). *Mepraia gajardoi* se encuentra cerca de precarios asentamientos de personas recolectoras de algas marinas, donde se alimenta preferentemente de aves marinas, mamíferos marinos, lagartos, perros, gatos y humanos (Sagua et al. 2000; González et al. 2015). Esta situación es epidemiológicamente relevante, especialmente si se considera que los vectores silvestres tienen prevalencias considerables; *M. spinolai* alcanza hasta un 76.1% (Coronado et al. 2009) y *M. gajardoi* hasta un 27.0% (Toledo et al. 2013). Bajo este escenario es necesario explorar las posibles áreas donde estas especies pueden ser detectadas e incrementar el conocimiento acerca de sus requerimientos de nicho ecológico.

El nicho ecológico es descrito como un conjunto de condidiones bióticas y abióticas donde un individuo puede sobrevivir y reproducirse (Wiens et al. 2010). Las variables del nicho tienen una expresión en el espacio geográfico (dualidad del nicho - biotopo, Colwell & Rangel 2009); así se

puede determinar la distribución geográfica de las especies a partir del conocimiento de sus requerimientos de nicho (Gaston 2003; Thuiller et al. 2005). Los modelos de distribución de especies (SDMs) son una herramienta utilizada para proyectar la distribución geográfica potencial de una especie a partir del conocimiento de los requerimientos de nicho. Estos modelos correlacionan las ocurrencias (georreferenciadas) de una especie con información ambiental (la mayoría de las veces información climática) identificando así hábitats idóneos para la colonización (Elith & Leathwick 2009; Soberón & Nakamura 2009). Es sabido que el clima es la el primer determinante para entender la distribución geográfica de las especies a gran escala espacial (Pearson & Dawson 2003; Soberón 2007; Peterson et al. 2011). Un supuesto que subyace a los modelos de distribución de especies es la conservación de nicho, la cual indica que las especies tienden a mantener los requerimientos del nicho en el espacio y tiempo (Wiens & Graham 2005; Wiens 2010). Si el nicho es conservado, entonces, es posible proyectar los requerimientos del nicho a otras regiones geográficas o a otros tiempos (Wiens & Graham 2005; Wiens 2010).

Los SDMs han sido usados ampliamente en ecología, evolución y conservación (Wiens 2010). Además, han sido

utilizado para modelar enfermedades infecciosas, modelando hospederos, parásitos, reservorios y/o vectores (Peterson 2006, 2011). Por ejemplo, se han realizado estudios para modelar vectores del virus de la Fiebre Amarilla (Liria & Navarro 2010), la enfermedad de Lyme (Mak et al. 2010), virus del Nilo Occidental (Peterson et al. 2004), dinámica espacial de vectores y humanos en casos de Dengue (Peterson et al. 2005), entre otros. La enfermedad de Chagas también ha sido modelada, el riesgo de la enfermedad ha sido modelado en Texas, Estados Unidos (Sarkar et al. 2010), sus reservorios (Peterson et al. 2002) y vectores (Beard et al. 2003; Bustamante et al. 2007; Carbajal et al. 2009; López-Cárdenas et al. 2010; Ceccarelli et al. 2015).

Una utilidad adicional de los SDMs es proyectar la distribución geográfica bajo condiciones de cambio climático, la que sirve, en el caso de las enfermedades infecciosas, para conocer la potencial colonización de los vectores y/o evaluar el riesgo de la enfermedad en el futuro. Por ejemplo, en la enfermedad de Chagas, los SDMs pueden revelar la distribución potencial de los vectores-reservorios; así se han definido áreas de potencial riesgo (Costa et al. 2014). Modelar bajo condiciones de cambio climático puede ser importante para anticipar la toma de decisiones sobre el

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control de enfermedades. Para modelar bajo condiciones futuras, se necesita información climática apropiada para este tipo de trabajo. A partir del año 2008, 20 grupos de modelación proveen un nuevo conjunto de modelos climáticos coordinados. Estos experimentos comprenden la quinta fase del proyecto de intercomparación de modelos acoplados CMIP5 (The fifth phase of the Coupled Model Intercomparison Project) (Taylor et al. 2009). Estos modelos son utilizados en el quinto informe de cambio climático del Panel Intergubernamental de Cambio Climático (IPCC 2013), los GCM (General Circulation Models). Estos modelos son desarrollados por diferentes grupos de investigación en el mundo, por ejemplo CSIRO (Commonwealth Scientific and Industrial Research Organization) es un GCM desarrollado por un grupo de investigadores australianos (Penalba & Rivera 2016). Cada GCM presenta diferentes escenarios climáticos o vías de concentración representativas (RCP), que representan, a su vez, vías de concentración de gases invernadero que se traduce en forzamiento radiativo (FR). El nivel de emisiones va a depender de la actividad humana, quedando finalmente cuatro escenarios, RCP 2.6, RCP 4.5, RCP 6.0, y RCP 8.5 (Figura 1). El número de cada vía tiene que ver con el cálculo aproximado del forzamiento radiativo para el año

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2100, expresado en W/m^2 (IPCC 2013). RCP 2.6 es el escenario donde se ejerce mayor mitigación frente al cambio climático, es el escenario más optimista. RCP 4.5 y 6.0 son escenarios de estabilización, es decir, que las emisiones de CO_2 aumentan pero en algún momento se estabilizan. Finalmente RCP 8.5 se considera el escenario más pesimista, donde las emisiones de CO_2 son altas y van en aumento. Los archivos de
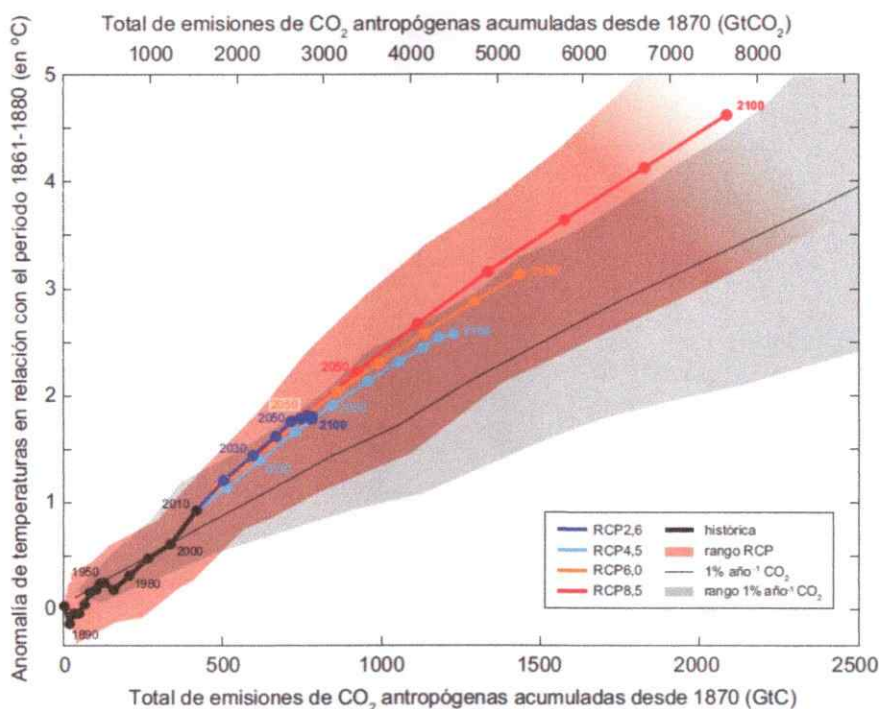

