

Future climate change and the distributional shift of the common vampire bat, *Desmodus rotundus*

Journal Club sessions

Paige Van de Vuurst and *et al.*, 2025. Scientific Reports (IF 3.8, H-Index 315, Q1)
Presented on March 24th, 2025



MSc. Mariana Alejandra Castro Mejía
SE Guerra-Palomares
Dr. CA García-Sepúlveda

Laboratorio de Genómica Viral y Humana
Facultad de Medicina
Universidad Autónoma de San Luis Potosí

Aim of manuscript and relevance

To assess the potential impacts of future climate change on the distribution of *Desmodus rotundus*, a common vampire bat species, and its role as a rabies virus reservoir.

The study explores how climate-induced changes in the bat's range could increase the risk of zoonotic disease transmission, particularly rabies, to new species, including humans.

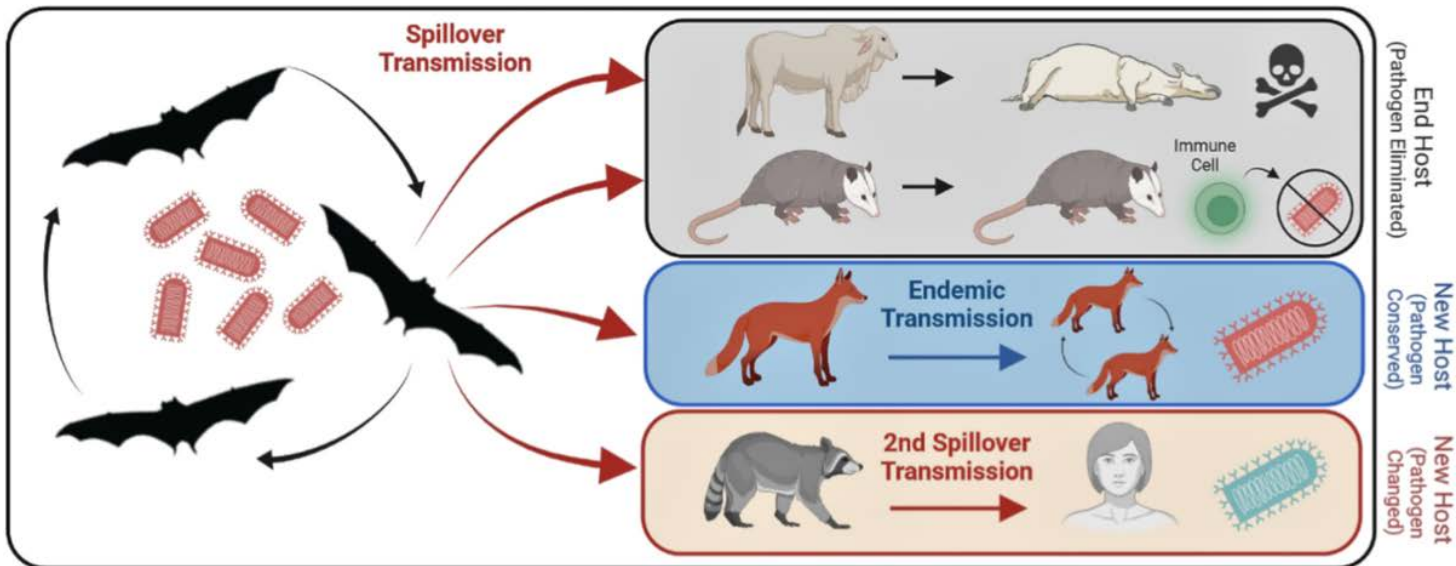


Climate change and zoonotic diseases

The Intergovernmental Panel on Climate Change (IPCC) has predicted that climate change will amplify negative health impacts across the globe, affecting the ecosystem stability.

This leads to shifts in species distribution, creating new species assemblages and increasing the risk of pathogen transmission to new hosts.

These changes can drive zoonotic diseases, causing economic losses due to the transmission of pathogens from wildlife to livestock.

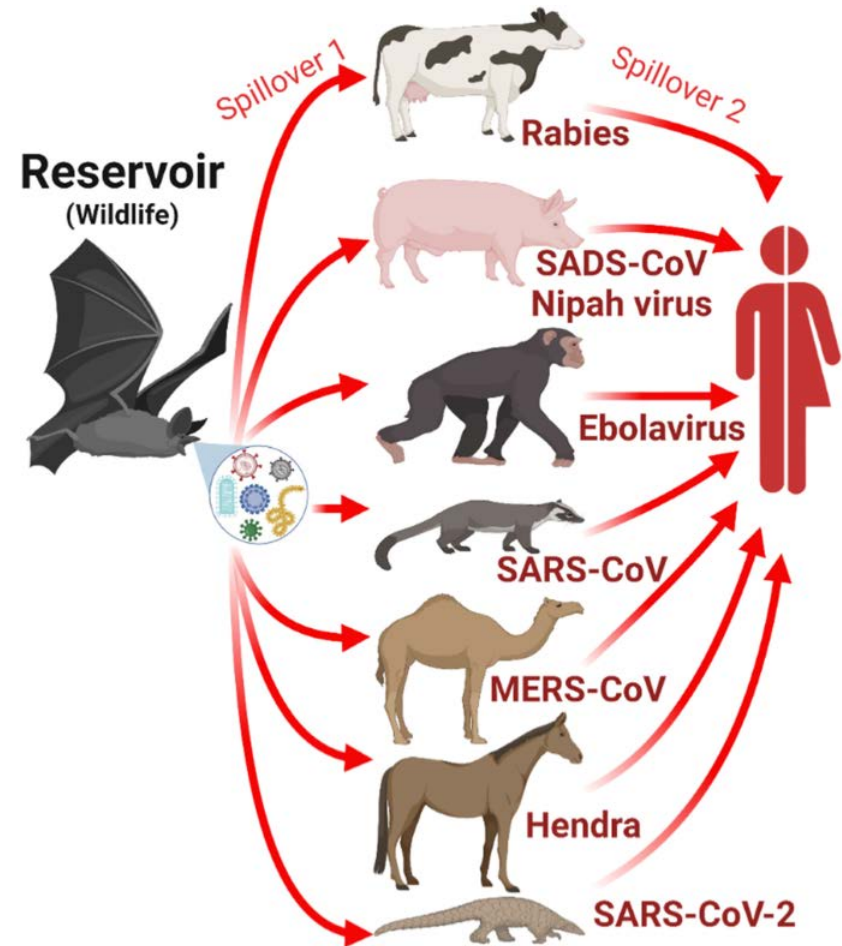


Spillover

Pathogen spillover, has been linked to some of the most lethal zoonotic diseases which impact humans.

Bats can tolerate infection by viruses that are highly pathogenic to livestock and humans.

Climate change impacts on health are not evenly distributed geographically.



Rabies virus (RAVB)

Rabies virus (RABV) is a significant bat-borne pathogen in Latin America, causing over \$8.6 billion in annual economic losses due to livestock deaths and lost human work hours.

