nature portfolio

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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 st	atistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a	Cor	nfirmed
		The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	\boxtimes	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	\boxtimes	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
	\boxtimes	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	\boxtimes	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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
	\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\times		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 commercial and custom code was used for data collection.

Data analysis

We used publicly available and appropriately cited software as described. Trinity v2.8.5, CD-HIT (v4.6), BUSCO (v5.2.2), MAFFT (v7.490), Mafft (v7.453) RAXML-NG (v1.0.1), IQ-Tree (v1.6.12), MEGA 11, BAMM (v2.5.0), BAMM tools (v2.1.7), TESS (v2.1), APE (v5.5), ENMeval (v0.3.1), MaxEnt (v3.4.4), RASP (v4.2), Hifiasm (v0.16.1), Soapdenovo2, BWA (v0.7.8), Merqury (v1.1), CEGMA (v2.5), , RepeatModeler (v1.0.5), RepeatScout (v1.0.5), Tandem Repeats Finder (v4.09), LTR FINDER (v4.09), RepeatMasker (v4.05), GlimmerHMM (v3.0.2), SNAP (v2.013.11.29), Geneid (v1.4), TBLASTN (v2.2.26), TopHat2 (v2.0.13), tRNAscan-SE (v1.4), INFERNAL (v1.1.2), ggplot2 (v2.2.1), VCFtools (v0.1.12b), LTRharvest (v1.07), LTRdigest (v1.5.8), SILIX (v1.2.11), Seurat (v.4.3.0), Monocle3 tools, Velocyto (v0.17.16), BLASTP (v2.2.28), Trimmomatic (v0.25), FLASH (v1.2.11), UPARSE (v7.1), UCHIME (v2.4.2), QIIME (v1.4.0), MetaGene (v3.12), jellyfish2.2.7, JuiceBox v1.11.08, , Genescan v1.0, InterProScan70 v5.39, , , BSTMatrix v2.0, BSTMatrix-ONT v1.1, BSTViewer V1.42, Bowtie2 v2.2.4, MetaGeneMark v2.10, eggNOG v4, HTSeq v0.6.1, DESeq2 v1.12.3, QIIME v1.9.1, PBBtools (https://github.com/bpucker/PBBtools/), Phylogenetic tree construction (https://github.com/bpucker/Tillandsioideae), trimAl v1.4.rev15 (https://vicfero.github.io/trimal/), ASTER (https://github.com/chaoszhang/ ASTER), Hifiasm (https://github.com/chhylp123/hifiasm), ALLHIC v 0.9.8 (https://github.com/tangerzhang/ALLHiC), Samtools v 0.1.19 (https://github.com/tangergithub.com/samtools/samtools), RepeatProteinMask v4.07 (https://github.com/rmhublev/RepeatMasker/blob/master/RepeatProteinMask) Augustus v3.2.3 (https://github.com/Gaius-Augustus/Augustus), Geneid v1.4 (https://genome.crg.cat/software/geneid/index.html), HISAT $v2.2.1\ (https://daehwankimlab.github.io/hisat2/download/), Stringtie\ v2.2.1\ (https://github.com/gpertea/stringtie), EvidenceModeler\ v1.1.1\ (https://github$ (https://github.com/EVidenceModeler/EVidenceModeler/releases), LASTZ (https://lastz.github.io/lastz/), OrthoFinder v2.3.7 (https:// github.com/davidemms/OrthoFinder), MUSCLE v3.8.31 (https://github.com/cran/muscle), TRIMAL v1.2 (https://vicfero.github.io/trimal/), RAxML v8.2.1 (https://github.com/stamatak/standard-RAxML), CAFE v2.1 (https://github.com/hahnlab/CAFE/blob/master/README.md), MCScanX v1.1.11 (https://github.com/wyp1125/MCScanx), PAML 4.9i (https://github.com/abacus-gene/paml), TransDecoder v5.7.1 (https:// transdecoder.github.io/), Diamond v2.0.15 (https://github.com/bbuchfink/diamond/releases/tag/v2.0.15), Nucleotide diversity (π) caculation (https://github.com/simonhmartin/genomics_general/blob/master/popgenWindows.py), SAW software (https://github.com/BGIResearch/ SAW), Stereopy tools (https://github.com/BGIResearch/stereopy), MEGAHIT v1.0.4 (https://github.com/voutcn/megahit).