Figura 1. Aumento de la temperatura media global en superficie como función del total de las emisiones globales acumuladas de CO_2 a partir de diversas líneas de evidencia (copiado de *Cambio Climático 2013-Bases Físicas*).

salida de los GCMs deben ser modificados para ser utilizados como archivos de entrada en los modelos de distribución

(Harris et al. 2014), es así como se baja la escala de los modelos GCMs (Ramírez-Villegas & Jarvis 2010) y también se generan las 19 variables bioclimáticas[1] (Ramírez-Villegas & Bueno-Cabrera 2009). Con esto se puede realizar una proyección de la distribución geográfica potencial para una especie hacia climas futuros.

Dado que *M. gajardoi* y *M. spinolai* se distribuyen en zonas geográficas con climas diferentes, y considerando el cambio climático propuesto para fines del siglo XXI donde se espera que la temperatura global aumente en promedio al menos 1°C, se proponen las siguientes hipótesis:

1. Bajo condiciones ambientales actuales, ambas especies tienen diferente nicho climático y por lo tanto proyectan su distribución potencial en zonas geográficas diferentes; específicamente, *M. spinolai* se limita al clima semi-árido mediterráneo y *M. gajardoi* al clima desértico costero.

Bio1: Temperatura media anual, Bio2: Rango medio diurno de temperatura, Bio3: Isotermalidad, Bio4: Estacionalidad de temperatura, Bio5: Temperatura máxima del mes más cálido, Bio6: Temperatura mínima del mes más frío, Bio7: Rango de temperatura anual, Bio8: Temperatura media del cuarto más húmedo, Bio9: Temparatura media del cuarto más seco, Bio10: Temperatura media del cuarto más caliente, Bio11: Temperatura media del cuarto más frío, Bio12: Precipitación anual, Bio13:Precipitación del mes más húmedo, Bio14: Precipitación del mes más seco, Bio15: Estacionalidad de la precipitación, Bio16: Precipitación del cuarto más húmedo, Bio17: Precipitación del cuarto más seco, Bio18: Precipitación del cuarto más caliente, Bio19: Precipitación del cuarto más frío.

2. Frente al cambio climático *M. spinolai* aumentará su área de distribución potencial hacia el sur, destacando zonas de interior y costa, llegando hasta la región del Bio-Bio. Por otro lado, *M. gajardoi*, aumentará su área de distribución potencial hacia el sur, colonizando solamente regiones costeras.

El objetivo principal de este trabajo es estudiar los nichos y estimar la distribución potencial de dos vectores silvestres de la enfermedad de Chagas en Chile, *M. spinolai* y *M. gajardoi*, bajo condiciones actuales y bajo diferentes escenarios de cambio climático.

Impact of climate change on geographical distribution of two wild vectors of Chagas disease in Chile, *Mepraia spinolai* and *Mepraia gajardoi* (Hemiptera: Reduviidae).

Abstract

Background: *Mepraia gajardoi* and *Mepraia spinolai* are endemic vector species of Chagas disease in Chile, inhabiting arid and semiarid areas, respectively. *Mepraia gajardoi* is distributed between 18° and 25°S, and *M. spinolai* between 26° and 34°S. Both species differ in habitat, *Trypanosoma cruzi* prevalence, morphology and genetics. *Mepraia spinolai* is considered more relevant in epidemiological terms because inhabits peridomiciliary areas and several notifications of home intrusion are reported every year. Less information is available for *M. gajardoi* at this point.

Methods: We model the ecological niche of *M. spinolai* and *M. gajardoi*, estimating their potential distributions from the current climate information and project their niches to future climatic conditions, using Maxent algorithm.

Results The potential distribution of both species was bounded to the range of their known distributions. For *M. spinolai*, climate change projections in the Representative Concentration Pathways RCP 4.5 and RCP 8.5 scenarios showed

loss of suitability areas, although appears new areas expanding its northern and southern range in Chile.

Conclusions: Our data suggest that future climatic conditions would broaden the range of *M. spinolai* distribution, opening new challenges for the 21st century in terms of vector control. More studies on the ecology, development and termic tolerance are necessary for *M. gajardoi*.

Keywords: Triatominae, Wild vectors, Ecological niche modelling, Climatic change, MaxEnt, Species distribution models

Background

Chagas disease or American tripanosomiasis is an endemic and zoonotic disease, affecting 7 to 8 million of people (World Health Organization 2013) and with an annual incidence between 28.000 and 41.000 in America (García & Hernández 2014). The causative agent of this disease is the protozoan *Trypanosoma cruzi*, transmitted by hematophagous insects of the subfamily Triatominae to mammals and viceversa (Panzera et al. 2004).

In Chile, there is a notification rate of new cases between 2.95 and 11.55 per hundred thousand inhabitants (García & Hernández 2014), and not exempt from vectorial transmission (Díaz et al. 2002). The vector species are *Triatoma infestans*, *Mepraia spinolai*, *M. gajardoi* and *M. parapatrica* (Frías-Lasserre 2010). These triatomines can be found in rural and suburban zones encompassing the northern desert and semiarid environments, between 18°30'S and 34°36'S (Bacigalupo et al. 2010). *Triatoma infestans*, considered a domestic vector in Chile, was declared controlled in 1999 after the interruption of vectorial transmission (Moncayo 2003); however, the wild vectors are still a problem in rural areas. For example, *M. spinolai* is abundant in stone quarries of periurban zones (Cattan et al. 2002), where it feeds on

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wild rodents, goats, dogs, cats, rabits and humans (Canals et al. 2001; Molina et al. 2004) and every year several home invasion by this vector species are notified to the authorities (data requested in www.portaltransparencia.cl). *Mepraia gajardoi* is abundant near seaweed collector settlements, where it preferably feeds on sea birds, marine mammals, lizards, dogs, cats and humans (Sagua et al. 2000; González et al. 2015). This situation is epidemiologically relevant, specially considering the fact that the prevalence of *T. cruzi* in natural populations of *M. spinolai* can reach up to 76.1% (Coronado et al. 2009) and 27.0% for *M. gajardoi* (Toledo et al. 2013). Under this scenario it is necessary to explore potential geographic areas where these species can be detected and thus, to increase the knowledge about niche requirements and geographic distributions.