The common vampire bat (*Desmodus rotundus*) transmits RABV to humans and livestock, with outbreaks frequently occurring in tropical and subtropical regions, where human infection risks are linked to livestock outbreaks.





Introduction

In the last 120 years, *D. rotundus* has expanded due to climate change, increasing the spread of RABV in livestock, particularly in Peru.

Climate change is expected to further shift its distribution, raising the risk of RABV spillover.

Ecological niche modeling (ENM) is used to predict these changes by assessing how environmental factors influence species distribution.

MAxEnt Software

An ecological niche modeling (MAxEnt) was used to predict the future distribution of *D. rotundus* across various climate scenarios in the Americas.

MaxEnt compares environmental conditions from occurrence locations with potential habitats, focusing on abiotic climate data to assess the species fundamental niche.

This approach avoids uncertainties from non-climate factors, offering a clearer view of future climate impacts.

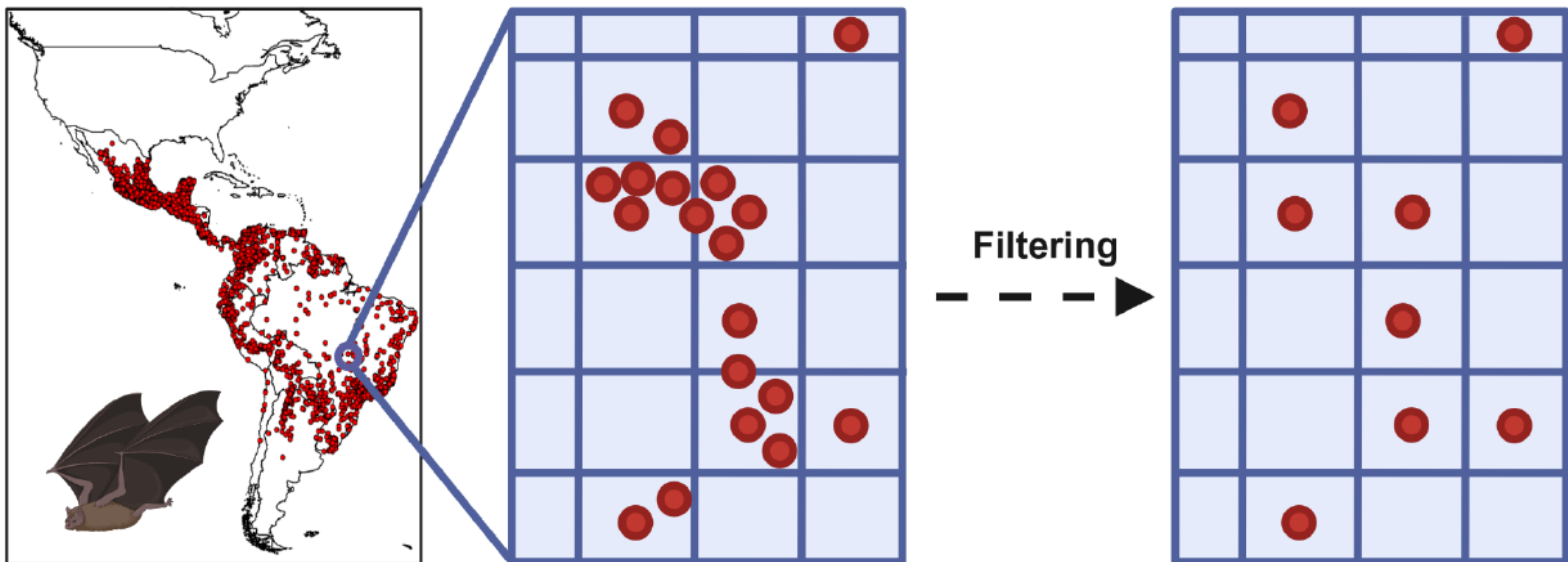


Occurrence location filtering

Occurrence data for *D. rotundus* was collected across Latin America from 1901 to 2023, with 74.6% of records geolocated.

To avoid bias and spatial autocorrelation, the data was filtered to one record per pixel at 5 km resolution.

Duplicate coordinates were removed to ensure accurate representation of climatic conditions for model calibration based on current climate data (1970-2000).

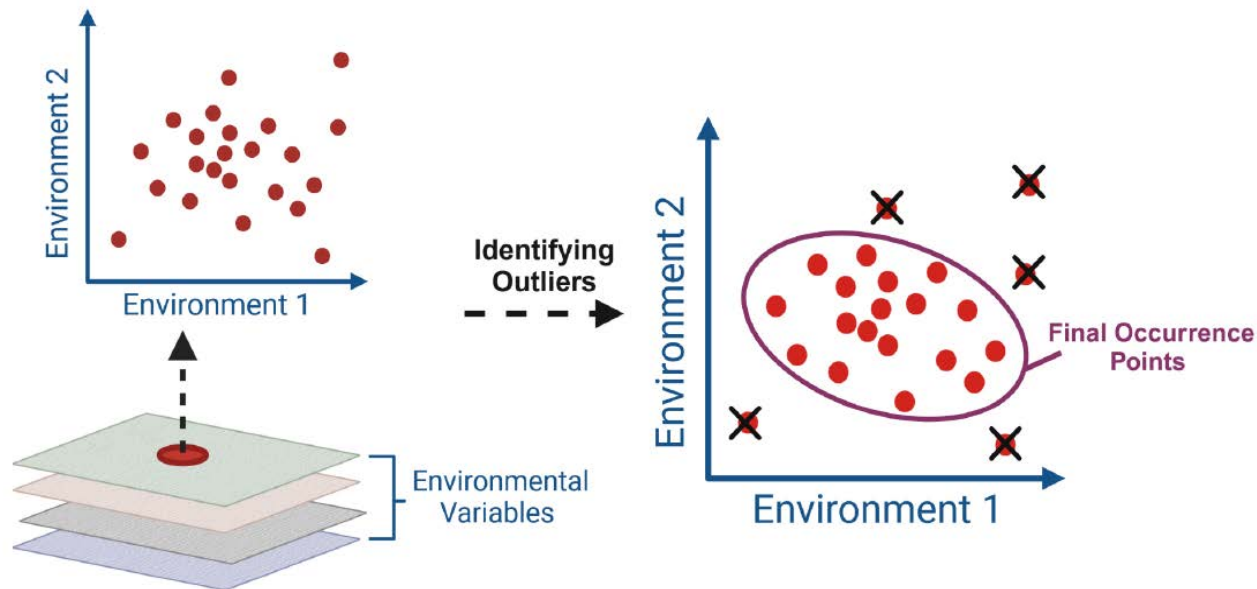


Occurrence location filtering

The occurrence locations of *D. rotundus* were matched with climate data from the WorldClim database at 5 km resolution.

Using current climate data (1970-2000), environmental variables were extracted, and a principal component analysis (PCA) was performed to summarize climate data variance.

