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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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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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 coeff AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)	icient)	
For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.	Ł	
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		
\boxtimes Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated		
Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.		
Software and code		
Policy information about <u>availability of computer code</u>		
Data collection Data was collected and subset using the commercial software Excel of Microsoft Office 2019 and the open source software R version 4.3	1.1.	

Data

Data analysis

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

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.

- 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 $\underline{\text{policy}}$

Data was analyzed using the open source software R version 3.6.2.

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	participant:
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Reporting on sex and ge	nder This information has not been collected.	
Population characteristic	See above.	
Recruitment	See above.	
Ethics oversight	See above.	
Note that full information on	the approval of the study protocol must also be provided in the manuscript.	
Field-specifi	c reporting	
Please select the one below	w 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	
or a reference copy of the docun	nent with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>	
Ecological, e	evolutionary & environmental sciences study design	
All studies must disclose o	n these points even when the disclosure is negative.	
Study description	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	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 existin 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	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	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	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	No data were excluded from the study.	
	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.	
Reproducibility	confidence intervals for each rate parameter estimate were determined with a dentist approach using 5,000 points sampled around	
Reproducibility Randomization	confidence intervals for each rate parameter estimate were determined with a dentist approach using 5,000 points sampled around	

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		Methods	
n/a	Involved in the study	n/a	Involved in the study
\boxtimes	Antibodies	\boxtimes	ChIP-seq
\boxtimes	Eukaryotic cell lines	\boxtimes	Flow cytometry
\boxtimes	Palaeontology and archaeology	\boxtimes	MRI-based neuroimaging
\boxtimes	Animals and other organisms		
\boxtimes	Clinical data		
\boxtimes	Dual use research of concern		
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