

## Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

### Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
  - Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted
  - Give  $P$  values as exact values whenever suitable.*
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's  $d$ , Pearson's  $r$ ), indicating how they were calculated

*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

Policy information about [availability of computer code](#)

Data collection	We did not use software to collect data.
Data analysis	We conducted all evolutionary analyses using R environment for statistical computing, version 3.6.0. We specify functions and packages necessary to replicate our results.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

### Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The complete dataset compiled for this study is included in the supplementary information.

# Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

## Study description

This study focuses on the evolution of live birth in phrynosomatid lizards. We assembled a multi-species dataset for this lineage on reproductive parity mode, thermal physiology, mass-specific metabolic rate, morphology, life history traits, and mass-specific production. We combined our dataset with an ultrametric tree for perform phylogenetic comparative methods to test evolutionary patterns associated with live birth.

## Research sample

Our dataset encompasses information for 125 phrynosomatid species. This dataset was gathered by newly collected and previously published data, and includes adult body mass, adult body size, field-body temperatures, preferred body temperatures, effectiveness in behavioral thermoregulation, critical thermal limits, mass-specific metabolic rate, offspring mass, offspring size, clutch/litter size, and annual mass-specific production.

## Sampling strategy

All phrynosomatid species for which we were able to obtain newly collected or previously published data of parity mode, thermal physiology, mass-specific metabolic rate, morphology, life history traits, and/or mass-specific production were included in this study.

## Data collection

We recorded all data (newly collected or previously published) in an Excel spreadsheet, which we supply in the supplement.

## Timing and spatial scale

We assembled our dataset between January 2020 and March 2020

## Data exclusions

No data were excluded for the analyses.

## Reproducibility

All evolutionary analyses were performed in triplicate, with qualitatively similar results.

## Randomization

For estimation of body temperature, preferred body temperature, critical thermal limits, adult body mass, adult body size, offspring mass, offspring size, a randomization procedure is not relevant.

## Blinding

Blinding was not relevant for obtain newly collected data, previously collected data, or for phylogenetic comparative methods.

Did the study involve field work?  Yes  No

## Field work, collection and transport

### Field conditions

To obtain body temperature measurements, our field work was limited to sunny days, and the lizards' known activity periods.

### Location

Data come from lizard populations in Mexico, and from 0 to 4151 m elev.

### Access & import/export

Permits supplied by the Dirección General de Vida Silvestre, México allowed us to conduct the field work presented in the study.

### Disturbance

Our experiments were non-invasive and not harmful for lizards, which were subsequently released to their site of capture.

## Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

### Materials & experimental systems

n/a	Involved in the study
<input checked="" type="checkbox"/>	Antibodies
<input checked="" type="checkbox"/>	Eukaryotic cell lines
<input checked="" type="checkbox"/>	Palaeontology and archaeology
<input type="checkbox"/>	Animals and other organisms
<input checked="" type="checkbox"/>	Human research participants
<input checked="" type="checkbox"/>	Clinical data
<input checked="" type="checkbox"/>	Dual use research of concern

### Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	ChIP-seq
<input checked="" type="checkbox"/>	Flow cytometry
<input checked="" type="checkbox"/>	MRI-based neuroimaging

## Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals

The study did not involve laboratory animals.

Wild animals

In this study we obtained newly collected data for 63 species (sample sizes were provided in Supplementary Data 2). We included only adults in our study. For laboratory experiments, animals were transported into individual bags to field laboratories. After each study in each population, animals were hydrated ad libitum and released to their habitat.

Field-collected samples

To obtain preferred body temperatures we maintained individuals in a thermal gradient during their activity time for one day. To obtain critical thermal limits, we maintained individuals at low and high temperatures for only for few minutes. Animals were kept in captivity no more than three days before being released back to the wild.

Ethics oversight

Experiments were non-invasive, and were covered by our permits.

Note that full information on the approval of the study protocol must also be provided in the manuscript.