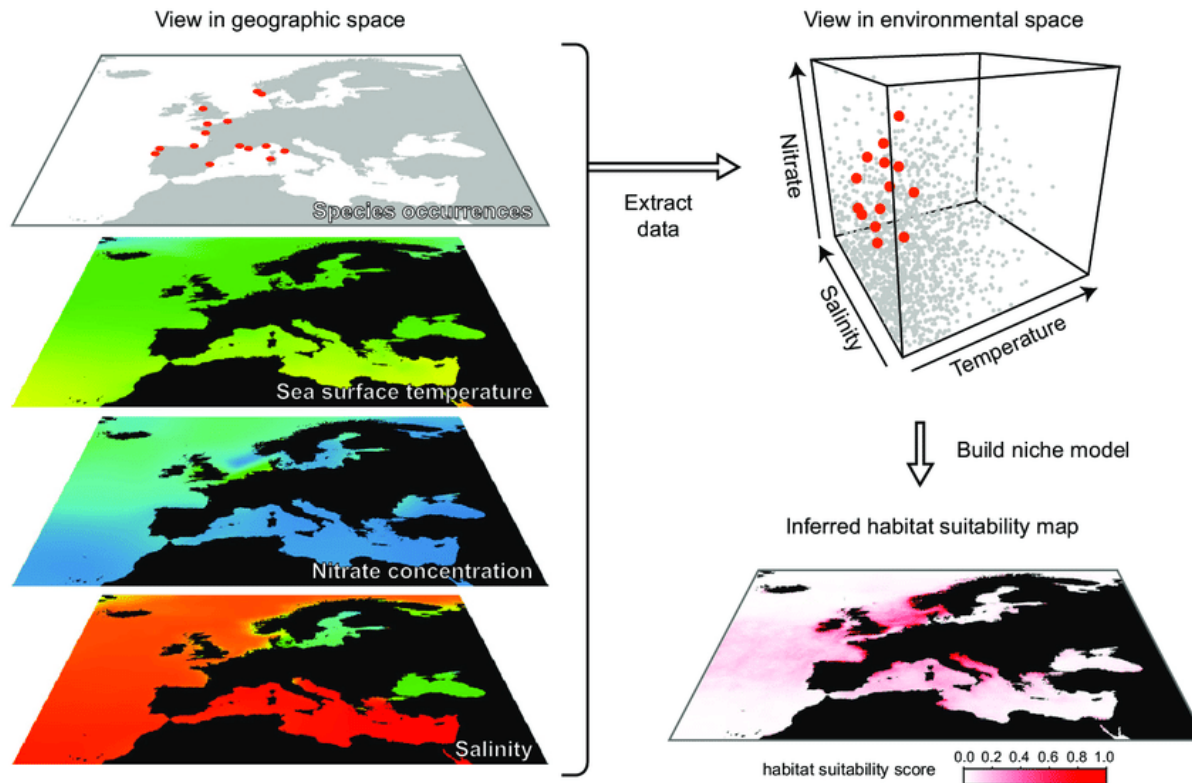
The first three principal components, representing 80.4% of the variance, were used to plot the species historical distribution in environmental space.



Ecological Niche Modeling

The main objective of ecological niche modeling is to predict how the distribution of *D. rotundus* will change under different climate change scenarios.

This is done by evaluating how the environmental conditions in areas where the species has already been observed may change in the future under various climate projections.

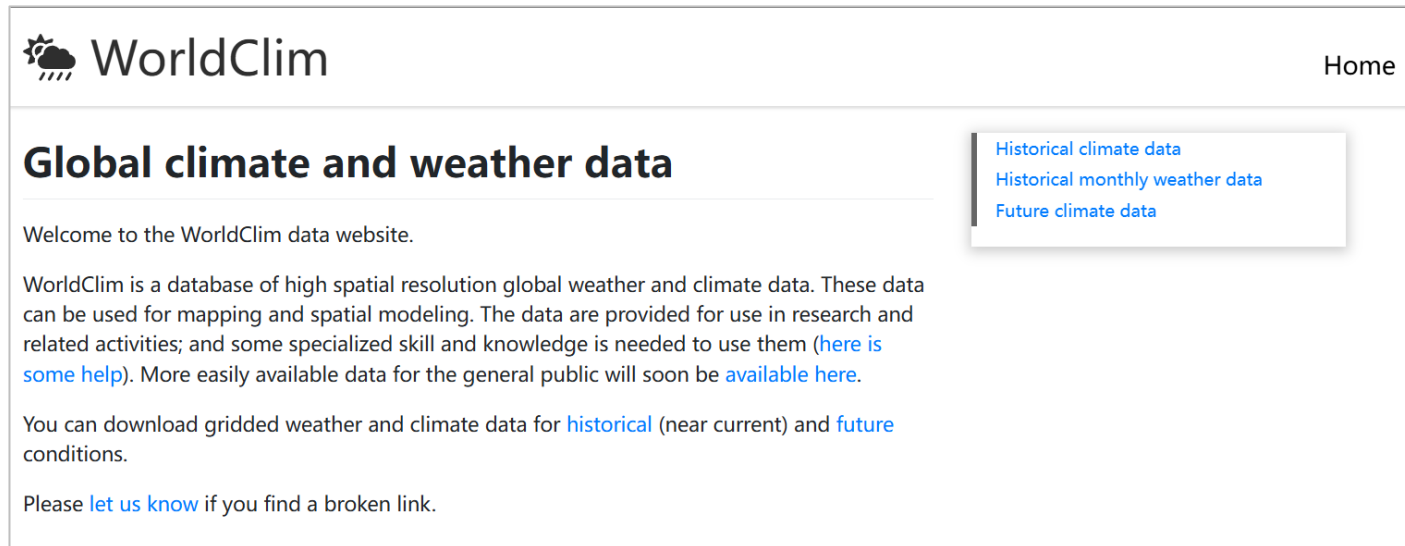


Selection of Climate Variables

19 climate metrics from the WorldClim dataset were used, including variables such as average temperature, precipitation and precipitation seasonality.

Some of these variables were highly correlated with each other, so a Pearson correlation analysis was performed to eliminate highly redundant variables ($\rho \geq 0.5$).

This reduced the climate variables to 7 that are considered important for the ecosystem of *D. rotundus*.



The screenshot shows the WorldClim website interface. At the top left is the WorldClim logo (a sun and cloud icon) and the text "WorldClim". At the top right is a "Home" link. Below the logo is the heading "Global climate and weather data". To the right of this heading is a dropdown menu with three options: "Historical climate data", "Historical monthly weather data", and "Future climate data". Below the heading is a welcome message: "Welcome to the WorldClim data website." followed by a paragraph: "WorldClim is a database of high spatial resolution global weather and climate data. These data can be used for mapping and spatial modeling. The data are provided for use in research and related activities; and some specialized skill and knowledge is needed to use them ([here is some help](#)). More easily available data for the general public will soon be [available here](#)." Below this is another paragraph: "You can download gridded weather and climate data for [historical](#) (near current) and [future](#) conditions." At the bottom is a note: "Please [let us know](#) if you find a broken link."