Species distribution models (SDMs) are proper tools to examine potential geographic distribution of species. These models correlate the occurrences (georeferenced) of a species with environmental information (mainly climatic information), identifying suitable areas for colonization based on their niche requirements (Elith & Leathwick 2009; Soberón & Nakamura 2009). The climate is key for the understanding of the geographical distribution of species in a large spatial

scale (Pearson & Dawson 2003; Soberón 2007; Peterson 2011), and in this case the climatic niche is examined.

Niche conservation - i.e. the tendency of species to maintain their requirements over space and time (Wiens & Graham 2005; Wiens 2010) - is frequently assumed when we use SDMs. If the niche is conserved, then, it is possible to project the niche requirements to other geographic regions or to other times (past or future) (Wiens & Graham 2005; Wiens 2010). Under this assumption, SDMs have been extended to the study of infectious diseases and host, parasite, reservoir and/or vector modelling (Peterson 2006, 2011). For example, the vectors of West Nile virus have been modeled (Peterson et al. 2004), also spatial dynamics of dengue vectors and human dengue cases (Peterson et al. 2005), among others. For Chagas disease, disease risk has been modeled (Sarkar et al. 2010), their reservoirs (Peterson et al. 2002) and mainly their vectors (Beard et al. 2003; Bustamante et al. 2007; Carbajal et al. 2009; López-Cárdenas et al. 2010; Ceccarelli et al. 2015). SDMs are also useful to project potential distribution under climate change conditions, which could help to identify spatial changes of infectious diseases (Costa et al. 2014). Modelling SDMs under future climate conditions can be important to make decisions about control and disease

surveillance, anticipating appropriate measures. For climate change projections, we used General Circulation Models (GCM), which are the result of the fifth phase of the Coupled Model Intercomparison Project CMIP5 (Taylor et al. 2009), part of the fifth Assessment Report (AR5) of the Intergovernmental Panel on Climate Change (IPCC 2013). Each GCM presents different climate scenarios or Representative Concentration Pathwayss (RCPs), which represents different ways of greenhouse gas concentrations resulting in radiative forcing, depending of human activity mitigation. Scenarios are: (i) RCP 2.6, considered an optimistic lending escenario and of maximun mitigation, (ii) RCP 4.5 and RCP 6.0, considered stabilization scenarios, in which there is increased radiative forcing but this stabilizes, and (iii) RCP 8.5, the most pessimistic scenario, in which higher levels of radiative forcing is recorded and the increase does not stop (Meinshausen et al. 2011).

Since *Mepraia spinolai* and *M. gajardoi* are distributed in different geographical areas with different climates (Di Castri & Hajek 1976; Frías 2010), and considering the climate change scenario proposed for the end of the century expecting global temperature increase of at least 1°C on average, it is

proposed that: (i) Under current environmental conditions, both species project their potential distribution in different geographical areas, i.e., *M. spinolai* limited to semi-arid Mediterranean climate and *M. gajardoi* to the coastal desert climate, and (ii) in a climate change scenario *M. spinolai* will increase its potential range to the south, highlighting hinterlands and coast, reaching the region of Bio-Bio, and *M. gajardoi* will increase its potential range southwards colonizing only coastal regions.

The aim of this study is to estimate the potential geographic distribution of two wild vectors of Chagas disease in Chile, *M. spinolai* and *M. gajardoi,* under current and future climate scenarios, using information of 19 bioclimatic variables obtained from Worldclim.

Methods

Study areas

This study was carried out considering the politic limits of Chile. We choose this country scale criterion because the wild vectors of Chagas disease included in this study are considered endemic species (Frías-Lasserre 2010). *Mepraia gajardoi* is distributed on north coastal zones, where the semiarid climate is common (Frías et al. 1998).

Triatomine species and ocurrence data

We obtained ocurrence data for both vector species from four different sources: field data, available literature, museum collections and reported sightings (Tables 1 and 2)

Table 1. Complete database for *Mepraia gajardoi* occurrences.

Locality	Coordenates		Source	Reference
Playa Corazones	-18.621111	-70.321667	MC	IEUMCE
Arica	-18.47816	-70.321777	MC	IEUMCE
Morro de Arica	-18.48944	-70.31855	MC	IEUMCE
Cueva Anzota	-18.55386	-70.330141	NT	SEREMI
Morro de Arica	-18.479722	-70.324167	NT	SEREMI
Punta de Piqueros	-23.467433	-70.617183	UFD	R. Campos
Punta de Lobos	-21.023458	-70.169527	PA	Frías et al. 1998
Bandurrias	-25.205556	-70.435278	PA	Frías et al. 1998
Piedras Negras	-22.632028	-70.260544	PA	Frías et al. 1998
Arica	-18.492299	-70.320289	PA	Moreno et al. 2005
Iquique	-20.232533	-70.136315	PA	Moreno et al. 2005
Antofagasta	-23.655803	-70.403037	PA	Moreno et al. 2005
Tocopilla	-22.085759	-70.197061	PA	Moreno et al. 2005
Guanera Culave	-18.598417	-70.335097	PA	Carvajal et al. 2007
Médano	-24.526944	-70.559444	PA	Botto-Mahan et al. 2008
Caleta Vitor	-18.7625	-70.342778	PA	Campos et al. 2013
Caleta San Marcos	-21.117205	-70.123718	PA	Toledo et al. 2013
Caleta Camarones	-19.204444	-70.268889	PA	Toledo et al. 2013
Caleta Río Seco	-21.001667	-70.164444	PA	Toledo et al. 2013

*The data were extracted from four different sources: unpublished field data (UFD), museum collections (MC), published articles (PA) and notifications to health services (NT). IEUMCE (Instituto Entomológico Universidad Metropolitana de las Ciencias de la Educación), SEREMI (Regional Ministerial Secretary).

Table 2. Partial database for *Mepraia spinolai* occurrences.