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

Data exclusions

Randomization

Replication

Blinding

No data were excluded from the analysis.

No analysis required being blind to groups.

We conformed the ability to replicate all code of this study.

Randomization dose not directly apply to the genome sequencing and assembly.

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

All data generated in this study are presented within the article and its supplementary information files. The source data are also provided alongside this paper. The genome sequencing and assembly data for T. duratii and V. erythrodactylon have been deposited in the National Center for Biotechnology Information (NCBI) under BioProject PRJNA1090265 (https://www.ncbi.nlm.nih.gov/datasets/genome/?bioproject=PRJNA1090265) and the corresponding genome annotation files are available on Figshare at the following URLs: https://figshare.com/articles/dataset/_i_Vriesea_erythrodactylon_i_genome/25887199; https://figshare.com/articles/ dataset/Tillandsia_duratii_genome/25887259. The transcriptome and 16S sequencing data can be accessed in NCBI under BioProjects PRJNA1090267 (https:// www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA1090267) and PRJNA1090269 (https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA1090269), respectively. The metagenome sequencing and assembly data are deposited under BioProject PRJNA1164103 in NCBI (https://www.ncbi.nlm.nih.gov/datasets/genome/? bioproject=PRJNA1164103), and with annotation files deposited on Figshare (https://figshare.com/articles/dataset/hong_genome_of_Bromeliaceae/25887490). Furthermore, the spatial transcriptomic data for tillandsioids are accessible in NCBI under BioProject PRJNA1163761 (https://www.ncbi.nlm.nih.gov/sra/ PRJNA1163761) and in the CNGB Sequence Archive (CNSA) of the China National GeneBank DataBase (CNGBdb) with accession number CNP0005627.

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Research involving n	uman participants, their data, or biological material	
Policy information about studies with <u>human participants or human data</u> . See also policy information about <u>sex, gender (identity/presentation),</u> and sexual orientation and race, ethnicity and racism.		
Reporting on sex and gender	n/a	
Reporting on race, ethnicity, on other socially relevant groupings	n/a	
Population characteristics	n/a	
Recruitment	n/a	
Ethics oversight	n/a	
Note that full information on the approval of the study protocol must also be provided in the manuscript.		
Field-specific r	eporting	
Please select the one below tha	t is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.	
X Life sciences	Behavioural & social sciences	
For a reference copy of the document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>		
Life sciences study design		
All studies must disclose on these points even when the disclosure is negative.		
	vere collected for analysis, representing 78% genera-richness of Tillandsioideae. V. erythrodactylon and T. duratii were selected eassembly, representing two types of tillandsioids.	

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
Antibodies	ChIP-seq
Eukaryotic cell lines	Flow cytometry
Palaeontology and archaeology	MRI-based neuroimaging
Animals and other organisms	•
Clinical data	
Dual use research of concern	
☐ ☐ Plants	
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Dual use research of concern	
Policy information about <u>dual use research of concer</u>	<u>n</u>
Hazards	
	of agents or technologies generated in the work, or the application of information presented
in the manuscript, pose a threat to:	
No Yes	
Public health	
National security	
Crops and/or livestock	
Ecosystems	
Any other significant area	
Experiments of concern	
Does the work involve any of these experiments of	concern:
No Yes	
Demonstrate how to render a vaccine ineffectiv	re
Confer resistance to therapeutically useful antib	piotics or antiviral agents
Enhance the virulence of a pathogen or render	a nonpathogen virulent
☐ Increase transmissibility of a pathogen	
Alter the host range of a pathogen	
Enable evasion of diagnostic/detection modaliti	es
Enable the weaponization of a biological agent of	or toxin

 \square Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	All plants used in ths study are currently being cultivated at the Shanghai Chenshan Botanical Garden and the Bromeliads Research Center of Zhejiang Academy of Agricultural Sciences in China.
Novel plant genotypes	n/a
Authentication	n/a