Click image to go to website

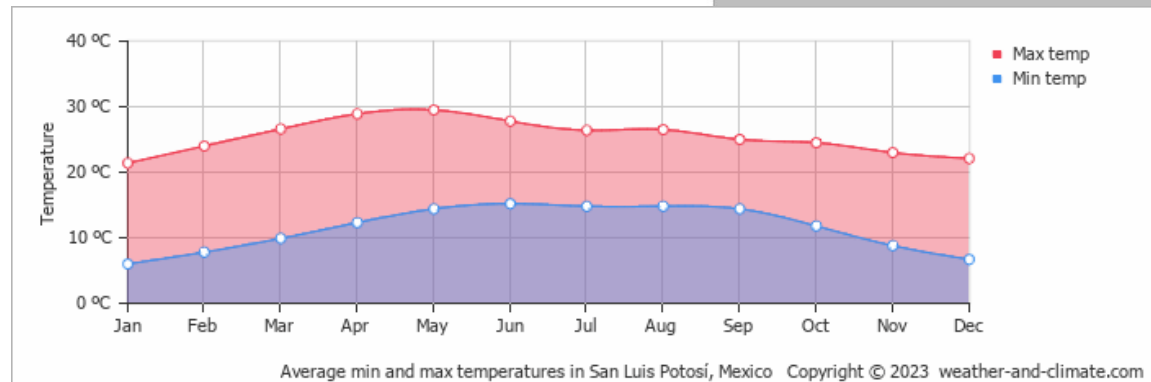
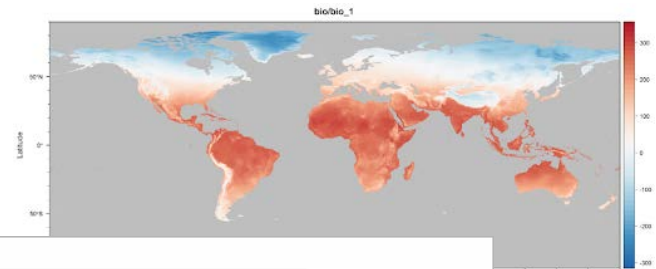
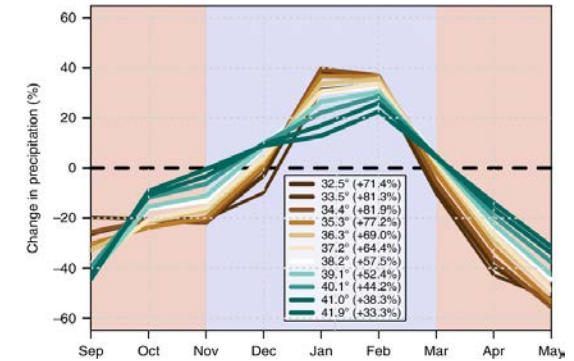
Filtering of Variables

Some variables were eliminated as they were not as relevant for modeling species' fundamental niche:

- The mean diurnal temperature range
- Maximum temperature of the warmest month
- Precipitation during the driest quarter

Ultimately, four climate variables were used:

- Precipitation seasonality.
- Annual precipitation.
- Minimum temperature of the coldest month.
- Isothermality.





Calibration Area Restriction

A restricted calibration area was defined to improve model accuracy and exclude areas where *D. rotundus* cannot live due to dispersal limitations.

This area was set with a 200 km buffer around occurrence locations, ten times the species' average range.

The model was calibrated using the *kuenm* package in R, which enables the creation of models with various parameterizations.

Additionally, parameters and feature classes were adjusted in MaxEnt software.

Ecological Niche Model Projection

The final ecological niche model was projected across the Americas and multiple future climate scenarios using six Global Circulation Models (GCMs).

The selected GCMs were chosen for their ability to capture climate variability and sensitivity to increased CO₂.

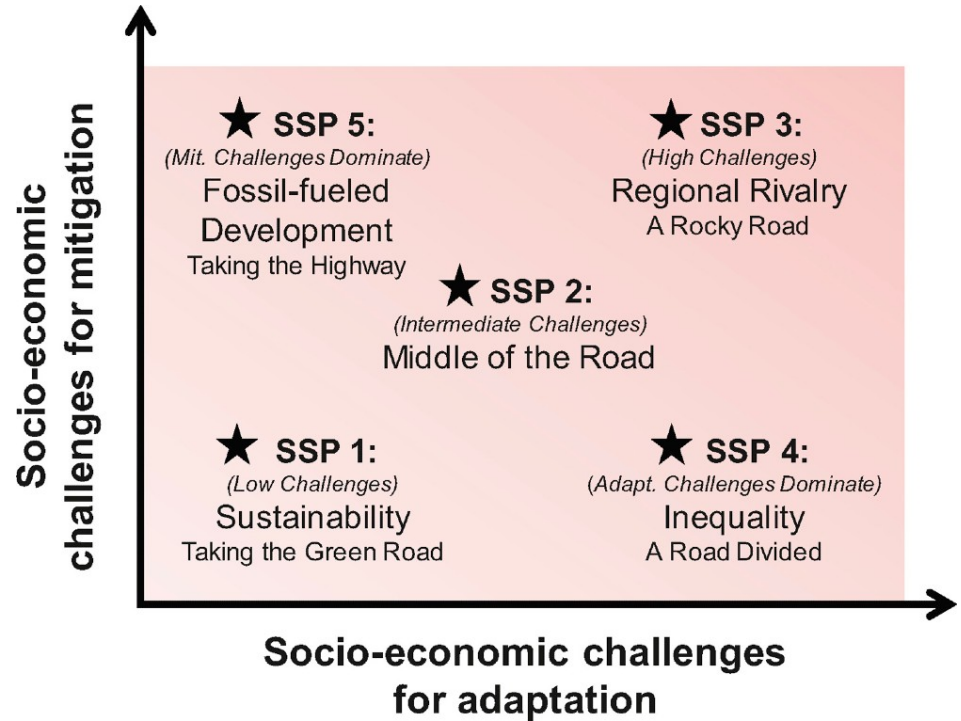
These models account for equilibrium climate sensitivity (ECS) and transient climate response (TCR) across different climate change scenarios.

Global Circulation Model Name	Abbreviation	ECS	TCR
Australian Community Climate and Earth System Simulator	ACC	4.7	2.1
Beijing Climate Center Climate System Model	BCC	3	1.7
Europe Wide Consortium Climate Model	EVeg	4.3	2.6
National Institute for Environmental Studies, University of Tokyo Model	MIROC	2.6	1.6
Max Planck Institute for Meteorology, Germany Model	MPI	3	1.8
United Kingdom Earth System Model	UK	5.3	2.8

Future Climate Scenarios and Model Projections

The model was projected across Shared Socio-economic Pathways (SSPs) to account for variations in climate change severity based on future greenhouse gas emissions and population growth.