Locality	Coordenates		Source	References
Calle Larga	-32.862127	-70.613307	NT	SEREMI
Llanos de Challe	-28.282694	-71.163556	UFD	A. Yañez
Los Tambos	-28.975880	-70.185307	UFD	C. Botto
Matancilla	-31.424693	-71.009567	UFD	A. Bacigalupo
Til Til	-33.101054	-70.905468	UFD	A. Bacigalupo
Putaendo	-32.614875	-70.681317	UFD	A. Bacigalupo
Petorca	-32.237043	-70.787373	UFD	A. Bacigalupo
Monte Grande	-30.0956	-70.4986	MC	IEUMCE
Carrizalillo	-29.097139	-71.407893	MC	MNHN
La Higuera	-29.386764	-71.056753	PA	Jovanny Bugueño 2013
Cachiyuyu	-29.036667	-70.898889	PA	Schaub & Schottelius 1984
Combarbalá	-31.17971	-71.005044	PA	Venegas et al. 1997
Valle Limarí	-30.55	-71.266667	PA	Schofield et al. 1998
Colina	-33.195277	-70.670897	PA	Canals et al. 1999
Vicuña	-30.031915	-70.708461	PA	Moreno et al. 2005
Reserva Nacional Las Chinchillas	-31.507778	-71.105278	PA	Botto et al. 2006
Inca de Oro	-26.640043	-69.593669	PA	Campos et al. 2011
Monte Patria	-30.854444	-70.6975	PA	Campos et al. 2013
Illapel	-31.630693	-71.1653	PA	Egaña et al. 2014

*The data were extracted from four different sources: unpublished field data (UFD), museum collections (MC), published articles (PA) and notifications to health services (NT). IEUMCE (Instituto Entomológico Universidad Metropolitana de las Ciencias de la Educación), MNHN (Museo Nacional de Historia Natural, Chile), SEREMI (Regional Ministerial Secretary).

All these data presented geographical coordinates to allow spatial location and thus to relate them to environmental data. Different research groups shared their database (2008 - 2016) providing field data for this study. We used 20 published scientific articles with georeferenced locations.

In relation to museum collections, we reviewed the collections of the Museo Nacional de Historia Natural (Santiago, Chile) and the Museo Entomológico de la Universidad Metropolitana de Ciencias de la Educación (Santiago, Chile). Finally, reported sightings of triatomines correspond to notification of home or garden intrusion to public health centers, including the collection of the specimen. We obtained this information through the website https://www.portaltransparencia.cl.

Environmental data

Climate data were obtained from WorldClim website http://www.worldclim.org (Hijmans et al. 2005). The layers are available in four different resolutions. We used data at 30-second spatial resolution, the smallest available resolution, because it describes the importance of local climate conditions for triatomines (Medone et al. 2015; Vega et al. 2015). We used climatic information of current and future layers. For the present layers, we used the 19 bioclimatic variables. These data were generated through interpolation of mean monthly climate data from weather stations (Hijmans et al. 2005). In the case of the future, we used the general circulation model GCM (Taylor et al. 2009),

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which belongs to the most recent global circulation models used in the last report of the IPCC (IPCC 2013). In addition, the GCMs have four Representative Concentration Pathways (RCPs) available, RCP 2.6, RCP 4.5, RCP 6.0 and RCP 8.5 (Martin et al. 2011). The RCPs are used to drive climate model simulations planned as part of the World Climate Research Programme's Fifth Coupled Model Intercomparison Project (CMIP5) (Taylor et al. 2009; Meinshausen et al. 2011). This model has 19 variables for the four RCPs. The models chosen are representative for the Southern Cone (Penalba & Rivas 2016).

We used PCA analysis (Qiao et al. 2014; Canals et al. 2016) to delete the multicollinerity between environmental variables. Thus we generated principal components, which represented the 19 variables of WorldClim. This analysis was performed to current and future environmental layers. For future conditions, we used two representative concentration pathways (RCPs), which are also obtained from worldclim and therefore have the 19 bioclimatic variables. In summary, analyses were performed for current, RCP 4.5 and RCP 8.5 layers. Then, we used PCA variables to build species distribution models for *M. spinolai* and *M. gajardoi*.

Niche analysis

We used the software Niche A (http://nichea.sourceforge.net/) to visualize the climate niche of both species in the environmental space. We generated the niches through occurrences and showed the convex polyhedron of the ocurrences points in a two-dimensional chart, using principal component 1 in X axis and principal component 2 in Y axis.

Species distribution modelling

SDMs were constructed using Maxent (Phillips 2004; Phillips et al. 2006). This software predicts species distribution, correlating environment data with species occurrence. Maxent is a machine-learning method that assesses the probability of distribution of a species by estimating probability distribution function of maximum entropy (Phillips et al. 2006). The method generally performs better than other software commonly used for SDMs and uses randomly selected pseudo-absences within an *a priori*-defined background area (Elith et al. 2006; Phillips et al. 2006; Ortega-Huerta & Peterson 2008). Maxent is also more robust to spatial errors in occurrence data and uses only presence dataset to predict species distributions (Phillips et al. 2006; Graham et al. 2008). We divided the occurrence data into two parts for

training and testing the model (75.0% and 25.0%, respectively). The performance of the model was evaluated using the AUC (area under the curve ROC, Receiver Operating Characteristic, Phillips et al. 2006). AUC ranges from 0.5 for a model that performs no better than chance to 1.0 if the model fits perfectly. The AUC quantifies the degree to which the model identifies presences more accurately than random (Phillips et al. 2006). For the species modelling distribution, we used the first four principal components, under current conditions, where the modeled climatic niche is projected under future climate scenarios (RCPs 4.5 and 8.5).

Results

Principal components analysis

For the PCA with current environmental variables, we obtained that the first four principal components explained 95.0% of the variance (Table 3). PC1, with a contribution of 45.0%, was positively correlated with Bio12, Bio14, Bio17 and Bio18 (annual precipitation, precipitation of driest month, precipitation of driest quarter, and precipitation of warmest quarter, respectively). PC2, with a contribution of 28.0%, was positively correlated with Bio1, Bio9, Bio10 and Bio11

(mean annual temperature, mean temperature of driest quarter, mean temperature of warmest quarter, and mean temperature of coldest quarter, respectively), and negatively correlated with the altitude. On the other hand, PC3, with a contribution of 12.0%, was negatively correlated with Bio4 and Bio7 (temperature seasonality and temperature annual range). Finally, PC4, with a contribution of 7.0%, was positively correlated with Bio3 (isothermality).

For future climate information, the results from PCA in the four RCPs were similar to those described for current environmental variables, explaining in all cases near to 95.0% of the variance. The variance contribution of each principal component was approximately: PC1 50.0%, PC2 25.0%, PC3 14.0% and PC4 7.0%. All principal components were correlated with the same variables as the PCs of the current bioclimatic variables, presenting coefficients with small differences in scores.

Table 3. Factor loadings of the principal components based on environmental data used in both species *M. spinolai* and *M. gajardoi*.

