

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 [Authors & Referees](#) 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

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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 to collect data. All datasets are downloaded from the original sources.

Data analysis

The analyses and mapping were both performed using MATLAB (R2016a). The boosted regression trees (BRT) models were fitted in R with extending 'gbm' library. Codes for data analysis have been uploaded on GitHub (<https://github.com/LilyXiangyi/ForestResponse>)

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/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

All data from public sources used in this study can be obtained from https://figshare.com/articles/Trade-off_between_gymnosperm_resistance_and_resilience_increases_forest_sensitivity_to_extreme_drought/12047241

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](https://www.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 assessed the spatial and temporal trade-off of resistance and resilience for gymnosperms and angiosperms to extreme drought using a global tree ring records from 2935 sites over the past century.
Research sample	The data we use are all obtained from publically available sources.
Sampling strategy	N/A
Data collection	Existing datasets are downloaded from the sources. All datasets include: raw data of tree-ring widths from https://www1.ncdc.noaa.gov/pub/data/paleo/treering/ ; the Climatic Research Unit (CRU), version TS 4.01 from https://crudata.uea.ac.uk/cru/data/hrg/ ; the gridded SPEI data (SPEIbase v2.5) from http://digital.csic.es/handle/10261/153475 ; the RegridDED Harmonized World Soil Database v1.2 from https://daac.ornl.gov/SOILS/guides/HWSD.html ; canopy height from https://webmap.ornl.gov/ogc/dataset.jsp?dg_id=10023_1 ; maximum rooting depth from https://wci.earth2observe.eu/thredds/catalog/usc/root-depth/catalog.html ; wood density from https://datadryad.org/handle/10255/dryad.235 ; SLA, Nm, and Pm from https://github.com/abhirupdatta/global_maps_of_plant_traits ; HSM and P50 from https://www.nature.com/articles/nature11688 ; isohydricity data from https://github.com/agkonings/isohydricity ; tree density from https://elischolar.library.yale.edu/yale_fes_data/1/ ; above ground biomass of tropical forest plots from http://www.forestplots.net/data-packages/brienen-et-al-2015 .
Timing and spatial scale	We used global tree ring sites and climate data from 1901-2015.
Data exclusions	We excluded chronologies of tree-ring widths not following criteria: availability of metadata (longitude, latitude, elevation, and species code), tree-ring series covering at least 25 years during 1901-2015, and types of tree-ring measurements providing total ring widths.
Reproducibility	N/A
Randomization	N/A
Blinding	N/A
Did the study involve field work?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> 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 | Involvement in the study |
|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |

Methods

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