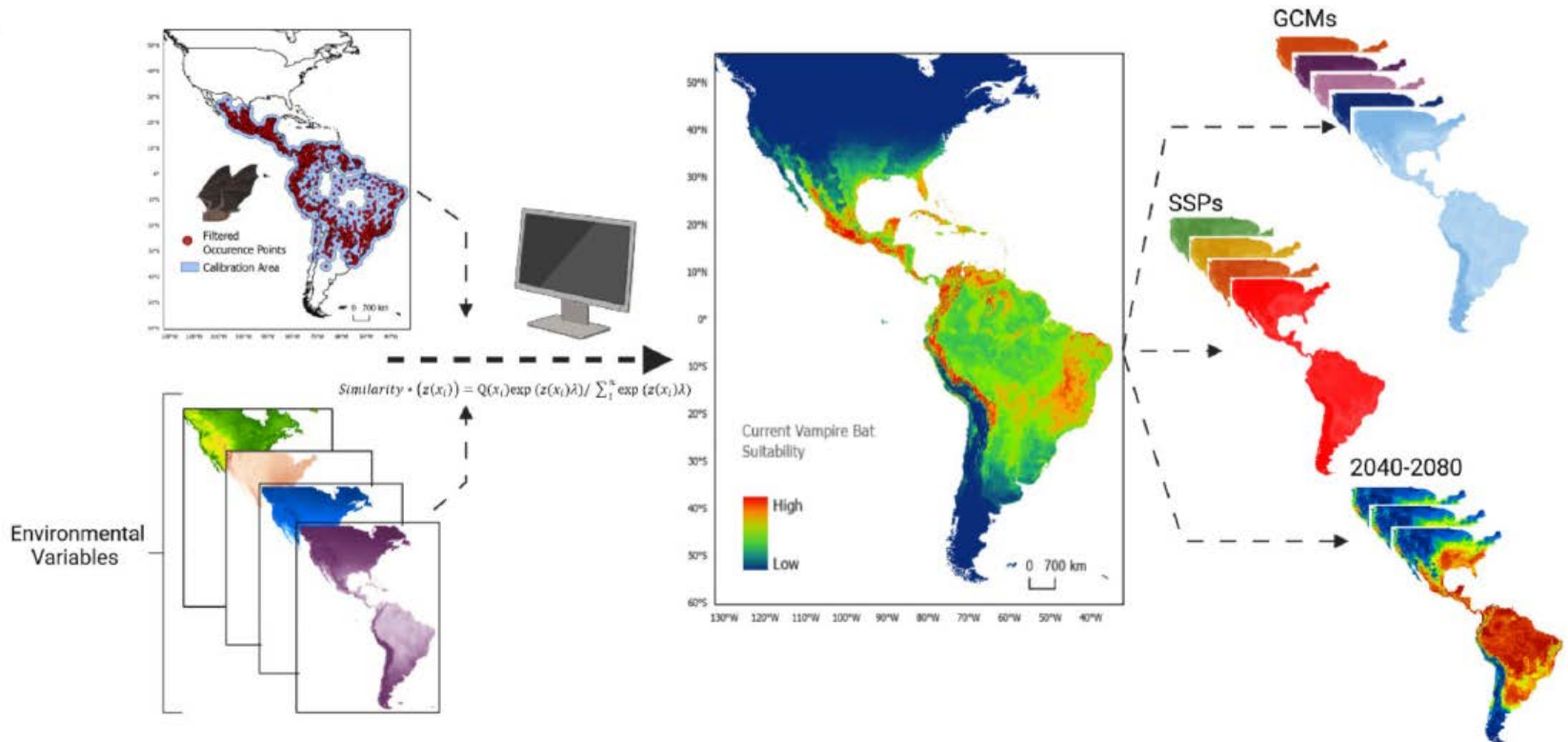
- SSP1 sustainable development.
- SSP2 middle-of-the-road pathway.
- SSP3 fragmentation.
- SSP5 high emissions future.



Future Climate Scenarios and Model Projections

Projections were made for three times periods: 2020-2040, 2041-2060, and 2061-2080.

The combination of GCMs, SSPs and time periods allow for a comprehensive assessment of the possible future distributions of *D. rotundus* in a variety of climates.





Projection without Extrapolation

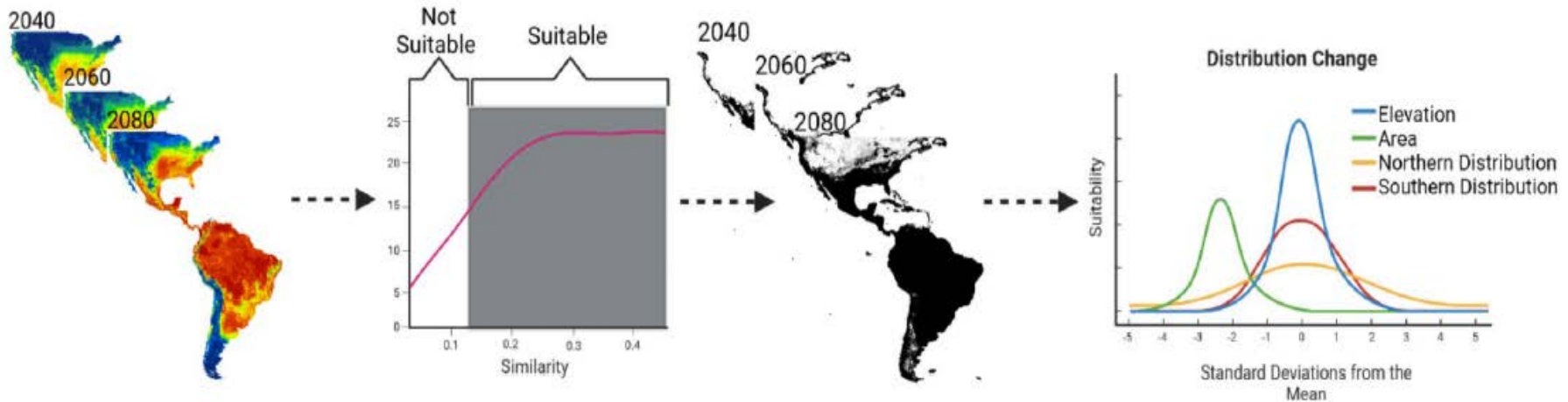
The MaxEnt model projected the species' future suitability without extrapolation to avoid incorrect assumptions about its physiological tolerances.

Extrapolation could suggest the species has broader tolerances than observed under the current climate, which contradicts the ecological niche conservatism hypothesis.

This hypothesis posits that species maintain their climatic tolerances over time, even during rapid changes.