	PC1	PC2	PC3	PC4
alt	-0.13	-0.31	-0.02	0.35
bio1	-0.19	0.33	0.05	0.06
bio2	-0.25	-0.12	-0.26	0.28
bio3	-0.24	-0.13	0.05	0.42
bio4	-0.02	0.01	-0.51	-0.36
bio5	-0.22	0.27	-0.18	0.02
bio6	-0.07	0.38	0.16	-0.03
bio7	-0.21	-0.07	-0.43	0.07
bio8	-0.18	0.22	0.24	0.21
bio9	-0.17	0.32	-0.10	-0.09
bio10	-0.19	0.33	-0.03	-0.01
bio11	-0.18	0.33	0.13	0.11
bio12	0.29	0.14	-0.11	0.20
bio13	0.24	0.17	-0.29	0.16
bio14	0.30	0.08	0.07	0.20
bio15	-0.24	-0.04	-0.17	0.34
bio16	0.24	0.17	-0.27	0.16
bio17	0.3	0.09	0.06	0.21
bio18	0.29	0.06	0.06	0.27
bio19	0.23	0.18	-0.28	0.11

*First four components explain 95% of variance.

Niche analysis

The graph of Figure 2 was constructed based on PC1 and PC2. The image shows the niche of *M. spinolai* represented by blue dots, which correspond to the values of the presences in the environmental space, and the larger polygon. Also, the niche of *M. gajardoi* is represented by red dots (presences), and a much smaller polygon.
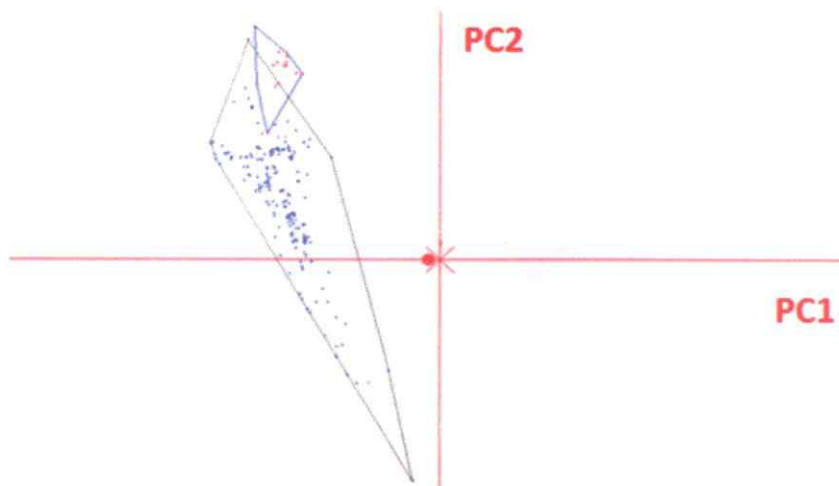
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Figure 2. Climatic niche of *M. spinolai* (gray polygon) and *M. gajardoi* (blue polygon) based on the first two principal components (PC1=X, PC2=Y).

Validation of SDMs

The average AUC value for the model of *M. spinolai* was 0.973 with standard deviation 0.003. In the case of *M. gajardoi*, the average value of AUC was 0.995 and standard deviation 0.002. These results indicate that the models perform significantly diffent than chance and thus they are validated at least for these scenarios.

Current and future SDMs for M. spinolai

The suitability area predicted under current conditions for *M. spinolai* shows that the potential distribution model matches very well with its known distribution (Figure 3), encompassing approximately from 27° to 34°S, covering an area of approximately 46,000 km². This area corresponds to the Mediterranean area in the arid and semi-arid climates of Chile (Di Castri & Hajek 1976). Suitable areas were observed in the inland valleys and, to a lesser extent, in the coastal areas. In general, the suitable areas are widely distributed in interior valleys, decreasing as they approach toward the coast and the Andes mountains.

On the other hand, there were modifications in the suitability areas in all future climate scenarios. RCP 4.5 (stabilization scenario) showed an increase in suitability areas to 94,000 km² (new areas), from 25° to 35°S including Antofagasta, Taracapá, Coquimbo, Valparaíso, Metropolitana and Maule regions. Nevertheless, there were loss of distribution areas 7,000 km² (lost areas) and maintainance of 40,000 km² (maintained areas), both in interior valleys. Meanwhile, the new areas, 54,000 km², are in interior valleys as well, but closer to the coast (Figure 4). RCP 8.5 (critical stage) maintains the total area suitable for *M.*

spinolai, although, showed a great loss of suitable area, corresponding to 28.000 km^2 (lost area), mainly in interior valleys among 30° to 33°S, including Coquimbo, Valparaíaso and Metropolitan regions. Regarding to new suitable areas, these are distributed among 30° to 34°S and correspond to 28,000 km^2 (new areas). Finally, adding the new areas the maintained suitable areas correspond to 19,000 km^2 (maintained areas) and focus on interior valleys among 30° to 33°S (Figure 5).
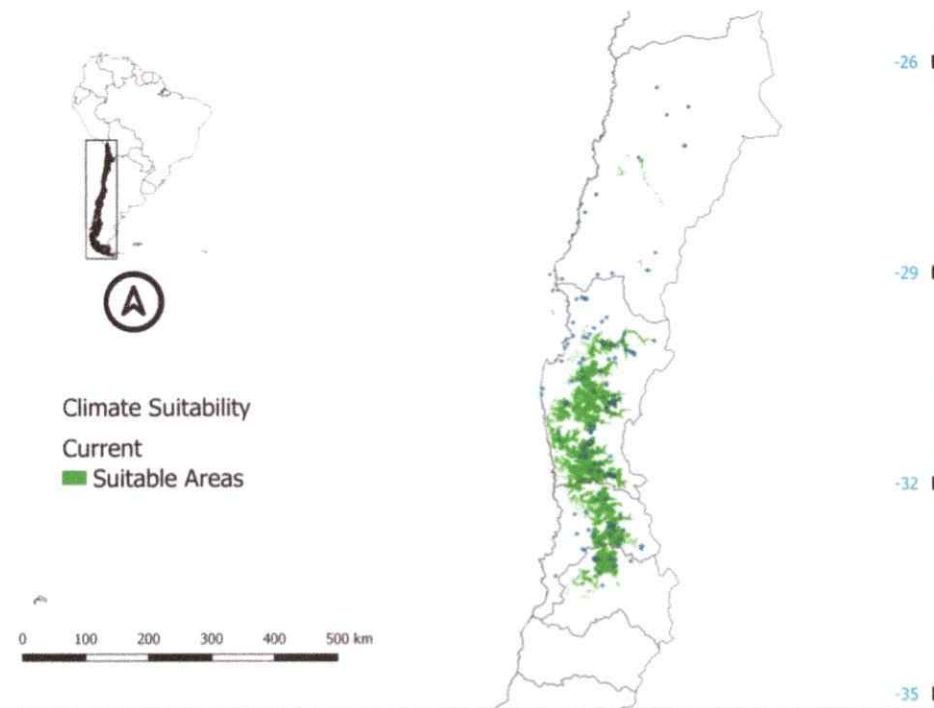

