

Reporting Summary

Nature Portfolio 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 Portfolio 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ | 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ | 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 No software was used for data collection.

Data analysis All the analyses were done in R and the packages that we used were: funrar, picante, MuMin and ggplot2. All the codes and complemetray packages are provided in the supplementary information.

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Provide your data availability statement here.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender NA

Reporting on race, ethnicity, or other socially relevant groupings NA

Population characteristics NA

Recruitment NA

Ethics oversight NA

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

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

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

Study description

We compiled a dataset comprising intrinsic and extrinsic variables of all chelonians to reveal their current risk patterns and abilities to track future changes. First, We use an updated threat status based on information from the Tortoise and Freshwater Turtle Specialist Group (TFTSG), the IUCN Red List, and regional assessments as indicators of species extinction risk. Second, based on the extinction risk assessment of the updated Red List, we conducted a binomial distribution test to examine which families of turtles and tortoises have a higher or lower proportion of threatened species than expected by chance alone. Third, we conducted Phylogenetic Generalized Least Squares test to find the best correlates of extinction risk. Fourth, we calculated the rates at which traits were evolving and compared them to the rates of change of these threats to predict whether turtles and tortoises can track climate change, extreme droughts, heatwaves, human expansion, and forest degradation in the next century. We combined the results from the binomial distribution test and the model-average analyses to predict the extinction risk probability of DD and NE species in the updated Red List.

Research sample

We retained 378 turtles and tortoises with a species-level identity.

Sampling strategy

We compiled the species list of chelonians based on the latest taxonomy checklists from the TFTSG 2018 (360 species), the Turtle Taxonomy Working Group 2021 (TTWG, 357 sp.), the Reptile Database 2024 (371 sp.), the IUCN Red List 2024-02 (272 sp.), and by consulting with experts in this field. For the *Chelonoidis nigra* species, we followed the TSTSG into categorizing each taxon as a species. There are seven newly described and provisionally accepted species listed in the Reptile Database that are not included in our study (e.g., *Chelodina ipudinapi*, *Elseya auramemoria*), because they have not yet been approved by the TTWG.

Data collection

Data was collected by Chuanwu Chen and Jiang Wang.

- We recorded range size from a recent study and supplemented it with information from the IUCN Red List and the TTWG 2021. Body size was collected from the TTWG 20 and supplemented with the published species traits of chelonians, as well as related publications. The information on activity time, diet, insular endemism, maximum lifespan and mean clutch size were derived from the two global datasets of the species traits, the book written by Lovich and Gibbons, the Reptile Database, the IUCN Red List, and related papers. We imputed missing values using the impute function in R package funspace.
- We constructed a phylogenetic tree for chelonians based on Colston et al.. This tree recognizes 357 species of extant or recently extinct chelonians and contains all 335 data-sufficient species in the updated Red List. For species that were previously classified as subspecies or subpopulations, We positioned them alongside their sister species. For some newly discovered species, we used the `add.species.to.genus` function (phytools) to incorporate the missing species midway along the branches of their respective genera.
- We grouped chelonians into aquatic (freshwater and marine) and terrestrial species based on the classification of the IUCN Red List, the published species traits dataset, books, and related papers, detailed in Table S1.
- We gathered threat information for each species from several sources (Table S1): the IUCN threat classification scheme; the Biology of Freshwater Turtles and Tortoises compiled by the IUCN/SSC TSTSG; the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES); the reports by the Turtle Conservation Coalition; and books. We reclassified threat types into five basic and recognized categories, including human exploitation (pet trade, human consumption, medicine), habitat destruction, pollution, invasive species, and climate change.
- We collected four climatic variables (mean annual temperature, mean annual precipitation, temperature seasonality, and precipitation seasonality) by mapping these bioclimatic data (WorldClim 1) across species distribution ranges. In addition, we measured the Standardized Precipitation Evapotranspiration Index (SPEI) to represent extreme droughts. Furthermore, we selected the Warm Spell Duration Index (WSDI) to represent heatwaves.

-For biogeographic distributions, We made our results comparable to global biogeographical studies on chelonians , by including Afrotropics, Australasia, Indomalaya, Nearctic, Neotropics, Palearctic and Marine. We classified species into those realms by intersecting their ranges with the shapefile of the World Wildlife Fund for Nature (WWF) biogeographical realms. We calculated the proportion of species distribution range belonging to each biogeographical realm using ArcGIS 10.7. A species was assigned to a realm when at least 80% of its range overlapped with that realm.

Timing and spatial scale

Data was collected from 2022-05-01 to 2024-11-20

Data exclusions

No data were excluded from the analyses.

Reproducibility

All the analyses can be reproducible with the provided data and code in supplementary material.

Randomization

We used the randomization to evaluate which families of turtles and tortoises have a higher or lower proportion of threatened species than expected by chance alone.

Blinding

Blinding was not relevant because we use all the species with available information.

Did the study involve field work? ☐ Yes ☒ No

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
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.