Post-projection analysis

1. MOP Analysis (Mobility-Oriented Parity): To identify areas with extrapolation risk where climate condition differ from training data.
2. Model Ensemble: To assess how climate change affects *D. rotundus* distribution.
3. Binarization of Maps: To evaluate suitable and unsuitable areas for the species.
4. Latitudinal and Elevation Changes: To determine how distribution may change across time and SSPs.



Results

304 models were effective in prediction with low omission rates ($E=0.05$)

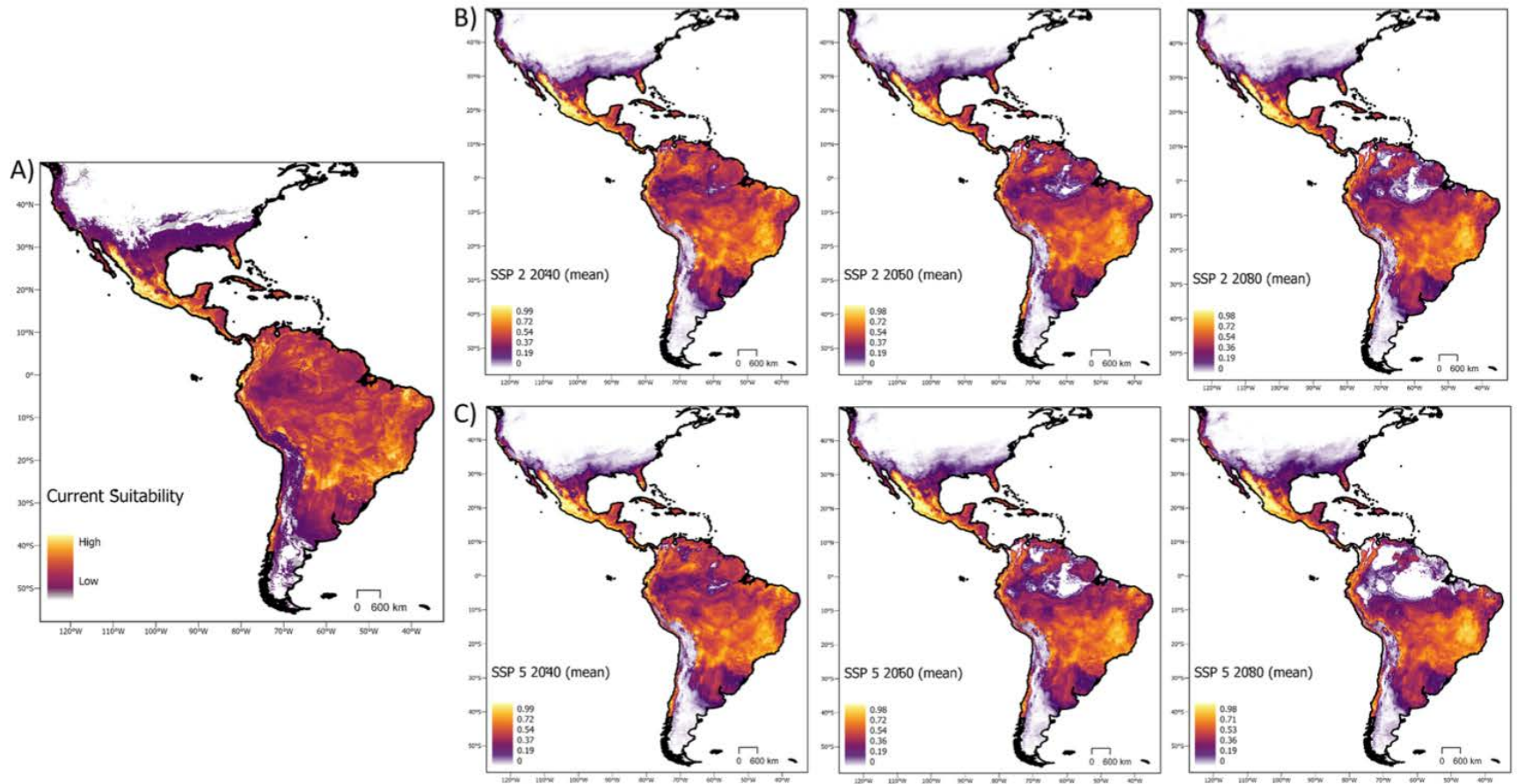
Minimum temperature of the coldest month (32.7%) and precipitation seasonality (32.6%) were the most relevant variables.

D. rotundus could expand its range into the southern United states and south-central portions of Argentina and Chile in the next 20-80 years.

Some CMs such as the MPI model and Eveg, showed greater variability in projected latitudes for *D. rotundus* suitability areas, especially to the north.

Areas with high livestock density and Amazon regions may face higher risks from species expansion and rabies transmission.