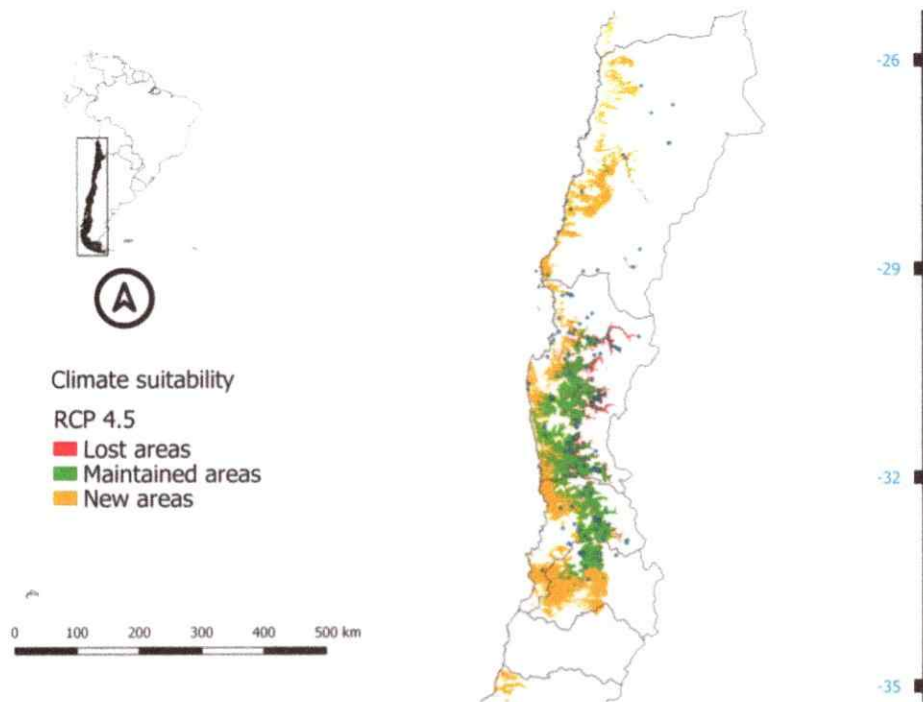Figure 3. Potential distribution for *Mepraia spinolai* under current climate conditions.

Figure 4. Potential distribution for *Mepraia spinolai* under future climate change scenario (RCP 4.5).
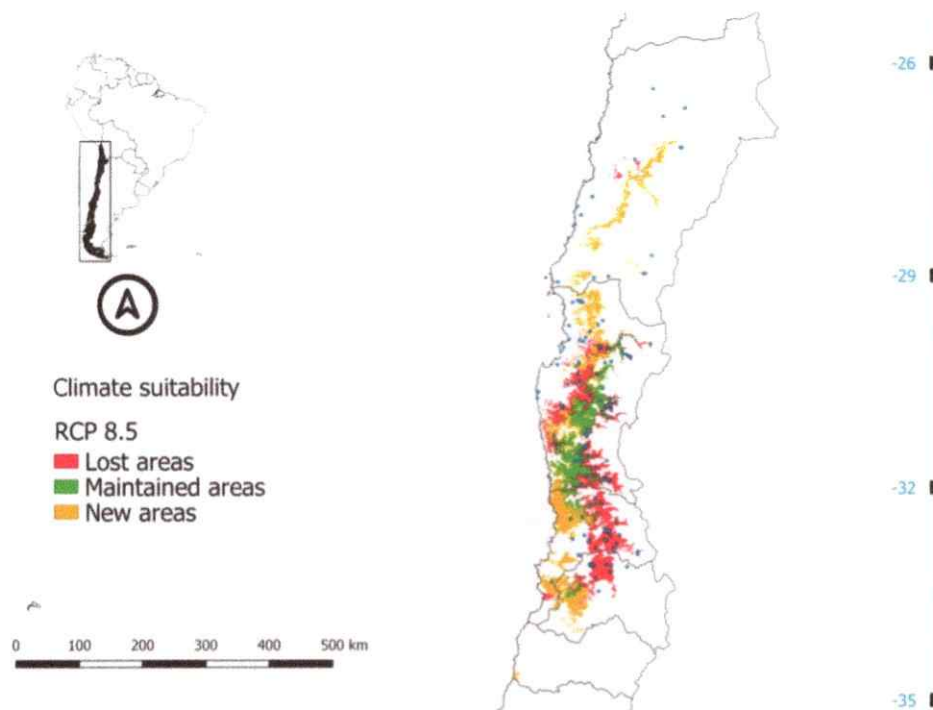
Figure 5. Potential distribution for *Mepraia spinolai* under future climate scenario (RCP 8.5).

Current and future SDMs for M. gajardoi

The potential distribution projected for *M. gajardoi* includes its known distribution. Figure 6 shows that it is a coastal species, with some suitable areas inland, but always near the coast, obtaining approximately 8,000 km². Distribution ranges from 18° and to 26°S, and it is limited by the desert area of Chile, specifically in the coast. Interestingly, the model predicts a distribution in the Reserva Nacional Pampa del Tamarugal, an inland area 55 km far from the coast. For future climate conditions predicted by RCP 4.5 and 8.5

scenarios, the potential geographic distribution was the same for both, suitable areas disappeared completely.

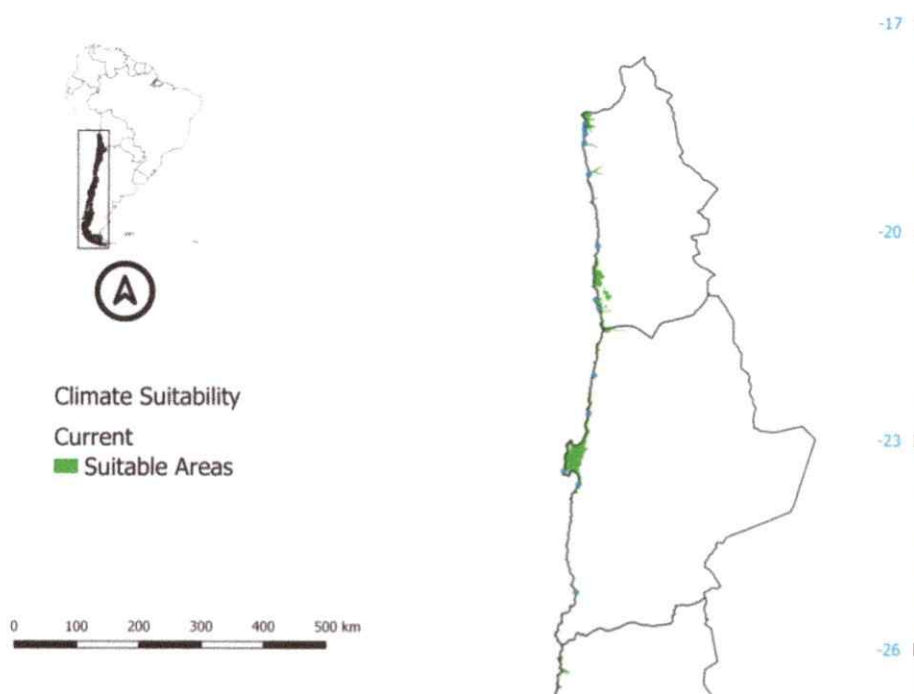Figure 6. Species distribution models for *Mepraia gajardoi* under current climate conditions.

