

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 |
| <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 type="checkbox"/> | <input checked="" 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 checked="" type="checkbox"/> | <input 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 checked="" type="checkbox"/> | <input 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 checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input 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

Data analysis

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](#)

The main Figures and main Tables are available in the article. The Supplementary Figure and Supplementary Table are available in the Supplementary Information of the article. The data generated and analyzed during the current study are provided as Supplementary Data and are available in the Dryad digital repository at <https://doi.org/10.5061/dryad.3ffbg79nx>.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	<input type="text" value="This information has not been collected."/>
Population characteristics	<input type="text" value="See above."/>
Recruitment	<input type="text" value="See above."/>
Ethics oversight	<input type="text" value="See above."/>

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	<input type="text" value="This study uses a phylogenetic comparative approach based on Hidden Markov Models of varying evolutionary complexity to test for correlation evolution between two plant characters and to estimate the rates of evolutionary transitions among the character states. One character has three levels and the other two levels. The experimental unit is the plant species and a total of 1,638 species were considered. The number of plant species per character state combination varied from 20 to 408 depending on state and dataset version. A total of six partially different dataset versions were analyzed."/>
Research sample	<input type="text" value="The research sample is a group of globally distributed plant species (angiosperms and gymnosperms) that reflect a large sample for which there is available combined data on mycorrhizal strategy, drought adaptation, and phylogeny. Data was collected from existing datasets provided by the Global Biodiversity Information Facility (https://doi.org/10.15468/dl.5mab9f), TRY – Plant Trait Database (Kattge et al. 2020. Glob Change Biol 26, 119-188), FungalRoot (Soudzilovskaia et al. 2020. New Phytol 227, 955-966), Bueno et al (2018) Mycorrhiza 29, 1-11, and Smith and Brown (2018) Am J Bot 105, 302-314."/>
Sampling strategy	<input type="text" value="Data were obtained from curated datasets in order to generate a large global sample of plant species with combined data on mycorrhizal strategy, drought adaptation, and phylogeny. Six partially different datasets were generated to account for data uncertainty. For each dataset version, the phylogenetic imbalance ratio (Gardner and Organ 2022 Syst Biol 70, 1061-1075) was calculated to determine the adequacy of the sample to test for correlated evolution. Finally, the 95% confidence intervals for each estimated rate parameter were determined."/>
Data collection	<input type="text" value="All data in existing datasets were downloaded by the author from an online database and from literature supporting information. These data were processed by the author using Excel and R software."/>
Timing and spatial scale	<input type="text" value="The data used in this study is based on multiple records collected over a century and reflect functional traits of extant plant species."/>
Data exclusions	<input type="text" value="No data were excluded from the study."/>
Reproducibility	<input type="text" value="18 different Hidden Markov Models were tested in this study. Each model was independently run on six partially different dataset versions, each one performed with five repeated starts, resulting in a total of 810 independent optimization exercises. The 95% confidence intervals for each rate parameter estimate were determined with a dentist approach using 5,000 points sampled around a specified distance from the maximum likelihood estimates."/>
Randomization	<input type="text" value="Allocation to groups was based on species traits and therefore non-randomly dependent on phylogenetic relationships. To account for this, the study employed Hidden Markov Models that consider hidden rate categories accounting for unobserved phylogenetic factors influencing state reconstruction and rate estimates."/>
Blinding	<input type="text" value="Data was assigned to each species using a complete blind approach, based solely on automated species name matches. Selection of estimated parameters was based on the goodness of fit (sample size-corrected Akaike information criterion), first among the five repeated starts of each model run, and second among the 18 different models of evolution."/>

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	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 and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

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