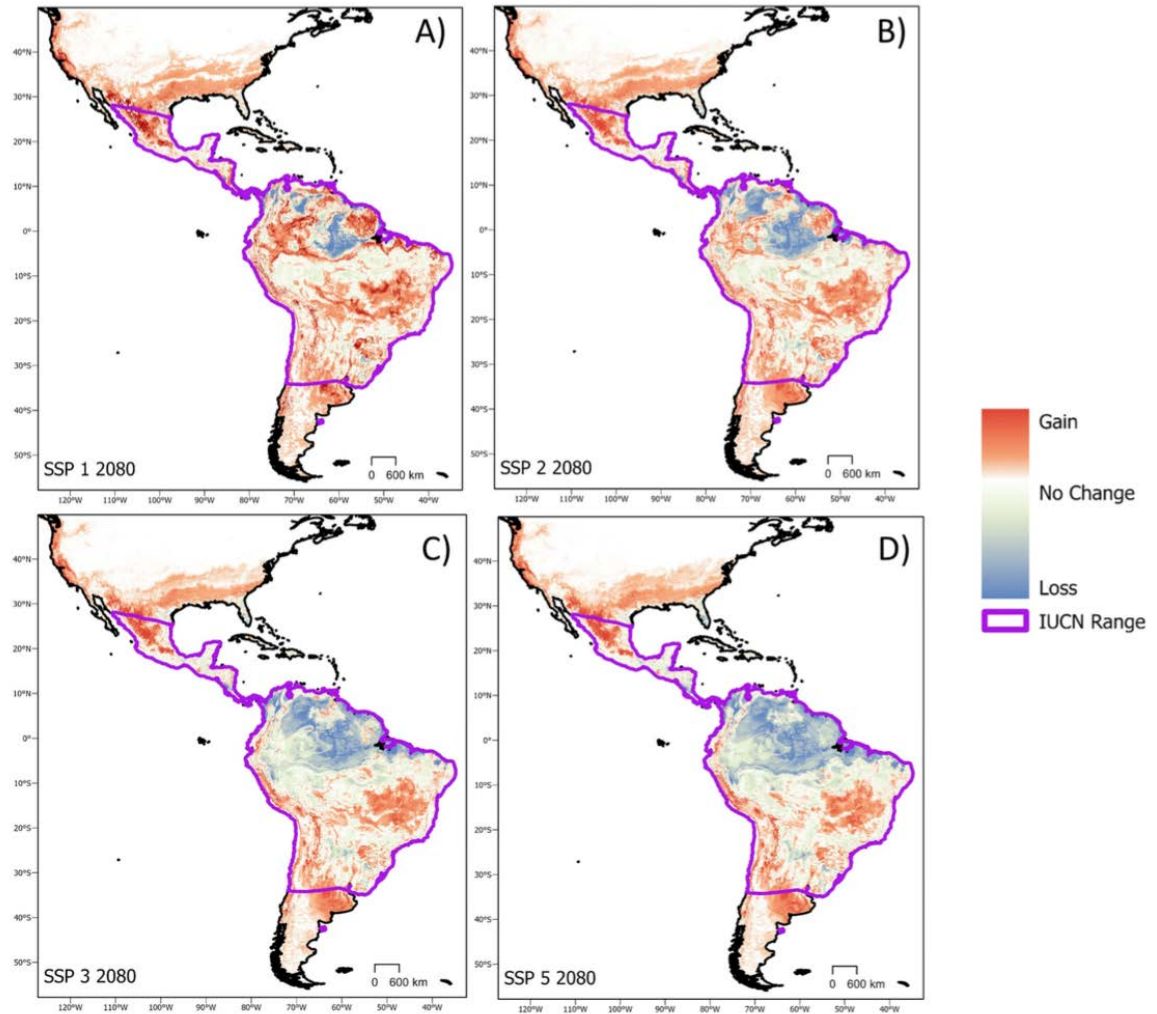
Suitable projections



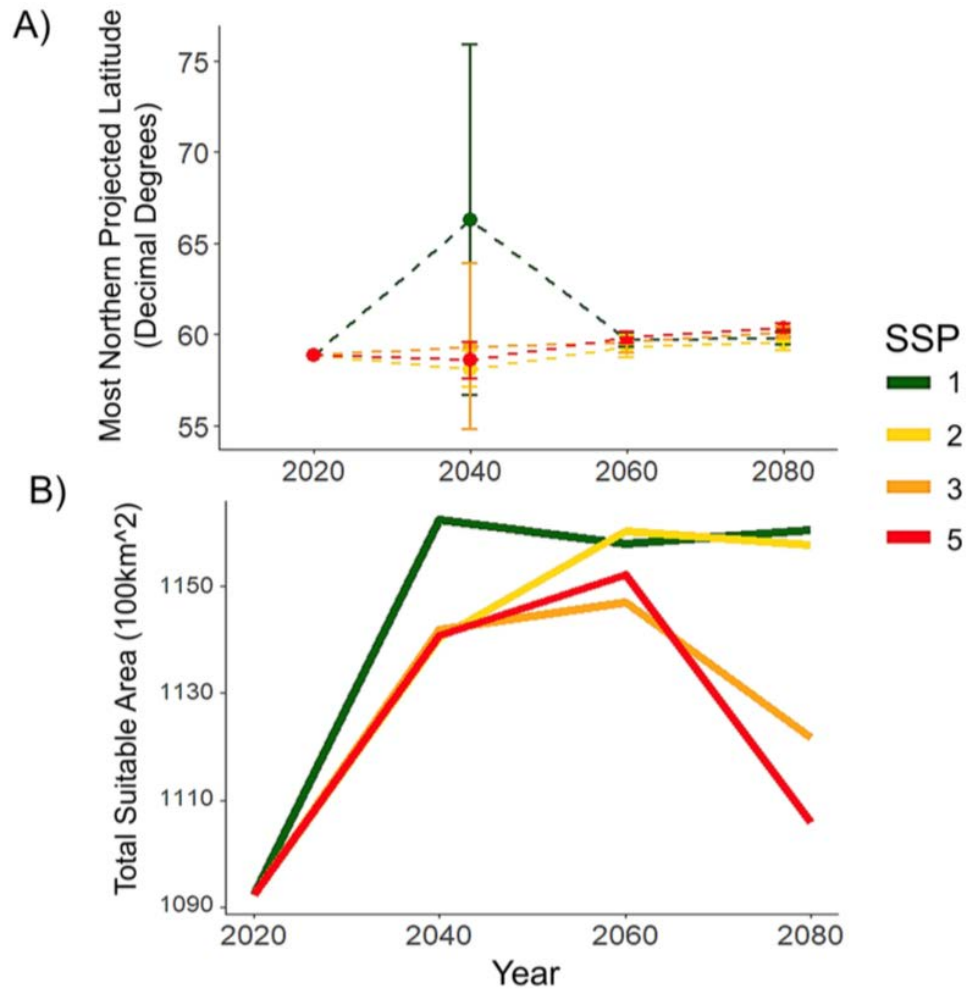
Habitat suitability projection for *D. rotundus* in SSP 2 and SSP 5 scenarios. Loss of suitable area in the Amazon is observed by 2060 and 2080, with expansion north and south in the worst-case scenario.

Change in future suitability

Future suitability change for *D. rotundus* shows a loss in the central Amazon and gains in western Mexico, Southern US, and central Argentina, with expansion north and south, under all climate scenarios.