Discussion

In this study, we assessed the habitat suitability of two endemic triatomine species from Chile, predicting their potential distribution under future climate scenarios. The niche model built for *M. spinolai* is associated with PC1, which is mainly correlated with annual precipitation,

precipitation of the driest month and precipitation of the driest quarter. Precipitation may be related to the presence of *M. spinolai* indirectly because rainfall influences the primary productivity (plant communities) and this, in turn, affects the abundance of small rodent species such as *Octodon degus* and *Phyllotis darwini*, hosts of *M. spinolai* (Rozas et al. 2005; Donoso et al. 2016). Other important variables that described the *M. spinolai* niche were PC2 associated with isothermality, temperature seasonality and temperature annual range. These variables are related to temperature, specifically with tolerance ranges of this species. In general, triatomines do not inhabit in sites with wide temperature range (Pereira et al. 2013). In the case of *M. spinolai*, laboratory evidence shows that its temperature range is between 15° and 42°C, preferably 24.2°C, and when environmental conditions are not favorable diapause is induced (Ehrenfeld et al. 1998). Furthermore, the habitat where this species is distributed does not present high annual temperature range. Finally, *M. spinolai* is a diurnal species that feeds at the hours of highest temperatures of the day; therefore, even higher temperature values might be harmful (Schenone et al. 1980).

Regarding the suitability areas shown in the model, the potential distribution of *M. spinolai* is limited to semiarid areas between 27° and 34°S. The semiarid climate is characterized by low rainfall, anticyclone effect over the coasts and by a temperature and humidity gradient, decreasing from the coast to the Andes (Huxman et al. 2004; Montecinos et al. 2016). The wild small mammals *Thylamys elegans*, *O. degus*, *P. darwini* and *Abrothrix olivaceus*, considered reservoirs of *T. cruzi*, inhabit in semiarid ecosystems (Rozas et al. 2005). Therefore, this implies that they are blood source of *M. spinolai*, which uses host burrows as habitat or shelter, but also rocky outcrops and bird nests (Canals et al. 2001). On the other hand, *M. spinolai* also inhabits peri-urban areas, where is abundant in stone quarries, a habitat offering high abundance of potential hosts (Cattan et al. 2002).

The model of *M. gajardoi* showed that is mainly related with PC1, which is associated with annual temperature, minimum temperature and mean temperature in general. Then, the model is explained mainly for temperature. This is related with the potential distribution of *M. gajardoi*, it occupies coastal areas between 18° and 26°S, where these sites are characterized by the Pacific anticyclone effect

that prevents precipitation (scarce rainfall) and high temperature differences (Ancapichún & Garcés-Vargas 2015), which would be an advantage for the suitable habitat of *M. gajardoi*. This species dwells in bird nests, and feeding habits include blood of small mammals, shorebirds and lizards (Sagua et al. 2000; Botto-Mahan et al. 2008).

Under future climate conditions *M. spinolai* loses suitable areas, where it is currently distributed, with different impact depending on the modeled scenario, although increases its distribution range, highlighting a potential distribution expansion in the north and south. Despite of the fact that future climate models have tremendous uncertainty, it is predicted for Chile that the number of droughts and rainfall will increase in the 21st century. Although rainfall will be more frequent, there will be less intense droughts in winter (Penalba & Rivera 2016). Furthermore, according to RCP 4.5 and RCP 8.5, it is predicted that the temperature will increase an average of 1.8° and 3.7°C, respectively (IPCC 2013). For Chile, the increase in temperature will be modest in the coast (0.5° to 1°C), but will increase towards the Andes, where it can increase up to 5°C in north and central Chile (Garreaud 2011). Therefore, considering niche conservatism, the impact of climate change on *M. spinolai* is

major depending on the scenario, being RCP 8.5 the one with high loss of suitable areas.

Future climate models project no suitable areas for *M. gajardoi*. We suggest that the geographical distribution of *M. gajardoi* hinders the work under niche modeling algorithm. Specifically, due to its limited distribution there may be a phenomenon like the roadside bias. This triatomine is in places with low thermal oscillation and rainfall (Di Castri & Hajek 1976); therefore, niche estimates might include low thermal tolerance and precipitation as important constraints in *M. gajardoi* potential distribution.

Some limitations of this type of studies include the inherent uncertainty of working with projections of a possible climate change (Martinez-Meyer 2005; Heikkenen et al. 2006). Furthermore, GCMs exhibit heterogeneity regarding the predicted areas, because, even though they can predict well the change that will occur globally, some specific areas might not be well represented. However, appropriate models for South America have been identified (Jiménez-Valverde et al. 2009). In the case of Chile, current weather observations (minimum 30 years) have not been compared versus the baseline of the GCM, to assess which model fits better for this region. In this study, we assumed that the problem presented

in scenarios RCP 2.6 and RCP 6.0 due to GCMs are models that predict future worldwide and do not necessarily reflect the reality that occurs at the analysed regional level. However, these models have been used to project future potential distributions in whole South America, and in United States, Mexico, Brasil and Argentina, all countries with large land areas. Hence, there are less problems in representing the climate of these regions, considering the original resolution of future models (Taylor et al. 2009). Unlike those countries, Chile is a long and narrow region bounded by the Pacific Ocean in the West and the Andes mountain range in the East, exhibiting different climates in a short stretch of land. For example, the area between the 18° and 25°S is subdivided into three types of climates: coastal desert, interior desert, and high desert (Di Castri & Hajek 1976), implying that climate change projections in face of this geographic complexity may present strong representation problems.

Finally, in this study we assume niche conservation, where the niches of the species under study do not change over time, thus species with strong conservation of the climatic niche must migrate or extinguish (Wiens 2010), i.e. the climatic requirements are maintained, and these can be

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projected to other realities as climatic change scenarios. However, other alternatives must be considered, where the species can modify its climatic niche due to phenotypic plasticity or local adaptation (Valladares et al. 2014). In this study that topic is not covered, however, future research should consider that phenotypic plasticity can be an attenuating factor of climate change and assist in short- and long-term adaptation (Nicotra et al. 2010; Chevin et al. 2010).

Conclusions

The climate requeriments of *M. spinolai* were related to low thermal oscillation, precipitation of coldest month and temperature seasonality. Its potential distribution was projected to semi-arid and Mediterranean climates, fitting the known distribution of this species, mainly located in inland valleys and in a lesser extent in the coast. The niche model of *M. gajardoi* was built mainly with temperature seasonality and temperature annual range. The potential distribution of *M. gajardoi* was limited to the oceanic coast climate of Chile. However, the fundamental niche of this especies is unknown, probably given that the habitat of *M.*

gajardoi is very specific, producing an effect like roadside bias, restricting the thermal tolerance for this species. It is recommended to develop laboratory experiments to assess its thermal range performance, and if possible, to include new presence points to ensure that all its environmental range is covered in future studies.

Under climate change, *M. spinolai* would increase its potential distribution to the north and south, although in the pessimistic scenario it shows notorious loss of suitable areas. *Mepraia gajardoi* does not show future suitability areas, because its climate niche was underestimated. Information about the habitat of these vectors species and the areas of geographic suitability for colonization would be useful for control of Chagas disease vectors. This would allow anticipating control measures and prevention campaigns, especially in areas where currently there are no wild triatomine reports and, therefore, no governmental programs focused on Chagas disease vectors.

Acknowledgments

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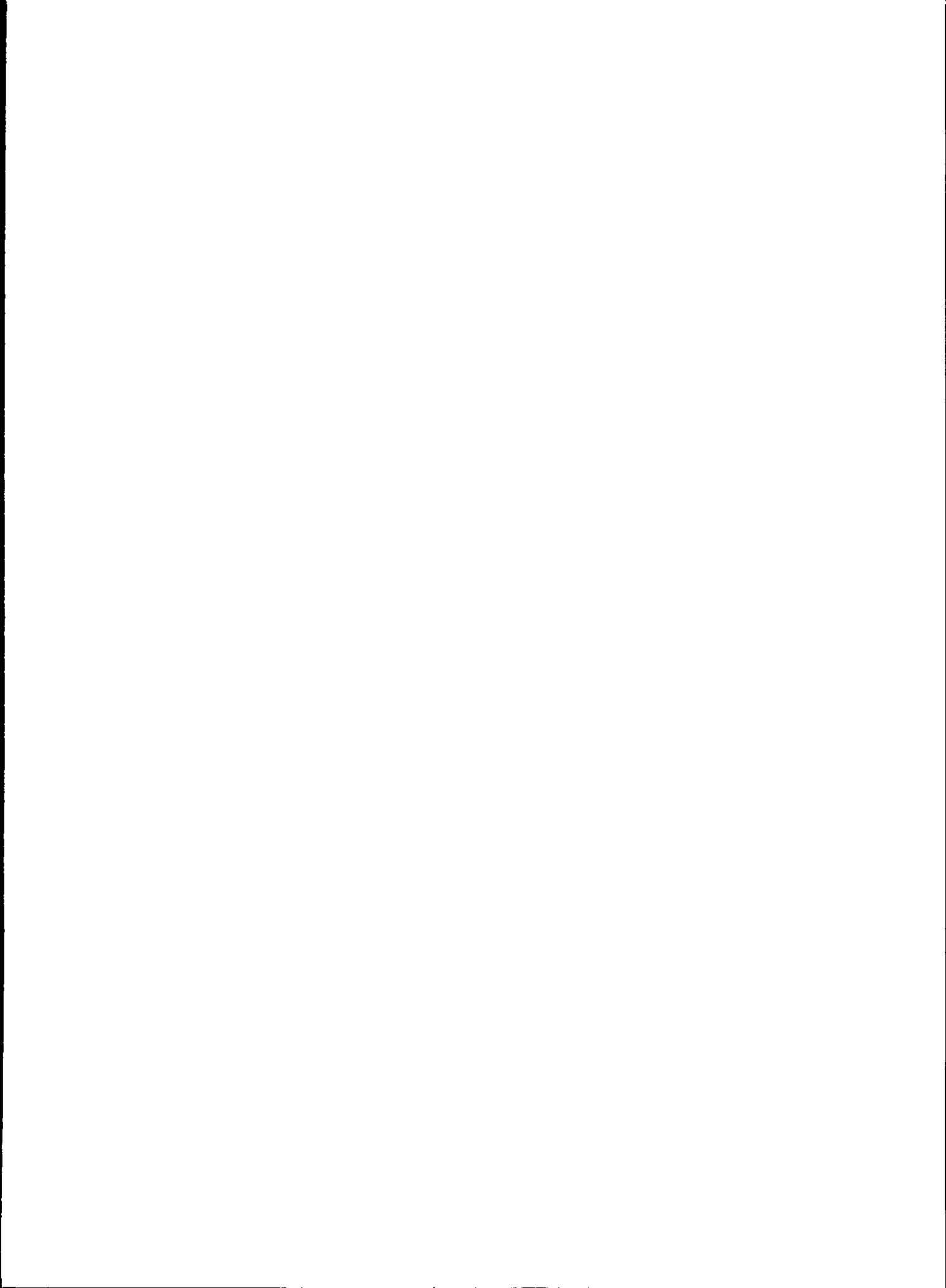
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CONCLUSIONES

- Los requerimientos climáticos de *M. spinolai* tienen que ver con baja oscilación térmica, precipitaciones en los meses más fríos y la estacionalidad de la temperatura. Su distribución potencial se proyecta a los climas semi-árido y mediterráneo, lo cual se ajusta a la distribución conocida para esta especie, ubicándose principalmente en zonas de valles de interior y en menor medida en la costa.

- El modelo de nicho para *M. gajardoi* se construye principalmente con las variables estacionalidad de la temperatura y rango de temperatura anual. Su distribución potencial se limita al clima oceánico costero de Chile. Sin embargo, el nicho fundamental de esta especie está subestimado, debido a que Maxent toma muestras en sitios muy particulares, restringiendo la tolerancia térmica para esta especie. Se recomienda realizar experimentos de laboratorio evaluando su rango térmico de desempeño.

- Frente al cambio climático, *M. spinolai* aumenta su distribución potencial hacia el sur y muestra una mayor probabilidad de ocurrencia en regiones donde actualmente

se distribuye esta especie, comparado con resultados del presente, mostrando aumento de a lo menos 10.000 km^2 para el futuro. *Mepraia gajardoi* no presenta zonas idóneas, esto se debería a que su nicho climático está subestimado.

- Conocer el hábitat de estas especies de vectores biológicos, y las zonas geográficas adecuadas de colonización, sería ventajoso para el control vectorial de la enfermedad de Chagas, debido a que esta información permite anticipar medidas de control y campañas de prevención.

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