Projected suitability changes for *D. rotundus*

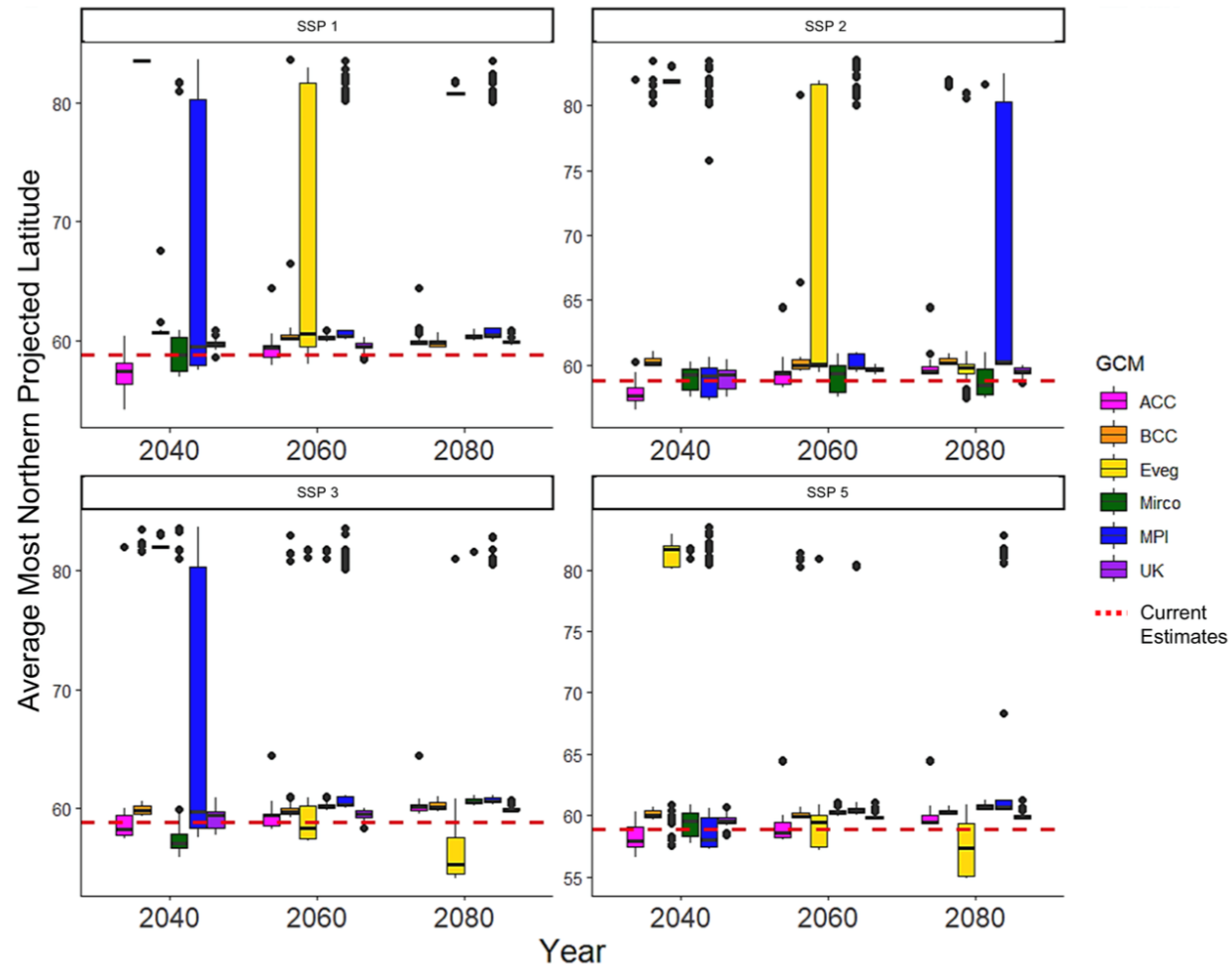


A: Significant increase in the most northern suitable latitude for all SSPs ($p = 0.001$).

B: Increase in total suitable area for *D. rotundus* across all projections ($p = 0.028$), with notable bell curve patterns in SSP3 and SSP5 (worst-case scenarios).

Global circulation model variability

Most future projections show northern suitable latitude for *D. rotundus* above current estimates, with higher variation in EVeg and MPI models due to low CO2 sensitivity and aerosol forcing differences.



Discussion

- The models showed that *D. rotundus* could expand its distribution northward and southward due to climate change.
- Keys areas in the Amazon rainforest could become unsuitable for the species due to changes in precipitation patterns.
- *D. rotundus*' distribution is influenced by the minimum temperature of the coldest month and precipitation seasonality, as the bat is sensitive to temperature and relies on tropical ecosystems.





Discussion

Climate change could alter the distribution of *D. rotundus* and facilitate the transmission of rabies to new species, including humans and livestock.

Areas like the southern U.S., Mexico, and parts of South America may face increased zoonotic disease risks due to expansion of rabies outbreaks.

The study used projections without extrapolation to avoid assuming rapid adaptation to unobserved climates.

This approach minimizes uncertainty by ensuring models do not predict ecologically unlikely areas.

It also highlighted that factors like land use and livestock density changes could significantly influence the results.

Conclusions

D. rotundus could expand its range in the next 20-80 years into new areas due to climate change, including the southern U.S. and parts of Argentina and Chile.

Some areas in higher latitudes may become suitable , while parts of the Amazon Rainforest may become unsuitable.

Dispersal success depends on resource availability, including pre density.

Recommendation: Implement preventive measures and educational programs in areas vulnerable to *D. rotundus* expansion, to reduce risks of human-wildlife conflict and rabies transmission.



Red de
Vigilancia de
Patógenos
Virales
Emergentes



Christian A. García-Sepúlveda — Laboratorio de Genómica Viral & Humana, Medicina UASLP

Sandra E. Guerra-Palomares — Laboratorio de Genómica Viral & Humana, Medicina UASLP

Dulce Ma. Hernández Piña — Laboratorio de Genómica Viral & Humana, Medicina UASLP

J. Manuel Mendoza Méndez — Laboratorio de Genómica Viral & Humana, Medicina UASLP

Andreu Comas García — Departamento de Microbiología, Medicina UASLP

Mauricio Comas García — Unidad de Microscopía de Alta Resolución, CICSAB Ciencias UASLP

Guillermo Espinosa Reyes — Centro de Investigación Aplicada en Ambiente y Salud (CIAAS), Medicina UASLP

Fernando Díaz-Barriga Martínez — Centro de Investigación Aplicada en Ambiente y Salud (CIAAS), Medicina UASLP

Juan Carlos Cuevas Tello — Algoritmos de Inteligencia Artificial Aplicados, Ingeniería UASLP

Ignacio Amezcua Osorio — Comité Estatal para el Fomento y Protección Pecuaria de San Luis Potosí.



www.genomica.uaslp.mx



GenomicaUASLP



GenomicaUASLP

Laboratorio de Genómica Viral & Humana BSL-3, Facultad de Medicina UASLP

- Dr. Christian A. García-Sepúlveda (Operaciones BSL-3, Virología Molecular)
- Dra. Sandra E. Guerra-Palomares (Virología molecular)
- Dr. Andreu Comas García (Epidemiología molecular)
- Dra. Sofia Bernal Silva (Virología molecular)
- Dr. Fernando Díaz-Barriga Martínez (Una salud integral)
- Dr. Mauricio Comas García (Microscopía electrónica y virología estructural)
- Dr. Roberto González Amaro (Inmunología)
- Dr. Juan Carlos Cuevas Tello (Aplicaciones de algoritmos de inteligencia artificial)

Laboratorio Nacional de Vacunología y Virus Tropicales, Escuela Nacional de Ciencias Biológicas IPN

- Dra. Ma. Isabel Salazar Sánchez (Virología molecular e inmunología)
- Dr. Jesús Miguel Torres Flores (Operaciones BSL-3)
- Dr. Joel Armando Vázquez Pérez (Virólogo especializado en Influenzavirus)
- Dr. Rosa Elena Sarmiento Silva (Viróloga especializada en virus respiratorios)

Departamento de Inmunología del Instituto de Investigaciones Biomédicas UNAM

- Dra. Clara Inés Espitia Pinzón (Operaciones BSL-3)
- Dr. Antonio García Knight (Inmunólogo viral con énfasis en virus emergentes)
- Dr. Renato León Rodríguez (Virología molecular)
- Dr. Wenceslao Coronado Aceves (Evaluación de fármacos in vitro e in vivo)
- Dra. Georgina Diaz Herrera (Médica Veterinaria pequeñas especies)
- Maestra Erika Segura Salinas (Evaluación de fármacos potenciales)